

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2057147
ToLID	<b>kaBotIsra</b>
Species	Botrylloides israeliense
Class	Ascidacea
Order	Stolidobranchia

Genome Traits	Expected	Observed
Haploid size (bp)	675,486,130	344,569,771
Haploid Number	16 (source: ancestor)	16
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q37

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . QV value is less than 40 for pri
- . Kmer completeness value is less than 90 for pri
- . BUSCO single copy value is less than 90% for pri
- . Assembly length loss > 3% for pri
- . More than 1000 gaps/Gbp for pri
- . Not 90% of assembly in chromosomes for pri

### Curator notes

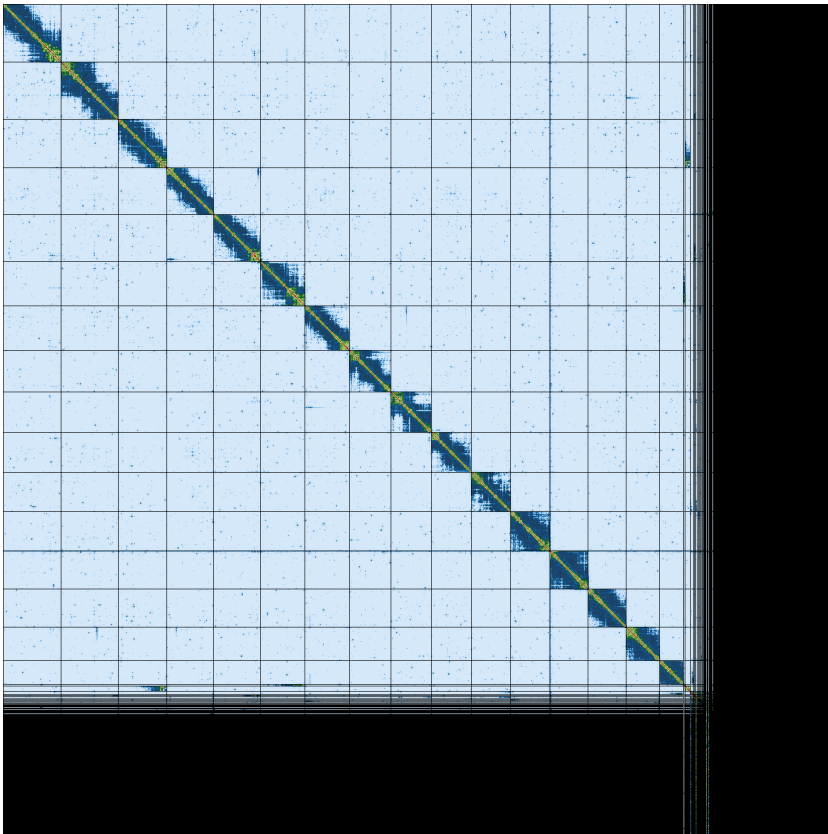
- . Interventions/Gb: 271
- . Contamination notes: "No presence of contaminants."
- . Other observations: "None"

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	529,144,227	344,569,771
GC %	39.98	39.73
Gaps/Gbp	1,220.84	1,062.19
Total gap bp	64,600	44,100
Scaffolds	936	850
Scaffold N50	22,475,165	16,807,710
Scaffold L50	10	9
Scaffold L90	115	133
Contigs	1,582	1,216
Contig N50	1,162,916	1,355,057
Contig L50	135	85
Contig L90	640	445
QV	39.2159	37.8718
Kmer compl.	87.5425	64.6732
BUSCO sing.	72.3%	85.7%
BUSCO dupl.	19.9%	1.7%
BUSCO frag.	1.7%	1.8%
BUSCO miss.	6.1%	10.8%

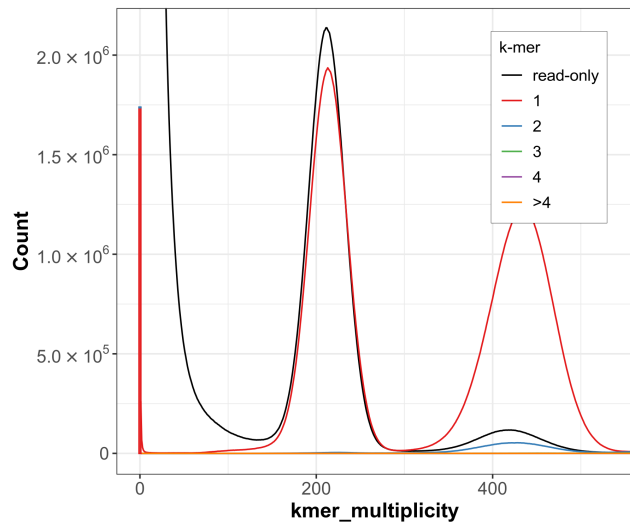
BUSCO: 5.8.2 (euk\_genome\_aug, augustus) / Lineage: metazoa\_odb10 (genomes:65, BUSCOs:954)

# HiC contact map of curated assembly

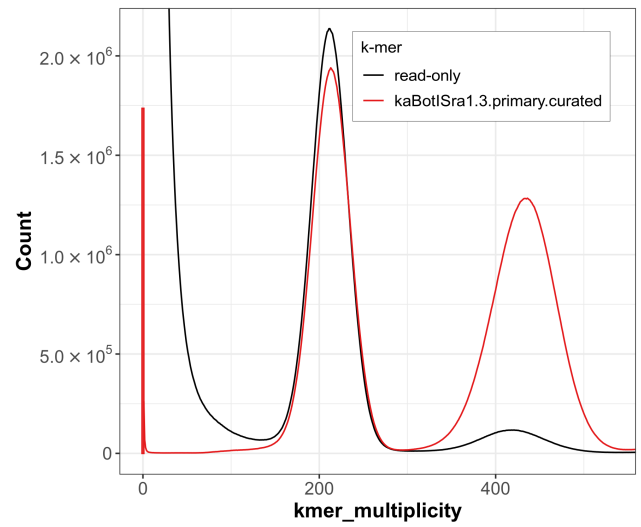


pri [\[LINK\]](#)

# K-mer spectra of curated assembly



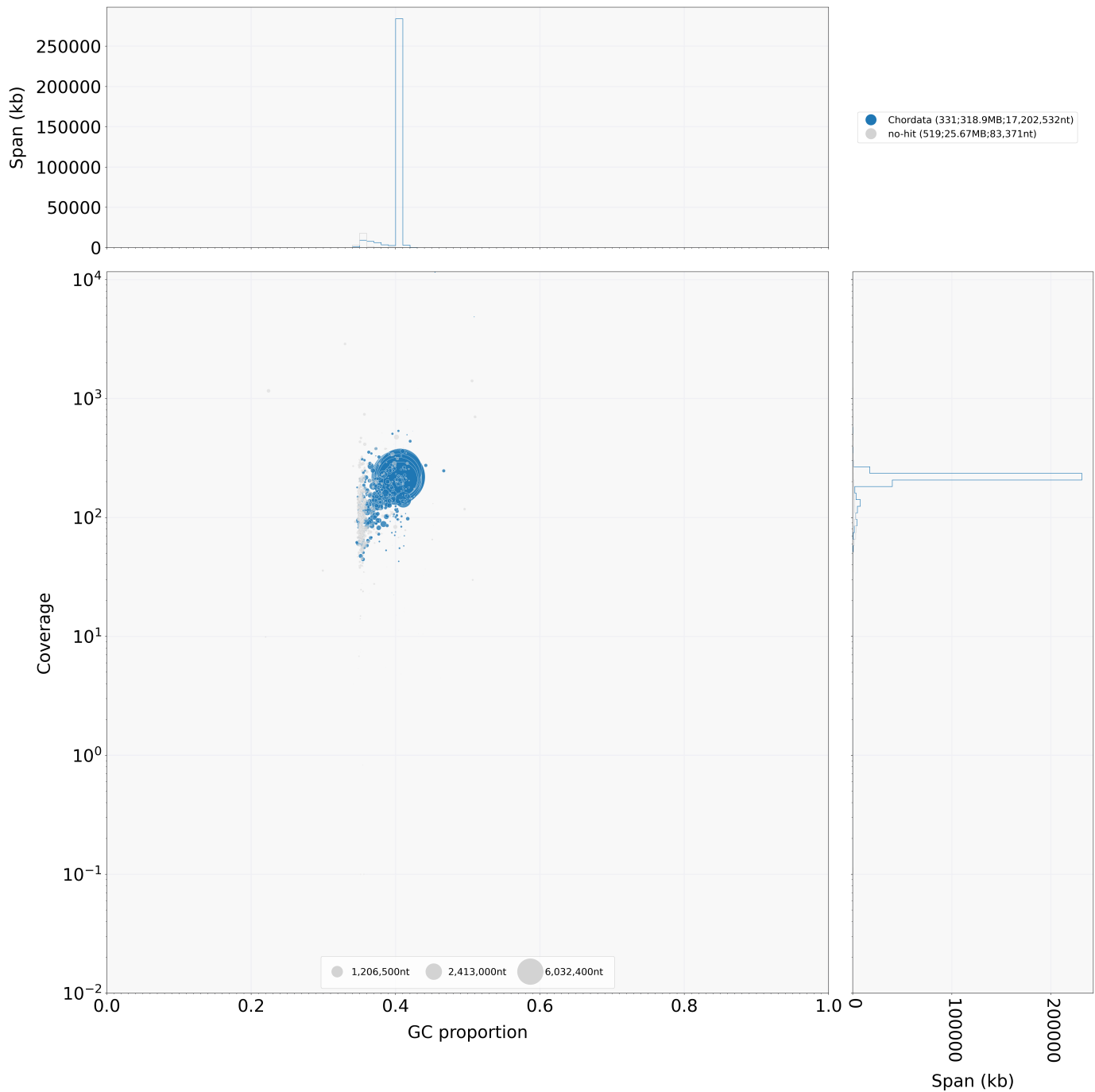
Distribution of k-mer counts per copy numbers found in asm



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

# Post-curation contamination screening

filename.blobDB.json.bestsum.phylum.p8.span.100.blobplot.bam0



**pri.** 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	ONT	Bionano	HiC
Coverage	391x	NA	97x

## Assembly pipeline

- **Necat**
  - |\_ *ver*: 0.0.1
  - |\_ *key param*: NA
- **purge\_dups**
  - |\_ *ver*: 1.2.5
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.1
  - |\_ *key param*: NA

## Curation pipeline

- **sanger-tol/curationpretext**
  - |\_ *ver*: 1.4.1
  - |\_ *key param*: NA
- **PretextView**
  - |\_ *ver*: 1.0.3
  - |\_ *key param*: NA

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