ERGA Assembly Report
v24.10.15

Tags: ERGA-BGE

TxID	1960102
ToLID	**jaActMedi1**
Species	Actinia mediterranea
Class	Anthozoa
Order	Actiniaria

Genome Traits	Expected	Observed
Haploid size (bp)	301,515,822	305,702,489
Haploid Number	6 (source: ancestor)	19
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q46

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 collapsed

Curator notes

. Interventions/Gb: 73
. Contamination notes: "No clear contaminants were found either using buscogenes or buscoregions (more sensitive) - did not rerun after addressing reviewers"
. Other observations: "The strength of the HiC signal, particularly along the diagonal was weaker than usual, and therefore as suggested by the reviewers, used the mq0 pretext map for the reviewing process. With a mq0 map we were able to localize all unlocs, and incorporate a few more scaffolds into the main assembly. The sex of the specimen was set to unknown in our lims system and we were not able to find any sex chromosomes based on ONT coverage either"

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	305,700,289	305,702,489
GC %	37.85	37.85
Gaps/Gbp	202.81	238.79
Total gap bp	12,400	14,600
Scaffolds	45	36
Scaffold N50	16,244,619	15,300,222
Scaffold L50	7	8
Scaffold L90	16	17
Contigs	107	109
Contig N50	5,958,017	5,958,017
Contig L50	16	16
Contig L90	54	54
QV	46.3055	46.3055
Kmer compl.	85.1608	85.1608
BUSCO sing.	94.8%	94.8%
BUSCO dupl.	0.4%	0.4%
BUSCO frag.	1.6%	1.6%
BUSCO miss.	3.2%	3.2%

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)
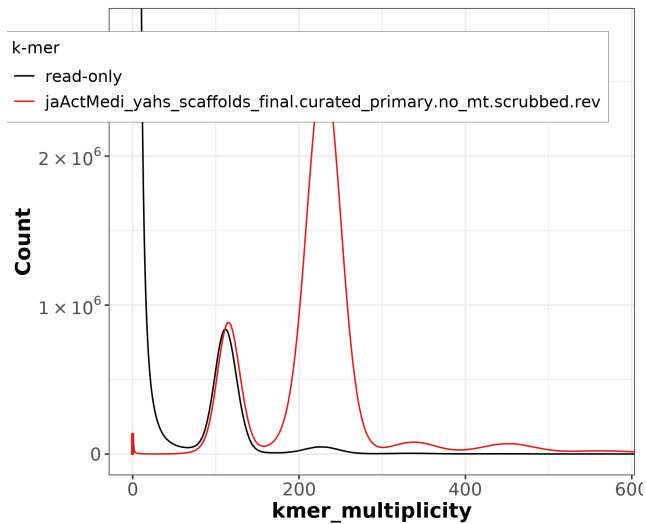BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)
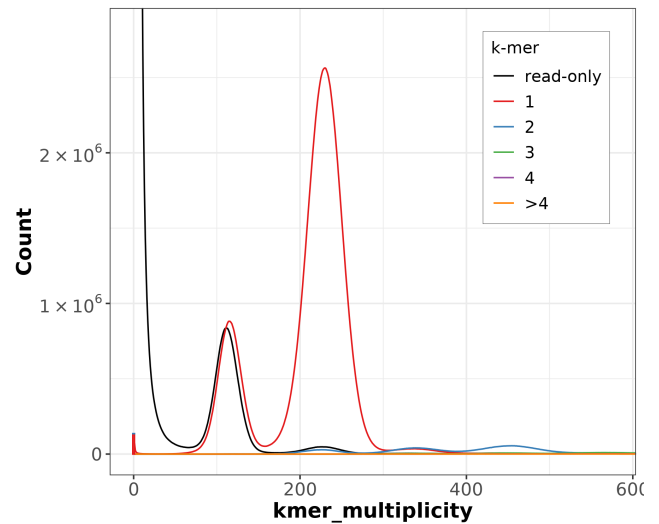
HiC contact map of curated assembly
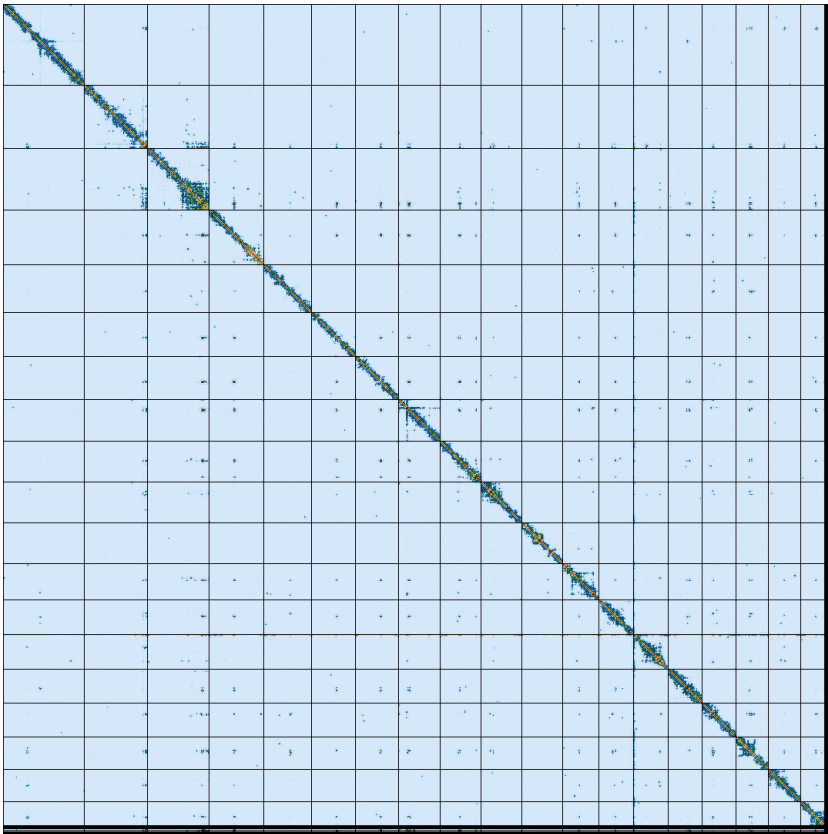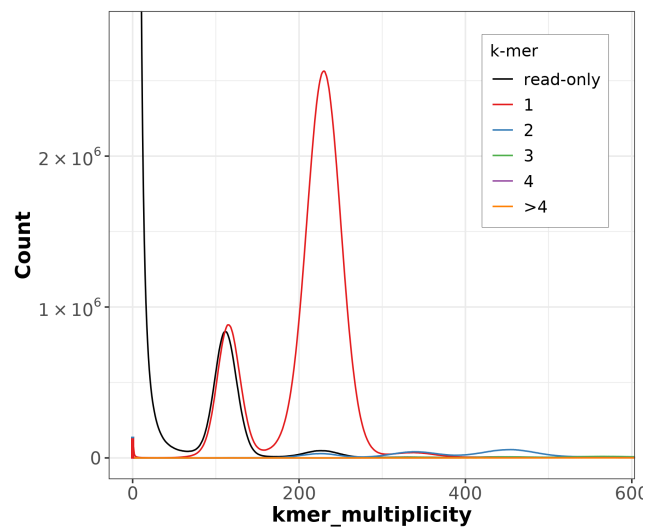

collapsed [LINK]

K-mer spectra of curated assembly

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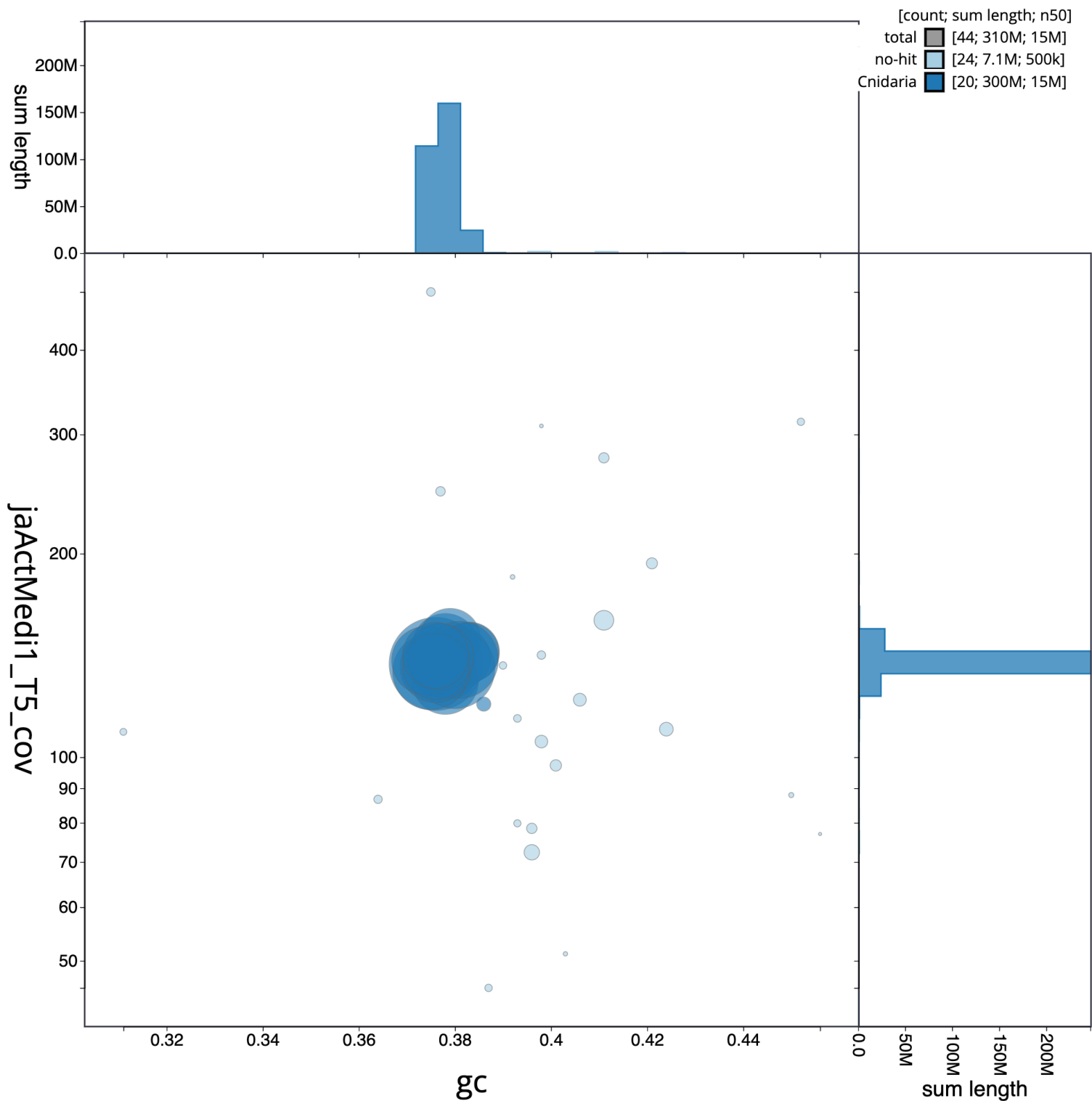their presence in reads/assemblies

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

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	133x	130x	93x

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
- **nextdenovo**
  |_ *ver:* 2.5.0
  |_ *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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