

# ERGA Assembly Report

v24.04.03\_beta

Tags: ATLASea[INVALID TAG]

|         |                       |
|---------|-----------------------|
| TxID    | 672921                |
| ToLID   | <b>tnTubPoly1.1</b>   |
| Species | Tubulanus polymorphus |
| Class   | Palaeonemertea        |
| Order   | Tubulaniformes        |

| Genome Traits     | Expected             | Observed    |
|-------------------|----------------------|-------------|
| Haploid size (bp) | 281,666,767          | 267,932,892 |
| Haploid Number    | 2 (source: ancestor) | 12          |
| Ploidy            | 2 (source: ancestor) | 2           |
| Sample Sex        | unknown              | unknown     |

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q48

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

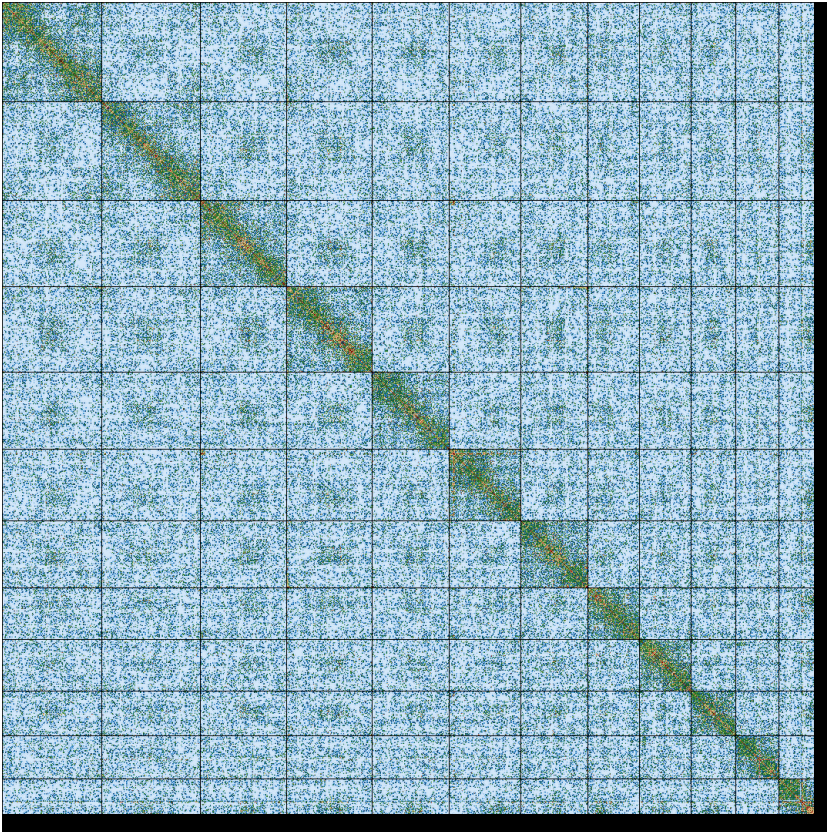
- . Interventions/Gb: None
- . Contamination notes: "None"
- . Other observations: "None"

## Quality metrics table

| Metrics      | Pre-curation collapsed | Curated collapsed |
|--------------|------------------------|-------------------|
| Total bp     | 267,933,645            | 267,932,892       |
| GC %         | 37.69                  | 37.69             |
| Gaps/Gbp     | 149.29                 | 253.79            |
| Total gap bp | 4,000                  | 9,600             |
| Scaffolds    | 124                    | 81                |
| Scaffold N50 | 16,924,479             | 24,873,478        |
| Scaffold L50 | 5                      | 5                 |
| Scaffold L90 | 12                     | 11                |
| Contigs      | 164                    | 149               |
| Contig N50   | 9,529,141              | 9,529,141         |
| Contig L50   | 11                     | 11                |
| Contig L90   | 34                     | 36                |
| QV           | 48.7773                | 48.8056           |
| Kmer compl.  | 81.3228                | 81.3225           |
| BUSCO sing.  | 97.6%                  | 97.6%             |
| BUSCO dupl.  | 0.4%                   | 0.4%              |
| BUSCO frag.  | 1.6%                   | 1.6%              |
| BUSCO miss.  | 0.4%                   | 0.4%              |

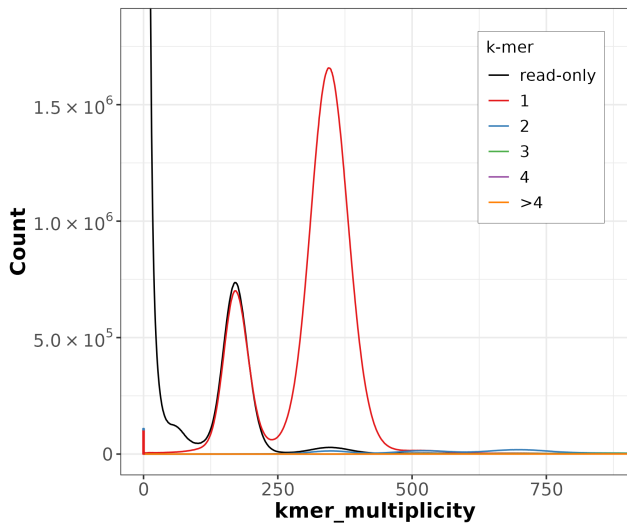
BUSCO 5.4.3 Lineage: eukaryota\_odb10 (genomes:70, BUSCOs:255)

# HiC contact map of curated assembly

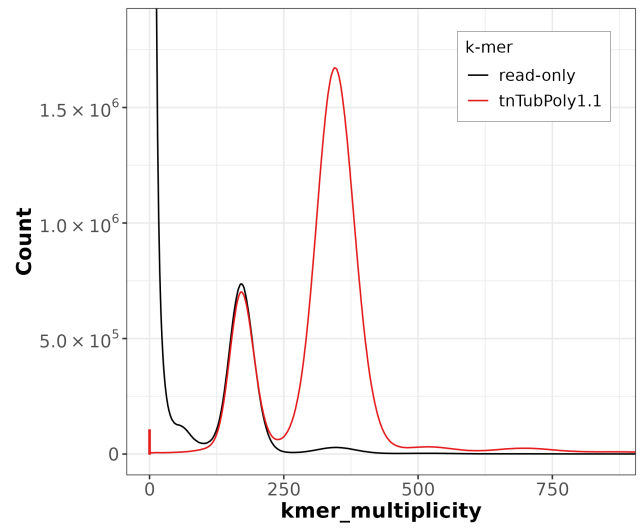


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

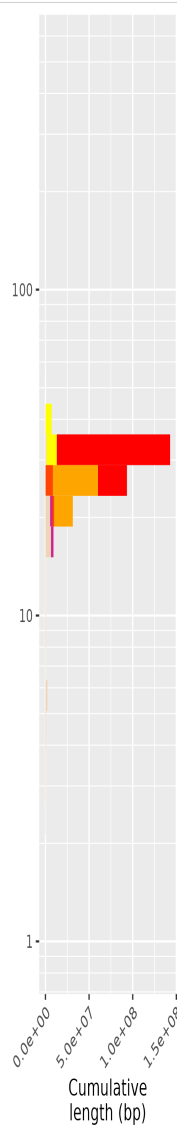
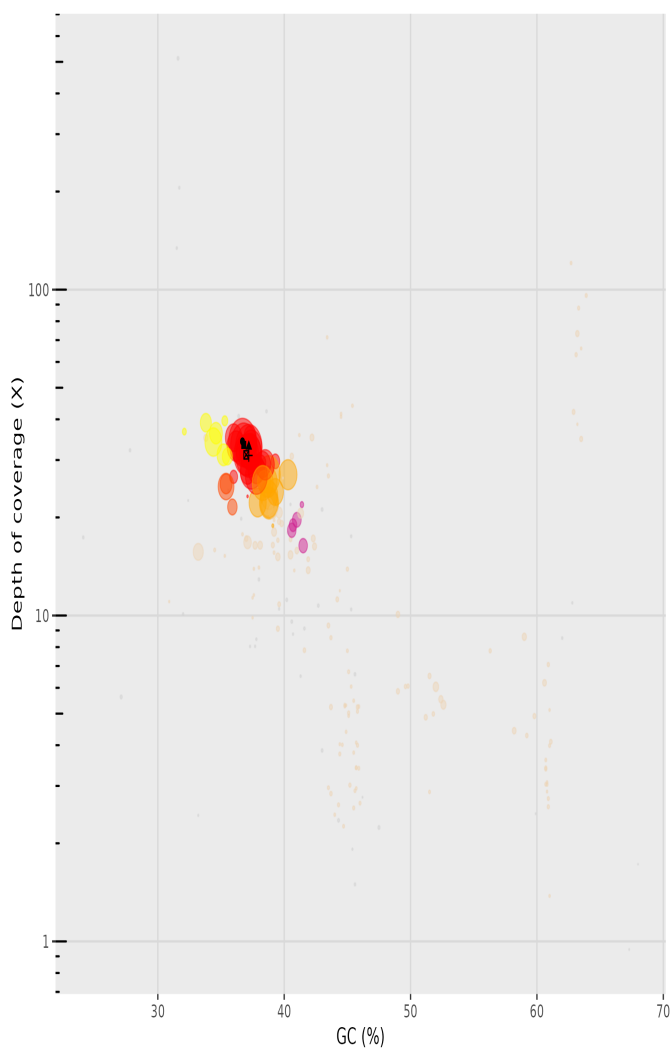
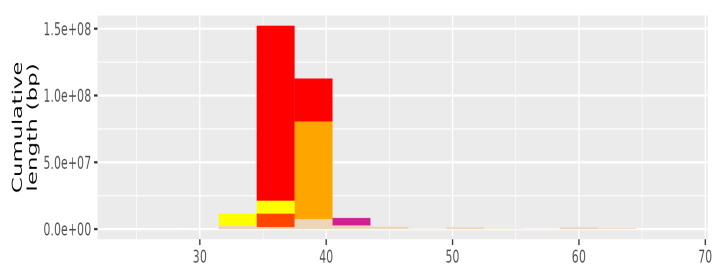


Distribution of k-mer counts per copy numbers found in asm



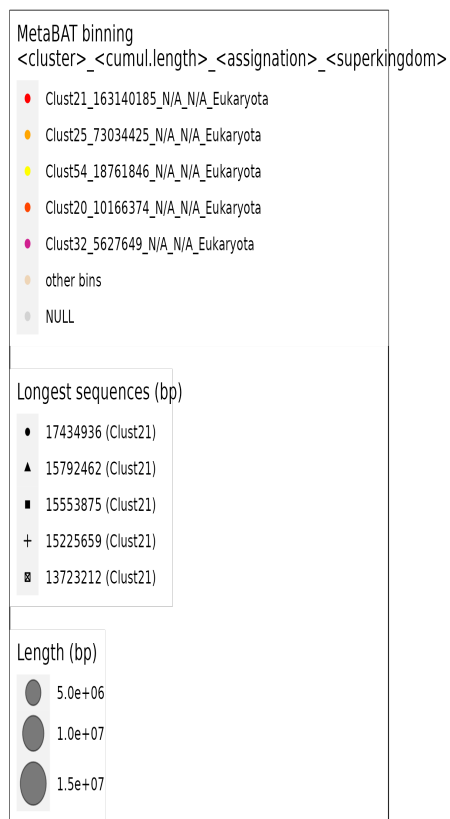
Distribution of k-mer counts coloured by their presence in reads/assemblies

# Post-curation contamination screening



## Decap Summary Graph

(45 0X contigs have been hidden)



**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 | ONT  |
|----------|-------------|------|
| Coverage | 36X         | 478X |

# Assembly pipeline

- **Hifiasm**
  - |\_ *ver:* 0.19.5-r593
  - |\_ *key param:* NA
- **purge\_dups**
  - |\_ *ver:* 1.2.5
  - |\_ *key param:* NA
- **yahs**
  - |\_ *ver:* 1.2
  - |\_ *key param:* NA

# Curation pipeline

- **Hifiasm**
  - |\_ *ver:* 0.19.5-r593
  - |\_ *key param:* NA
- **purge\_dups**
  - |\_ *ver:* 1.2.5
  - |\_ *key param:* NA
- **yahs**
  - |\_ *ver:* 1.2
  - |\_ *key param:* NA

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Date and time: 2024-07-23 17:14:46 CEST