

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3229189
ToLID	ilNycAphr2
Species	Nychiodes aphrodite
Class	Insecta
Order	Lepidoptera

Genome Traits	Expected	Observed
Haploid size (bp)	668,888,793	691,271,241
Haploid Number	30 (source: ancestor)	22
Ploidy	2 (source: ancestor)	2
Sample Sex	ZW	ZW

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q63

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

Curator notes

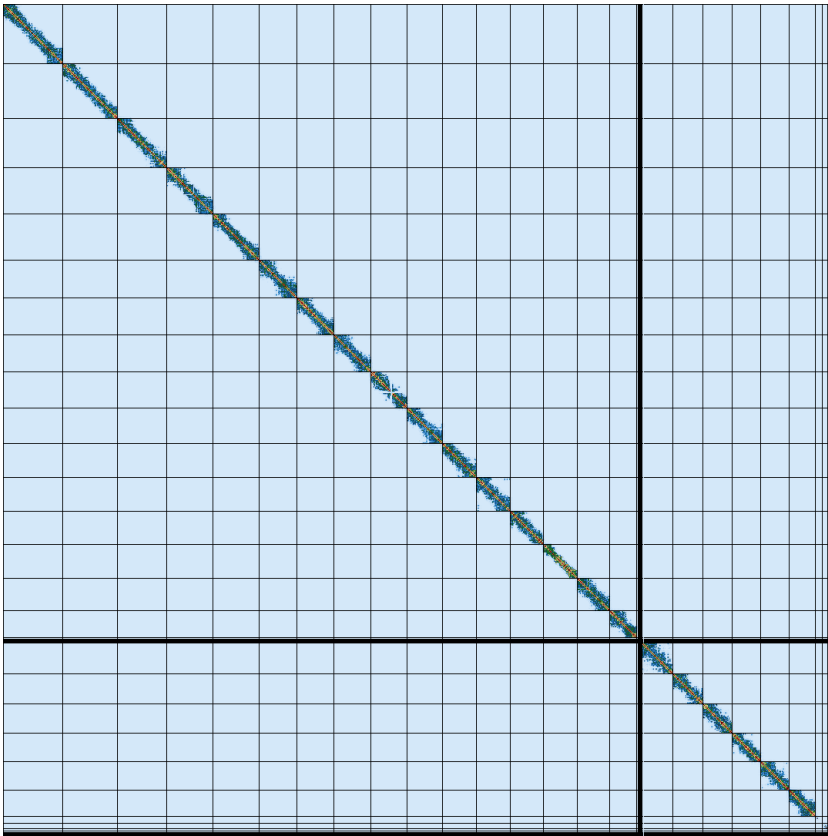
- . Interventions/Gb: 12
- . Contamination notes: "We removed a total of 49 contaminant scaffolds/contigs detected with BTK and FCS-GX. As FCS its faster, it was used to obtain the blobplot shown."
- . Other observations: "We curated the hifiasm primary. Curation made 4 cuts in contigs, 1 break at a gap and 3 joins. We both sex chromosomes, the Z chromosome and the W. The mitogenome was assembled with FOAMv0.5 into a single circular contig of 15,485 bp. Note that the MT is not present in the assembly under review and it will be added just before the ENA upload."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	700,508,710	691,271,241
GC %	36.62	36.4
Gaps/Gbp	1.43	4.34
Total gap bp	200	600
Scaffolds	195	144
Scaffold N50	29,429,818	29,451,812
Scaffold L50	10	10
Scaffold L90	21	20
Contigs	196	147
Contig N50	28,094,440	28,094,440
Contig L50	10	10
Contig L90	21	21
QV	61.9876	63.3307
Kmer compl.	87.5682	86.766
BUSCO sing.	97.9%	97.9%
BUSCO dupl.	0.5%	0.5%
BUSCO frag.	0.2%	0.2%
BUSCO miss.	1.4%	1.4%

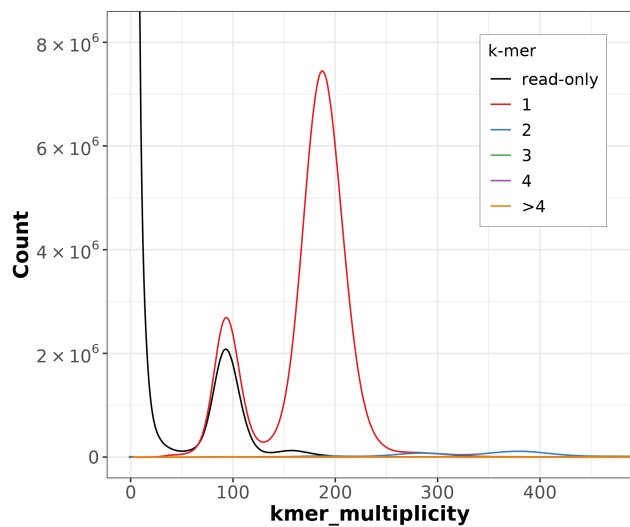
BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: lepidoptera_odb10 (genomes:16, BUSCOs:5286)

HiC contact map of curated assembly

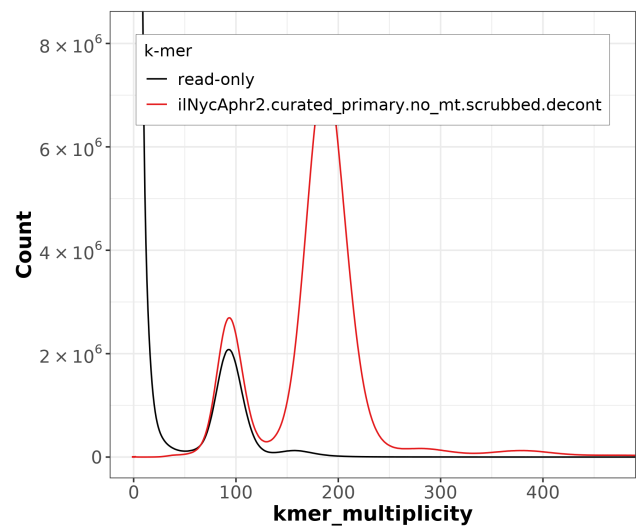


pri [\[LINK\]](#)

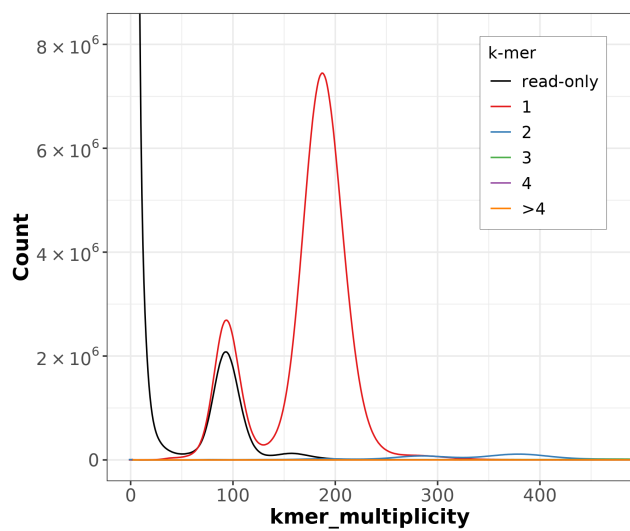
K-mer spectra of curated assembly



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

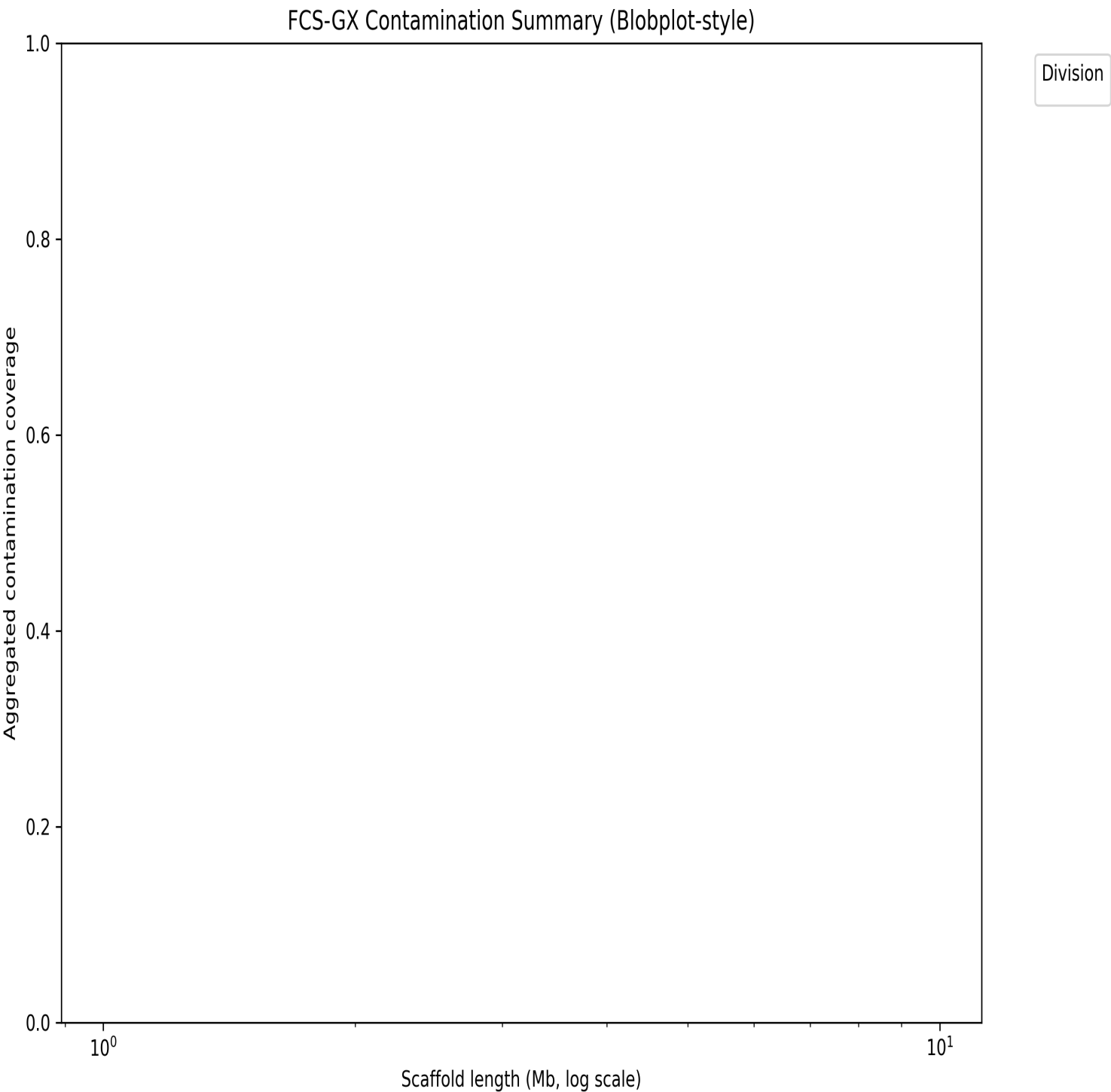


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



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	Illumina	Omni-C
Coverage	96	63	61

Assembly pipeline

- **CLAWS pipeline**
 - |_ *ver*: 2.3.0
 - |_ *key param*: NA
- **Trim_galore**
 - |_ *ver*: 0.6.7
 - |_ *key param*: NA
- **Filtlong**
 - |_ *ver*: 0.2.1
 - |_ *key param*: NA
- **hifiasm**
 - |_ *ver*: 0.24.0
 - |_ *key param*: NA
- **YaHS**
 - |_ *ver*: 1.2a
 - |_ *key param*: NA
- **FOAM pipeline**
 - |_ *ver*: 0.5
 - |_ *key param*: NA
- **mitos**
 - |_ *ver*: 2.1.3
 - |_ *key param*: NA

Curation pipeline

- **Blobtoolkit dtol nextflow pipeline**
 - |_ *ver*: 0.6
 - |_ *key param*: NA
- **FCS-GX**
 - |_ *ver*: v0.5.5
 - |_ *key param*: NA
- **PretextViewAI**
 - |_ *ver*: 1.0.5
 - |_ *key param*: NA

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