ERGA Assembly Report
v24.10.15

Tags: ERGA-BGE

TxID	2828945
ToLID	**ilHipCypr1**
Species	Hipparchia cypriensis
Class	Insecta
Order	Lepidoptera

Genome Traits	Expected	Observed
Haploid size (bp)	382,535,333	387,821,496
Haploid Number	29 (source: ancestor)	28
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	ZZ

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q65

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

. Kmer completeness value is less than 90 for pri

Curator notes

. Interventions/Gb: 5
. Contamination notes: "33 contaminants (pseudomonadota, bacillota, nematoda) detected with blobtools and removed."
. Other observations: "Curation made 0 cuts in contigs, 1 break at a gap and 1 join. Z identified by alignment to ilHipSeme1.2. Performed diploid curation. Hap2 was incomplete. Put longest, no-gap haps into primary assembly and the rest into alt."
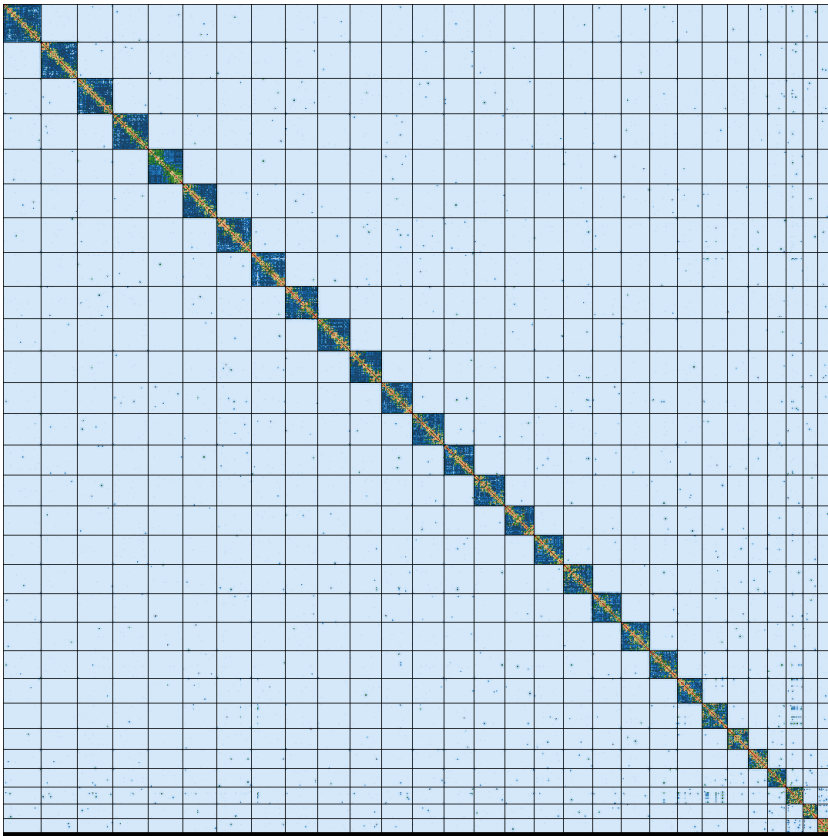
Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	391,457,550	387,821,496
GC %	37.09	36.95
Gaps/Gbp	5.11	2.58
Total gap bp	400	200
Scaffolds	110	54
Scaffold N50	14,412,884	14,456,993
Scaffold L50	13	13
Scaffold L90	25	25
Contigs	112	55
Contig N50	14,412,884	14,456,993
Contig L50	13	13
Contig L90	25	25
QV	62.7713	65.8841
Kmer compl.	67.8475	68.1245
BUSCO sing.	98.2%	98.8%
BUSCO dupl.	0.3%	0.3%
BUSCO frag.	0.3%	0.1%
BUSCO miss.	1.2%	0.8%

Warning! BUSCO versions or lineage datasets are not the same across results:
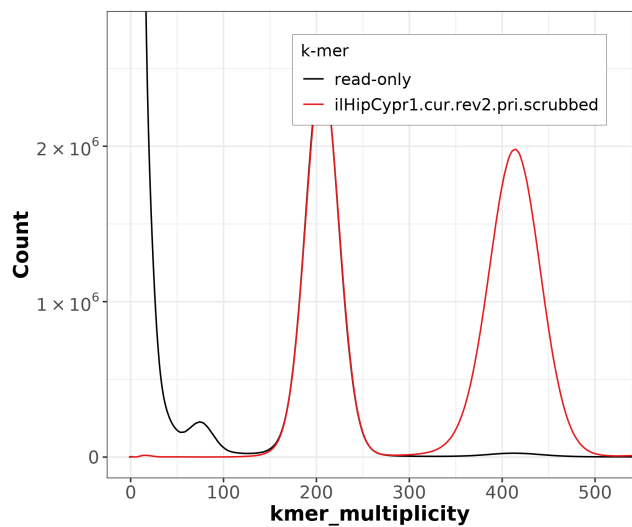BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: lepidoptera_odb10 (genomes:16, BUSCOs:5286)
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: lepidoptera_odb12 (genomes:79, BUSCOs:5760)
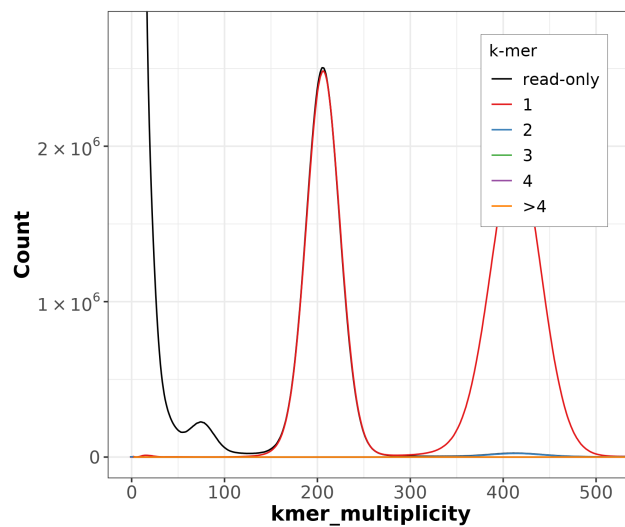
HiC contact map of curated assembly
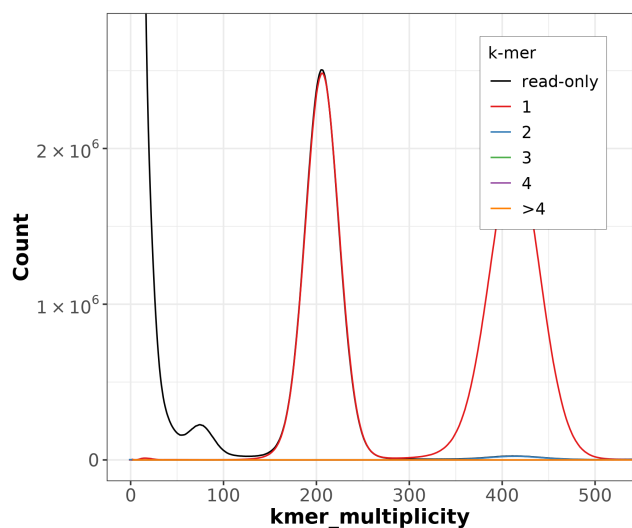

pri [LINK]

K-mer spectra of curated assembly

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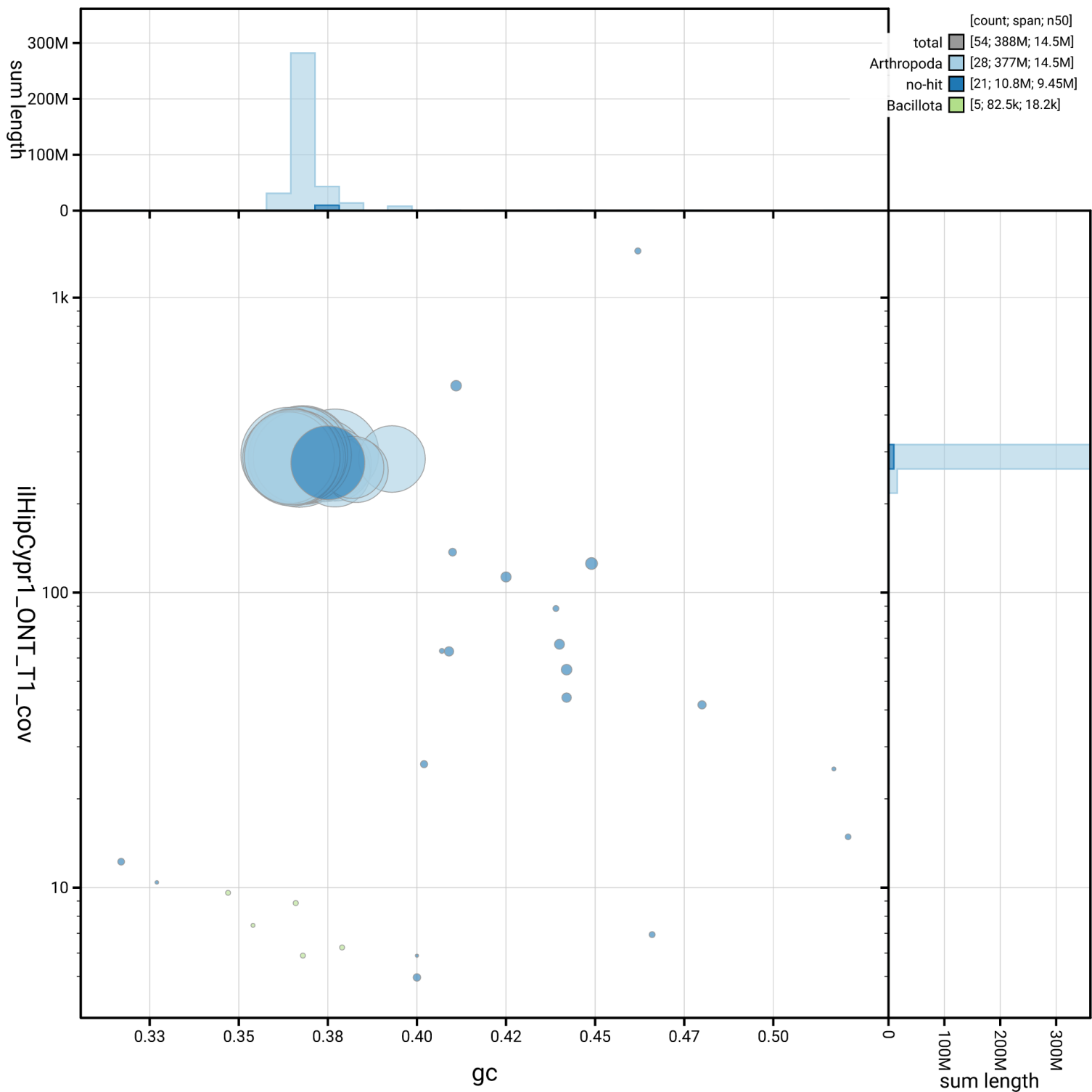

Distribution of k-mer counts per copy numbers found in asm

Distribution of k-mer counts per copy numbers found in asm

Post-curation contamination screening

pri. 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	ONT	Illumina	Omni-C
Coverage	300x	198x	137x

Assembly pipeline

- **Filtlong**
    |_ *ver:* 0.2.1
    |_ *key param:* --min_length 1000 --min_mean_q 80
- **Hifiasm**
    |_ *ver:* 0.24.0
    |_ *key param:* --telo-m AACCT"
- **YaHS**
    |_ *ver:* 1.2a
    |_ *key param:* --no-contig-ec
- **CLAWS pipeline**
    |_ *ver:* 2.3.0
    |_ *key param:* NA
- **Blobtoolkit Nextflow pipeline (latest)**
    |_ *ver:* 0.6
    |_ *key param:* NA
- **FOAM pipeline**
    |_ *ver:* 0.5
    |_ *key param:* NA
- **mitos**
    |_ *ver:* 2.1.3
    |_ *key param:* NA

Curation pipeline

- **GRIT_Rapid**
    |_ *ver:* 2.0
    |_ *key param:* NA
- **PretextViewAI**
    |_ *ver:* 1.0.4
    |_ *key param:* NA

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