

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3014478
ToLID	imAmeSpall1
Species	Ameles spallanzania
Class	Insecta
Order	Mantodea

Genome Traits	Expected	Observed
Haploid size (bp)	2,583,211,628	2,608,886,360
Haploid Number	8 (source: ancestor)	14
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	XX

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 6.8.Q62
Obtained EBP quality metric for hap2: 6.8.Q62

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

- . Observed Haploid Number is different from Expected
- . Observed sex is different from Sample sex

Curator notes

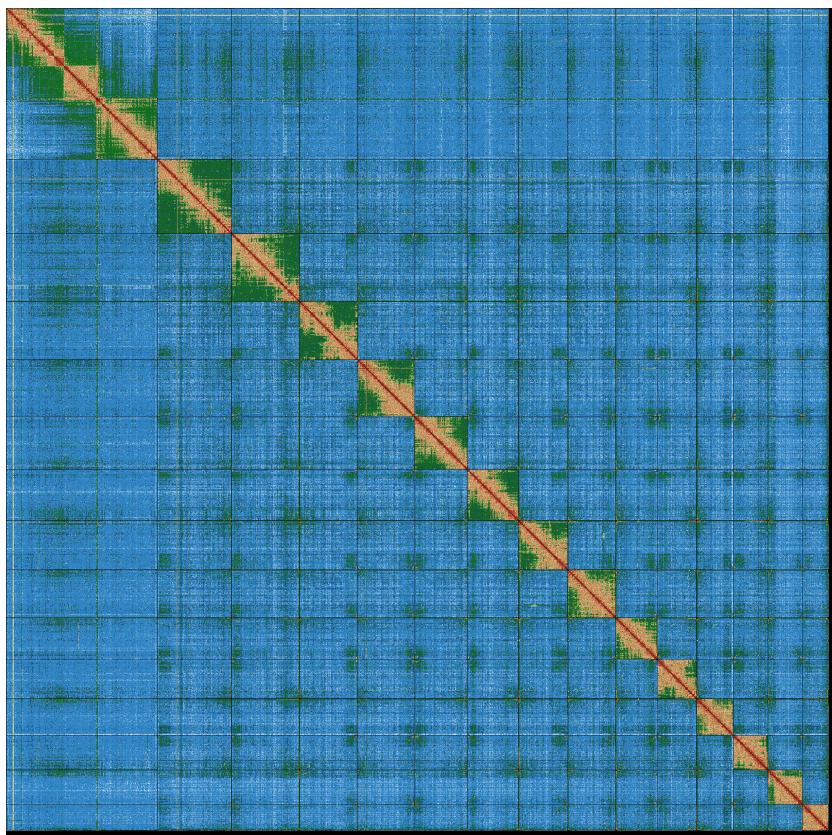
- . Interventions/Gb: None
- . Contamination notes: "Decontamination was done with NCBI FCS pipeline and confirmed with Blob toolkit"
- . Other observations: "This genome assembly was produced by assembling PacBio HiFi data from two different individuals with Hifiasm, purging with purge_dups and then scaffolding with Yahs. Both assemblies are presented as requested. Curation made 18 cuts in contigs, 14 breaks at gaps and 80 joins for the Hap1 and 17 cuts in contigs, 6 breaks at gaps and 413 joins for the Hap2. The sex chromosomes were assigned based on an alignment with the species *Deroplatys truncata* (GCA_030765065.1)"

Quality metrics table

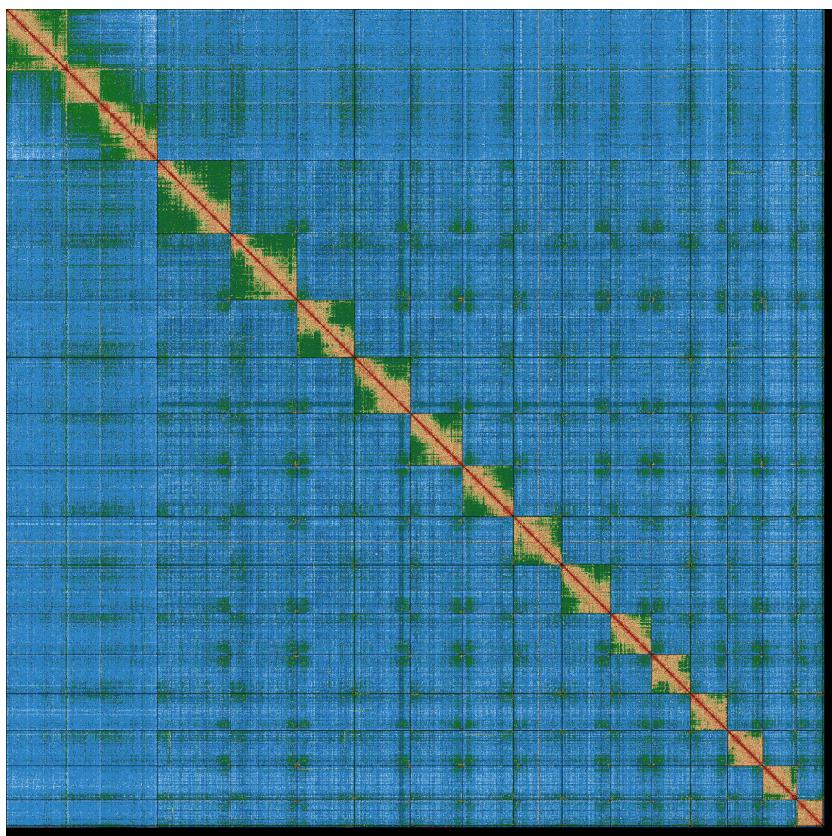
Metrics	Pre-curation hap1	Pre-curation hap2	Curated hap1	Curated hap2
Total bp	2,609,282,592	2,583,173,298	2,608,886,360	2,582,360,386
GC %	37.88	37.88	37.88	37.88
Gaps/Gbp	378.65	341.83	551.19	499.54
Total gap bp	197,600	176,600	287,600	258,000
Scaffolds	646	819	260	418
Scaffold N50	17,033,530	17,239,675	166,772,640	161,208,364
Scaffold L50	41	38	6	6
Scaffold L90	161	176	13	13
Contigs	1,634	1,702	1,698	1,708
Contig N50	3,996,391	4,133,618	3,764,138	4,054,688
Contig L50	180	159	189	162
Contig L90	757	708	805	719
QV	62.6925	62.6457	62.6942	62.6448
Kmer compl.	94.9093	95.5045	94.8929	95.4991
BUSCO sing.	96.0%	96.2%	95.8%	96.1%
BUSCO dupl.	3.2%	2.7%	3.3%	2.7%
BUSCO frag.	0.1%	0.3%	0.2%	0.3%
BUSCO miss.	0.7%	0.8%	0.7%	0.9%

BUSCO: 5.8.0 (euk_genome_min, miniprot) / Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

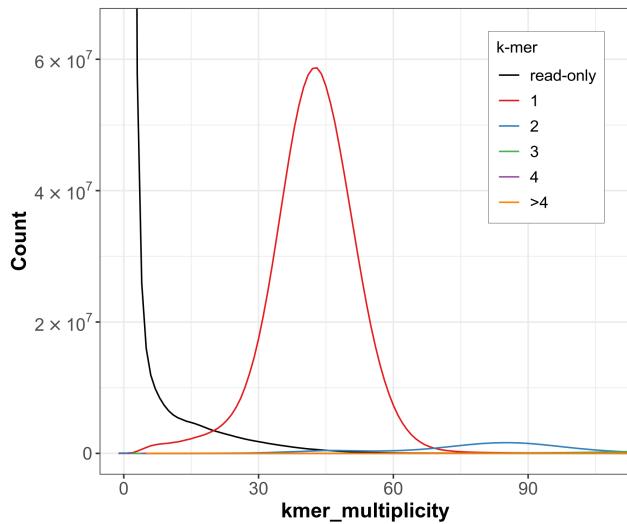


hap1 [\[LINK\]](#)

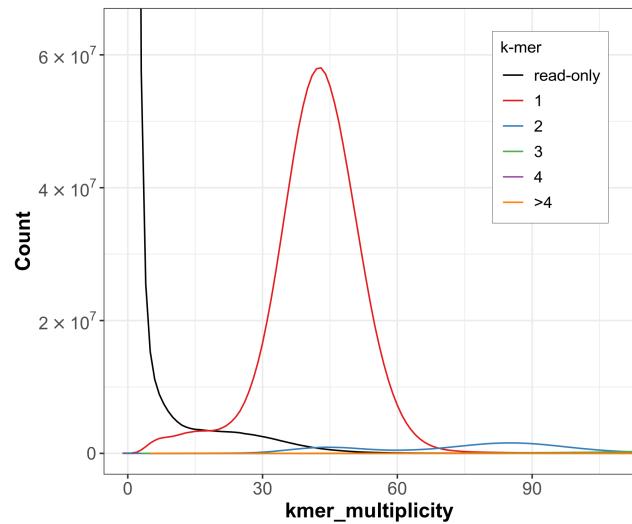


hap2 [\[LINK\]](#)

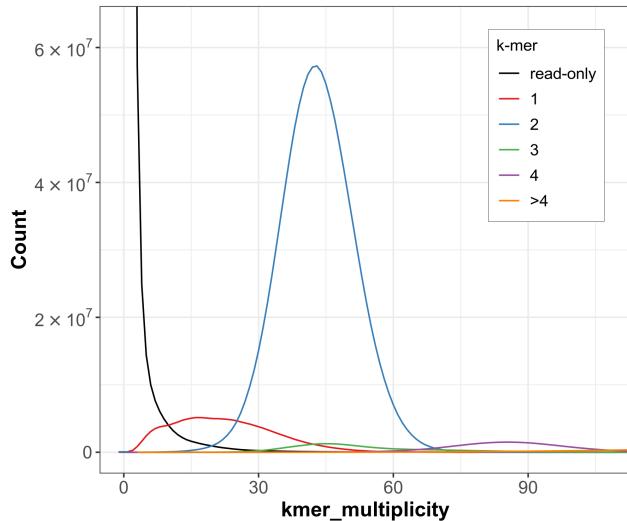
K-mer spectra of curated assembly



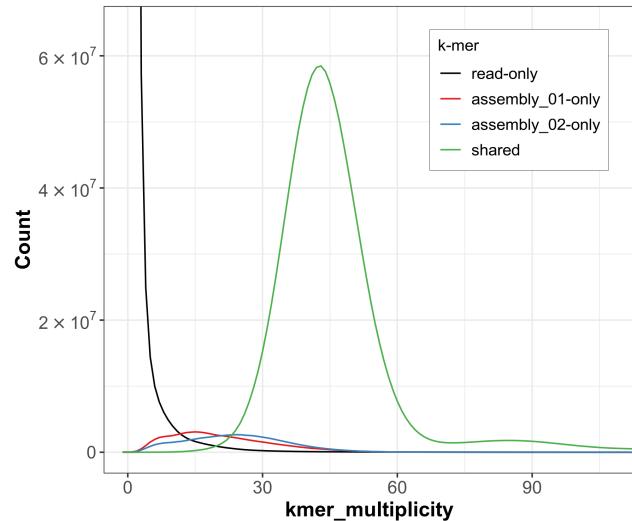
Distribution of k-mer counts per copy numbers found in **assembly_02** (hapl.)



Distribution of k-mer counts per copy numbers found in **assembly_01** (hapl.)

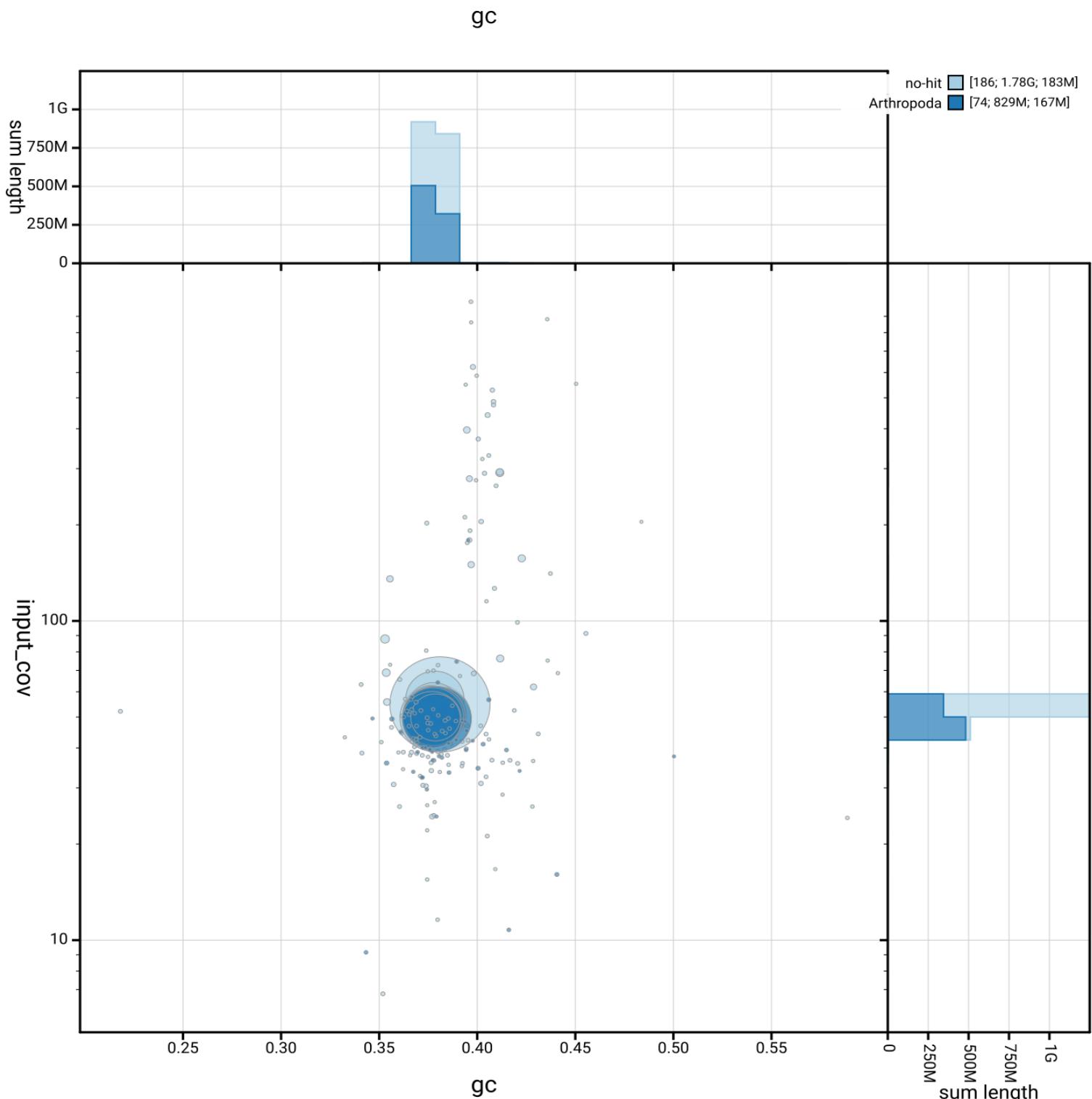


Distribution of k-mer counts per copy numbers found in **asm** (dipl.)



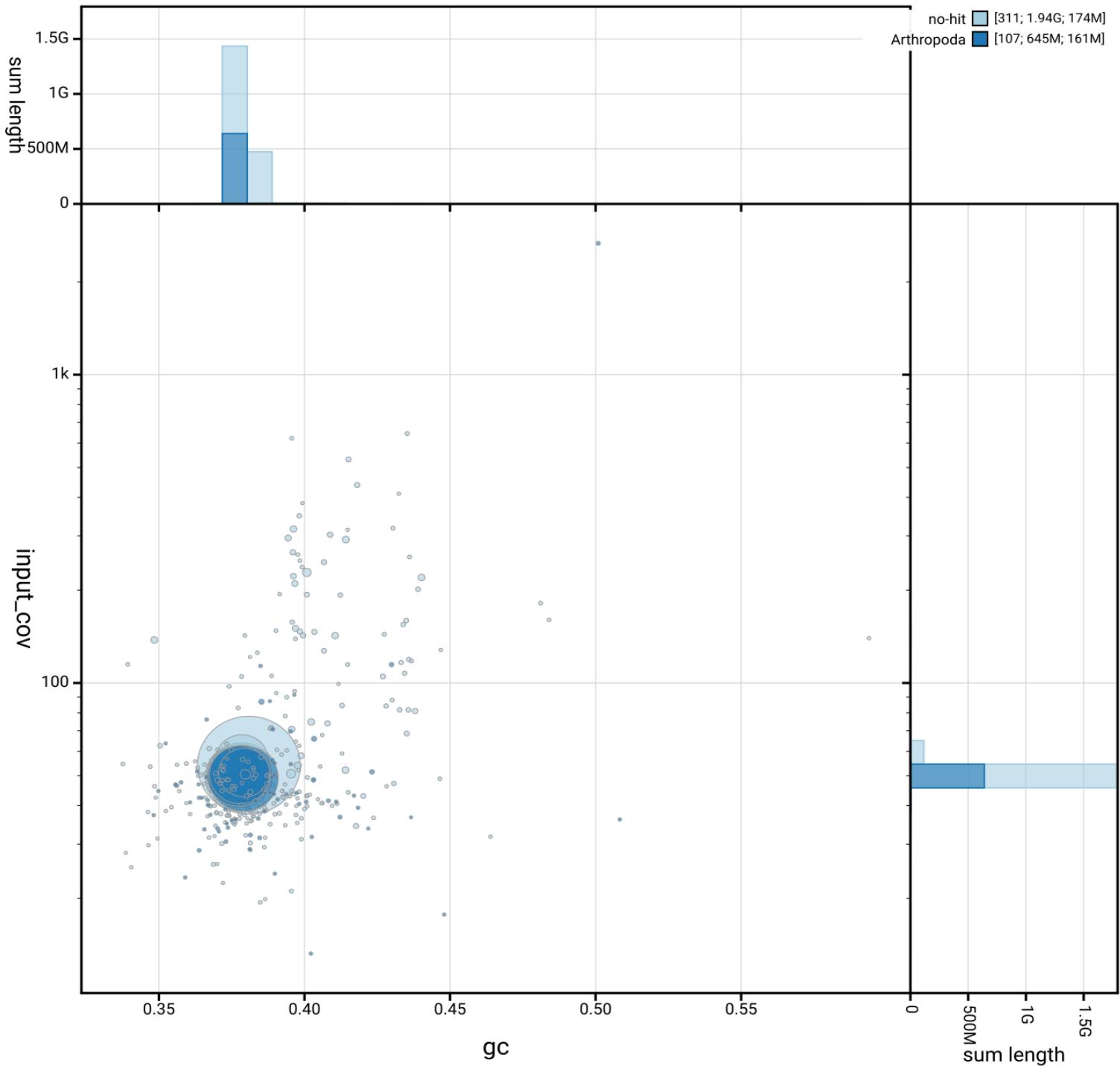
Distribution of k-mer counts coloured by their presence in reads/assemblies

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.

gc



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	HiC
Coverage	29.54X	145.70X	

Assembly pipeline

- **Hifiasm**
 - |_ ver: Galaxy Version 0.24.0+galaxy0
 - |_ key param: VGP Galaxy workflow VGP3 v 0.3.2
- **purge_dups**
 - |_ ver: Galaxy Version 1.2.6+galaxy0
 - |_ key param: VGP Galaxy workflow VGP6 v 0.8
- **YaHS**
 - |_ ver: Galaxy Version 1.2a.2+galaxy2
 - |_ key param: VGP Galaxy workflow VGP8 v 2.0

Curation pipeline

- **PretextMap**
 - |_ ver: Galaxy Version 0.1.9+galaxy1
 - |_ key param: VGP workflow VGP PretextMap generation v2
- **PretextView**
 - |_ ver: 1.0.0
 - |_ key param: NA

Submitter: Marcella Sozzoni

Affiliation: UNIFI

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