ERGA Assembly Report
v24.10.15

Tags: ERGA-BGE

TxID	3350002
ToLID	**idIrwNobi7**
Species	Irwiniella nobilipennis
Class	Insecta
Order	Diptera

Genome Traits	Expected	Observed
Haploid size (bp)	305,332,931	373,623,222
Haploid Number	6 (source: ancestor)	6
Ploidy	3 (source: ancestor)	2
Sample Sex	XX	XX

EBP metrics summary and curation notes

Obtained EBP quality metric for : 7.7.Q72

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

. Observed Haploid size (bp) has >20% difference with Expected
. Observed Ploidy is different from Expected

. Kmer completeness value is less than 90 for

Curator notes

. Interventions/Gb: 13
. Contamination notes: "Removed one Pseudomonas contig from initial 12 contigs. This corresponds to the shoulder on left of het/1n peak in merqury plot. Due to this, genomescope did not estimate genome size accurately. Loss in k-mer completeness due to contaminant removal."
. Other observations: "No Hi-C was produced for this species (funding ran dry, I think). The draft assembly was aligned to idTheUnic2.1 (GCA_949987705) and idTheNobi1.1 (GCA_963855945) assemblies, which confirmed order of contigs inferred based on repeats types and read overlaps. The pre-curation WGA is shown in the image (instead of contact map). 2 contig joins made in SUPER_2 and 3 contig joins made in SUPER_X with 0 gap characters. The result is all sequence placed into T2T chromosomes."
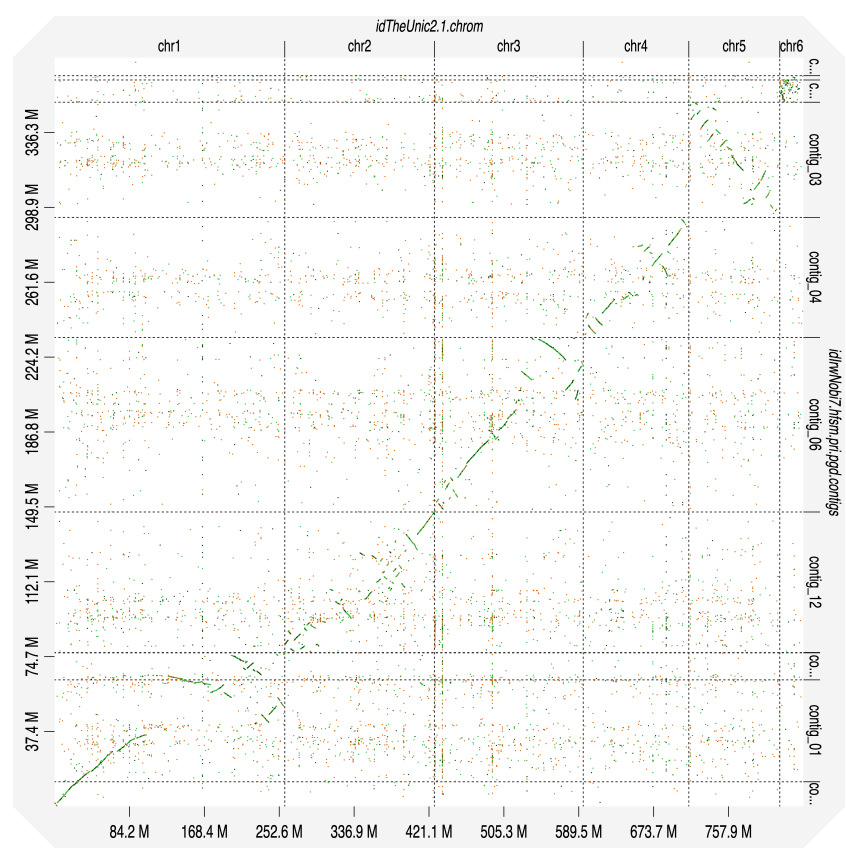
Quality metrics table

Metrics	Pre-curation <pri>	Curated <pri>
Total bp	373,685,851	373,623,222
GC %	35.99	35.98
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	12	6
Scaffold N50	59,897,714	70,131,851
Scaffold L50	3	3
Scaffold L90	6	5
Contigs	12	6
Contig N50	59,897,714	70,131,851
Contig L50	3	3
Contig L90	6	5
QV	71.8728	72.1545
Kmer compl.	91.1877	83.947
BUSCO sing.	98.8%	98.3%
BUSCO dupl.	0.2%	0.7%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.9%	0.9%

Warning! BUSCO versions or lineage datasets are not the same across results:
BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: arthropoda_odb10 (genomes:90, BUSCOs:1013)
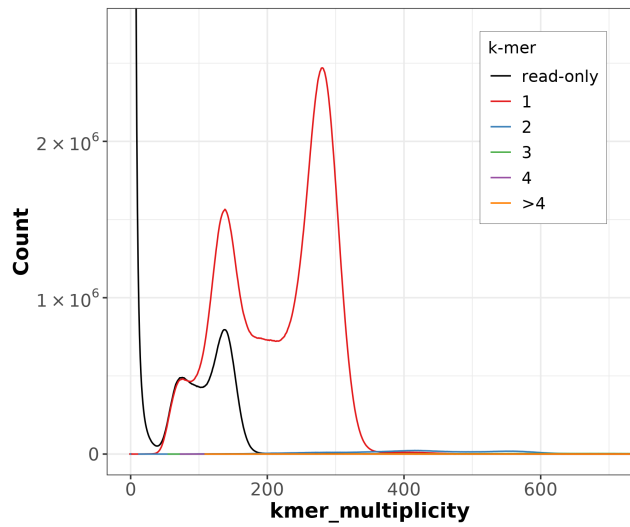BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)
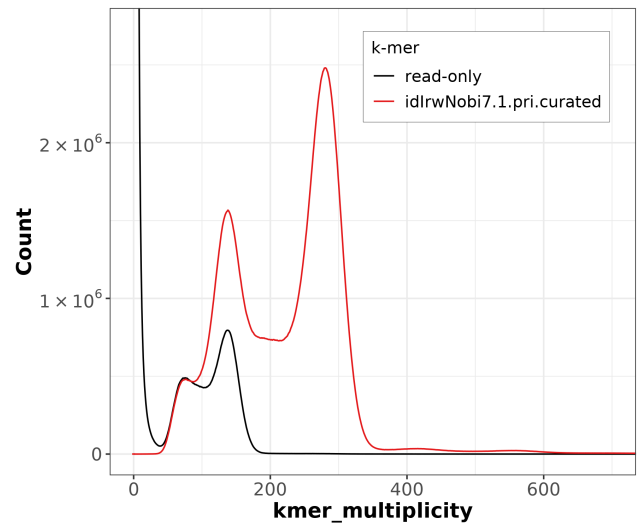
HiC contact map of curated assembly

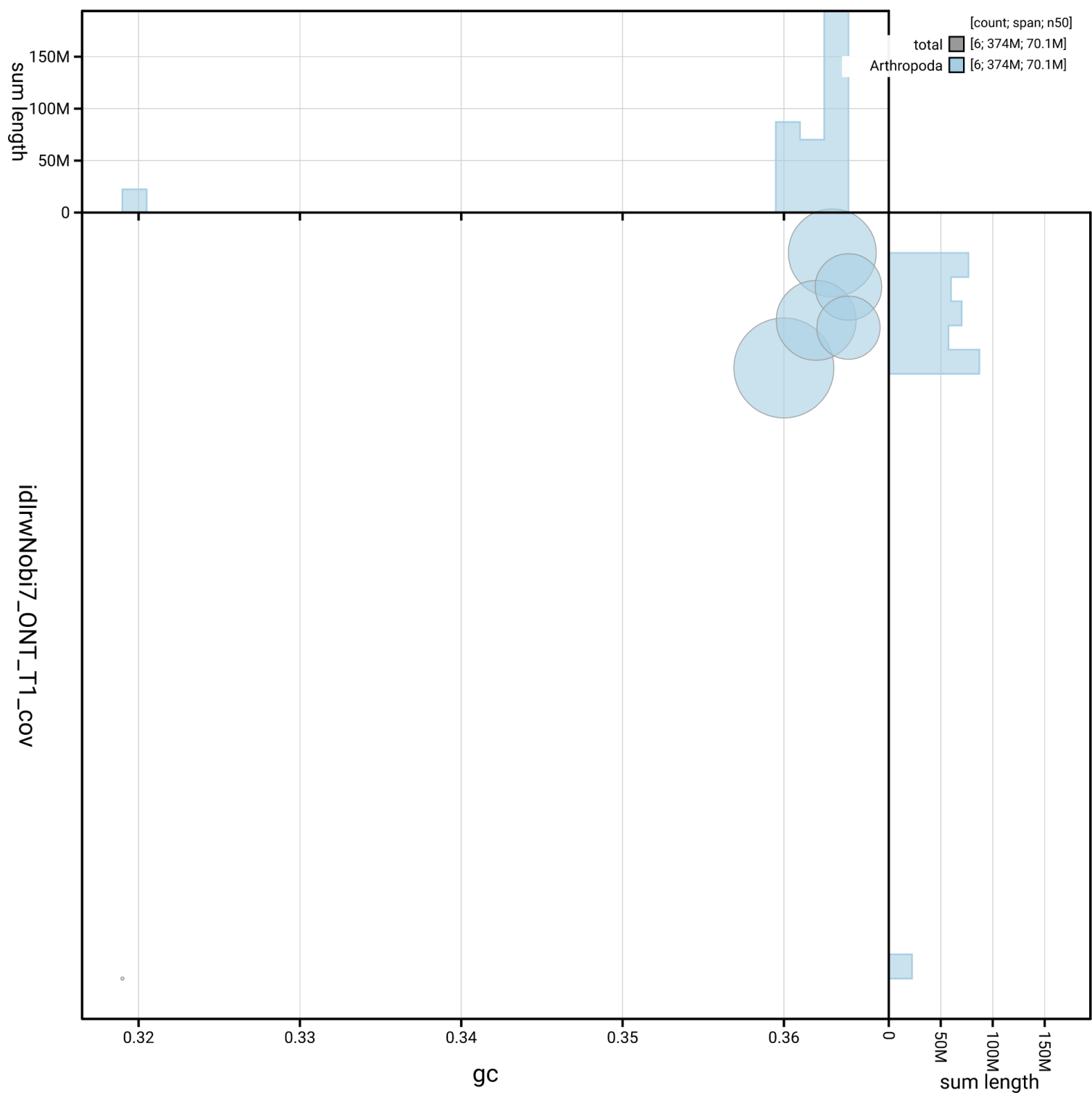File link is missing!

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

. 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
Coverage	347x

Assembly pipeline

- **CLAWS**
  |_ *ver:* v2.3
  |_ *key param:* NA
- **Filtlong**
  |_ *ver:* v0.2.1
  |_ *key param:* --min_length 1000 --min_mean_q 99 -t 58000000000
- **Hifiasm**
  |_ *ver:* 0.24.0
  |_ *key param:* --ont
- **purge_dups**
  |_ *ver:* 1.2.6
  |_ *key param:* NA

Curation pipeline

- **D-GENIES**
  |_ *ver:* None
  |_ *key param:* NA
- **Blobtoolkit Nextflow**
  |_ *ver:* None
  |_ *key param:* NA

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Date and time: 2026-02-24 19:45:47 CET