

Genome Annotation Report

Taxon Info	
TxID	105859
Species	<i>Antedon mediterranea</i>
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
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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%

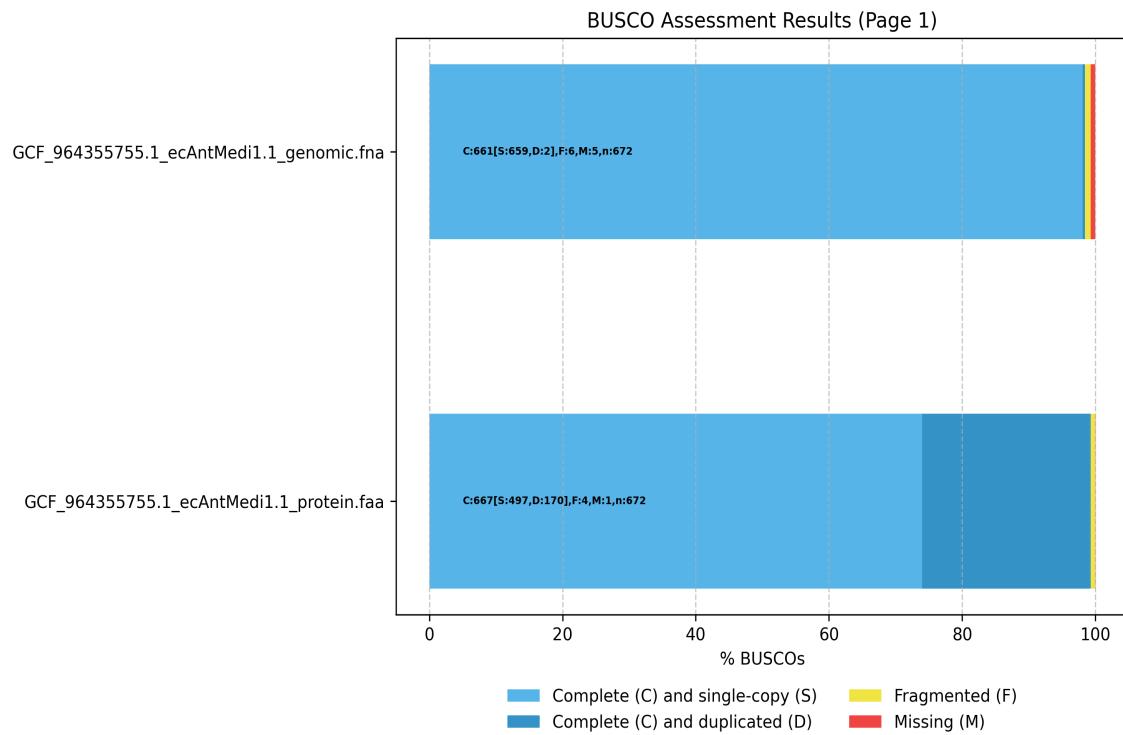
OMArk	
OMA_clade	Eleutherozoa
num_conserved_hogs	8933
single	5266 (58.95%)
duplicated	1867 (20.90%)
duplicated_unexpected	1865 (20.88%)
duplicated_expected	2 (0.02%)
missing	1800 (20.15%)
num_proteins_in_proteome	25416
total_consistent	18127 (71.32%)
consistent_partial_hits	4198 (16.52%)
consistent_fragmented	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	

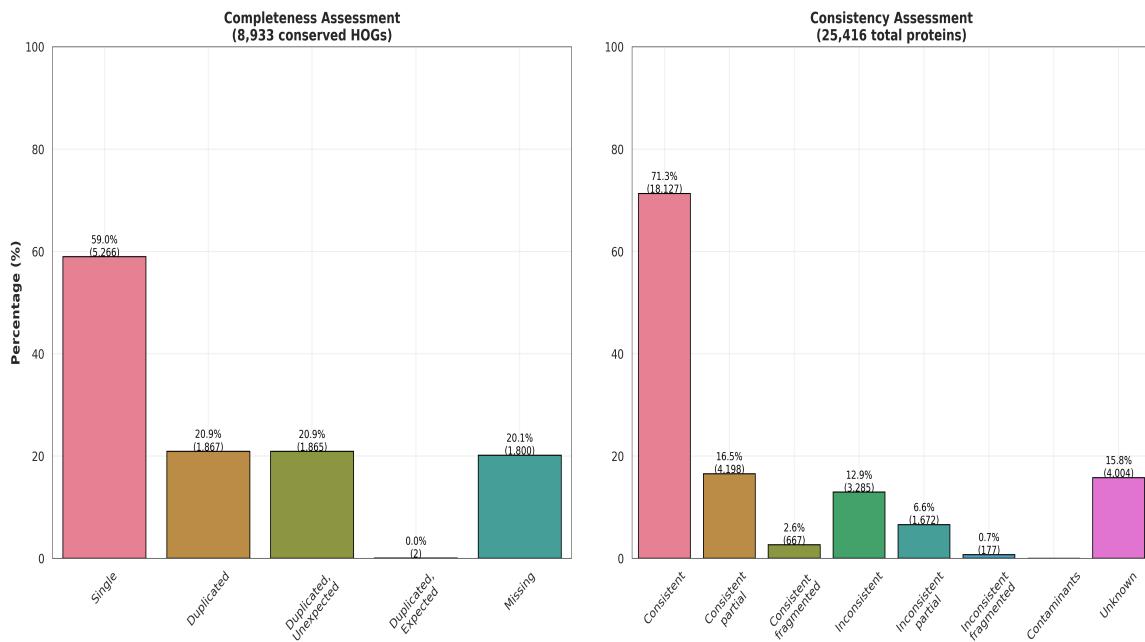
psauron_score	99.4
true_count	25270
false_count	146
median_score	0.99642
max_score	1.0
min_score	0.00168

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%)



OMARK Assessment Result



Protein Distribution and Length Relationship by In-Frame Score

