

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

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

Genome Traits	Expected	Observed
Haploid size (bp)	1,485,957,015	1,505,308,508
Haploid Number	11 (source: ancestor)	17
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	X1X2

## 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
- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for collapsed

## Curator notes

- . Interventions/Gb: 83
- . Contamination notes: "Wolbachia endosymbiont removed by FCS-GX"
- . Other observations: "Mitohifi failed to assemble mtDNA. I was unable to assign X1X2 chromosomes through wga or synteny with Parasteatoda\_tepidariorum or Dysdera\_tilosensis.

<https://bmcecoevol.biomedcentral.com/articles/10.1186/s12862-021-01750-8> shows X1X2, and 17 chr total."

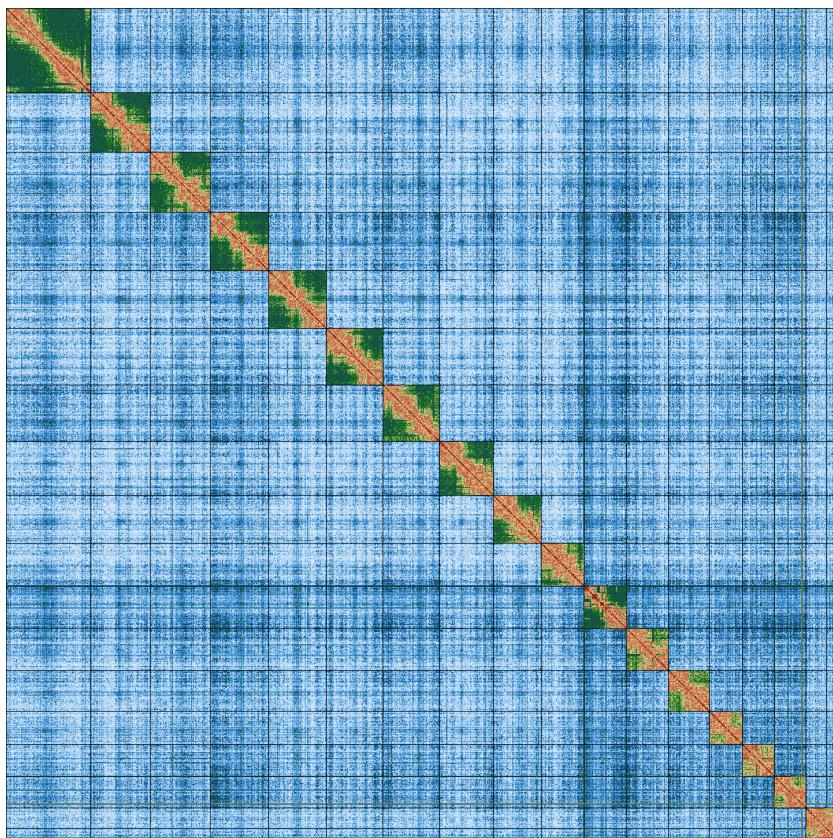
# Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,527,716,421	1,505,308,508
GC %	41.58	41.55
Gaps/Gbp	39.27	60.45
Total gap bp	12,000	18,200
Scaffolds	101	43
Scaffold N50	97,804,034	101,994,854
Scaffold L50	7	7
Scaffold L90	16	15
Contigs	161	134
Contig N50	29,532,000	29,532,000
Contig L50	16	16
Contig L90	49	49
QV	66.1	69.4
Kmer compl.	88.47	88.15
BUSCO sing.	92.3%	92.7%
BUSCO dupl.	5.1%	4.8%
BUSCO frag.	0.6%	0.2%
BUSCO miss.	2.0%	2.2%

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

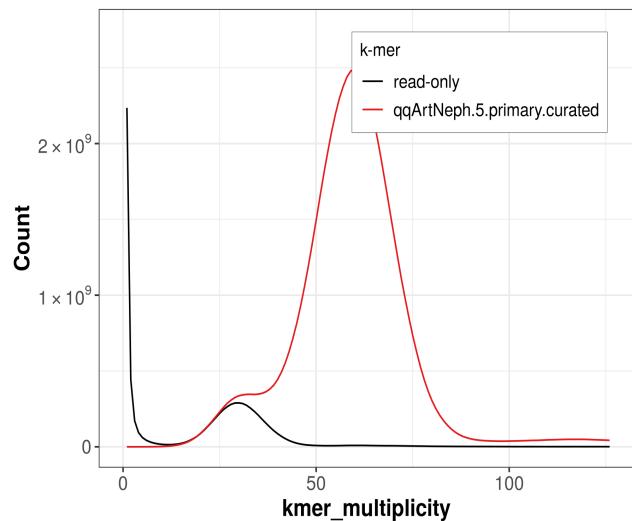
BUSCO: 5.8.3 (euk\_genome\_min, miniprot) / Lineage: arachnida\_odb10 (genomes:10, BUSCOs:2934)  
 BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: arachnida\_odb10 (genomes:10, BUSCOs:2934)

# HiC contact map of curated assembly

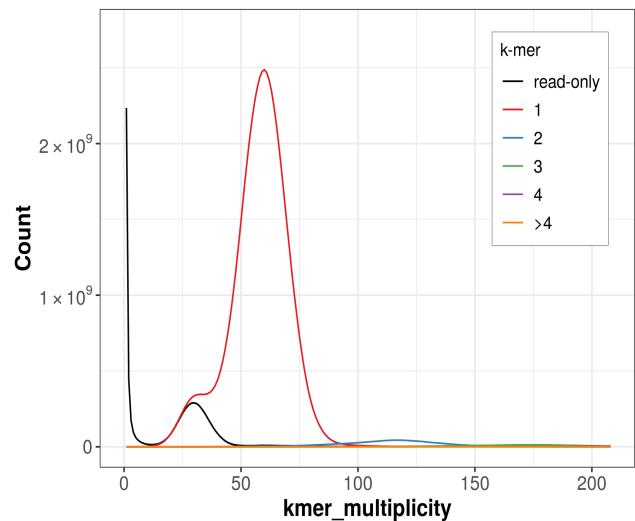


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

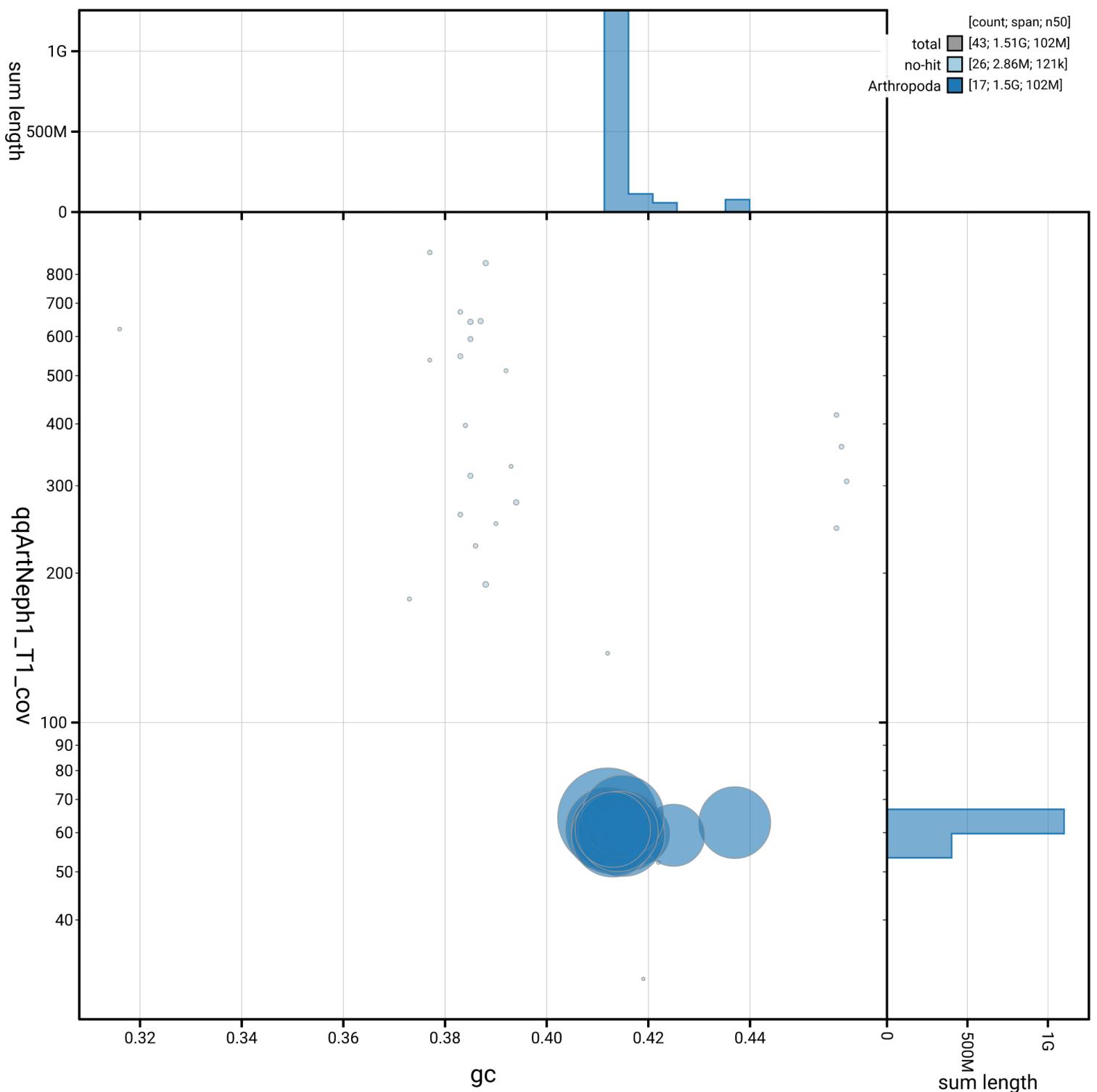


Distribution of k-mer counts coloured by their presence in reads/assemblies



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
- **Hifiasm**
  - |\_ ver: 0.25.0-r726
  - |\_ key param: NA
- **purge\_dups**
  - |\_ ver: 1.2.5
  - |\_ key param: NA
- **YaHS**
  - |\_ ver: 1.2a.1
  - |\_ key param: NA

## Curation pipeline

- **Sanger-tol/curationpretext**
  - |\_ ver: 1.5.0
  - |\_ key param: NA
- **PretextView**
  - |\_ ver: 1.0.4
  - |\_ key param: NA
- **sanger-tol/agp-tpf-utils**
  - |\_ ver: commit: 35ea45dbcd8f3ece7a91104e5813541b55beb2ff
  - |\_ key param: NA
- **mahesh-panchal/sanger-tol-ear**
  - |\_ ver: commit: 4d9020a088
  - |\_ key param: NA

Submitter: Mahesh Binzer-Panchal

Affiliation: SciLifeLab

Date and time: 2025-11-27 09:31:13 CET