

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1849190
ToLID	<b>icAntGang</b>
Species	Anthroherpon ganglbaueri
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	289,632,189	243,270,400
Haploid Number	11 (source: ancestor)	11
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

## EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 6.7.Q65

Obtained EBP quality metric for hap2: 5.7.Q65

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

- . Assembly length loss > 3% for hap1
- . Assembly length loss > 3% for hap2
- . More than 1000 gaps/Gbp for hap2

### Curator notes

- . Interventions/Gb: 107
- . Contamination notes: "No contaminants were found"
- . Other observations: "Chromosomes arms were reconstructed with alignment with a species from the same family ( Leptodirus hochenwartii, GCA\_947310635.1)."

# Quality metrics table

Metrics	Pre-curation hap1	Pre-curation hap2	Curated hap1	Curated hap2
Total bp	529,803,353	273,308,231	242,249,656	243,270,400
GC %	35.25	33.32	32.5	32.56
Gaps/Gbp	1,162.7	1,737.96	986.59	1,771.69
Total gap bp	123,200	95,000	47,800	86,200
Scaffolds	3,677	599	13	11
Scaffold N50	2,249,664	13,642,877	26,729,212	27,310,071
Scaffold L50	30	9	4	4
Scaffold L90	1,929	32	9	9
Contigs	4,293	1,074	252	442
Contig N50	626,861	919,243	1,585,153	981,229
Contig L50	174	104	54	90
Contig L90	2,452	379	158	257
QV	56.925	60.7798	65.8548	65.0701
Kmer compl.	94.5129	93.912	91.0109	91.2776
BUSCO sing.	95.9%	98.2%	97.3%	97.7%
BUSCO dupl.	2.7%	1.3%	0.9%	1.2%
BUSCO frag.	0.3%	0.2%	0.1%	0.0%
BUSCO miss.	1.2%	0.3%	1.8%	1.1%

Warning! BUSCO versions or lineage datasets are not the same across results:

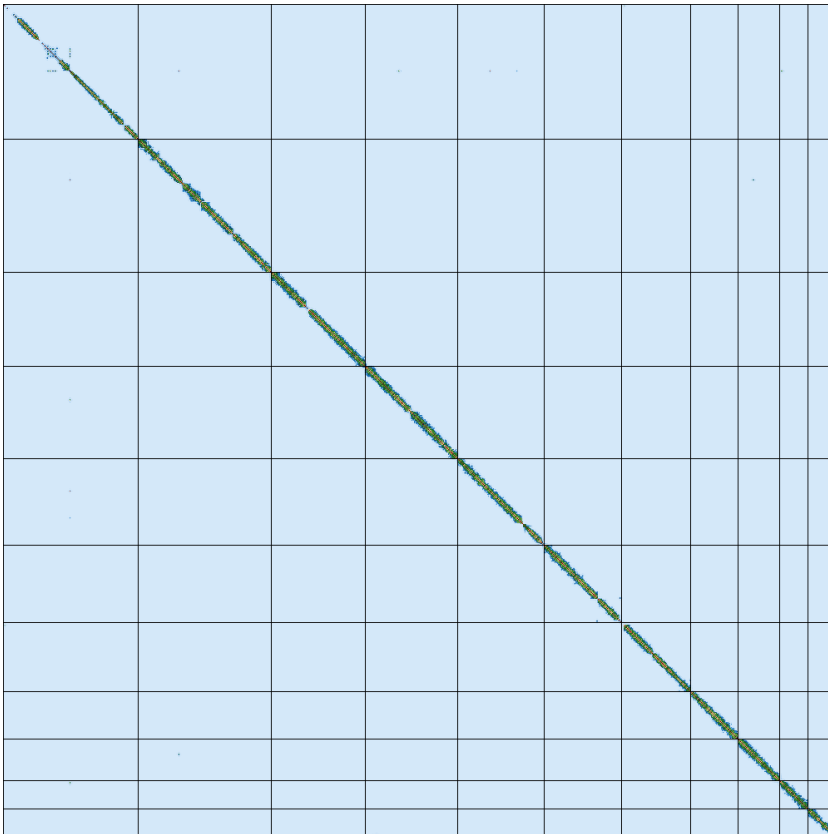
BUSCO: 5.8.0 (euk\_genome\_met, metaeuk) / Lineage: arthropoda\_odb10 (genomes:90, BUSCOs:1013)

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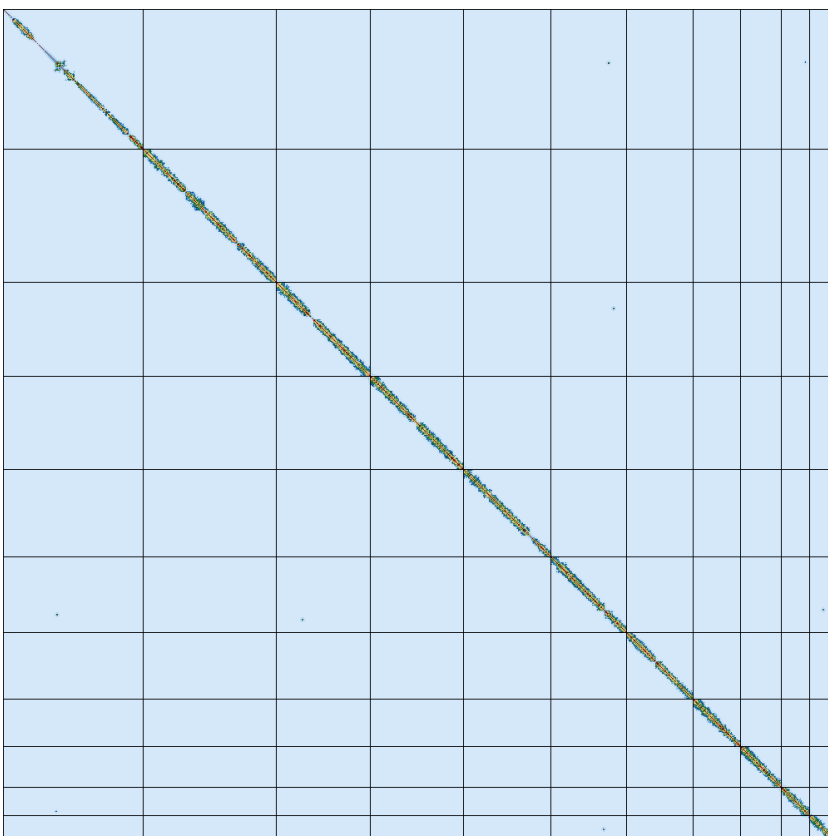
BUSCO: 5.8.0 (euk\_genome\_min, miniprot) / Lineage: insecta\_odb10 (genomes:75, BUSCOs:1367)

BUSCO: 5.8.0 (euk\_genome\_min, miniprot) / Lineage: insecta\_odb10 (genomes:75, BUSCOs:1367)

# HiC contact map of curated assembly

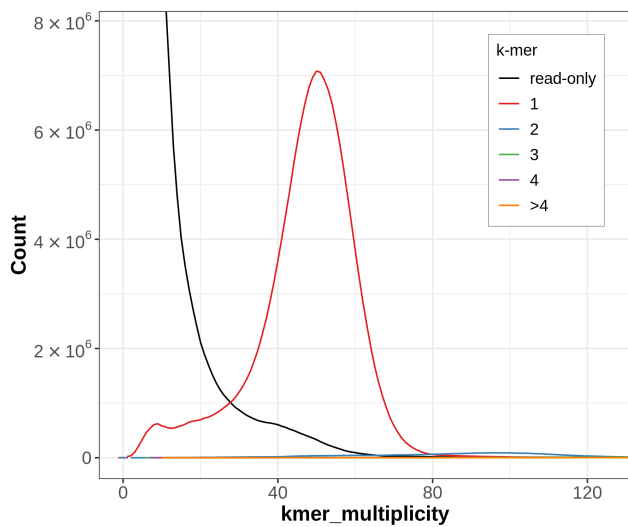


hap1 [\[LINK\]](#)

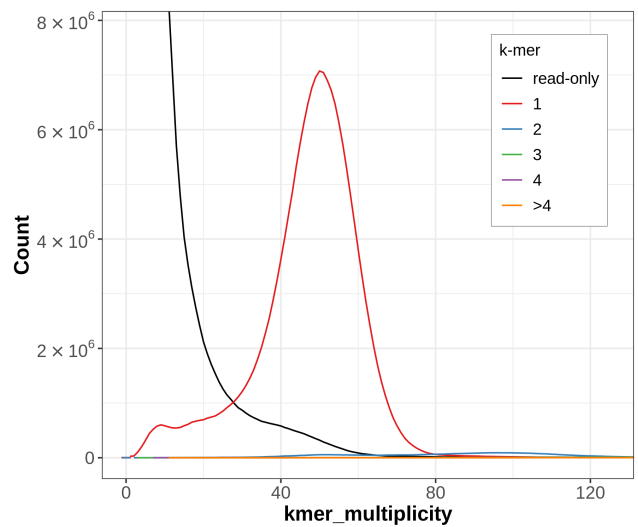


hap2 [\[LINK\]](#)

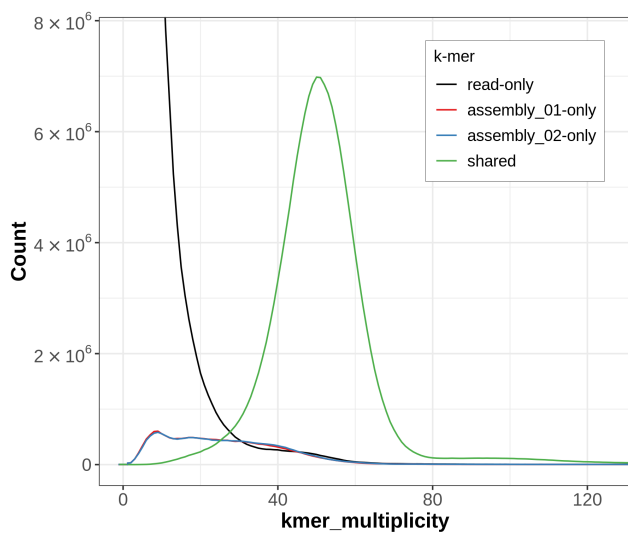
# K-mer spectra of curated assembly



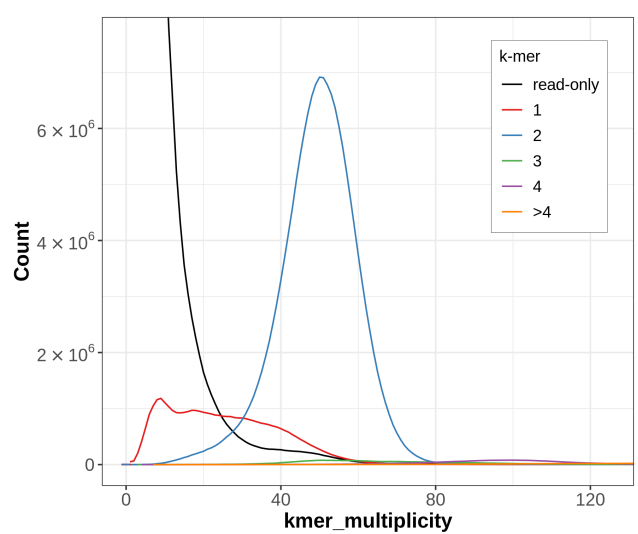
Distribution of k-mer counts per copy numbers found in **KmerCompletenessCnSpectra/assembly\_01** (hap1.)



Distribution of k-mer counts per copy numbers found in **KmerCompletenessCnSpectra/assembly\_02** (hap1.)

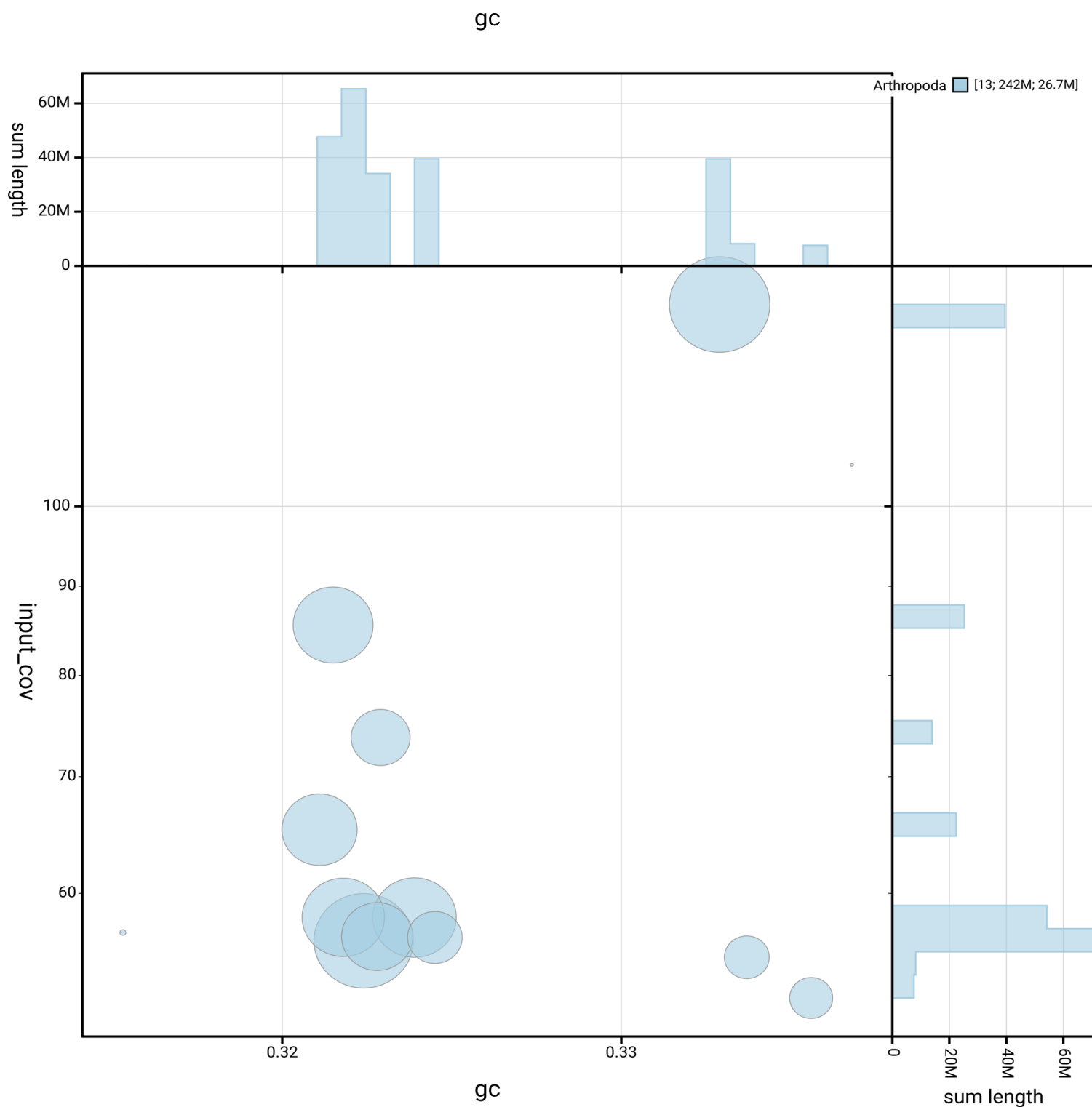


Distribution of k-mer counts coloured by their presence in reads/assemblies

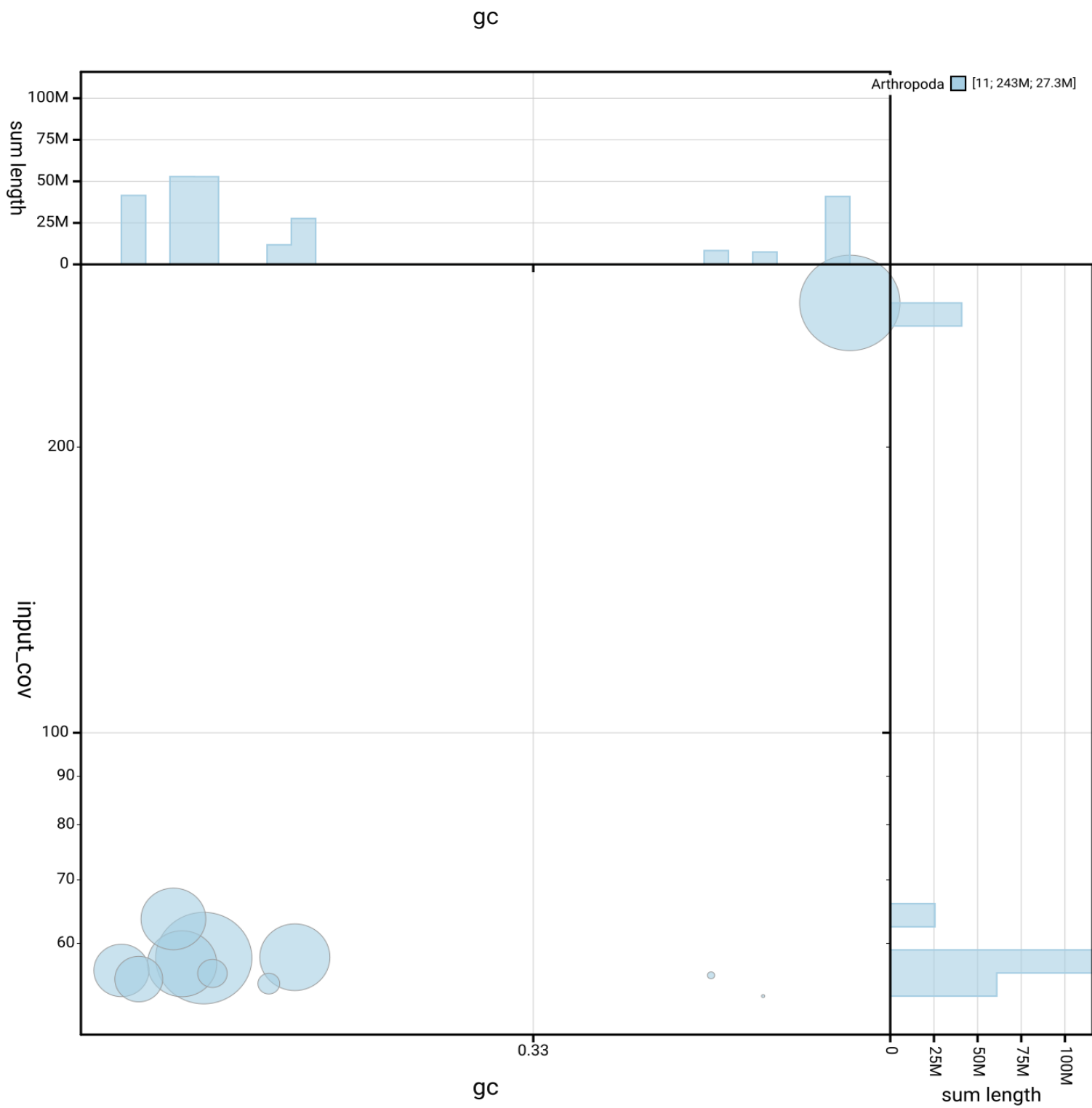


Distribution of k-mer counts per copy numbers found in asm (dipl.)

# 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	HiC
Coverage	34.80X	NA

## Assembly pipeline

- **Hifiasm**
  - |\_ *ver*: Galaxy Version 0.24.0+galaxy0
  - |\_ *key param*: VGP Galaxy workflow VGP3 v 0.2.8
- **purge\_dups**
  - |\_ *ver*: Galaxy Version 1.2.6+galaxy0
  - |\_ *key param*: VGP Galaxy workflow VGP6 v 0.5
- **YaHS**
  - |\_ *ver*: Galaxy Version 1.2a.2+galaxy2
  - |\_ *key param*: VGP Galaxy workflow VGP8 v 1.4

## 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

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