

# ERGA Assembly Report

v24.02.09\_beta

Tags: ERGA-BGE

ToLID	<b>fValHis1</b>
Species	<b>Valencia hispanica</b>
Class	Actinopteri
Order	Cyprinodontiformes

Genome Traits	Expected	Observed
Haploid size (bp)	1,348,231,524	1,291,680,485
Haploid Number	24 (source: ['ancestor'])	24
Ploidy	2 (source: ['ancestor'])	2
Sample Sex	ZW	ZW

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q50

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

### Curator notes

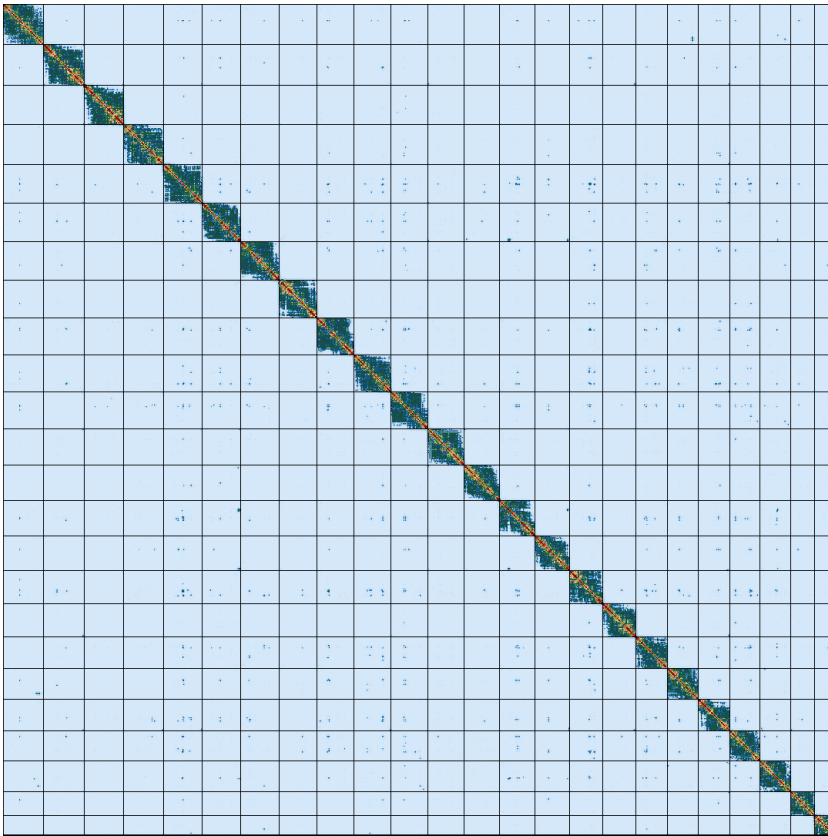
- . Interventions/Gb: 2
- . Contamination notes: "No contaminants found"
- . Other observations: "Yahs did a very good initial job. Manual curation was minimal"

# Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,291,679,885	1,291,680,485
GC %	40.09	40.09
Gaps/Gbp	52.64	54.97
Total gap bp	13,600	14,200
Scaffolds	31	28
Scaffold N50	56,937,854	56,937,854
Scaffold L50	11	11
Scaffold L90	21	21
Contigs	99	99
Contig N50	38,296,799	38,296,799
Contig L50	14	14
Contig L90	41	41
QV	50.5814	50.5814
Kmer compl.	98.05	98.05
BUSCO sing.	97.8%	97.8%
BUSCO dupl.	0.8%	0.8%
BUSCO frag.	0.4%	0.4%
BUSCO miss.	1.0%	1.0%

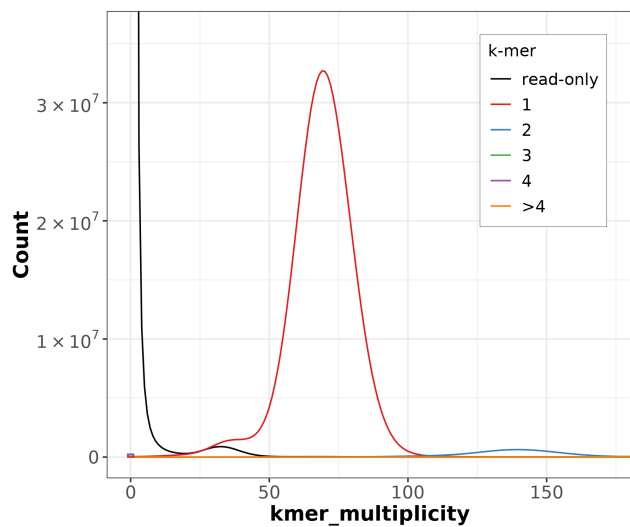
BUSCO 5.4.0 Lineage: actinopterygii\_odb10 (genomes:26, BUSCOs:3640)

# HiC contact map of curated assembly

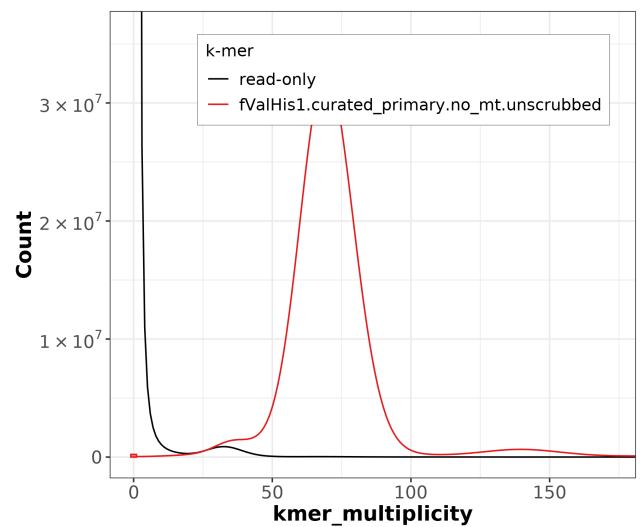


collapsed [\[LINK\]](#)

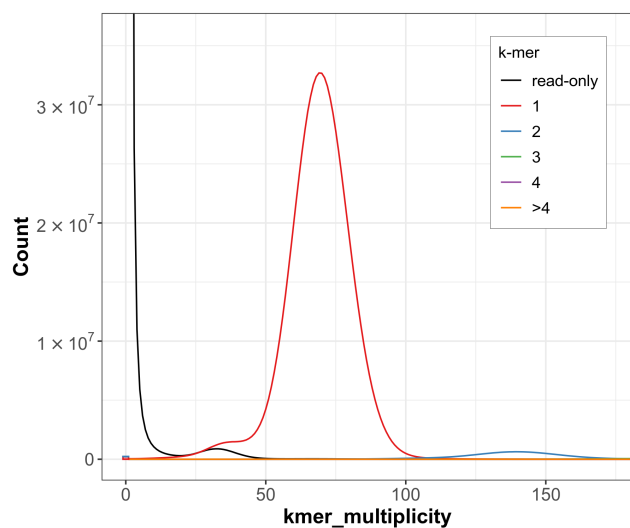
# K-mer spectra of curated assembly



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

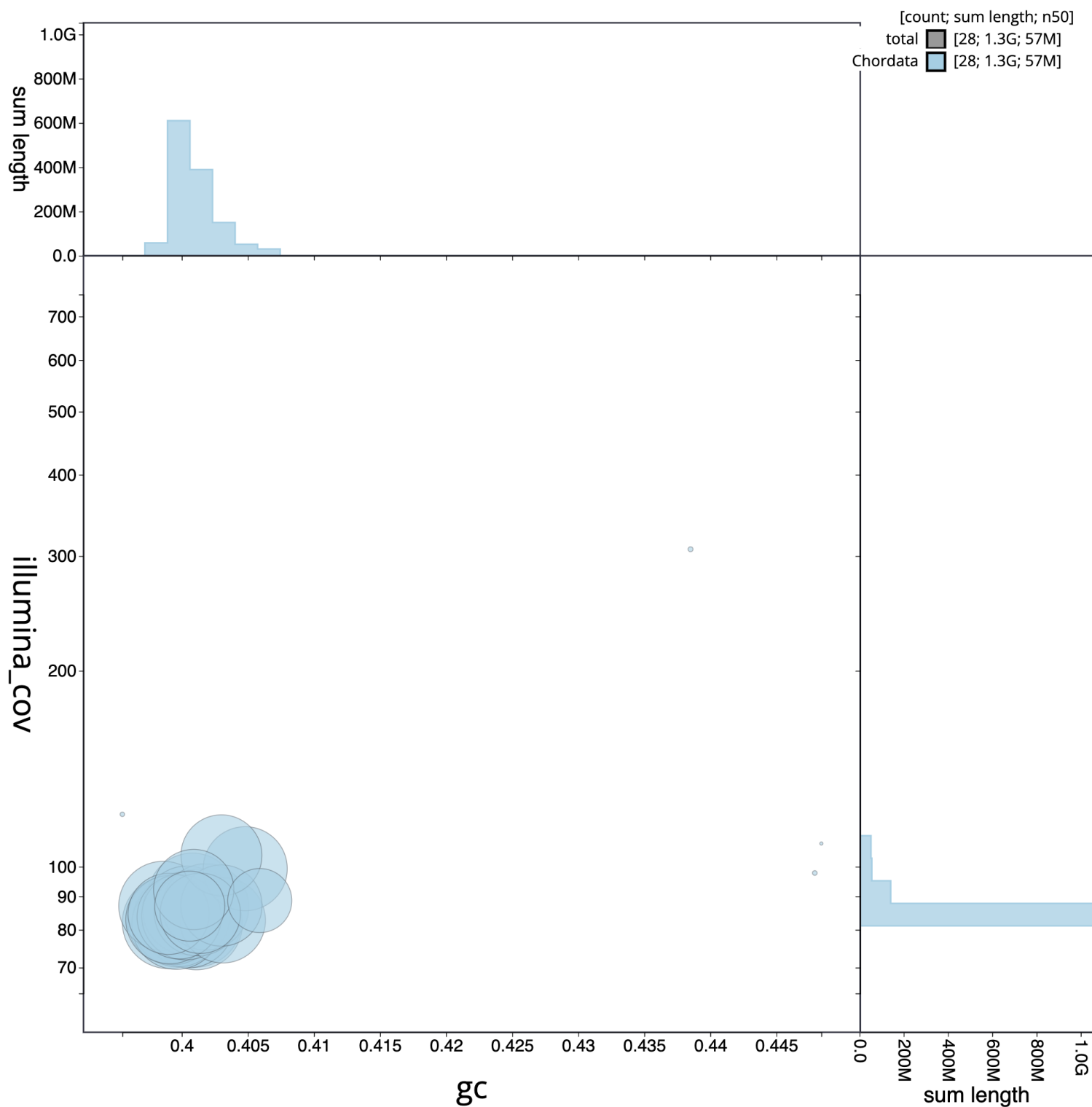


Distribution of k-mer counts coloured by their presence in reads/assemblies



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	ONT	Illumina	OmniC
Coverage	74x	83x	70x

## Assembly pipeline

- **Trim\_Galore**
  - |\_ *ver*: 0.6.7
  - |\_ *key param*: "--gzip -q 20"
  - |\_ *key param*: "--paired"
  - |\_ *key param*: "--retain\_unpaired"
- **Filtlong**
  - |\_ *ver*: 0.2.1
  - |\_ *key param*: NA
- **nextdenovo**
  - |\_ *ver*: 2.5.0
  - |\_ *key param*: NA
- **hypo**
  - |\_ *ver*: 1.0.3
  - |\_ *key param*: NA
- **purge\_dups**
  - |\_ *ver*: 1.2.6
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.2a
  - |\_ *key param*: NA

## Curation pipeline

- **PretextView**
  - |\_ *ver*: 0.2.5
  - |\_ *key param*: NA

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