ERGA Assembly Report

v24.10.15

Tags: ERGA-Pilot

TxID	30301
ToLID	**kaBotSchl1**
Species	Botryllus schlosseri
Class	Ascidiacea
Order	Stolidobranchia

Genome Traits	Expected	Observed
Haploid size (bp)	536,801,721	525,542,369
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
. BUSCO single copy value is less than 90% for pri
. Assembly length loss > 3% for pri

Curator notes

. Interventions/Gb: None
. Contamination notes: "No presence of contaminants."
. Other observations: "Manual Curation by Jo Wood (Sanger Institute)"

Quality metrics table

| Metrics	Pre-curation pri	Curated pri
Total bp	669,506,172	525,542,369
GC %	40.46	40.47
Gaps/Gbp	648.24	913.34
Total gap bp	86,800	96,000
Scaffolds	560	411
Scaffold N50	29,857,706	28,655,804
Scaffold L50	10	8
Scaffold L90	49	15
Contigs	994	891
Contig N50	1,847,095	1,823,425
Contig L50	112	90
Contig L90	373	311
QV	42.6514	41.8891
Kmer compl.	75.4032	62.9441
BUSCO sing.	84.5%	89.7%
BUSCO dupl.	7.8%	0.6%
BUSCO frag.	1.5%	1.3%
BUSCO miss.	6.3%	8.4%

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

HiC contact map of curated assembly
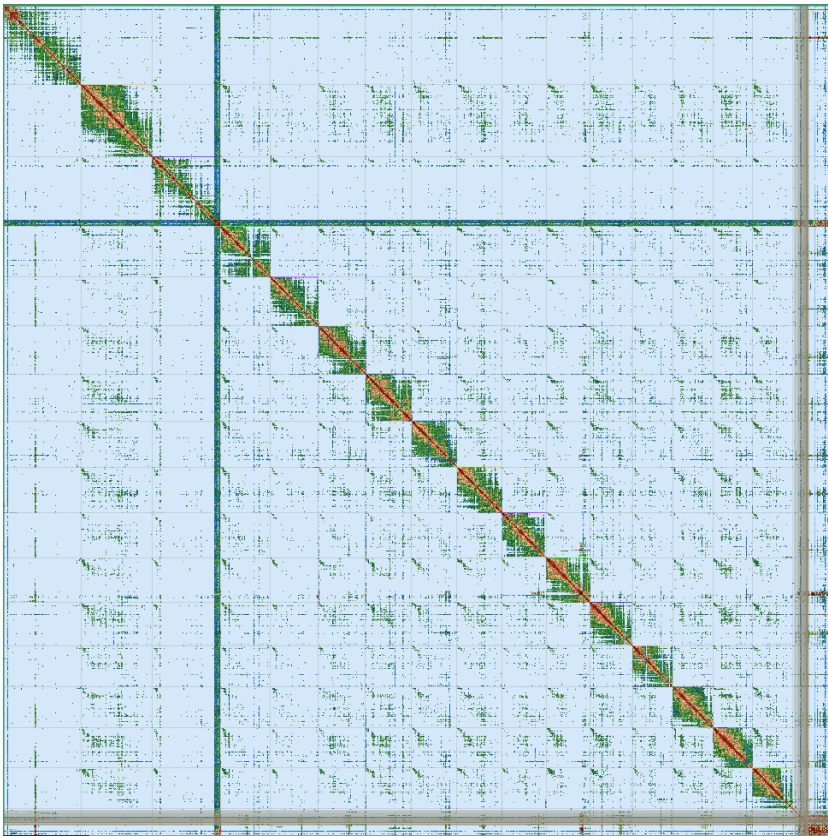
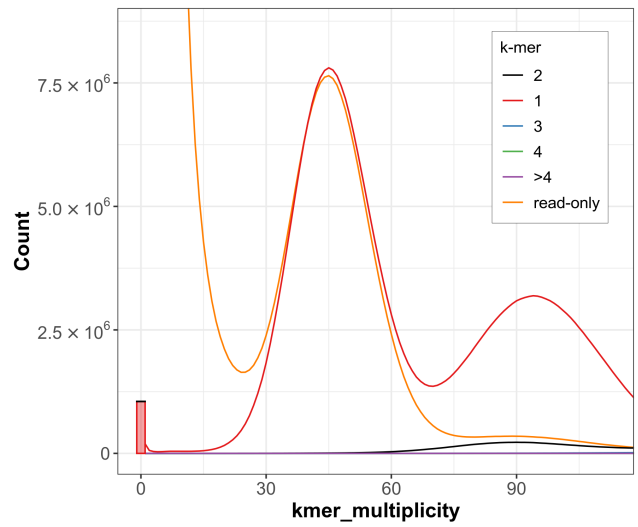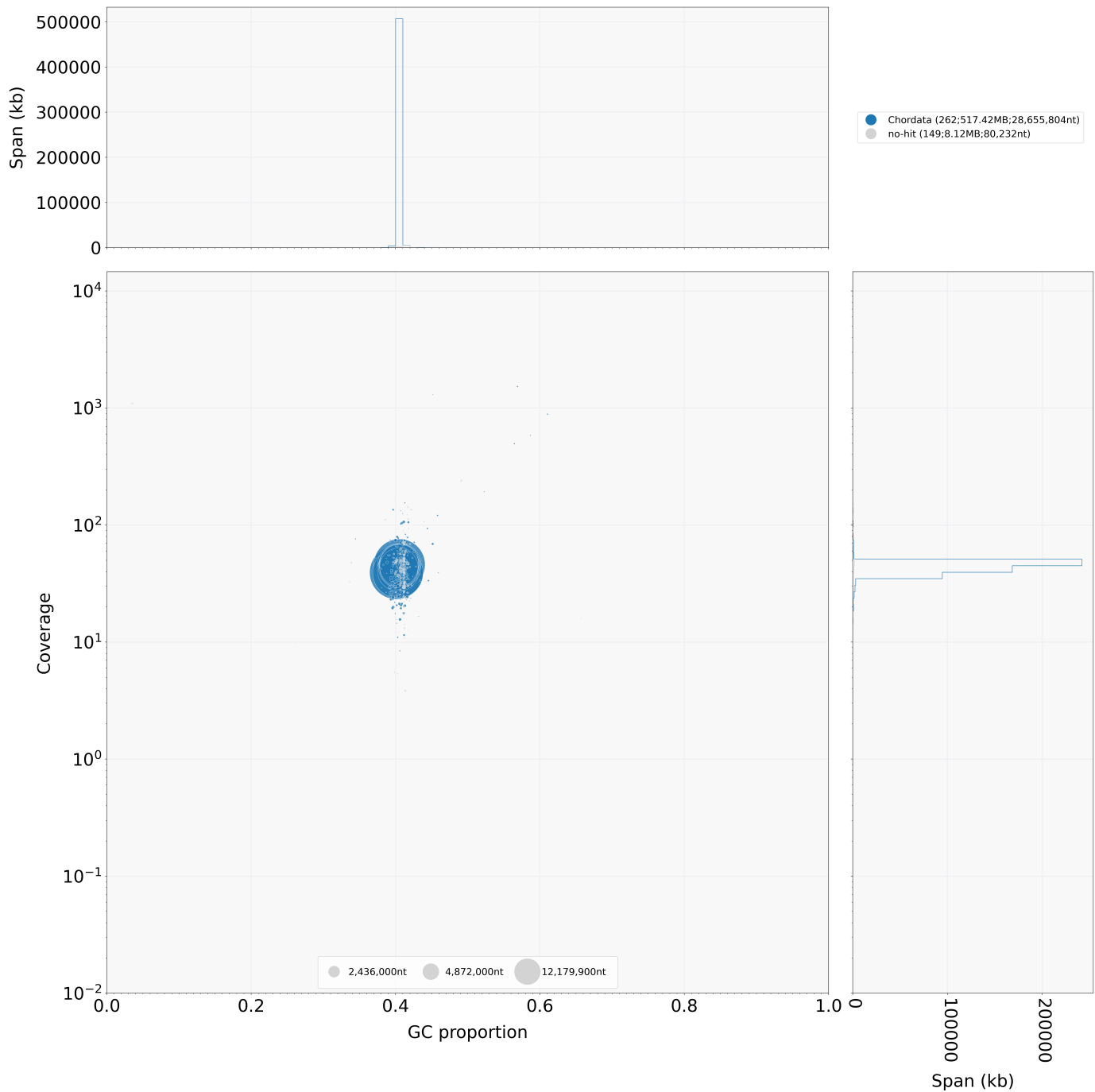**pri** [LINK]

K-mer spectra of curated assembly
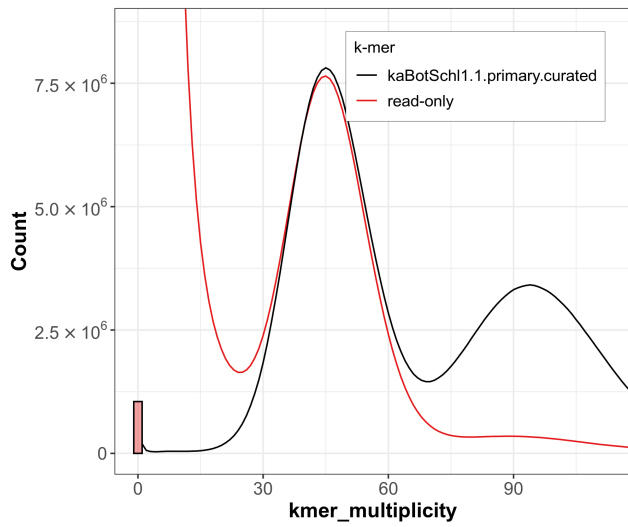
Distribution of k-mer counts coloured by their presence in reads/assemblies

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

Legend:
- Chordata (262;517.42MB;28,655,804nt)
- no-hit (149;8.12MB;80,232nt)

Bubble size legend: 2,436,000nt, 4,872,000nt, 12,179,900nt

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	135x	NA	141x

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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