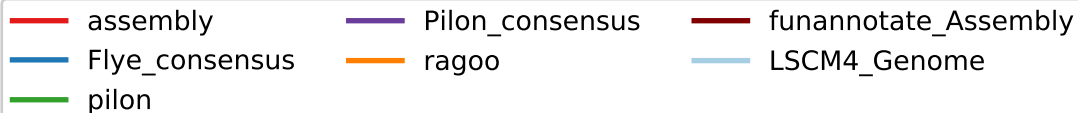# Report

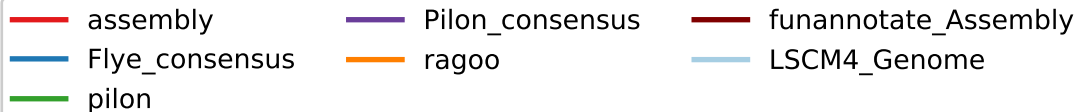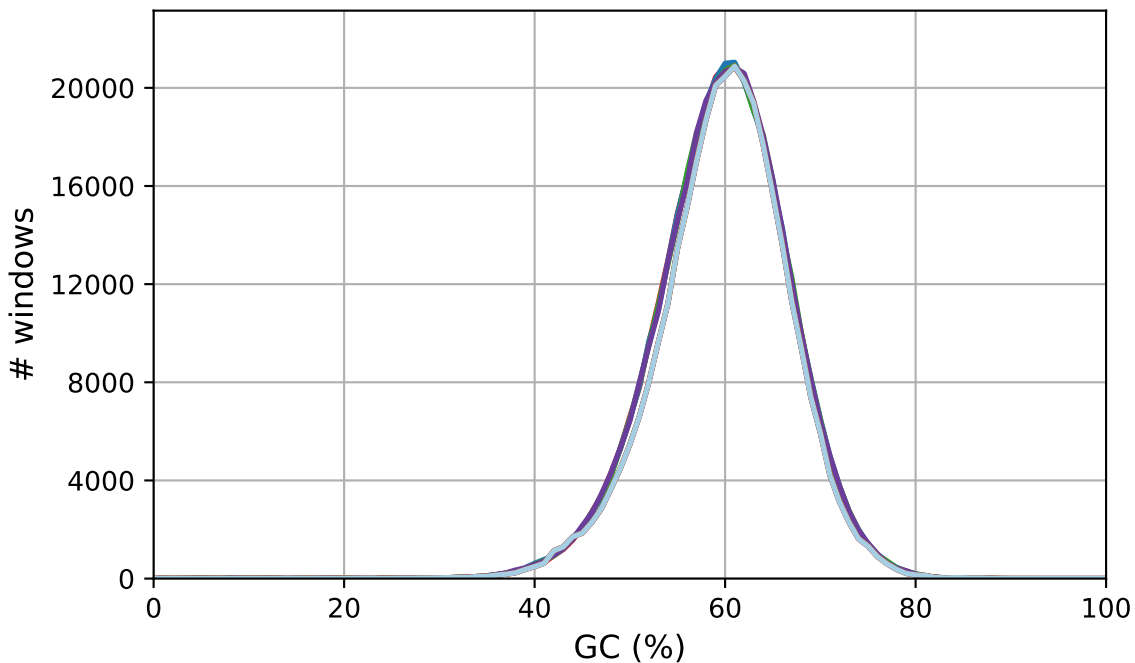|	assembly	Flye_consensus	pilon	Pilon_consensus	ragoo	funannotate_Assembly	LSCM4_Genome
# contigs (>= 0 bp)	170	170	170	170	55	43	43
# contigs (>= 1000 bp)	144	144	144	144	52	43	43
# contigs (>= 5000 bp)	90	90	90	90	44	40	40
# contigs (>= 10000 bp)	60	60	60	60	39	38	38
# contigs (>= 25000 bp)	52	52	52	52	36	36	36
# contigs (>= 50000 bp)	47	47	47	47	36	36	36
Total length (>= 0 bp)	34478885	34563691	34529424	34564601	32522116	32471852	32471852
Total length (>= 1000 bp)	34461536	34546308	34512059	34547226	32520056	32471852	32471852
Total length (>= 5000 bp)	34309228	34394036	34359761	34395024	32496008	32462717	32462717
Total length (>= 10000 bp)	34102624	34187188	34153346	34188586	32461854	32449926	32449926
Total length (>= 25000 bp)	33986021	34070618	34036994	34072170	32421283	32421283	32421283
Total length (>= 50000 bp)	33803297	33887739	33854040	33889288	32421283	32421283	32421283
# contigs	170	170	170	170	55	43	43
Largest contig	2721432	2727781	2725357	2727751	2700836	2700836	2700836
Total length	34478885	34563691	34529424	34564601	32522116	32471852	32471852
GC (%)	59.72	59.73	59.75	59.74	59.83	59.82	59.82
N50	1020162	1023034	1022025	1023058	1095675	1095675	1095675
N75	666564	668283	667593	668440	670411	670411	670411
L50	12	12	12	12	10	10	10
L75	24	24	24	24	21	21	21
# N's per 100 kbp	3.19	3.18	3.64	3.64	0.48	0.48	0.48

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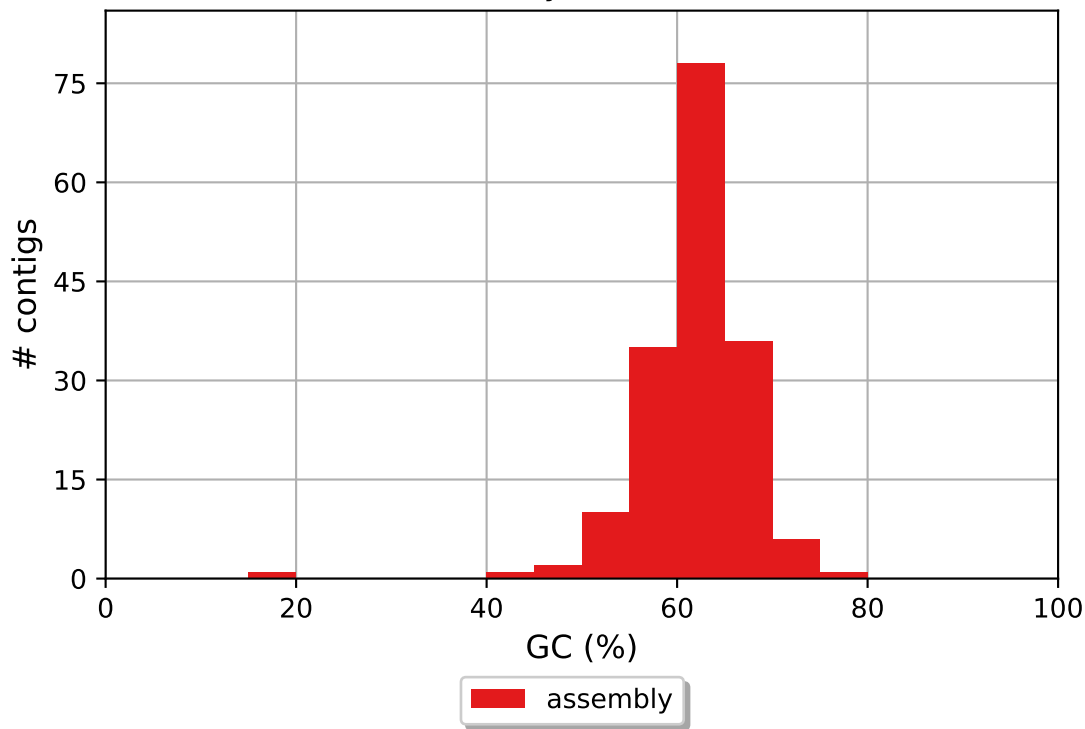(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

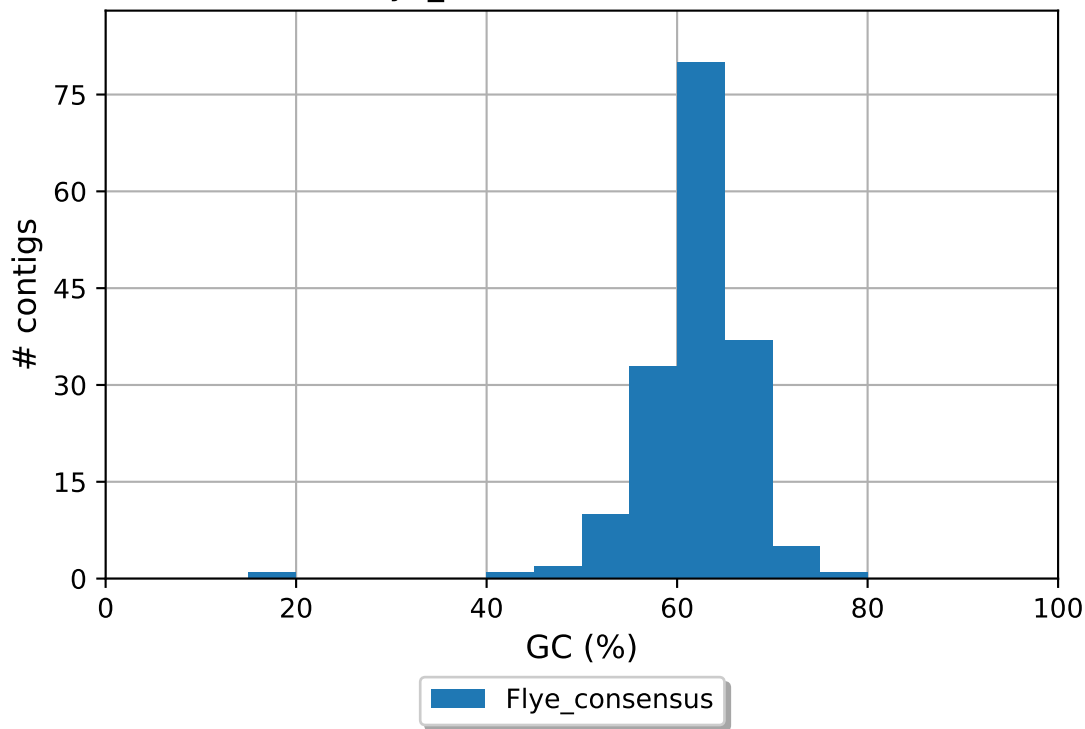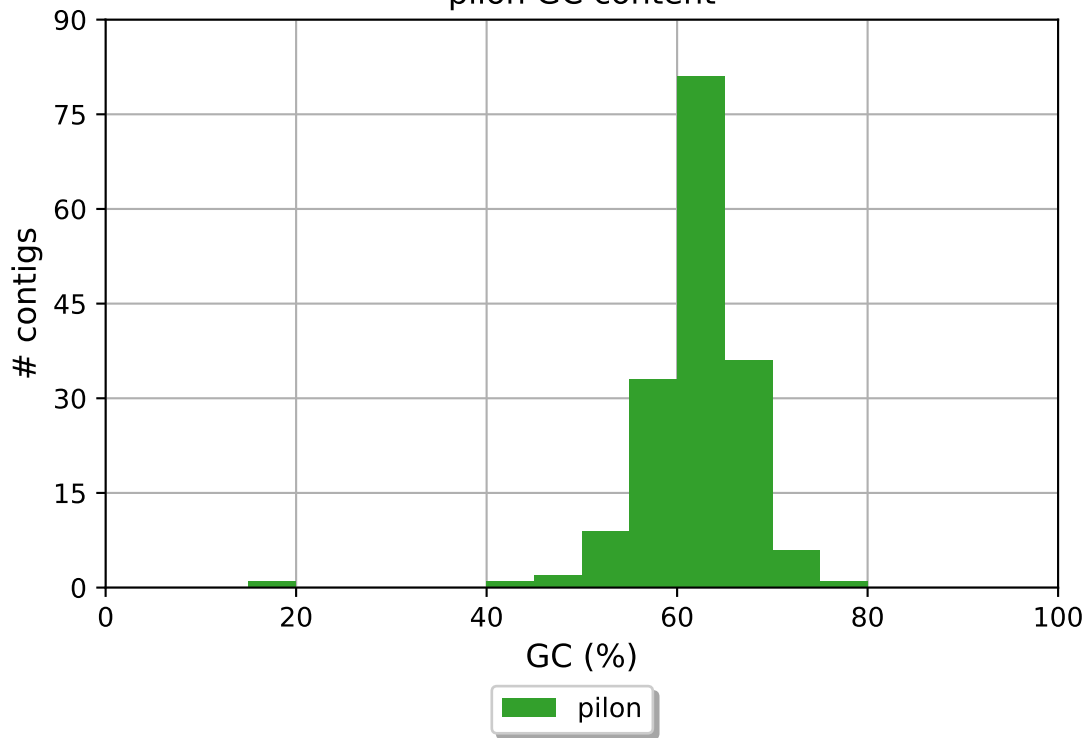|		
assembly	Pilon_consensus	funannotate_Assembly
Flye_consensus	ragoo	LSCM4_Genome
pilon		
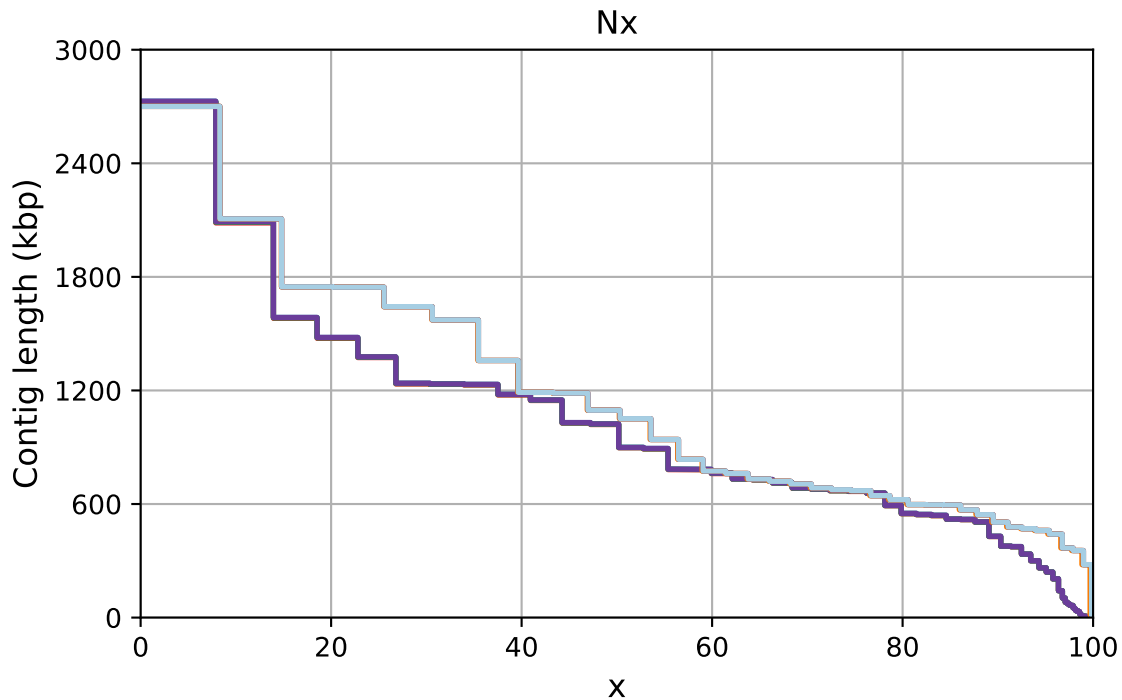
Cumulative length
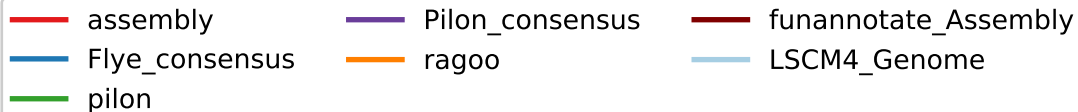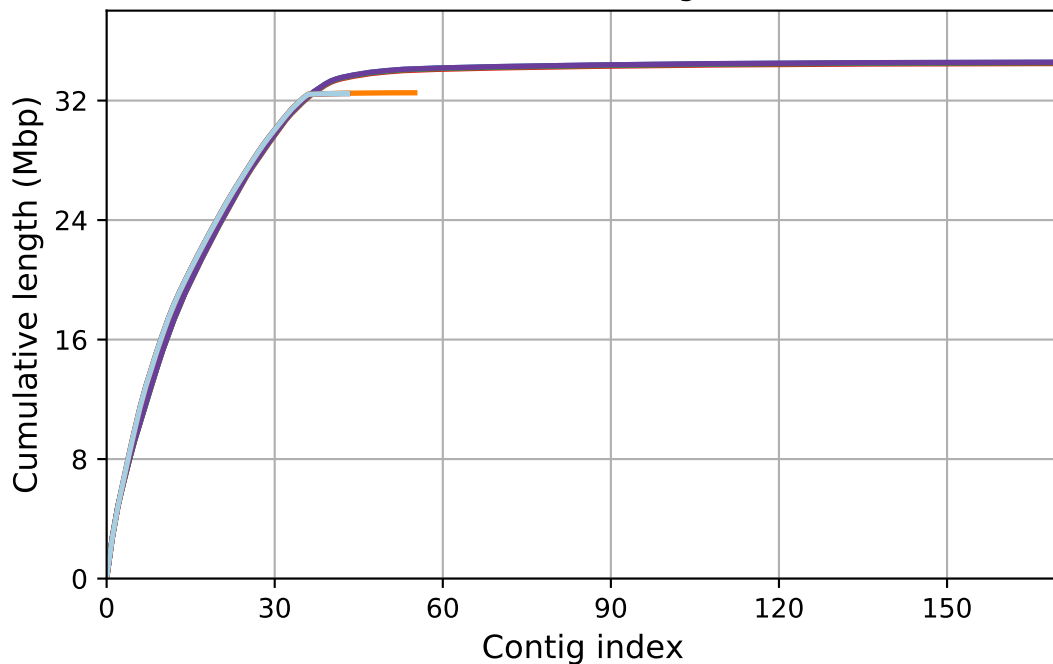
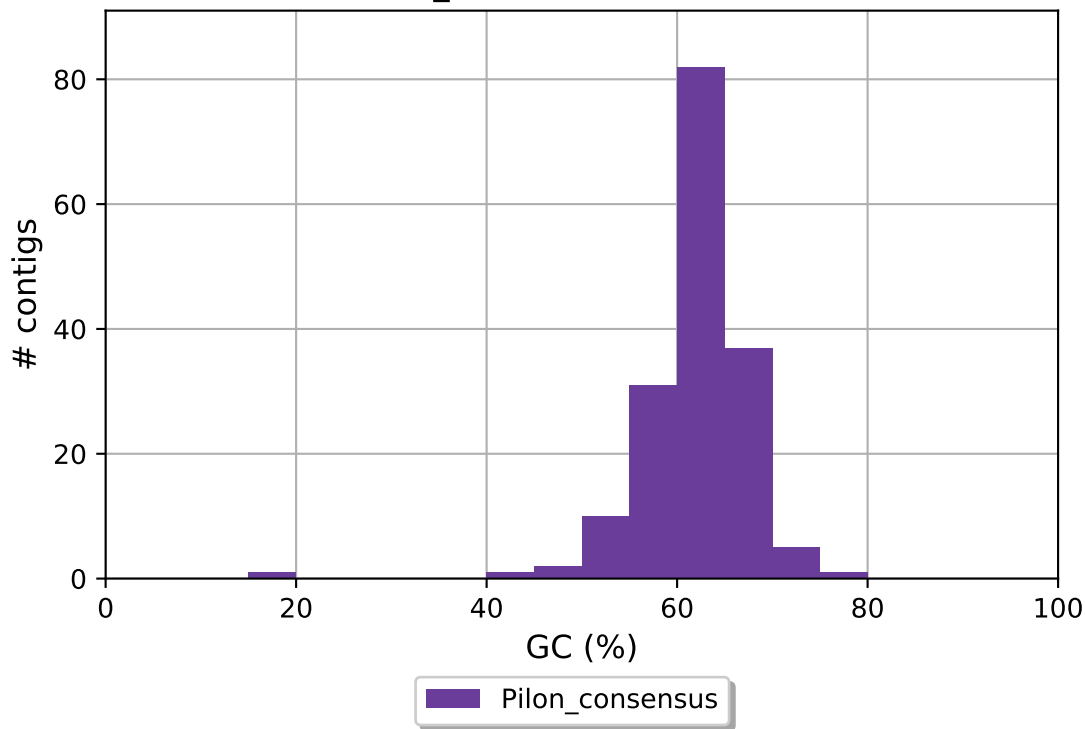## GC content

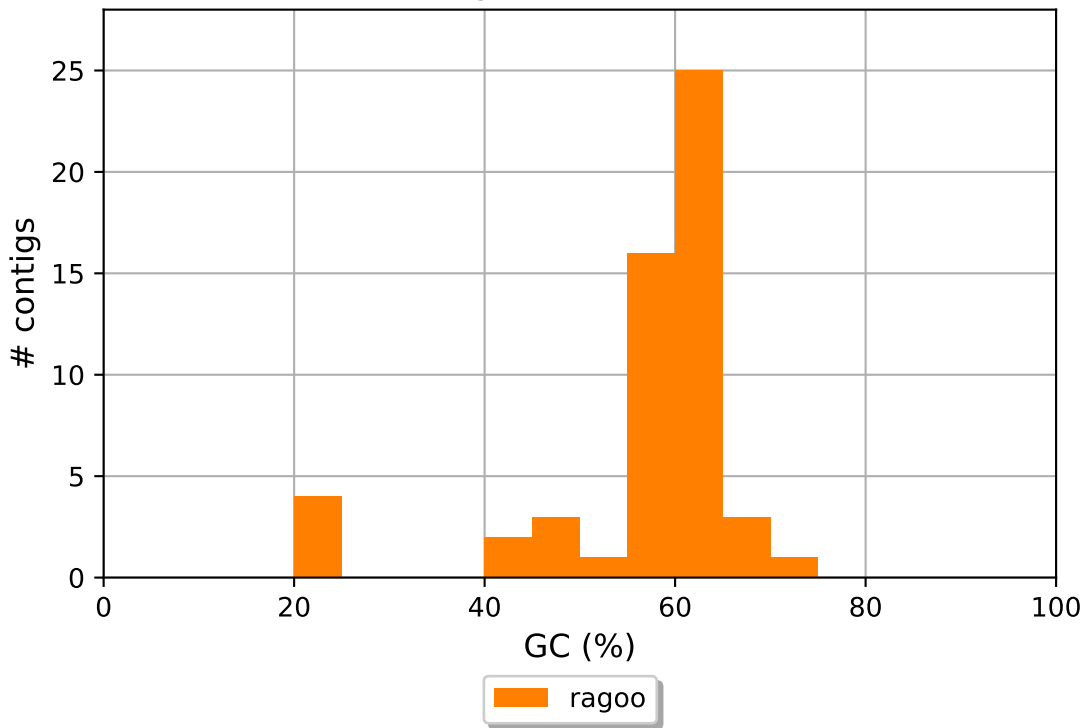assembly GC content
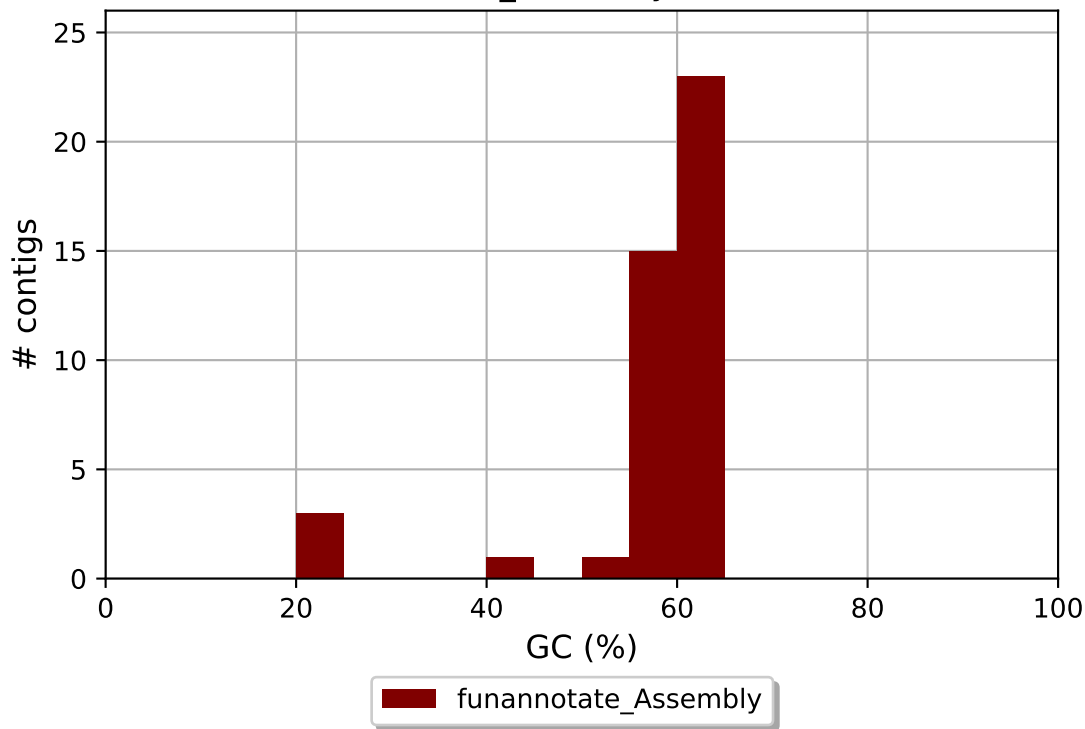
Flye_consensus GC content
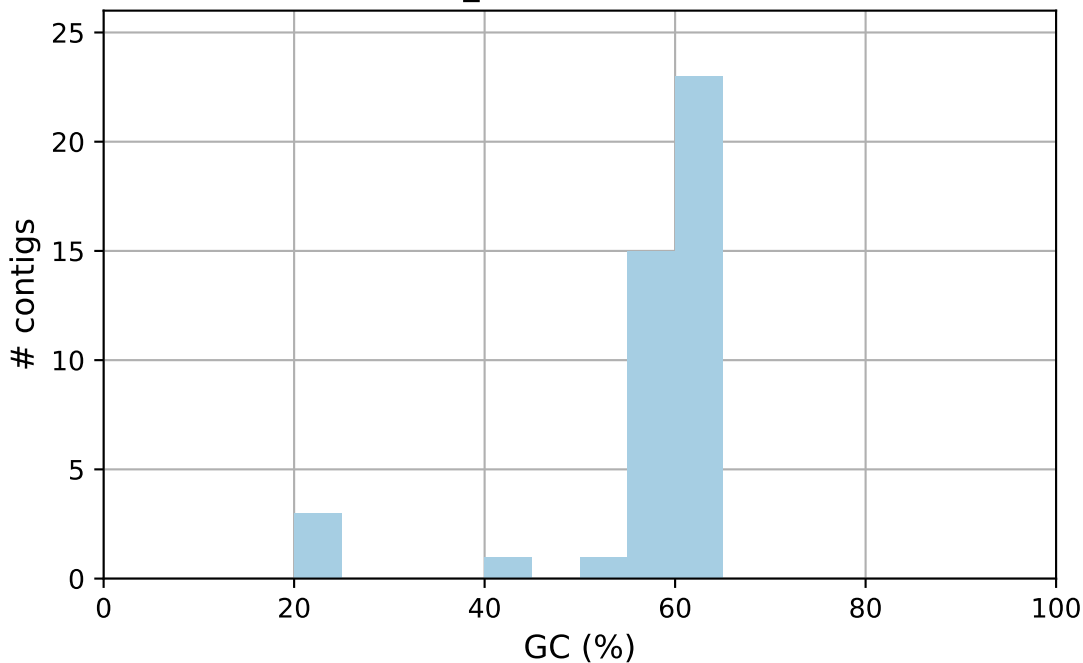
pilon GC content

Pilon_consensus GC content

ragoo GC content

funannotate_Assembly GC content

LSCM4_Genome GC content