

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1656920
ToLID	kaSymBrak
Species	<i>Symplegma brakenhielmi</i>
Class	Asciidiacea
Order	Stolidobranchia

Genome Traits	Expected	Observed
Haploid size (bp)	639,728,327	562,276,130
Haploid Number	16 (source: ancestor)	16
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q41

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

- . Kmer completeness value is less than 90 for pri
- . Assembly length loss > 3% for pri
- . More than 1000 gaps/Gbp for pri

Curator notes

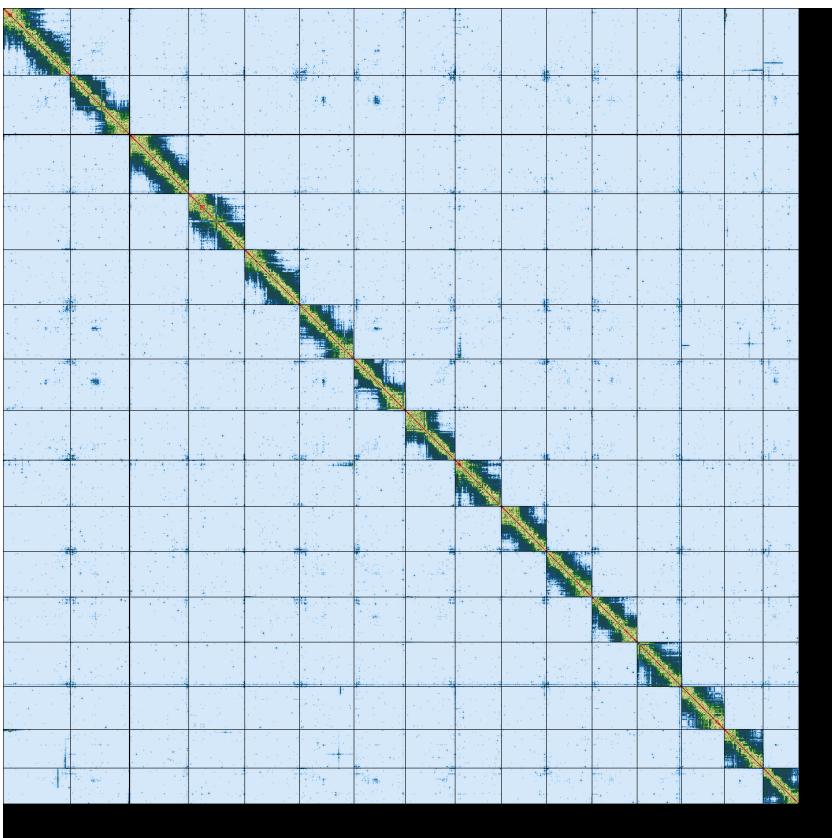
- . Interventions/Gb: 219
- . Contamination notes: "From the BlobTools analysis, chromosomes SUPER_12 and SUPER_16 are classified as "Arthropoda" instead of "Chordata," thus identifying them as contaminants. Both align to the same sequence, with an alignment length of 6,051 in both cases."
- . Other observations: "Report EAR after revisions."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	600,884,103	562,276,130
GC %	40.66	40.22
Gaps/Gbp	1,214.88	1,412.12
Total gap bp	73,000	95,600
Scaffolds	1,101	700
Scaffold N50	30,480,455	33,584,967
Scaffold L50	9	8
Scaffold L90	28	15
Contigs	1,831	1,494
Contig N50	1,215,688	1,243,442
Contig L50	135	125
Contig L90	595	508
QV	39.7478	41.8443
Kmer compl.	84.7795	80.5569
BUSCO sing.	88.4%	90.3%
BUSCO dupl.	4.1%	1.9%
BUSCO frag.	2.2%	1.8%
BUSCO miss.	5.3%	6.1%

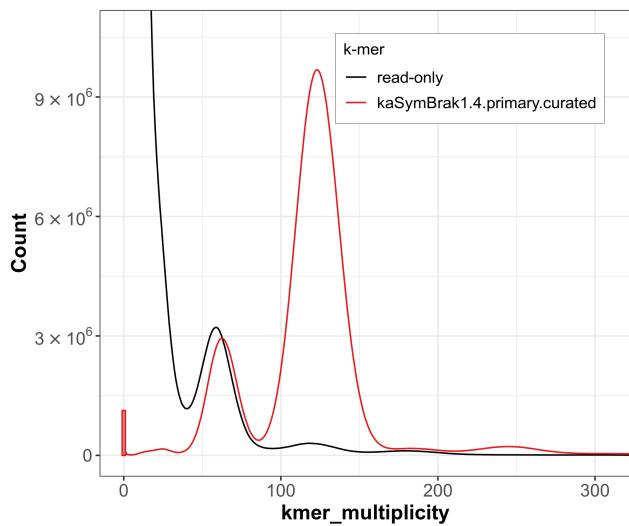
BUSCO: 5.8.2 (euk_genome_aug, augustus) / Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

HiC contact map of curated assembly

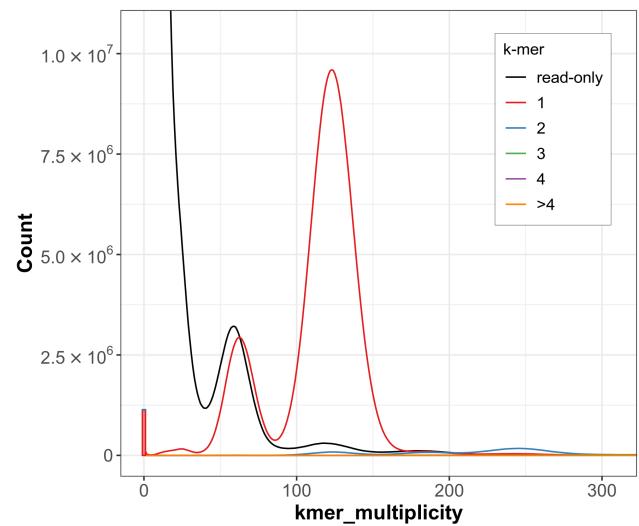


pri [LINK]

K-mer spectra of curated assembly



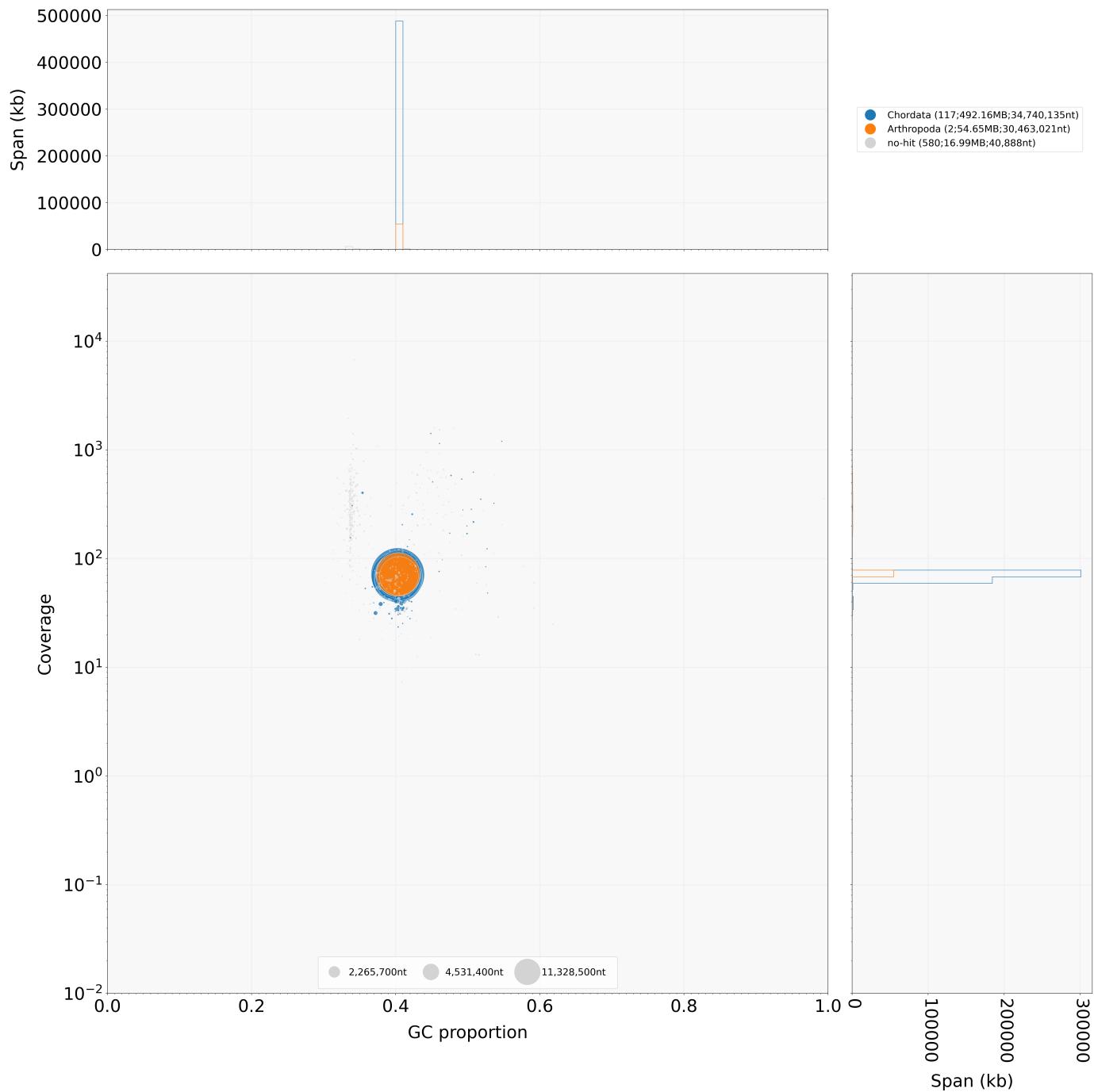
Distribution of k-mer counts coloured by their presence in reads/assemblies



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



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	HiC
Coverage	169x	NA	104x

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: 1.5.0
 - |_ key param: NA
- **PretextView**
 - |_ ver: 1.0.3
 - |_ key param: NA

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