

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2066575
ToLID	<b>qqLycPrae</b>
Species	Lycosa praegrandis
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	2,631,755,056	2,580,375,041
Haploid Number	12 (source: ancestor)	12
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.8.Q66

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

- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for pri
- . Assembly length loss > 3% for pri

### Curator notes

- . Interventions/Gb: None
- . Contamination notes: "No presence of contaminants."
- . Other observations: "Hard to determine the sex or identify sex chromosomes. Earlier papers (from the 1950's) suggest a 22A+X1X2 configuration, but species in this group could have from 1 to 10 X chromosomes. Most Lycosidae have a X1X2/X1X1X2X2 configuration. Identifying the sex chromosomes for this Genus requires lab work, and can't be done at this stage."

# Quality metrics table

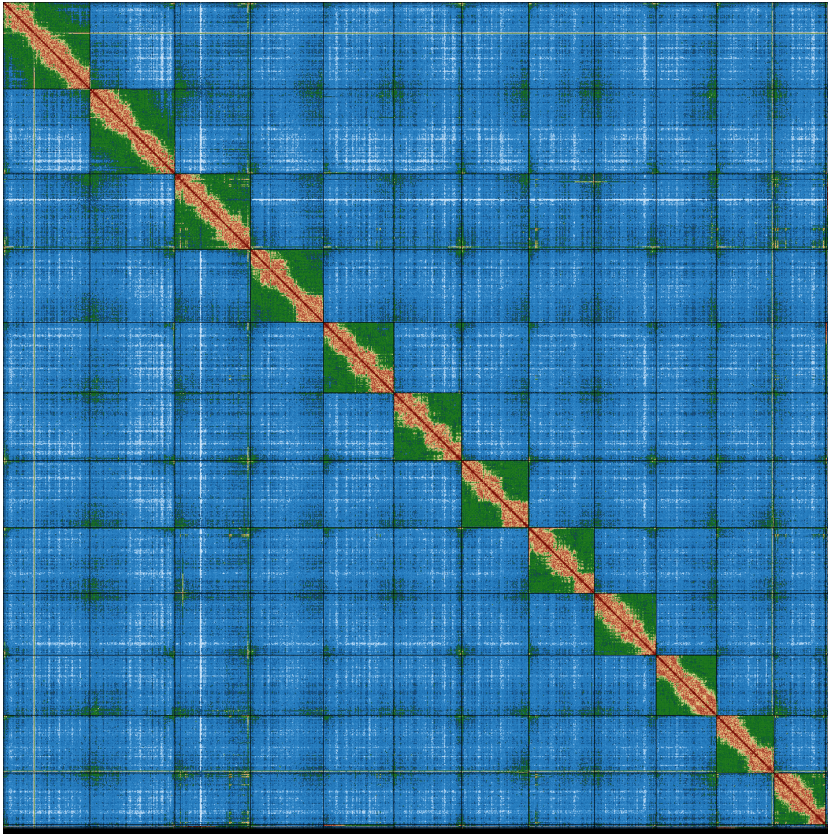
Metrics	Pre-curation pri	Curated pri
Total bp	2,669,554,149	2,580,375,041
GC %	31.69	31.67
Gaps/Gbp	99.27	107.35
Total gap bp	53,000	55,400
Scaffolds	152	131
Scaffold N50	216,947,197	213,744,341
Scaffold L50	6	6
Scaffold L90	11	11
Contigs	417	408
Contig N50	24,969,355	25,468,180
Contig L50	29	28
Contig L90	125	120
QV	66.6874	66.0
Kmer compl.		82.35
BUSCO sing.	96.1%	90.4%
BUSCO dupl.	0.1%	5.0%
BUSCO frag.	0.7%	0.2%
BUSCO miss.	3.2%	4.4%

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

BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: basidiomycota\_odb10 (genomes:133, BUSCOs:1764)

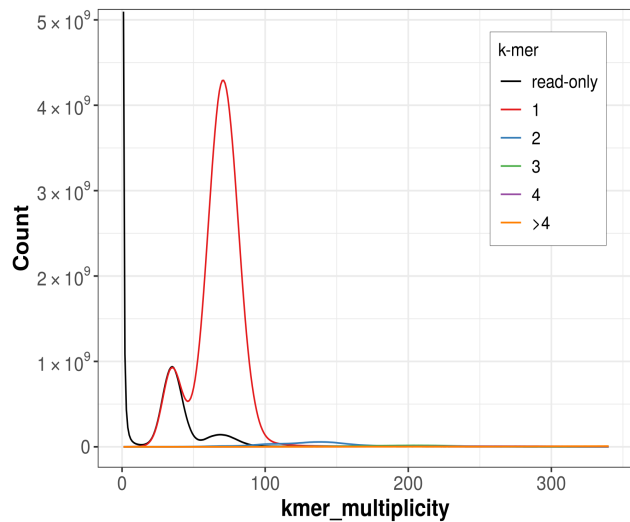
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: arachnida\_odb10 (genomes:10, BUSCOs:2934)

# HiC contact map of curated assembly

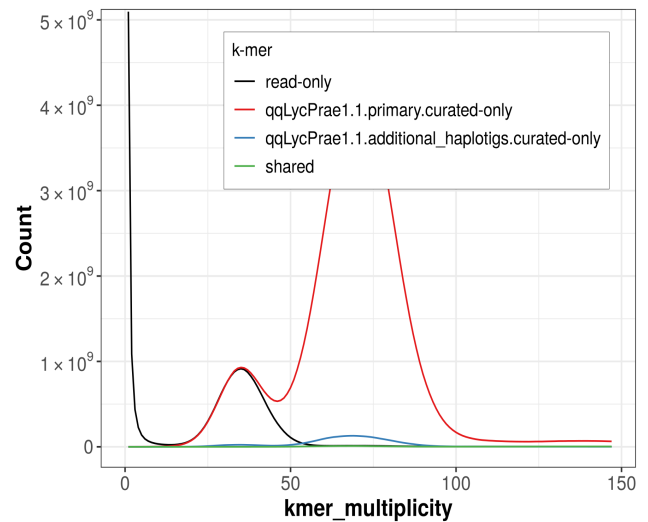


pri [\[LINK\]](#)

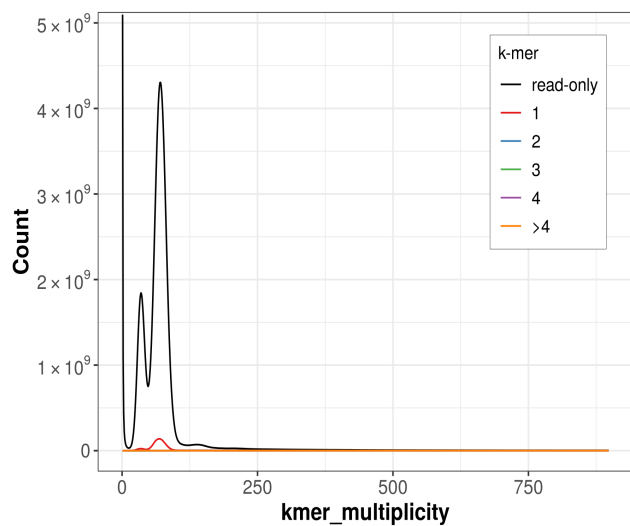
# K-mer spectra of curated assembly



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

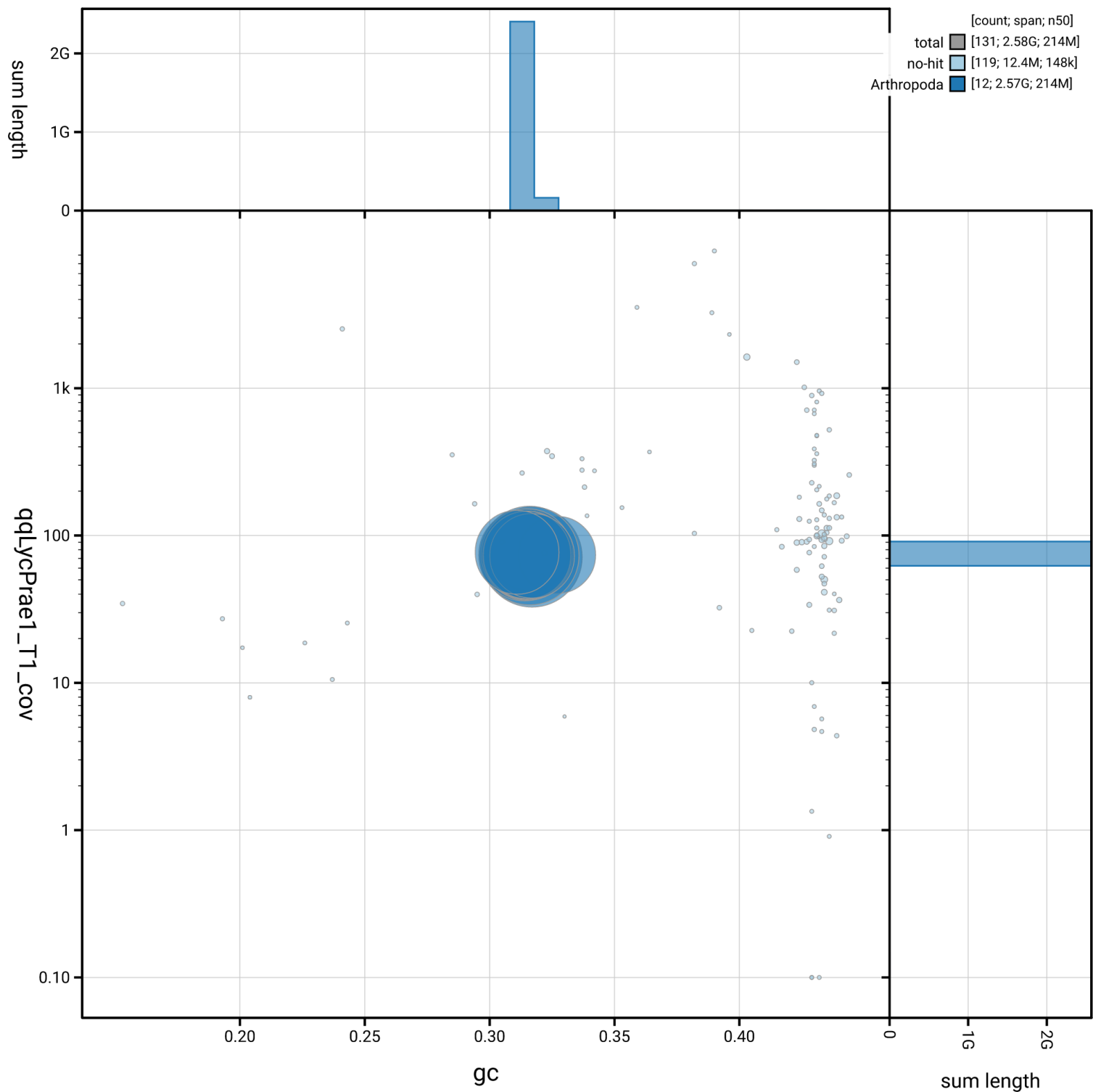


Distribution of k-mer counts coloured by their presence in reads/assemblies



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	HiFi	Bionano	OmniC
Coverage	71x	NA	134x

# Assembly pipeline

- **Hifiasm**
  - |\_ *ver*: 0.20.0-r639
  - |\_ *key param*: NA
- **purge\_dups**
  - |\_ *ver*: 1.2.5
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.2.2
  - |\_ *key param*: NA

# Curation pipeline

- **sanger-tol/curationpretext**
  - |\_ *ver*: v1.5.0-g5fd8e6e
  - |\_ *key param*: NA
- **Nextflow**
  - |\_ *ver*: 25.04.2
  - |\_ *key param*: NA
- **pretextmap**
  - |\_ *ver*: 0.1.9
  - |\_ *key param*: NA
- **HiGlass**
  - |\_ *ver*: 0.10.4
  - |\_ *key param*: NA
- **PretextViewAI**
  - |\_ *ver*: 1.0.5
  - |\_ *key param*: NA

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