

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2068848
ToLID	<b>qqArtNeph1</b>
Species	Artema nephilit
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	1,485,957,015	1,509,413,142
Haploid Number	11 (source: ancestor)	17
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.8.Q69

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

- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for collapsed

### Curator notes

- . Interventions/Gb: None
- . Contamination notes: "Wolbachia endosymbiont removed by FCS-GX"
- . Other observations: "There are some repeats with half-coverage, but I don't find a corresponding haplotig, or if the repeat should be collapsed."

# Quality metrics table

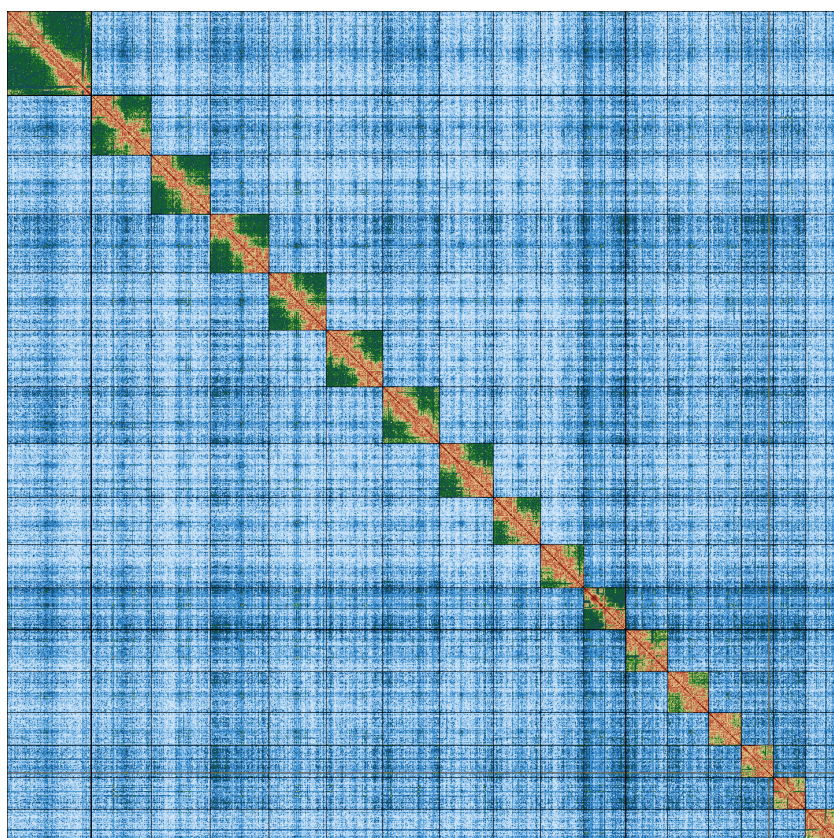
Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,527,716,421	1,509,413,142
GC %	41.58	41.57
Gaps/Gbp	39.27	44.39
Total gap bp	12,000	13,400
Scaffolds	101	78
Scaffold N50	97,804,034	102,440,379
Scaffold L50	7	7
Scaffold L90	16	15
Contigs	161	145
Contig N50	29,532,000	29,532,000
Contig L50	16	16
Contig L90	49	48
QV	66.1	69.4
Kmer compl.	88.47	88.18
BUSCO sing.	92.3%	92.7%
BUSCO dupl.	5.1%	4.9%
BUSCO frag.	0.6%	0.2%
BUSCO miss.	2.0%	2.1%

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

BUSCO: 5.8.3 (euk\_genome\_min, miniprot) / Lineage: arachnida\_odb10 (genomes:10, BUSCOs:2934)

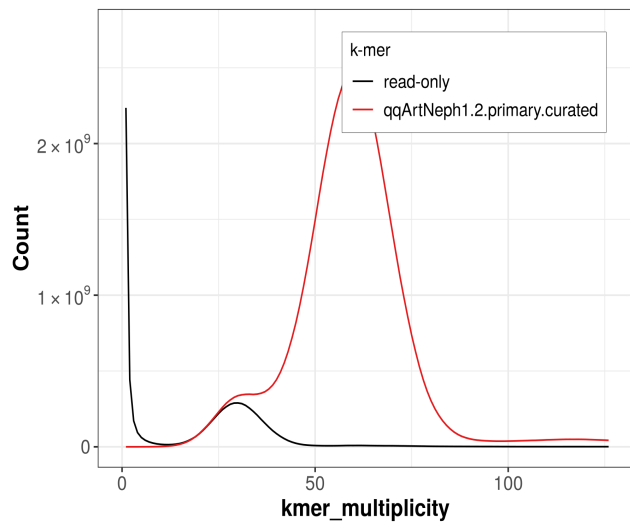
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: arachnida\_odb10 (genomes:10, BUSCOs:2934)

# HiC contact map of curated assembly

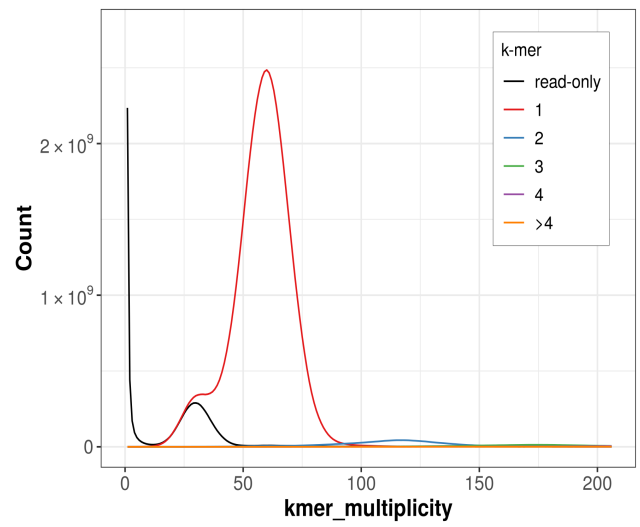


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

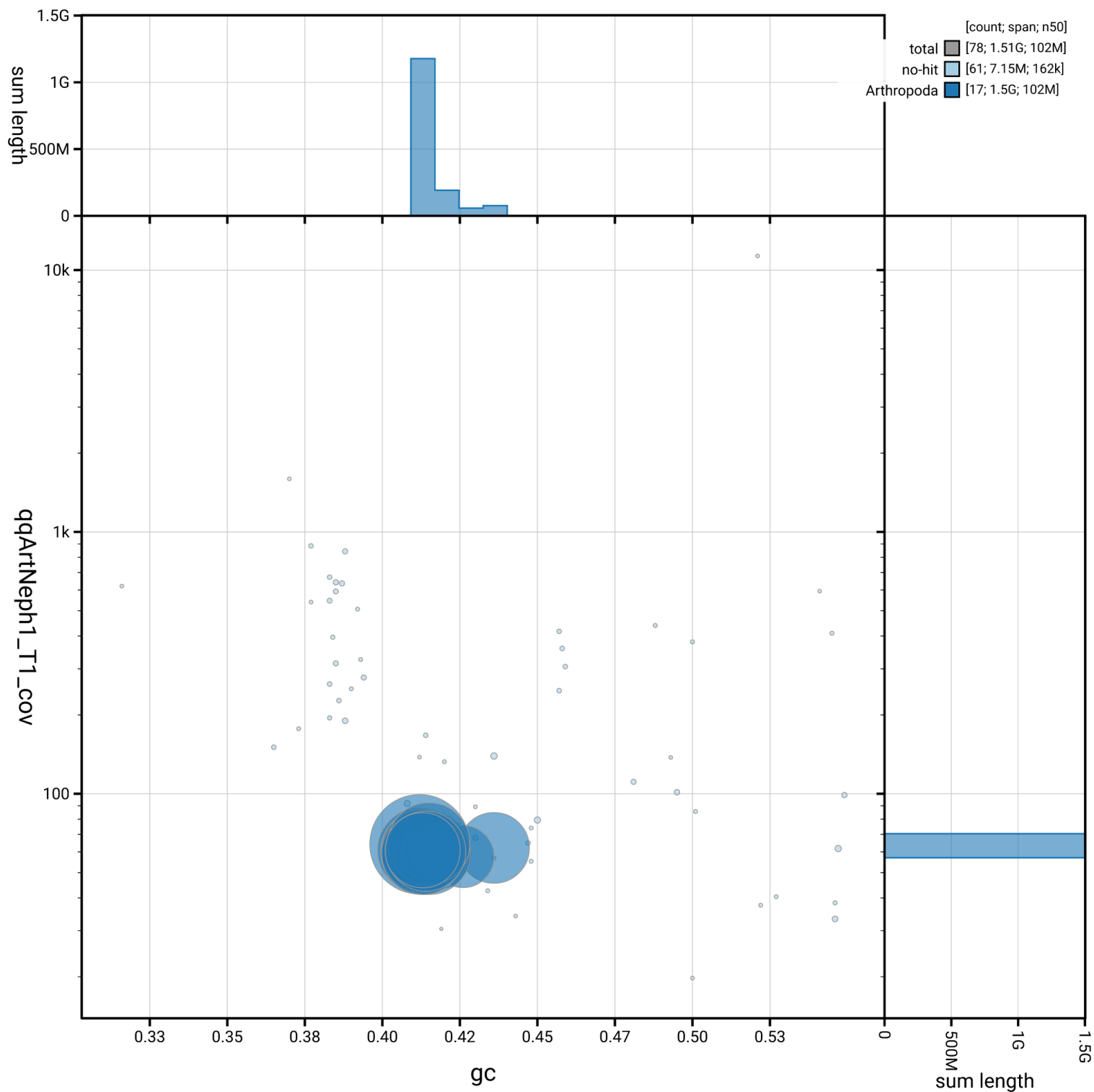


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

# 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	hifi	hic
Coverage	60x	235x

# Assembly pipeline

- **NBIS/Earth-Biogenome-Project-pilot**
  - |\_ *ver*: commit:855f10a4de2cbfbb20122d2afce4ea6233c1336c
  - |\_ *key param*: NA

# Curation pipeline

- **Sanger-tol/curationpretext**
  - |\_ *ver*: 1.5.0
  - |\_ *key param*: NA
- **PretextView**
  - |\_ *ver*: 1.0.4
  - |\_ *key param*: NA
- **mahesh-panchal/sanger-tol-ear**
  - |\_ *ver*: commit: 4d9020a088
  - |\_ *key param*: NA

Submitter: Mahesh Binzer-Panchal  
Affiliation: SciLifeLab

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