

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| | |
|---------|--------------------|
| TxID | 470614 |
| ToLID | iqDecAlbi3 |
| Species | Decticus albifrons |
| Class | Insecta |
| Order | Orthoptera |

| Genome Traits | Expected | Observed |
|-------------------|----------------------|---------------|
| Haploid size (bp) | 5,749,217,804 | 6,526,031,816 |
| Haploid Number | 16 (source: direct) | 16 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | X0 | X0 |

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 8.8.Q71

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

- . Kmer completeness value is less than 90 for pri

Curator notes

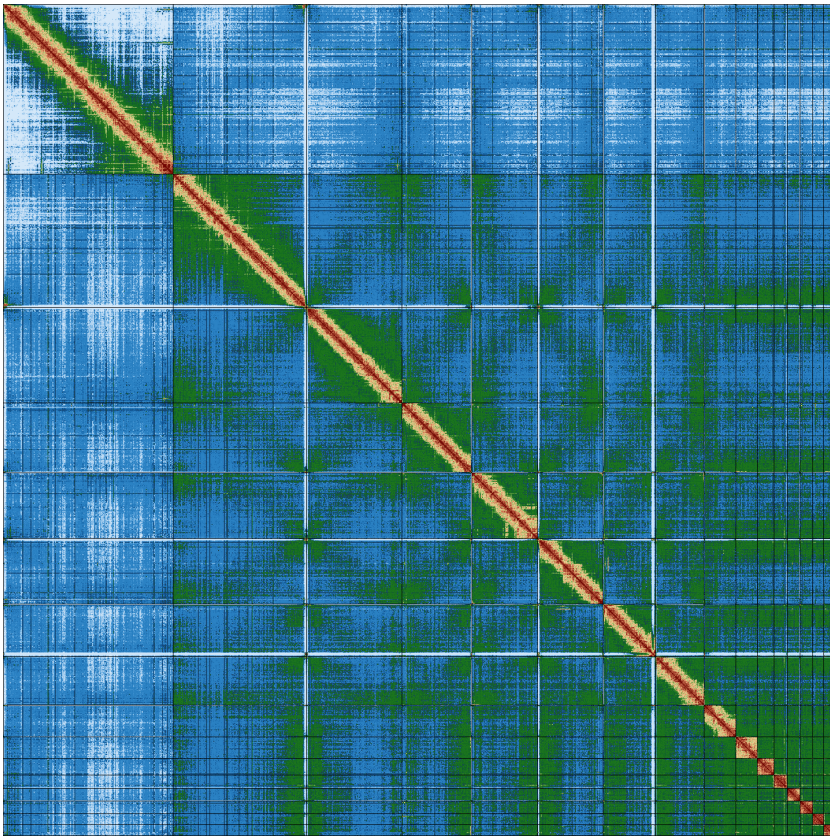
- . Interventions/Gb: None
- . Contamination notes: "Just one contig determind from fcsgx: ptg0001071_1 1 138374 138374 EXCLUDE plnt:plants 100 Lactuca sativa"
- . Other observations: "our first bioblitz data set - very high quality. SUPER_1 is the X chromosome. The sample is male but seems be X0."

Quality metrics table

| Metrics | Pre-curation pri | Curated pri |
|--------------|---------------------|----------------|
| Total bp | 6,526,460,112 | 6,526,031,816 |
| GC % | 40.85 | 40.85 |
| Gaps/Gbp | 0 | 7.2 |
| Total gap bp | 0 | 9,400 |
| Scaffolds | 85 | 37 |
| Scaffold N50 | 169,784,744 | 547,912,991 |
| Scaffold L50 | 15 | 4 |
| Scaffold L90 | 39 | 10 |
| Contigs | 85 | 84 |
| Contig N50 | 169,784,744 | 169,784,744 |
| Contig L50 | 15 | 15 |
| Contig L90 | 39 | 39 |
| QV | 71.1703 | 71.17 |
| Kmer compl. | 82.2097 | 82.2091 |
| BUSCO sing. | 93.5% | 93.4% |
| BUSCO dupl. | 4.2% | 4.2% |
| BUSCO frag. | 1.0% | 1.0% |
| BUSCO miss. | 1.3% | 1.3% |

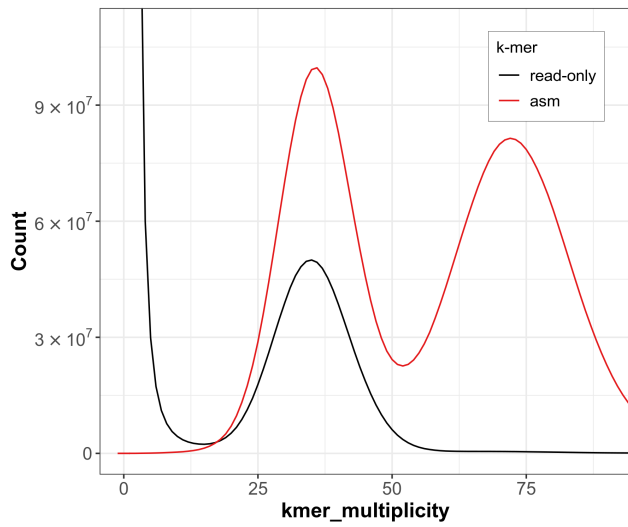
BUSCO: 5.8.3 (euk_genome_min, miniprot) / Lineage: insecta_odb12 (genomes:79, BUSCOs:3114)

HiC contact map of curated assembly

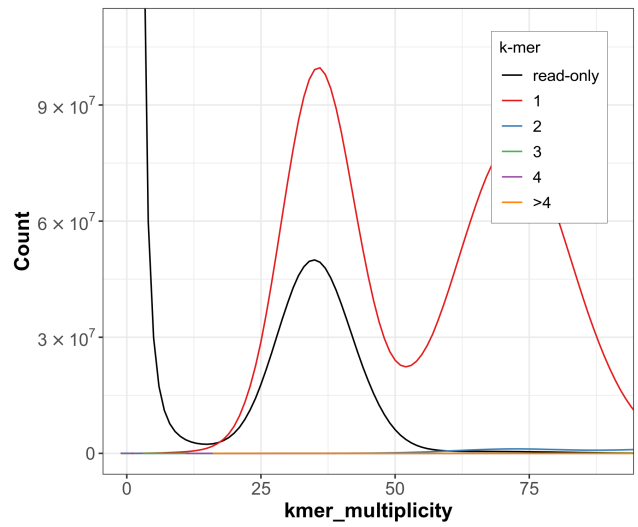


pri [\[LINK\]](#)

K-mer spectra of curated assembly

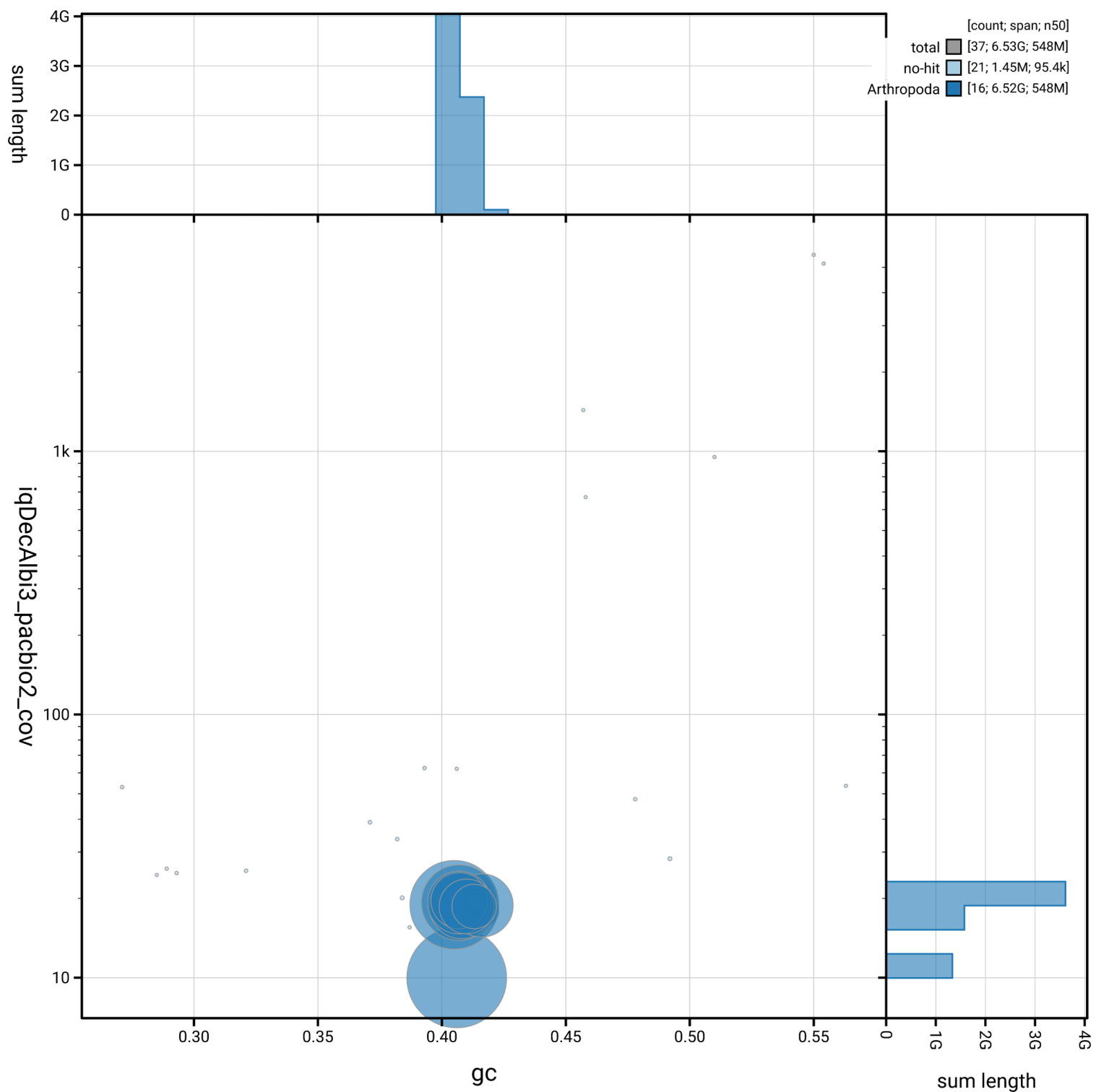


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



pri. 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 | HiC |
|----------|------|-----|
| Coverage | 66x | 73x |

Assembly pipeline

- **Hifiasm**
 - |_ *ver*: 0.25.0-r726
 - |_ *key param*: HiC
 - |_ *key param*: 13
- **purge_dups**
 - |_ *ver*: 1.2.5
 - |_ *key param*: NA

Curation pipeline

- **GRIT_Rapid**
 - |_ *ver*: 1a3d79a8
 - |_ *key param*: NA

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