

# Report

	MycOvi_Canu	MycOvi_HiFi_Flye	MycOvi_Hifiiasm	MycOvi_Nano_Flye
# contigs (>= 0 bp)	1	1	1	3
# contigs (>= 1000 bp)	1	1	1	3
# contigs (>= 5000 bp)	1	1	1	2
# contigs (>= 10000 bp)	1	1	1	2
# contigs (>= 25000 bp)	1	1	1	1
# contigs (>= 50000 bp)	1	1	1	1
Total length (>= 0 bp)	1034958	1014841	1014842	1020358
Total length (>= 1000 bp)	1034958	1014841	1014842	1020358
Total length (>= 5000 bp)	1034958	1014841	1014842	1017019
Total length (>= 10000 bp)	1034958	1014841	1014842	1017019
Total length (>= 25000 bp)	1034958	1014841	1014842	994273
Total length (>= 50000 bp)	1034958	1014841	1014842	994273
# contigs	1	1	1	3
Largest contig	1034958	1014841	1014842	994273
Total length	1034958	1014841	1014842	1020358
Reference length	1081520	1081520	1081520	1081520
GC (%)	29.25	29.23	29.22	29.24
Reference GC (%)	29.03	29.03	29.03	29.03
N50	1034958	1014841	1014842	994273
NG50	1034958	1014841	1014842	994273
N90	1034958	1014841	1014842	994273
NG90	1034958	1014841	1014842	994273
auN	1034958.0	1014841.0	1014842.0	969372.8
auNG	990400.6	952273.0	952274.8	914553.0
L50	1	1	1	1
LG50	1	1	1	1
L90	1	1	1	1
LG90	1	1	1	1
# misassemblies	58	40	40	60
# misassembled contigs	1	1	1	1
Misassembled contigs length	1034958	1014841	1014842	994273
# local misassemblies	7	20	20	7
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 1 part	0 + 1 part	2 + 1 part
Unaligned length	471031	383083	383528	441728
Genome fraction (%)	50.210	58.031	57.990	51.519
Duplication ratio	1.038	1.006	1.006	1.036
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	3352.07	3749.07	3749.80	3421.49
# indels per 100 kbp	497.49	205.17	205.00	401.41
Largest alignment	57826	65945	65945	57905
Total aligned length	563830	631677	631233	576971
NA50	3367	16611	16611	6007
NGA50	1656	14998	14998	1832
NA90	-	-	-	-
NGA90	-	-	-	-
auNA	13396.4	19857.6	19816.2	13812.2
auNGA	12819.7	18633.3	18594.5	13031.1
LA50	30	18	18	26
LGA50	41	20	20	35
LA90	-	-	-	-
LGA90	-	-	-	-

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

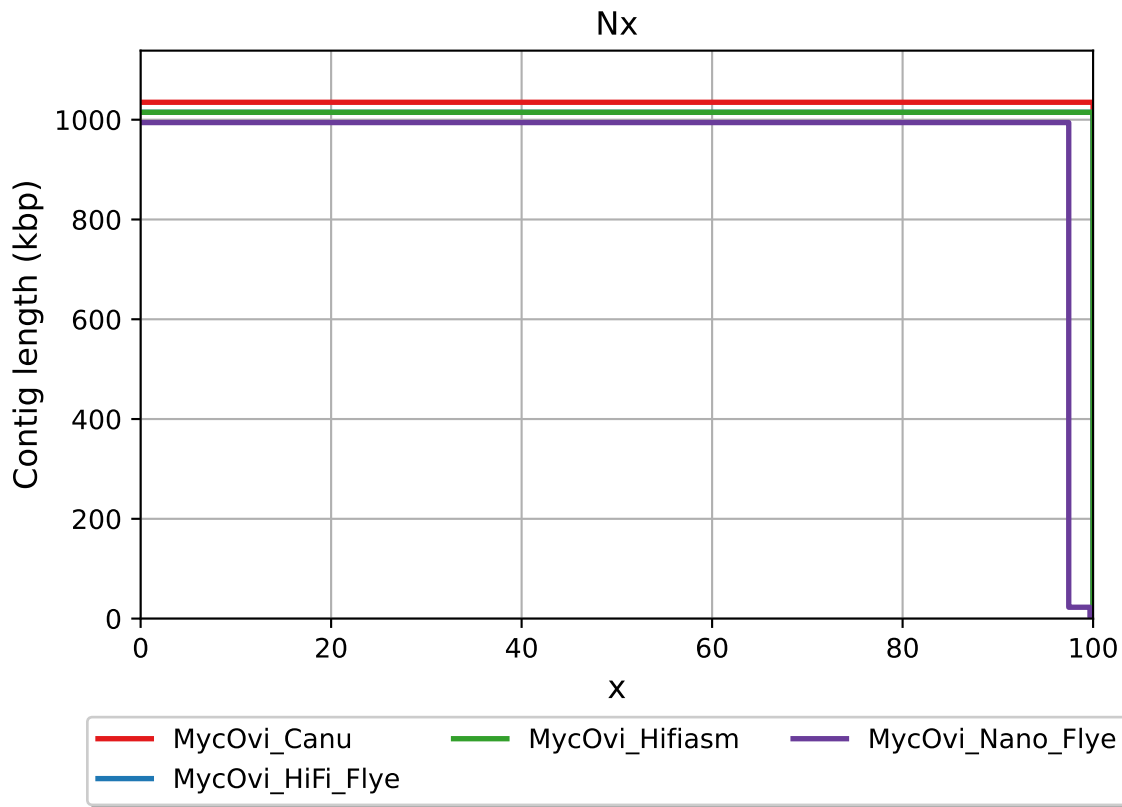
	MycOvi_Canu	MycOvi_HiFi_Flye	MycOvi_Hifiasm	MycOvi_Nano_Flye
# misassemblies	58	40	40	60
# contig misassemblies	58	40	40	60
# c. relocations	58	40	40	60
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	1	1	1	1
Misassembled contigs length	1034958	1014841	1014842	994273
# local misassemblies	7	20	20	7
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# mismatches	18900	23682	23670	19741
# indels	2805	1296	1294	2316
# indels (<= 5 bp)	2732	1205	1203	2243
# indels (> 5 bp)	73	91	91	73
Indels length	4839	3184	3179	4059

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).

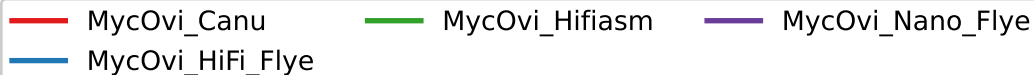
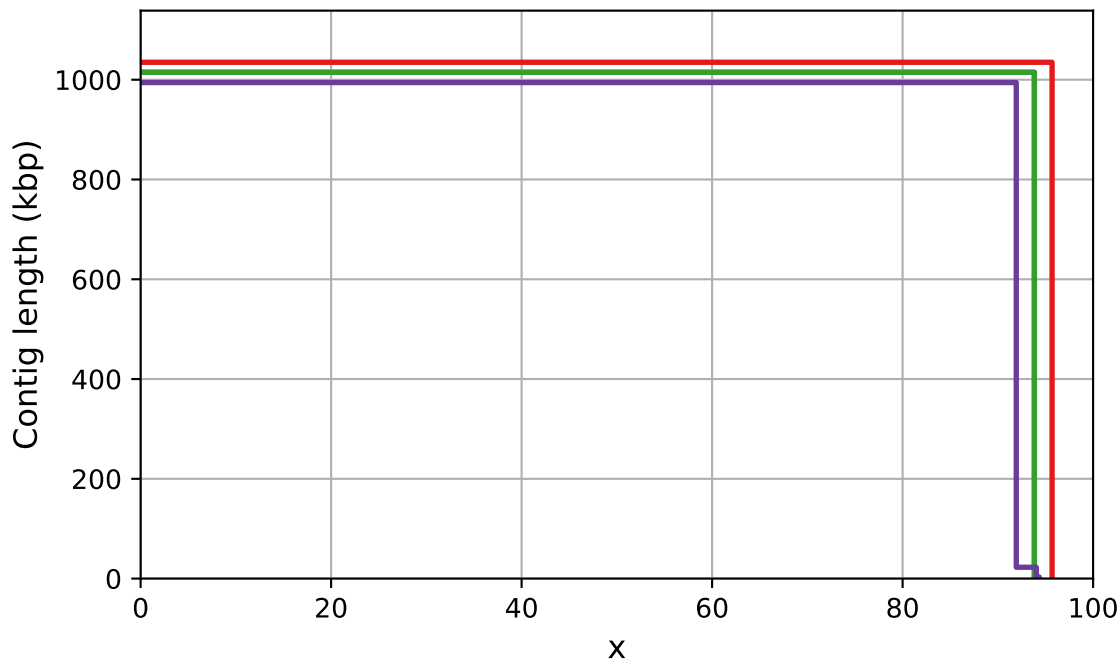
## Unaligned report

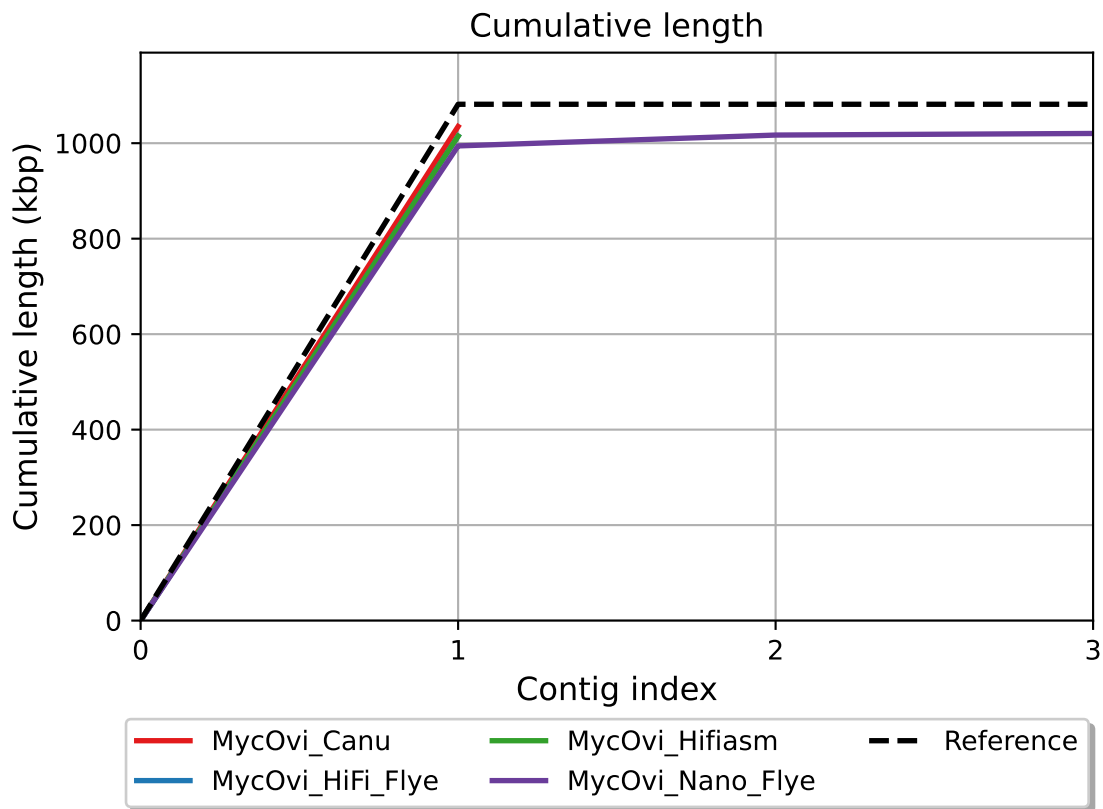
	MycOvi_Canu	MycOvi_HiFi_Flye	MycOvi_Hifiasm	MycOvi_Nano_Flye
# fully unaligned contigs	0	0	0	2
Fully unaligned length	0	0	0	26085
# partially unaligned contigs	1	1	1	1
Partially unaligned length	471031	383083	383528	415643
# N's	0	0	0	0

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).

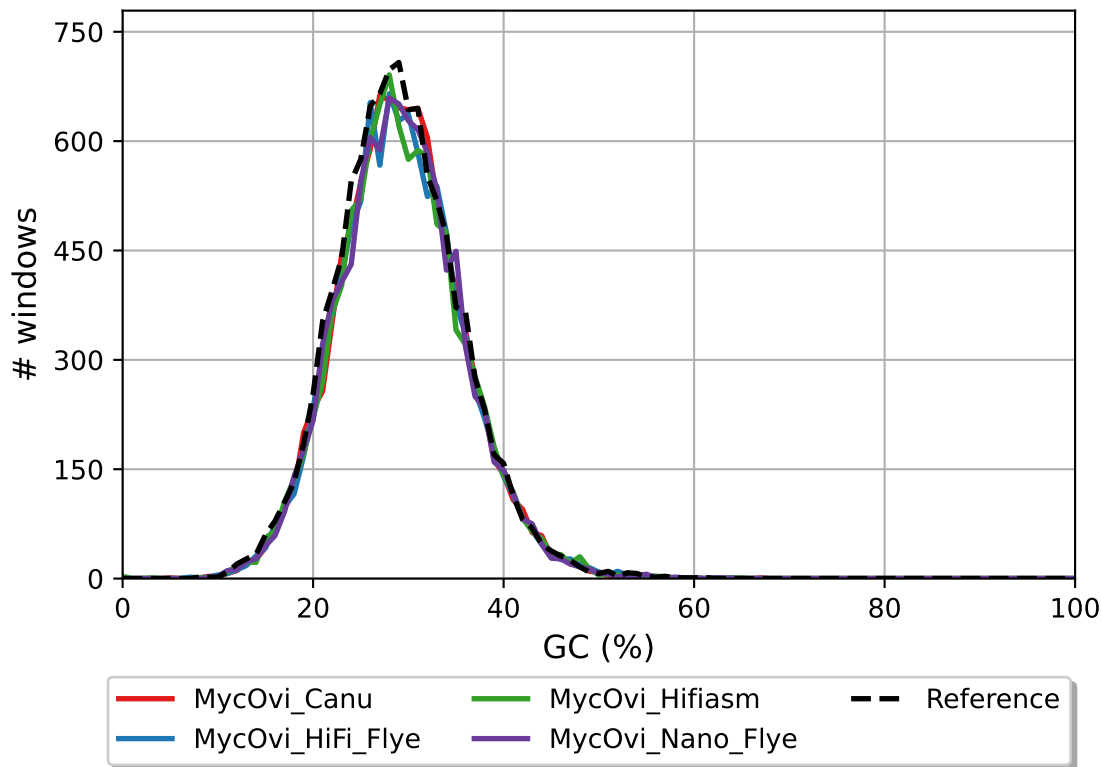


# NGx

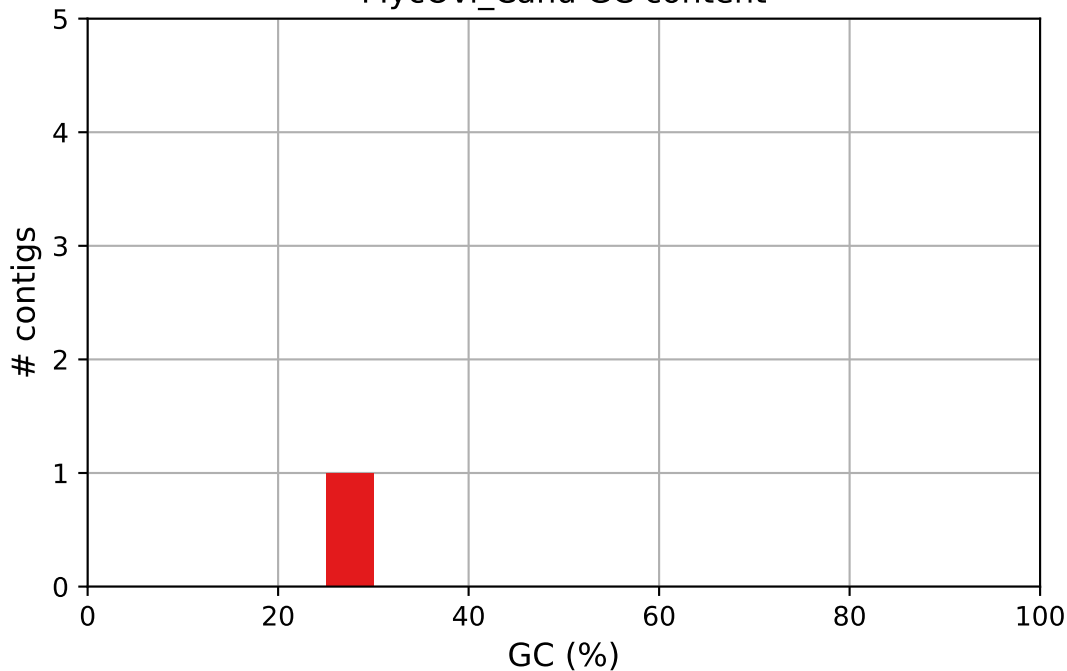




GC content



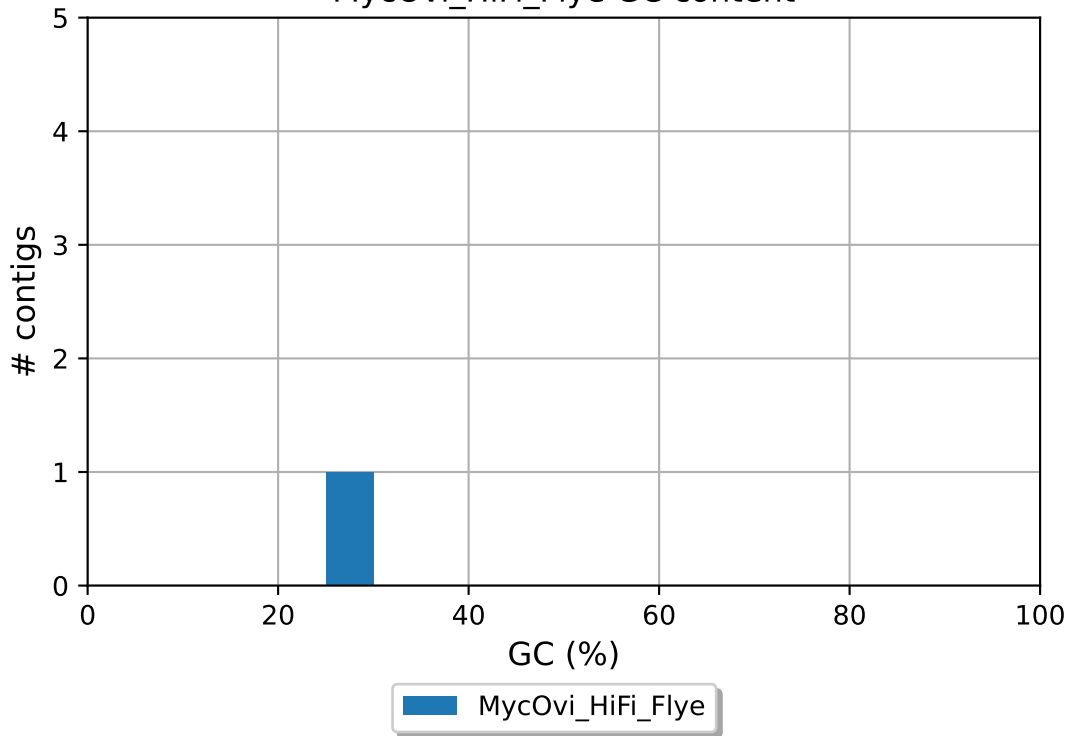
MycOvi\_Canu GC content



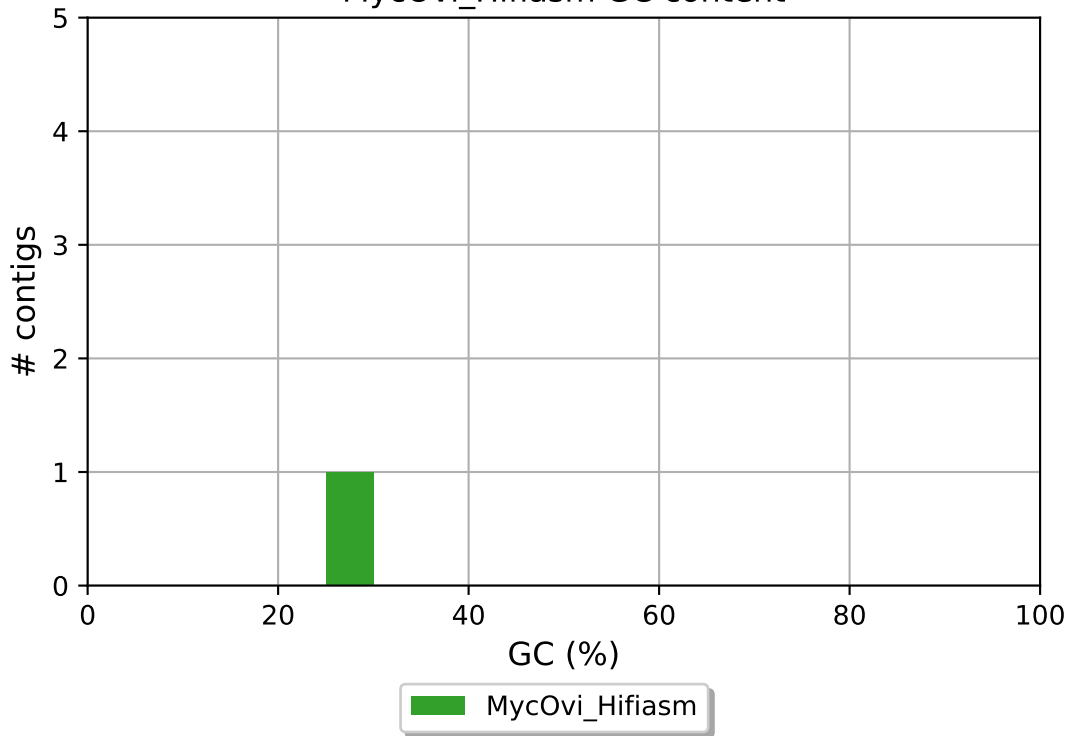
 MycOvi\_Canu



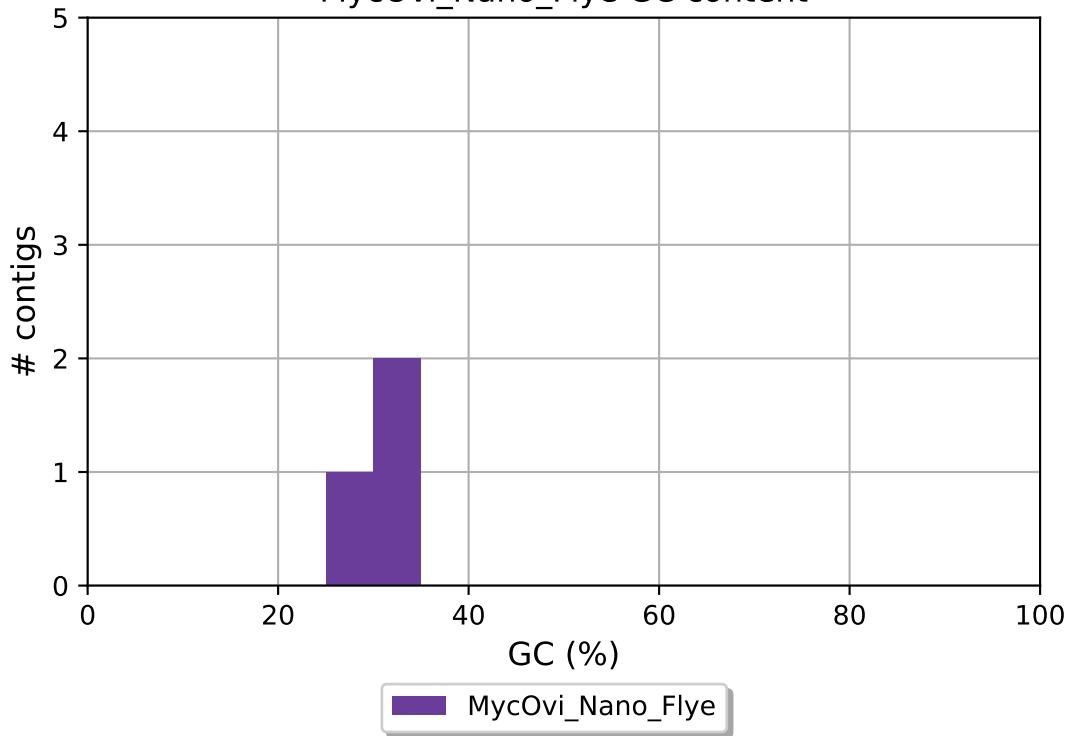
MycOvi\_HiFi\_Flye GC content



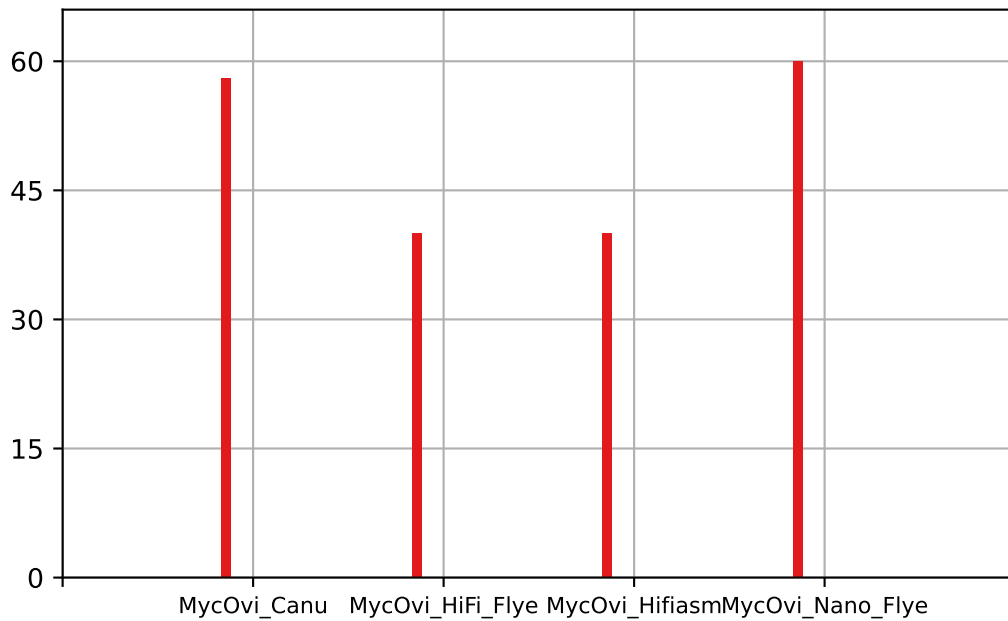
MycOvi\_Hifiasm GC content



MycOvi\_Nano\_Flye GC content

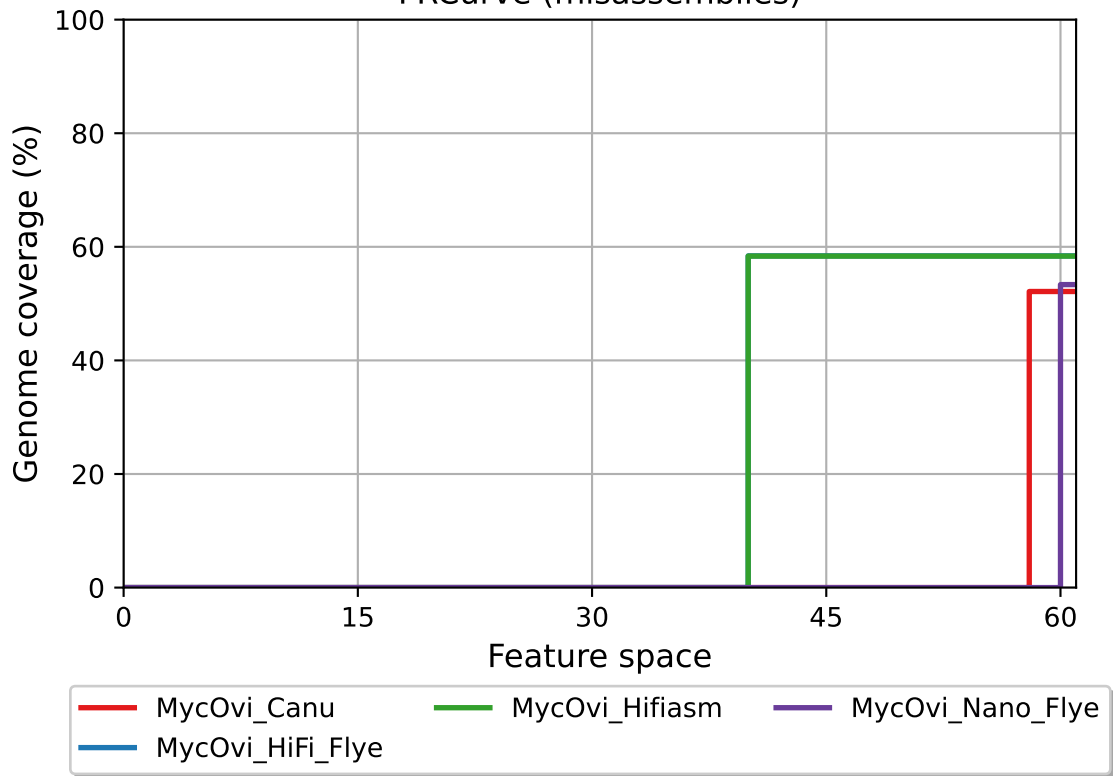


## Misassemblies

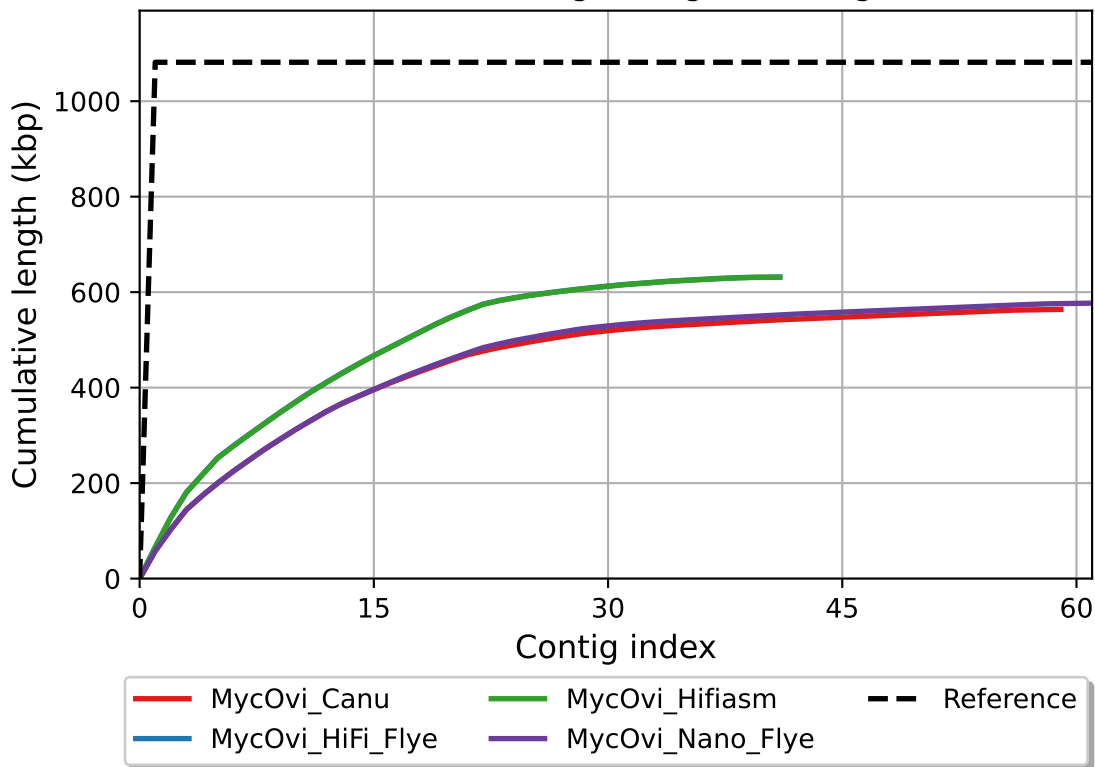


 # relocations

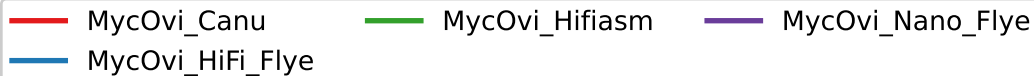
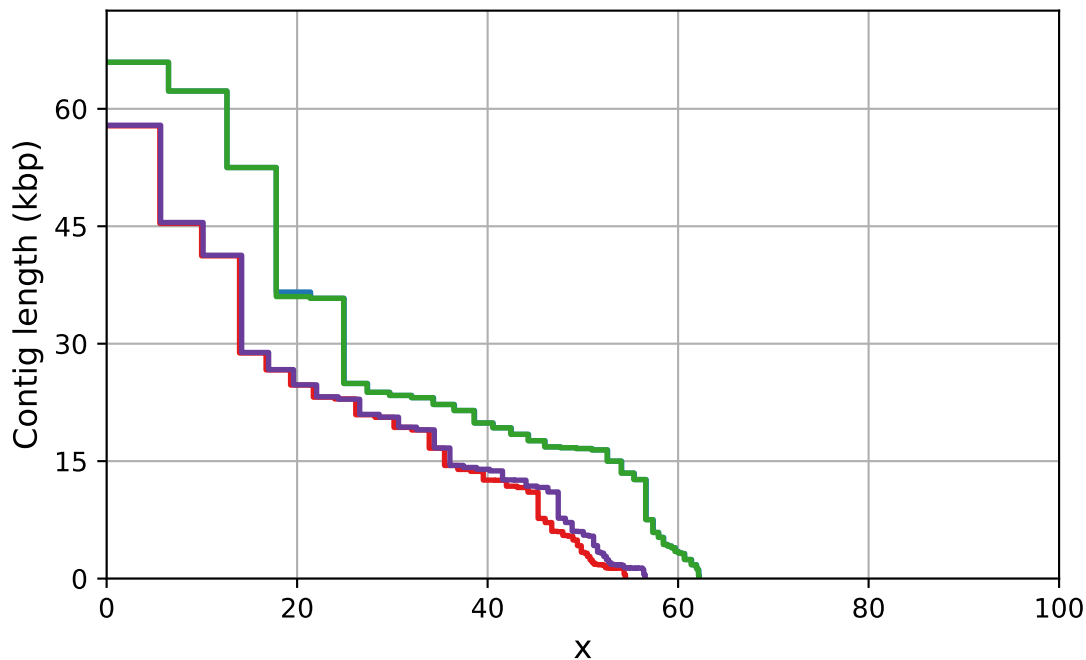
FRCurve (misassemblies)



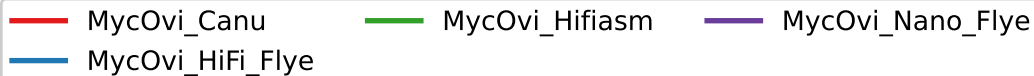
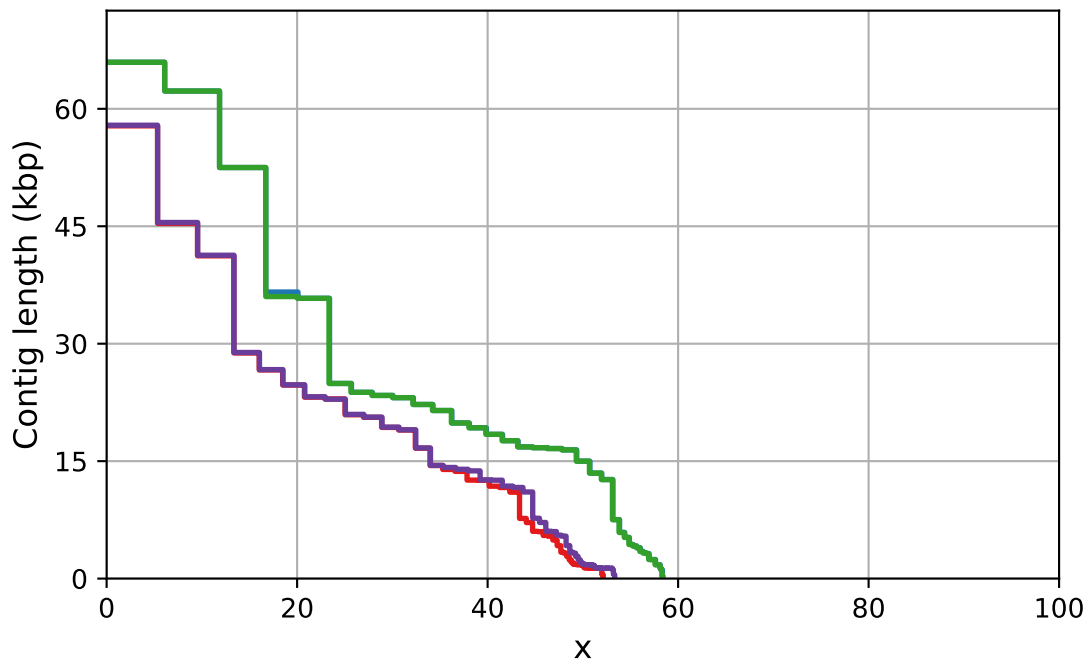
Cumulative length (aligned contigs)



## NAx



## NGAx





Genome fraction, %

