

Report

	Flye_Scaffold	Canu_Scaffold
# contigs (>= 0 bp)	11	29
# contigs (>= 1000 bp)	11	29
# contigs (>= 5000 bp)	10	29
# contigs (>= 10000 bp)	10	29
# contigs (>= 25000 bp)	10	28
# contigs (>= 50000 bp)	8	18
Total length (>= 0 bp)	34875698	36011764
Total length (>= 1000 bp)	34875698	36011764
Total length (>= 5000 bp)	34871541	36011764
Total length (>= 10000 bp)	34871541	36011764
Total length (>= 25000 bp)	34871541	35993267
Total length (>= 50000 bp)	34792138	35622420
# contigs	11	29
Largest contig	12202900	8146704
Total length	34875698	36011764
Reference length	34204973	34204973
GC (%)	22.73	22.76
Reference GC (%)	22.44	22.44
N50	8062995	5609440
NG50	8062995	5609440
N90	4041305	3928465
NG90	4041305	5029427
auN	8120809.9	5910377.3
auNG	8280050.8	6222578.0
L50	2	3
LG50	2	3
L90	5	6
LG90	5	5
# misassemblies	675	739
# misassembled contigs	9	26
Misassembled contigs length	34816006	35887505
# local misassemblies	165	163
# scaffold gap ext. mis.	0	2
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 9 part	0 + 14 part
Unaligned length	424840	551682
Genome fraction (%)	97.158	97.080
Duplication ratio	1.036	1.067
# N's per 100 kbp	1.43	3.33
# mismatches per 100 kbp	142.23	144.76
# indels per 100 kbp	211.18	217.17
Largest alignment	1455203	1455185
Total aligned length	34390152	35396359
NA50	404377	401924
NGA50	405183	405106
NA90	78836	34547
NGA90	94458	90261
auNA	476707.3	463025.2
auNGA	486055.0	487483.3
LA50	27	28
LGA50	26	26
LA90	94	116
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_Scaffold	Canu_Scaffold
# misassemblies	675	739
# contig misassemblies	672	729
# c. relocations	276	298
# c. translocations	384	419
# c. inversions	12	12
# scaffold misassemblies	3	10
# s. relocations	2	6
# s. translocations	1	4
# s. inversions	0	0
# misassembled contigs	9	26
Misassembled contigs length	34816006	35887505
# local misassemblies	165	163
# scaffold gap ext. mis.	0	2
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	48913	51241
# indels	72624	76869
# indels (<= 5 bp)	68542	71786
# indels (> 5 bp)	4082	5083
Indels length	168977	191401

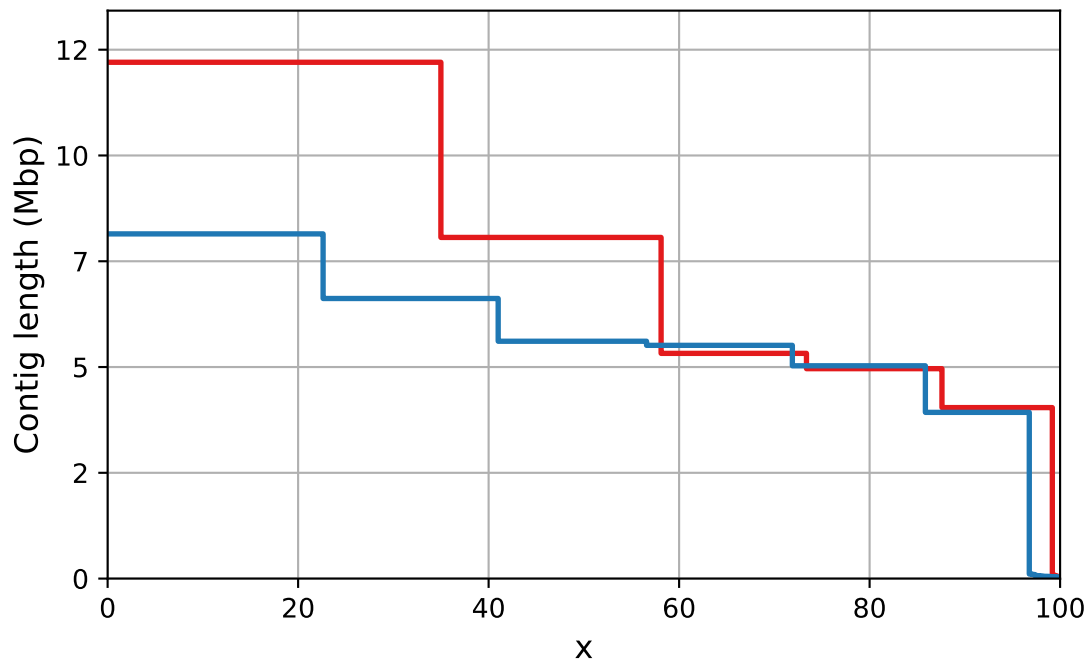
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	Flye_Scaffold	Canu_Scaffold
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	9	14
Partially unaligned length	424840	551682
# N's	500	1200

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

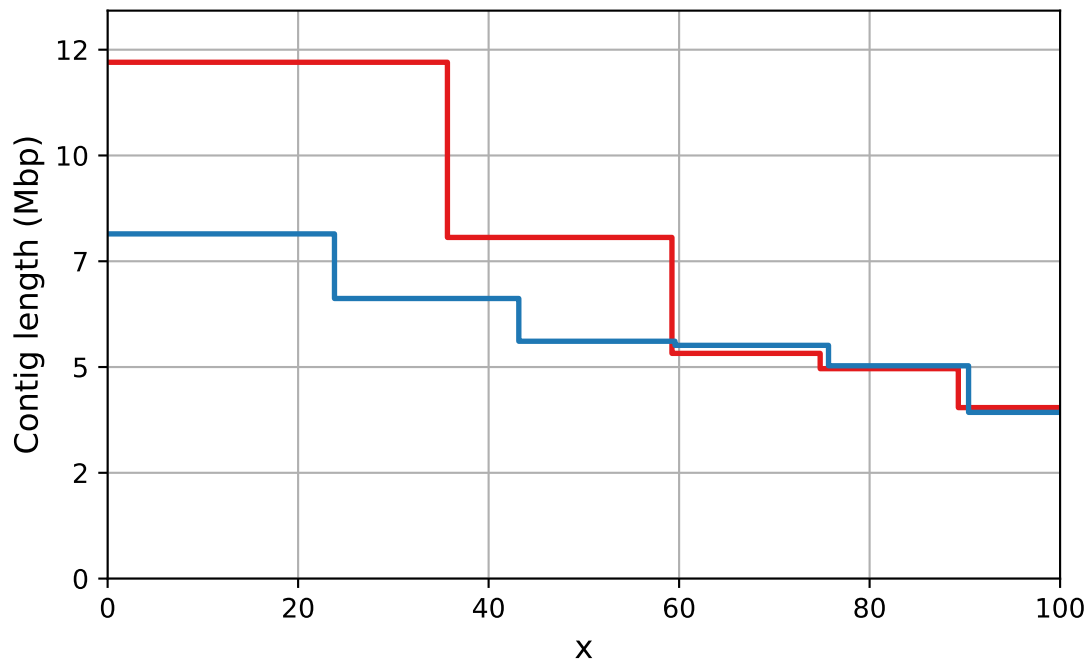
Nx



Flye\_Scaffold

Canu\_Scaffold

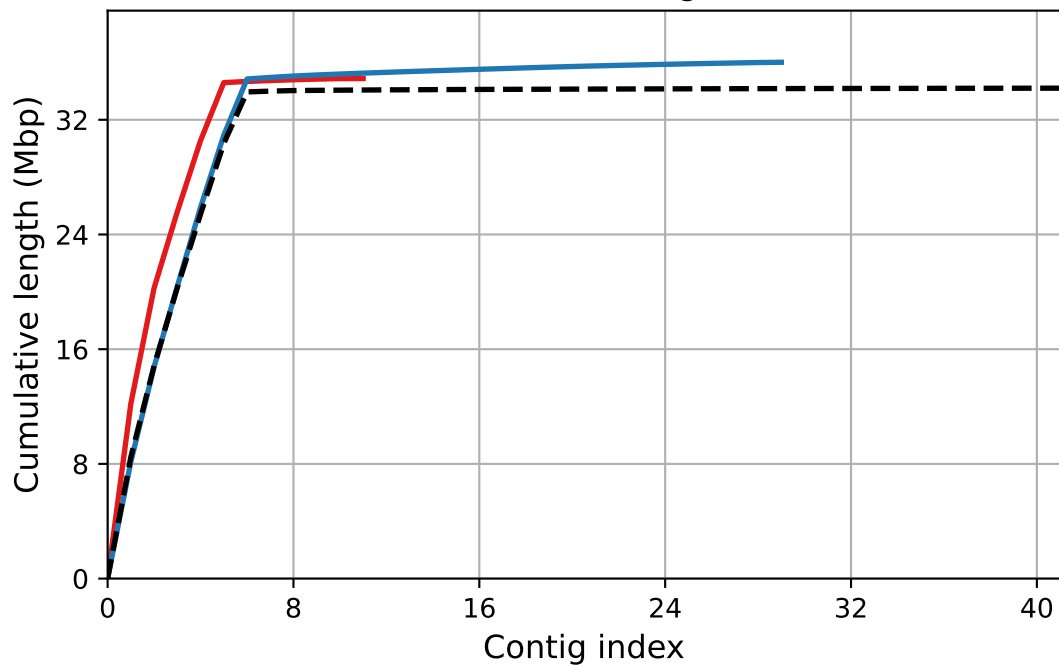
NGx



Flye\_Scaffold

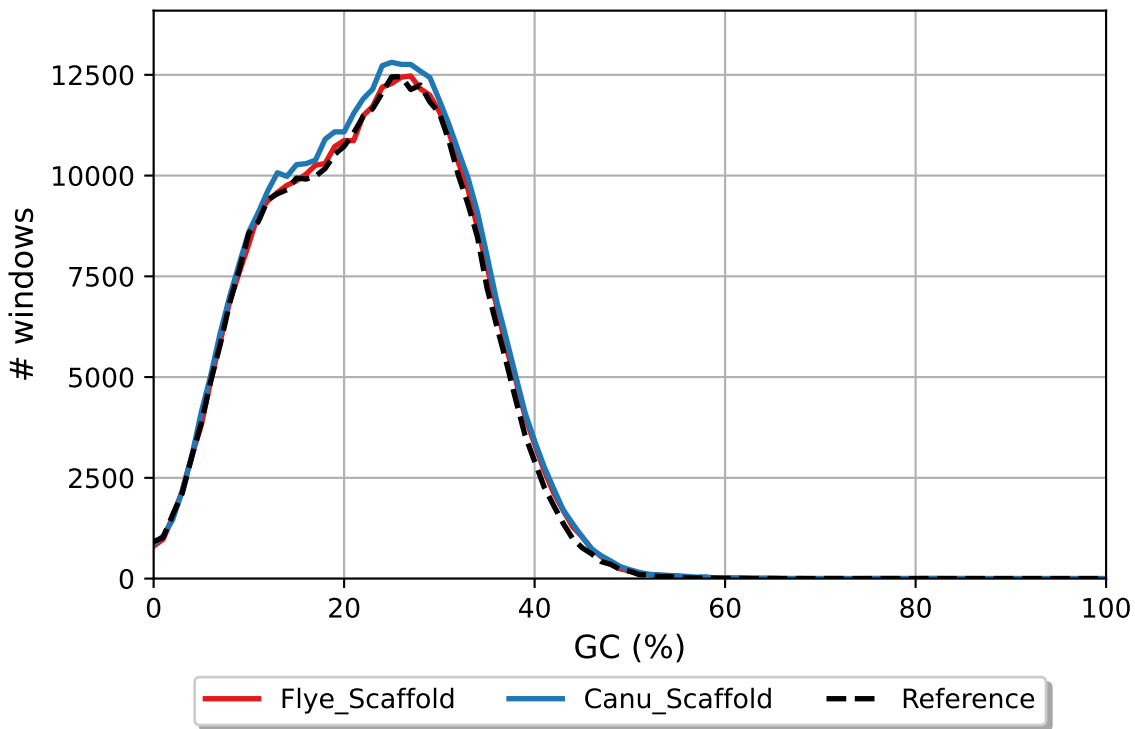
Canu\_Scaffold

Cumulative length

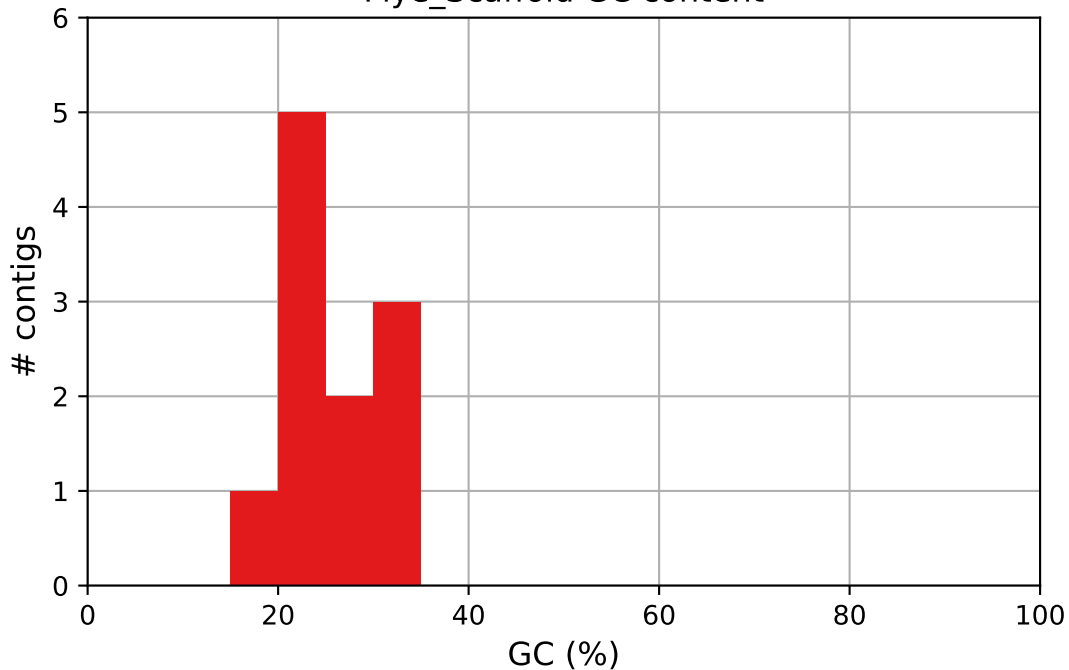


Flye\_Scaffold Canu\_Scaffold Reference

GC content



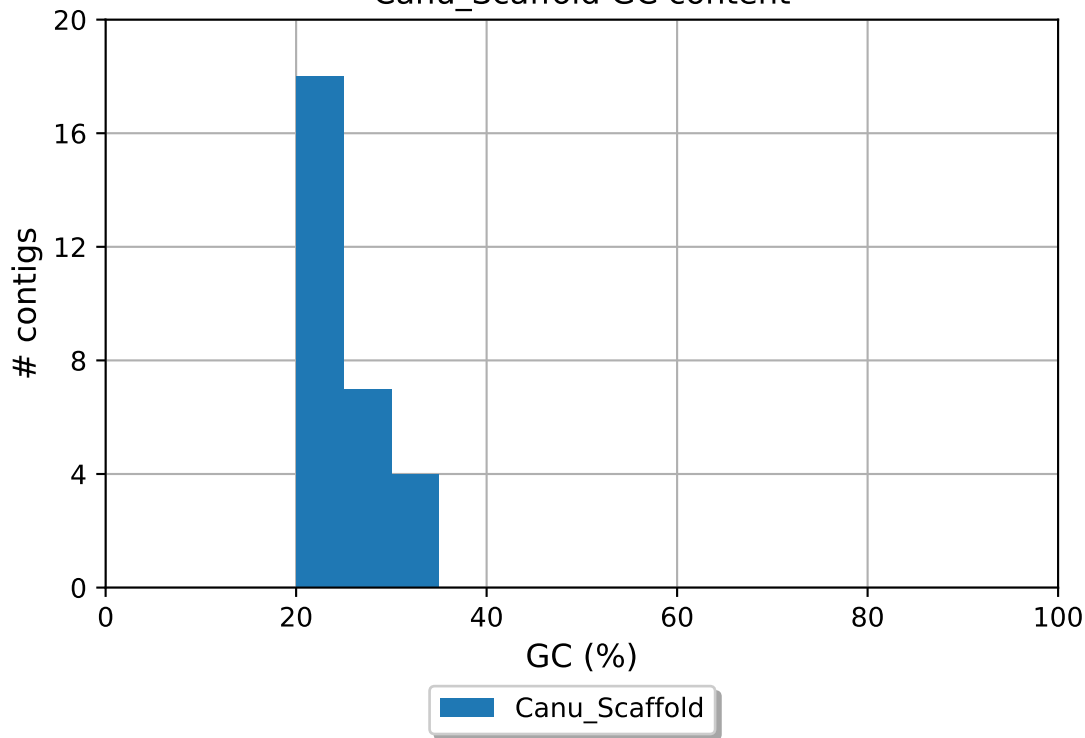
Flye\_Scaffold GC content



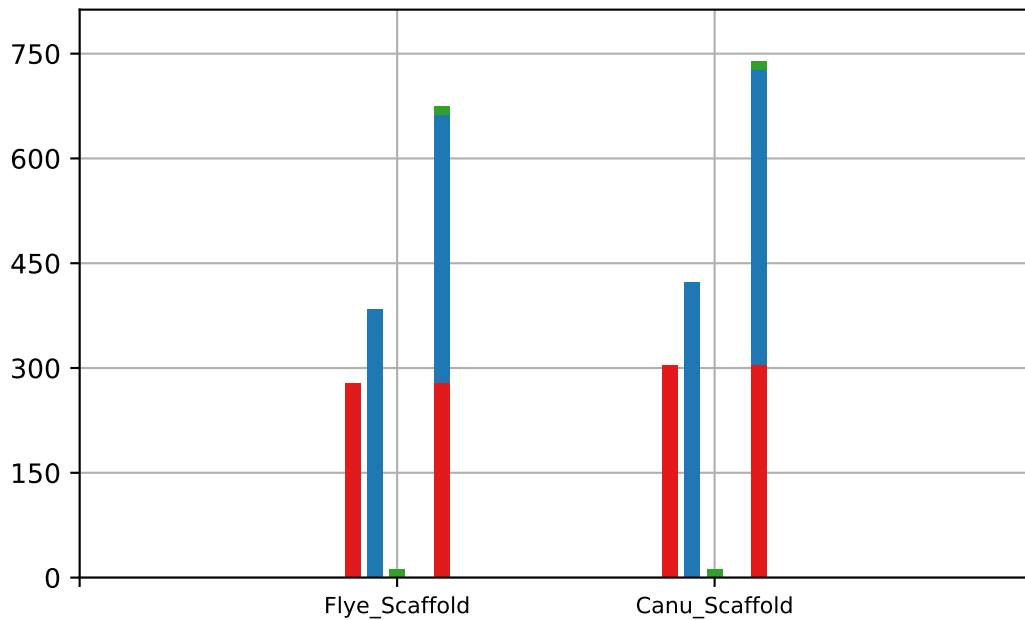
Flye\_Scaffold



Canu\_Scaffold GC content



## Misassemblies



# relocations

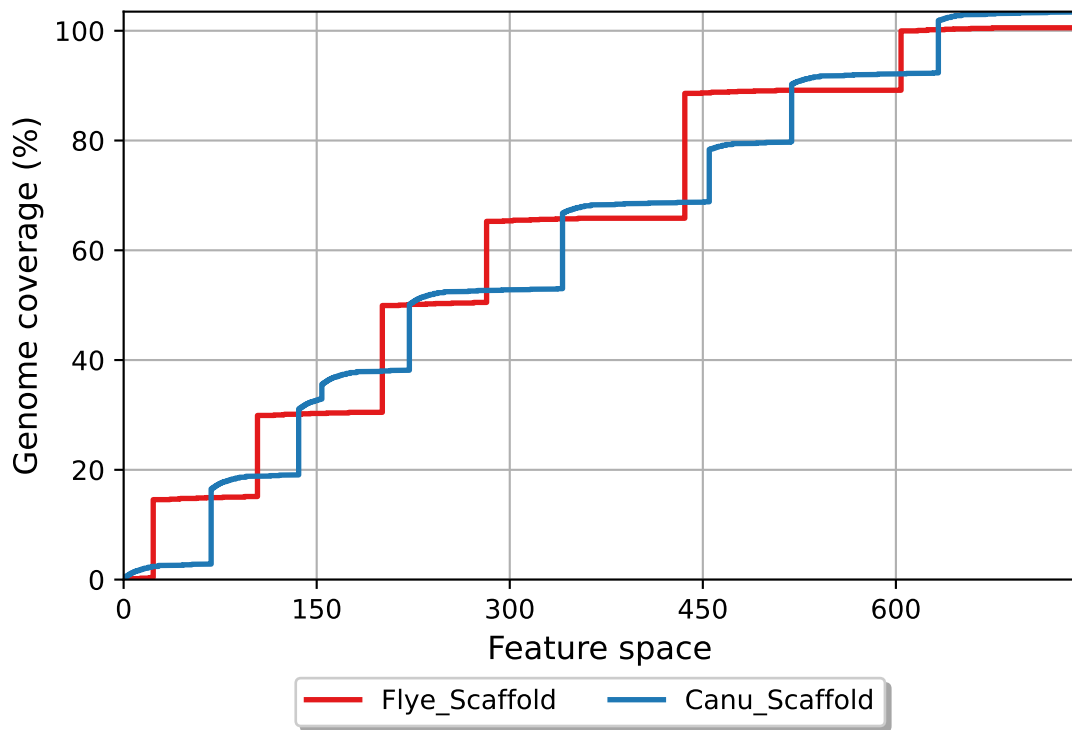


# translocations

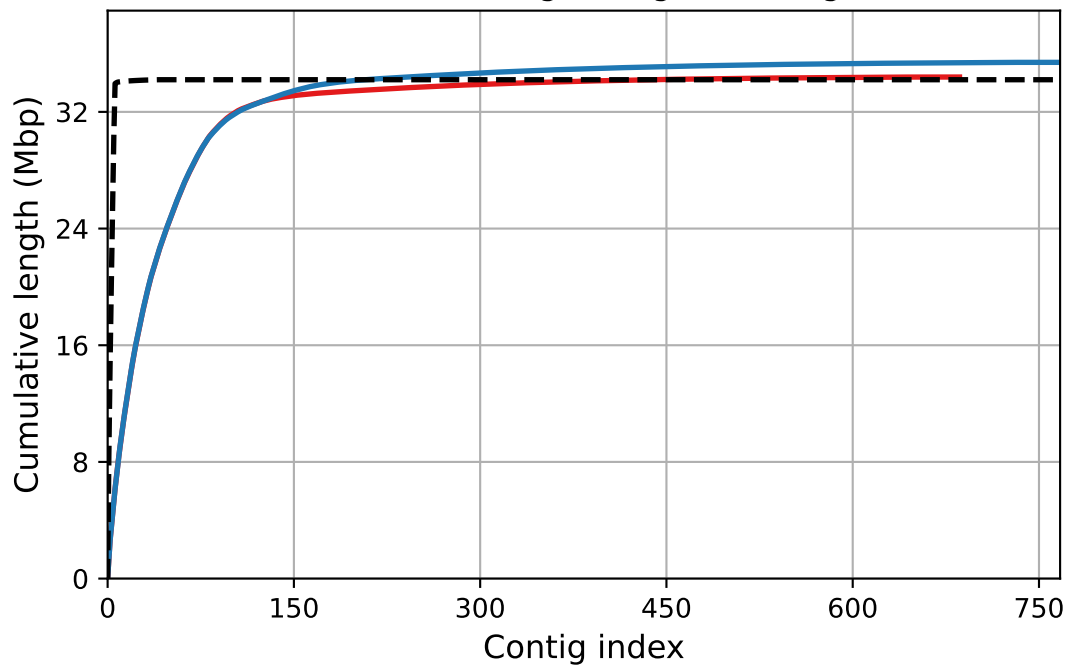


# inversions

FRCurve (misassemblies)

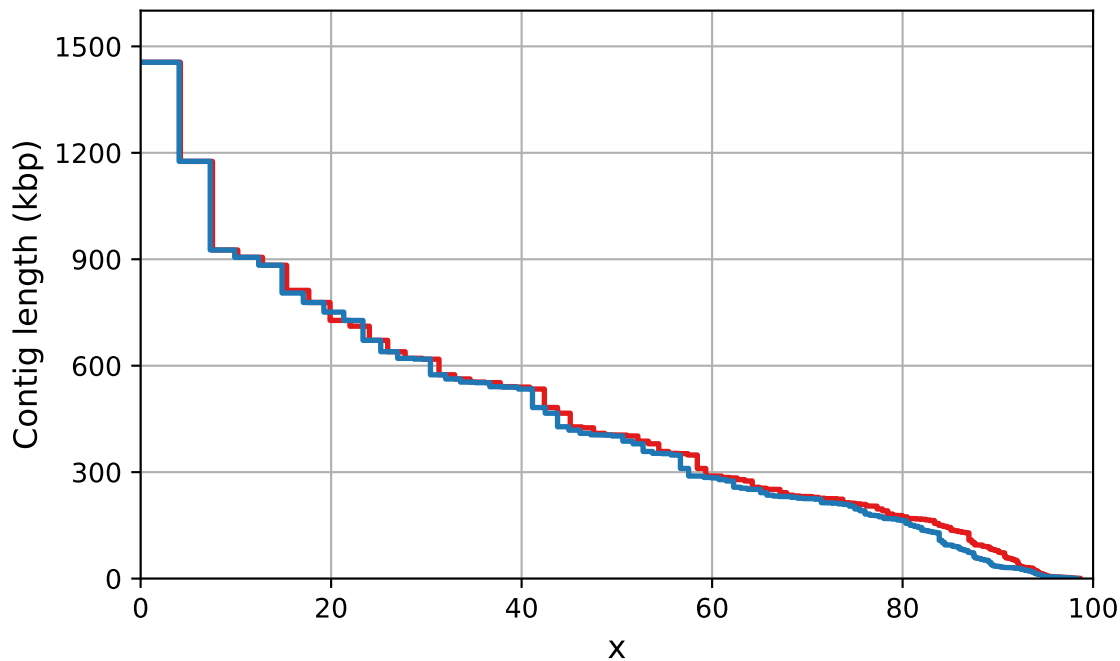


Cumulative length (aligned contigs)



Flye\_Scaffold    Canu\_Scaffold    Reference

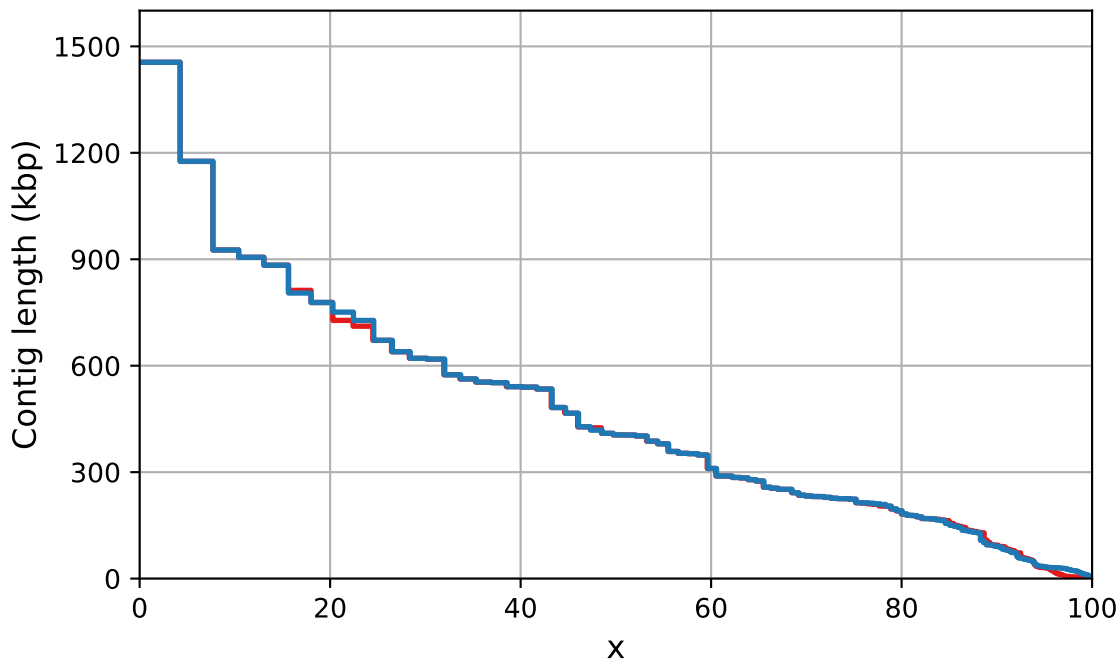
# NAx



Flye\_Scaffold

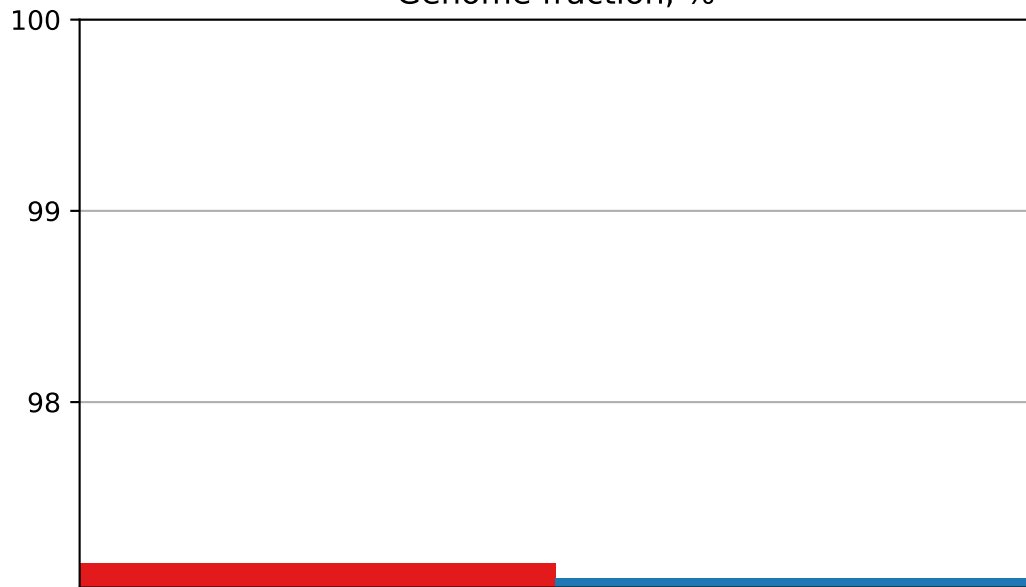
Canu\_Scaffold

# NGAx



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Genome fraction, %



Flye\_Scaffold



Canu\_Scaffold