

Report

	flye-ont-ecoli	racon_ont_ecoli	velvet_ecoli	wengan_ont_ecoli
# contigs (>= 0 bp)	1	1	788	1
# contigs (>= 1000 bp)	1	1	350	1
# contigs (>= 5000 bp)	1	1	244	1
# contigs (>= 10000 bp)	1	1	156	1
# contigs (>= 25000 bp)	1	1	47	1
# contigs (>= 50000 bp)	1	1	10	1
Total length (>= 0 bp)	4594810	4590330	4563900	4641085
Total length (>= 1000 bp)	4594810	4590330	4495927	4641085
Total length (>= 5000 bp)	4594810	4590330	4217462	4641085
Total length (>= 10000 bp)	4594810	4590330	3540826	4641085
Total length (>= 25000 bp)	4594810	4590330	1864395	4641085
Total length (>= 50000 bp)	4594810	4590330	587899	4641085
# contigs	1	1	372	1
Largest contig	4594810	4590330	71245	4641085
Total length	4594810	4590330	4511775	4641085
Reference length	4641652	4641652	4641652	4641652
GC (%)	51.16	51.07	50.74	50.79
Reference GC (%)	50.79	50.79	50.79	50.79
N50	4594810	4590330	19872	4641085
NG50	4594810	4590330	19331	4641085
N90	4594810	4590330	6908	4641085
NG90	4594810	4590330	5384	4641085
auN	4594810.0	4590330.0	25281.7	4641085.0
auNG	4548440.7	4539575.5	24574.3	4640518.1
L50	1	1	65	1
LG50	1	1	68	1
L90	1	1	218	1
LG90	1	1	237	1
# misassemblies	4	2	0	2
# misassembled contigs	1	1	0	1
Misassembled contigs length	4594810	4590330	0	4641085
# local misassemblies	0	0	0	0
# 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 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0
Genome fraction (%)	100.000	100.000	97.140	99.979
Duplication ratio	0.990	0.989	1.001	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	489.53	400.21	2.17	4.24
# indels per 100 kbp	928.35	1096.50	0.31	10.99
Largest alignment	3935672	4589578	71217	4640327
Total aligned length	4594801	4590329	4511718	4641085
NA50	3935672	4589578	19872	4640327
NGA50	3935672	4589578	19331	4640327
NA90	656590	4589578	6908	4640327
NGA90	656590	4589578	5384	4640327
auNA	3464915.5	4588826.2	25280.1	4639569.2
auNGA	3429948.7	4538088.3	24572.7	4639002.5
LA50	1	1	65	1
LGA50	1	1	68	1
LA90	2	1	218	1
LGA90	2	1	237	1

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

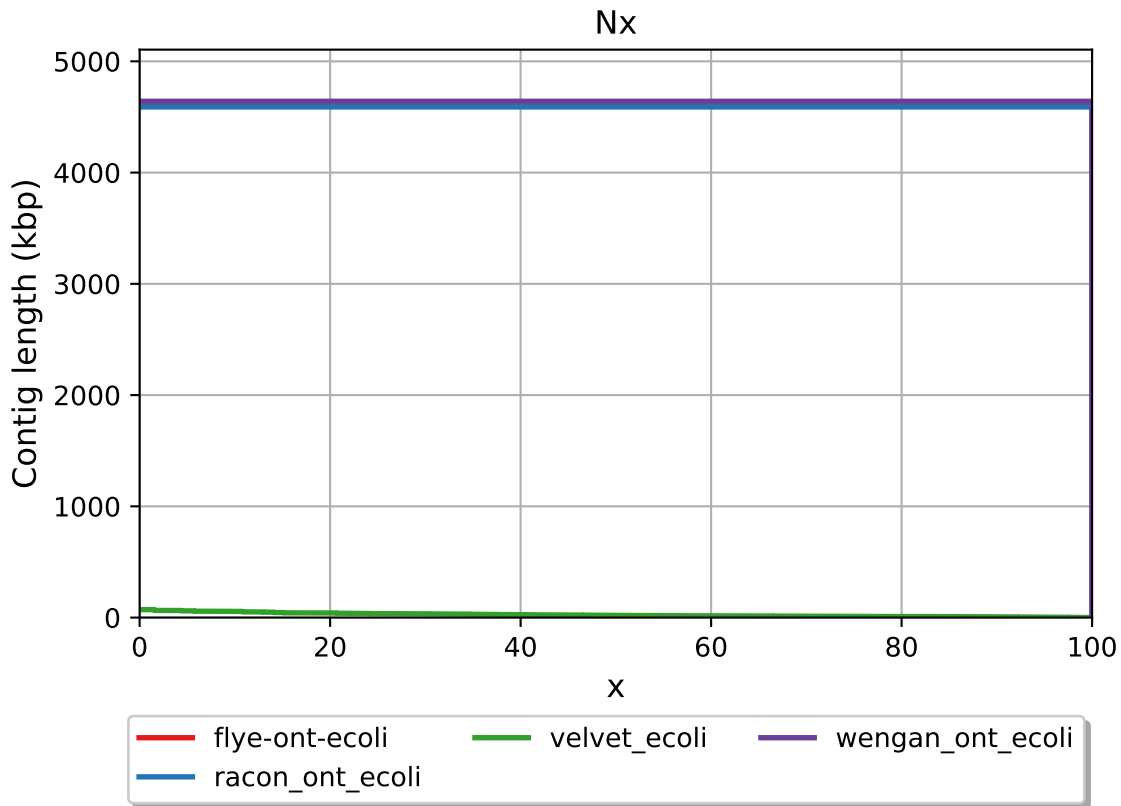
	flye-ont-ecoli	racon_ont_ecoli	velvet_ecoli	wengan_ont_ecoli
# misassemblies	4	2	0	2
# contig misassemblies	4	2	0	2
# c. relocations	2	2	0	2
# c. translocations	0	0	0	0
# c. inversions	2	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	1	1	0	1
Misassembled contigs length	4594810	4590330	0	4641085
# local misassemblies	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# mismatches	22493	18371	98	197
# indels	42656	50333	14	510
# indels (<= 5 bp)	42648	50291	14	505
# indels (> 5 bp)	8	42	0	5
Indels length	50034	64377	15	1029

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).

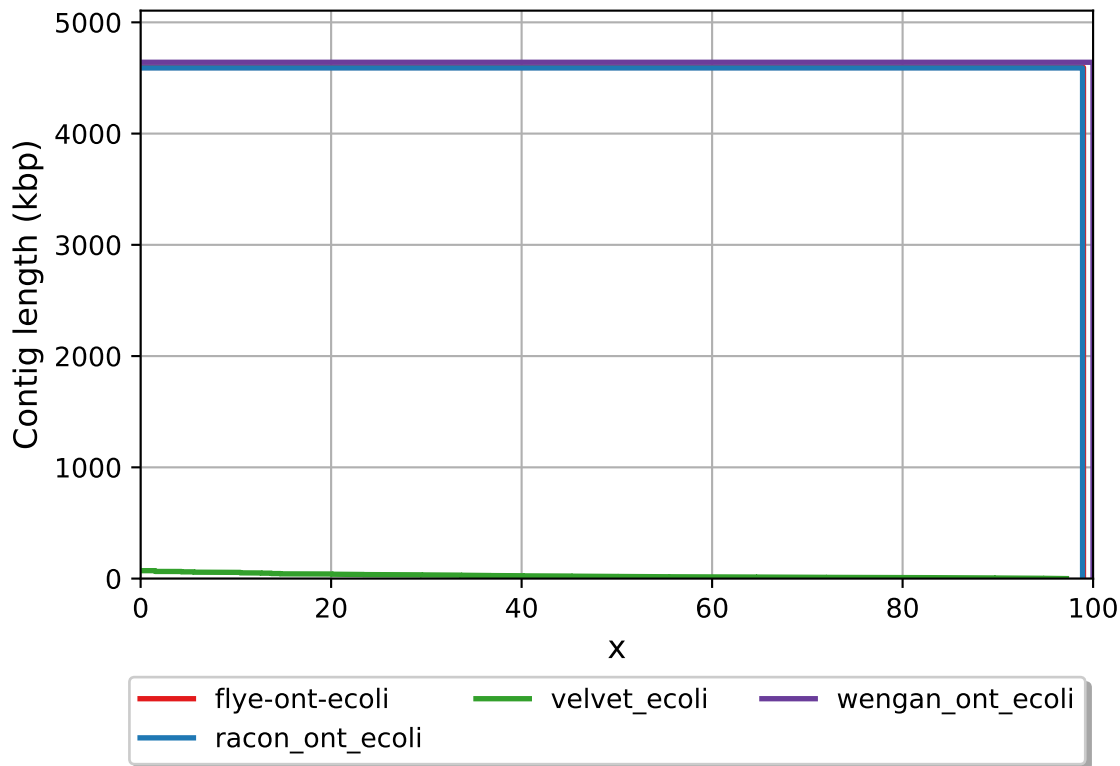
Unaligned report

	flye-ont-ecoli	racon_ont_ecoli	velvet_ecoli	wengan_ont_ecoli
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

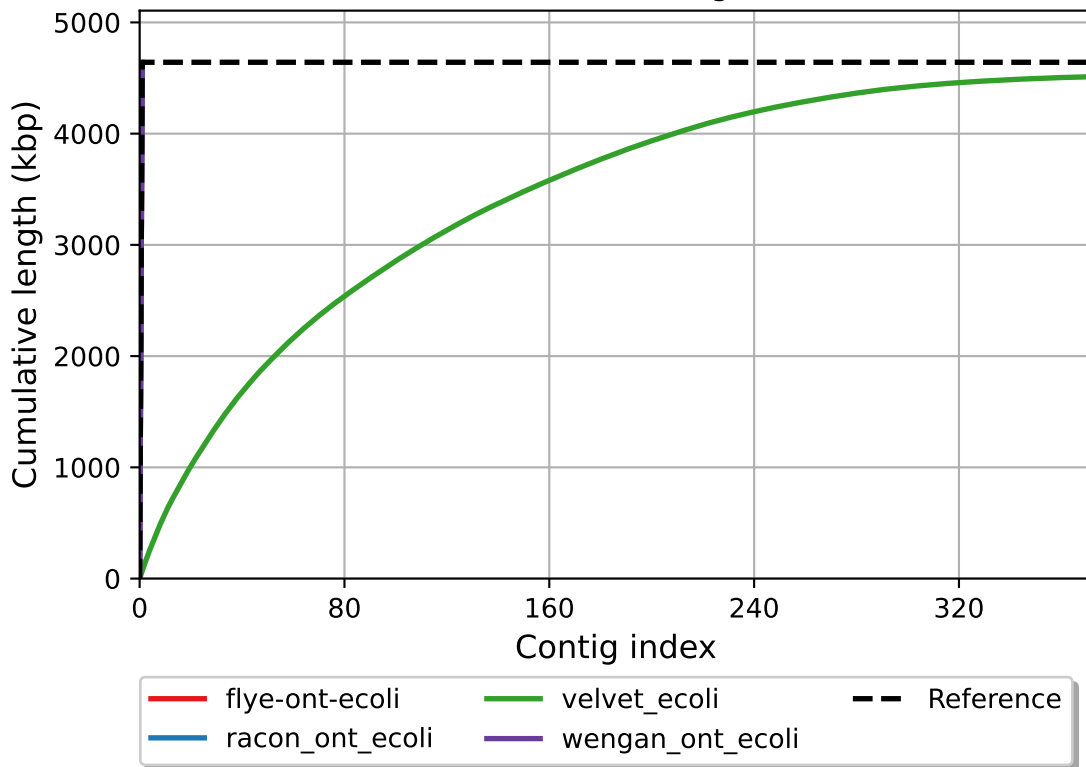
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



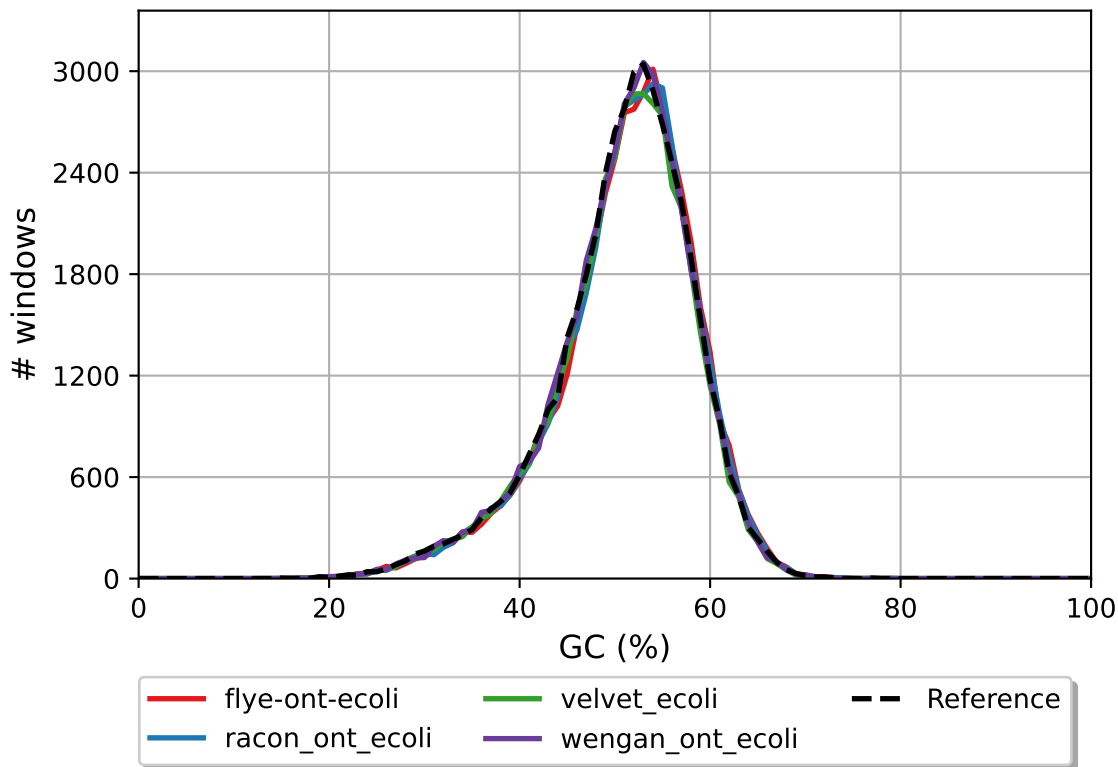
NGx



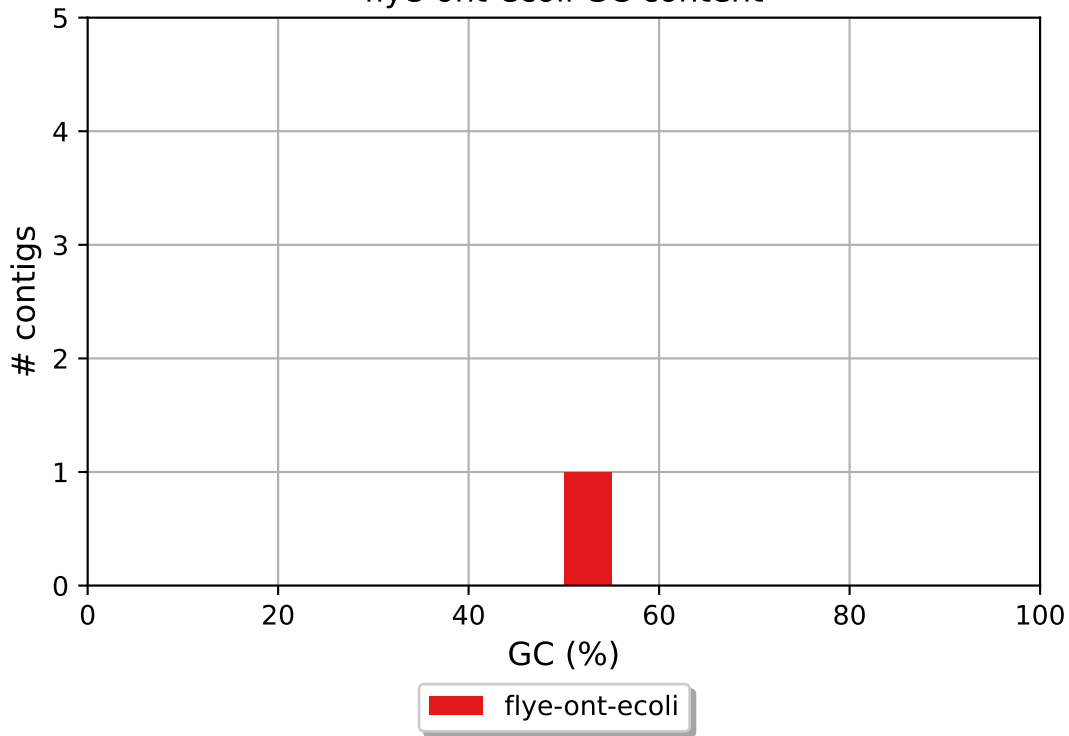
Cumulative length



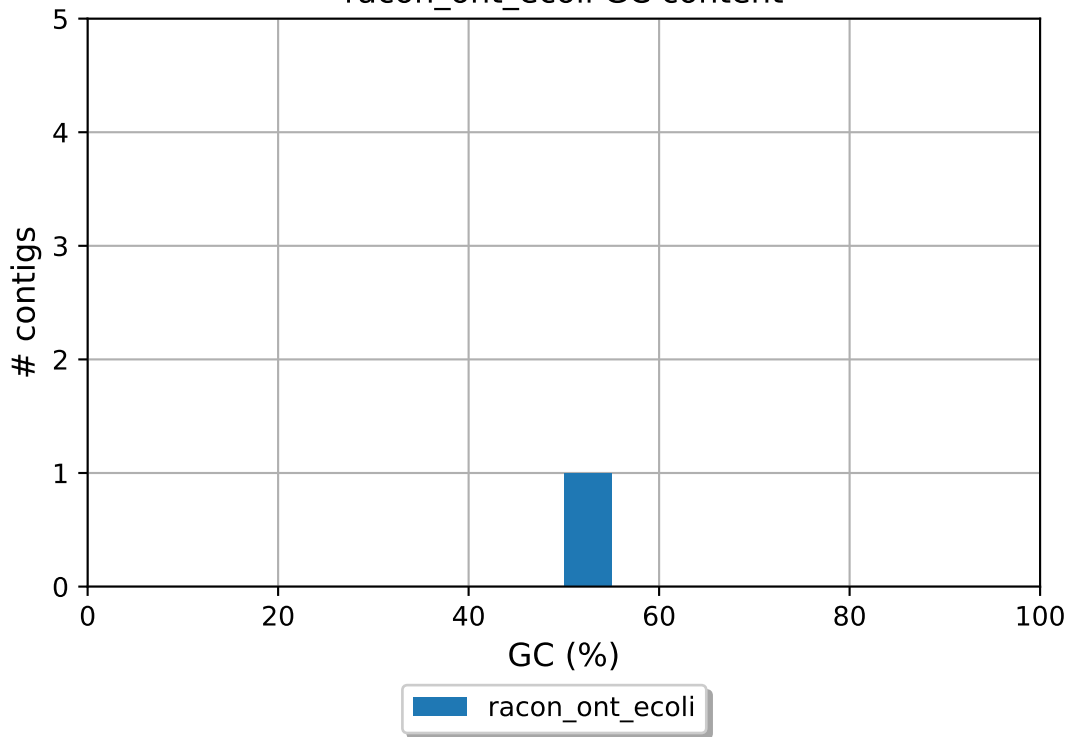
GC content



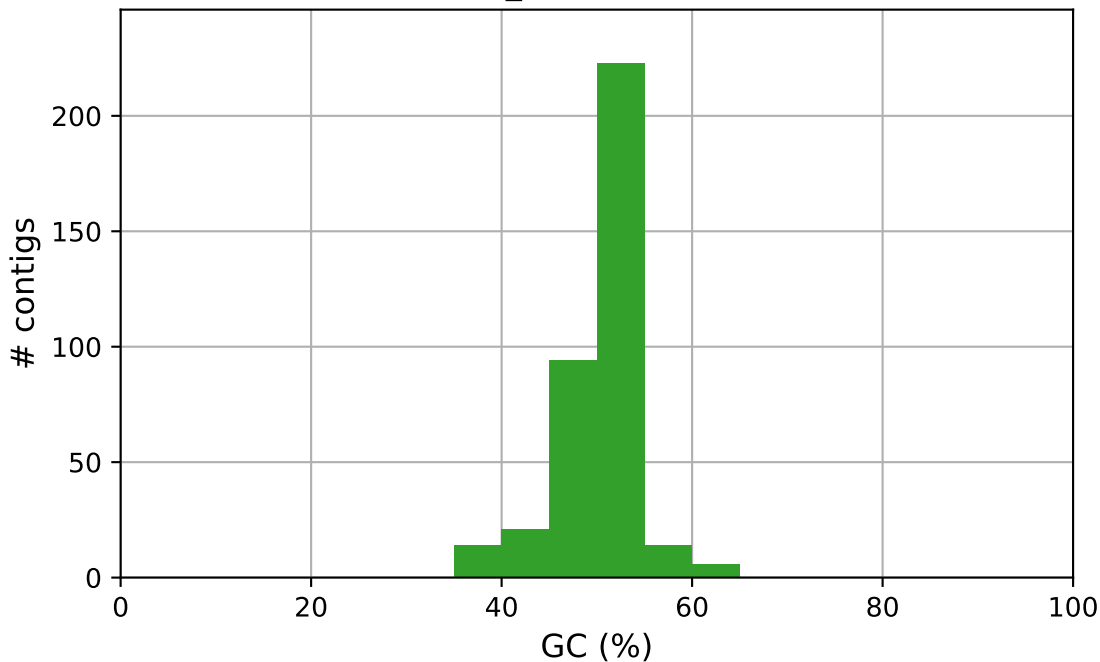
flye-ont-ecoli GC content



racon_ont_ecoli GC content

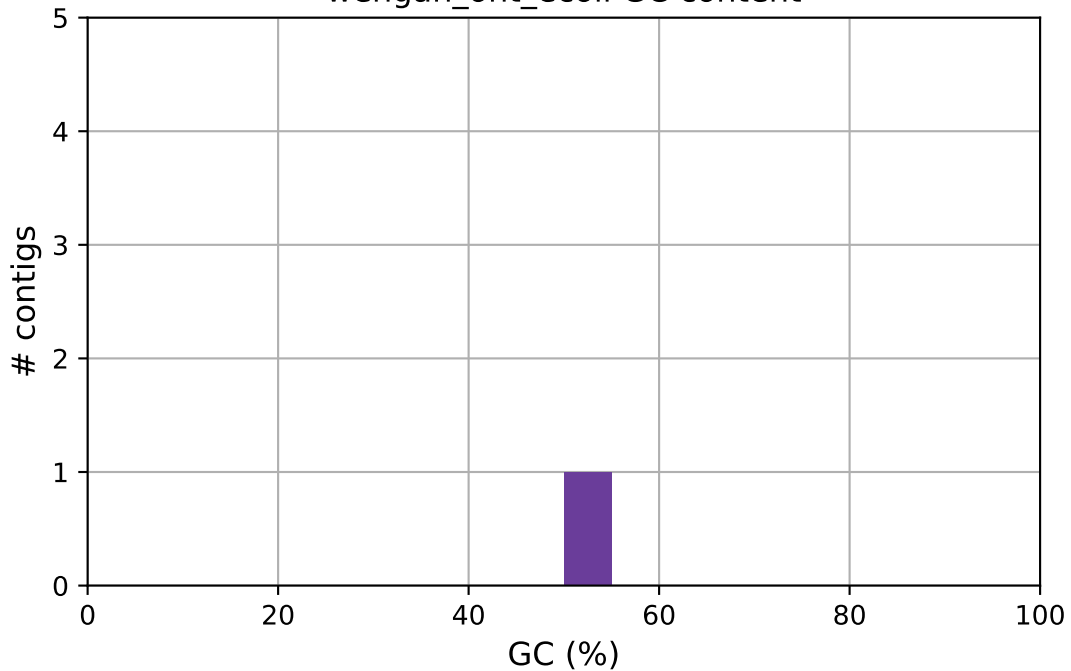


velvet_ecoli GC content



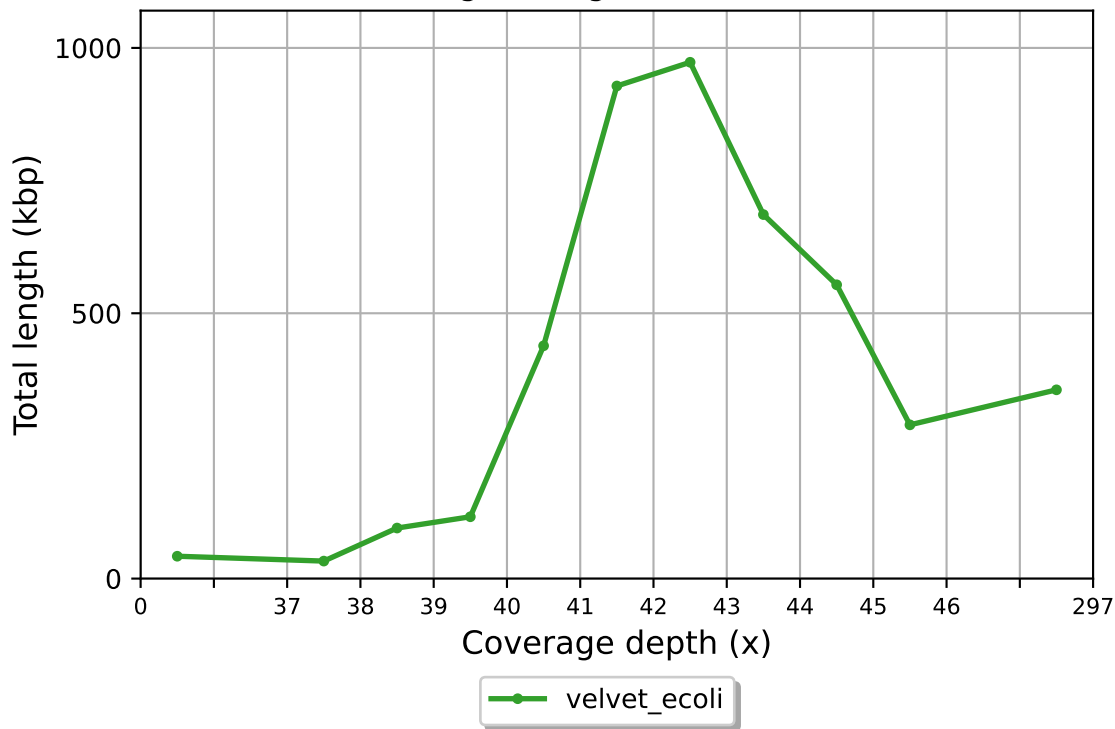
■ velvet_ecoli

wengan_ont_ecoli GC content

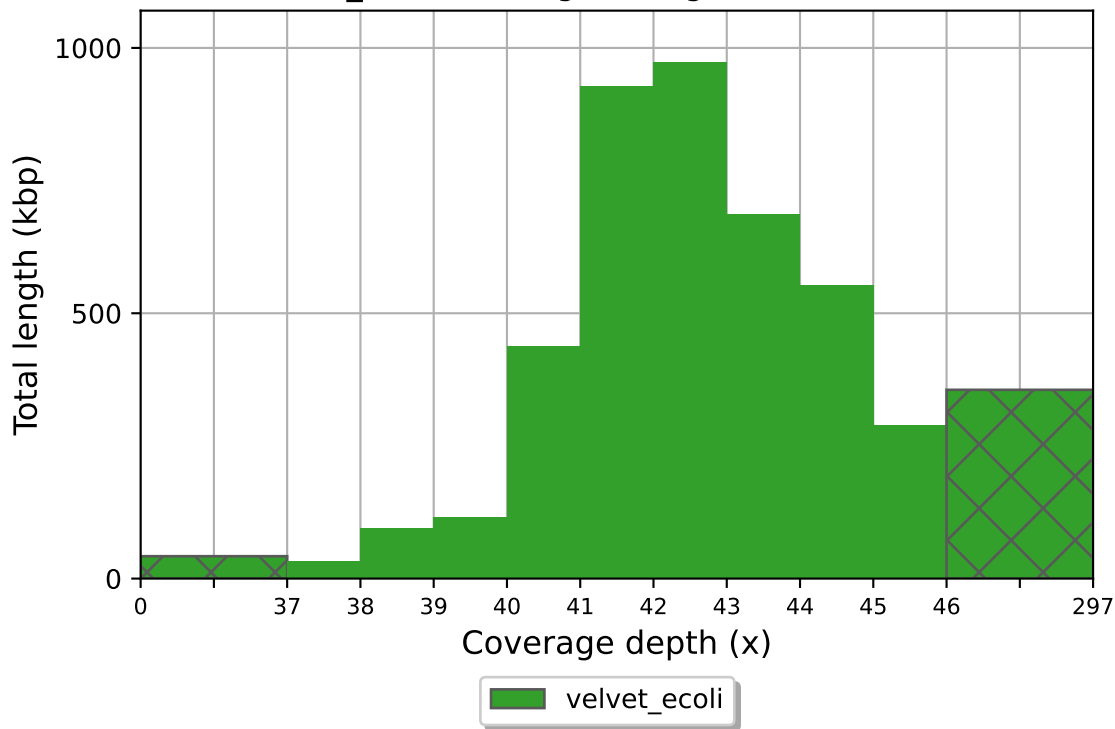


wengan_ont_ecoli

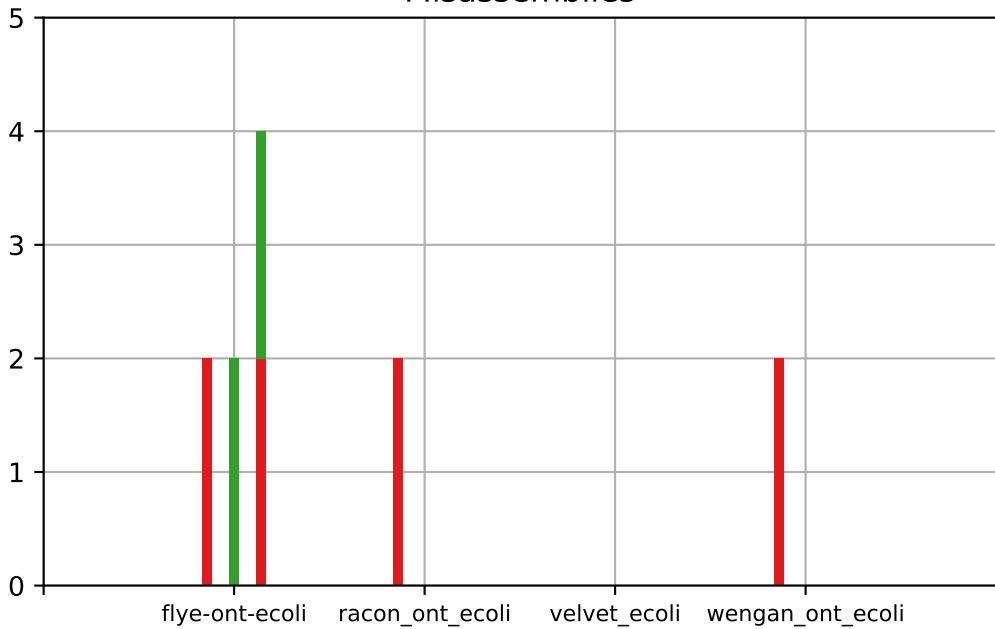
Coverage histogram (bin size: 1x)



velvet_ecoli coverage histogram (bin size: 1x)



Misassemblies

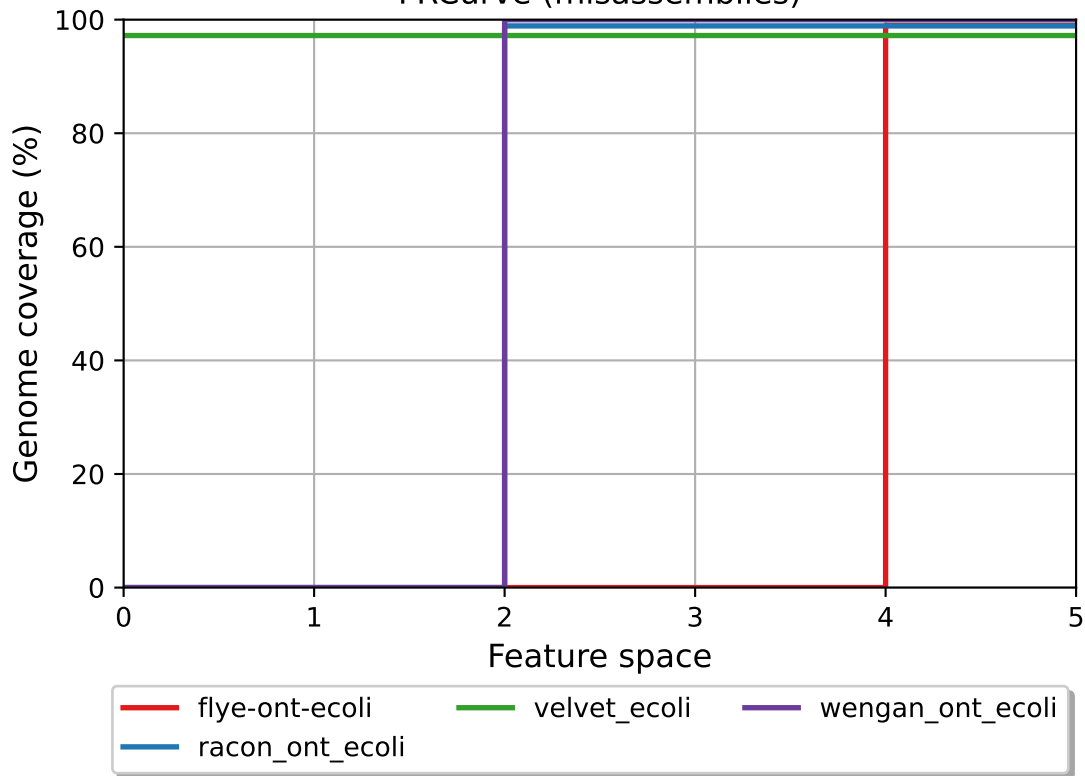


relocations

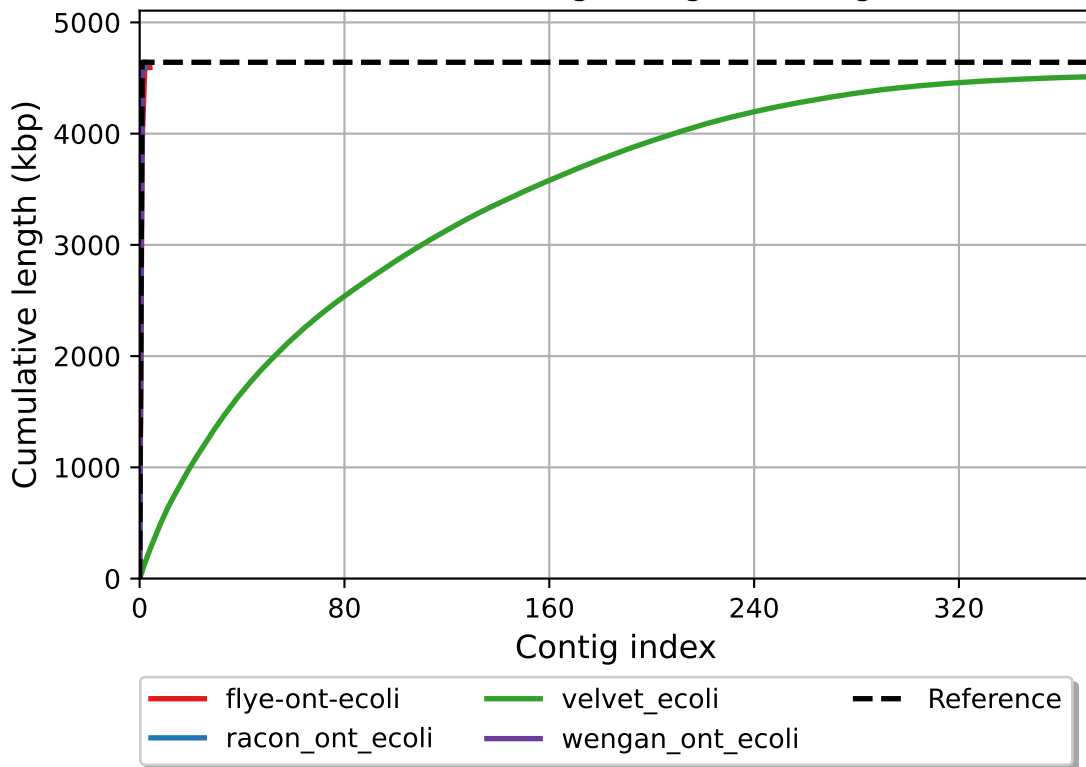


inversions

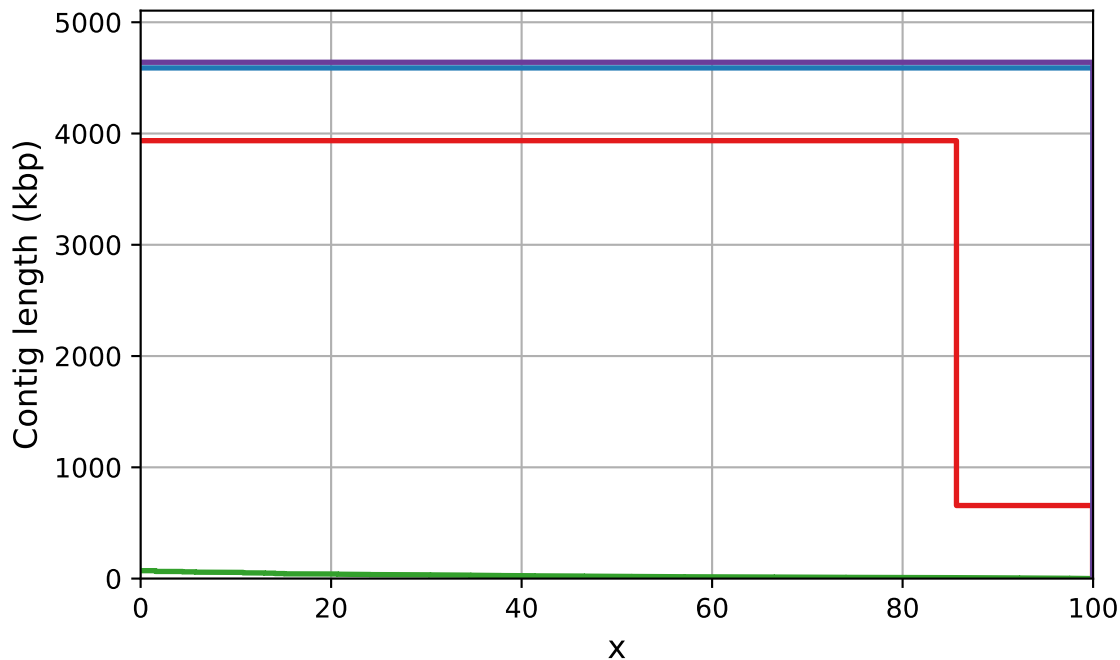
FRCurve (misassemblies)



Cumulative length (aligned contigs)

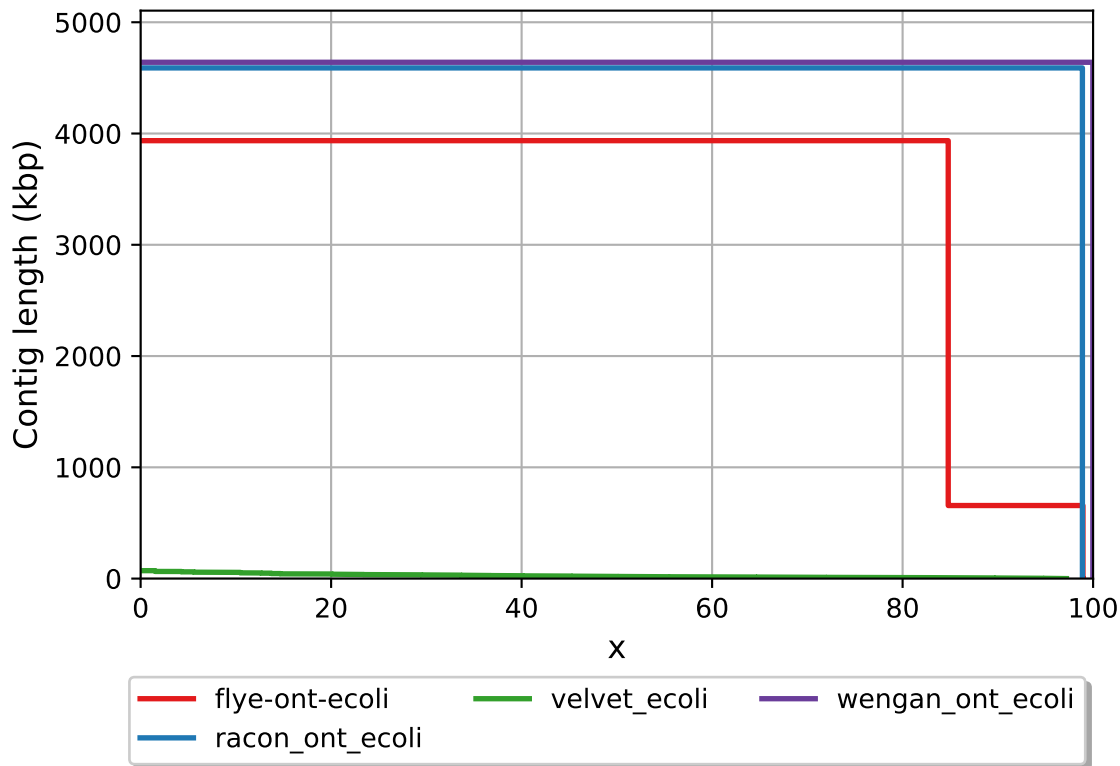


NAx

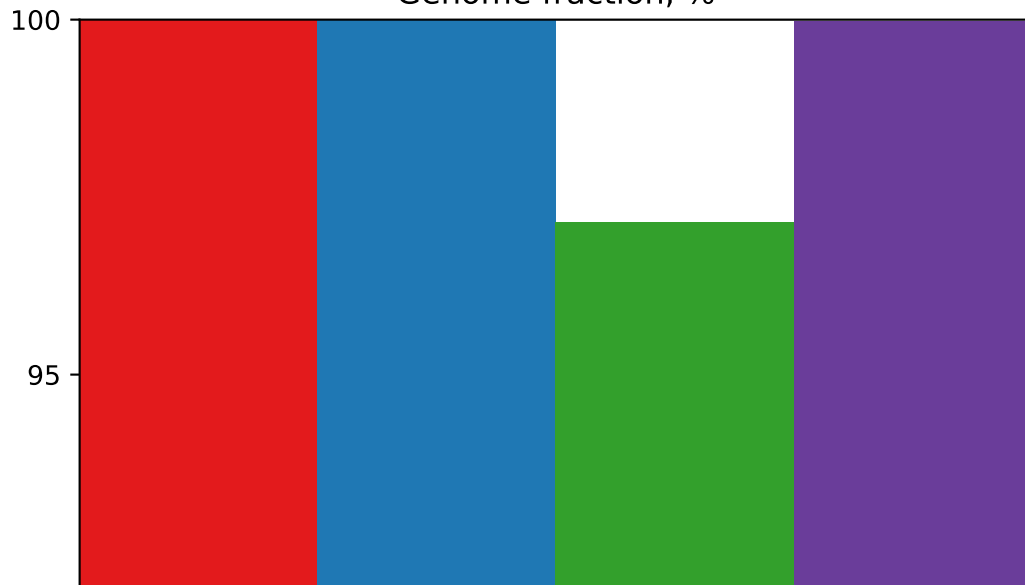


flye-ont-ecoli velvet_ecoli wengan_ont_ecoli
racon_ont_ecoli

NGAx



Genome fraction, %



flye-ont-ecoli
racon_ont_ecoli

velvet_ecoli

wengan_ont_ecoli