

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1963931
ToLID	icLapAnag1
Species	Laparocerus anagae
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	500,646,919	514,188,479
Haploid Number	11 (source: ancestor)	11
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	X0

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 7.7.Q67

Obtained EBP quality metric for hap2: 7.7.Q70

The following metrics were automatically flagged as below EBP recommended standards or different from expected:

- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for hap1
- . Kmer completeness value is less than 90 for hap2
- . Assembly length loss > 3% for hap2

Curator notes

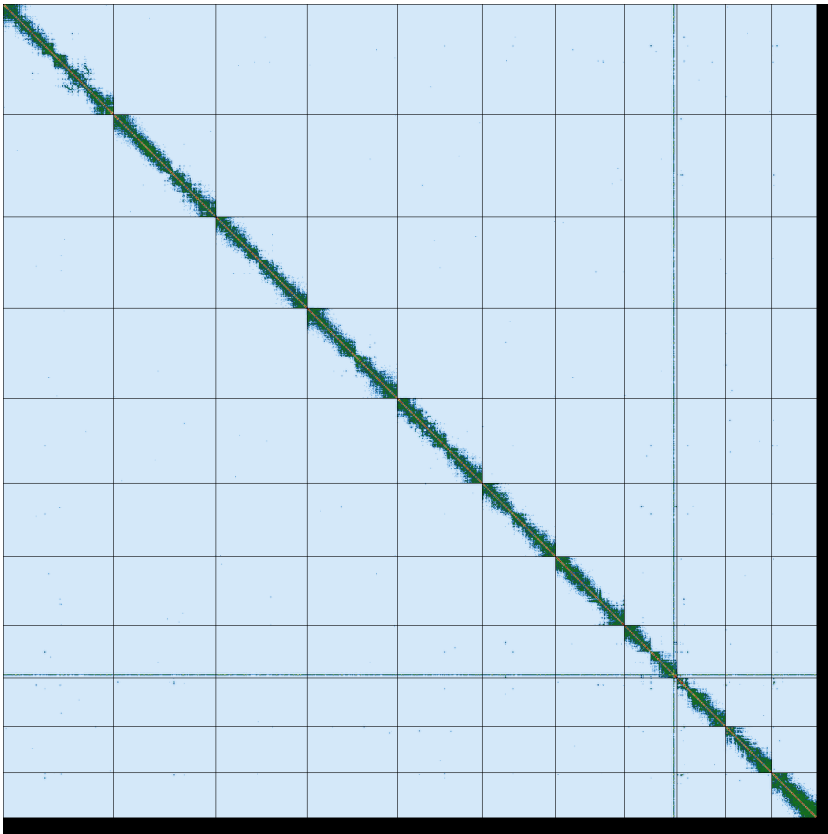
- . Interventions/Gb: 23
- . Contamination notes: "FCS-GX detected 146 contaminated contigs in haplotype 1 and 91 contaminated contigs in haplotype 2. The Proteobacteria Rahnella victoriana was fully assembled to a circle. Mitochondrial genome was removed from the assembly"
- . Other observations: "The PacBio reads were subsampled to 50X. The sex chromosome is potentially hlsu11 which is part of the hap1 assembly. It has no corresponding haplotype and shows half coverage. Though I don't know how to tag this sex chromosome - I could not find much information about sex chromosomes in weevils."

Quality metrics table

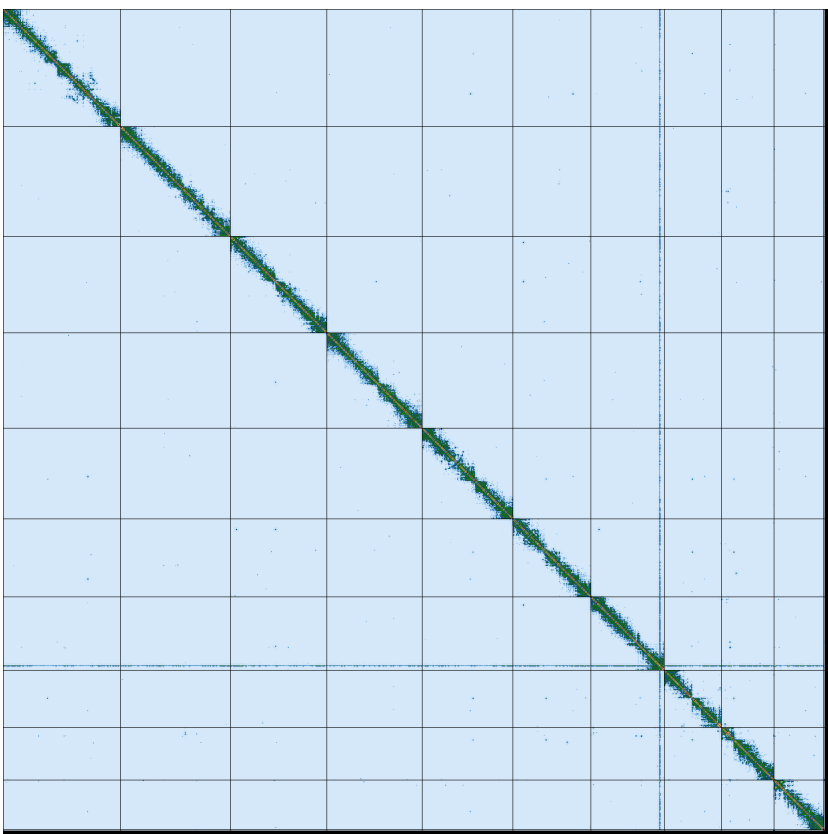
Metrics	Pre-curation hap1	Pre-curation hap2	Curated hap1	Curated hap2
Total bp	486,377,018	510,740,606	514,188,479	481,753,495
GC %	32.9	33.18	32.88	33.22
Gaps/Gbp	67.85	48.95	68.07	58.12
Total gap bp	6,600	5,000	7,000	5,600
Scaffolds	264	113	264	108
Scaffold N50	55,537,056	52,413,696	52,580,765	55,302,066
Scaffold L50	4	5	5	4
Scaffold L90	9	10	10	9
Contigs	297	138	299	136
Contig N50	24,718,012	25,762,000	25,606,415	25,935,046
Contig L50	9	9	9	8
Contig L90	23	21	24	20
QV	66.9104	71.0195	67.1519	70.7657
Kmer compl.	63.6013	67.5989	67.4921	63.717
BUSCO sing.	91.6%	96.6%	96.6%	91.8%
BUSCO dupl.	0.9%	0.9%	1.0%	0.8%
BUSCO frag.	1.1%	1.1%	1.0%	1.1%
BUSCO miss.	6.4%	1.4%	1.4%	6.3%

BUSCO: 5.8.3 (euk_genome_min, miniprot) / Lineage: endopterygota_odb12 (genomes:76, BUSCOs:3754)

HiC contact map of curated assembly

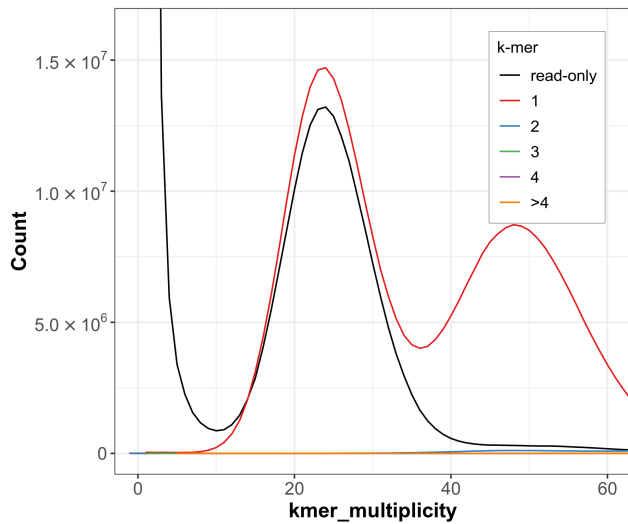


hap1 [\[LINK\]](#)

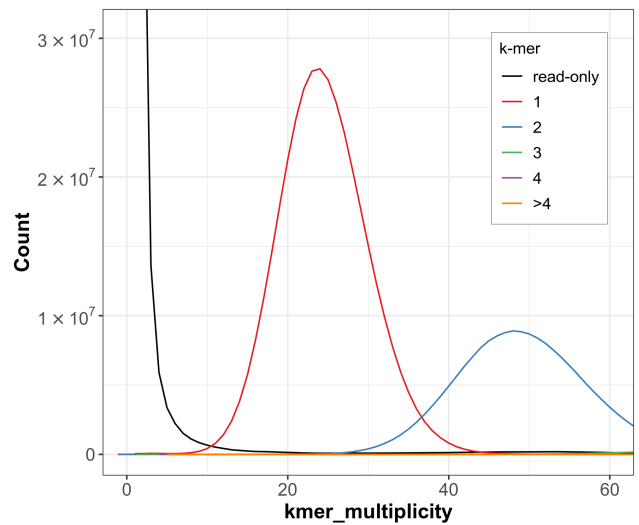


hap2 [\[LINK\]](#)

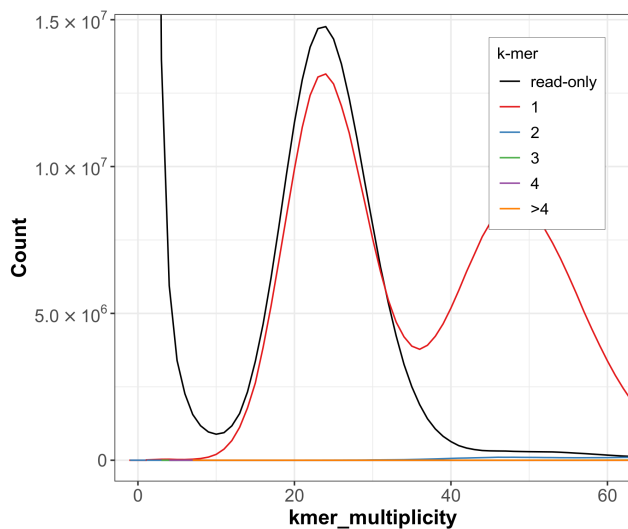
K-mer spectra of curated assembly



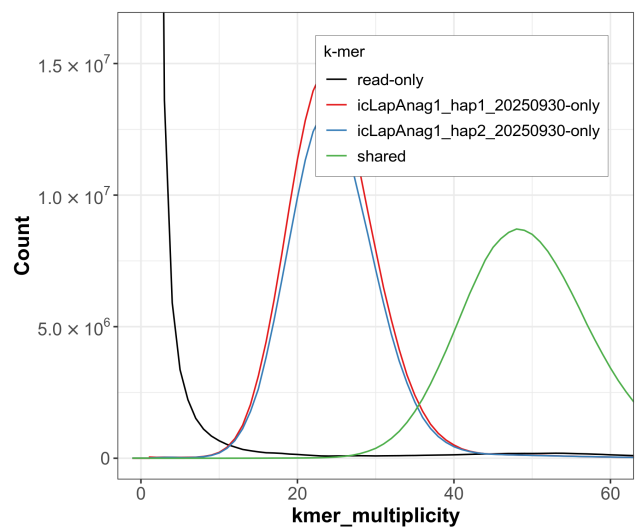
Distribution of k-mer counts per copy numbers found in
icLapAnag1_hap1_20250930 (hap1.)



Distribution of k-mer counts per copy numbers found in
asm (dipl.)

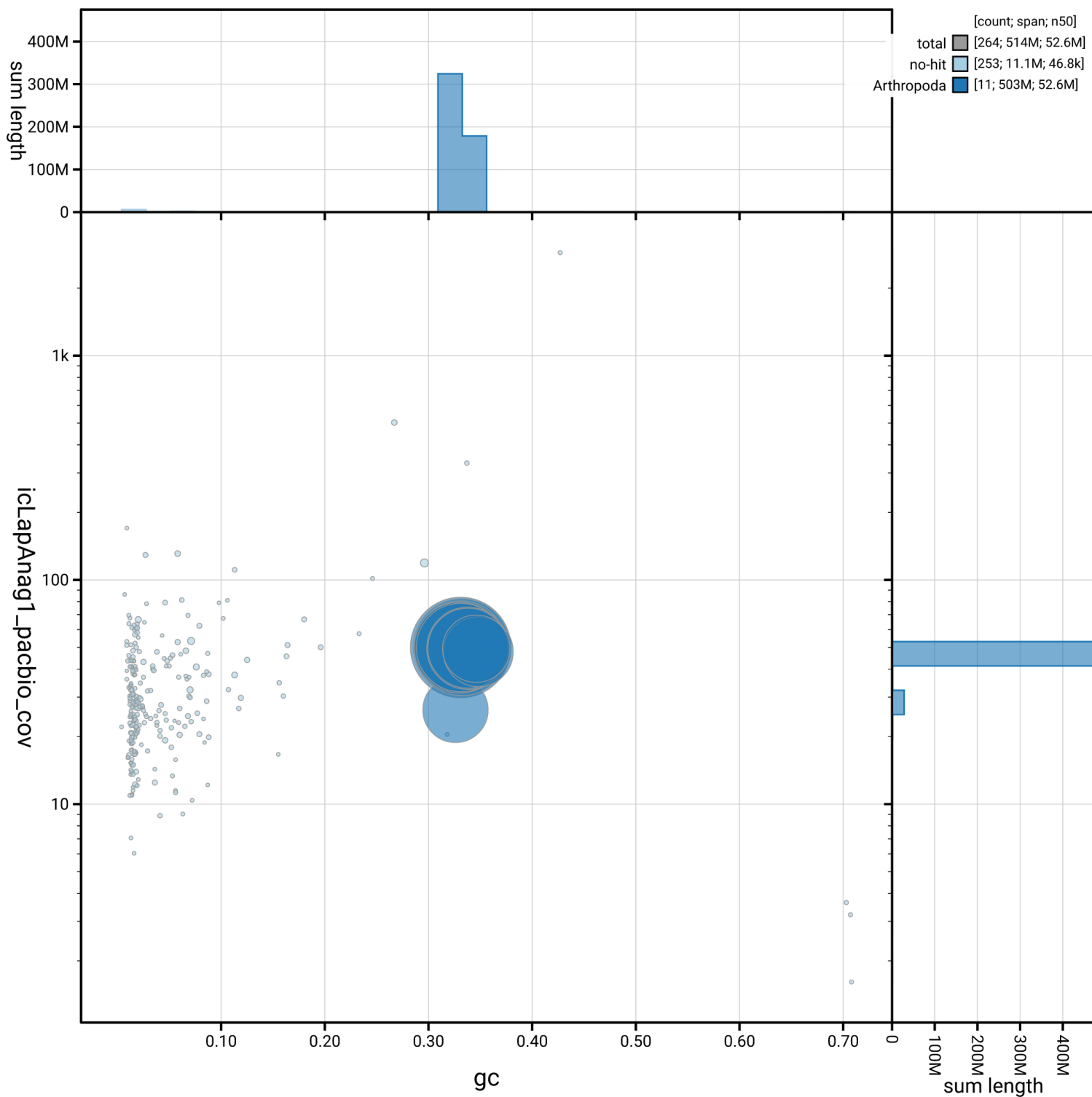


Distribution of k-mer counts per copy numbers found in
icLapAnag1_hap2_20250930 (hap1.)

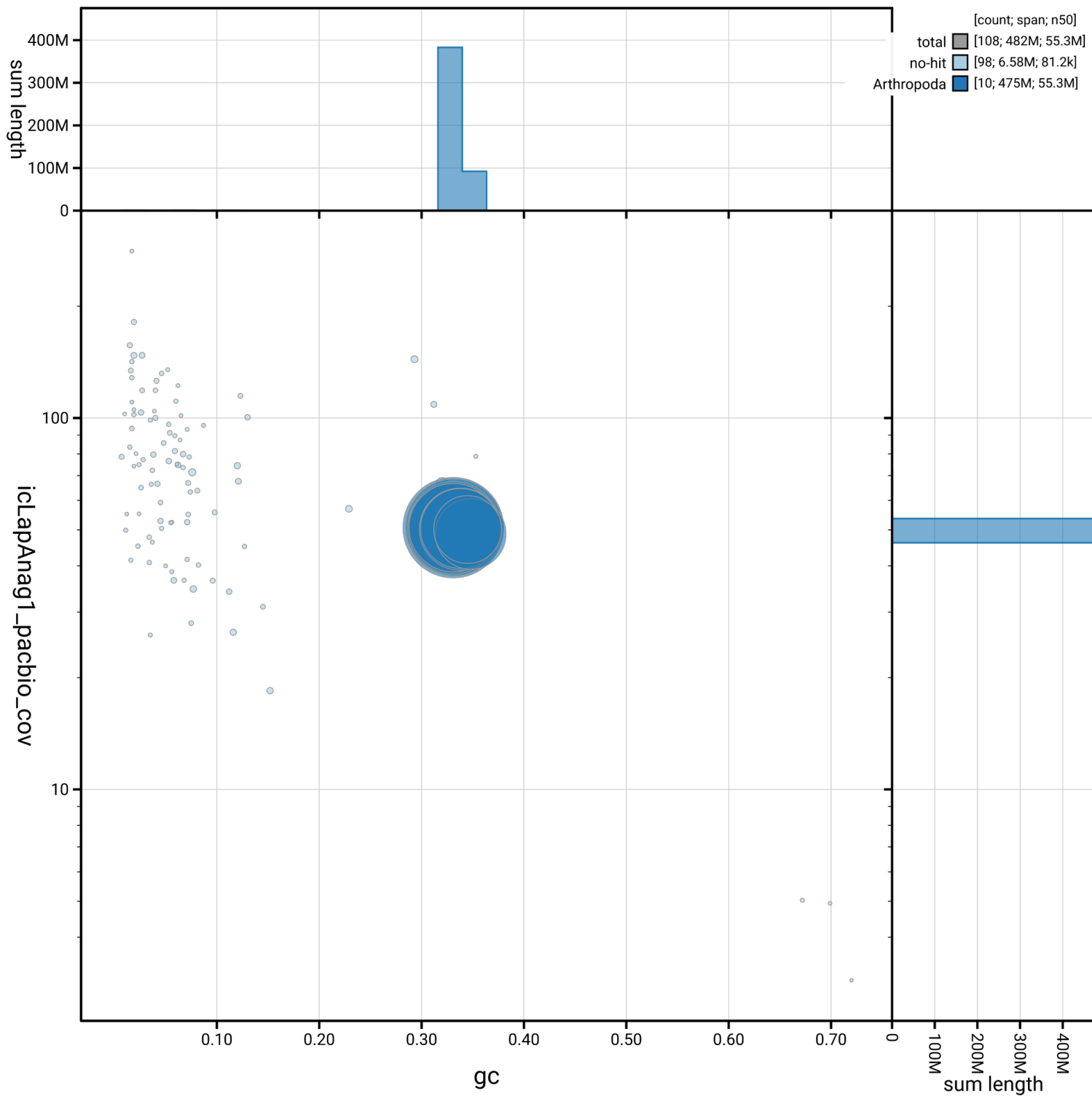


Distribution of k-mer counts coloured by
their presence in reads/assemblies

Post-curation contamination screening



hap1. Bubble plot circles are scaled by sequence length, positioned by coverage and GC proportion, and coloured by taxonomy. Histograms show total assembly length distribution on each axis.



hap2. Bubble plot circles are scaled by sequence length, positioned by coverage and GC proportion, and coloured by taxonomy. Histograms show total assembly length distribution on each axis.

Data profile

Data	HiFi	Bionano	OmniC
Coverage	317x	NA	49x

Assembly pipeline

- **Hifiasm**
 - |_ *ver*: 0.25.0-r726
 - |_ *key param*: HiC
 - |_ *key param*: 12
- **purge_dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA
- **YaHS**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA

Curation pipeline

- **GRIT_Rapid**
 - |_ *ver*: 2.0
 - |_ *key param*: NA

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Date and time: 2025-10-01 10:02:22 CEST