

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1526741
ToLID	xbXylDors1
Species	Xylophaga dorsalis
Class	Bivalvia
Order	Myida

Genome Traits	Expected	Observed
Haploid size (bp)	453,366,001	451,794,626
Haploid Number	19 (source: ancestor)	18
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	ubnknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q51

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

- . Observed Haploid Number is different from Expected
- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for collapsed
- . More than 1000 gaps/Gbp for collapsed

Curator notes

- . Interventions/Gb: 367
- . Contamination notes: "We found contaminants in the yabs scaffolded assembly within six small scaffolds which were removed from the curated assembly submitted for review. The contaminants corresponded mostly to bacterial sequences (Pseudomonadota, Bacillota)"
- . Other observations: "The reviewing process led to several changes in many of the super scaffolds, with six additional haplotigs found and removed. We found it very difficult to localize a number of these scaffolds (mostly centromeric) which were set as unlocs. The sex of the specimen was set to -unknown- in our lms system. We could find the sex chromosome in the assembly. We found a large haplotig (4 Mbases) which was removed before remapping."

Quality metrics table

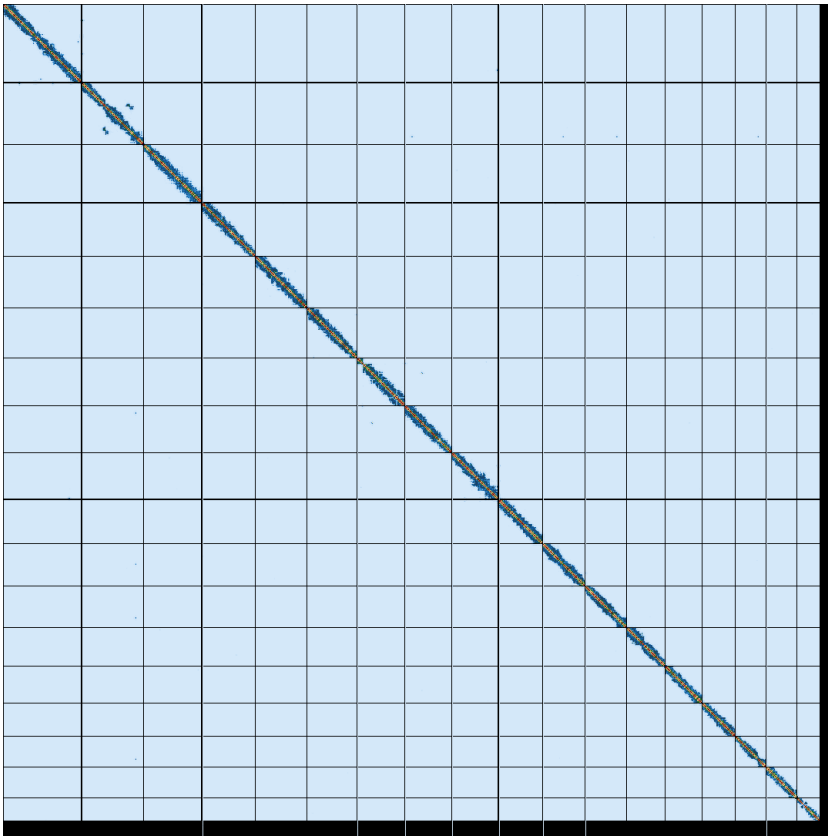
Metrics	Pre-curation collapsed	Curated collapsed
Total bp	456,718,437	451,794,626
GC %	38.08	38.08
Gaps/Gbp	1,907.08	2,078.38
Total gap bp	174,200	187,800
Scaffolds	392	320
Scaffold N50	24,961,909	25,438,142
Scaffold L50	8	8
Scaffold L90	18	16
Contigs	1,263	1,259
Contig N50	1,293,548	1,253,263
Contig L50	83	85
Contig L90	509	510
QV	51.1047	51.104
Kmer compl.	68.8674	68.4412
BUSCO sing.	90.5%	91.2%
BUSCO dupl.	1.5%	0.7%
BUSCO frag.	4.6%	4.6%
BUSCO miss.	3.4%	3.5%

Warning! BUSCO versions or lineage datasets are not the same across results:

BUSCO: 5.4.0 (euk_genome_met, metaeuk) / Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

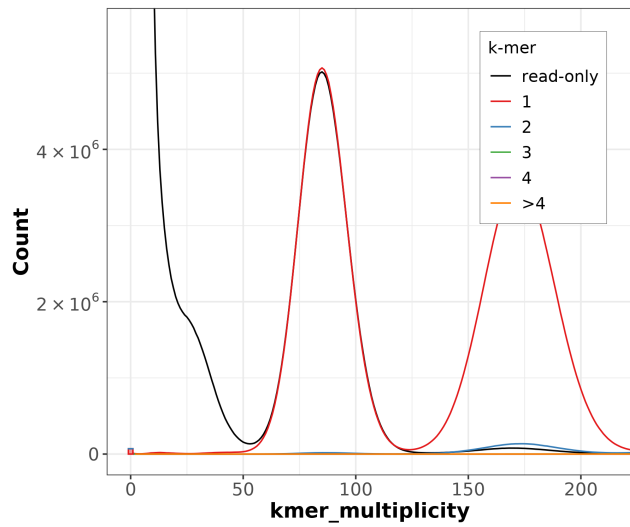
BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

HiC contact map of curated assembly

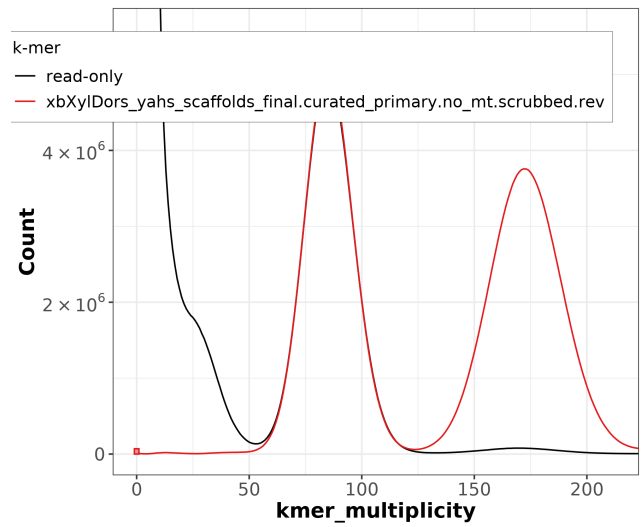


collapsed [\[LINK\]](#)

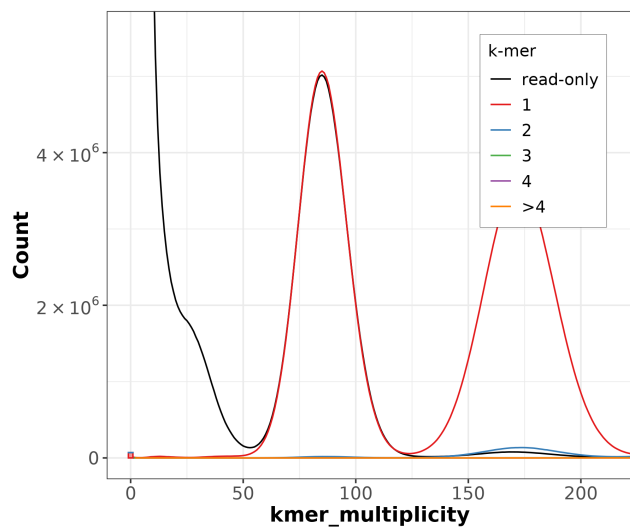
K-mer spectra of curated assembly



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

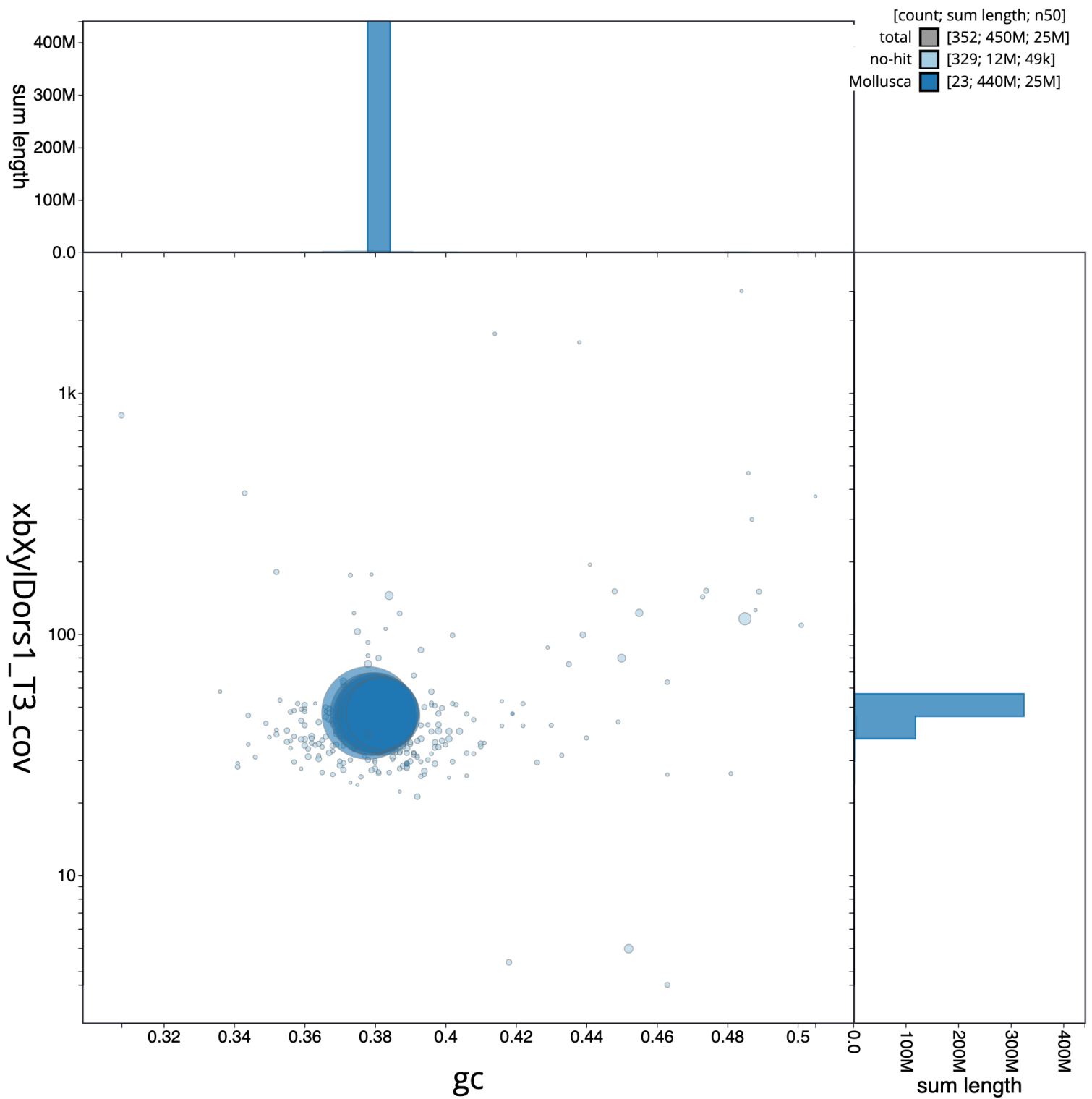


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



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	ONT	Illumina	OmniC
Coverage	93x	230x	178x

Assembly pipeline

- **Trim_galore**
 - |_ *ver*: 0.6.7
 - |_ *key param*: --gzip
 - |_ *key param*: =q 20
 - |_ *key param*: --paired
 - |_ *key param*: retain_unpaired
- **Filtlong**
 - |_ *ver*: 0.2.1
 - |_ *key param*: NA
- **Flye**
 - |_ *ver*: 2.9.1-b1780
 - |_ *key param*: NA
- **hypo**
 - |_ *ver*: 1.0.3
 - |_ *key param*: NA
- **purge_dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA
- **YaHS**
 - |_ *ver*: 1.2a
 - |_ *key param*: NA

Curation pipeline

- **PretextView**
 - |_ *ver*: 0.2.5
 - |_ *key param*: NA
- **GRIT_Rapid**
 - |_ *ver*: 2.0
 - |_ *key param*: NA

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