

Report

	Canu_Polished	Flye_Repaired
# contigs (>= 0 bp)	29	12
# contigs (>= 1000 bp)	29	12
# contigs (>= 5000 bp)	29	11
# contigs (>= 10000 bp)	29	11
# contigs (>= 25000 bp)	28	11
# contigs (>= 50000 bp)	18	9
Total length (>= 0 bp)	35997303	34821575
Total length (>= 1000 bp)	35997303	34821575
Total length (>= 5000 bp)	35997303	34817418
Total length (>= 10000 bp)	35997303	34817418
Total length (>= 25000 bp)	35978808	34817418
Total length (>= 50000 bp)	35607977	34738027
# contigs	29	12
Largest contig	8143141	8060236
Total length	35997303	34821575
Reference length	34204973	34204973
GC (%)	22.76	22.73
Reference GC (%)	22.44	22.44
N50	5606788	5603593
NG50	5606788	5603593
N90	3926766	4039478
NG90	5028520	4039478
auN	5907817.2	5989400.2
aUNG	6217385.0	6097369.2
L50	3	3
LG50	3	3
L90	6	6
LG90	5	6
# misassemblies	741	652
# misassembled contigs	26	10
Misassembled contigs length	35873046	34761865
# local misassemblies	163	157
# scaffold gap ext. mis.	2	1
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 14 part	0 + 10 part
Unaligned length	553592	418606
Genome fraction (%)	97.059	97.154
Duplication ratio	1.066	1.034
# N's per 100 kbp	2.18	1.26
# mismatches per 100 kbp	142.25	136.90
# indels per 100 kbp	117.35	108.87
Largest alignment	1454400	1454560
Total aligned length	35379816	34343729
NA50	387049	404186
NGA50	404880	404961
NA90	34537	78783
NGA90	90226	94427
auNA	460561.4	477059.3
aUNGA	484694.7	485659.1
LA50	28	27
LGA50	26	26
LA90	117	94
LGA90	89	87

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

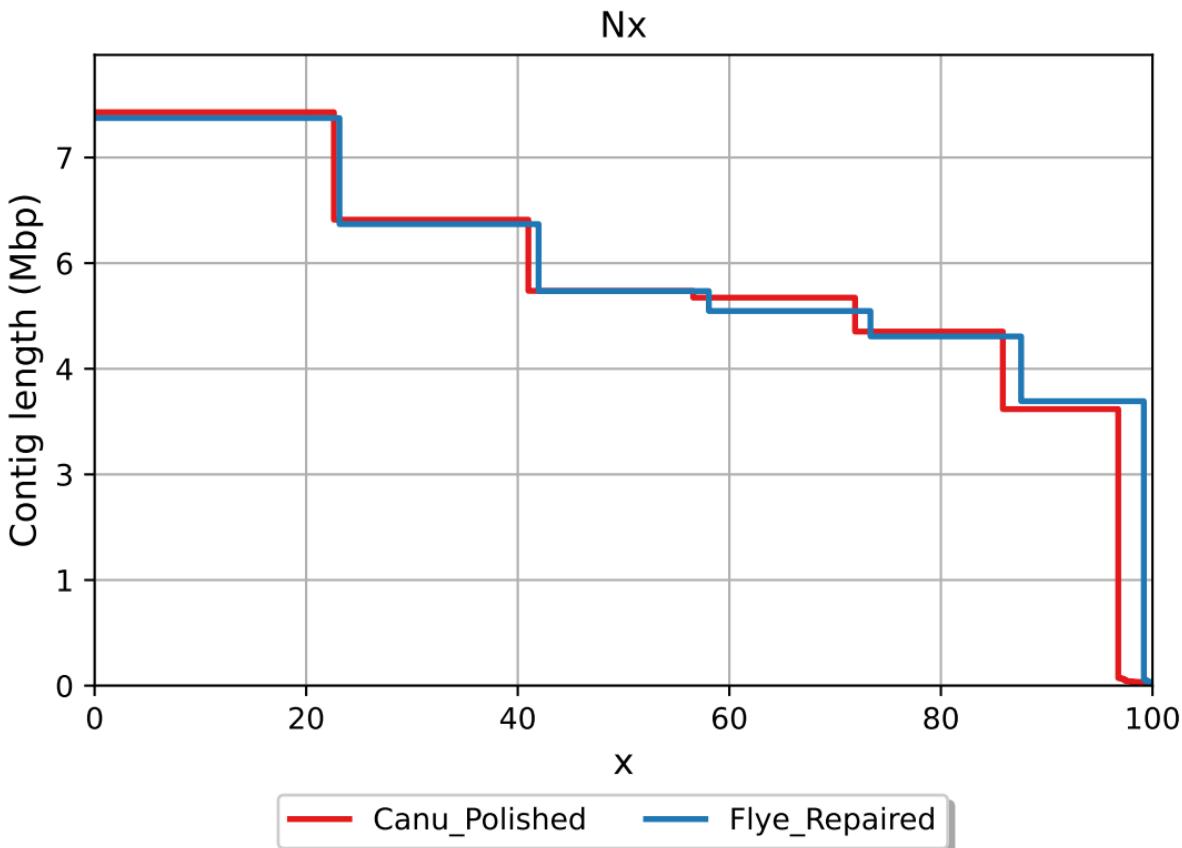
	Canu_Polished	Flye_Repaired
# misassemblies	741	652
# contig misassemblies	731	648
# c. relocations	296	261
# c. translocations	424	375
# c. inversions	11	12
# scaffold misassemblies	10	4
# s. relocations	5	2
# s. translocations	5	2
# s. inversions	0	0
# misassembled contigs	26	10
Misassembled contigs length	35873046	34761865
# local misassemblies	163	157
# scaffold gap ext. mis.	2	1
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	50328	47016
# indels	41517	37389
# indels (<= 5 bp)	36525	33324
# indels (> 5 bp)	4992	4065
Indels length	143403	122141

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).

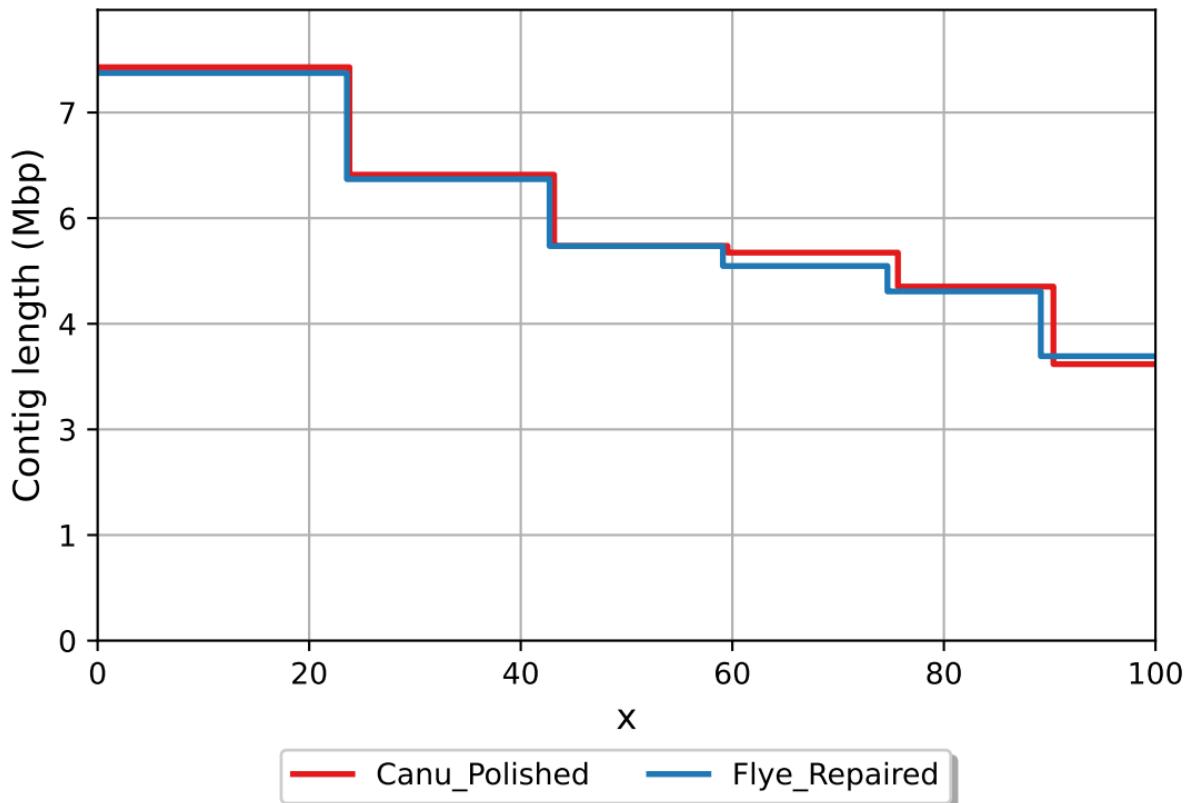
Unaligned report

	Canu_Polished	Flye_Repaired
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	14	10
Partially unaligned length	553592	418606
# N's	786	438

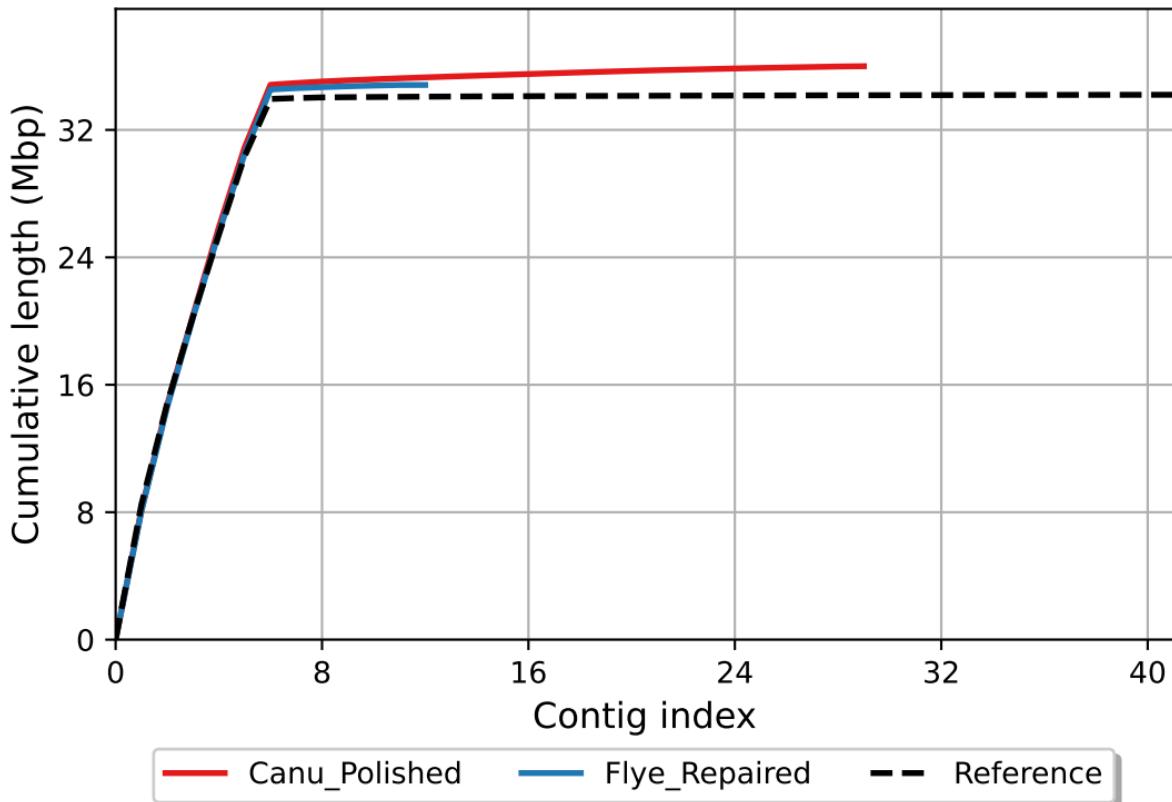
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



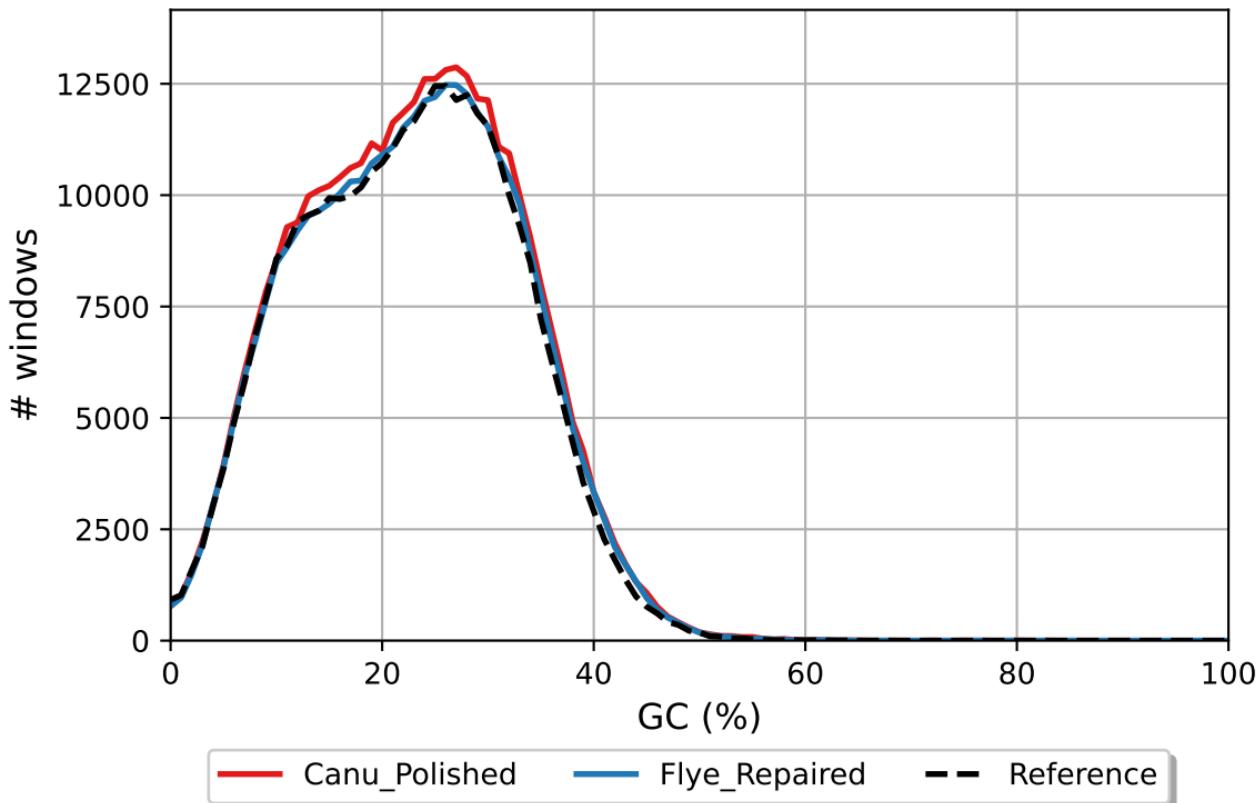
NGx



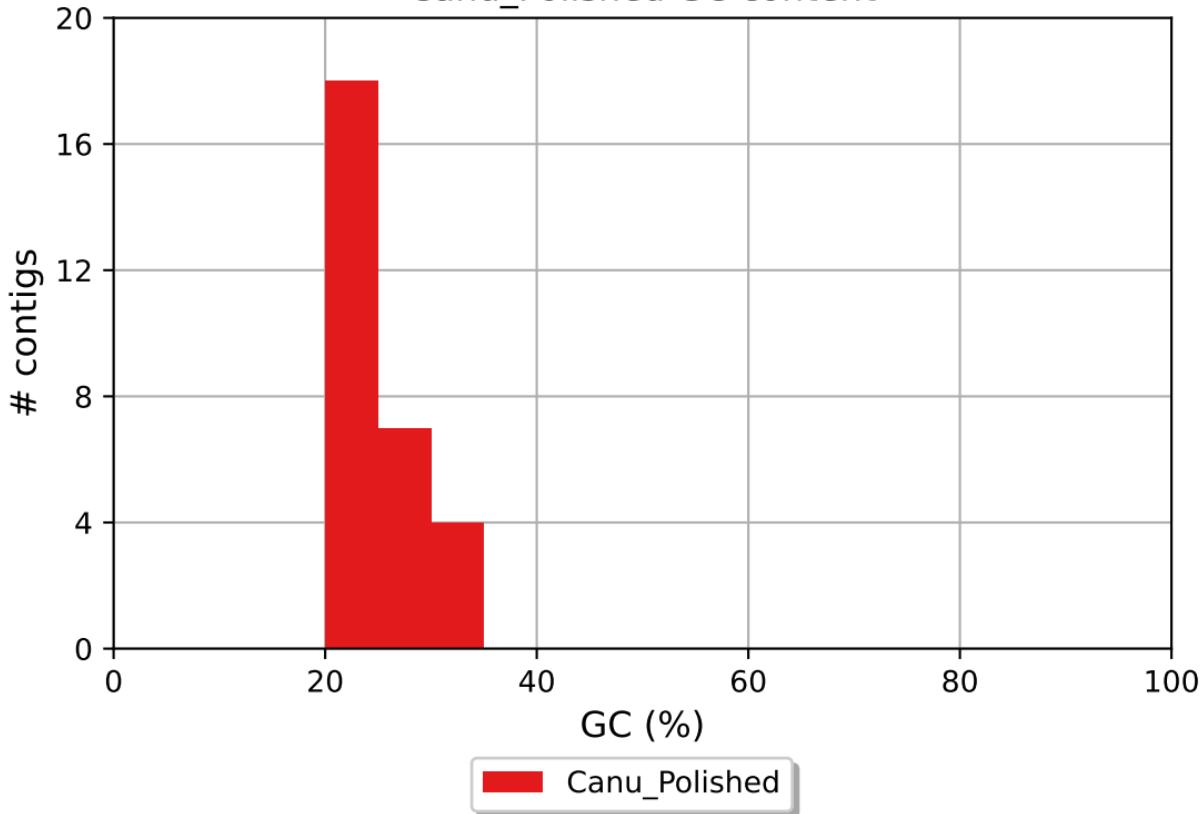
Cumulative length



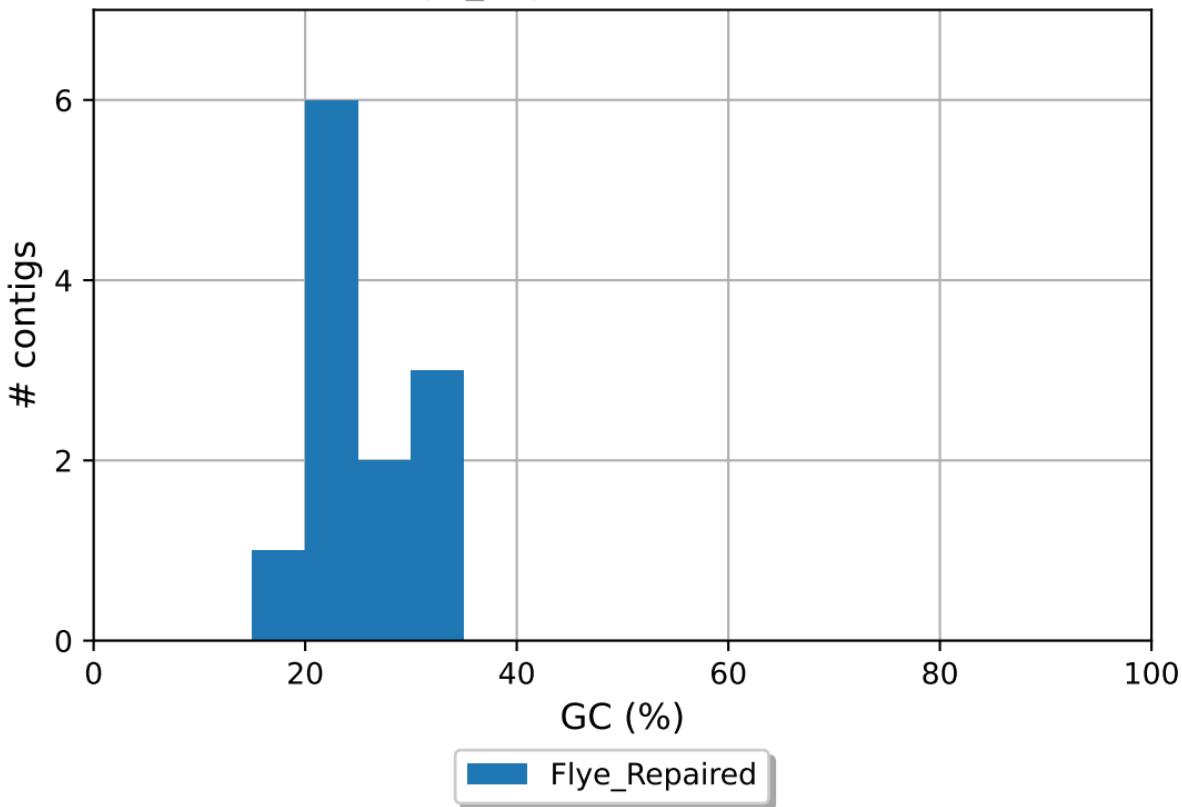
GC content



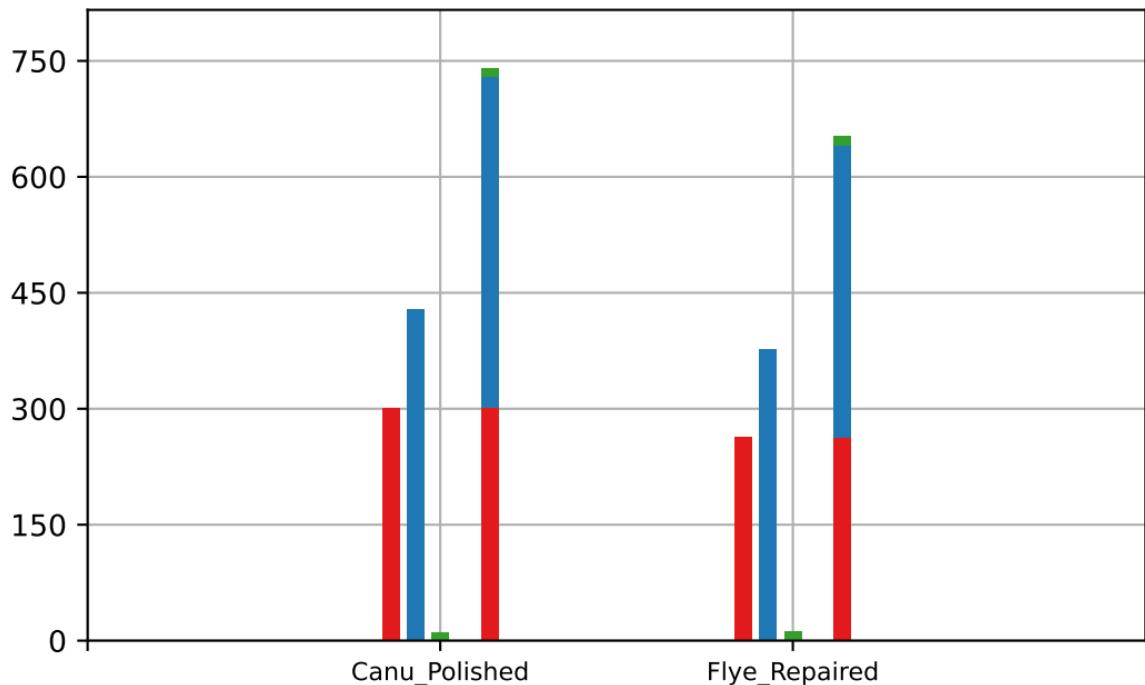
Canu_Polished GC content



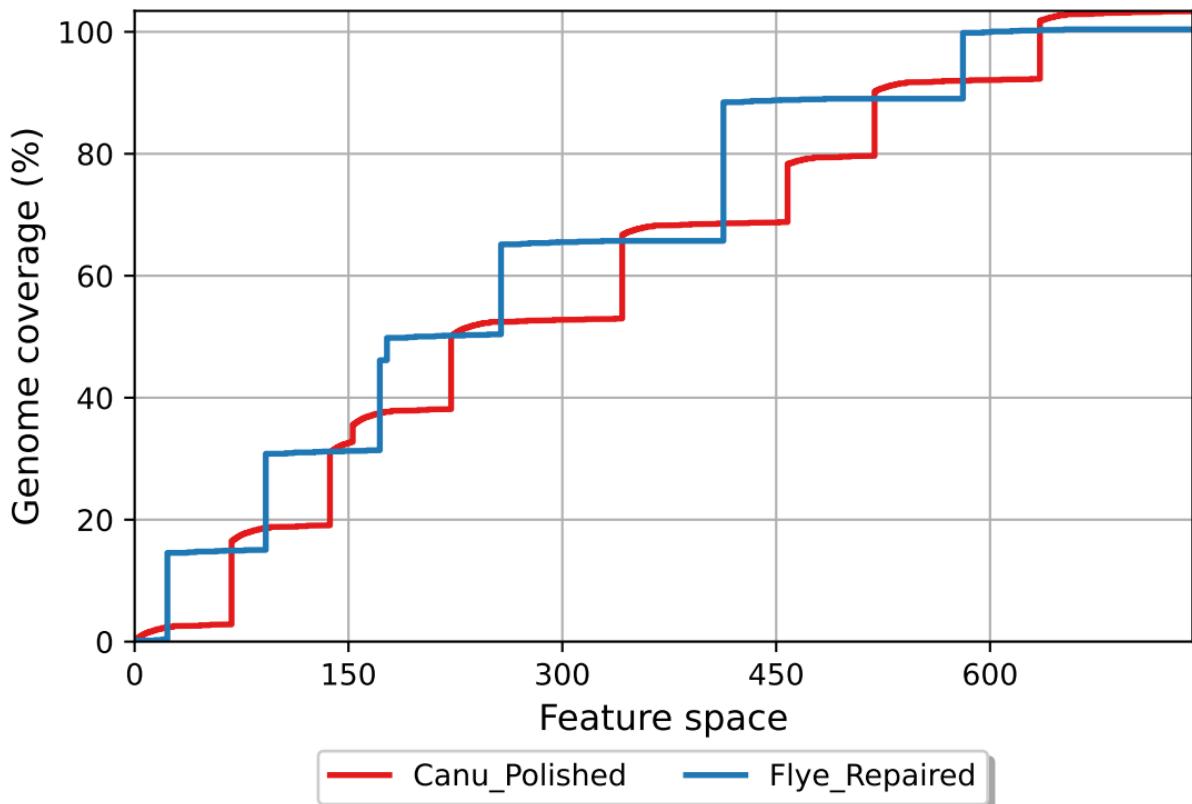
Flye_Repaired GC content



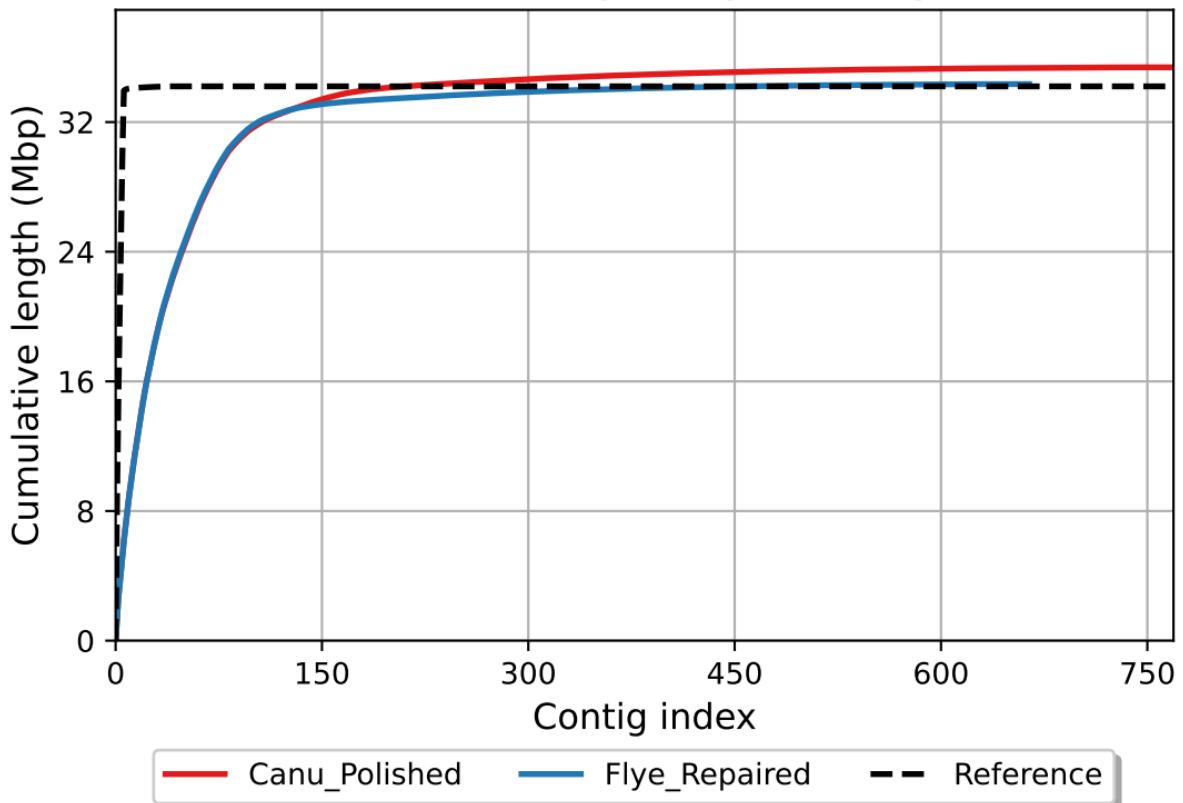
Misassemblies



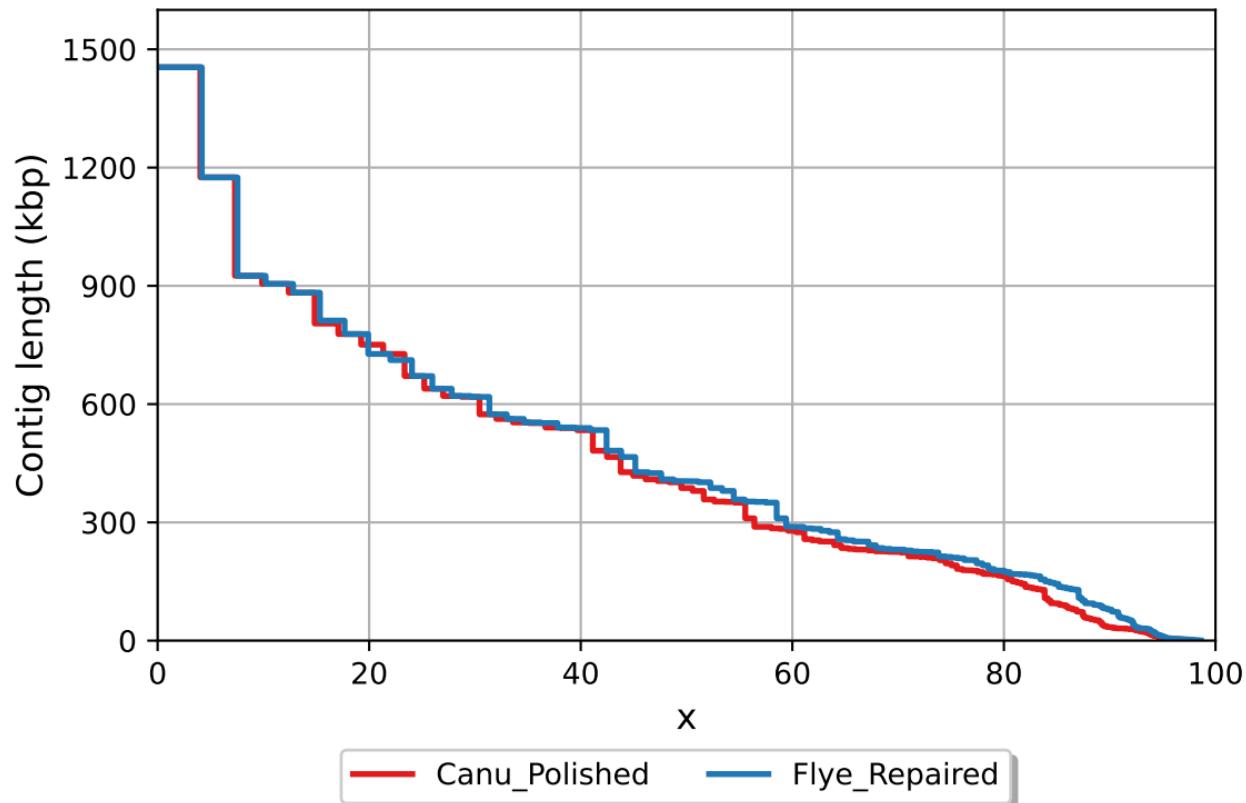
FRCurve (misassemblies)



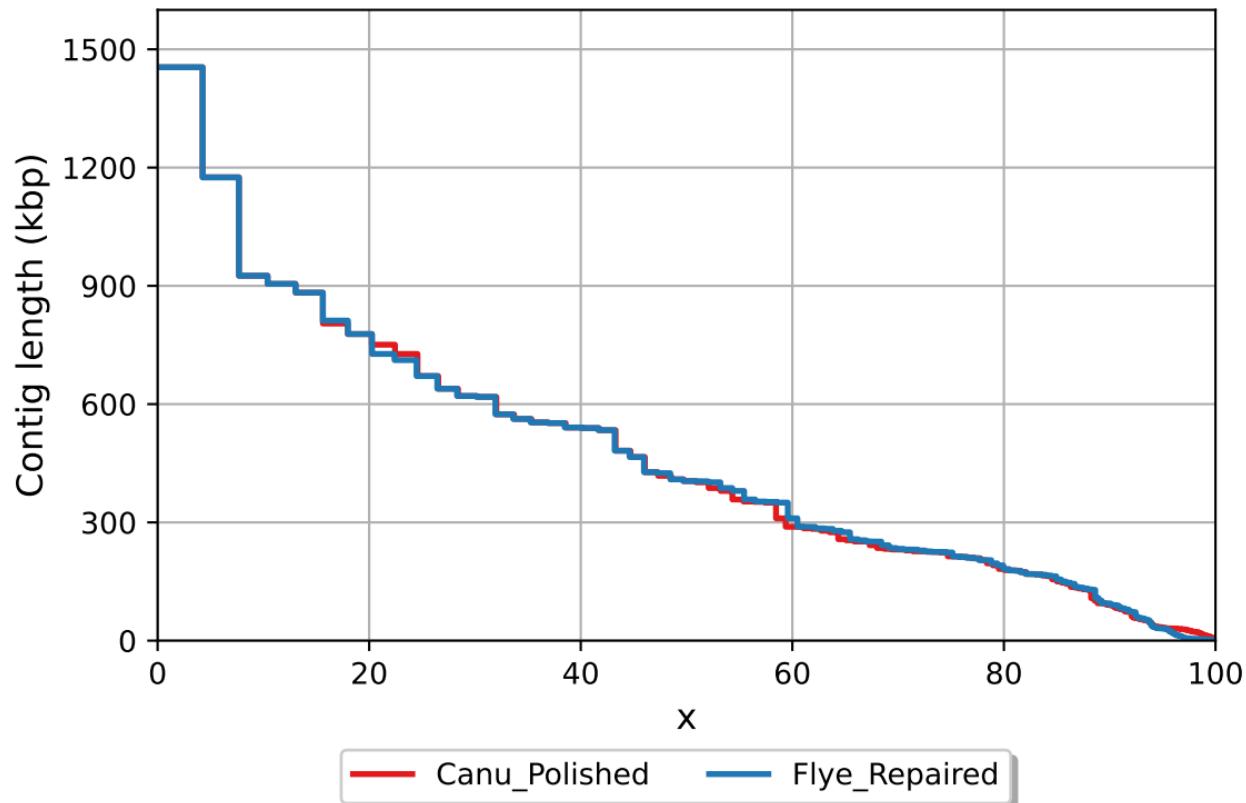
Cumulative length (aligned contigs)



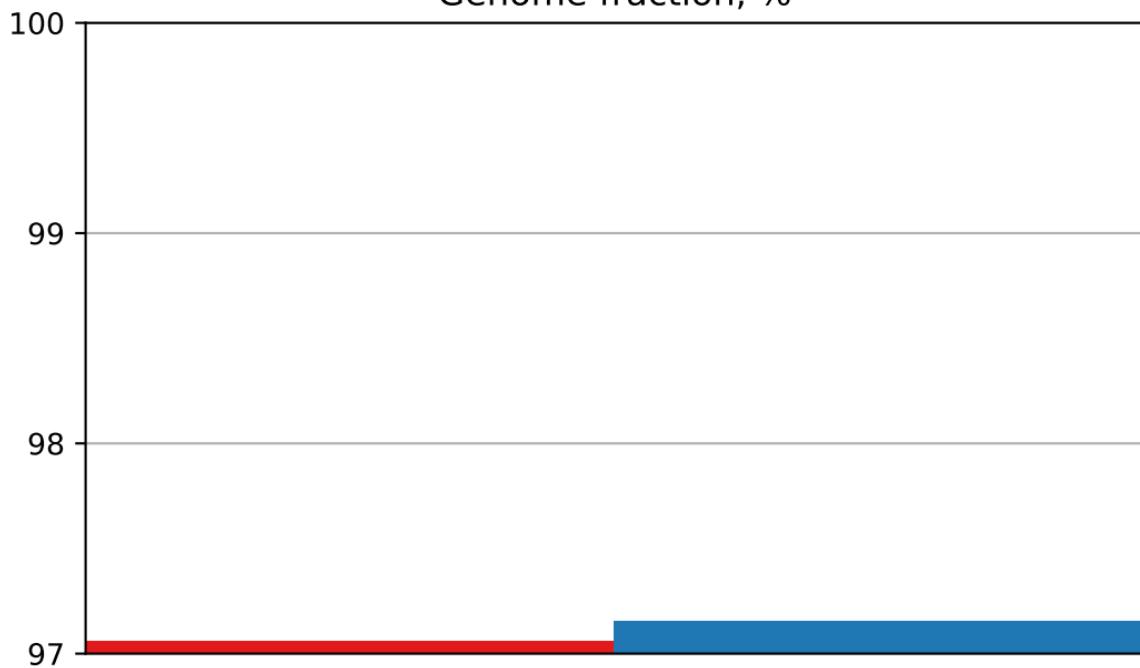
NAx



NGAx



Genome fraction, %



Canu_Polished Flye_Repaired