

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	305,700,689
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

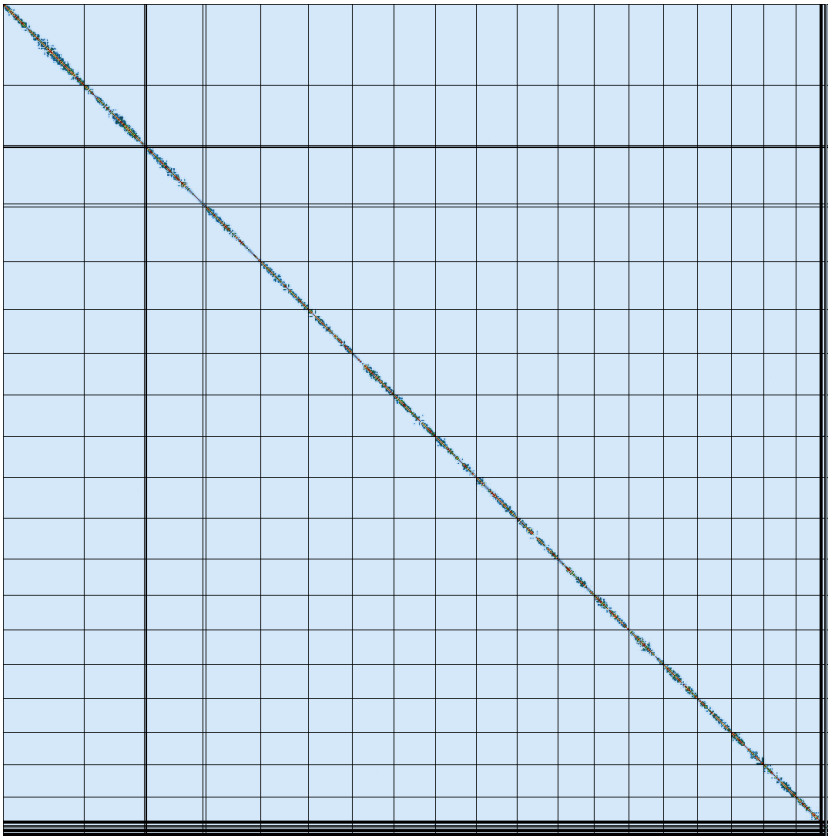
- . Interventions/Gb: 30
- . Contamination notes: "No clear contaminants were found either using buscogenes or buscoregions (more sensitive)"
- . Other observations: "The strength of the HiC signal, particularly along the diagonal was weaker than usual, which somewhat limited our curation, but in general the yahs scaffolding seemed to be quite acceptable and we only made 9 changes to the yahs scaffolds. 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	305,700,689
GC %	37.85	37.85
Gaps/Gbp	202.81	209.36
Total gap bp	12,400	12,800
Scaffolds	45	44
Scaffold N50	16,244,619	15,129,518
Scaffold L50	7	8
Scaffold L90	16	17
Contigs	107	108
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%

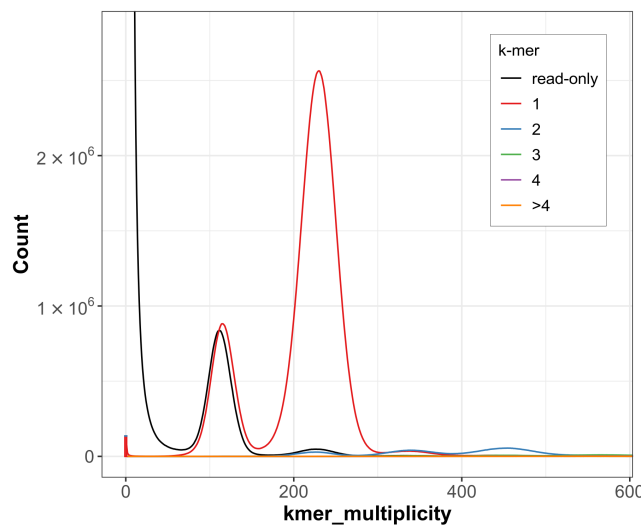
BUSCO: 5.4.0 (euk_genome_met, metaeuk) / Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

HiC contact map of curated assembly

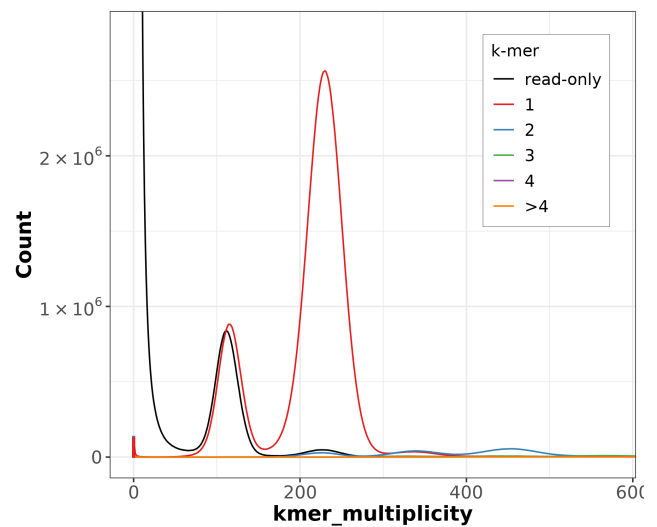


collapsed [\[LINK\]](#)

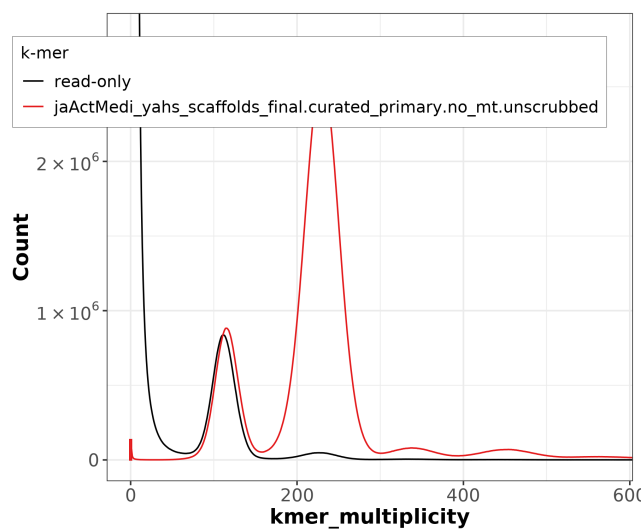
K-mer spectra of curated assembly



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

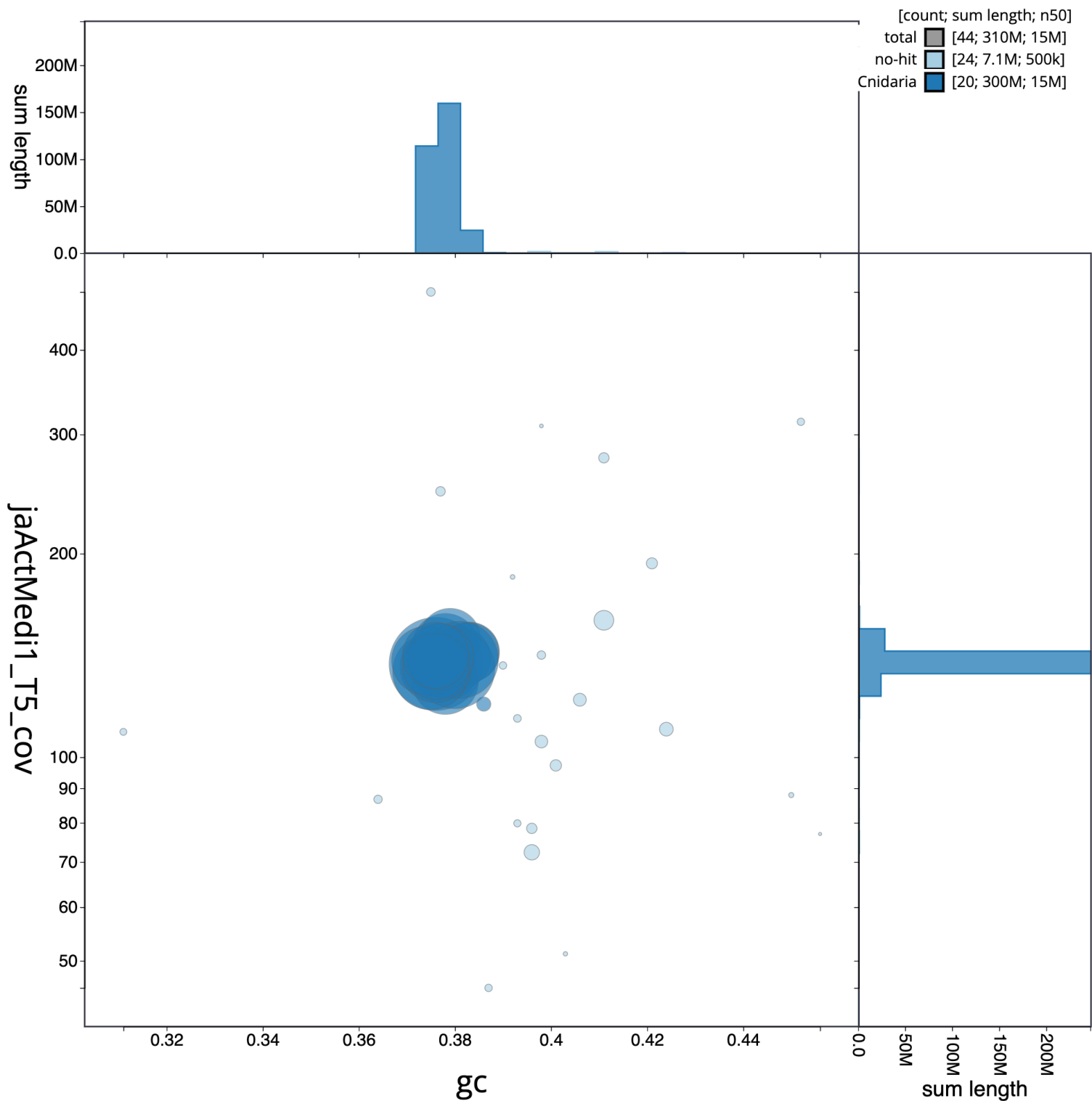


Distribution of k-mer counts per copy numbers found in asm



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

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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