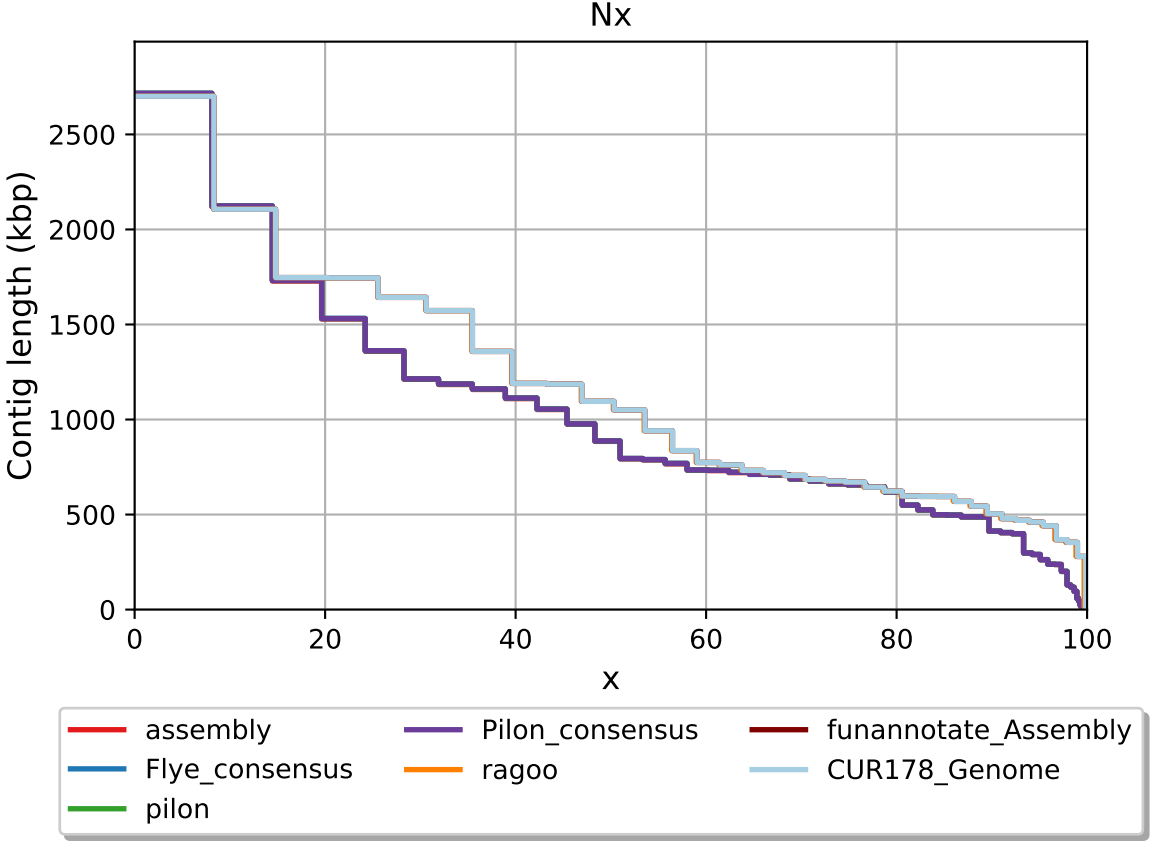
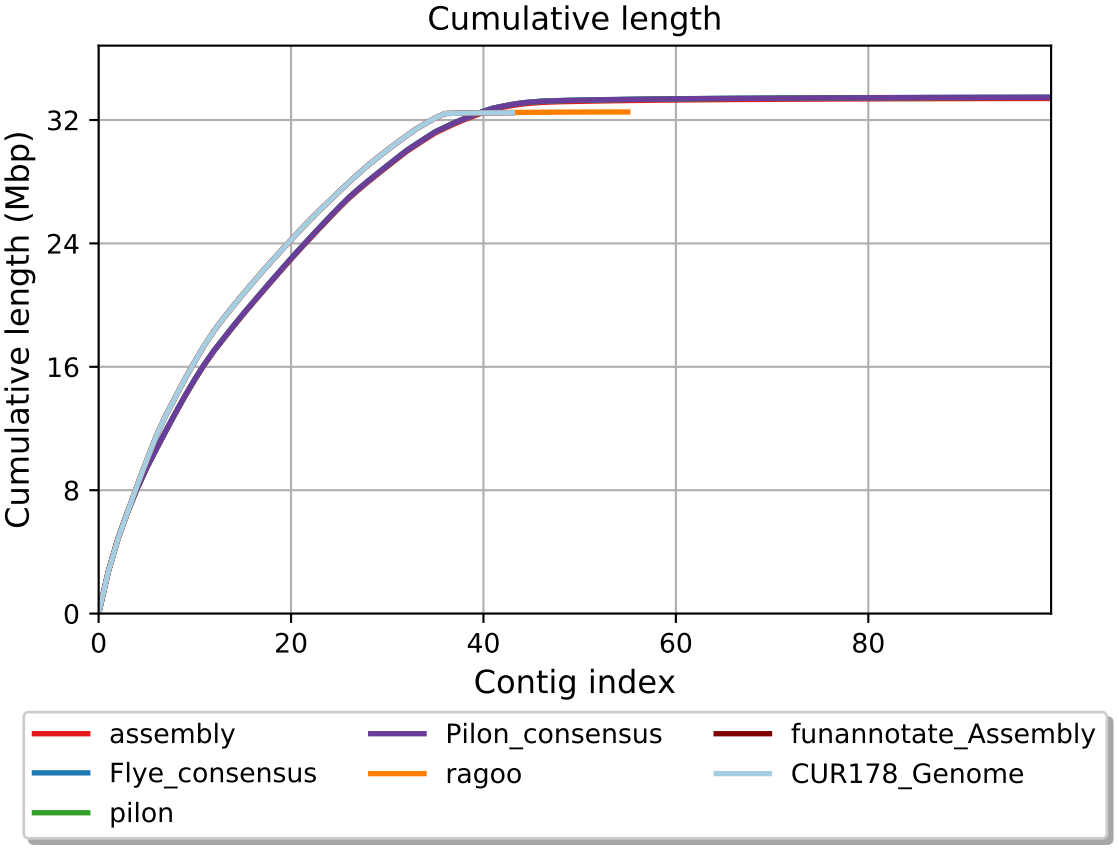
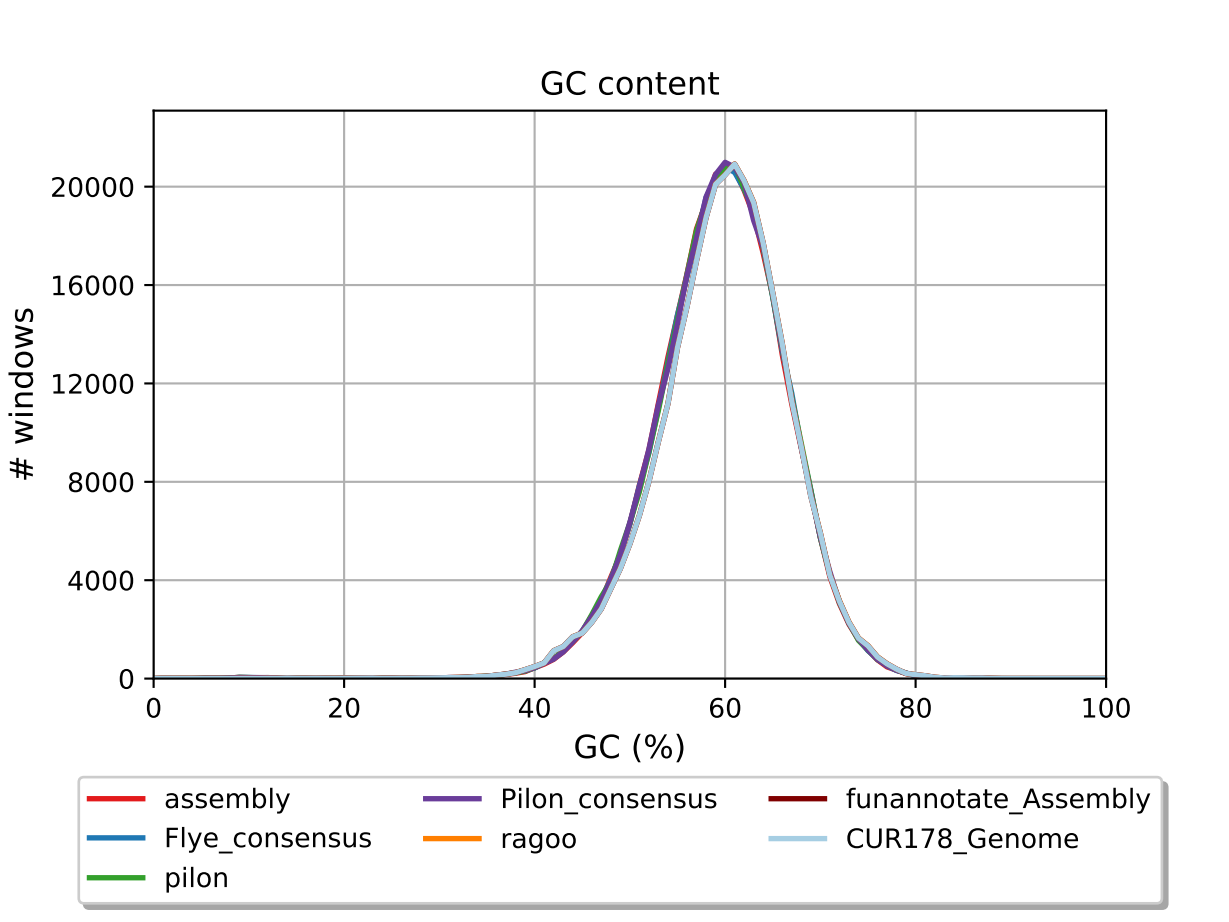
Report

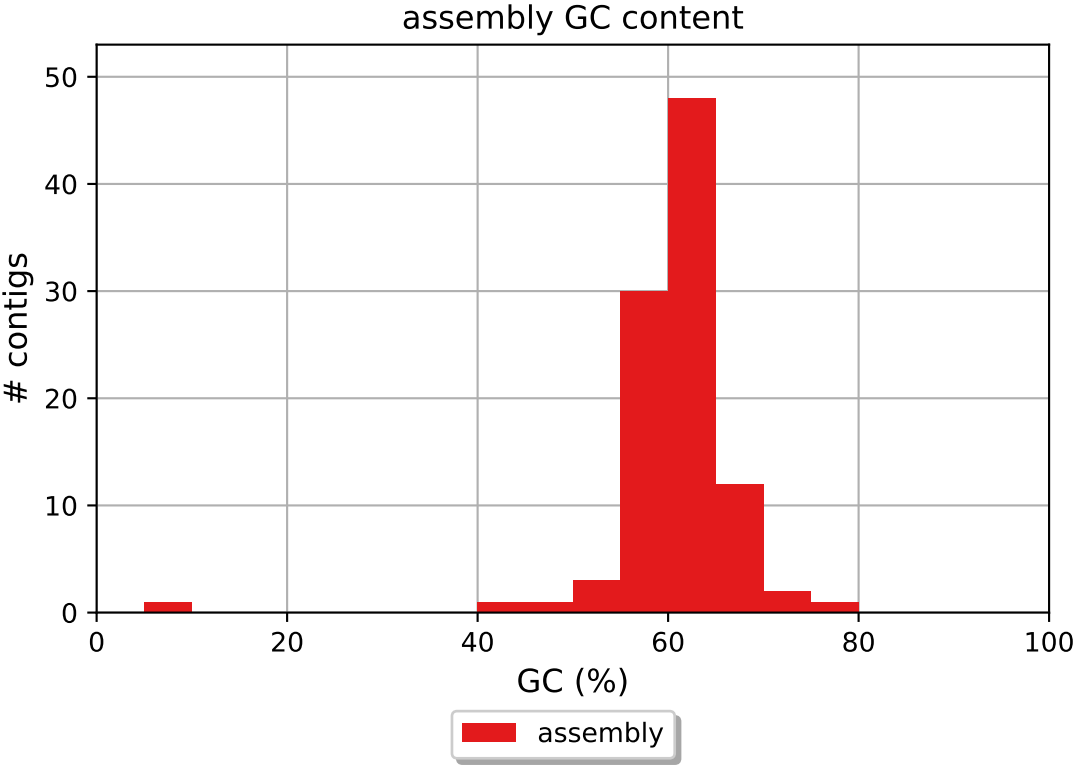
	assembly	Flye_consensus	pilon	Pilon_consensus	ragoo	funannotate_Assembly	CUR178_Genome
# contigs (>= 0 bp)	99	99	99	99	55	43	43
# contigs (>= 1000 bp)	92	92	92	92	52	43	43
# contigs (>= 5000 bp)	63	63	63	63	44	40	40
# contigs (>= 10000 bp)	53	53	53	53	39	38	38
# contigs (>= 25000 bp)	47	47	47	47	36	36	36
# contigs (>= 50000 bp)	45	45	45	45	36	36	36
Total length (>= 0 bp)	33395910	33475539	33467098	33469083	32522116	32471852	32471852
Total length (>= 1000 bp)	33391012	33470631	33462192	33464173	32520056	32471852	32471852
Total length (>= 5000 bp)	33315689	33395291	33386780	33388801	32496008	32462717	32462717
Total length (>= 10000 bp)	33244585	33324131	33315599	33317607	32461854	32449926	32449926
Total length (>= 25000 bp)	33165662	33245247	33236849	33238962	32421283	32421283	32421283
Total length (>= 50000 bp)	33094689	33174149	33165736	33167870	32421283	32421283	32421283
# contigs	99	99	99	99	55	43	43
Largest contig	2710265	2716464	2715805	2716217	2700836	2700836	2700836
Total length	33395910	33475539	33467098	33469083	32522116	32471852	32471852
GC (%)	59.56	59.59	59.59	59.60	59.83	59.82	59.82
N50	885010	887310	887008	887250	1095675	1095675	1095675
N75	655307	656926	656799	656947	670411	670411	670411
L50	12	12	12	12	10	10	10
L75	24	24	24	24	21	21	21
# N's per 100 kbp	3.89	3.88	2.50	2.50	0.48	0.48	0.48

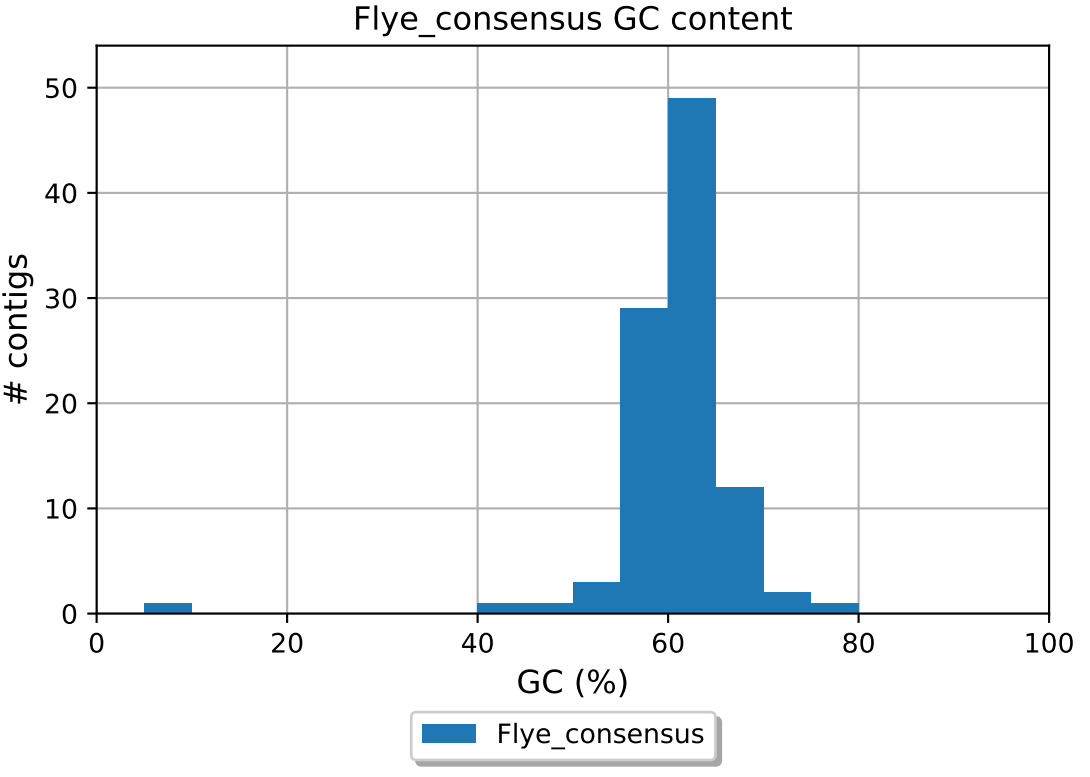
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

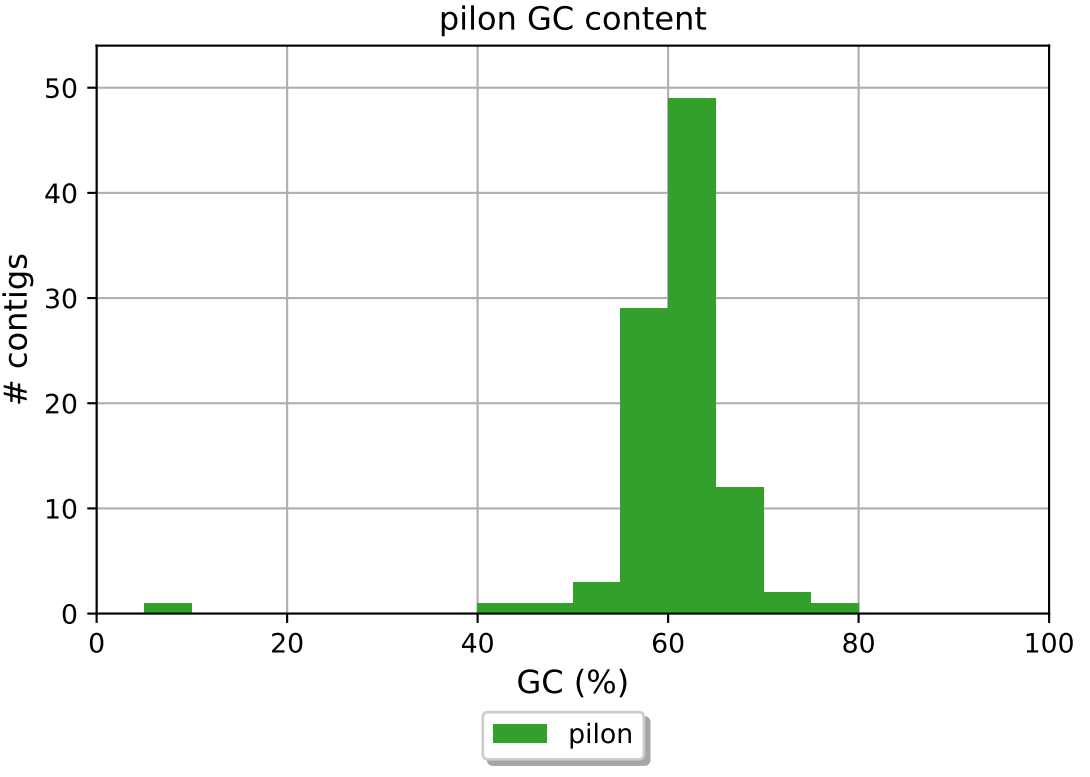

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
assembly
Flye_consensus
pilon
Pilon_consensus
ragoo
funannotate_Assembly
CUR178_Genome

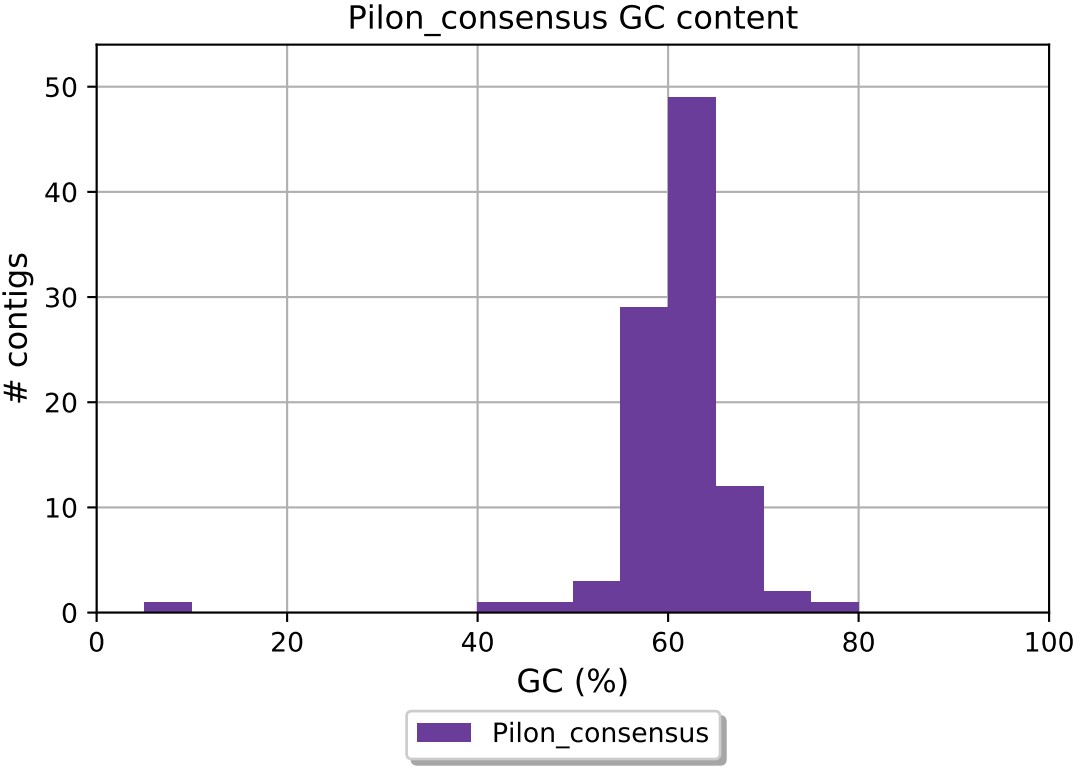

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
20
40
60
80
Contig index
assembly
Flye_consensus
pilon
Pilon_consensus
ragoo
funannotate_Assembly
CUR178_Genome

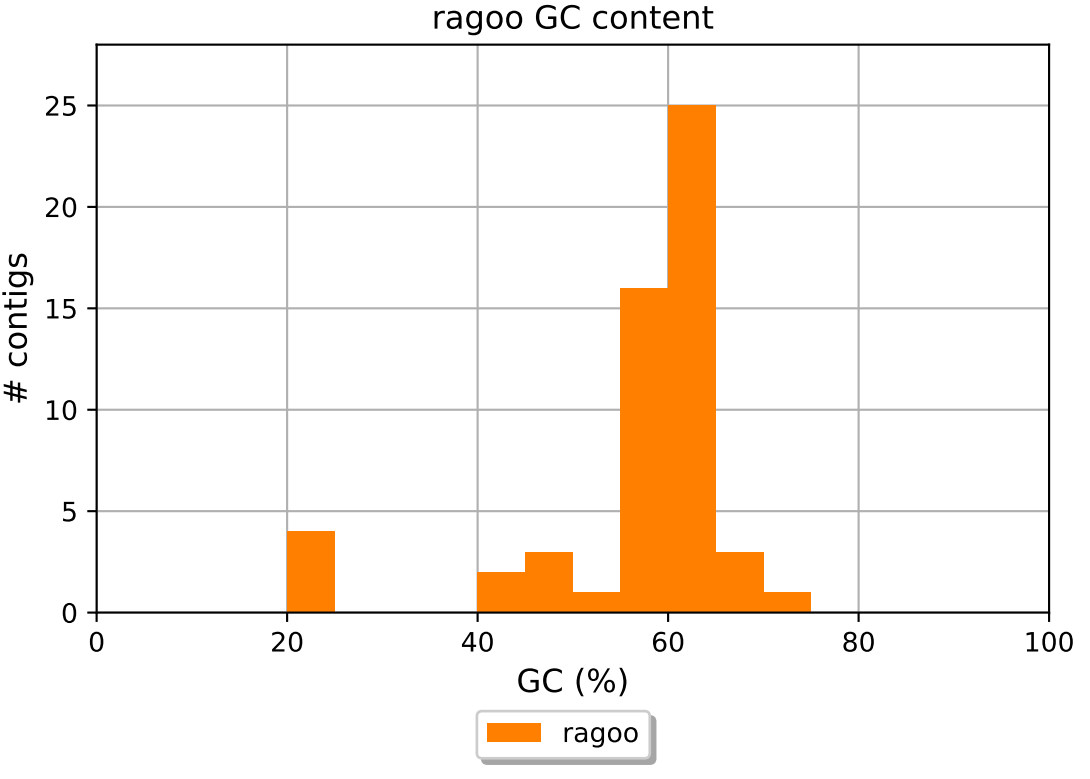

GC content
windows
GC (%)
0
4000
8000
12000
16000
20000
0
20
40
60
80
100
assembly
Flye_consensus
pilon
Pilon_consensus
ragoo
funannotate_Assembly
CUR178_Genome

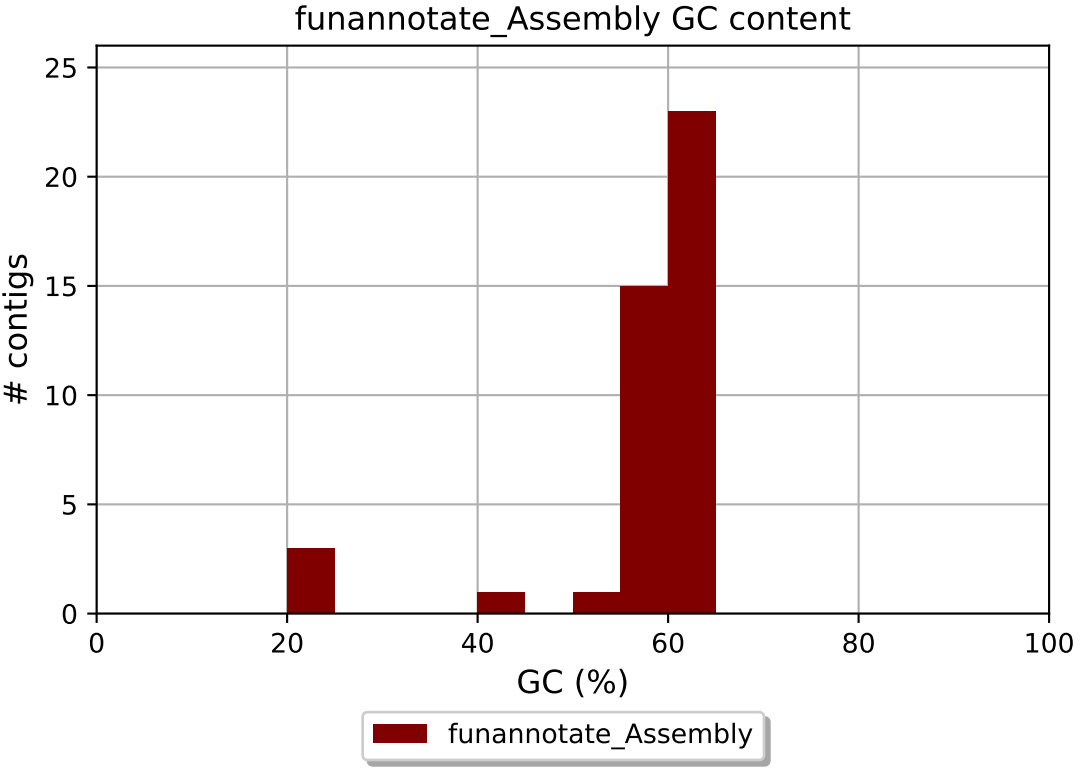

assembly GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
assembly

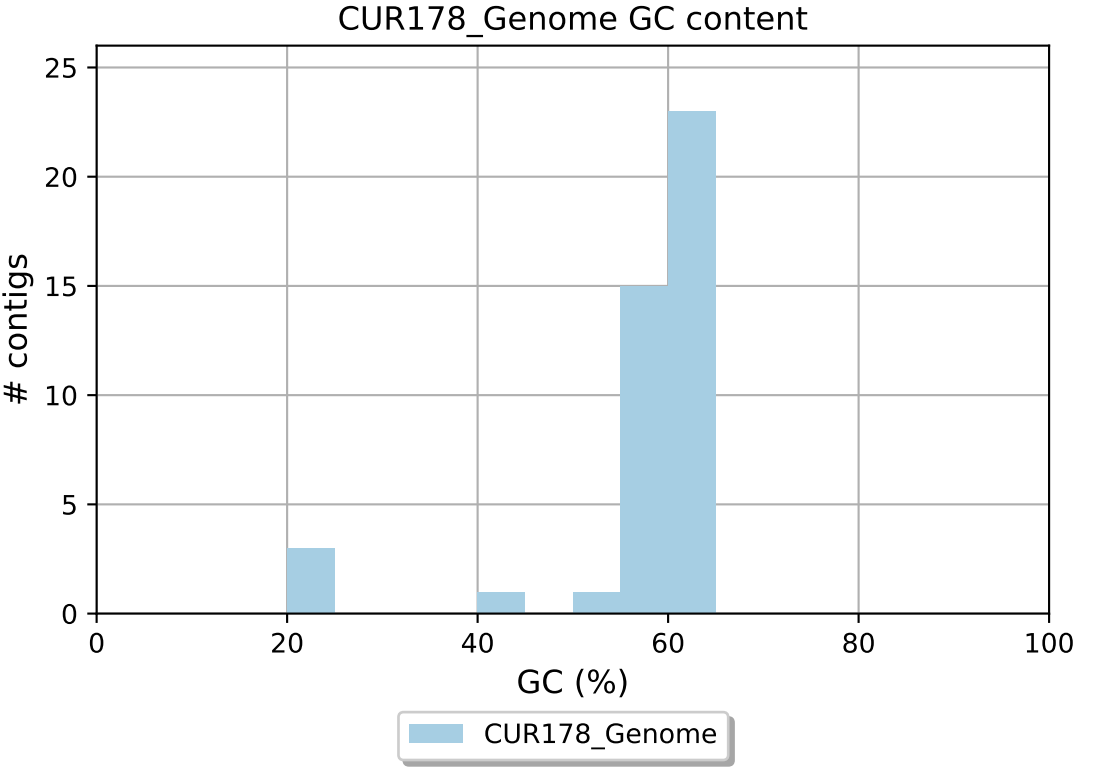

Flye_consensus GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
Flye_consensus


pilon GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
pilon


Pilon_consensus GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
Pilon_consensus


ragoo GC content
contigs
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
ragoo


funannotate_Assembly GC content
contigs
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
funannotate_Assembly


CUR178_Genome GC content
contigs
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
CUR178_Genome