

Genome Analysis Report

General Statistics	
num_genes	36391
num_genes_without_introns	12967 (35.63%)
mean_gene_length	2359.57
median_gene_length	1562.0
num_exons	149704
mean_exons_per_gene	4.11
median_exons_per_gene	2.0
num_exon_3n	76783 (51.29%)
num_exon_3n1	36932 (24.67%)
num_exon_3n2	35989 (24.04%)
mean_cds_length	1091.43
median_cds_length	873.0
total_cds_length	39718072
percentage_cds_coverage	10.64%
num_introns	113313
mean_intron_length	407.27
median_intron_length	149.0
short_intron_<120_3n0_without_stop	4324 (3.82)%
long_intron_>120_3n0_without_stop	1189 (1.05)%
short_intron_<120_3n1_without_stop	4197 (3.70)%
long_intron_>120_3n1_without_stop	1293 (1.14)%
short_intron_<120_3n2_without_stop	4308 (3.80)%

long_intron_>120_3n2_without_stop	1252 (1.10)%
short_intron_<120_3n0_with_stop	12079 (10.66)%
long_intron_>120_3n0_with_stop	20325 (17.94)%
short_intron_<120_3n1_with_stop	11654 (10.28)%
long_intron_>120_3n1_with_stop	20481 (18.07)%
short_intron_<120_3n2_with_stop	11737 (10.36)%
long_intron_>120_3n2_with_stop	20474 (18.07)%

BUSCO	
lineage_dataset	poales_odb12
complete	97.6%
single_copy	96.7%
multi_copy	0.9%
fragmented	0.4%
missing	2.0%
num_markers	6282
domain	eukaryota

OMArk	
OMA_clade	Oryza
num_conserved_hogs	15087
single	13319 (88.28%)
duplicated	1350 (8.95%)
duplicated_unexpected	1101 (7.30%)
duplicated_expected	249 (1.65%)

missing	418 (2.77%)
num_proteins_in_proteome	36387
total_consistent	30364 (83.45%)
consistent_partial_hits	1803 (4.96%)
consistent_fragmented	1625 (4.47%)
total_inconsistent	2284 (6.28%)
inconsistent_partial_hits	517 (1.42%)
inconsistent_fragmented	1444 (3.97%)
total_contaminants	0 (0.00%)
contaminants_partial_hits	0 (0.00%)
contaminants_fragmented	0 (0.00%)
total_unknown	3739 (10.28%)

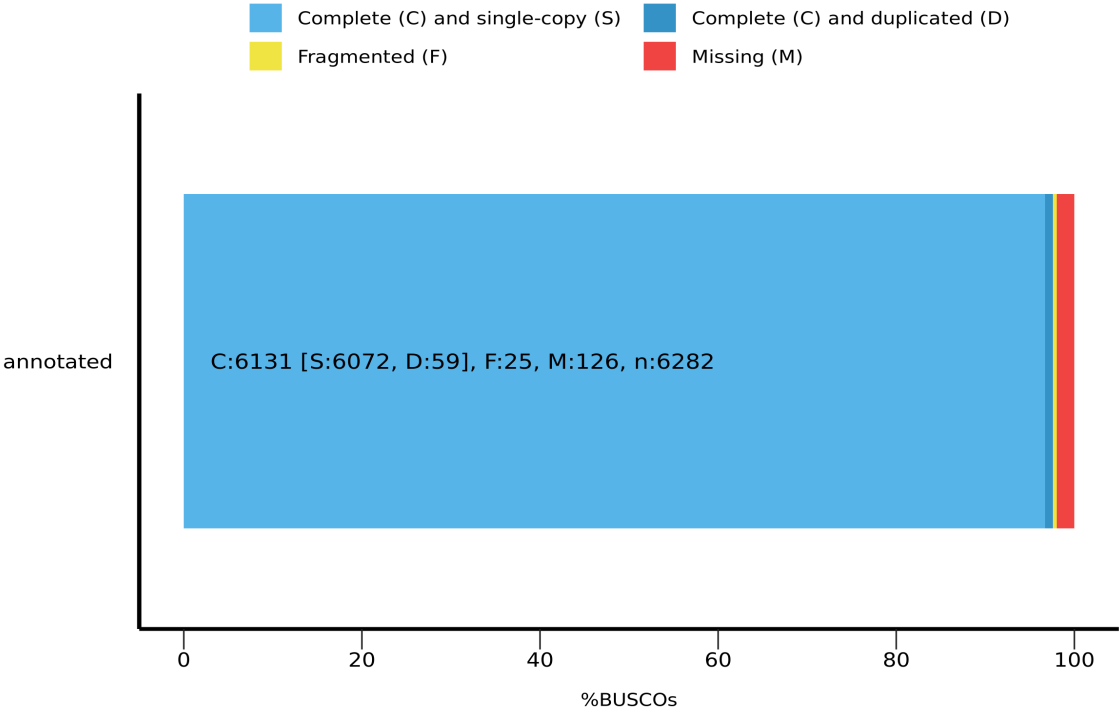
PSAURON	
psauron_score	83.8
true_count	30492
false_count	5895
median_score	0.98278
max_score	1.0
min_score	0.00022

Best Reciprocal Hits	
num_best_reciprocal_hits	29149
num_splitting_genes_08	924 (3.17%)
num_splitting_genes_05	0 (0.0%)

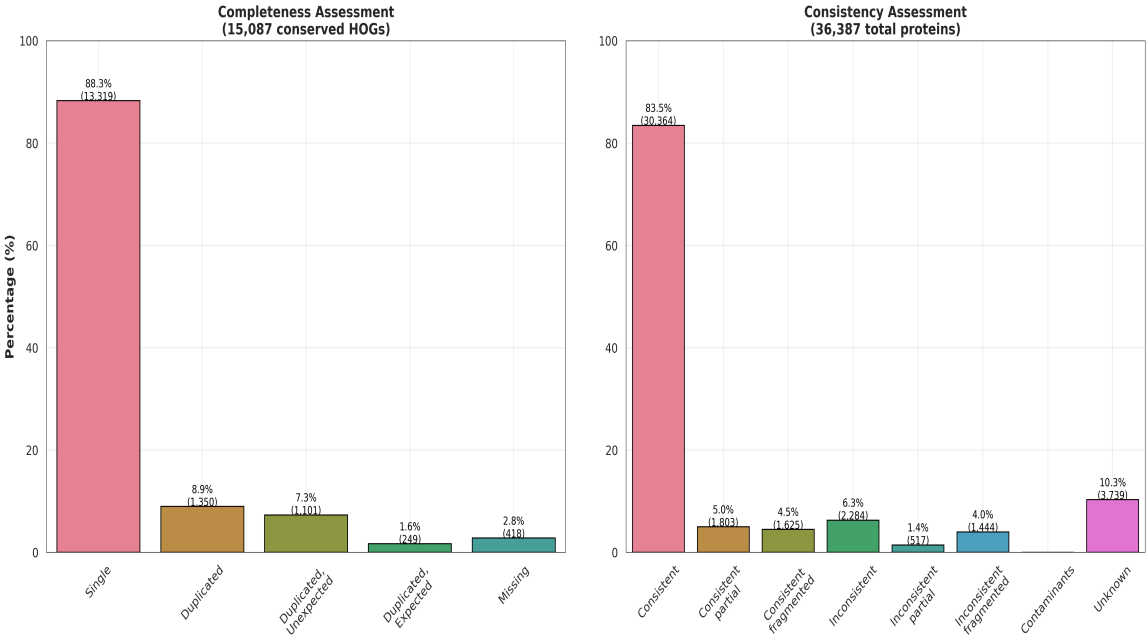
num_fusion_genes_12	414 (1.42%)
num_fusion_genes_15	454 (1.56%)
KL_divergence_normalized	0.0101
JS_divergence_normalized	0.0022
Wasserstein_distance	2.872448

RNASeq	
mapping_rate	96.27%
primary_mapping_rate	95.83%
properly_paired	92.47%
num_gene_unsupported	9445 (25.95%)
num_exon_unsupported	20233 (13.52%)
num_intron_supported	107182
num_intron_supported_canonical	107102 (99.93%)
num_intron_supported_non_canonical	80 (0.07%)

BUSCO Assessment Results



OMARK Assessment Result



Distribution of In-Frame Scores by PSAURON

