ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	597850
ToLID	**iyAntRoge3**
Species	Anthophora rogenhoferi
Class	Insecta
Order	Hymenoptera

Genome Traits	Expected	Observed
Haploid size (bp)	445,419,612	441,476,508
Haploid Number	9 (source: ancestor)	17
Ploidy	1 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 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 Ploidy is different from Expected

. Not 90% of assembly in chromosomes for collapsed

Curator notes

. Interventions/Gb:
. Contamination notes: ""
. Other observations: "The assembly was produced with hifiasm in Hi-C mode, decontaminated with FCS-GX, and haplotigs purged with purge_dups. Scaffolding was performed with YaHS. Mitochondria was assembled with Oatk."

Quality metrics table

| Metrics	Pre-curation collapsed	Curated collapsed
Total bp	442,215,395	441,476,508
GC %	40.41	40.42
Gaps/Gbp	36.18	36.24
Total gap bp	3,200	3,200
Scaffolds	1,085	1,085
Scaffold N50	16,560,000	17,437,000
Scaffold L50	9	10
Scaffold L90	350	350
Contigs	1,101	1,101
Contig N50	10,497,625	10,497,625
Contig L50	13	13
Contig L90	366	366
QV	65.2913	65.284
Kmer compl.	91.9202	91.9158
BUSCO sing.	98.7%	99.1%
BUSCO dupl.	0.5%	0.2%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.6%	0.6%

BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: hymenoptera_odb10 (genomes:40, BUSCOs:5991)
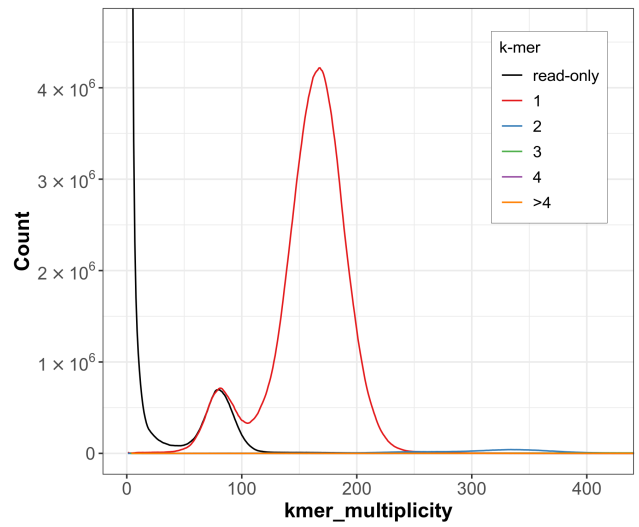
HiC contact map of curated assembly
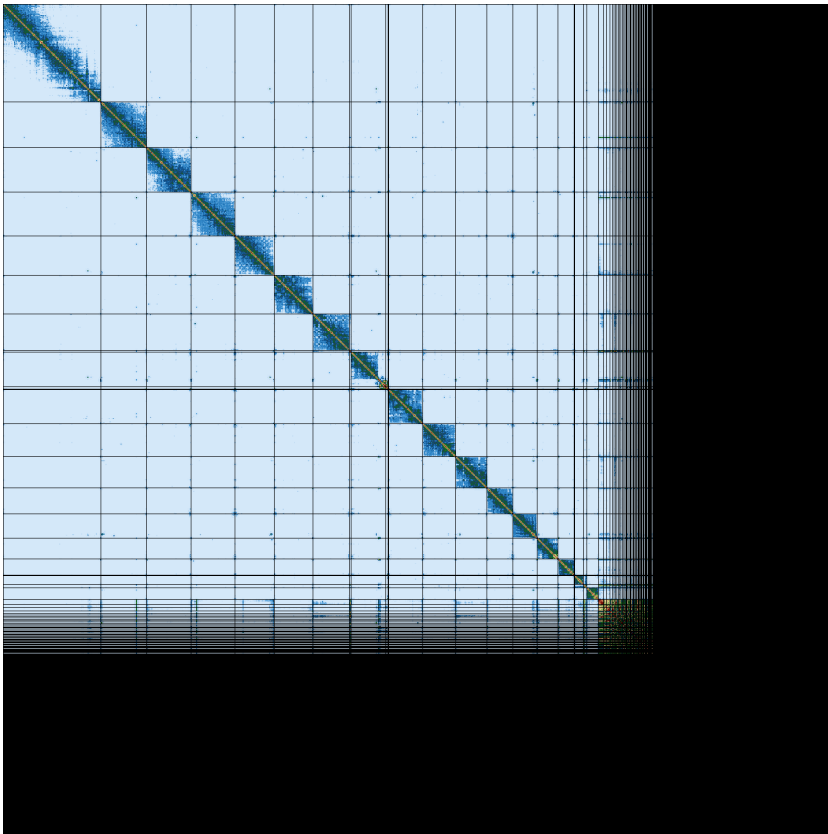
collapsed [LINK]
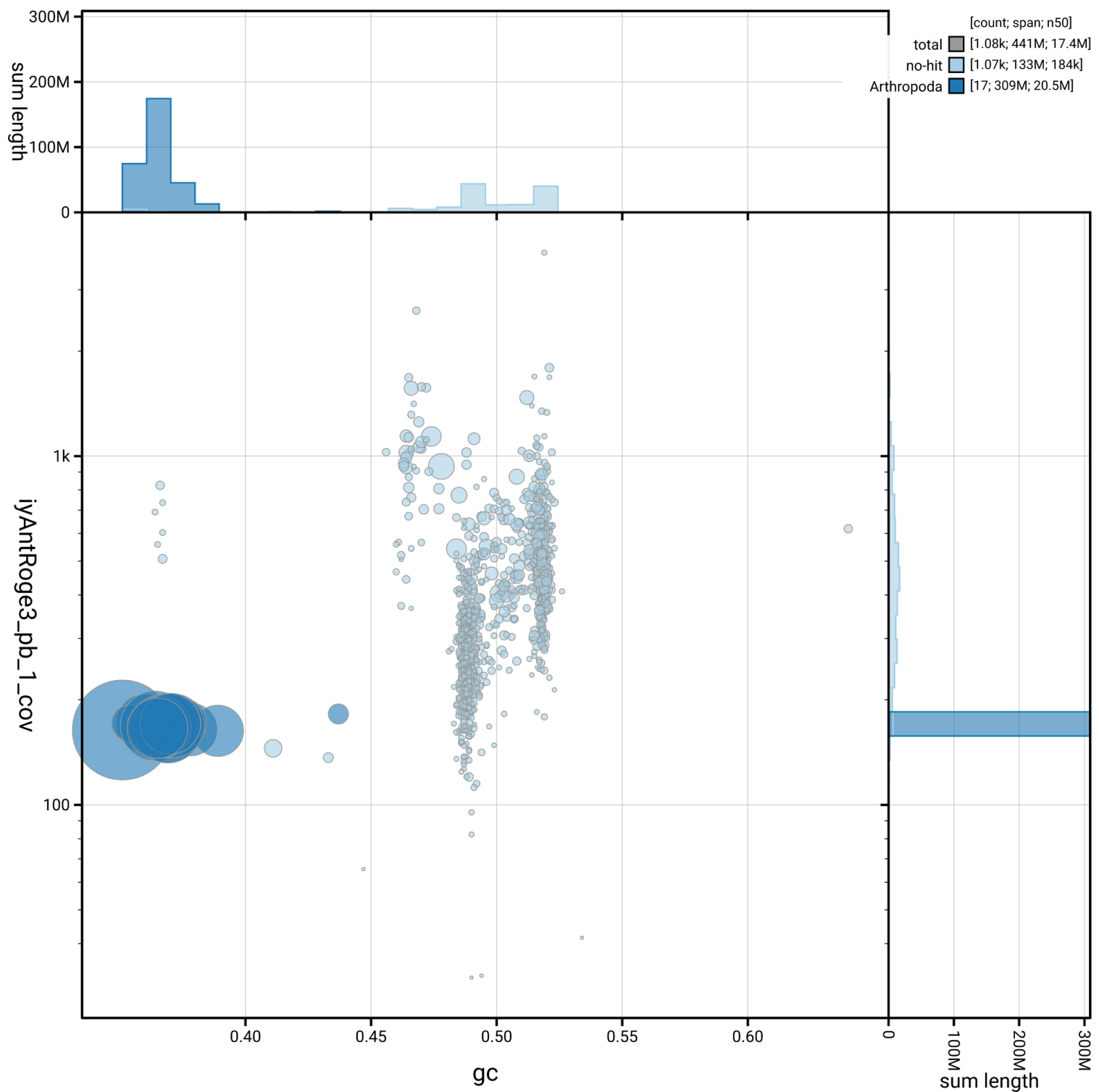
K-mer spectra of curated assembly
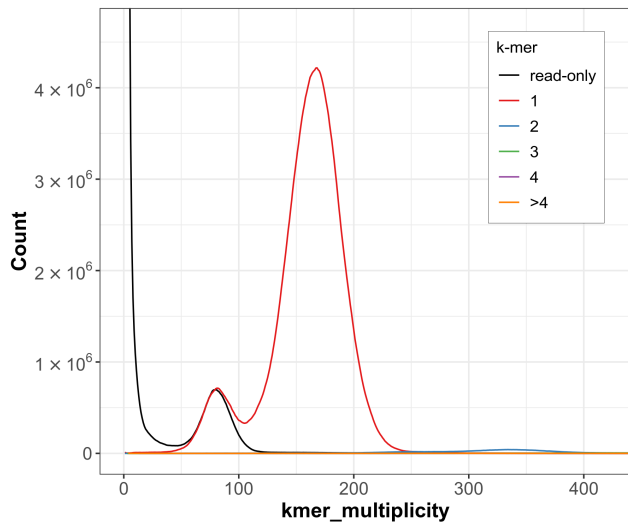
Distribution of k-mer counts per copy
numbers found in asm

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

Post-curation contamination screening

collapsed. 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	PacBio HiFi	Arima HiC v2
Coverage	50x	27x

Assembly pipeline

- **hifiasm-hic**
  |_ *ver:* 0.25.0-r726
  |_ *key param:* --h1
  |_ *key param:* --h2
- **purge_dups**
  |_ *ver:* 1.2.5
  |_ *key param:* NA
- **YaHS**
  |_ *ver:* 1.2a.2
  |_ *key param:* NA
- **NBIS/Earth-Biogenome-Project-pilot**
  |_ *ver:* 99c8937
  |_ *key param:* NA
- **sanger-tol/blobtoolkit**
  |_ *ver:* 0.8.0
  |_ *key param:* NA
- **Oatk**
  |_ *ver:* 1.0
  |_ *key param:* -m hymenoptera.fam

Curation pipeline

- **sanger-tol/curationpretext**
  |_ *ver:* 1.4.2
  |_ *key param:* NA
- **sanger-tol/agp-tpf-utils**
  |_ *ver:* 1.2.3
  |_ *key param:* NA

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