

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1380992
ToLID	xbPinRudi
Species	Pinna rudis
Class	Bivalvia
Order	Pterioda

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

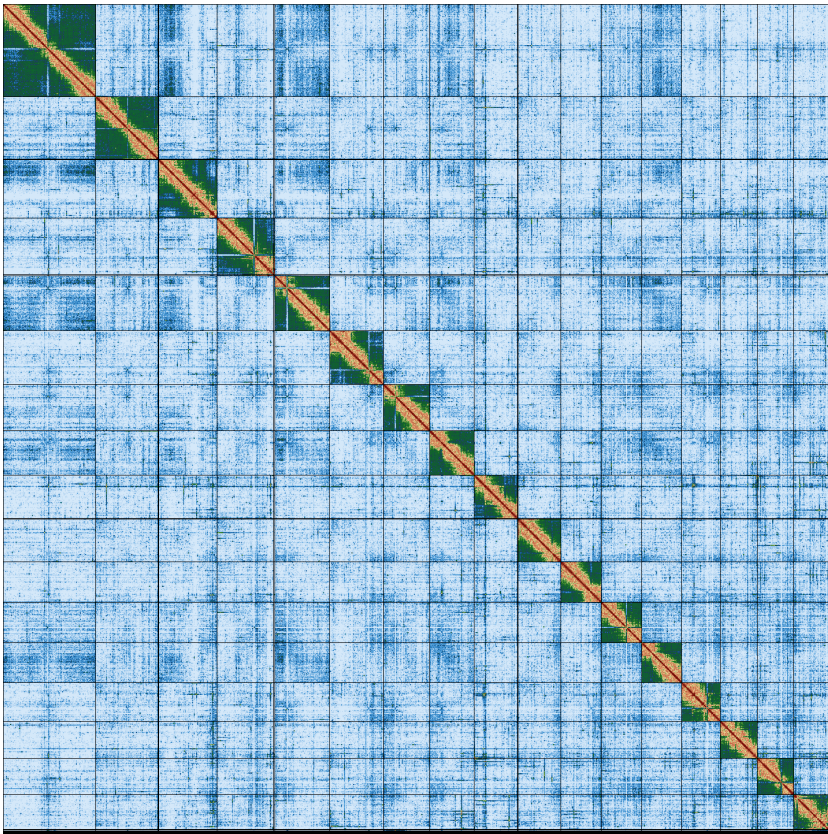
- . Interventions/Gb: None
- . Contamination notes: "There are no signs of contamination in the data"
- . Other observations: "Assembly comes out smaller than the expected size of around 1.2Gb. The haploid number of 14 given in GoaT is likely to be incorrect. Correct number seems to be 17."

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%

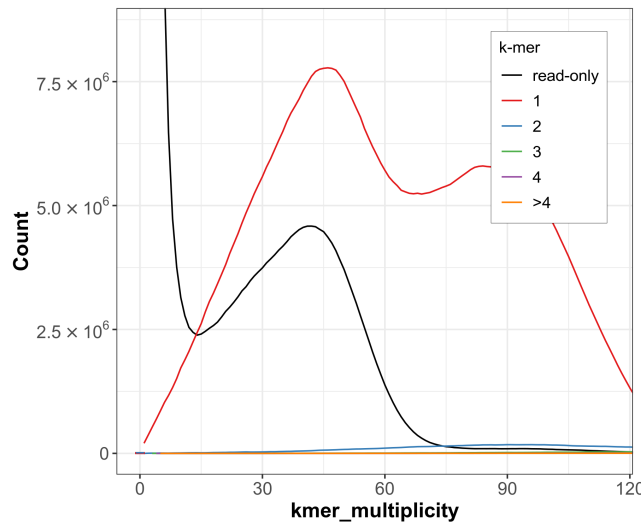
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

HiC contact map of curated assembly

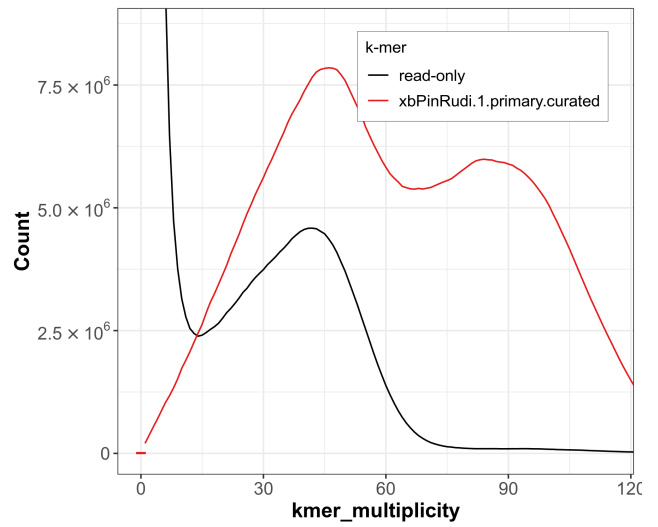


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

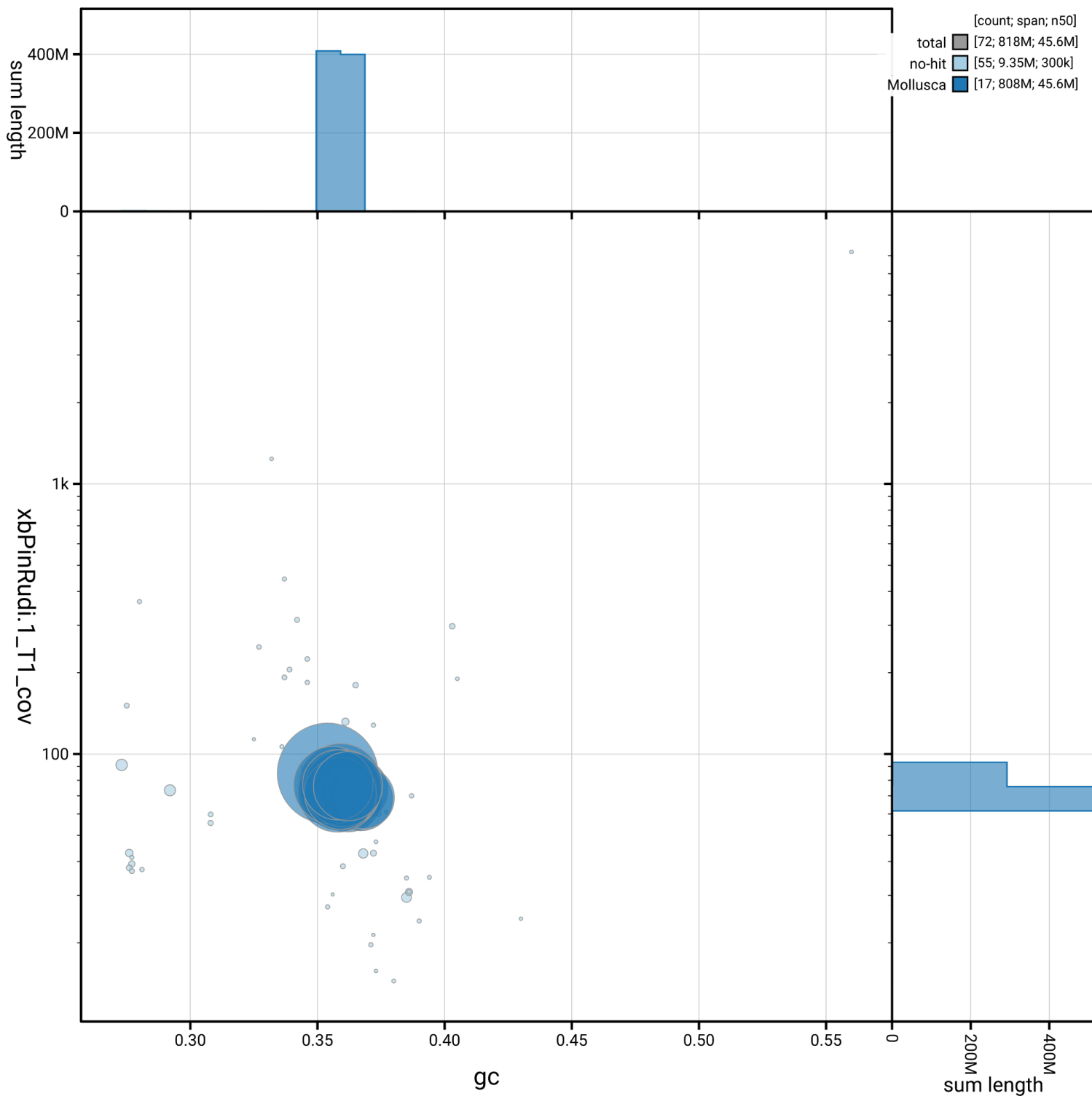


Distribution of k-mer counts per copy numbers found in asm



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