

ERGA Assembly Report

v24.09.10

Tags: ATLASea[INVALID TAG]

| | |
|---------|---------------------|
| TxID | 1443217 |
| ToLID | keGlaTala1.1 |
| Species | Glandiceps talaboti |
| Class | Enteropneusta |
| Order | NA |

| Genome Traits | Expected | Observed |
|-------------------|----------------------|-------------|
| Haploid size (bp) | 513,604,706 | 590,507,926 |
| Haploid Number | 4 (source: ancestor) | 9 |
| 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:

- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for collapsed
- . Not 90% of assembly in chromosomes for collapsed

Curator notes

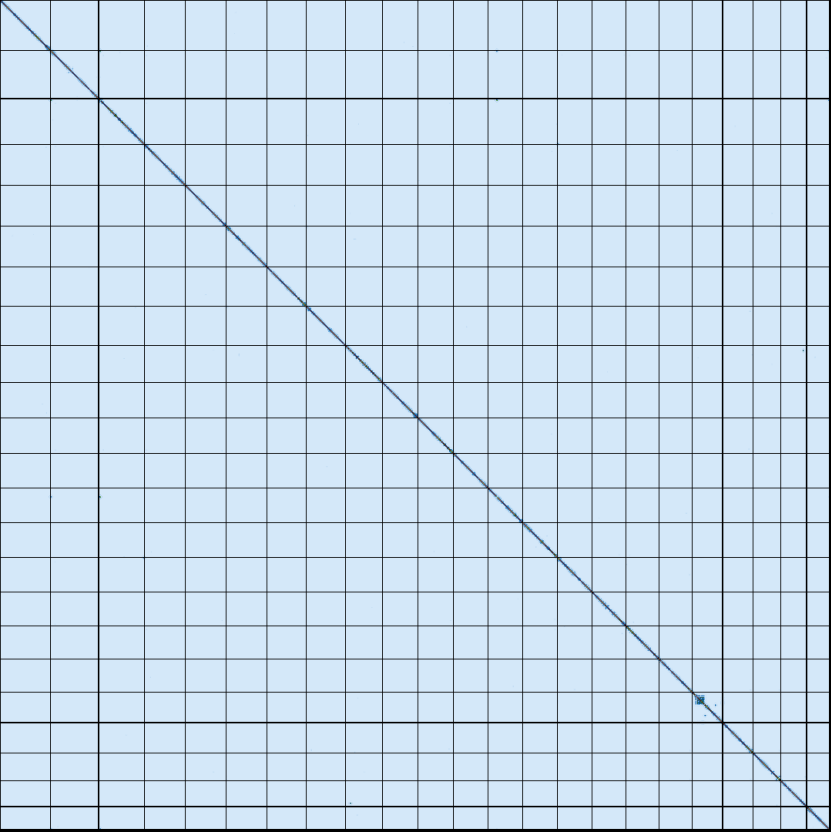
- . Interventions/Gb: 102
- . Contamination notes: "49 contigs were identified as bacterial sequences and removed, totaling 2.1 Mb, with the largest being 99 Kb "
- . Other observations: "A few modifications were made: 33 regions totaling 6.15 Mb were tagged as haplotigs "

Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|--------------|------------------------|-------------------|
| Total bp | 596,685,097 | 590,507,926 |
| GC % | 35.7 | 35.7 |
| Gaps/Gbp | 254.74 | 254.02 |
| Total gap bp | 15,200 | 17,200 |
| Scaffolds | 71 | 49 |
| Scaffold N50 | 25,083,287 | 25,083,287 |
| Scaffold L50 | 11 | 10 |
| Scaffold L90 | 21 | 20 |
| Contigs | 223 | 199 |
| Contig N50 | 6,057,000 | 6,057,000 |
| Contig L50 | 28 | 28 |
| Contig L90 | 99 | 98 |
| QV | 48.5375 | 57.0432 |
| Kmer compl. | 71.5043 | 71.2741 |
| BUSCO sing. | 97.4% | 97.5% |
| BUSCO dupl. | 0.7% | 0.5% |
| BUSCO frag. | 1.3% | 1.3% |
| BUSCO miss. | 0.6% | 0.7% |

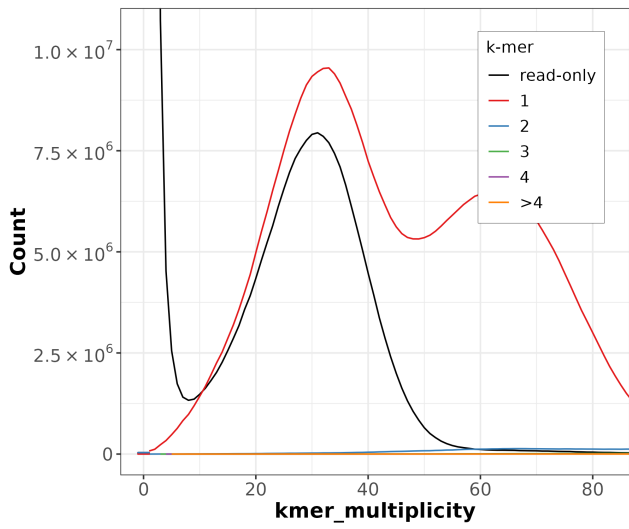
BUSCO 5.4.3 Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

HiC contact map of curated assembly

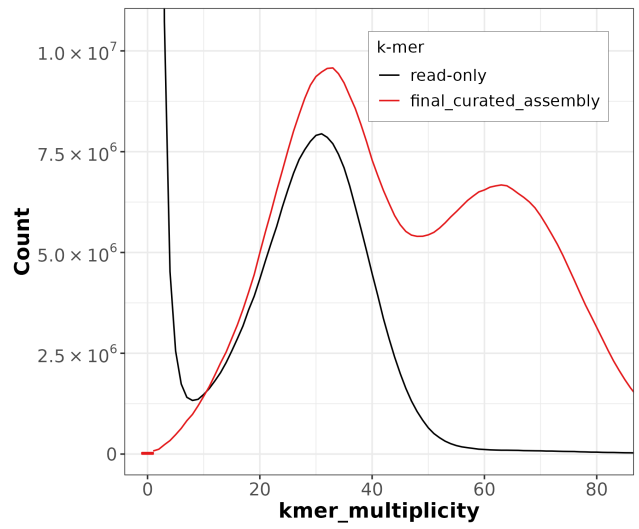


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

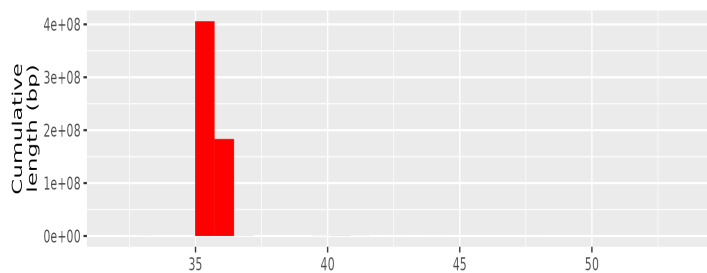


Distribution of k-mer counts per copy numbers found in asm

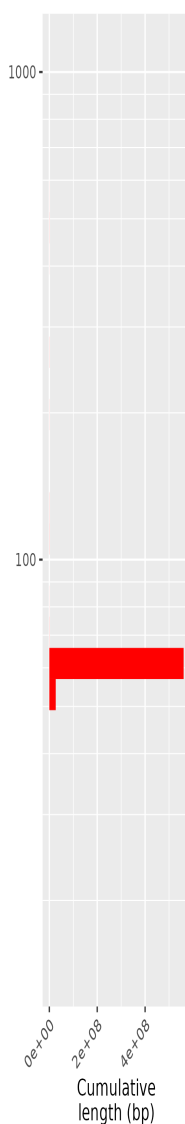
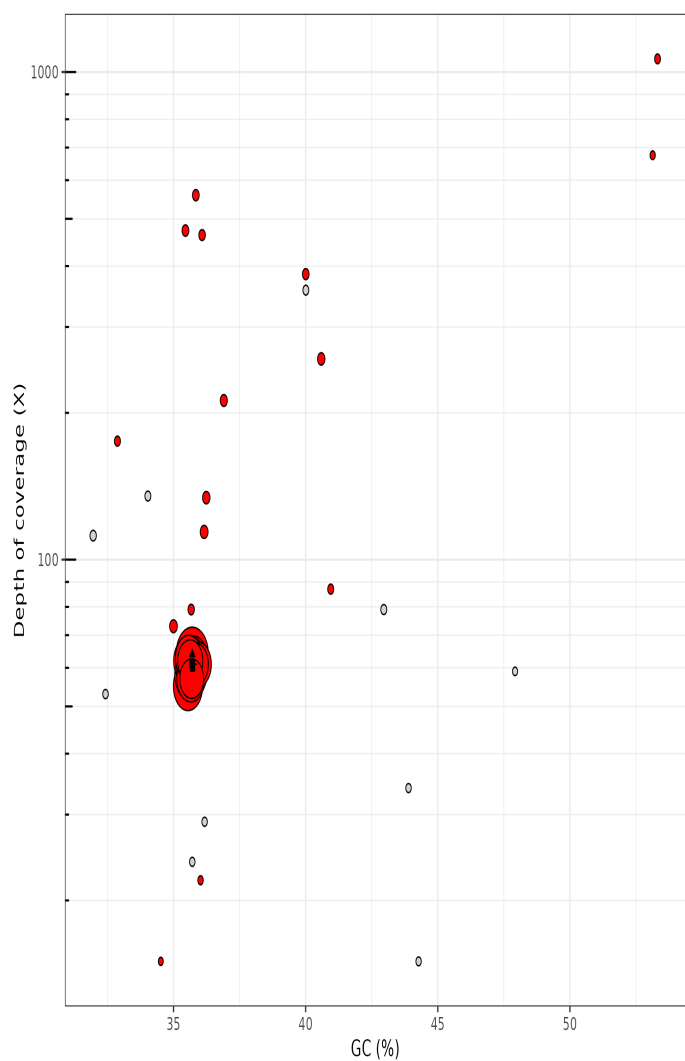


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



Length (bp)

○ 1e+07

○ 2e+07

○ 3e+07

Longest sequences (bp)

● keGlāTala1_1 - 35921338 (Eukaryota)

▲ keGlāTala1_2 - 33943121 (Eukaryota)

■ keGlāTala1_3 - 32312036 (Eukaryota)

+ keGlāTala1_4 - 29028597 (Eukaryota)

▣ keGlāTala1_5 - 28985948 (Eukaryota)

superkingdom

● Eukaryota

○ N/A

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 | 62 | 69 |

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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