

# Genome Analysis Report

General Statistics	
num_transcripts	36391
num_genes_without_introns	12968 (35.64%)
mean_gene_length	2359.57
median_gene_length	1562.0
num_exons	149725
mean_exons_per_gene	4.11
median_exons_per_gene	2.0
num_exon_3n	76783 (51.28%)
num_exon_3n1	36932 (24.67%)
num_exon_3n2	36010 (24.05%)
mean_cds_length	1091.4
median_cds_length	873.0
total_cds_length	39717145
percentage_cds_coverage	10.64%
num_introns	113334
mean_intron_length	407.2
median_intron_length	149.0
short_intron_<120_3n0_without_stop	4324 (3.82)%
long_intron_>120_3n0_without_stop	1185 (1.05)%
short_intron_<120_3n1_without_stop	4205 (3.71)%
long_intron_>120_3n1_without_stop	1291 (1.14)%
short_intron_<120_3n2_without_stop	4319 (3.81)%

long_intron_>120_3n2_without_stop	1249 (1.10)%
short_intron_<120_3n0_with_stop	12073 (10.65)%
long_intron_>120_3n0_with_stop	20332 (17.94)%
short_intron_<120_3n1_with_stop	11652 (10.28)%
long_intron_>120_3n1_with_stop	20486 (18.08)%
short_intron_<120_3n2_with_stop	11733 (10.35)%
long_intron_>120_3n2_with_stop	20485 (18.07)%

BUSCO	
lineage_dataset	poales_odb10
complete	97.6%
single_copy	95.8%
multi_copy	1.8%
fragmented	0.2%
missing	2.2%
num_markers	4896
domain	eukaryota

OMArk	
OMA_clade	Oryza
num_conserved_hogs	15087
single	13316 (88.26%)
duplicated	1353 (8.97%)
duplicated_unexpected	1101 (7.30%)
duplicated_expected	252 (1.67%)

missing	418 (2.77%)
num_proteins_in_proteome	36387
total_consistent	30365 (83.45%)
consistent_partial_hits	1803 (4.96%)
consistent_fragmented	1625 (4.47%)
total_inconsistent	2283 (6.27%)
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	30494
false_count	5893
median_score	0.98278
max_score	1.0
min_score	0.00022

Best Reciprocal Hits	
num_best_reciprocal_hits	29185
num_splitting_genes_08	932 (3.19%)
num_splitting_genes_05	0 (0.0%)

num_fusion_genes_12	437 (1.5%)
num_fusion_genes_15	482 (1.65%)
KL_divergence_normalized	0.0105
JS_divergence_normalized	0.0023
Wasserstein_distance	2.480915

RNASeq	
mapping_rate	96.27%
primary_mapping_rate	95.83%
properly_paired	92.47%
num_gene_unsupported	9445 (25.95%)
num_exon_unsupported	20232 (13.51%)
num_intron_supported	107202
num_intron_supported_canonical	107131 (99.93%)
num_intron_supported_non_canonical	71 (0.07%)



