ERGA Assembly Report

v24.09.10

Tags: ERGA-BGE

TxID	166086		
ToLID	rHemHip1		
Species	Hemorrhois hippocrepis		
Class	Lepidosauria		
Order	Squamata		

Genome Traits	Expected	Observed
Haploid size (bp)	1,677,182,640	1,806,509,314
Haploid Number	18 (source: ancestor)	18
Ploidy	3 (source: ancestor)	2
Sample Sex	ZW	ZW

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.8.Q50

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

. Observed Ploidy is different from Expected

Curator notes

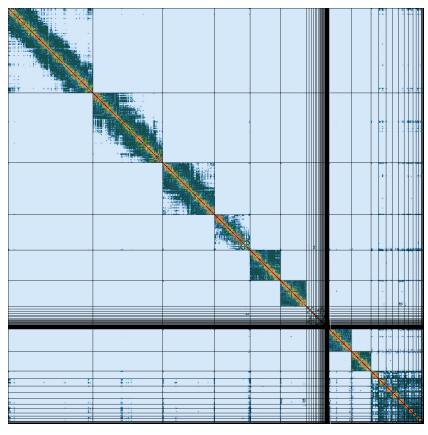
- . Interventions/Gb: 5
- . Contamination notes: "No contaminants detected with blobtoolkit INSDC pipeline in the precurated assembly."
- . Other observations: "Curation made 4 cuts in contigs, 5 breaks at gaps and 0 joins. The W contigs were found in the purge_dups' hap.fa and placed back into the nextdenovo asseembly before yahs scaffolding. After curation and review, the W was assembled into 1 contig of 11.9 Mb and 37 unlocalized scaffolds totalling 99,702,411 bp. Consistently with the cytogenetic information we identified 10 microchromosomes (SUPER_7-SUPER_16). Although there are 4 scaffolds with clear contcats with them is not possible to place them into a unique SUPER. The link provided for the pretextmap points to a folder where reviewers can add additional save_states if required. Finally, the mitogenome has been assembled independently with FOAM into a 21,416 bp circular contig with high accuracy."

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed	
Total bp	1,810,545,746	1,806,509,314	
GC %	41.21	41.21	
Gaps/Gbp	24.3 19.93		
Total gap bp	8,800	7,200	
Scaffolds	112	110	
Scaffold N50	153,613,959	153,613,759	
Scaffold L50	4	4	
Scaffold L90	11	14	
Contigs	156	146	
Contig N50	47,232,710	54,718,507	
Contig L50	12	11	
Contig L90	40	35	
QV	50.2312	50.2958	
Kmer compl.	95.6393	95.62	
BUSCO sing.	96.5%	96.5%	
BUSCO dupl.	1.0%	1.0%	
BUSCO frag.	0.7%	0.7%	
BUSCO miss.	1.8%	1.8%	

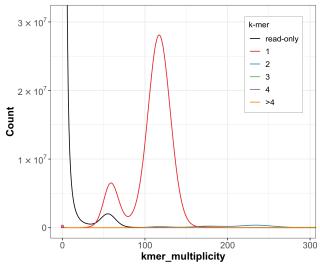
BUSCO 5.4.0 Lineage: vertebrata_odb10 (genomes:67, BUSCOs:3354)

HiC contact map of curated assembly

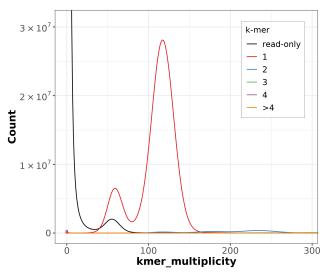


collapsed [LINK]

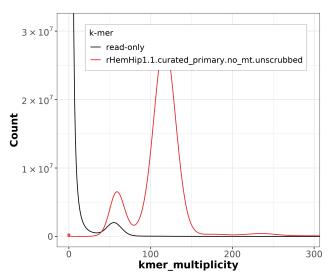
K-mer spectra of curated assembly



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

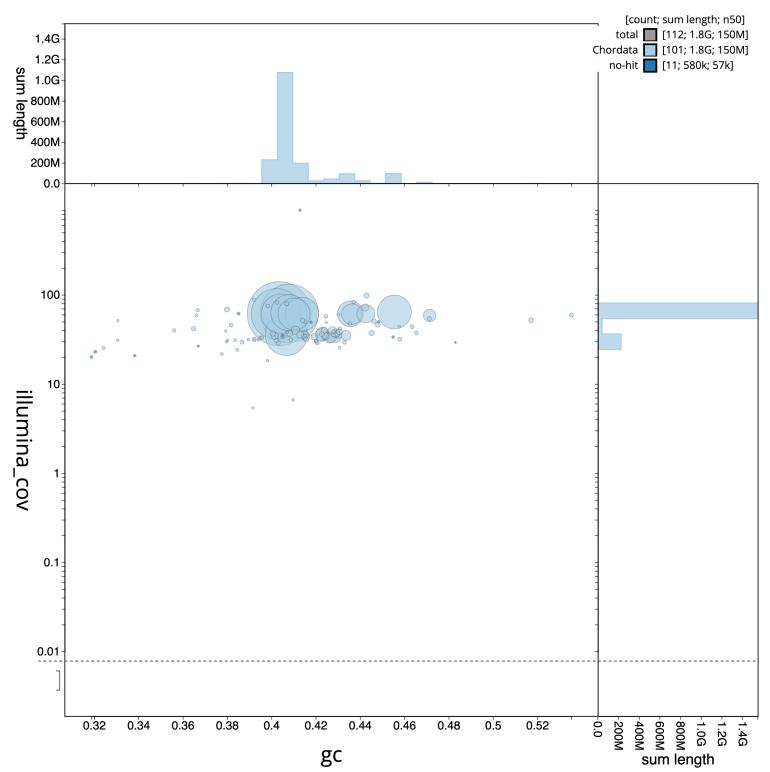


Distribution of k-mer counts per copy numbers found in asm



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	ONT	Illumina	OmniC
Coverage	84x	60x	53x

Assembly pipeline

```
- CLAWS pipeline
   |_ ver: 2.2.0
   _ key param: NA
- Trim_galore
   |_ ver: 0.6.7
   _ key param: NA
- Filtlong
    _ ver: 0.2.1
    |_ key param: NA
- flye
   |_ ver: 2.9.1
    _ 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
- Blobtoolkit INSDC pipeline
    |_ ver: 1.0
    | key param: NA
- FOAM pipeline
   _ ver: 0.5
    _ key param: NA
- mitos
    |_ ver: 2.1.3
    _ key param: NA
```

Curation pipeline

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