

Report

	Canu_Polished	Flye_Polished
# contigs (>= 0 bp)	41	16
# contigs (>= 1000 bp)	41	16
# contigs (>= 5000 bp)	41	15
# contigs (>= 10000 bp)	41	15
# contigs (>= 25000 bp)	40	15
# contigs (>= 50000 bp)	26	13
Total length (>= 0 bp)	35841794	34744195
Total length (>= 1000 bp)	35841794	34744195
Total length (>= 5000 bp)	35841794	34740038
Total length (>= 10000 bp)	35841794	34740038
Total length (>= 25000 bp)	35823352	34740038
Total length (>= 50000 bp)	35281531	34660719
# contigs	41	16
Largest contig	5923086	12156340
Total length	35841794	34744195
Reference length	34204973	34204973
GC (%)	22.86	22.81
Reference GC (%)	22.44	22.44
N50	3340021	3382267
NG50	3340021	3382267
N90	1245950	1728463
NG90	1766319	2027319
auN	3324743.8	6221091.3
auNG	3483843.8	6319163.2
L50	4	3
LG50	4	3
L90	11	8
LG90	10	7
# misassemblies	731	670
# misassembled contigs	38	15
Misassembled contigs length	35718446	34740038
# local misassemblies	166	160
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 20 part	0 + 14 part
Unaligned length	531612	424097
Genome fraction (%)	97.068	97.170
Duplication ratio	1.062	1.030
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	134.18	135.84
# indels per 100 kbp	146.76	140.94
Largest alignment	1447687	1448980
Total aligned length	35247025	34216551
NA50	400139	400519
NGA50	403196	402898
NA90	34220	78414
NGA90	83308	90812
auNA	460105.7	470908.9
auNGA	482123.3	478332.6
LA50	28	27
LGA50	26	26
LA90	117	95
LGA90	90	89

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_Polished
# misassemblies	731	670
# contig misassemblies	731	670
# c. relocations	297	272
# c. translocations	425	387
# c. inversions	9	11
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	38	15
Misassembled contigs length	35718446	34740038
# local misassemblies	166	160
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	47293	46479
# indels	51728	48225
# indels (<= 5 bp)	34557	35938
# indels (> 5 bp)	17171	12287
Indels length	273216	225352

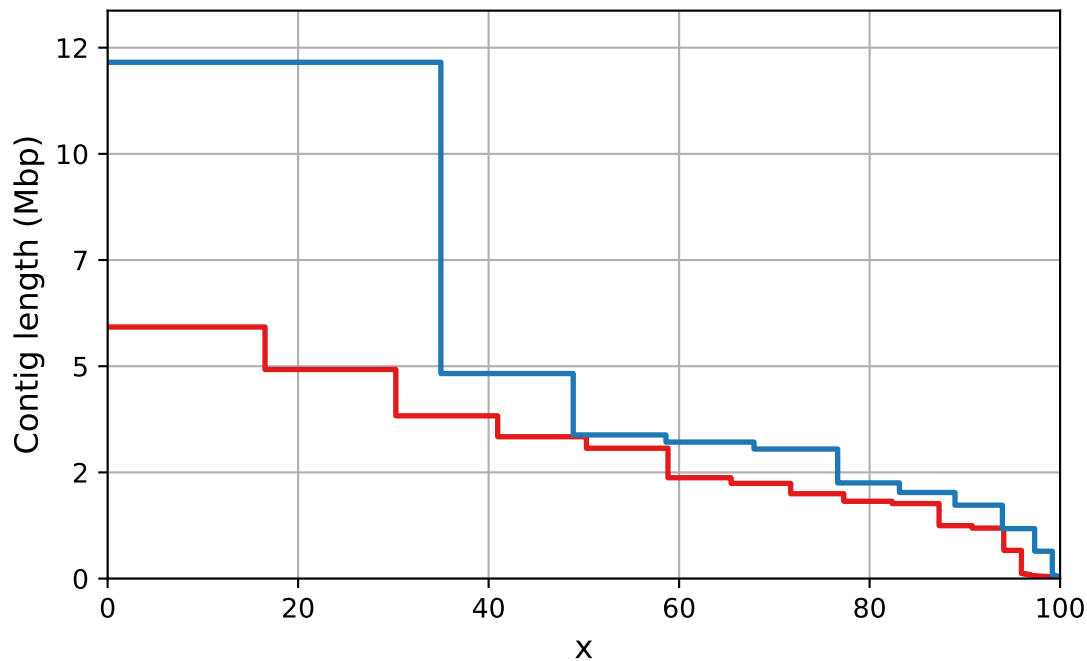
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Canu_Polished	Flye_Polished
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	20	14
Partially unaligned length	531612	424097
# N's	0	0

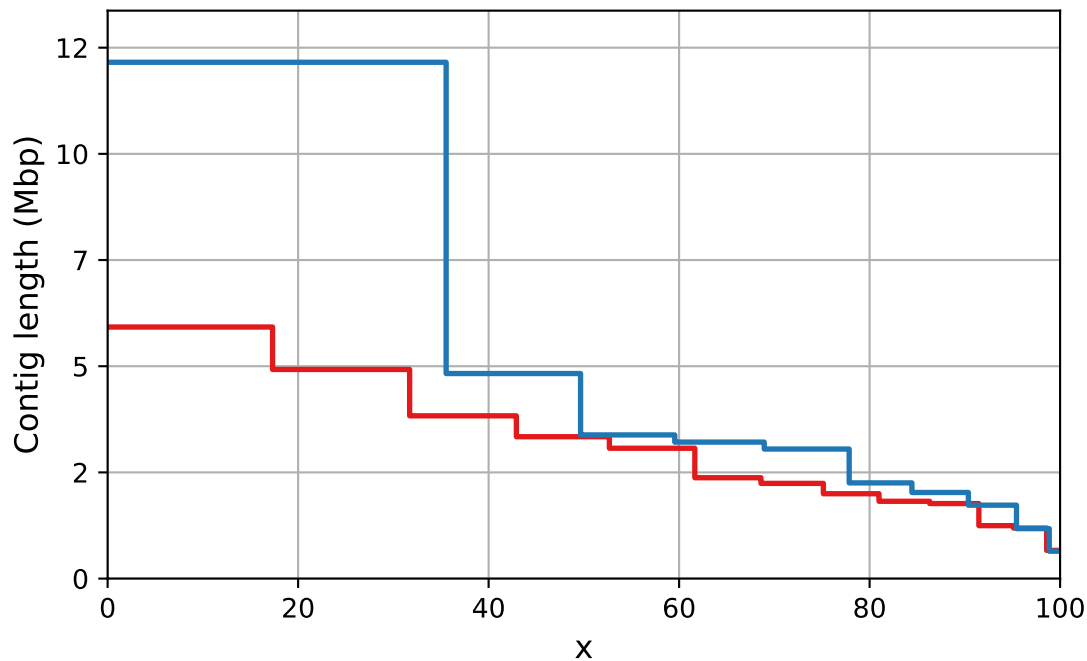
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



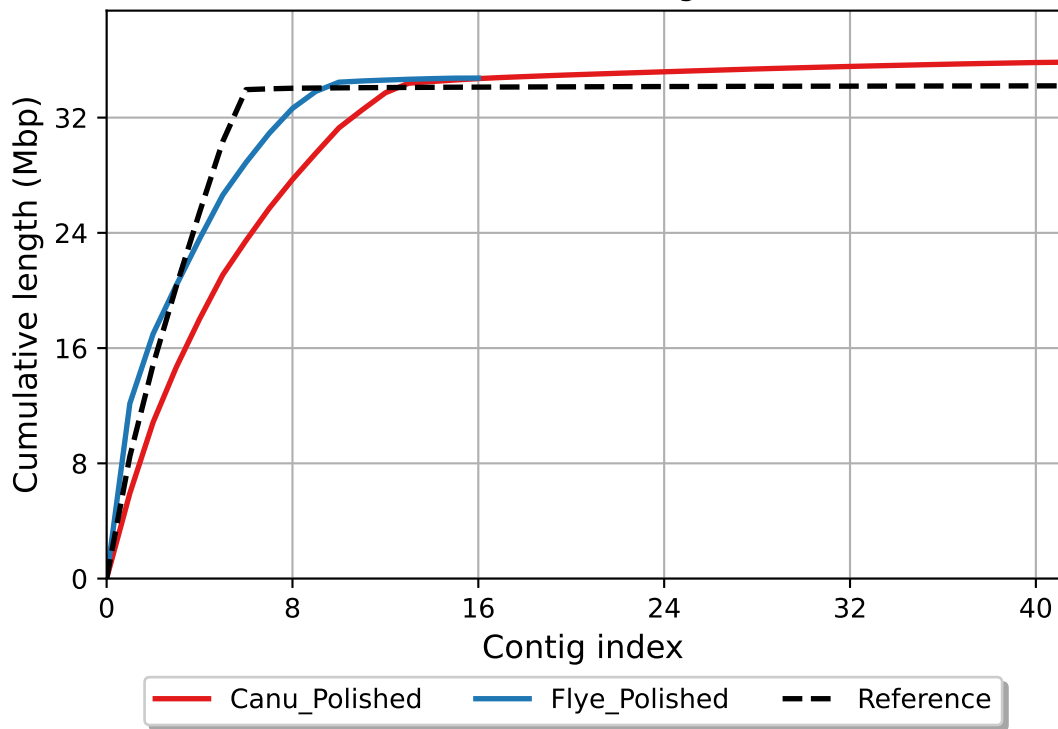
— Canu_Polished — Flye_Polished

NGx

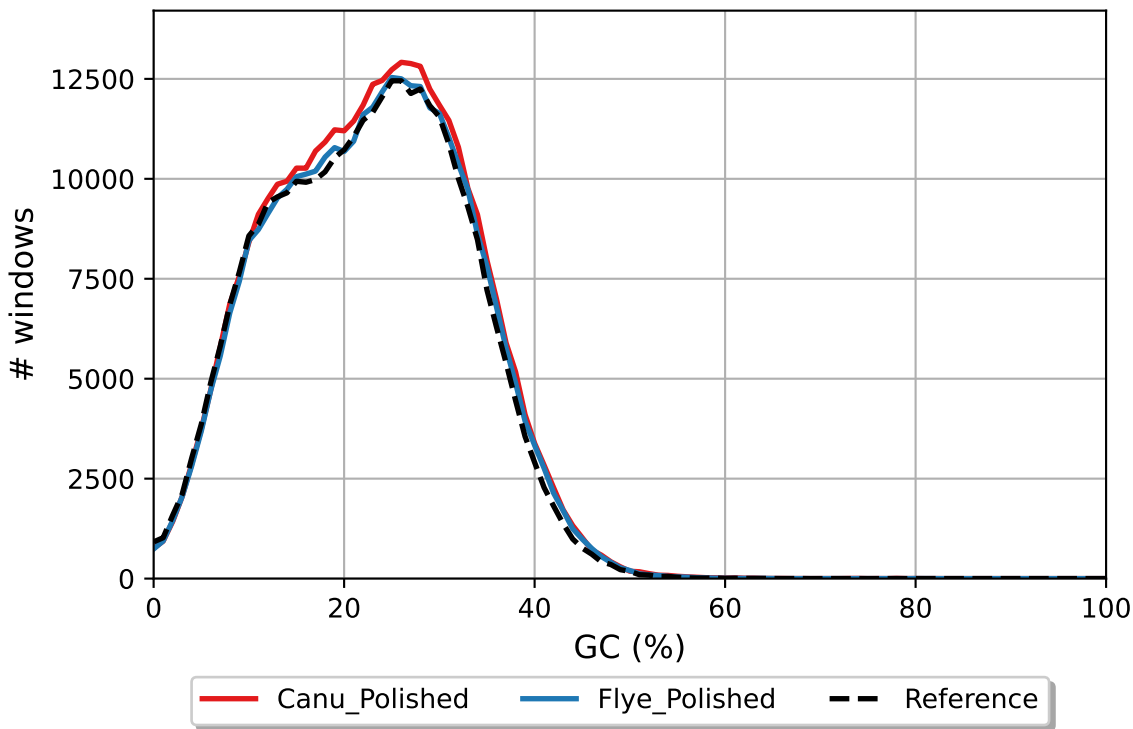


— Canu_Polished — Flye_Polished

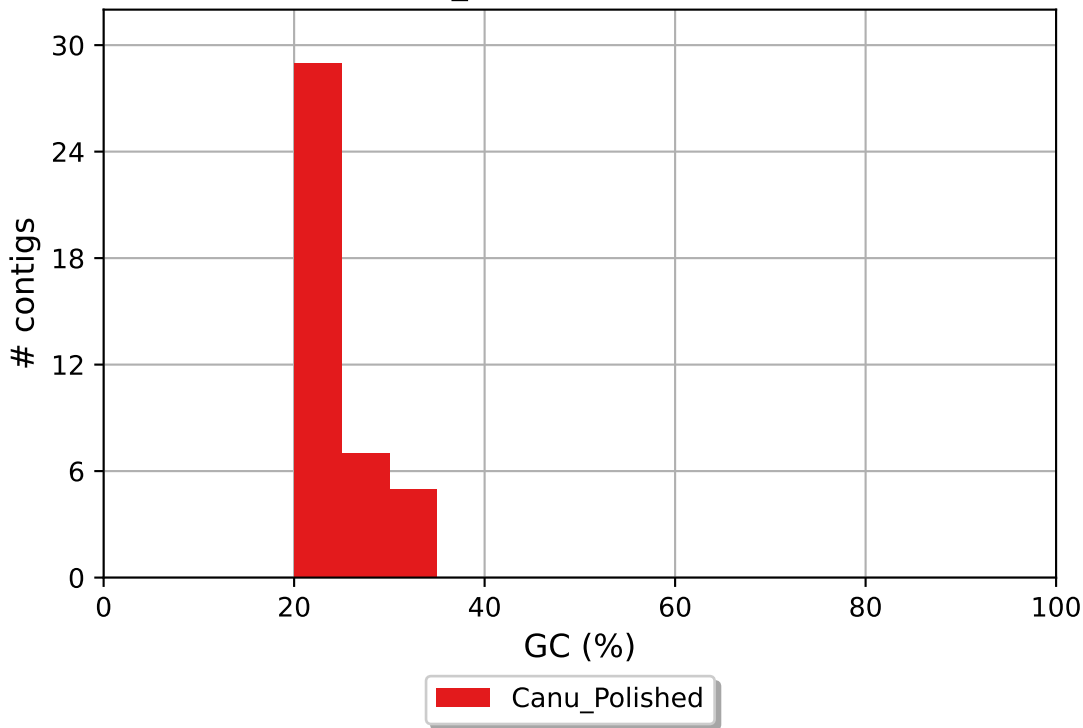
Cumulative length



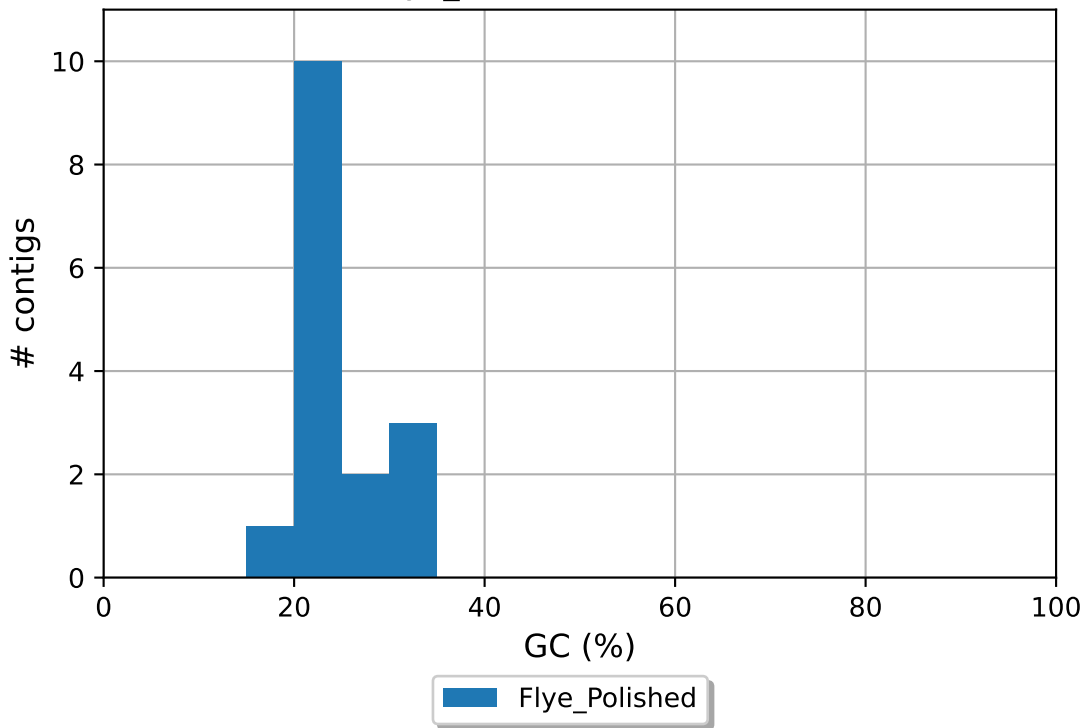
GC content



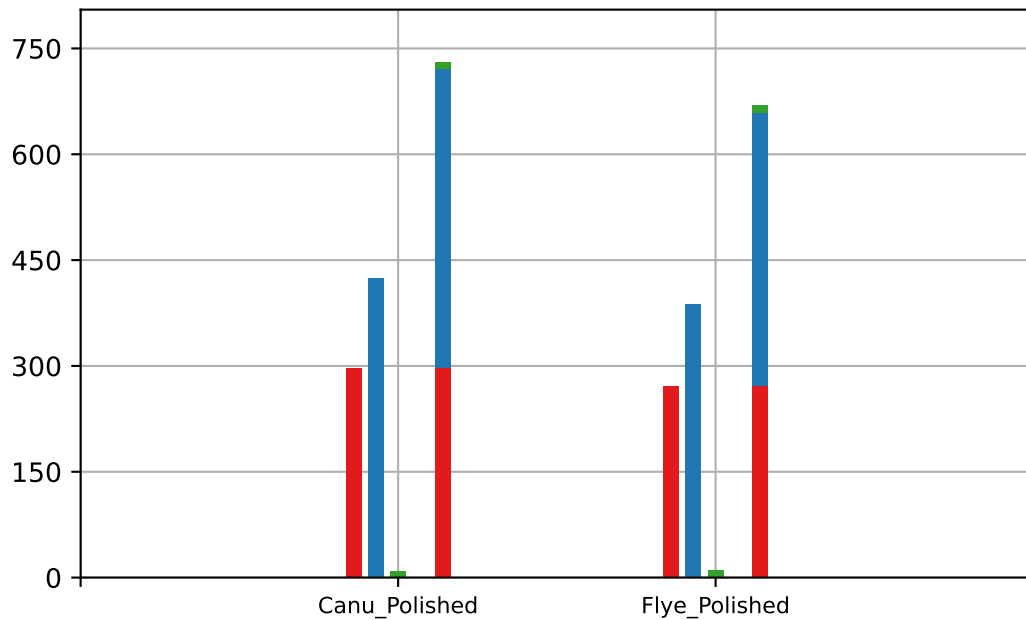
Canu_Polished GC content



Flye_Polished GC content

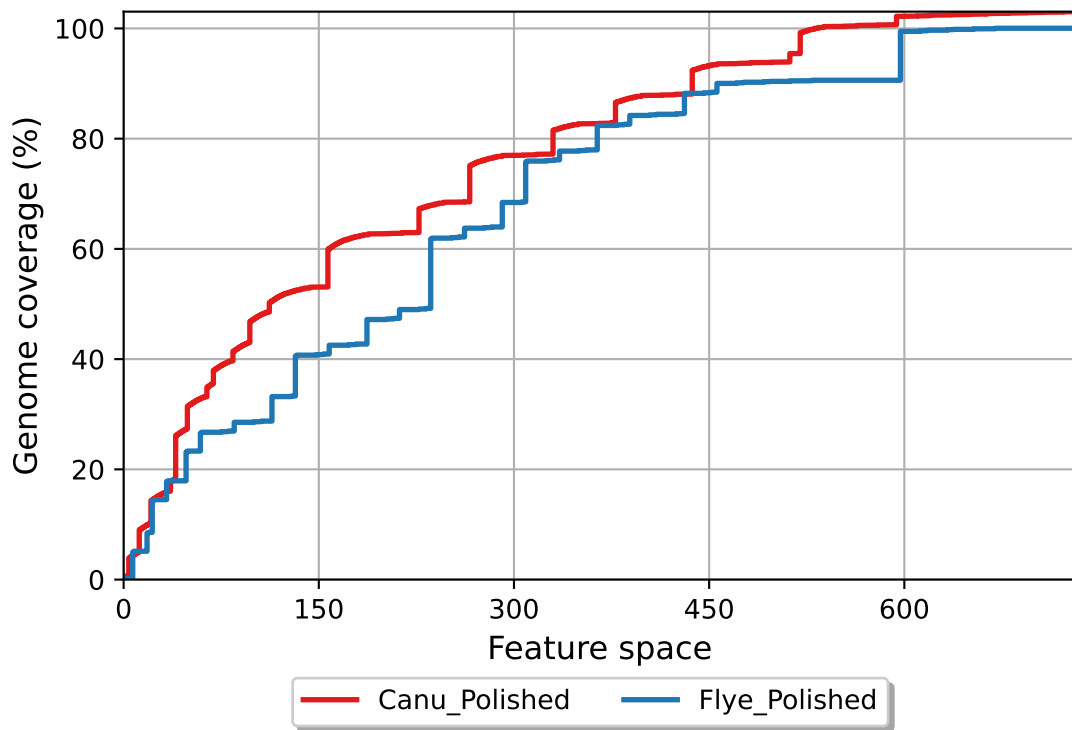


Misassemblies

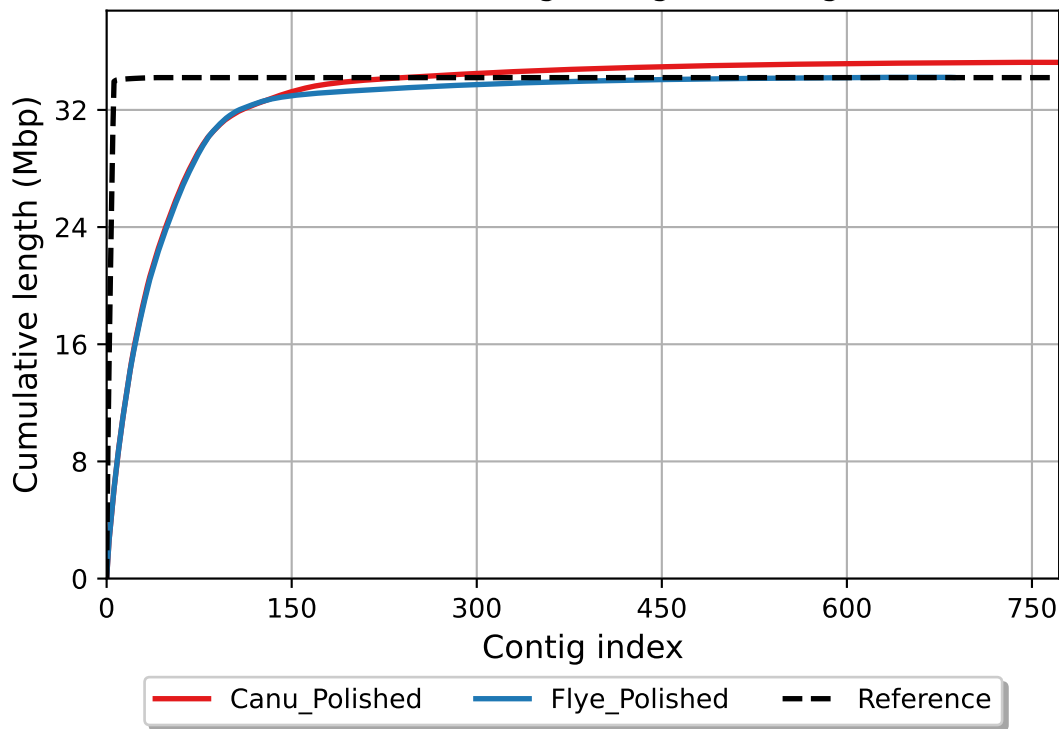


■ # relocations ■ # translocations ■ # inversions

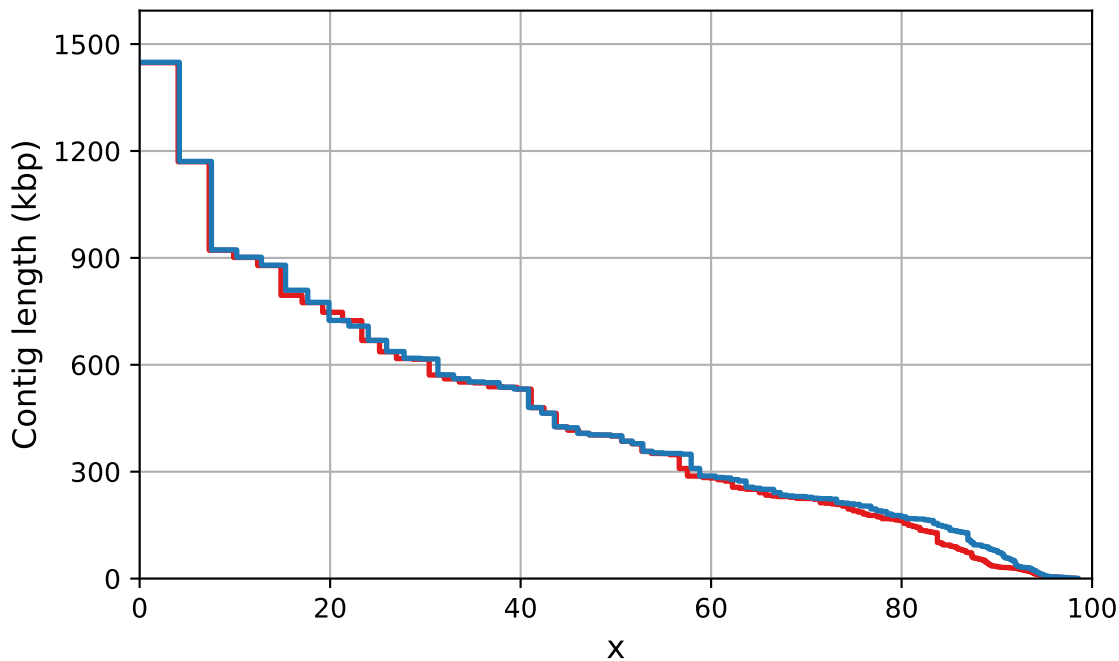
FRCurve (misassemblies)



Cumulative length (aligned contigs)

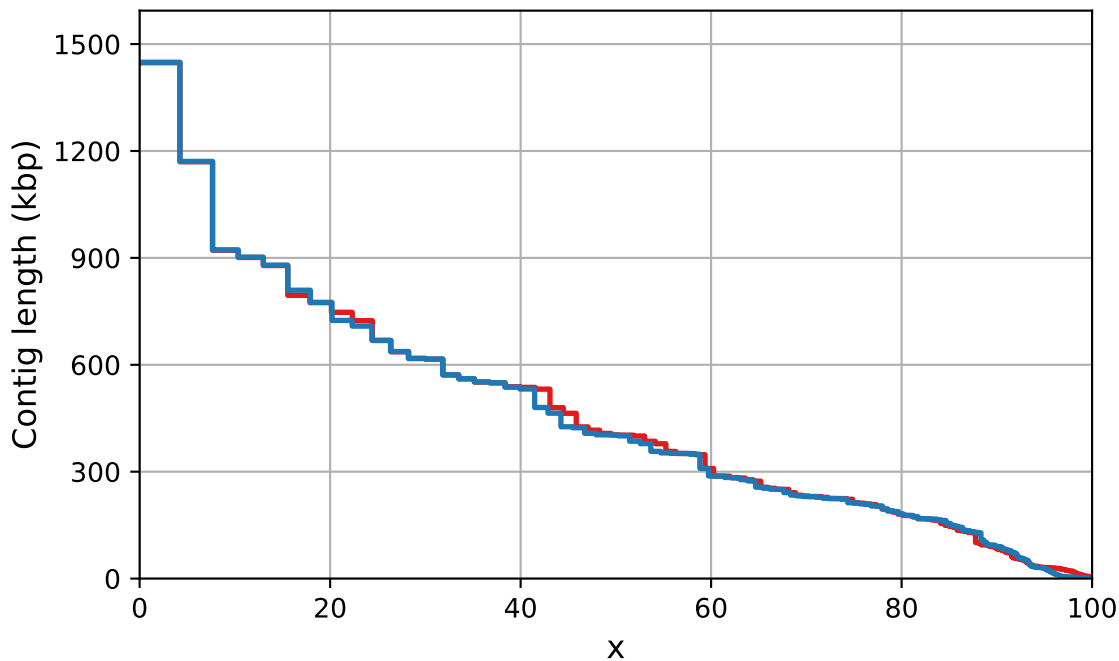


NAx



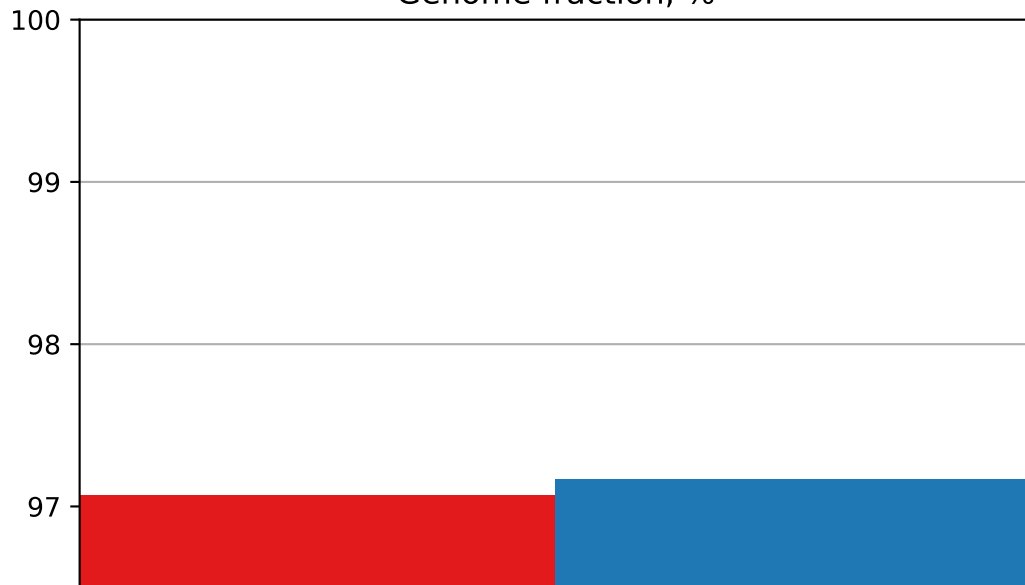
Canu_Polished Flye_Polished

NGAx



Canu_Polished Flye_Polished

Genome fraction, %



Canu_Polished



Flye_Polished