ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3065877
ToLID	**icHerPorc**
Species	Herpes porcellus
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	860,627,567	775,827,564
Haploid Number	11 (source: ancestor)	13
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q49

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 pri
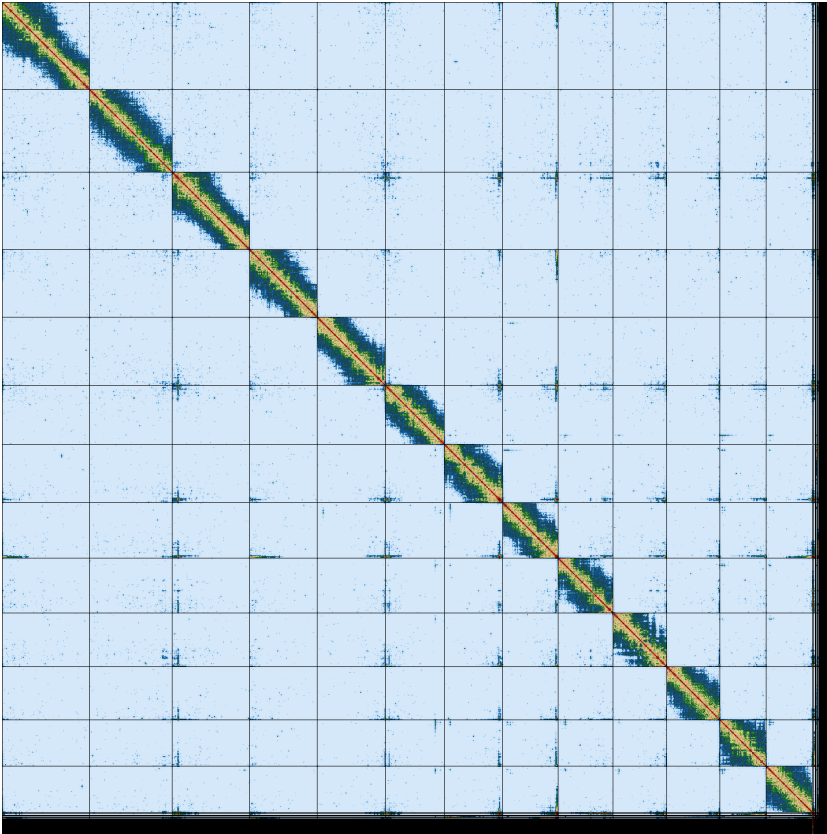. BUSCO single copy value is less than 90% for pri

Curator notes

. Interventions/Gb: 20
. Contamination notes: "No presence of contaminants."
. Other observations: "None"

Quality metrics table

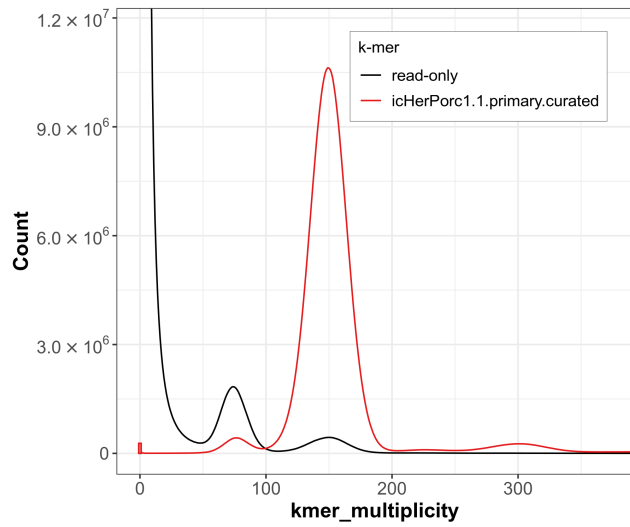| Metrics	Pre-curation pri	Curated pri
Total bp	776,183,321	775,827,564
GC %	33.36	33.36
Gaps/Gbp	182.95	193.34
Total gap bp	14,200	16,200
Scaffolds	159	151
Scaffold N50	54,968,996	54,968,996
Scaffold L50	6	6
Scaffold L90	12	12
Contigs	301	301
Contig N50	8,297,486	8,297,486
Contig L50	29	29
Contig L90	98	98
QV	49.1387	49.1367
Kmer compl.	86.6404	86.6333
BUSCO sing.	89.7%	89.8%
BUSCO dupl.	0.6%	0.5%
BUSCO frag.	1.0%	1.0%
BUSCO miss.	8.7%	8.7%

BUSCO: 5.8.2 (euk_genome_aug, augustus) / Lineage: arthropoda_odb10 (genomes:90, BUSCOs:1013)

HiC contact map of curated assembly

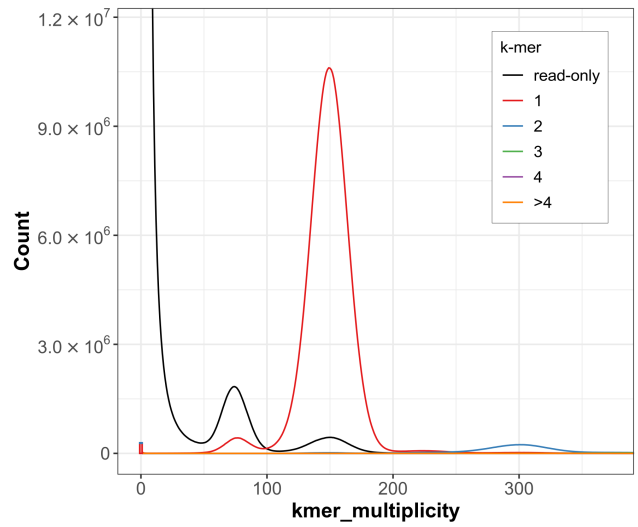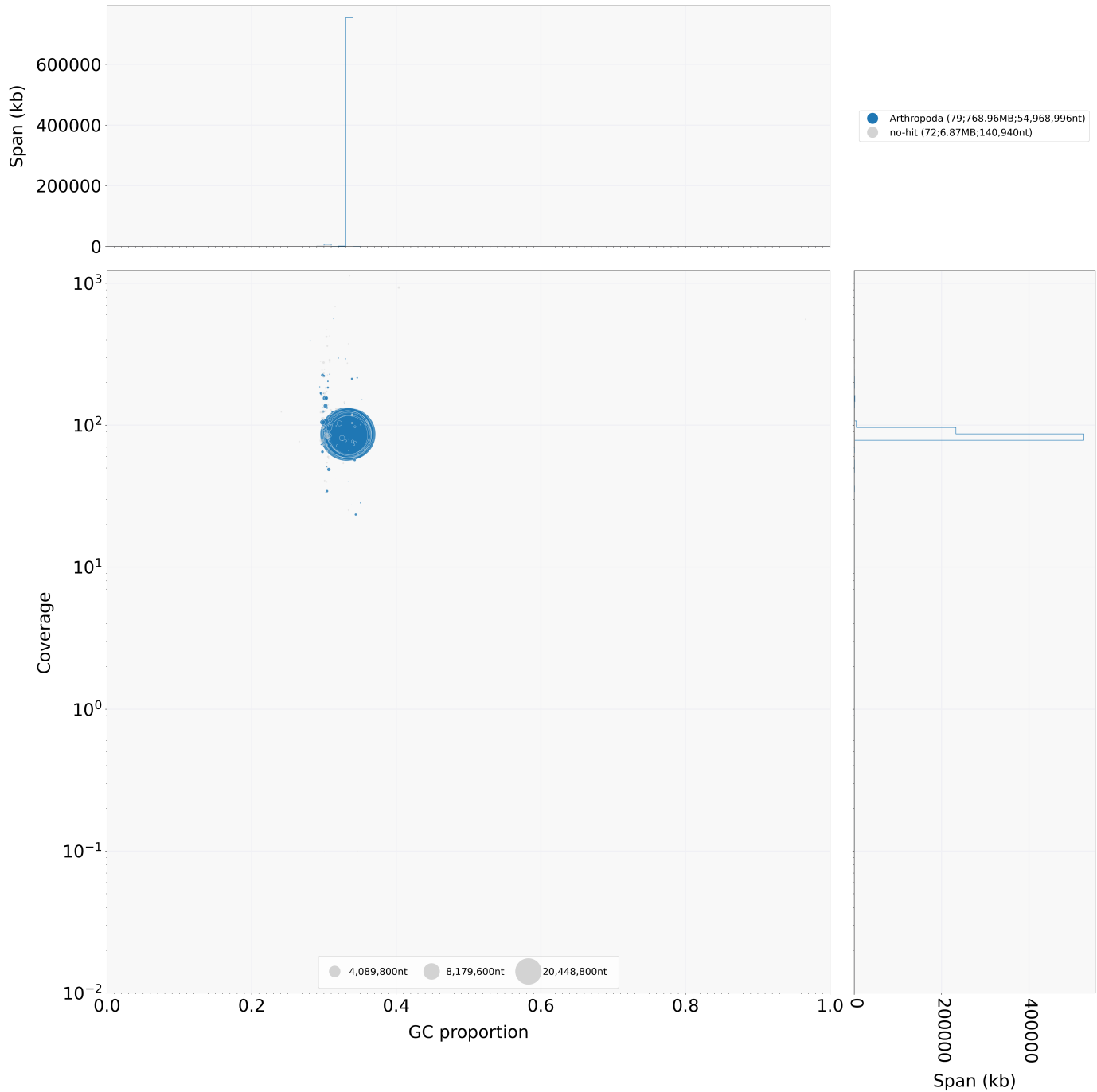**pri** [LINK]

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

filename.blobDB.json.bestsum.phylum.p8.span.100.blobplot.bam0

- Arthropoda (79;768.96MB;54,968,996nt)
- no-hit (72;6.87MB;140,940nt)

4,089,800nt   8,179,600nt   20,448,800nt

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	ONT	Bionano	OmniC
Coverage	174x	NA	48x

Assembly pipeline

- **Necat**
    |_ *ver:* 0.0.1
    |_ *key param:* NA
- **purge_dups**
    |_ *ver:* 1.2.5
    |_ *key param:* NA
- **YaHS**
    |_ *ver:* 1.1
    |_ *key param:* NA

Curation pipeline

- **sanger-tol/curationpretext**
    |_ *ver:* 1.4.1
    |_ *key param:* NA
- **PretextView**
    |_ *ver:* 1.0.3
    |_ *key param:* NA

Submitter: Carmela Gissi
Affiliation: UNIBA

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