

Report

	4222_RB2_FLYE_MEDAKA_PILON_RAGTAG_GC	B8_RB11_out_ragtag_ragtag.scaffold	G11_RB6_2022_out_ragtag_ragtag.scaffold
# contigs (>= 0 bp)	21	22	24
# contigs (>= 1000 bp)	21	22	24
# contigs (>= 5000 bp)	21	22	23
# contigs (>= 10000 bp)	21	21	23
# contigs (>= 25000 bp)	21	20	21
# contigs (>= 50000 bp)	20	20	20
Total length (>= 0 bp)	15192876	15185003	15364824
Total length (>= 1000 bp)	15192876	15185003	15364824
Total length (>= 5000 bp)	15192876	15185003	15361584
Total length (>= 10000 bp)	15192876	15175298	15361584
Total length (>= 25000 bp)	15192876	15151083	15336220
Total length (>= 50000 bp)	15159425	15151083	15292693
# contigs	21	22	24
Largest contig	1359012	1349481	1407955
Total length	15192876	15185003	15364824
Reference length	15074320	15074320	15074320
GC (%)	48.04	48.03	47.96
Reference GC (%)	48.02	48.02	48.02
N50	936923	989449	971839
NG50	963931	989449	971839
N75	775097	737257	746866
NG75	775097	737257	770431
L50	8	7	7
LG50	7	7	7
L75	12	12	12
LG75	12	12	11
# misassemblies	29	148	159
# misassembled contigs	12	19	18
Misassembled contigs length	8193210	14969946	13484855
# local misassemblies	39	159	177
# scaffold gap ext. mis.	0	1	2
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	1	2
# unaligned contigs	0 + 15 part	0 + 20 part	2 + 21 part
Unaligned length	124049	519580	1023928
Genome fraction (%)	99.733	97.178	94.879
Duplication ratio	1.005	1.004	1.005
# N's per 100 kbp	0.00	1.32	2.60
# mismatches per 100 kbp	11.21	423.07	486.53
# indels per 100 kbp	8.37	186.08	190.22
Largest alignment	1122352	951516	951855
Total aligned length	15052939	14656043	14333695
NA50	854172	239738	195720
NGA50	854172	240170	195720
NA75	421761	135509	102806
NGA75	421761	143900	103962
LA50	8	19	18
LGA50	8	18	18
LA75	14	40	45
LGA75	14	39	43

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

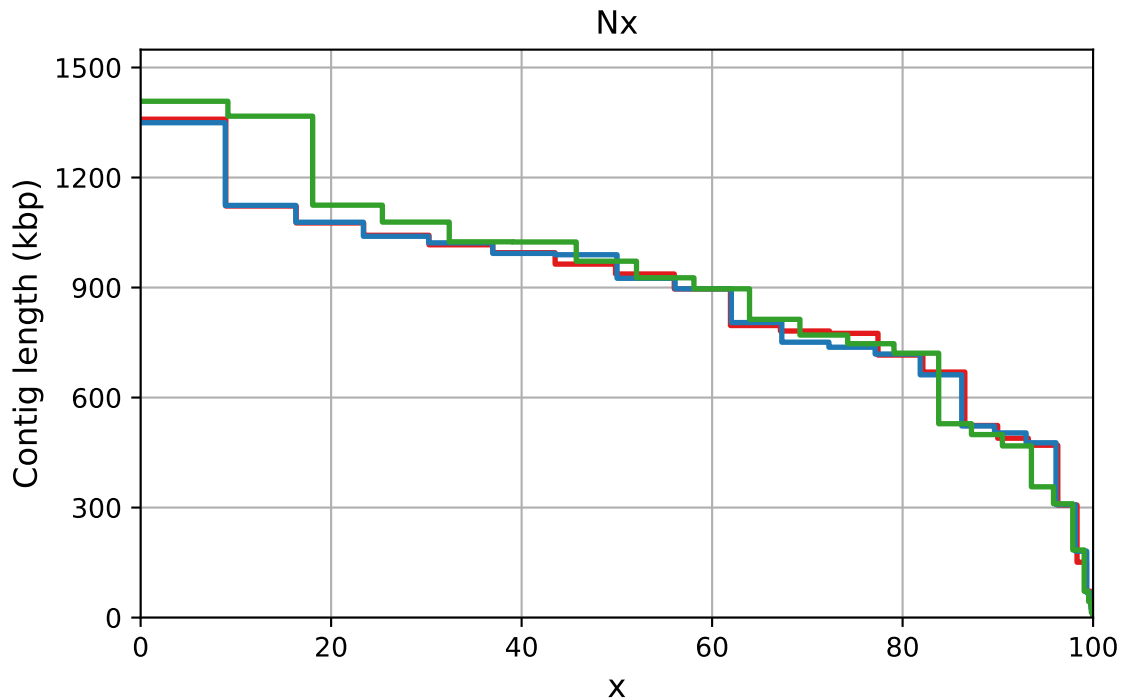
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# misassemblies	29	148	159
# contig misassemblies	29	148	159
# c. relocations	23	84	92
# c. translocations	6	50	56
# c. inversions	0	14	11
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	12	19	18
Misassembled contigs length	8193210	14969946	13484855
# local misassemblies	39	159	177
# scaffold gap ext. mis.	0	1	2
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	1	2
# mismatches	1682	61826	69419
# indels	1256	27194	27140
# indels (<= 5 bp)	1209	24569	24175
# indels (> 5 bp)	47	2625	2965
Indels length	3658	78851	83866

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

	4222_RB2_FLYE_MEDAKA_PILON_RAGTAG_GC	B8_RB11_out_ragtag_ragtag.scaffold	G11_RB6_2022_out_ragtag_ragtag.scaffold
# fully unaligned contigs	0	0	2
Fully unaligned length	0	0	14616
# partially unaligned contigs	15	20	21
Partially unaligned length	124049	519580	1009312
# N's	0	200	400

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).

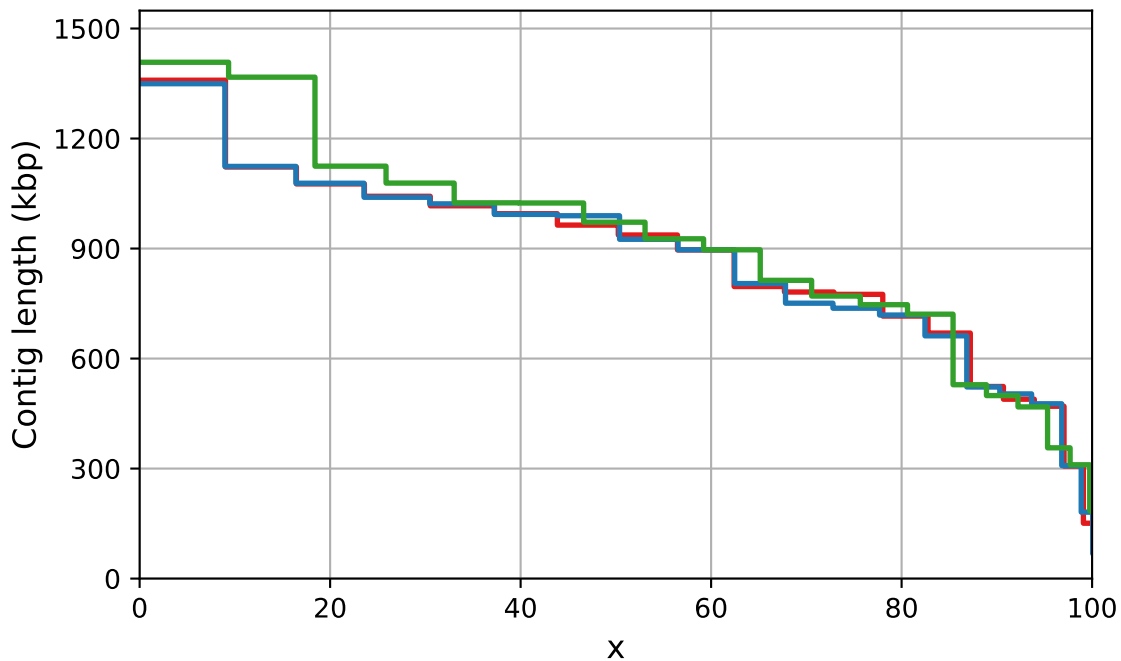


KA_PILON_RAGTAG_GC

B8_RB11_out_ragtag_ragtag.scaffold

G11_RB6_202

NGx

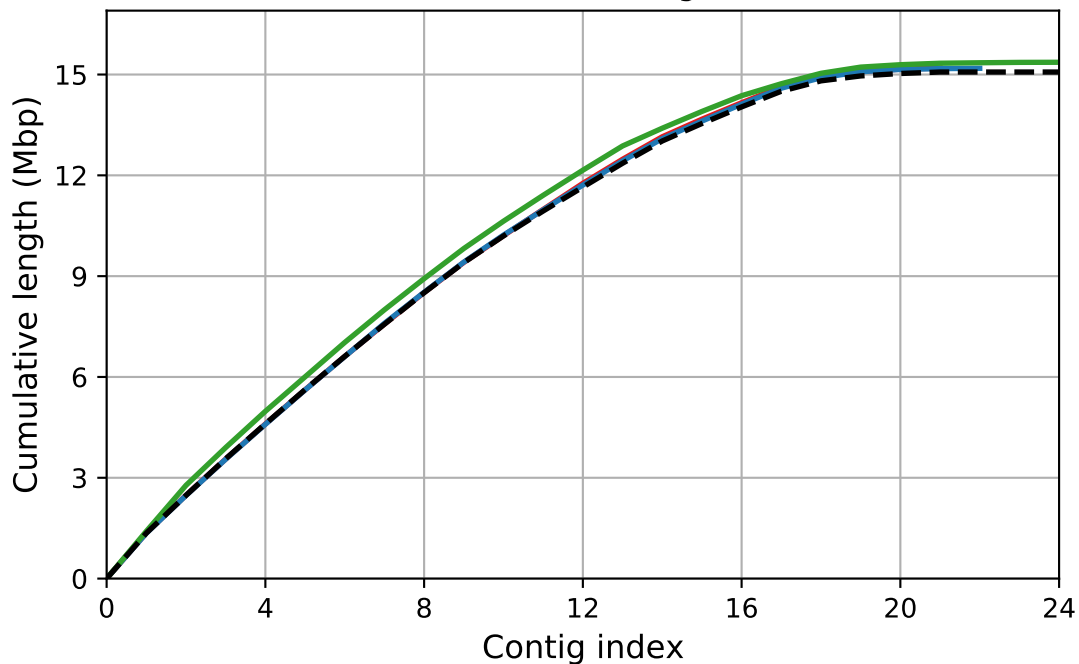


KA_PILON_RAGTAG_GC

B8_RB11_out_ragtag_ragtag.scaffold

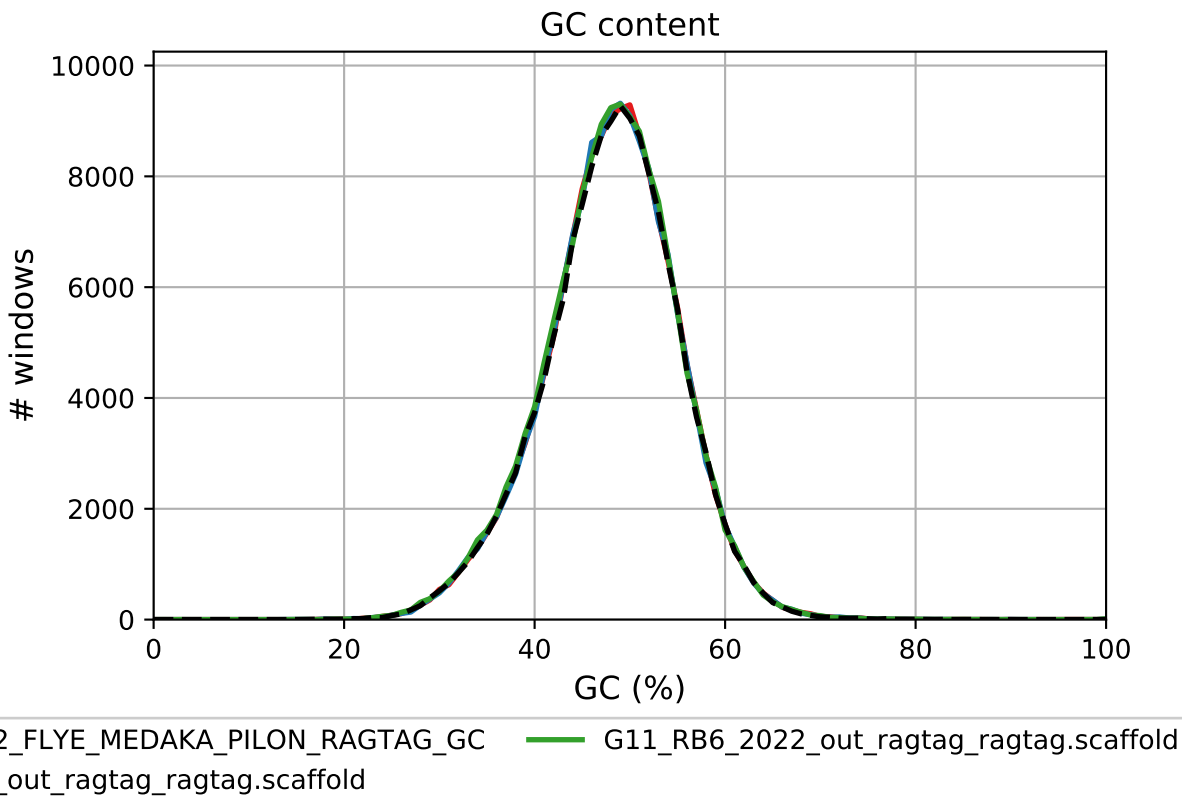
G11_RB6_202

Cumulative length

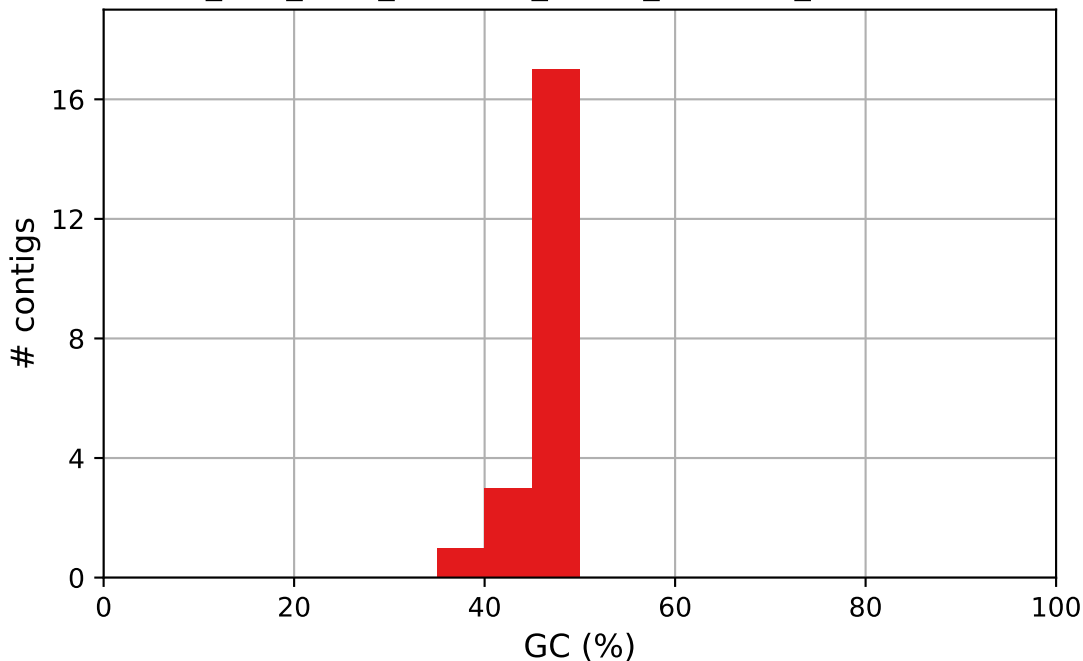


2_FLYE_MEDAKA_PILON_RAGTAG_GC
_out_ragtag_ragtag.scaffold

G11_RB6_2022_out_ragtag_ragtag.scaffold

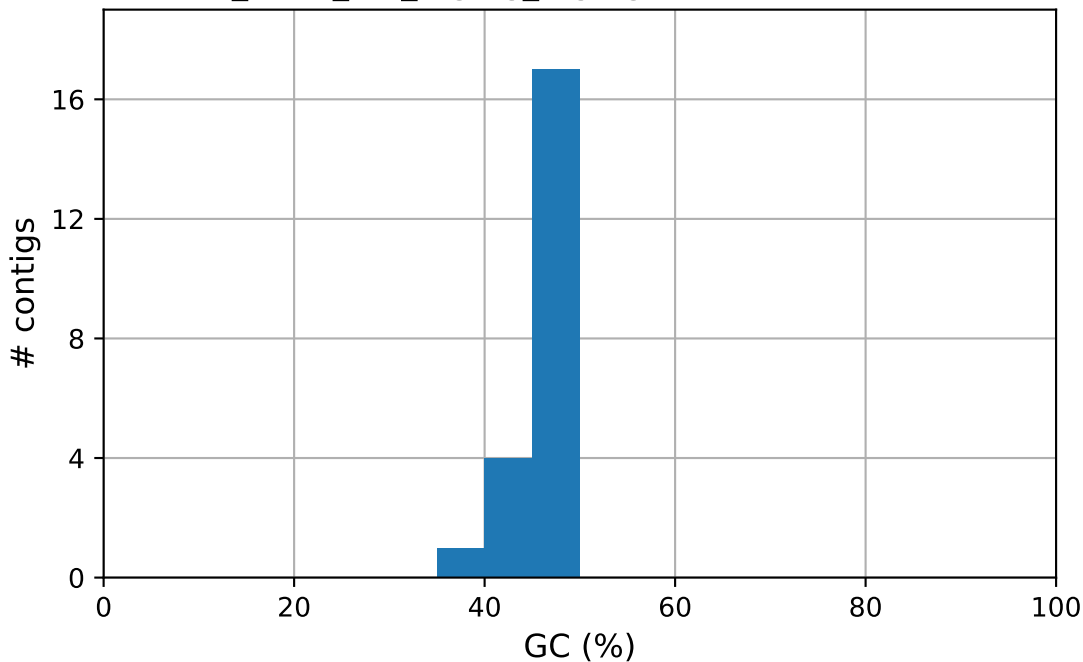


4222_RB2_FLYE_MEDAKA_PILON_RAGTAG_GC GC content



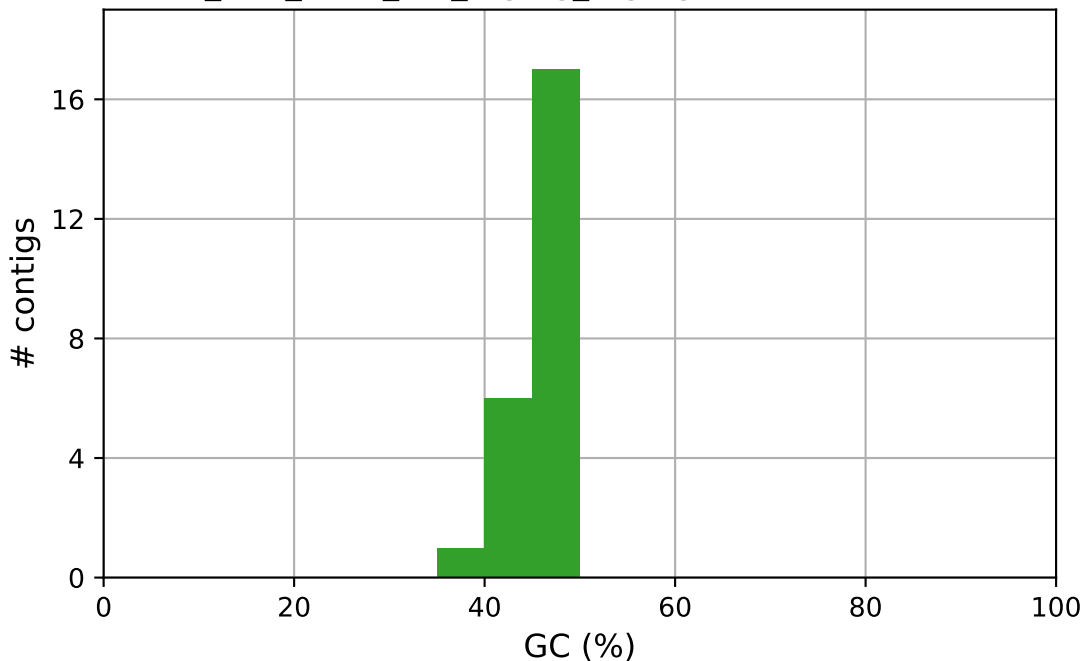
4222_RB2_FLYE_MEDAKA_PILON_RAGTAG_GC

B8_RB11_out_ragtag_ragtag.scaffold GC content



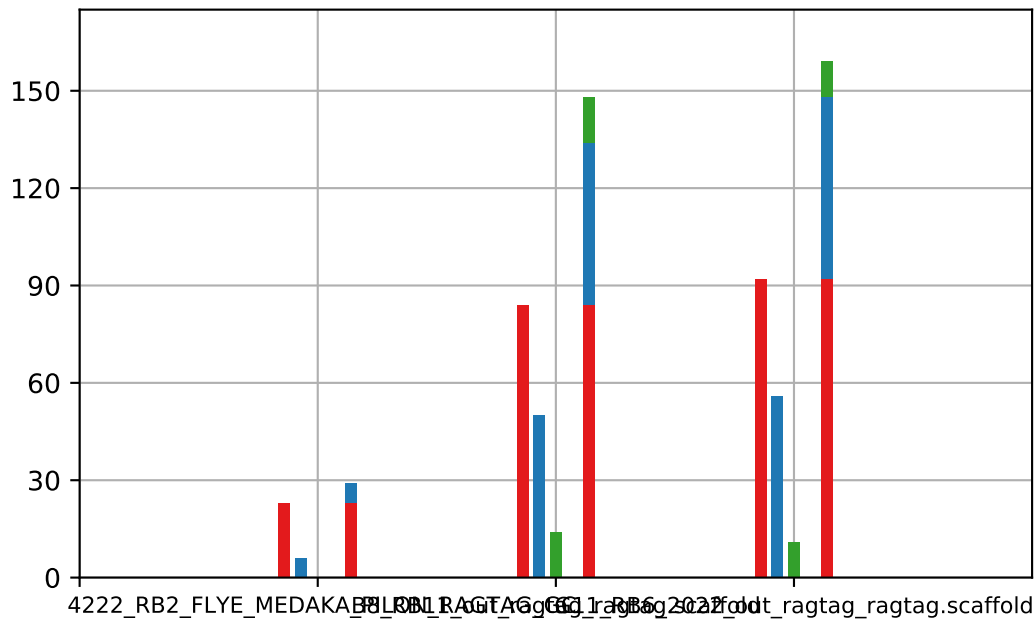
B8_RB11_out_ragtag_ragtag.scaffold

G11_RB6_2022_out_ragtag_ragtag.scaffold GC content

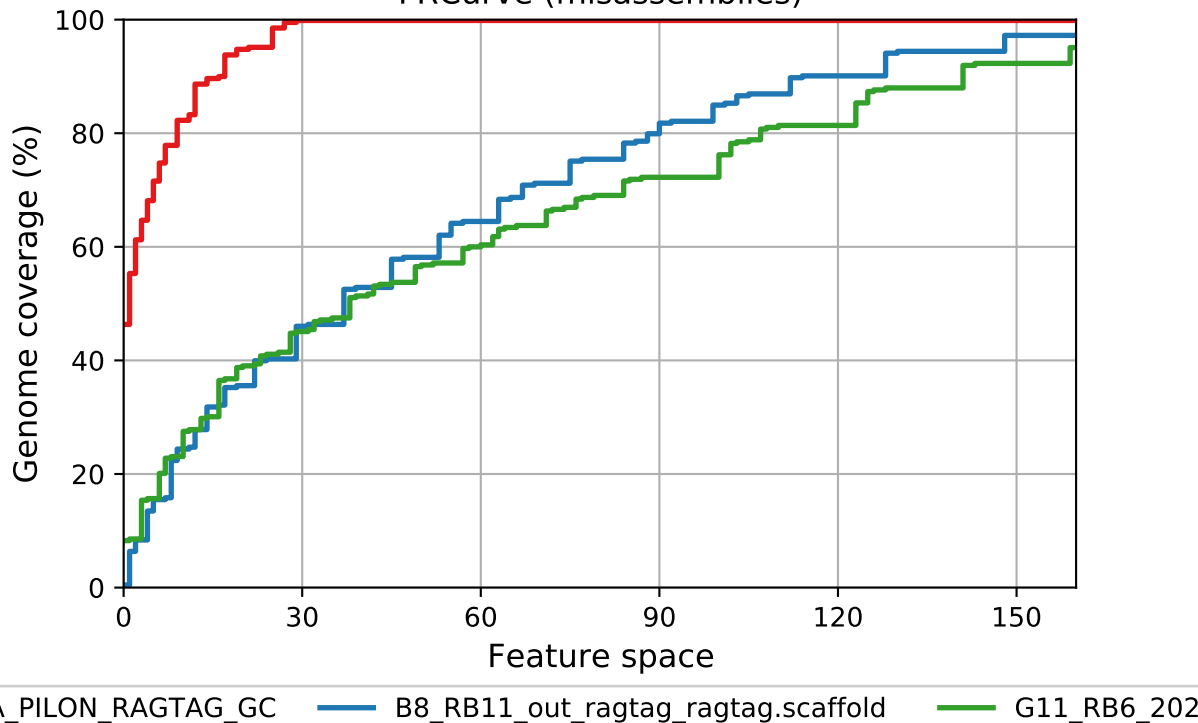


G11_RB6_2022_out_ragtag_ragtag.scaffold

Misassemblies



FRCurve (misassemblies)

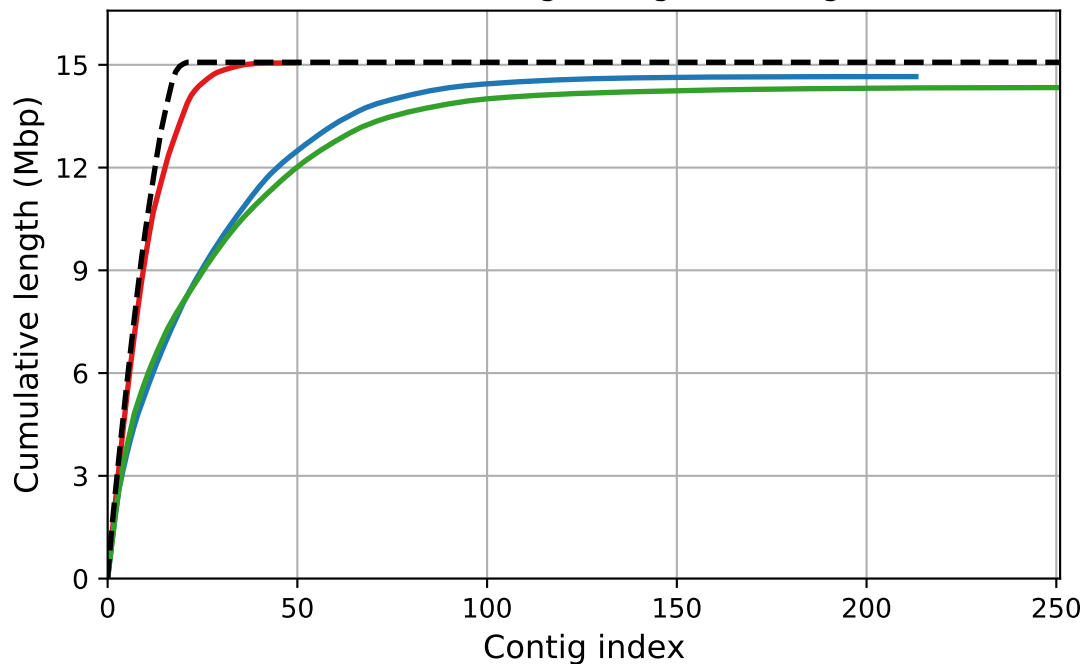


KA_PILON_RAGTAG_GC

B8_RB11_out_ragtag_ragtag.scaffold

G11_RB6_202

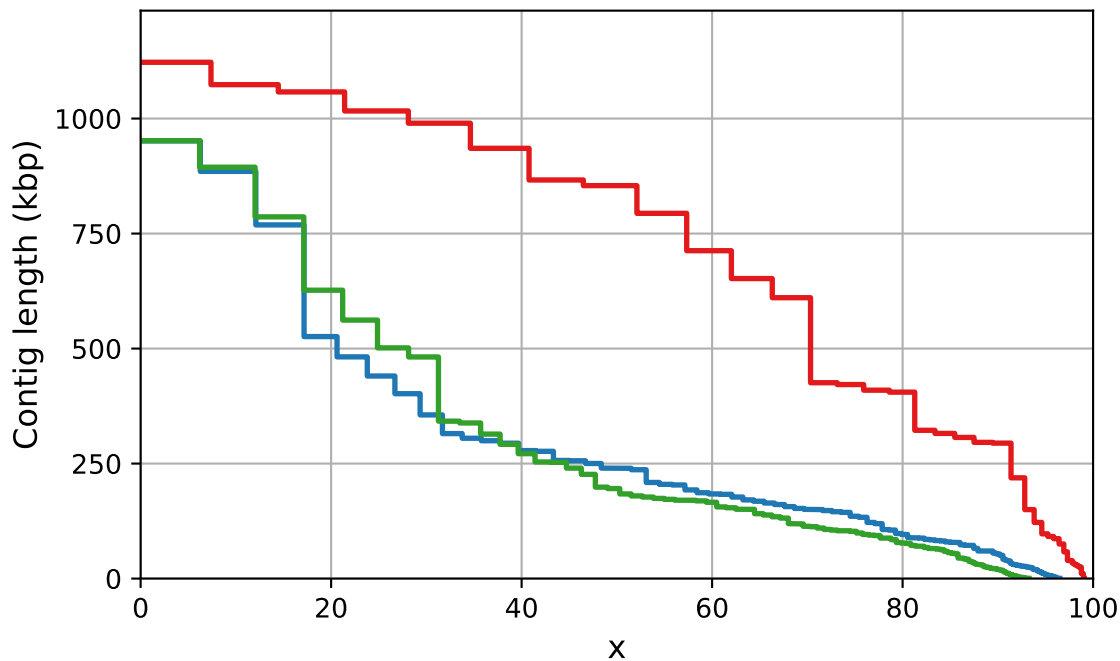
Cumulative length (aligned contigs)



2_FLYE_MEDAKA_PILON_RAGTAG_GC
_out_ragtag_ragtag.scaffold

G11_RB6_2022_out_ragtag_ragtag.scaffold

NAx

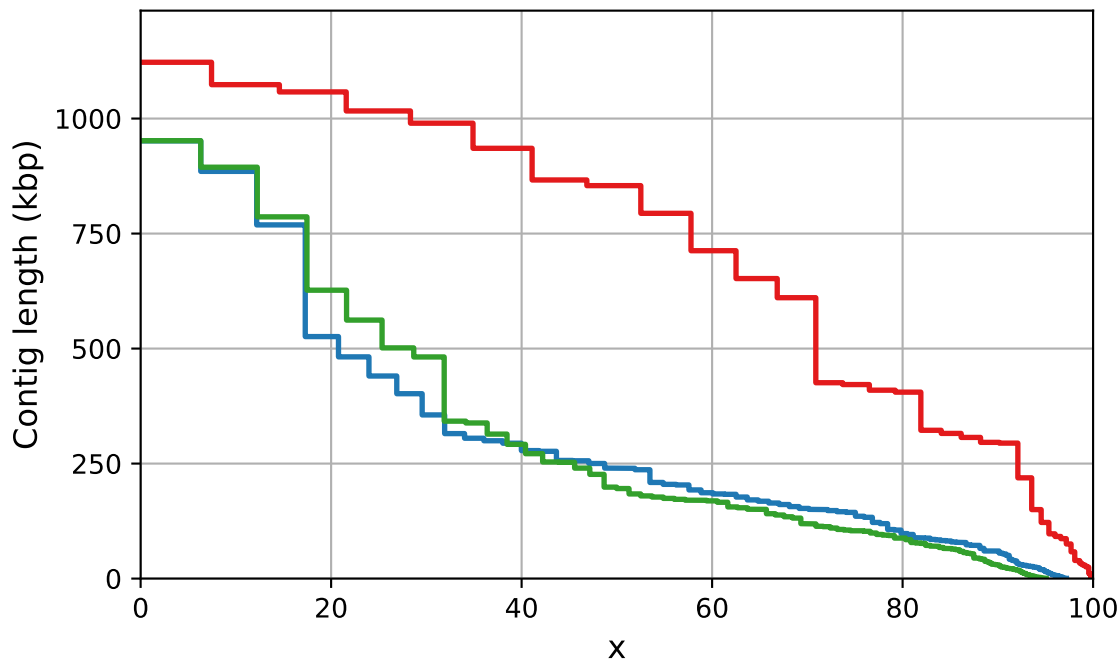


KA_PILON_RAGTAG_GC

B8_RB11_out_ragtag_ragtag.scaffold

G11_RB6_202

NGAx



KA_PILON_RAGTAG_GC

B8_RB11_out_ragtag_ragtag.scaffold

G11_RB6_202

Genome fraction, %

100

95

90

KA_PILON_RAGTAG_GC



B8_RB11_out_ragtag_ragtag.scaffold



G11_RB6_202

