Report

	canu_raw	canu_scaffold	canu_medaka_polished
# contigs (>= 0 bp)	41	29	29
# contigs (>= 1000 bp)	41	29	29
# contigs (>= 5000 bp)	41	29	29
# contigs (>= 10000 bp)	41	29	29
# contigs (>= 25000 bp)	40	28	28
# contigs (>= 50000 bp)	26	18	18
Total length (>= 0 bp)	35577586	36011764	35906896
Total length (>= 1000 bp)	35577586	36011764	35906896
Total length (>= 5000 bp)	35577586	36011764	35906896
Total length (>= 10000 bp)	35577586	36011764	35906896
Total length (>= 25000 bp)	35559156	35993267	35888397
Total length (>= 50000 bp)	35019221	35622420	35518355
# contigs	41	29	29
Largest contig	5884780	8146704	8126513
Total length	35577586	36011764	35906896
Reference length	34204973	34204973	34204973
GC (%)	23.04	22.76	22.80
Reference GC (%)	22.44	22.44	22.44
N50	3312350	5609440	5589158
NG50	3312350	5609440	5589158
N90	1236530	3928465	3917967
NG90	1756805	5029427	5009411
auN	3299140.5	5910377.3	5893519.9
auNG	3431531.9	6222578.0	6186761.4
L50	4	3	3
LG50	4	3	3
L90	11	6	6
LG90	10	5	5
# misassemblies	721	739	731
# misassembled contigs	38	26	26
Misassembled contigs length	35454535	35887505	35782662
# local misassemblies	164	163	167
# scaffold gap ext. mis.	0	2	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 20 part	0 + 14 part	0 + 14 part
Unaligned length	554700	551682	546647
Genome fraction (%)	97.060	97.080	97.083
Duplication ratio	1.054	1.067	1.064
# N's per 100 kbp	0.00	3.33	1.31
# mismatches per 100 kbp	125.02	144.76	137.57
# indels per 100 kbp	419.22	217.17	255.48
Largest alignment	1435619	1455185	1451587
Total aligned length	34961051	35396359	35295972
NA50	396866	401924	400956
NGA50	399719	405106	404265
NA90	33921	34547	34573
NGA90	77740	90261	90099
auNA	455858.8	463025.2	462539.2
auNGA	474152.0	487483.3	485553.5
LA50	28	28	28
LGA50	26	26	26
LA90	117	116	115
LGA90	93	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

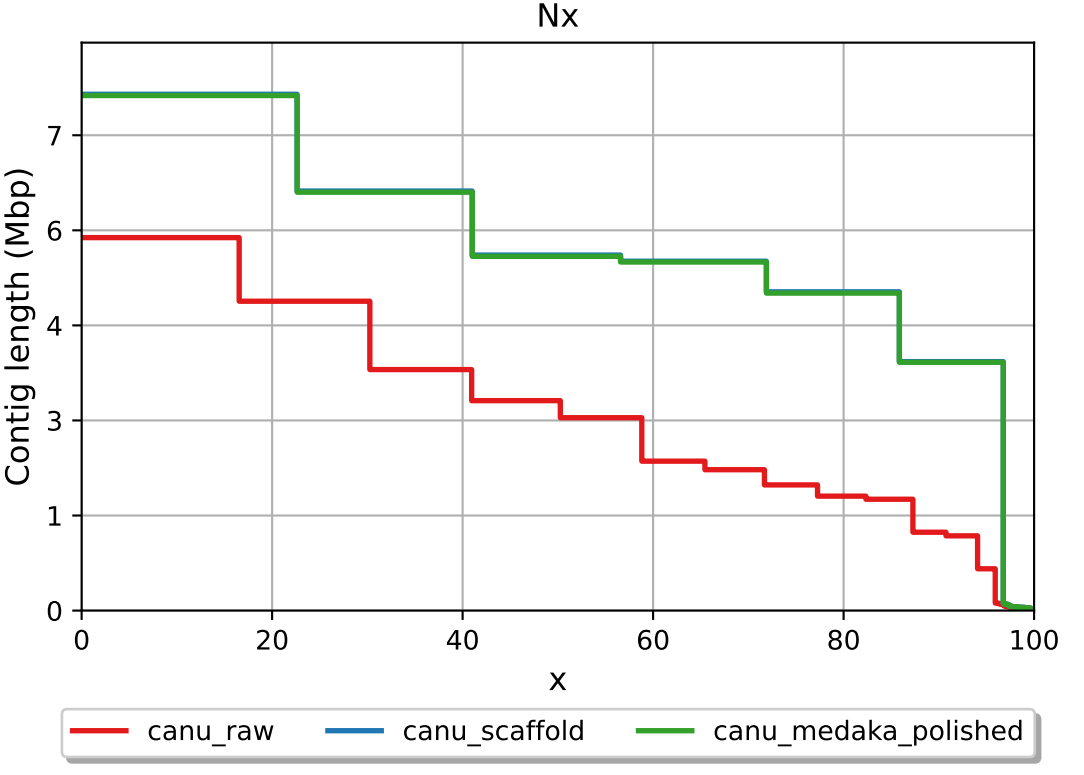
	canu_raw	canu_scaffold	canu_medaka_polished
# misassemblies	721	739	731
# contig misassemblies	721	729	723
# c. relocations	288	298	297
# c. translocations	421	419	414
# c. inversions	12	12	12
# scaffold misassemblies	0	10	8
# s. relocations	0	6	4
# s. translocations	0	4	4
# s. inversions	0	0	0
# misassembled contigs	38	26	26
Misassembled contigs length	35454535	35887505	35782662
# local misassemblies	164	163	167
# scaffold gap ext. mis.	0	2	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	43709	51241	48558
# indels	146564	76869	90173
# indels (<= 5 bp)	122855	71786	85085
# indels (> 5 bp)	23709	5083	5088
Indels length	529209	191401	217368

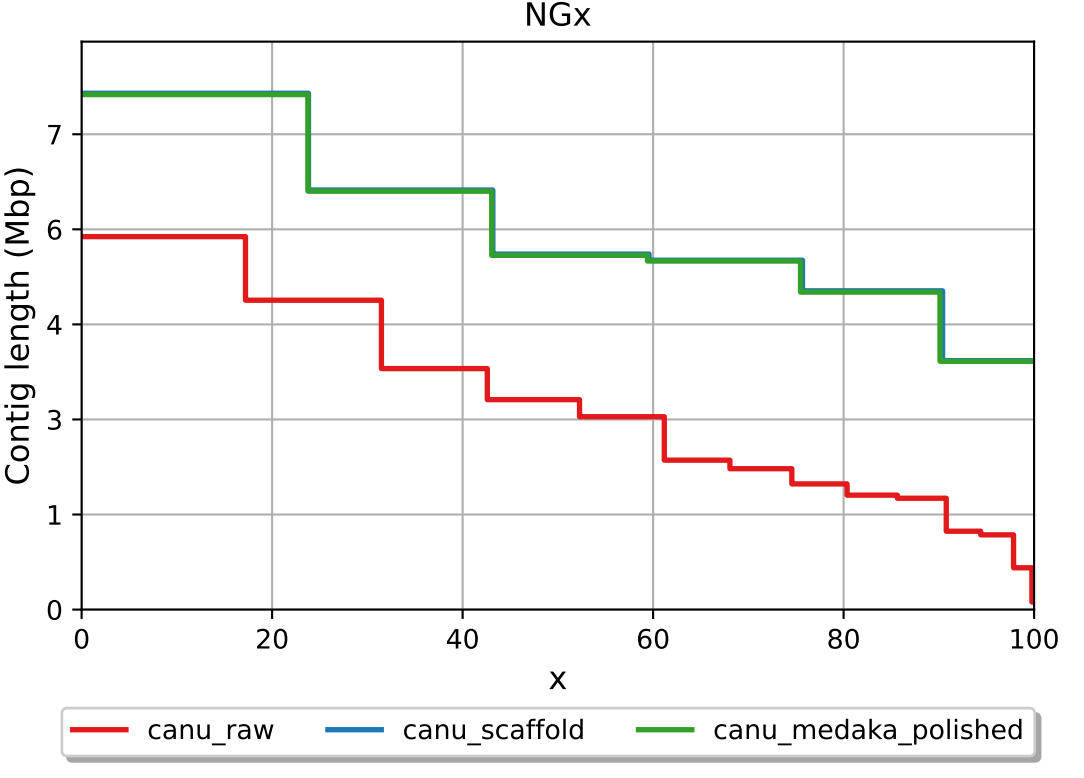
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

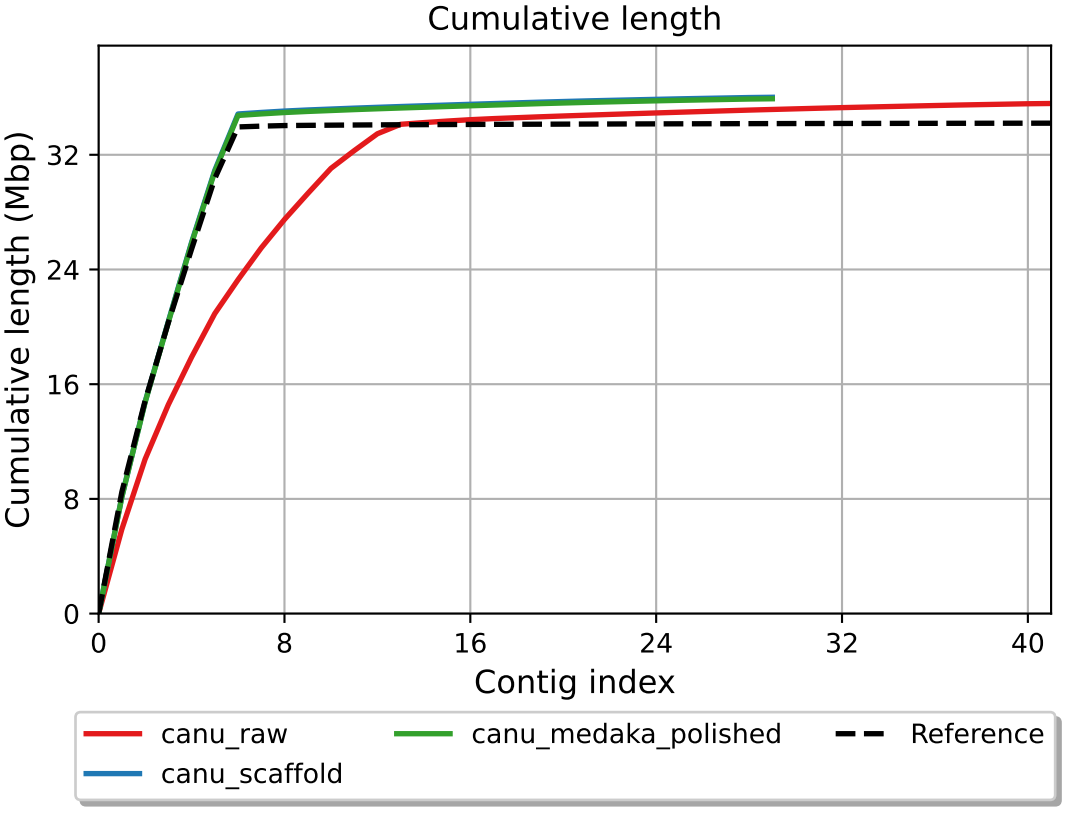
Unaligned report

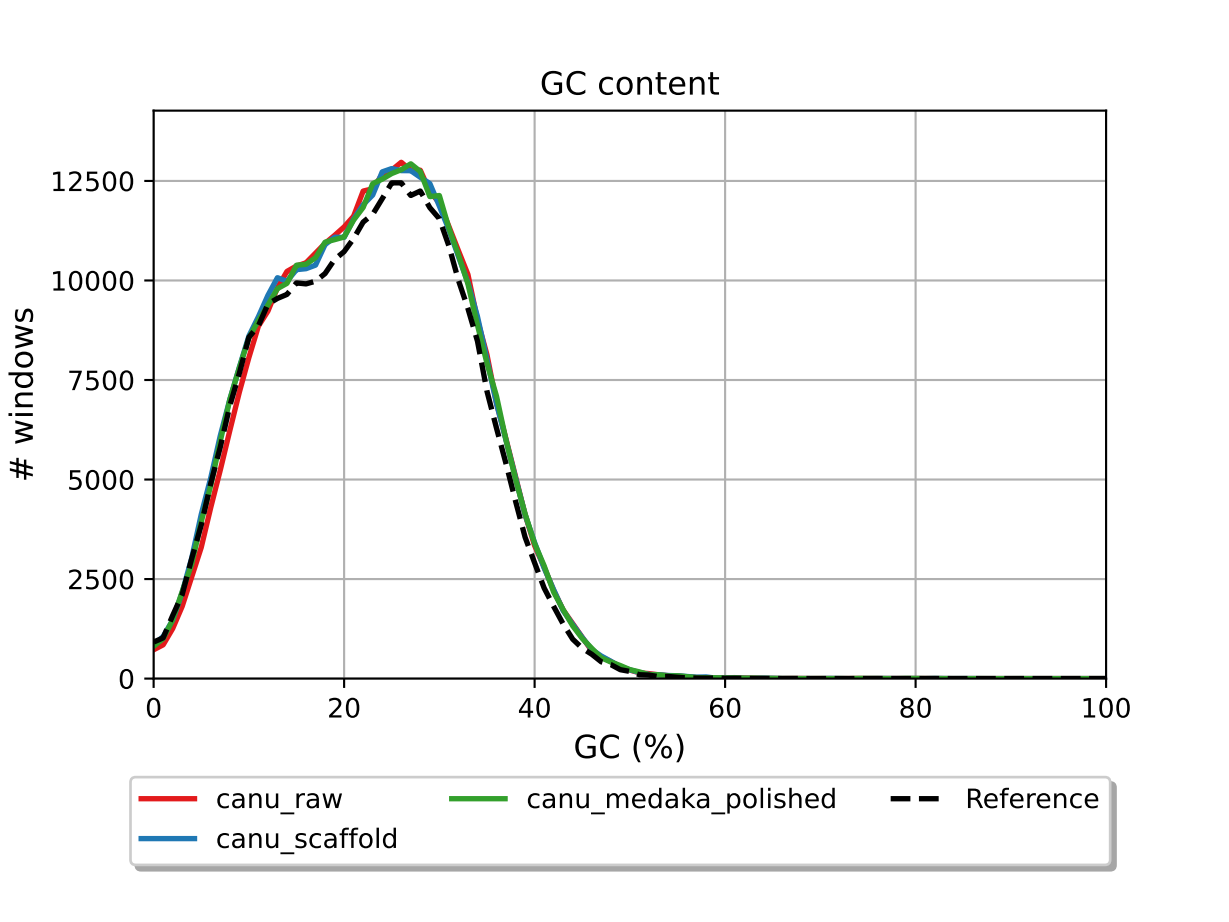
	canu_raw	canu_scaffold	canu_medaka_polished
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	20	14	14
Partially unaligned length	554700	551682	546647
# N's	0	1200	469

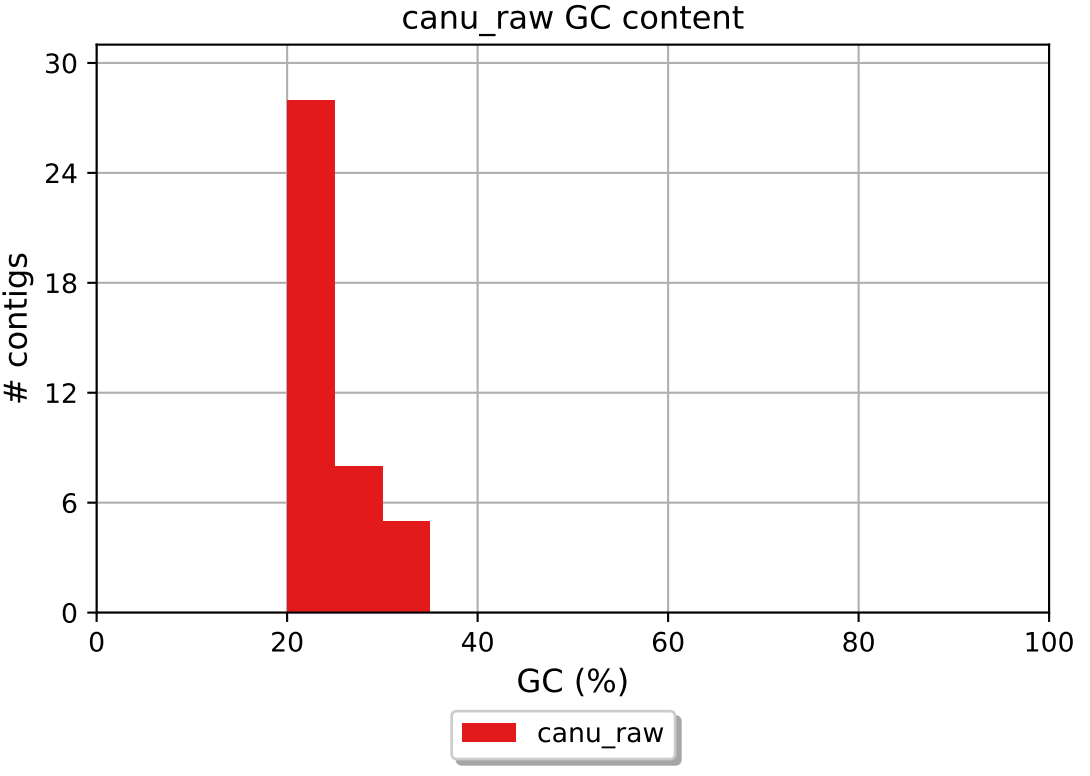
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

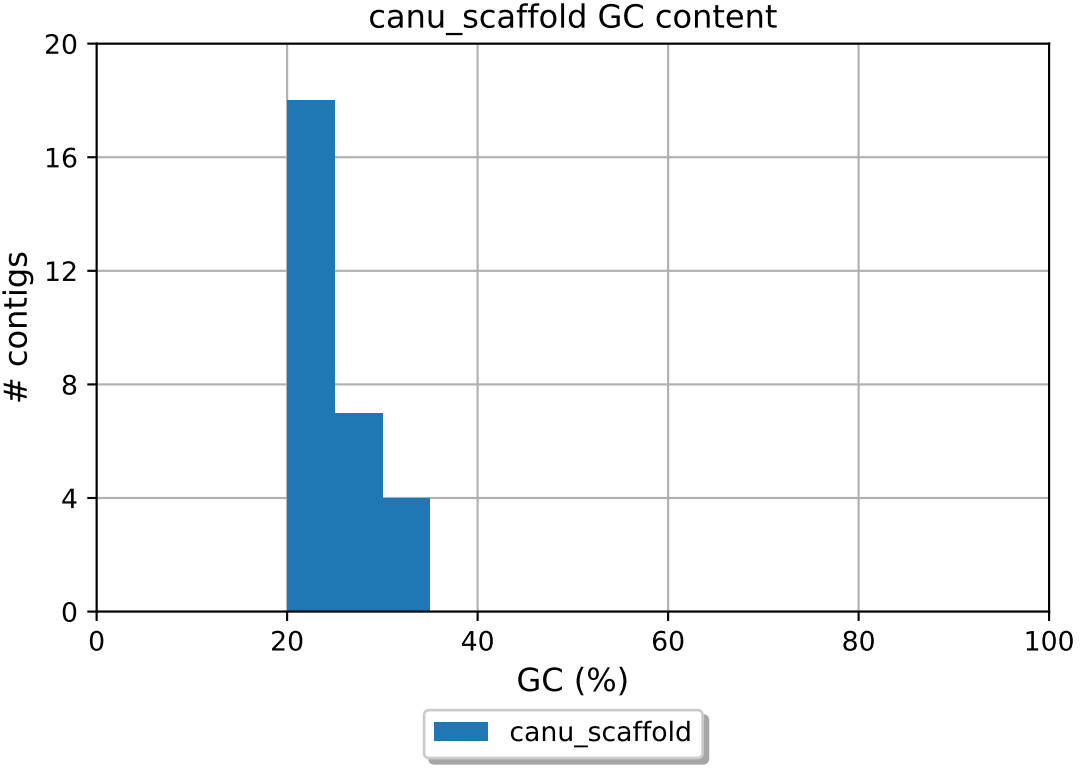

Nx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
canu_raw
canu_scaffold
canu_medaka_polished

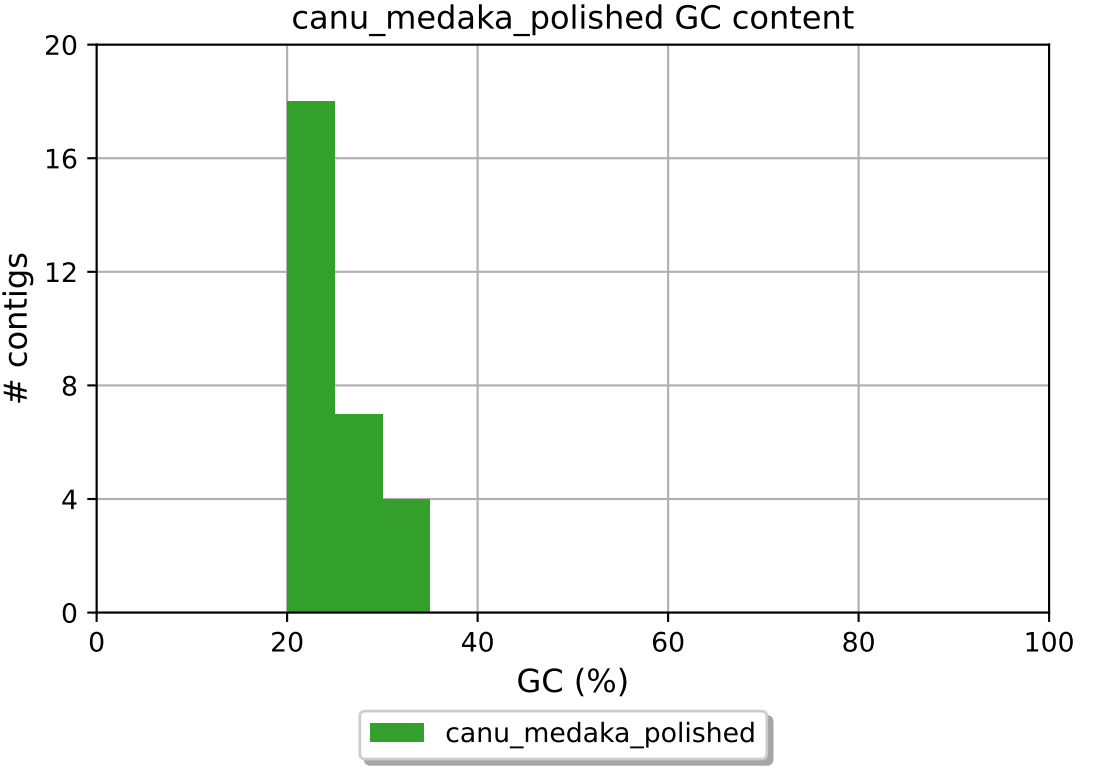

NGx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
canu_raw
canu_scaffold
canu_medaka_polished

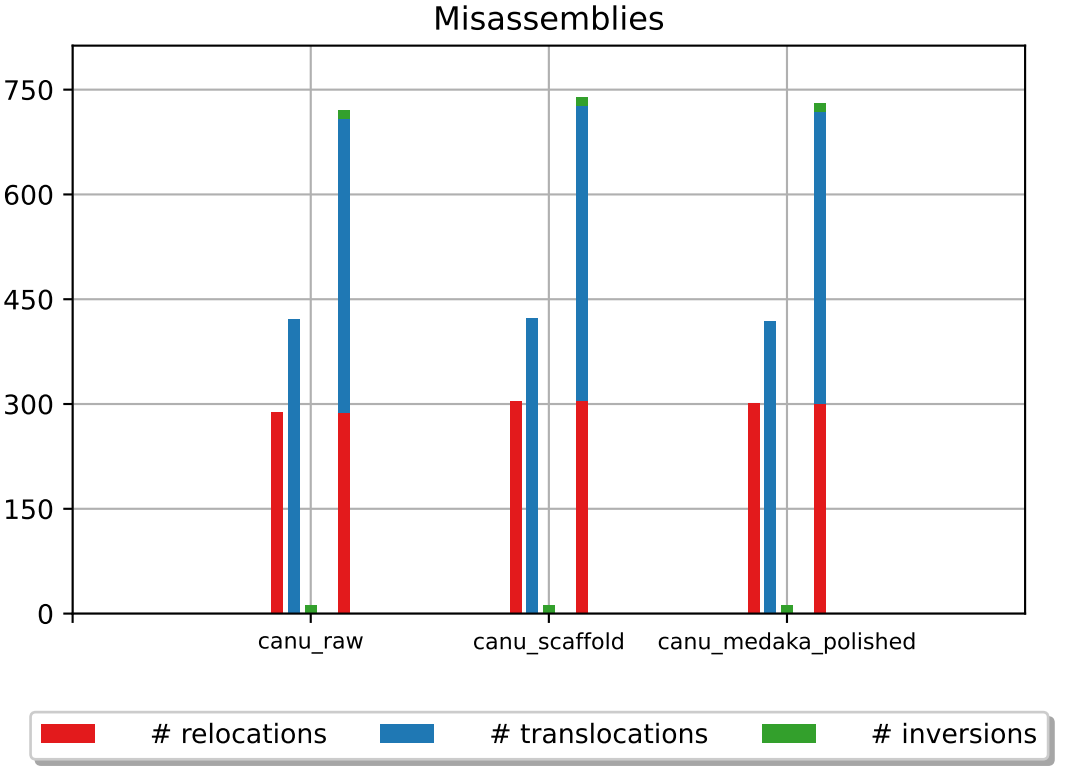

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
canu_raw
canu_scaffold
canu_medaka_polished
Reference

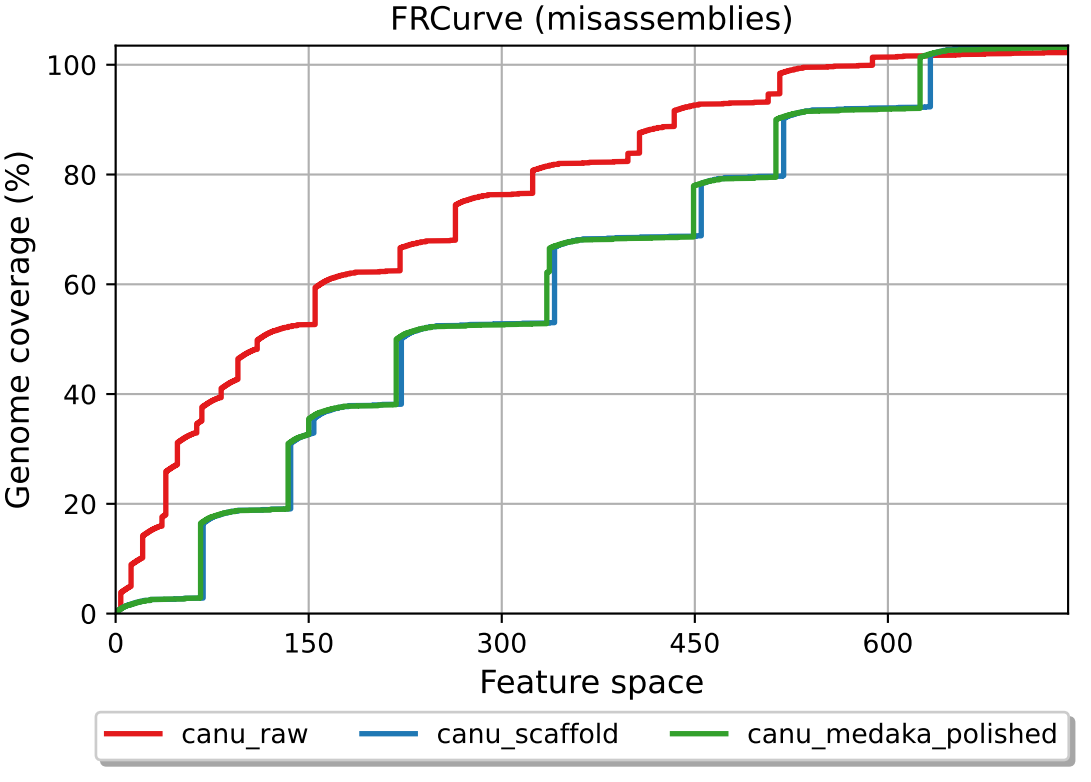

GC content
windows
GC (%)
0
2500
5000
7500
10000
12500
0
20
40
60
80
100
canu_raw
canu_scaffold
canu_medaka_polished
Reference

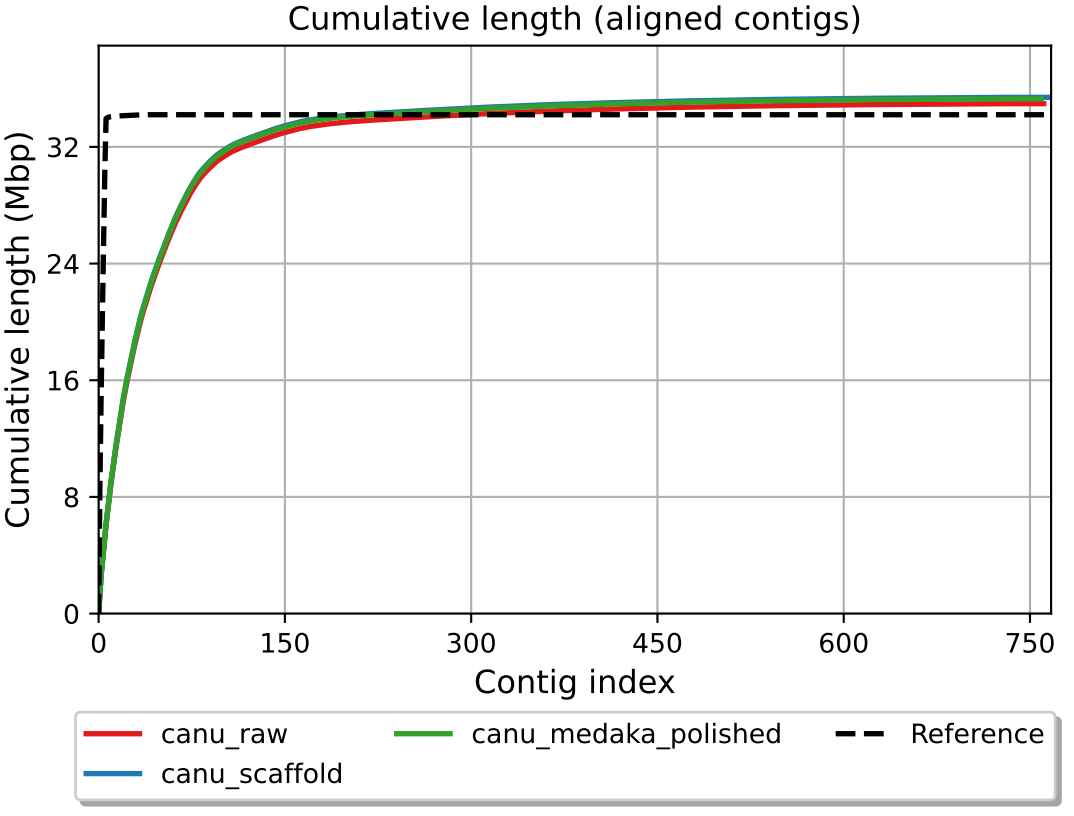

canu_raw GC content
contigs
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
canu_raw

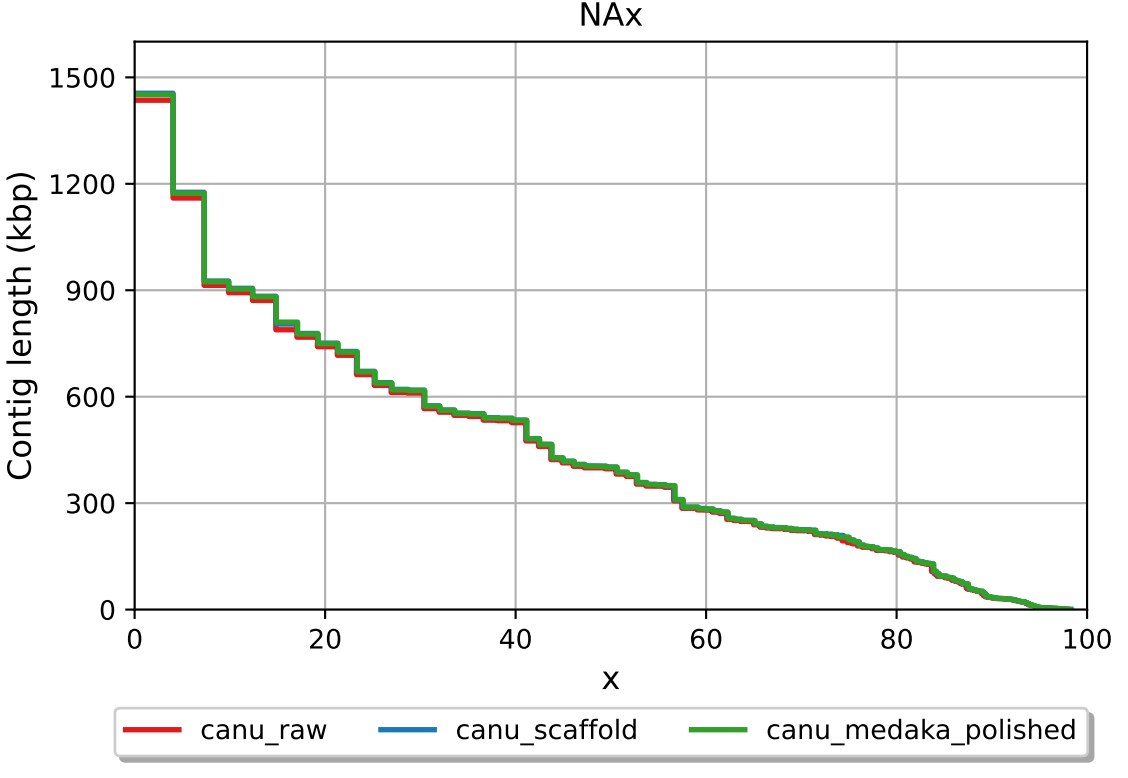

canu_scaffold GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
canu_scaffold

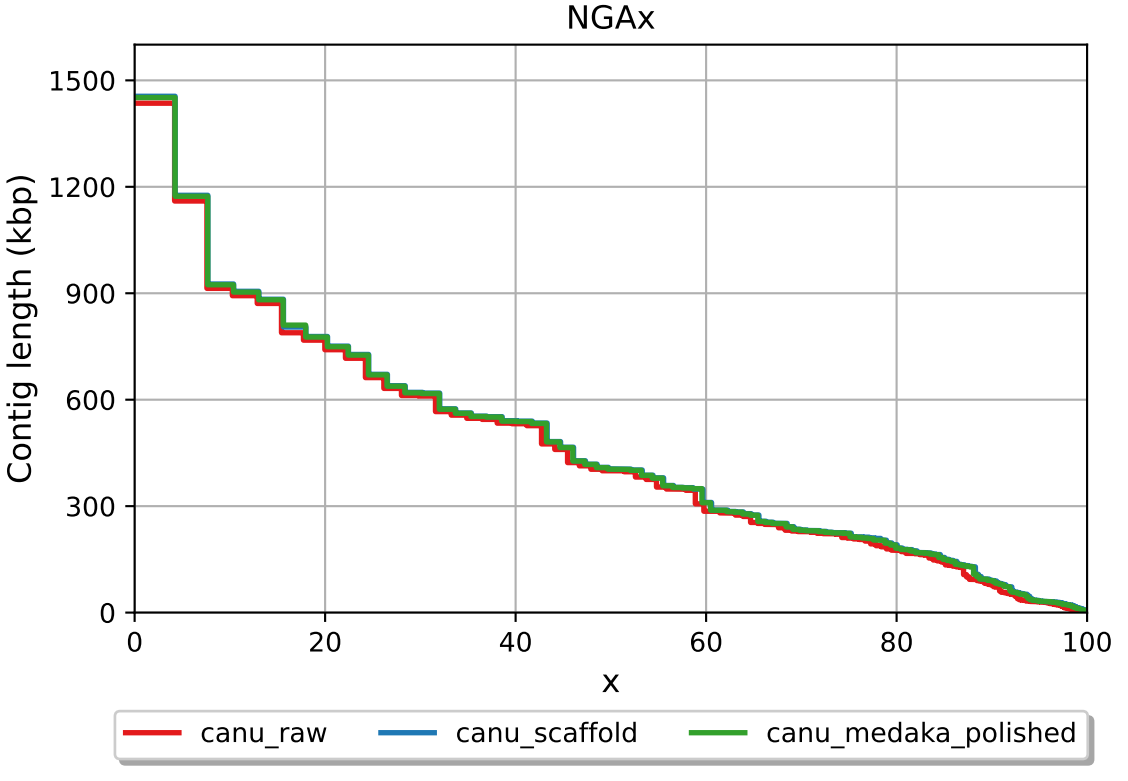

canu_medaka_polished GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
canu_medaka_polished

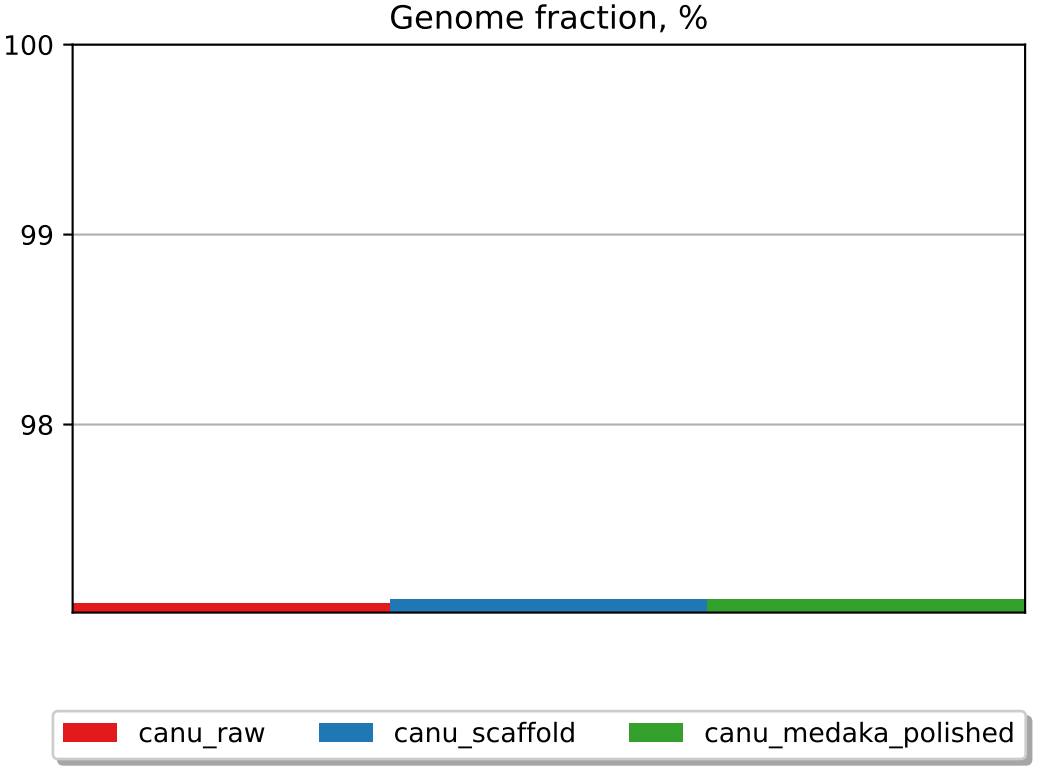

Misassemblies
750
600
450
300
150
0
canu_raw
canu_scaffold
canu_medaka_polished
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
150
300
450
600
Feature space
canu_raw
canu_scaffold
canu_medaka_polished


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


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
canu_raw
canu_scaffold
canu_medaka_polished


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
canu_raw
canu_scaffold
canu_medaka_polished


Genome fraction, %
100
99
98
canu_raw
canu_scaffold
canu_medaka_polished