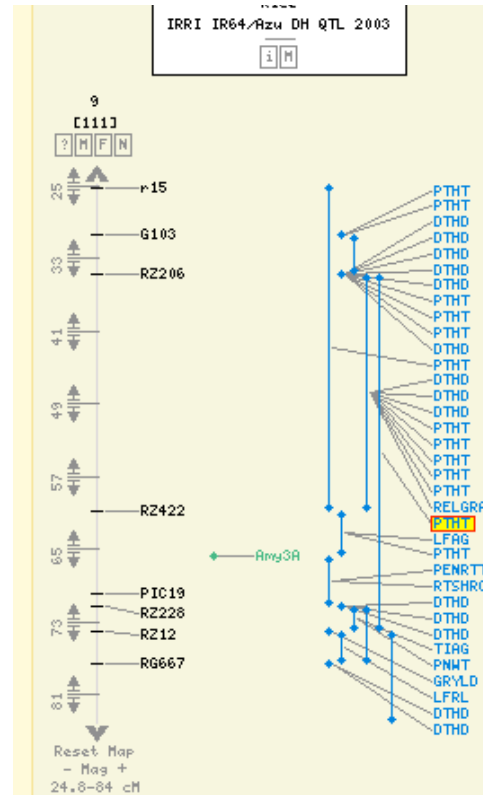
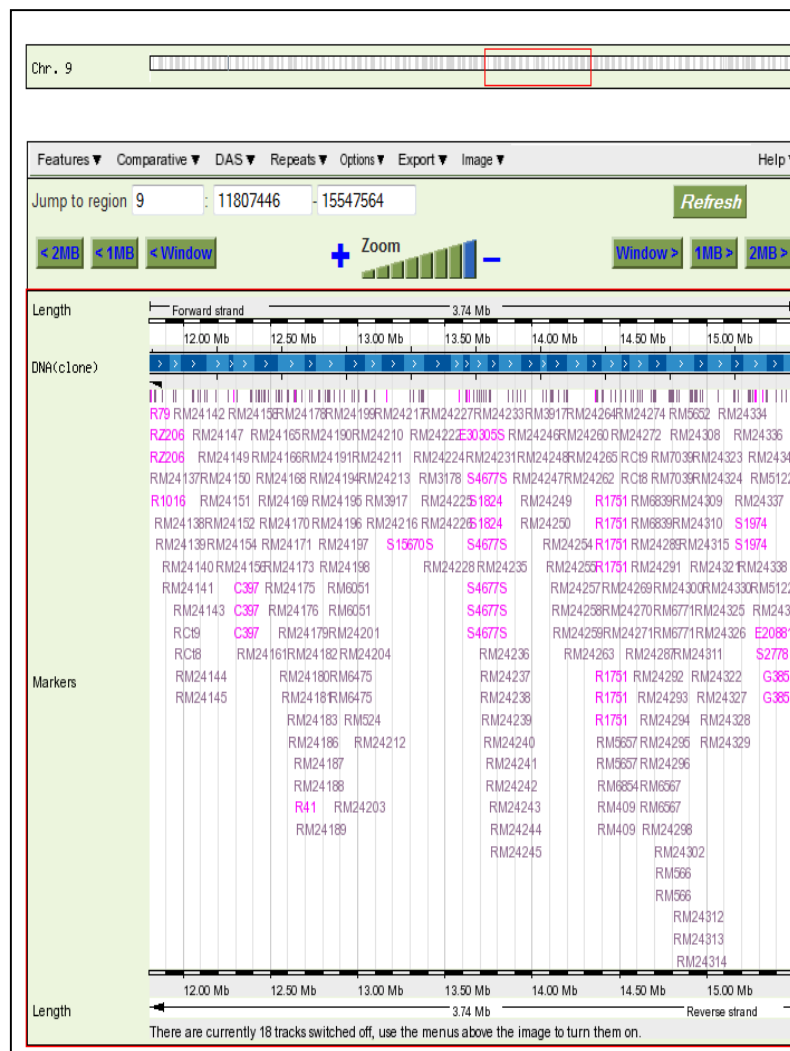


Supplemental Figure 1.



CMap View of QTLs on IR64Azucena mapping population Chr 9, showing highlighted QTL CQAX26, flanked by markers RZ206, RZ422.

[illegible]

A: P14 I31: 153 SSR and 15 RFLP markers within 11.8 – 15.5 genomic region.

B: P15 I4: Marker detailed info provided by Gramene, using RM566 as an example.

Supplementary Figure 3



D

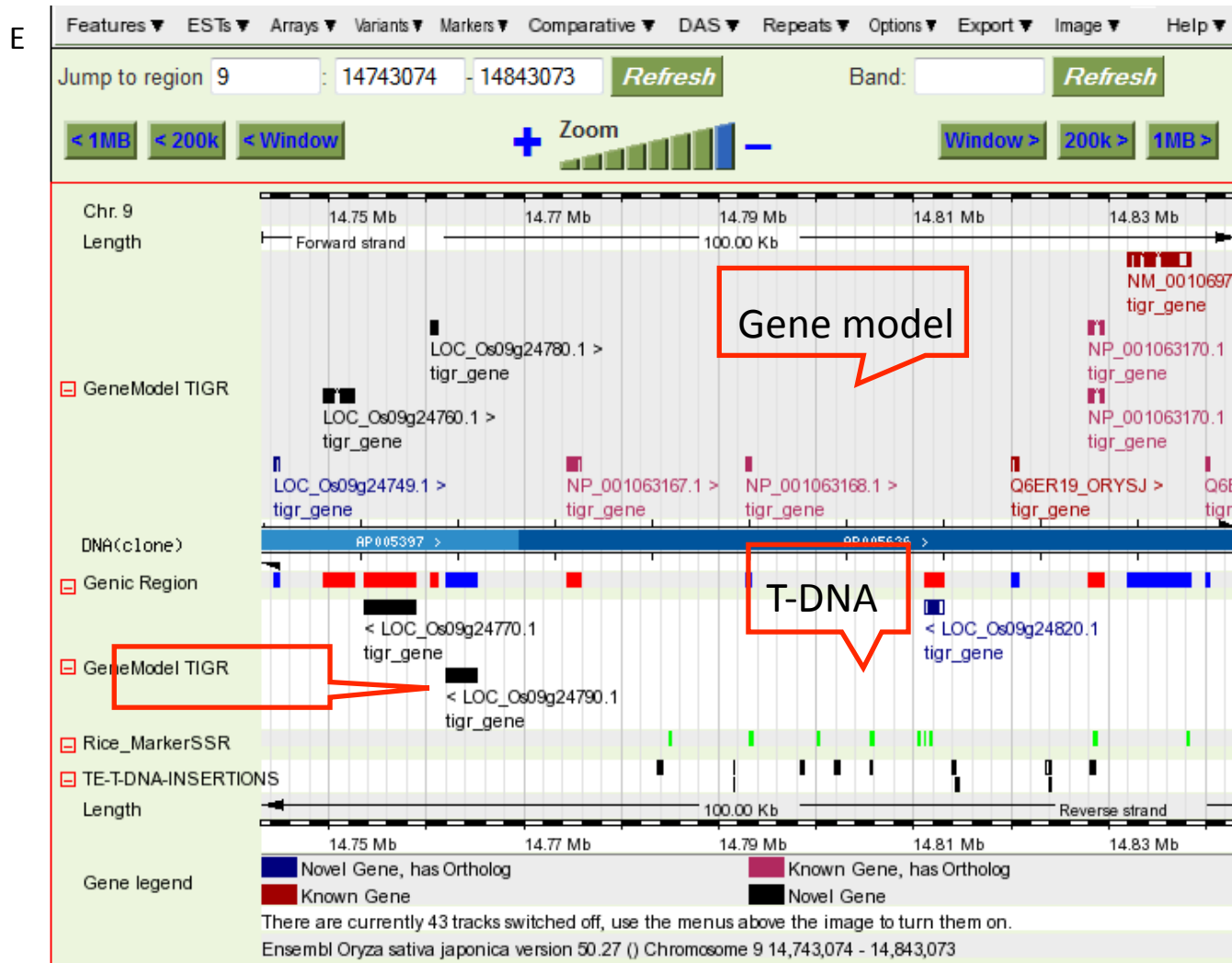
New Count Results

Gramene Gene ID	Chromosome Name	Gene Start (bp)	Gene End (bp)	Strand
LOC_Os09g24810	9	14792755	14793393	1
LOC_Os09g24880	9	14859622	14860185	1
LOC_Os09g25100	9	15026139	15027688	1
LOC_Os09g24890	9	14863763	14864002	1
LOC_Os09g25060	9	14974931	14976712	-1
LOC_Os09g24850	9	14832051	14838356	1
LOC_Os09g24720	9	14728630	14730118	-1
LOC_Os09g24770	9	14753593	14758908	-1
LOC_Os09g25130	9	15059396	15060349	1
LOC_Os09g24740	9	14737436	14742086	1
LOC_Os09g24900	9	14866361	14869926	1
LOC_Os09g24970	9	14916135	14917910	1
LOC_Os09g24749	9	14744411	14744847	1
LOC_Os09g25070	9	14991802	14993887	-1

P15, l10-12, l22-23: 41 Gene models within 14.7 – 15.1 Mb Genomic region:

C: Genome Browser detail viewer; D: Gene model retrieved by Mart.

Supplemental Figure 4



E: Gene models and T-DNA display within 14.7 -14.8 (0.1) Mb genomic region.

Supplemental Figure 5

F a) LOC_Os09g24810

URL: http://www.gramene.org/Oryza_sativa_japonica/geneview?gene=LOC_Os09g24810

Ensembl Gene Report for LOC_Os09g24810

Gene	NP_001063168.1 (RefSeq_peptide)
Gene References	TIGR Locus: LOC_Os09g24810 mini zinc finger 3, putative ... more IRGSP Gene: Os09g0414500

Orthologue Prediction


The following gene(s) have been identified as putative orthologues:

Species
Arabidopsis thaliana

1-to-many [AT1G74660-TAIR-G](#) (Novel Ensembl prediction) [[MultiContigView](#)] [[Align](#)]
MIF1 (MINI ZINC FINGER 1); DNA binding / transcription factor; Constitutive overexpression of MIF1 caused dramatic developmental defects, seedlings were non-responsive to gibberellin (GA) for cell elongation, hypersensitive to the [GA synthesis inhibitor](#) paclobutrazol (PAC) and abscisic acid (ABA), and hyposensitive to auxin, brassinosteroid and cytokinin, but normally responsive to ethylene.
[Target %id: 42; Query %id: 38]

b) LOC_Os09g25150

URL: http://pathway.gramene.org/RICE/NEW-IMAGE?type=GENE&object=LOC_OS09G25150.1



O. sativa japonica Gene: LOC_Os09g25150.1

ID: LOC_OS09G25150.1

Chromosome: Chromosome 9


Map Position: 15,075,603 <- 15,078,106 (nucleotides) 65.51 (centisomes)

Sequence Length: 2504 bp / 2501/3 AAs

Products: [dihydroflavonol-4-reductase, putative, expressed](#)

Reactions Catalyzed by Enzymes:
[a 3β-hydroxy-δ⁵-steroid + NAD⁺ = a 3-oxo-δ⁵-steroid + NADH + H⁺](#),
[campest-4-en-3β-ol = campest-4-en-3-one](#)

Pathways Involving Enzymes: [brassinosteroid biosynthesis II](#)

Gene-Reaction Schematic: 

1.1.1.145

1.1.1.145

LOC_Os09g25150.1

F: Annotation or pathway evidence of two identified candidate genes.