

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1380992
ToLID	<b>xbPinRudi</b>
Species	Pinna rudis
Class	Bivalvia
Order	Pterioidea

Genome Traits	Expected	Observed
Haploid size (bp)	1,264,691,974	817,629,743
Haploid Number	14 (source: ancestor)	17
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q62

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . Observed Haploid Number is different from Expected

## Curator notes

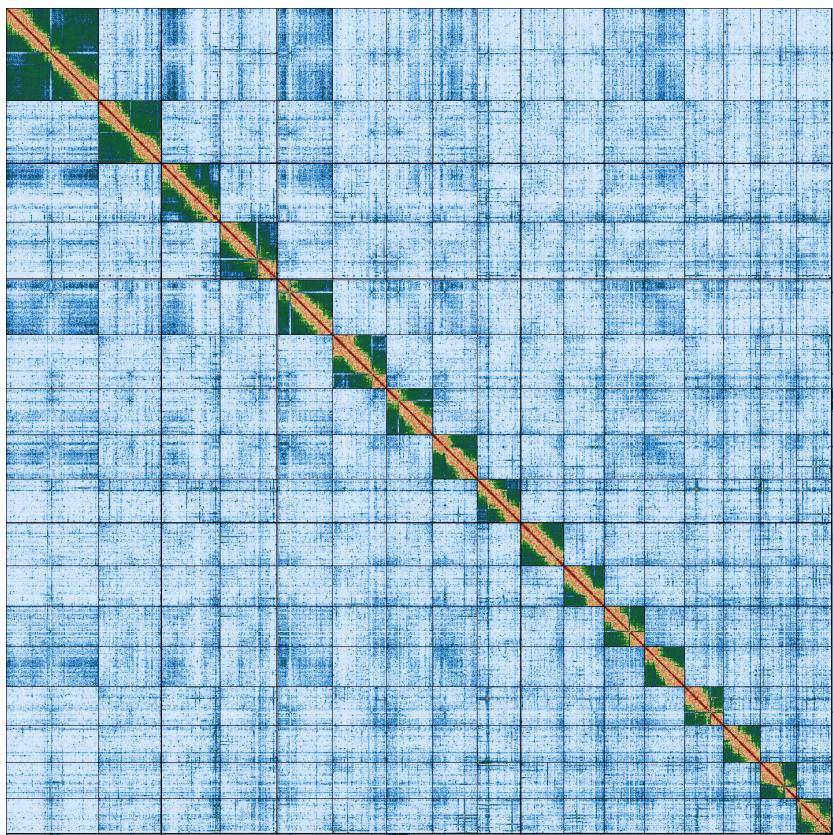
- . Interventions/Gb: None
- . Contamination notes: "There are no signs of contamination in the data"
- . Other observations: "Assembly comes out smaller than the expected size of around 1.2Gb. The haploid number of 14 given in GoaT is likely to be incorrect. Correct number seems to be 17."

## Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	825,238,288	817,629,743
GC %	35.96	35.96
Gaps/Gbp	350.2	379.14
Total gap bp	57,800	62,000
Scaffolds	92	72
Scaffold N50	43,106,870	45,632,123
Scaffold L50	8	7
Scaffold L90	16	15
Contigs	381	382
Contig N50	3,852,967	3,898,541
Contig L50	66	65
Contig L90	208	207
QV		62.9718
Kmer compl.	% Covered	
BUSCO sing.	95.7%	96.4%
BUSCO dupl.	2.1%	1.2%
BUSCO frag.	0.4%	0.3%
BUSCO miss.	1.8%	2.1%

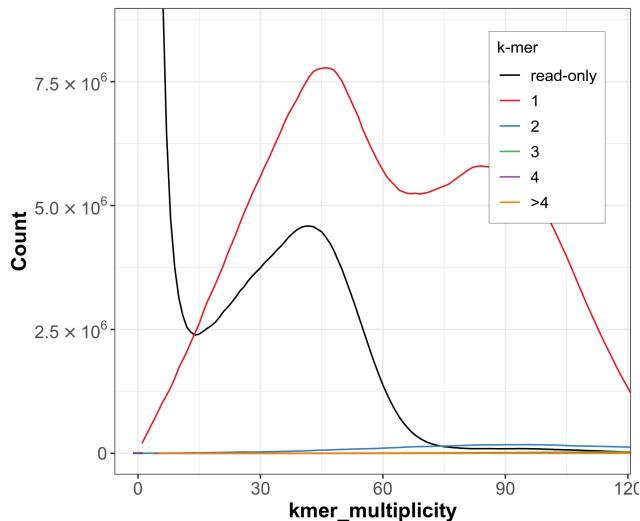
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: metazoa\_odb10 (genomes:65, BUSCOs:954)

# HiC contact map of curated assembly

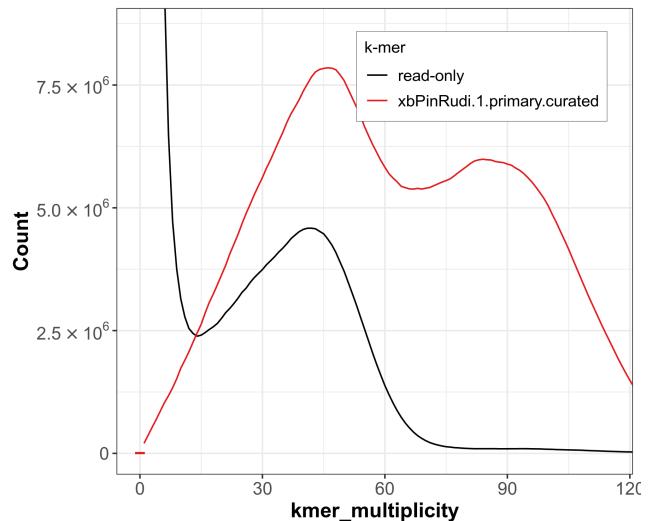


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

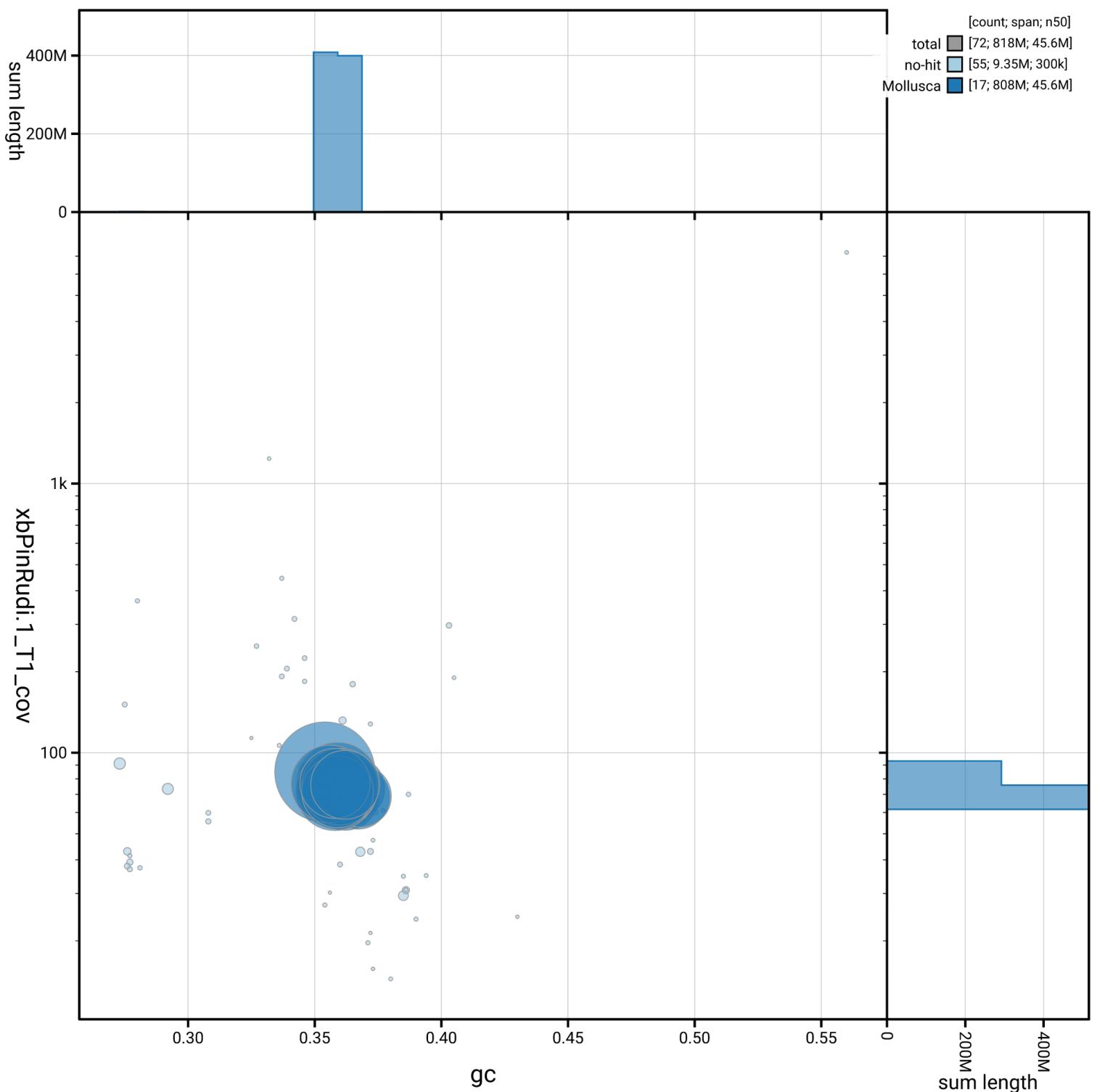


Distribution of k-mer counts per copy numbers found in asm



Distribution of k-mer counts 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	HiFi	OmniC
Coverage	76x	286x

## Assembly pipeline

```
- Hifiasm
  |_ ver: 0.25.0-r726
  |_ key param: NA
- purge_dups
  |_ ver: 1.2.6
  |_ key param: NA
- NBIS/Earth-Biogenome-Project-pilot
  |_ ver: e6e9c1621b
  |_ key param: NA
- sanger-tol/blobtoolkit
  |_ ver: 0.9.0
  |_ key param: NA
- YaHS
  |_ ver: 1.2.2
  |_ key param: NA
```

## Curation pipeline

```
- agp-tpf-utils
  |_ ver: 1.2.3
  |_ key param: NA
- sanger-tol/curationpretext
  |_ ver: 1.5.1
  |_ key param: NA
```

Submitter: Tomas Larsson

Affiliation: SciLifeLab

Date and time: 2026-02-03 11:55:50 CET