

# ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	28791
ToLID	<b>fCypLut1_hap1</b>
Species	<i>Cyprinella lutrensis</i>
Class	Actinopteri
Order	Cypriniformes

Genome Traits	Expected	Observed
Haploid size (bp)	802,987,641	926,985,129
Haploid Number	25 (source: direct)	25
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q57

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

### Curator notes

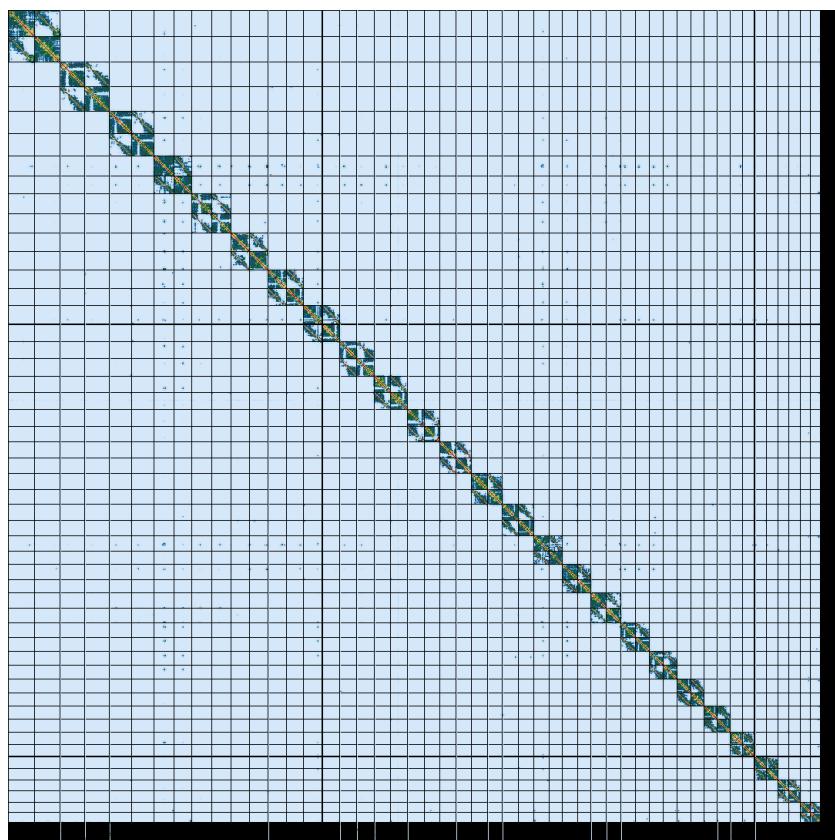
- . Interventions/Gb: 154
- . Contamination notes: "
- . Other observations: "The assembly of *Cyprinella lutrensis* (fCypLut1) was generated as part of the Vertebrate Genomes Project (<https://vertebratogenomesproject.org/>). Both haplotypes were analyzed and manually improved using Pretext. "

## Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	905,396,741	926,985,129
GC %	38.58	38.61
Gaps/Gbp	875.86	900.77
Total gap bp	158,600	167,000
Scaffolds	470	456
Scaffold N50	36,464,699	36,156,036
Scaffold L50	9	11
Scaffold L90	21	23
Contigs	1,263	1,291
Contig N50	1,162,085	1,164,858
Contig L50	210	206
Contig L90	659	668
QV	57.4847	57.5044
Kmer compl.	74.3347	74.9648
BUSCO sing.	94.9%	
BUSCO dupl.	0.5%	
BUSCO frag.	1.2%	
BUSCO miss.	3.5%	

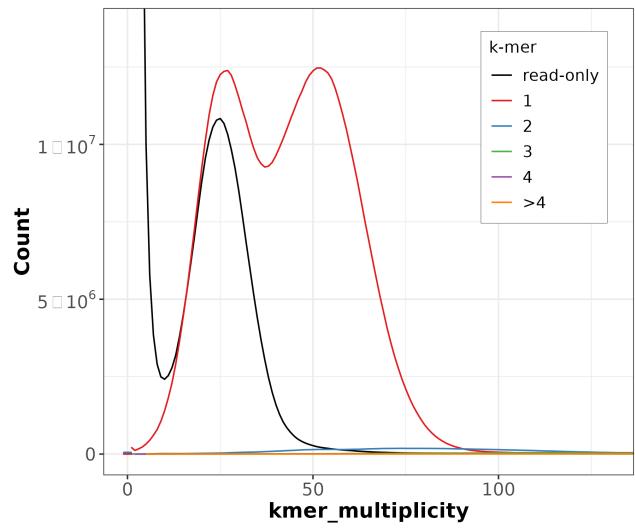
BUSCO: 5.8.2 (euk\_genome\_met, metaeuk) / Lineage: actinopterygii\_odb12 (genomes:75, BUSCOs:7207)

# HiC contact map of curated assembly

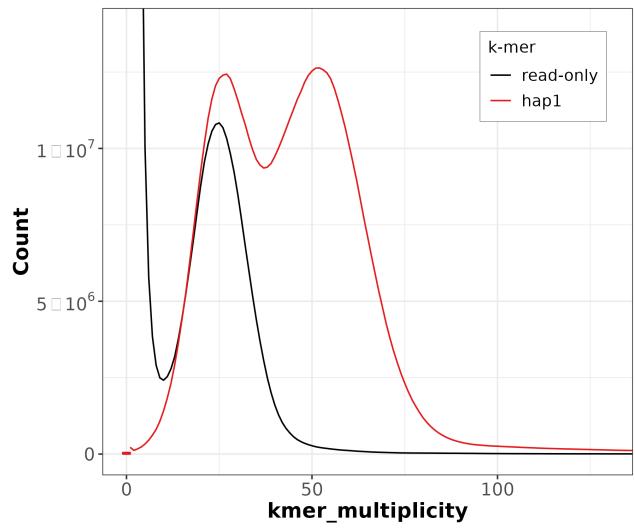


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

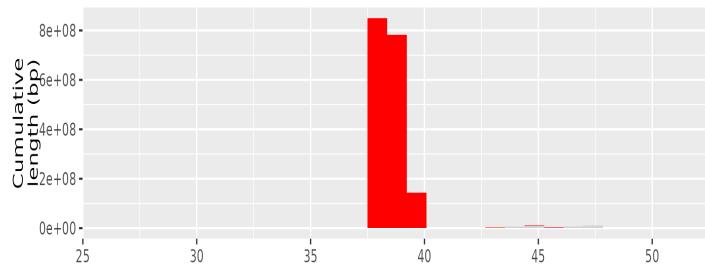


Distribution of k-mer counts per copy numbers found in asm



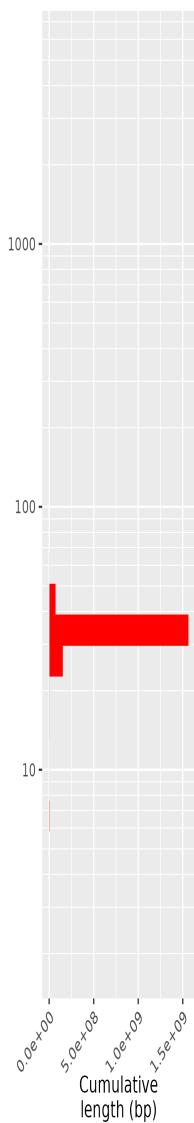
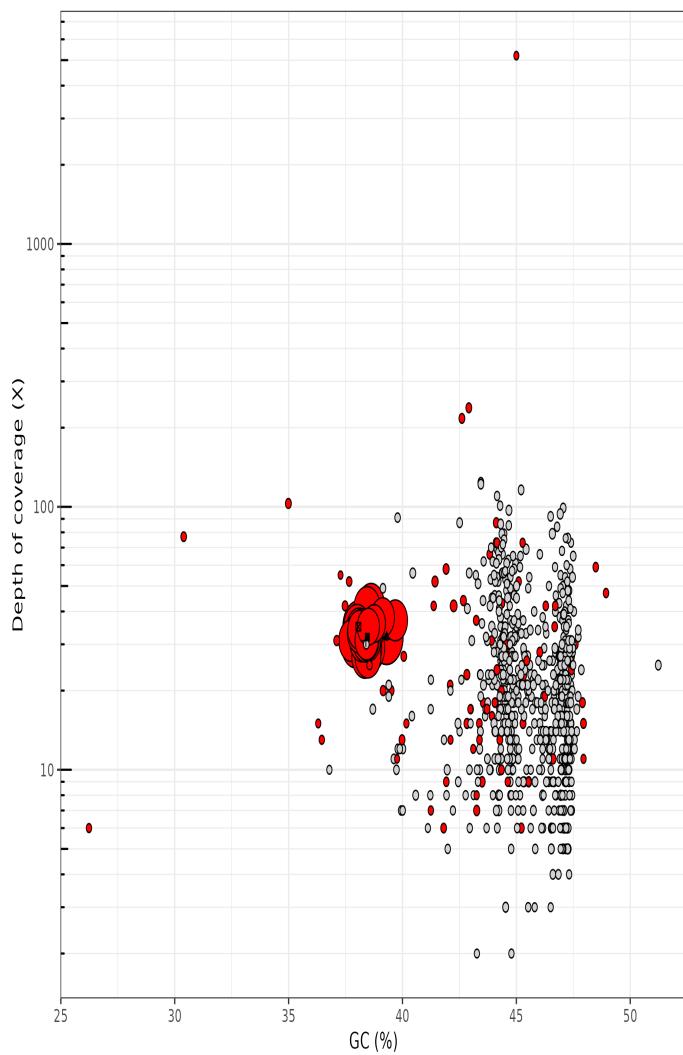
Distribution of k-mer counts coloured by their presence in reads/assemblies

# Post-curation contamination screening



TAPAs summary Graph

(1 0X contig has been hidden)



Length (bp)

- 1e+07
- 2e+07
- 3e+07
- 4e+07
- 5e+07

superkingdom

- Eukaryota
- N/A

Longest sequences (bp)

- Hap1\_fCypLut1\_1 - 57444818 (Eukaryota)
- ▲ Hap2\_fCypLut1\_1 - 56629774 (Eukaryota)
- Hap1\_fCypLut1\_2 - 53729220 (Eukaryota)
- + Hap2\_fCypLut1\_2 - 53125133 (Eukaryota)
- ▣ Hap1\_fCypLut1\_3 - 49364229 (Eukaryota)

**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	Long reads	Arima
Coverage	NA	NA

## 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

```
- PretextMap
  |_ ver: 0.1.9
  |_ key param: NA
- PretextView
  |_ ver: 0.2.5
  |_ key param: NA
```

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Date and time: 2025-10-20 08:59:17 CEST