

ERGA Assembly Report

v24.08.26

Tags: ERGA-BGE

TxID	2934182
ToLID	xgPhyFlav1
Species	Phyllidia flava
Class	Gastropoda
Order	Nudibranchia

Genome Traits	Expected	Observed
Haploid size (bp)	3,011,504,214	3,343,225,297
Haploid Number	12 (source: ancestor)	28
Ploidy	2 (source: ancestor)	2
Sample Sex	XX	XX

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 7.8.Q6

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

- . Observed Haploid Number is different from Expected
- . QV value is less than 40 for hap1
- . Kmer completeness value is less than 90 for hap1
- . Assembly length loss > 3% for hap1

Curator notes

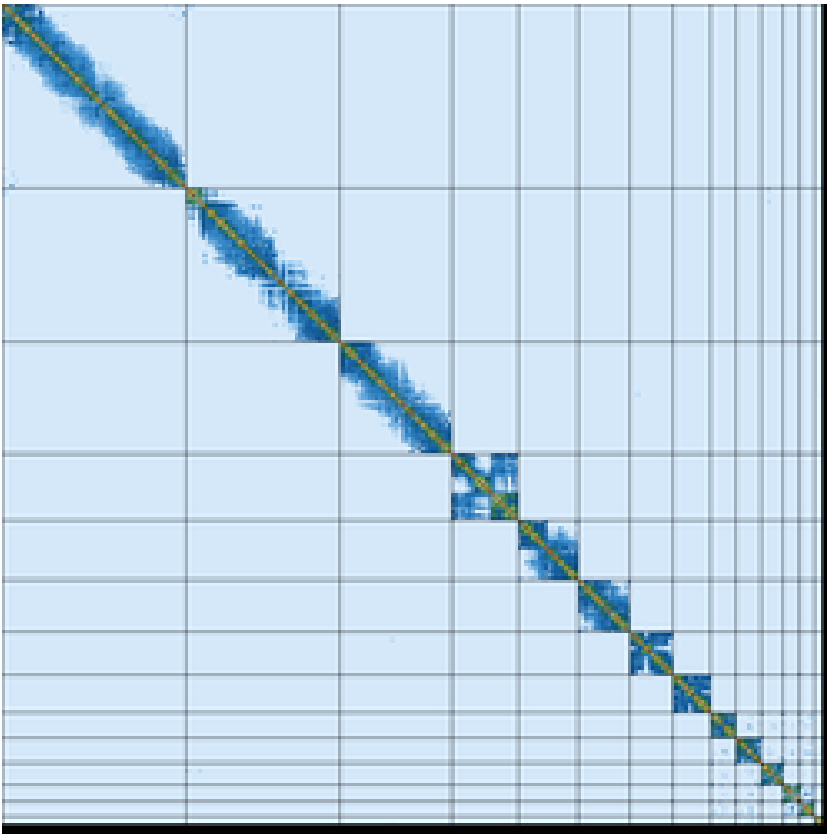
- . Interventions/Gb: 2
- . Contamination notes: "No presence of contaminants. Mitochondrial genome was removed from the assembly"
- . Other observations: "Large collapsed repeat in chr5, haplotypic inversion in chr12"

Quality metrics table

Metrics	Pre-curation hap1	Curated hap1
Total bp	3,660,021,265	3,343,225,297
GC %	41.62	41.09
Gaps/Gbp	34.97	22.13
Total gap bp	1,874,523	138,686
Scaffolds	973	104
Scaffold N50	111,683,922	125,437,426
Scaffold L50	12	10
Scaffold L90	35	24
Contigs	1,101	178
Contig N50	73,275,821	77,716,104
Contig L50	16	14
Contig L90	85	43
QV	68.0694	6
Kmer compl.	95.5615	9
BUSCO sing.	95.3%	95.2%
BUSCO dupl.	0.7%	0.7%
BUSCO frag.	1.1%	1.1%
BUSCO miss.	2.9%	3.0%

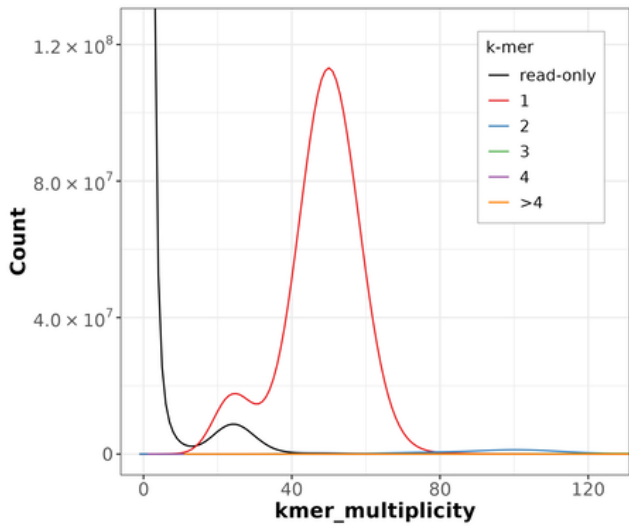
BUSCO 5.4.7 Lineage: mammalia_odb10 (genomes:24, BUSCOs:9226)

HiC contact map of curated assembly

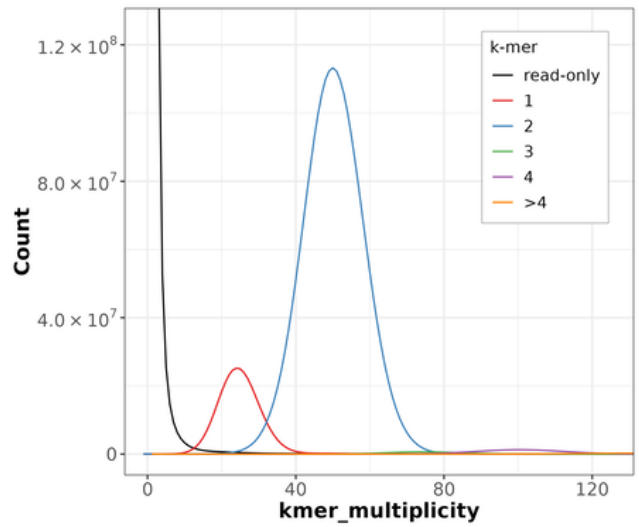


hap1 [\[LINK\]](#)

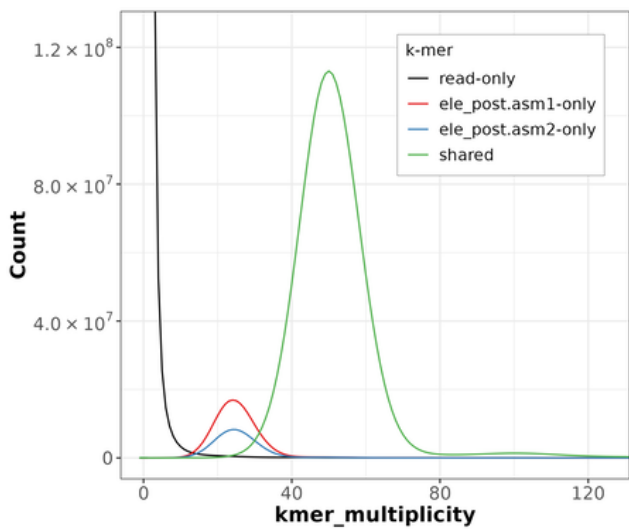
K-mer spectra of curated assembly



dataset_a95c0e30-e3ee-4059-830c-e735aceecf0b.dat



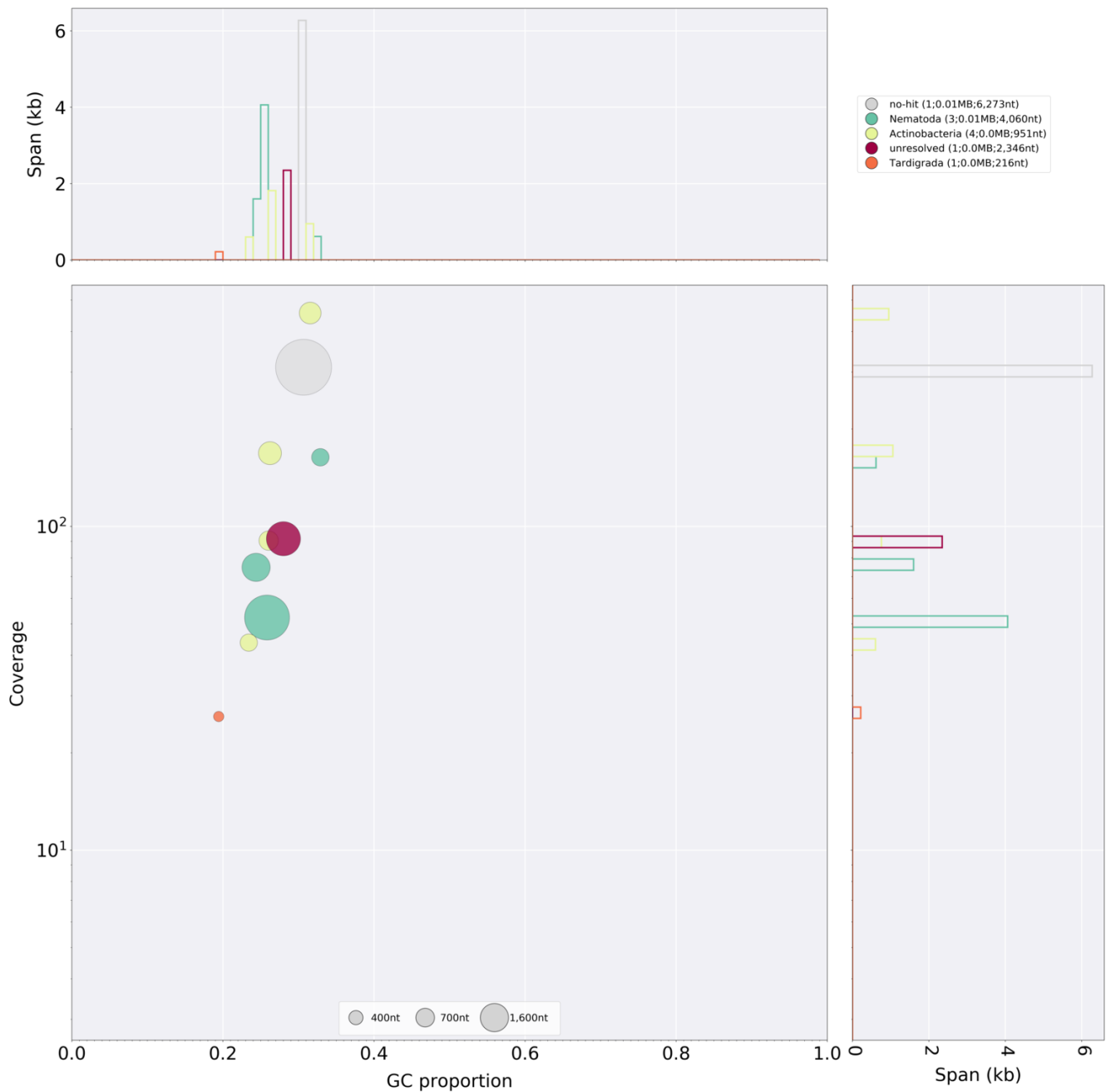
dataset_d0f465df-7b4b-4011-a131-e707c50b6695.dat



dataset_56f39779-5c88-4801-8bc1-b21787fcaa45.dat

Post-curation contamination screening

example/test.test.blobDB.json.bestsum.phylum.p7.span.100.blobplot.bam0



hap1. 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	Bionano	OmniC
Coverage	40x	10x	90x

Assembly pipeline

- **Hifiasm**
 - |_ *ver*: 0.19.4
 - |_ *key param*: HiC
 - |_ *key param*: 10
- **purge_dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA
- **Bionano_solve**
 - |_ *ver*: Galaxy_3.7.0
 - |_ *key param*: NA
- **YaHS**
 - |_ *ver*: 1.1
 - |_ *key param*: NA

Curation pipeline

- **GRIT_Rapid**
 - |_ *ver*: 2.0
 - |_ *key param*: NA
- **HiGlass**
 - |_ *ver*: 1.0
 - |_ *key param*: NA

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