

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1662264
ToLID	<b>qqLevThor3</b>
Species	Leviellus thorelli
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	2,048,663,629	2,190,932,837
Haploid Number	12 (source: ancestor)	13
Ploidy	2 (source: ancestor)	2
Sample Sex	female	female

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.8.Q51

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

- . Observed Haploid Number is different from Expected

### Curator notes

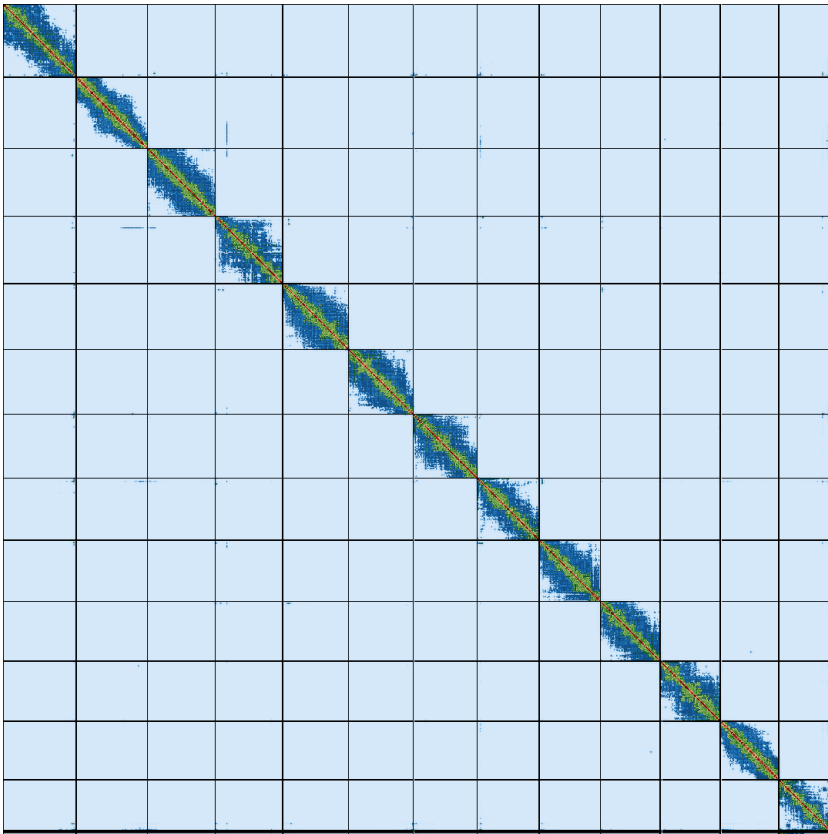
- . Interventions/Gb: 26
- . Contamination notes: "Scaffold\_22 (1.5 MBases) was removed from the yahs scaffolded assembly because it was identified as pseudomonadota (which include symbionts of many arthropod species). The contaminant was removed from the yahs scaffolded assembly and is not present in the curated pretext which was shared."
- . Other observations: "The HiC signal along the diagonal is quite strong. We were able to place several scaffolds to many of the super scaffolds but we found it very difficult to localize most of them. The sex of the specimen was set to -female- in our lims system. We could find the sex chromosome in the assembly"

# Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	2,192,434,344	2,190,932,837
GC %	34.31	34.31
Gaps/Gbp	356.68	369.25
Total gap bp	156,400	161,800
Scaffolds	149	130
Scaffold N50	162,679,147	167,117,025
Scaffold L50	6	7
Scaffold L90	12	12
Contigs	931	939
Contig N50	5,371,768	5,371,768
Contig L50	119	119
Contig L90	422	422
QV	51.5219	51.5224
Kmer compl.	95.3695	95.2763
BUSCO sing.	93.5%	93.8%
BUSCO dupl.	2.7%	2.4%
BUSCO frag.	1.0%	0.9%
BUSCO miss.	2.8%	2.9%

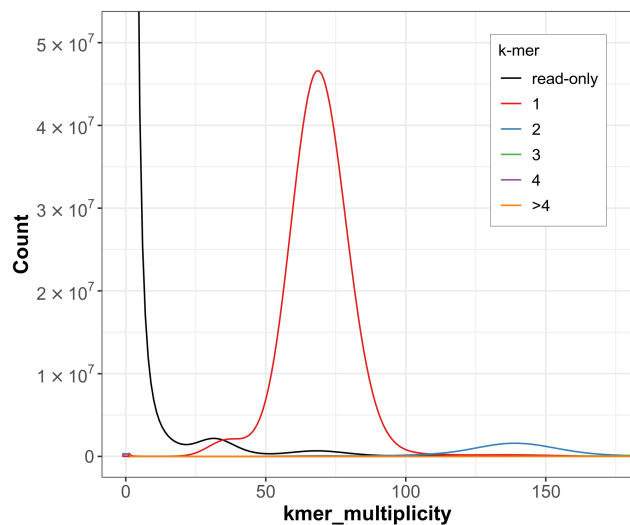
BUSCO: 5.4.0 (euk\_genome\_met, metaeuk) / Lineage: metazoa\_odb10 (genomes:65, BUSCOs:954)

# HiC contact map of curated assembly

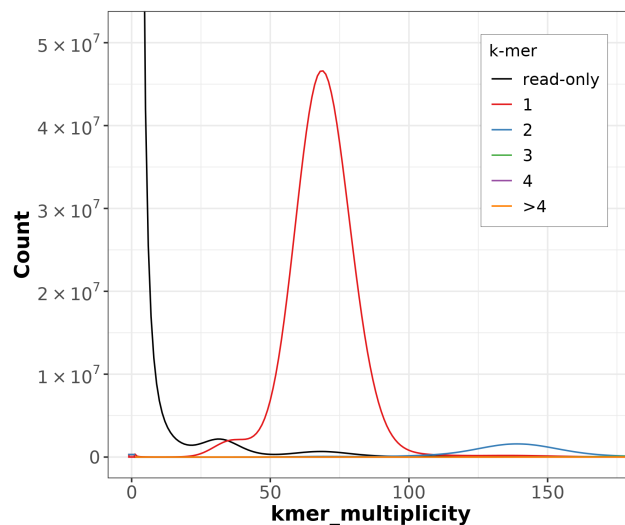


collapsed [\[LINK\]](#)

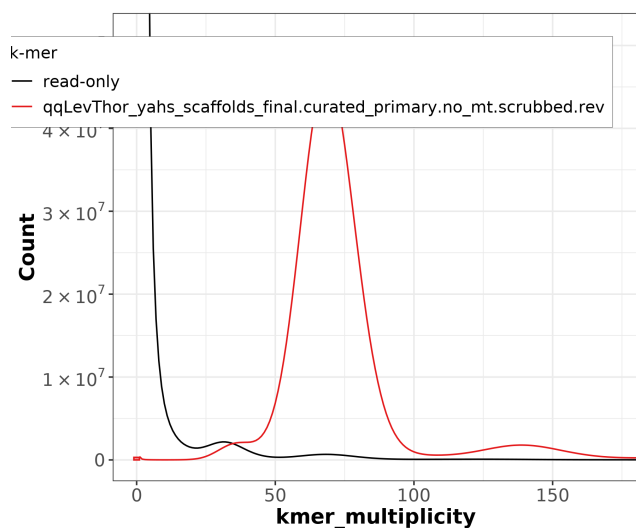
# K-mer spectra of curated assembly



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

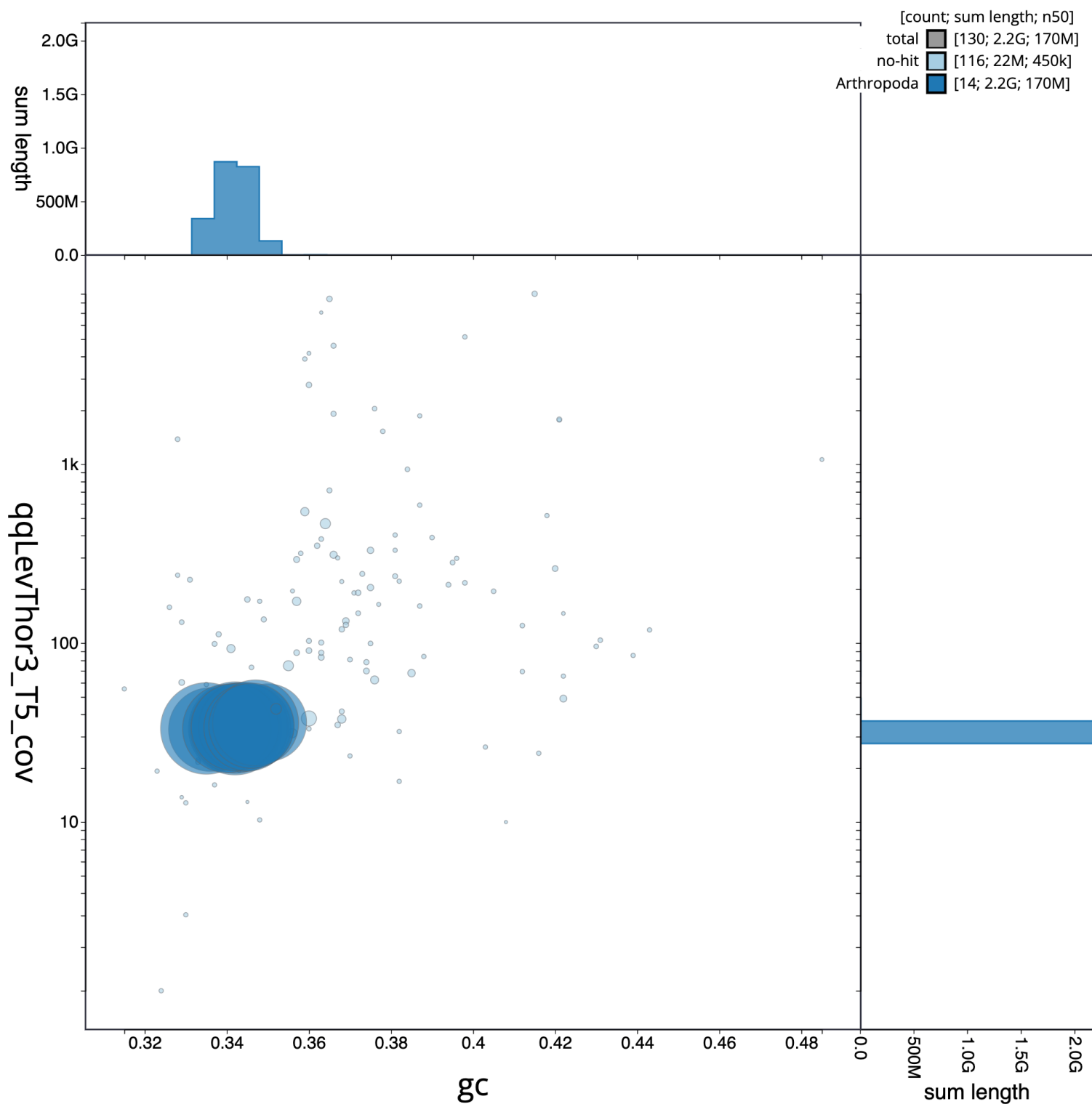


Distribution of k-mer counts per copy numbers found in asm



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

# 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	ONT	Illumina	OmniC
Coverage	40x	62x	125x

# Assembly pipeline

- **Trim\_galore**
  - |\_ *ver*: 0.6.7
  - |\_ *key param*: --gzip
  - |\_ *key param*: =q 20
  - |\_ *key param*: --paired
  - |\_ *key param*: retain\_unpaired
- **Filtlong**
  - |\_ *ver*: 0.2.1
  - |\_ *key param*: NA
- **nextdenovo**
  - |\_ *ver*: 2.5.0
  - |\_ *key param*: NA
- **hypo**
  - |\_ *ver*: 1.0.3
  - |\_ *key param*: NA
- **purge\_dups**
  - |\_ *ver*: 1.2.6
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.2a
  - |\_ *key param*: NA

# Curation pipeline

- **PretextView**
  - |\_ *ver*: 0.2.5
  - |\_ *key param*: NA
- **GRIT\_Rapid**
  - |\_ *ver*: 2.0
  - |\_ *key param*: NA

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