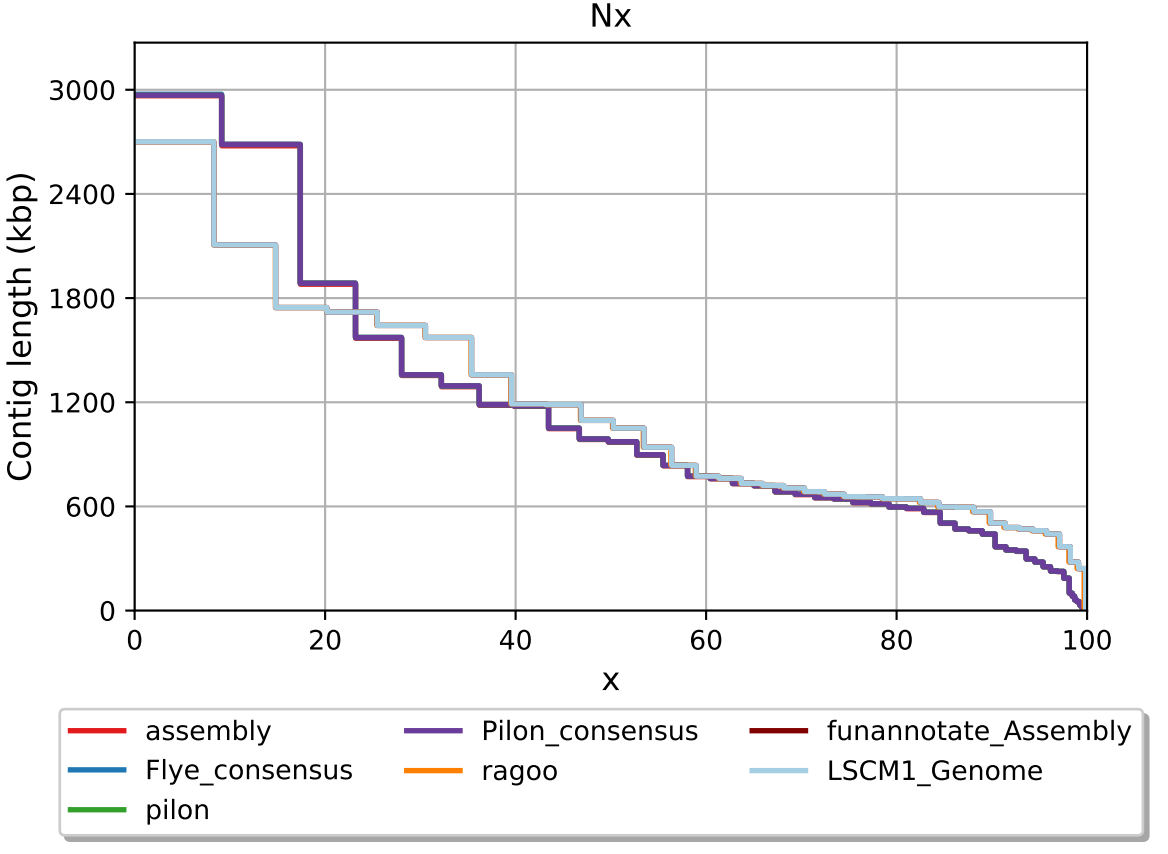
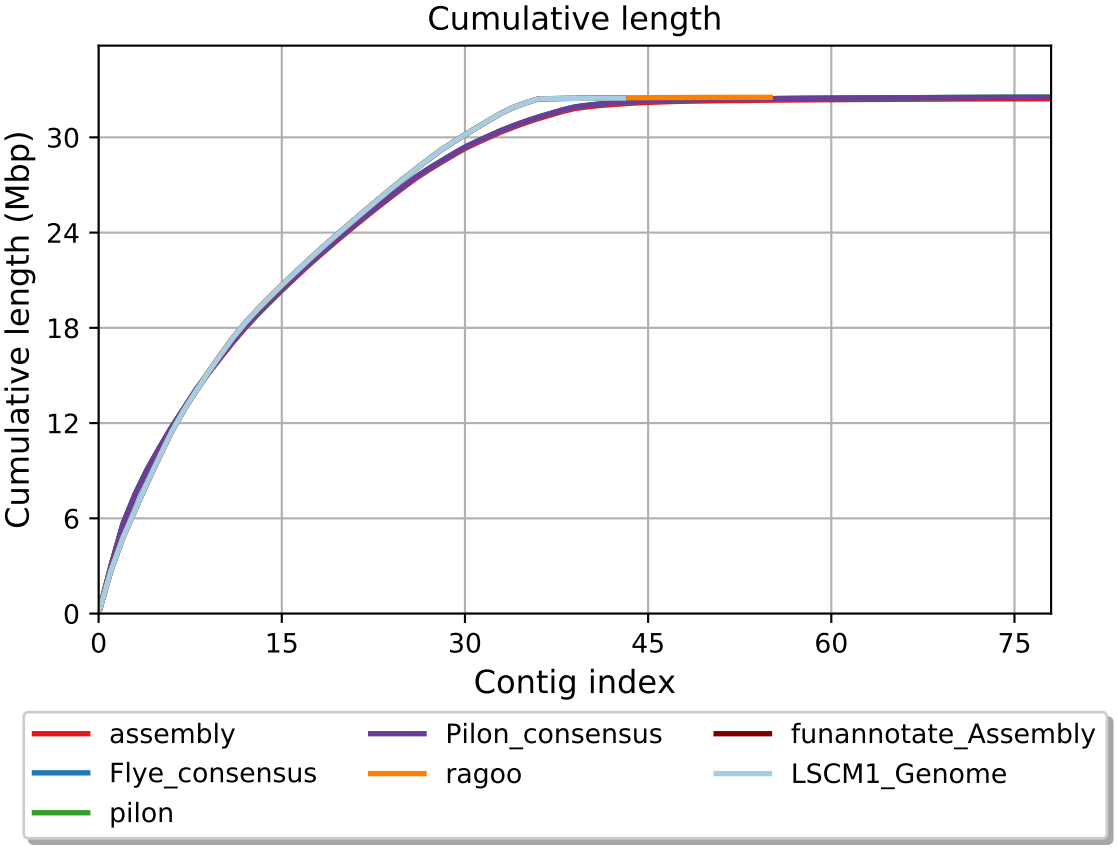
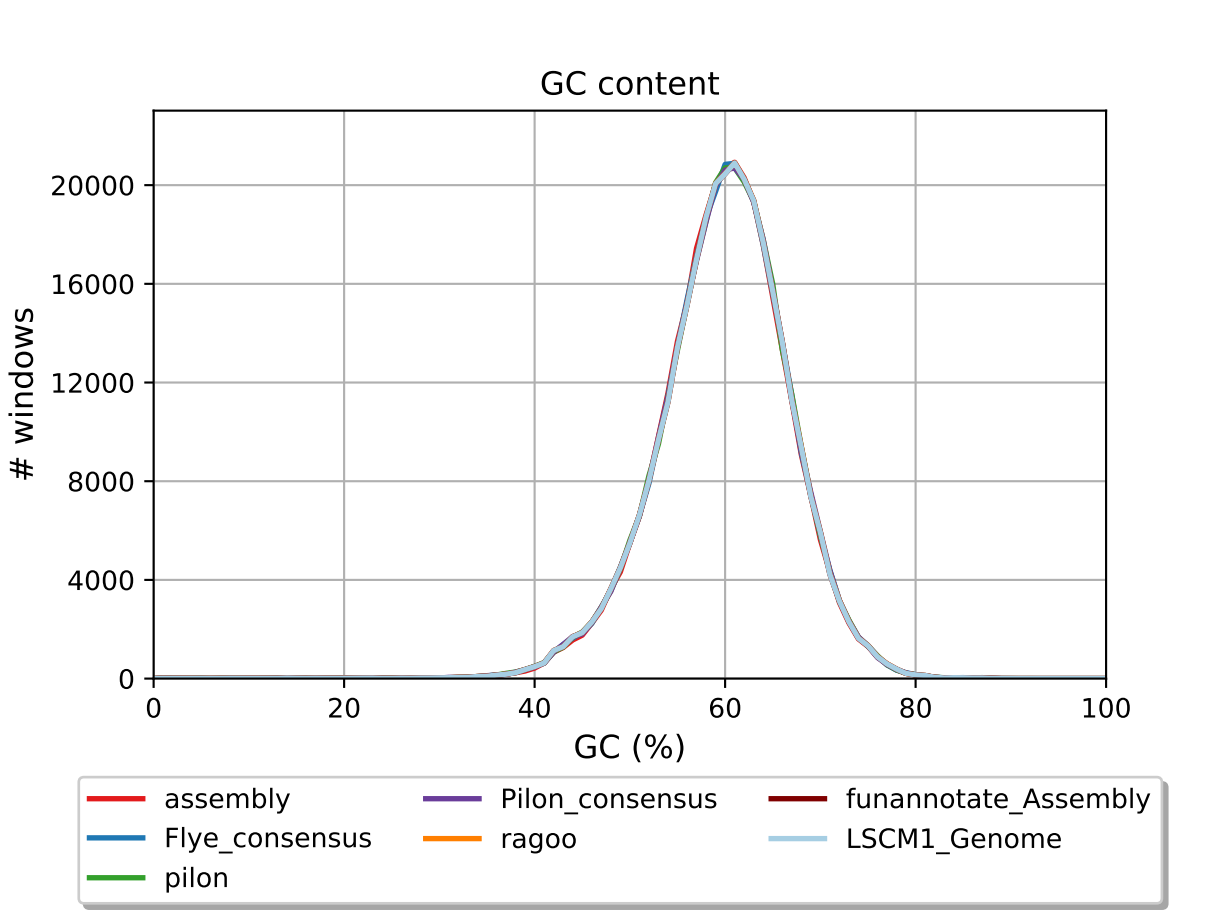
Report

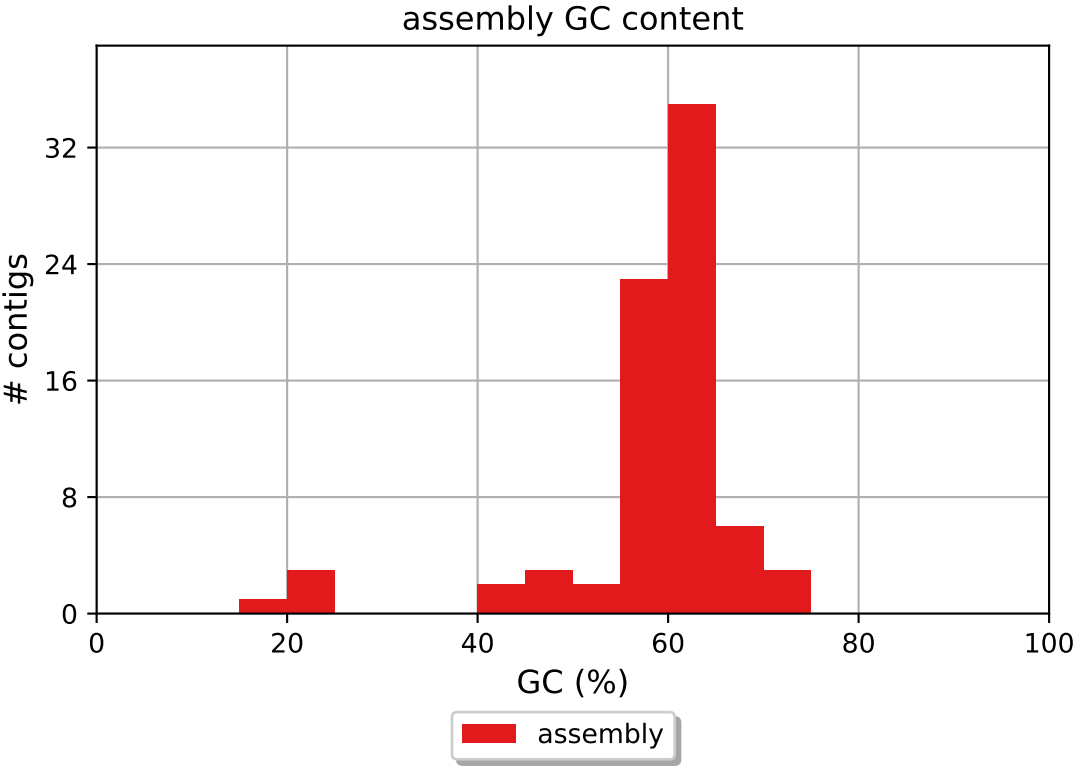
	assembly	Flye_consensus	pilon	Pilon_consensus	ragoo	funannotate_Assembly	LSCM1_Genome
# contigs (>= 0 bp)	78	78	78	78	55	43	43
# contigs (>= 1000 bp)	75	75	75	75	52	43	43
# contigs (>= 5000 bp)	61	61	61	61	44	40	40
# contigs (>= 10000 bp)	52	52	52	52	39	38	38
# contigs (>= 25000 bp)	47	47	47	47	36	36	36
# contigs (>= 50000 bp)	43	43	43	43	36	36	36
Total length (>= 0 bp)	32426734	32523284	32525493	32522116	32522116	32471852	32471852
Total length (>= 1000 bp)	32424674	32521224	32523433	32520056	32520056	32471852	32471852
Total length (>= 5000 bp)	32377939	32474521	32476621	32473327	32496008	32462717	32462717
Total length (>= 10000 bp)	32318650	32415179	32417287	32413989	32461854	32449926	32449926
Total length (>= 25000 bp)	32257264	32353761	32355931	32352630	32421283	32421283	32421283
Total length (>= 50000 bp)	32117658	32213947	32216068	32212752	32421283	32421283	32421283
# contigs	78	78	78	78	55	43	43
Largest contig	2965689	2974001	2968943	2968532	2700836	2700836	2700836
Total length	32426734	32523284	32525493	32522116	32522116	32471852	32471852
GC (%)	59.81	59.82	59.82	59.83	59.83	59.82	59.82
N50	969483	972711	973083	972880	1095675	1095675	1095675
N75	642109	644114	644270	644248	656112	656112	656112
L50	11	11	11	11	10	10	10
L75	21	21	21	21	21	21	21
# N's per 100 kbp	1.85	1.84	0.48	0.48	0.48	0.48	0.48

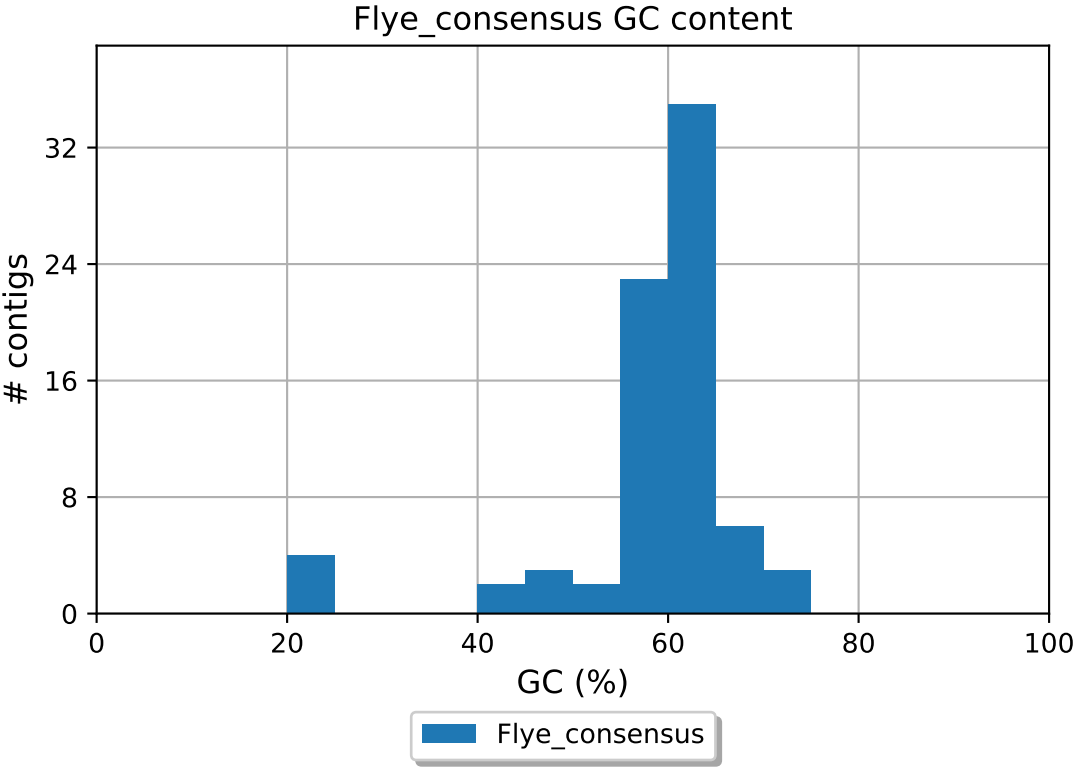
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

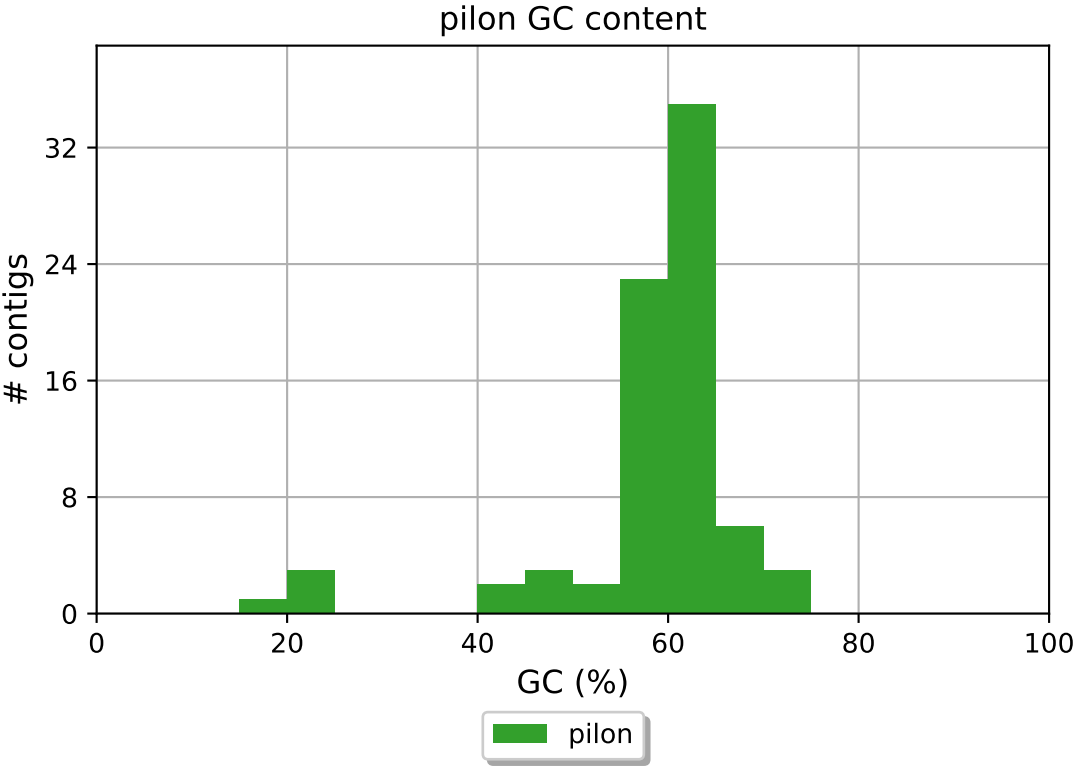

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
assembly
Flye_consensus
pilon
Pilon_consensus
ragoo
funannotate_Assembly
LSCM1_Genome

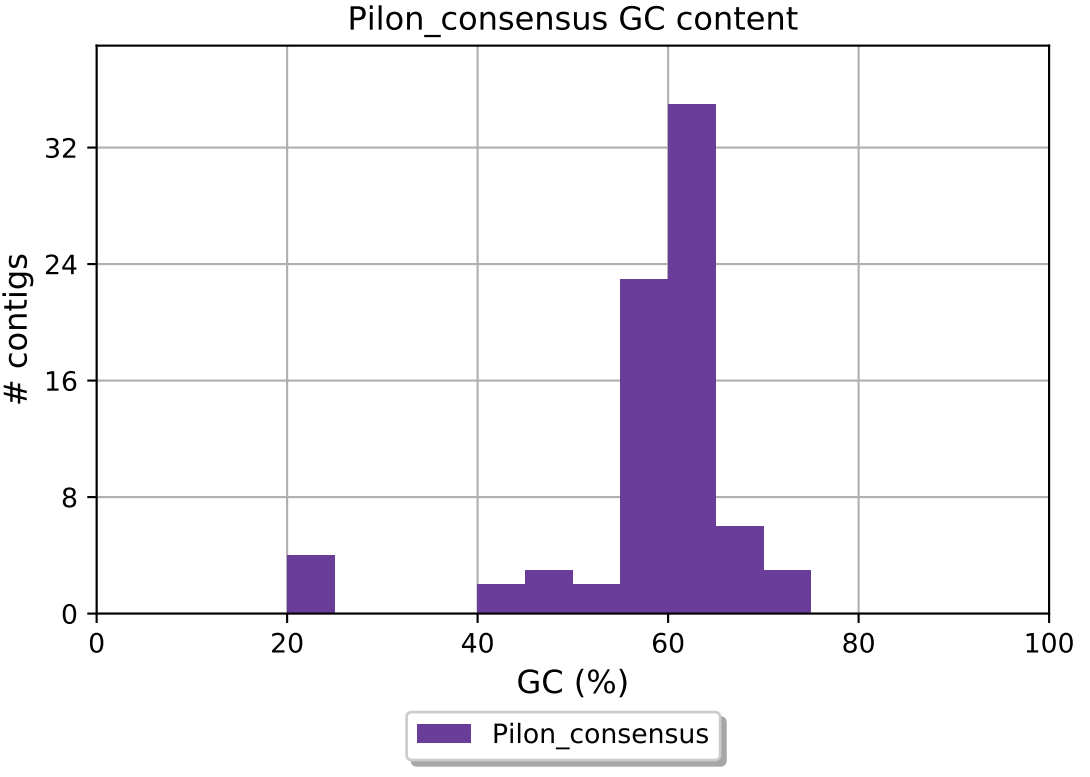

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
15
30
45
60
75
Contig index
assembly
Flye_consensus
pilon
Pilon_consensus
ragoo
funannotate_Assembly
LSCM1_Genome

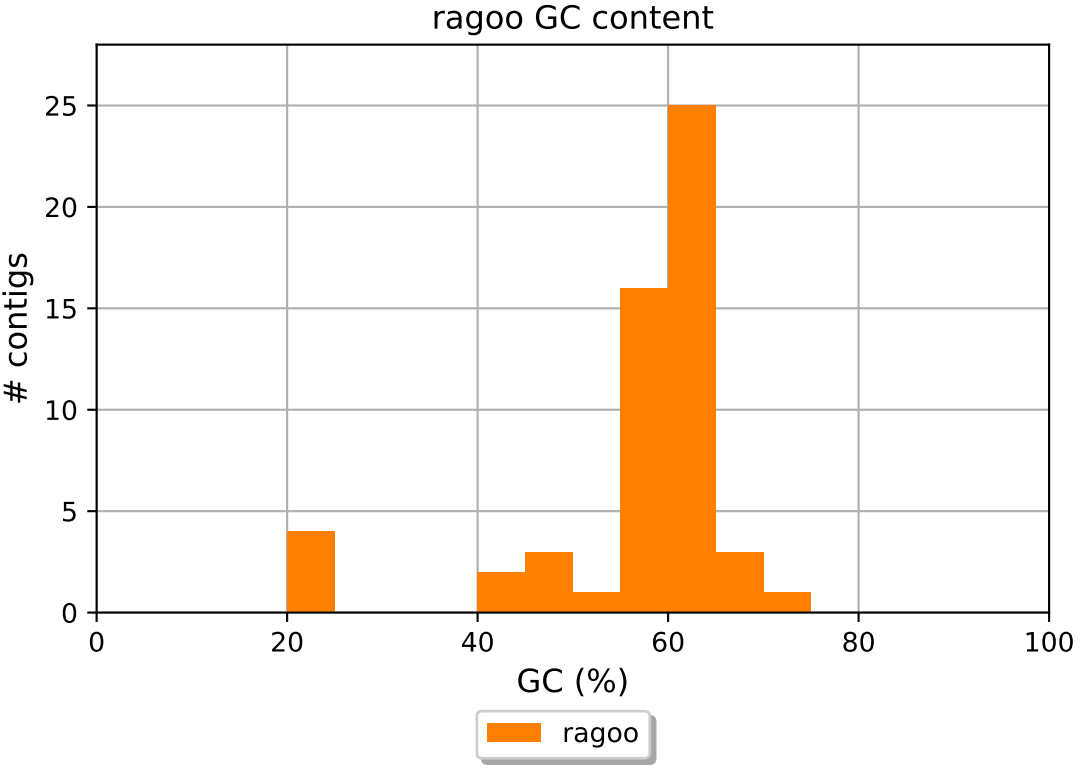

GC content
windows
GC (%)
0
4000
8000
12000
16000
20000
0
20
40
60
80
100
assembly
Flye_consensus
pilon
Pilon_consensus
ragoo
funannotate_Assembly
LSCM1_Genome

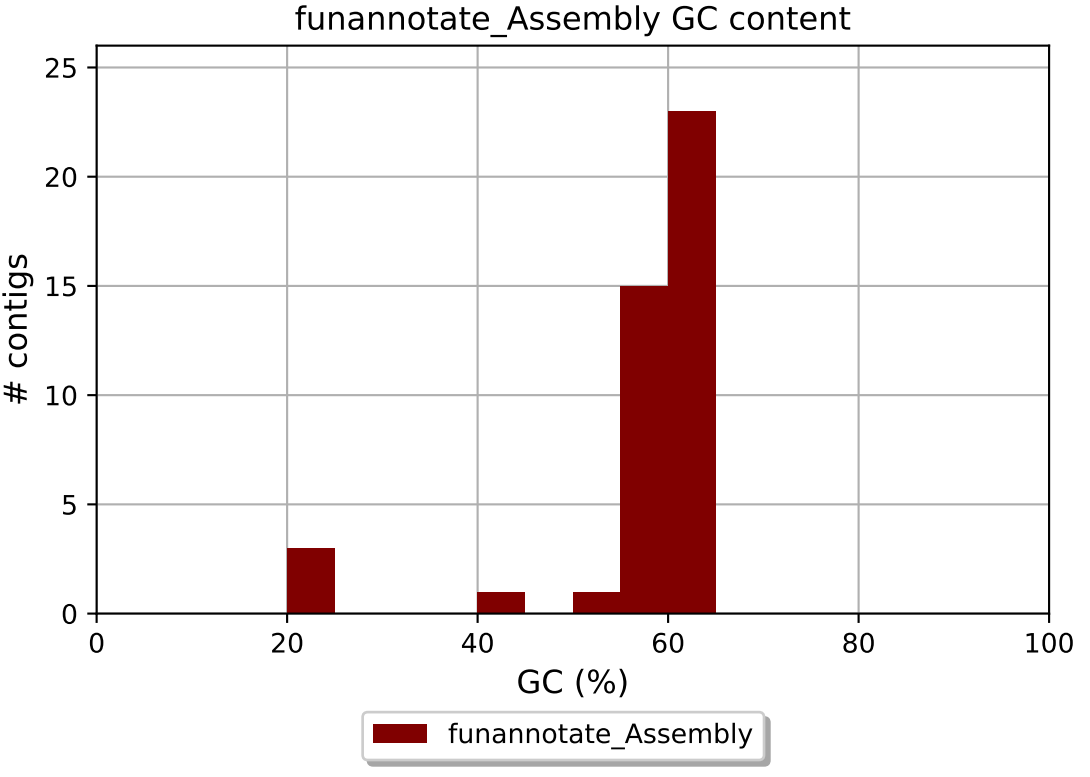

assembly GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
assembly

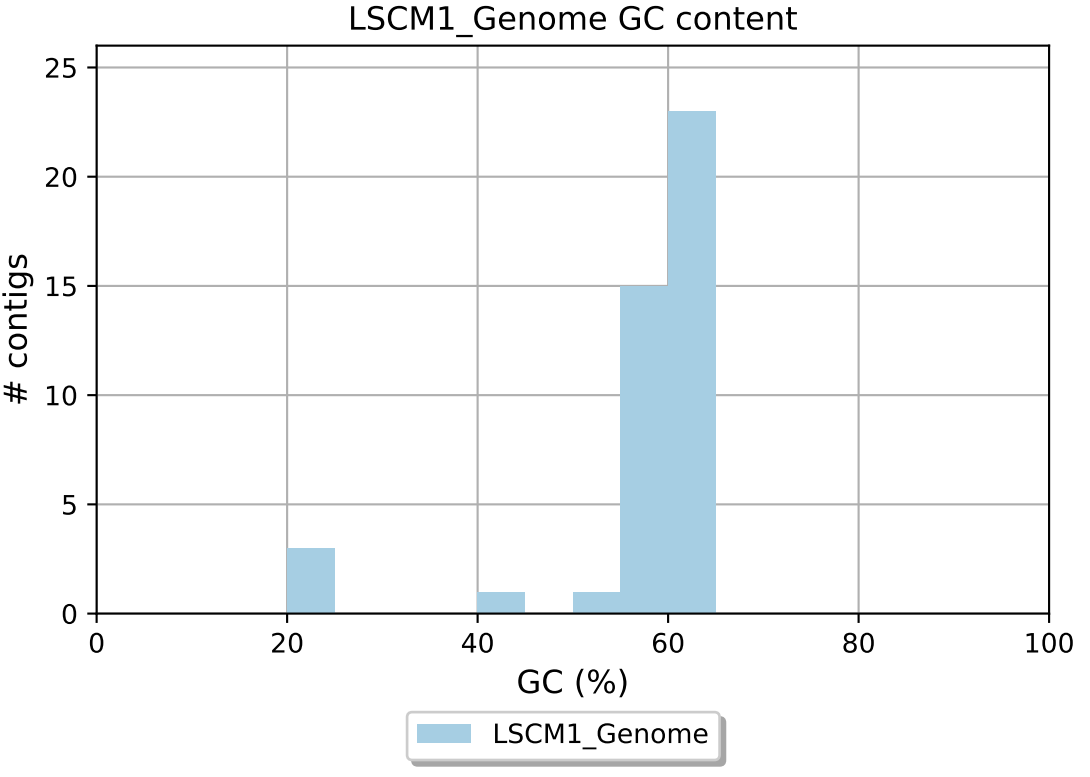

Flye_consensus GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
Flye_consensus


pilon GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
pilon


Pilon_consensus GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
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


LSCM1_Genome GC content
contigs
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
LSCM1_Genome