ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

| TxID | 69427 | |
|---------|-----------------|--|
| ToLID | xgAlbTers5 | |
| Species | Albinaria teres | |
| Class | Gastropoda | |
| Order | Stylommatophora | |

| Genome Traits | Expected | Observed |
|-------------------|-----------------------|---------------|
| Haploid size (bp) | 1,601,490,426 | 1,732,817,941 |
| Haploid Number | 20 (source: ancestor) | 31 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | Unknown | unknown |

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q56

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

- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for collapsed

Curator notes

. Interventions/Gb: None

. Contamination notes: "None"

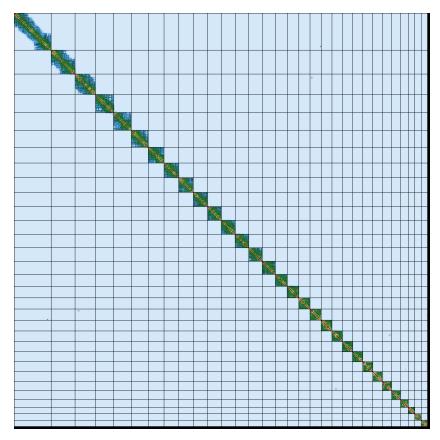
. Other observations: "None"

Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|--------------|------------------------|----------------------|
| Total bp | 1,733,434,212 | 1,732,817,941 |
| GC % | 38.99 | 38.99 |
| Gaps/Gbp | 192.68 | 196.79 |
| Total gap bp | 33,400 | 35,100 |
| Scaffolds | 86 | 82 |
| Scaffold N50 | 57,406,542 | 57,406,542 |
| Scaffold L50 | 12 | 12 |
| Scaffold L90 | 27 | 26 |
| Contigs | 420 | 423 |
| Contig N50 | 7,880,036 | 7,880,036 |
| Contig L50 | 74 | 74 |
| Contig L90 | 224 | 224 |
| QV | 56.8685 | 56.8677 |
| Kmer compl. | 77.8995 | 77.8852 |
| BUSCO sing. | 96.1% | 96.1% |
| BUSCO dupl. | 3.5% | 3.5% |
| BUSCO frag. | 0.0% | 0.0% |
| BUSCO miss. | 0.4% | 0.4% |

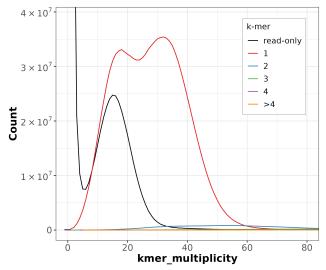
BUSCO 5.4.3 Lineage: eukaryota_odb10 (genomes:70, BUSCOs:255)

HiC contact map of curated assembly

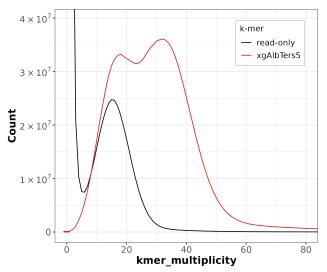


collapsed [LINK]

K-mer spectra of curated assembly

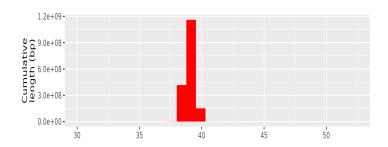


Distribution of k-mer counts per copy numbers found in asm

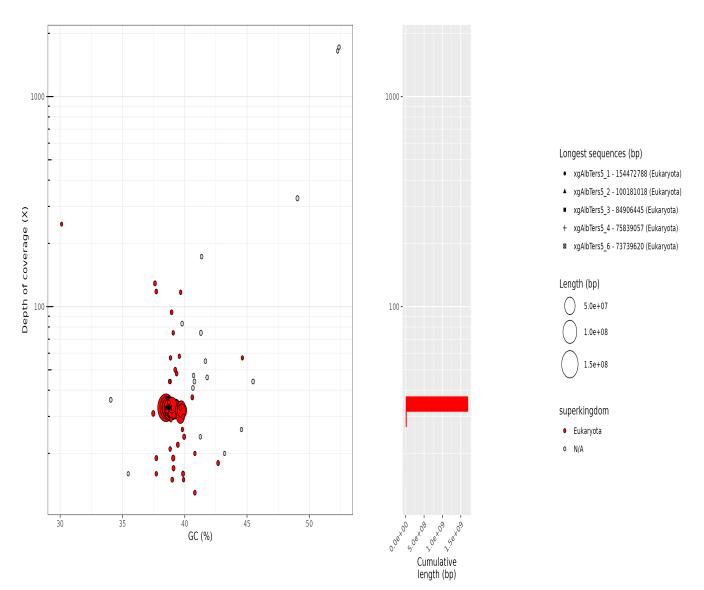


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



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 | PACBIO Hifi | Arima (4-enz) |
|----------|-------------|---------------|
| Coverage | 36 | 33 |

Assembly pipeline

Curation pipeline

Submitter: Lola Demirdjian Affiliation: Genoscope

Date and time: 2024-07-25 15:02:42 CEST