

# Genome Annotation Report

| Taxon Info |                      |
|------------|----------------------|
| TxID       | 105859               |
| Species    | Antedon mediterranea |
| Phylum     | Echinodermata        |
| Class      | Crinoidea            |
| Order      | Comatulida           |
| ToLID      | ecAntMedi1.1_ncbi    |

## Warnings

### 1. Number of genes

No warnings

### 2. Predicted CDS

No warnings

### 3. BUSCO/OMark completeness

No warnings

### 4. Intron length distribution

- Excess short 3n intron > 34% (35.58%)

### 5. RNA-Seq support

- Genome mapping rate < 90.0% (82.6%)
- Percent intron supported < 75.0% (0.0%)

| Summary   |       |
|-----------|-------|
| num_genes | 24442 |

|                                     |   |
|-------------------------------------|---|
| num_transcripts                     | 25416                                   |
| num_transcripts_without_introns     | 1228 (4.83%)                            |
| mean_exons_per_transcript           | 11.55                                   |
| mean_exons_per_multiexon_transcript | 12.08                                   |
| mean_cds_length                     | 2071.59                                 |
| median_cds_length                   | 1395.0                                  |
| mean_intron_length                  | 1394.05                                 |
| median_intron_length                | 447.0                                   |
| BUSCO_annotation                    | C:99.3[S:74.0,D:25.3],F:0.6,M:0.1       |
| BUSCO_assembly                      | C:98.4[S:98.1,D:0.3],F:0.9,M:0.7,E:26.0 |
| PSAURON_score                       | 99.4                                    |
| num_intron_supported                | 0 (0.0%)                                |

| General Statistics                    |          |
|---------------------------------------|----------|
| num_genes                             | 24442    |
| mean_gene_length                      | 10165.06 |
| median_gene_length                    | 4233.5   |
| num_transcripts                       | 25416    |
| mean_transcripts_per_gene             | 1.48     |
| median_transcripts_per_gene           | 1.0      |
| num_exons                             | 313568   |
| mean_exons_per_transcript             | 11.55    |
| median_exons_per_transcript           | 8.0      |
| mean_exons_per_multiexon_transcript   | 12.08    |
| median_exons_per_multiexon_transcript | 9.0      |

|  |                 |
|--|-----------------|
| num_transcripts_without_introns                          | 1228 (4.83%)    |
| num_exon_3n  | 136217 (43.44%) |
| num_exon_3n1   | 89437 (28.52%)  |
| num_exon_3n2   | 87914 (28.04%)  |
| mean_cds_length  | 2071.59         |
| median_cds_length  | 1395.0          |
| total_cds_length   | 52651413        |
| percentage_cds_coverage                                  | 14.85%          |
| num_introns  | 279614          |
| mean_intron_length                                       | 1394.05         |
| median_intron_length                                     | 447.0           |
| mean_introns_per_transcript                              | 10.55           |
| median_introns_per_transcript                            | 7.0             |
| short_intron_3n/short_intron                             | 6113 (35.58%)   |
| long_intron_3n/long_intron                               | 86931 (33.13%)  |
| stopless_short_intron_3n/stopless_short_intron           | 479 (25.77%)    |
| stopless_short_intron_3n1/stopless_short_intron          | 644 (34.64%)    |
| stopless_short_intron_3n2/stopless_short_intron          | 736 (39.59%)    |
| stop_containing_short_intron_3n/short_containing_intron  | 5634 (36.77%)   |
| stop_containing_short_intron_3n1/short_containing_intron | 4730 (30.87%)   |
| stop_containing_short_intron_3n2/short_containing_intron | 4960 (32.37%)   |

| BUSCO           |               |
|-----------------|---------------|
| lineage_dataset | metazoa_odb12 |
| n_markers       | 672           |

|             |   |
|-------------|---|
| BUSCO Assem | C:98.4[S:98.1,D:0.3],F:0.9,M:0.7,E:26.0 |
| BUSCO Annot | C:99.3[S:74.0,D:25.3],F:0.6,M:0.1       |
| Delta BUSCO | 0.9%                                    |

| OMArk                     |                |
|---------------------------|----------------|
| OMA_clade                 | Eleutherozoa   |
| num_conserved_hogs        | 8933           |
| single                    | 5266 (58.95%)  |
| duplicated                | 1867 (20.90%)  |
| duplicated_unexpected     | 1865 (20.88%)  |
| duplicated_expected       | 2 (0.02%)      |
| missing                   | 1800 (20.15%)  |
| num_proteins_in_proteome  | 25416          |
| total_consistent          | 18127 (71.32%) |
| consistent_partial_hits   | 4198 (16.52%)  |
| consistent_fragmented     | 667 (2.62%)    |
| total_inconsistent        | 3285 (12.92%)  |
| inconsistent_partial_hits | 1672 (6.58%)   |
| inconsistent_fragmented   | 177 (0.70%)    |
| total_contaminants        | 0 (0.00%)      |
| contaminants_partial_hits | 0 (0.00%)      |
| contaminants_fragmented   | 0 (0.00%)      |
| total_unknown             | 4004 (15.75%)  |

| PSAURON |
|---------|
|---------|

|               |         |
|---------------|---------|
| psaaron_score | 99.4    |
| true_count    | 25270   |
| false_count   | 146     |
| median_score  | 0.99642 |
| max_score     | 1.0     |
| min_score     | 0.00168 |

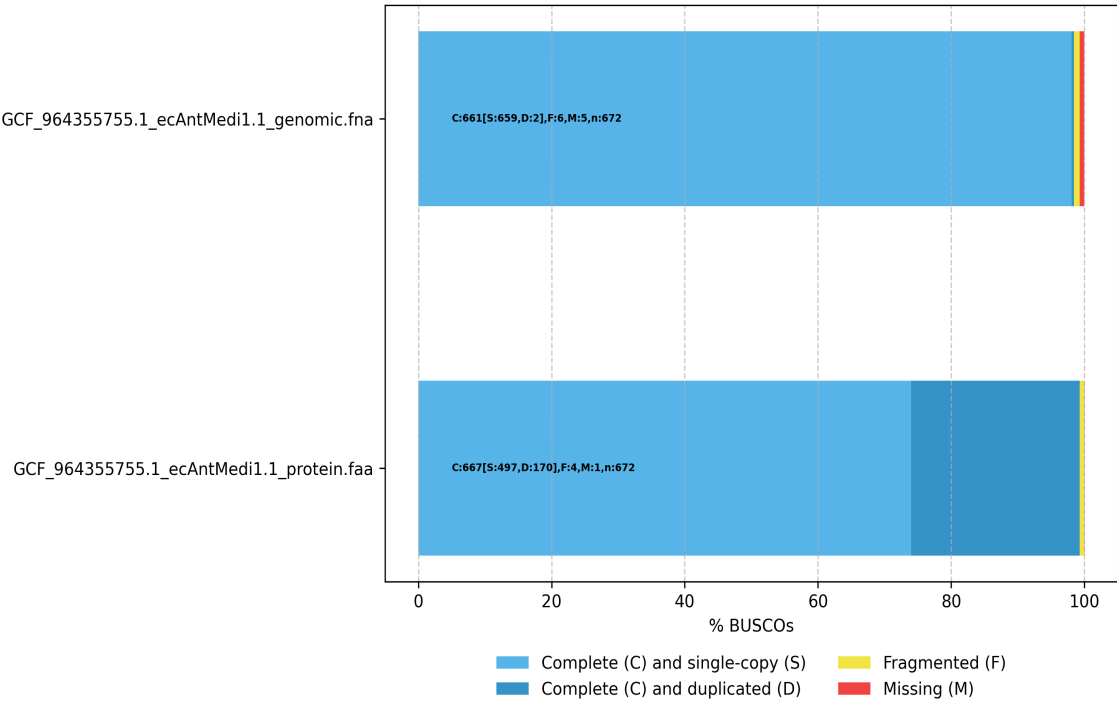
### Best Reciprocal Hits

|                               |            |
|-------------------------------|------------|
| num_best_reciprocal_hits      | 18057      |
| num_split_gene_length_<0.75x  | 11 (0.06%) |
| num_fusion_gene_length_>1.25x | 0 (0.0%)   |
| KL_divergence_normalized      | 0.0001     |
| JS_divergence_normalized      | 0.0        |
| Wasserstein_distance          | 0.255469   |

### RNASeq

|                                    |                 |
|------------------------------------|-----------------|
| mapping_rate                       | 82.6%           |
| primary_mapping_rate               | 81.52%          |
| properly_paired                    | 76.99%          |
| num_gene_supported                 | 18387 (83.37%)  |
| num_exon_supported                 | 287195 (91.59%) |
| num_exact_intron_boundary          | 0 (0.0%)        |
| num_intron_supported_canonical     | 0 (0.00%)       |
| num_intron_supported_non_canonical | 0 (0.00%)       |

BUSCO Assessment Results (Page 1)



OMARK Assessment Result

