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RESEARCH ARTICLE

Deciphering the inheritance and QTL-seq aided mapping of the candidate locus governing pericarp pigmentation in Manipur black rice

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Abstract

Manipur black rice is a speciality rice characterised by black pigmented pericarp due to anthocyanin accumulation. We have investigated the inheritance of black pericarp pigmentation through classical genetic analysis in a Manipur black rice cultivar, *Chakhao Poireiton*. Total anthocyanin content was quantified using cyanidin-3-glucoside and peonidin-3-glucoside as standards in an $F_{2:3}$ population generated from the cross, Pusa 1652/*Chakhao Poireiton*. Also, mapping of the putative candidate loci was attempted using QTL-seq approach. The trait genetics indicated supplementary gene action with a segregation ratio of 9 (black): 3 (brown): 4 (white). QTL-seq analysis identified a genomic region between 26.82 to 27.97Mb on chromosome 4 as associated with pericarp colour. The identified region was found to carry three putative genes, LOC_Os04g47040, LOC_Os04g47059 and LOC_Os04g47080 with functions associated with pericarp colouration. Besides, 10 SNPs with modifier effect were identified in the intergenic region between LOC_Os04g47040 and LOC_Os04g47059, indicating possible regulation of trait in the upstream of LOC_Os04g47059, which needs further validation. Segregation pattern and the putative candidate loci identified in this study implicate future advancements toward breeding black rice.

Keywords: Pericarp pigmentation, mapping, Manipur black rice, QTL-seq, anthocyanin, annotation.

Introduction

Pigmented rice is a special class of rice having coloured outer bran layer (pericarp). Naturally, the pigmented rice shows varying range of pigmentations such as red, brown, deep purple and black, which are rich in phytochemicals such as anthocyanins, proanthocyanins (Finocciaro et al. 2010; Kim et al. 2014), phenolic acids, flavonoids (Pengkumsri et al. 2015) and minerals (Hurtada et al. 2018; Kang et al. 2011). Among these, black rice is a rich source of anthocyanin (Lee et al. 2010; Hosoda et al. 2018; Bhuvaneswari et al. 2020). Anthocyanins belong to the flavonoid group of water-soluble secondary metabolites which confer different hues of colours (blue, purple, red) to fruits, vegetables and cereals (He and Giusti 2010). The major biological property for which anthocyanins are valued is their antioxidant activity (Castañeda-Ovando et al. 2009; Nimse and Pal 2015). Based on animal and human clinical trials, potential health benefits of anthocyanins from natural foods, including pigmented rice have been reported (Pojer et al. 2013; Khoo et al. 2017; Samyor et al. 2017; Callcott et al. 2019).

Genetics of pigmented rice has been under investigation for a long time. In a black rice cultivar of Korea, *Heugnambyeo*, Rahman et al. (2013) reported that the pericarp pigmentation

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showed digenic inheritance with a segregation ratio of 9 black: 3 brown: 4 white. Prior to this, Hu et al. (1996) reported two genes *viz., Ra* and *Rb* located on chromosomes 4 and 1, respectively, encoding for basic helix-loop-helix (bHLH) transcription factors that regulate anthocyanin biosynthetic pathway in rice. In plants, anthocyanin compounds are produced through a multistep biosynthetic pathway involving various pathway genes that are under the control of several regulatory genes. Subsequently, several such regulatory genes have been identified in black rice to control the temporal and spatial expression of the pathway genes (Sakamoto et al. 2001; Wang and Shu 2007; Shih et al. 2008). Further, on fine mapping, a 2-bp deletion (GT) in exon 7 of *Ra* was reported to be responsible for purple/black pericarp pigmentation (Wang and Shu 2007). Maeda et al. (2015) identified three pericarp colour genes *viz., Kala1*, *Kala3* and *Kala4* located on chromosomes 1, 3 and 4, respectively, in a black rice variety of Japan, *Hong XieNuo*. Further, *Kala4* (LOC_Os04g47059) was identified to be essential for inducing black pericarp.

Among the black rice of India, the most popular is the *Chakhao* rice cultivated over ages in Manipur, a north-eastern state. In an earlier study, we have reported that the pericarp pigmentation of *Chakhao* landraces varied from white to dark/deep purple. The population structure of pigmented genotypes was distinct, with total anthocyanin content varying from 29.8 to 275.8 mg.100g^{-1} dry weight (Bhuvaneswari et al. 2020). However, unlike the other black rices, the genetic basis of black pericarp colour in Manipur black rice remains to be deciphered, which has significant implications for its genetic improvement. Therefore, the present study was aimed at understanding the inheritance of black pericarp pigmentation in one of the popular landraces, *Chakhao Poireiton* and mapping the genomic region underlying the trait.

Materials and methods

Population development

A direct cross between *Chakhao Poireiton* as female and a white pericarp genotype, Pusa 1652 as male was made to generate F_1 seeds during *Kharif* 2017 at the Division of Genetics, ICAR-Indian Agricultural Research Institute (IARI), New Delhi. Additionally, a reciprocal cross with Pusa 1652 as female and *Chakhao Poireiton* as male was also attempted. The F_1 plants were raised during the offseason 2017-2018 at IARI-Rice Breeding and Genetics Research Centre, Aduthurai, Tamil Nadu. During *Kharif* 2018, an F_2 population comprising of 150 plants from the direct cross and 161 plants from the reciprocal cross were raised. At grain maturity, the F_2 population from the reciprocal cross were scored for pericarp colour and classified as white (no pigmentation), light brown, variegated brown, dark brown and black. The progeny rows of each of the F_2 plants were raised as $F_{2:3}$ families to ascertain the zygosity based on the segregation for pericarp colour in both the F_2 populations. Ten random plants from each of the $F_{2:3}$ families were scored for grain pericarp colour.

Estimation of total anthocyanin content (TAC)

TAC was estimated using high-performance liquid chromatography (HPLC) with two replications from seeds harvested from 161 individual F_2 plants generated from the reciprocal cross along with parental lines. Based on a previous report (Bhuvaneswari et al. 2020), cyanidin 3-glucoside (C_3G) and peonidin 3-glucoside (P_3G) were used as standard reference compounds. The anthocyanin content was determined in mg.100g^{-1} grain dry weight basis.

Constitution of extreme bulks

Leaf samples were collected from the F_2 plants at the vegetative phase and genomic DNA was extracted as per Murray and Thompson (1980). Before storing, the extracted DNA was quantified by NABi, a UV-Vis nanospectrophotometer (MicroDigital Co., Ltd., Republic of Korea). After the anthocyanin profiling, 20 F_2 progenies having extremely high TAC content (> 100mg.100g^{-1} DW) and 20 plants with extremely low TAC content (< 100mg.100g^{-1} DW) were identified for developing bulks. Equal concentrations of genomic DNA (300 ng/µL) from the selected 20 individuals with high TAC were pooled together to form the black pericarp (BP) bulk. Similarly, pooled DNA from the lowest TAC individuals formed the white pericarp (WP) bulk. The DNA of the black rice check, *Chakhao Poireiton* was designated as CP.

Whole genome re-sequencing and QTL-seq analysis

The two DNA bulks (BP and WP) along with the DNA of the parent (CP) were sequenced using Illumina Hiseq 2500 platform with an average read length of 150 bp to an average depth of 25x. The QTL-seq pipeline of Takagi et al. (2013) was employed to identify the genomic region governing BP in *Chakhao Poireiton*. The quality check and filtering of raw reads from CP, BP and WP bulk were assessed using FastQC v0.11.5 (Andrews 2010). The high-quality reads (HQRs, Q≥30; P≥90, whole genome GC%=43) with an average read length of 150 bp from *Chakhao Poireiton* were aligned to the reference genome (Nipponbare) using the Burrows-Wheeler Aligner (BWA; Li and Durbin 2009). The generated sequence alignment/map (SAM) format files were converted to binary alignment/map (BAM) format and single nucleotide polymorphism (SNP) calling was done using SAMtools (Li et al. 2009). The package Coval (Kosugi et al. 2013) was used to refine the SNP calls. The SNPs identified were replaced in the Nipponbare genome to generate the reference sequence of *Chakhao Poireiton*. The newly generated reference sequence of *Chakhao Poireiton* was used to map the reads of BP and WP bulks. The SNP index was calculated separately for each bulk at all the SNP positions identified using the following formula (Abe et al. 2012).

SNP index = No. of reads harbouring SNPs in a bulk in comparison to reference sequence / Total no. of reads

A sliding window approach was carried out with a window size of 2Mb with an increment of 10kb. The SNP index was plotted against genomic positions across 12 chromosomes for both bulks. Further, ΔSNP index (SNP index of BP bulk – SNP index of WP bulk) was calculated and plotted against the physical position. The statistical confidence intervals of ΔSNP index for all the SNP positions with given read depths were also plotted (Takagi et al. 2013).

In silico search for putative candidate genes

In the genomic region associated with the pericarp colour, in silico search was carried out to identify the presence of genes associated with target trait using the database of Rice Genome Annotation Project (http://rice.uga.edu/).

Results and discussion

Pigmented rices are generally not grown widely in the world and hence had little commercial focus. Recently, due to increasing reports on nutraceutical properties with potential health benefits, demand for pigmented rice is on the rise among rice consumers (Wuryandani et al. 2018; Melini et al. 2019). The rice grains' deep colour (black/deep purple) is imparted by flavonoid compounds and anthocyanins whereas proanthocyanins are responsible for red pigmentation (Khoo et al. 2017; Hosoda et al. 2018; Sweeney et al. 2006). Anthocyanins are synthesized through the phenylpropanoid pathway, catalysed by multiple enzymes namely, chalcone synthase (CHS), chalcone isomerase (CHI), flavonoid-3-hydroxylase (F3H), di-hydroflavonol-4-reductase (DFR), anthocyanin synthase (ANS) and UDP flavonoid-3-glycosyltransferase (UF3GT). Since the expression of these genes are under the regulatory control of several other genes the inheritance of pigmentation is complex and challenging to investigate. In India, Manipur black rice is recently conferred with a geographical identification tag (GI No. 602; GoI 2019), recognizing its commercial and geographical importance. Manipur black rice are generally low-yielding; hence, breeding interventions to improve its yield and agronomic performance have become mandatory. However, to maintain the essential grain qualities such as pericarp pigmentation in the breeding process, knowledge on its inheritance pattern is essentially required. Therefore, this study forms the pioneer report on the genetic control of black pigmentation in Manipur black rice.

Table 1. The range of anthocyanin content in different pericarp colour categories of $F_{2:3}$ individual plant harvested grains

Visual class	No. of $F_{2:3}$ plants	TAC (mg/100g DW)	Reclassification*
Black	50	40.0 to 377.0	Black (81)
Dark brown	31	20.9 to 192.9	
Variegated brown	20	9.6 to 19.6	Brown (38)
Brown	18	5.4 to 18.3	
Light brown	5	0.3 to 4.0	White (42)
White	37	0.0 to 3.1	
Total	161		

*Reclassified based on non-overlapping TAC.

The pericarp of F_1 seeds from the direct cross, *Chakhao Poireiton*/Pusa 1652 was black pigmented, while the pericarp of F_1 seeds from the reciprocal cross, Pusa 1652/*Chakhao Poireiton* was white (Fig. 1). The difference in expression of pericarp pigmentation in reciprocal crosses depicted that the pericarp colour development in rice has maternal effect. The seeds harvested from the F_1 plants (F_2 seeds) in both the crosses showed dark brown colour indicating semi-dominance nature of pericarp pigmentation. Further, the F_3 seeds harvested from 161 F_2 plants of the reciprocal cross were classified into categories such as 50 black, 31 dark brown, 20 variegated brown, 18 brown, 5 light brown and 37 white (Table 1). On estimation, TAC was found to vary from 0 to 377.0 mg.100g^{-1} among the harvested seeds. However, the TAC values overlapped across the pericarp colour categories generated through visual scoring, particularly among the adjacent classes. To reduce the overlap, based on TAC, the population was reclassified into three distinct classes viz., 20.9–377.0 mg.100g^{-1} with black/dark brown grains, 5.4–19.6

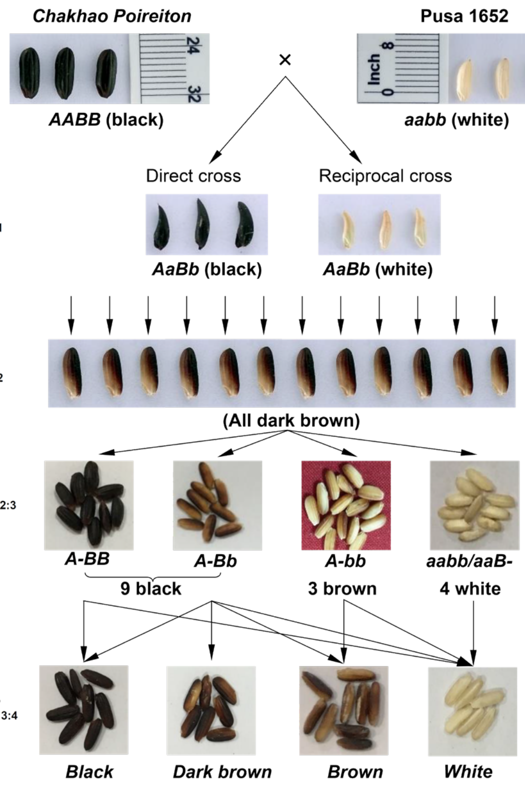

Fig. 1. Segregation of black pericarp pigmentation in different filial generations of cross between Chakhao Poireiton and Pusa 1652

Table 2. Expression of pericarp pigmentation and test of goodness of fit in early generations of the cross, Pusa 1652/*Chakhao Poireiton*

Generation	Pericarp colour	Frequency		Ratio	χ^2 value	p-value
		Observed	Expected			
F_1	White		-	-	-	
$F_{1:2}$	Dark brown		-	-	-	
	Black	81	40.3	9		
$F_{2:3}$	Brown	38	30.2	3	3.1	0.21ns
	white	42	90.6	4		

ns, non-significant

mg 100^{-1}g having variegated brown to brown grains, and 0-4.0 mg 100^{-1}g with light brown to white grains. The black and dark brown seed colour categories were combined as one class and named 'black', variegated brown and brown categories were classified as 'brown' and light brown and white were combined to form the 'white' class. The frequency of the classes was modified to 81 black, 38 brown and 41 white. The goodness of fit test indicated that the segregation fitted well (p=0.21) with the genetic ratio of 9 black: 3 brown: 4 white (Table 2) suggesting that two genes with supplementary gene action could govern the pericarp colour in *Chakhao Poireiton*. In an earlier study too, a similar pattern of inheritance of pericarp pigmentation was reported based on C_3G quantification in Korean black rice genotypes, '*Kewha*' and '*Heugnambyeo*' (Rahman et al. 2013).

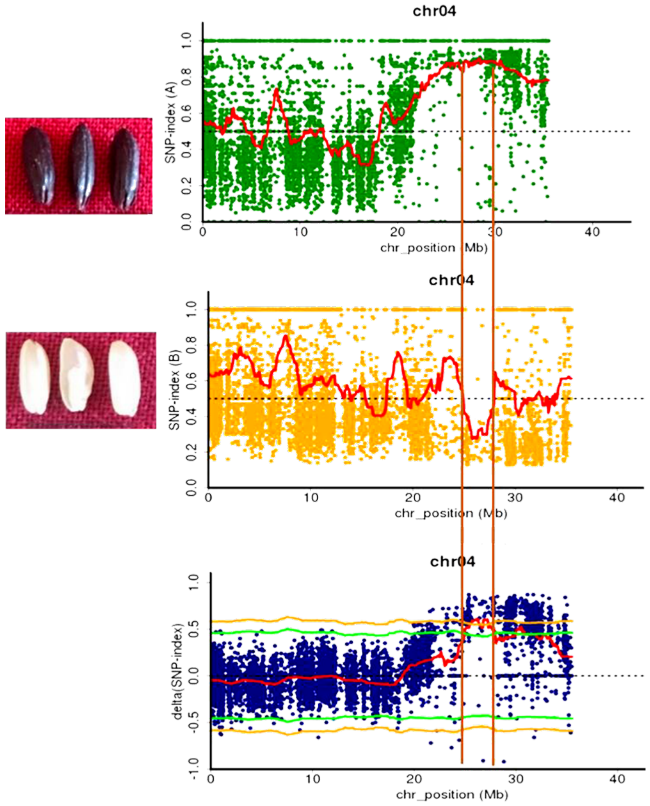

Fig. 2. SNP index plots of black pericarp bulk (A), white pericarp bulk (B) and ΔSNP index plot of Chromosome 4 showing the major genomic region (26.82-27.97 Mb) associated with black pericarp pigmentation in *Chakhao Poireiton*

To verify the genetic ratio, phenotyping for pericarp pigmentation was carried out on 161 $F_{3:4}$ families. All the plants originating from white class were uniformly white with no segregation for pericarp colouration. Alternately, the $F_{3:4}$ seeds derived from the black pericarped $F_{2:3}$ plants were either non-segregating black or segregated into black and white categories. All the dark brown pericarp genotypes were segregated into different visual categories such as black, variegated brown, brown, light brown and white. Brown pericarped genotypes were either non-segregating or segregated into brown and white (Fig. 1). The possible allelic combination of digenic segregation for different colour categories is presented in Supplementary Table S1.

Although the visual selection for black colour pericarp would be highly effective in identifying plants with high anthocyanin content in genetic improvement programmes, the trait showed maternal effect and semi-dominance inheritance. This could potentially delay phenotypic selection by one generation under normal breeding cycle, and could lead to longer breeding period. Therefore, identifying the underlying genes could be of utmost importance for fast-tracking of black rice genetic improvement program. Since the pericarp pigmentation in *Chakhao Poireiton* showed qualitative inheritance, we have employed a rapid approach called QTL-seq for mapping the candidate loci using a segregating population from the cross, Pusa 1652/*Chakhao Poireiton*. QTL-seq is a rapid and high throughput approach that uses next generation sequencing (NGS) techniques to rapidly delineate genomic regions from two bulked populations (Takagi et al. 2013). It is analogous to bulked segregant analysis (BSA, Michelmore et al. 1991), a rapid method to identify tightly linked loci from contrasting bulks for the target traits in a segregating population. BSA is cumbersome and time consuming in the event of several polymorphic loci between the parents and in the absence of tightly linked markers.The whole genome resequencing of three samples namely, CP, BP and WP resulted in the generation of 58.1, 61.2 and 50.6 million HQRs. A total of 58.1 million HQRs were aligned to the reference sequence of Nipponbare and a total of 2761500 SNPs were identified. These SNPs were replaced in the Nipponbare genome sequence to generate the reference sequence of *Chakhao Poireiton*. Alignment of the HQRs of both the bulks

Table 3. Anthocyanin pigmentation related loci present on chromosome 4 identified by QTL-seq approach in *Chakhao Poireiton*

Physical Position (bp)	Locus ID	Putative function
27878857-27909919	LOC_Os04g47040	Anthocyanin regulatory Lc protein, putative, expressed
27919179-27941819	LOC_Os04g47059	TRANSPARENT TESTA 8, putative, expressed
27955640-27949384	LOC_Os04g47080	Anthocyanin regulatory Lc protein, putative, expressed

to the parental sequence of *Chakhao Poireiton* resulted in identification of 1426434 and 1422445 SNPs/InDels in BP bulk and WP bulk, respectively. The SNP index for each of the bulks was generated separately and was used to generate chromosome wise ΔSNP index (Supplementary Fig. 1). The sliding window analysis performed with the window size of 2Mb and increment of 10kb led to the identification of a putative candidate region on chromosome 4 at the physical position between 26.82-27.97 Mb (Fig.2) governing pericarp colour. There was a total of 957 SNPs within the genomic region identified.

The annotation of 957 SNPs found in the putative region is provided in Supplementary Table S2. These SNPs originated from 51 annotated genes including retrotransposon proteins, OsSAUR19, DUF584, AP2 domain containing protein, thioesterase family protein, glycosyl transferase 8 domain containing protein, trehalose phosphatase, LTPL121-protease inhibitor/seed storage/LTP family protein precursor etc. Among these, three loci LOC_Os04g47040, LOC_Os04g47059 and LOC_Os04g47080 have been identified to be associated with pericarp colouration (Table 3). A total of 38 SNPs was present in downstream and intergenic region in LOC_Os04g47040, while LOC_Os04g47059, contained a total of 53 SNPs in intron and upstream/promoter region. Interestingly, no SNPs were present in the LOC_Os04g47080. Putative functions of LOC_Os04g47040 and LOC_Os04g47059 were indicated to be that of the anthocyanin regulatory *Lc* genes. The gene LOC_Os04g47040 is orthologous to the maize R (*Lc*) gene (Ludwig et al. 1989; Hu et al. 2000) and LOC_Os04g47059/*OSB2* is a bHLH transcription factor coding gene known to govern seed coat colour development in rice (Sakamoto et al. 2001; Oikawa et al. 2015). Earlier a 2-bp deletion in the exon 7 of *Ra* gene encoding a *Myc* transcription factor corresponding to LOC_Os04g47080 was reported to be associated with pericarp pigmentation in purple rice cultivar '*Yunanheixiannuo*' of China (Wang and Shu 2007) and black rice cultivar '*Hugnambyeo*' of Korea (Rahman et al. 2013). However, we could not identify any deletion in LOC_Os04g47080 of *Chakhao Poireiton*. Oikawa et al. (2015) identified *Kala4* (LOC_Os04g47059) as a causal gene for black pericarp pigmentation in the Japanese black rice cultivar 'Hong XieNuo' and reported rearrangements in its promoter region. In the current study, we observed 51 SNPs in the intronic region of LOC_Os04g47059 and one SNP in the promoter region. Additionally, 10 SNPs were identified in the region between LOC_Os04g47040 and LOC_Os04g47059, indicating existence of significant variation in the upstream region of the gene LOC_Os04g47059. Functionally, the genes identified in this study are regulatory genes that are already recognised to be involved in pericarp pigmentation in black rice (Seol et al. 2016). Further, analysis of promoter region and other regulatory elements located upstream of LOC_Os04g47059 needs to be carried out to unveil the regulatory mechanism involved in the expression of the trait in *Chakhao Poireiton*. In rice, R2R3-MYB and homologs of the basic helix-loop-helix (bHLH)-type transcription factors were reported to be the regulatory genes in involved in pigmentation traits (Sakamoto et al. 2001; Sun et al. 2018). The expression of these transcription factors could be tissue specific.

To conclude, the black pericarp pigmentation in Manipur black rice genotype, *Chakhao Poireiton* was identified to be governed by digenic supplementary gene action. Although the QTL-seq strategy could identify a single genomic region on chromosome 4 that signifies the regulatory control of the pericarp pigmentation, the structural gene that is responsible for the trait is yet to be identified. Further, the inheritance pattern also supported the involvement of additional gene. Therefore, to identify the other gene governing pericarp pigmentation, analysis of intermediate bulks constituted with the individuals carrying intermediate anthocyanin content *viz.,* black, dark brown, light brown and white is required. For which a modified pooling strategy to constitute four bulks based on the varying phenotypic classes needs to be carried out (Yang et al. 2019). In *Chakhao Poireiton*, the locus on chromosome 4 is involved in governing the pericarp pigmentation as reported from other black rice genotypes in various other studies. Identification of candidate genes bears significant practical implications in Manipur black rice improvement programmes.

Authors' Contribution

Conceptualization of research (AKS, GKS); Contribution of experimental materials (AKS, SB); Design of experiments (AKS, GKS, SB); Execution of experiments and data collection (SB, GKS, SS, HB, MN, PKB); Analysis of data and interpretation (RKE, SB); Preparation of manuscript (SB, RKE, KKV, GKS)

Supplementary materials

Supplementary materials include Supplementary Fig. 1 and Supplementary Tables S1 and S2.

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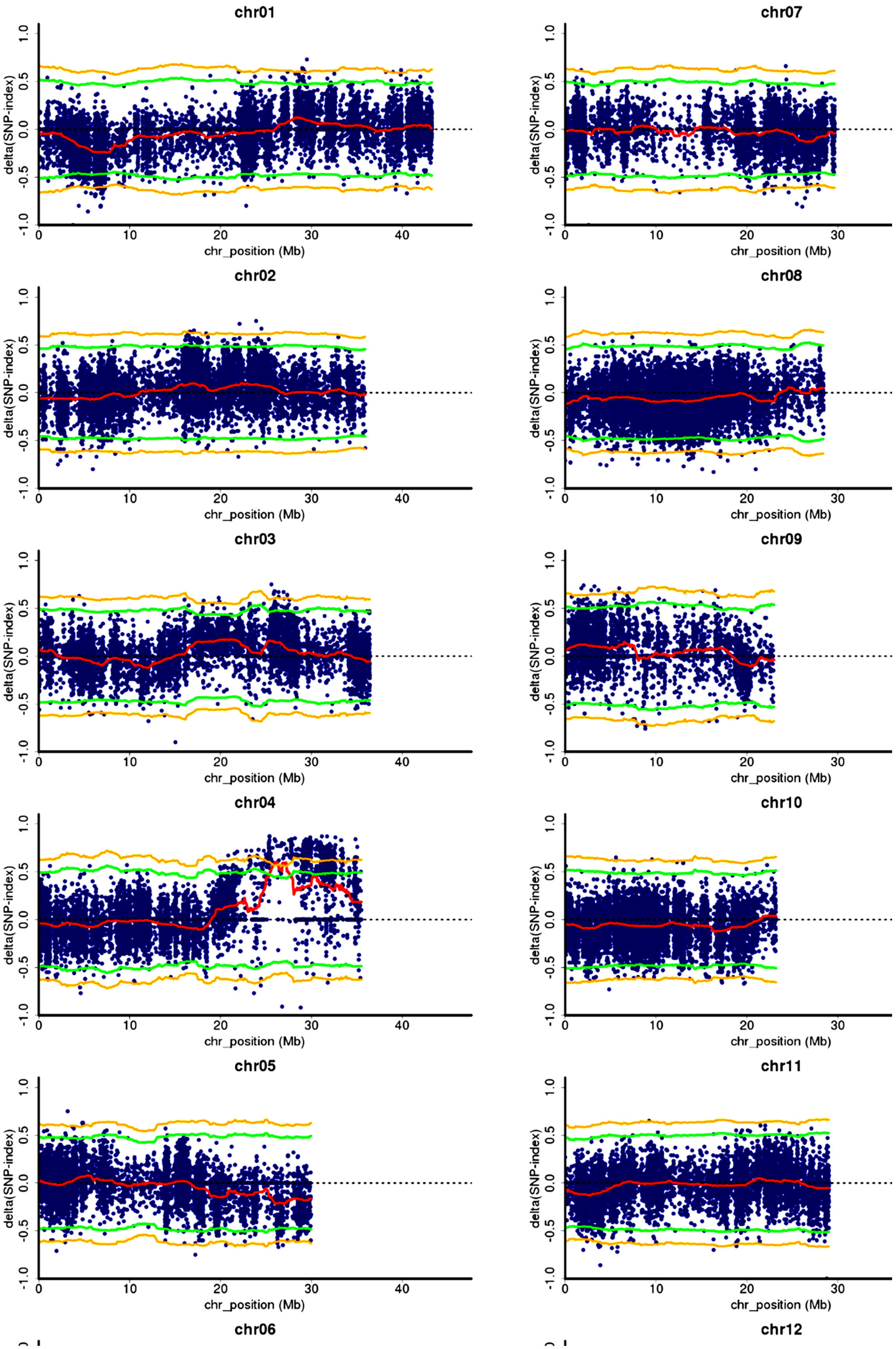

Supplementary Fig. 1. QTL-seq basedΔSNP index plot obtained for BP and WP bulks across 12 chromosomes

Supplementary Table 1. Allelic combinations in $F_{2:3}$ genotypes for different colour categories

Gametes	AB	Ab	aB	Ab
AB	AABB Black	AABb Dark brown	AaBB Black	AaBb Dark brown
Ab	AABb Dark brown	AAbb Brown	AaBb Dark brown	Aabb Brown
aB	AaBB Black	AaBb Dark brown	aaBB White	aaBb White
Ab	AaBb Dark brown	Aabb Brown	aaBb White	aabb White

Supplementary Table 2. Annotation of Chromosome 4 region with significant ΔSNP index

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25155678	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25155761	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25155888	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25155953	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25155957	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25155972	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25156111	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25156213	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25156310	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25156700	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25156826	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25156830	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25157054	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25157113	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25157138	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g42500
25179704	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179714	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179759	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179764	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179792	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179817	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179827	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g42540
25179868	C	T	missense_variant	MODERATE	LOC_Os04g42560
25179905	G	A	synonymous_variant	LOW	LOC_Os04g42560
25179918	C	T	missense_variant	MODERATE	LOC_Os04g42560
25179924	T	C	missense_variant	MODERATE	LOC_Os04g42560
25179968	G	T	missense_variant	MODERATE	LOC_Os04g42560
25180043	G	A	synonymous_variant	LOW	LOC_Os04g42560
25180044	G	T	missense_variant	MODERATE	LOC_Os04g42560
25180058	T	C	synonymous_variant	LOW	LOC_Os04g42560
25180108	T	G	missense_variant	MODERATE	LOC_Os04g42560
25242889	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g42670
25262604	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25262651	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25262737	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25262825	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25262910	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25263026	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g42700

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25263199	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25263400	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25263418	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25263421	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42700
25263469	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g42710
25263690	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g42710
25263726	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g42710
25263794	G	A	missense_variant	MODERATE	LOC_Os04g42710
25263803	C	T	missense_variant	MODERATE	LOC_Os04g42710
25263957	A	G	synonymous_variant	LOW	LOC_Os04g42710
25264087	G	A	missense_variant	MODERATE	LOC_Os04g42710
25264229	A	G	splice_donor_variant&intron_variant	HIGH	LOC_Os04g42710
25264284	G	C	missense_variant	MODERATE	LOC_Os04g42710
25265018	A	T	synonymous_variant	LOW	LOC_Os04g42710
25265460	A	G	missense_variant	MODERATE	LOC_Os04g42710
25265770	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42710
25271485	G	A	intergenic_region	MODIFIER	LOC_Os04g42710-LOC_Os04g42720
25271519	G	A	intergenic_region	MODIFIER	LOC_Os04g42710-LOC_Os04g42720
25271579	T	C	intergenic_region	MODIFIER	LOC_Os04g42710-LOC_Os04g42720
25271596	G	T	intergenic_region	MODIFIER	LOC_Os04g42710-LOC_Os04g42720
25289821	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25289840	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25289869	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25289879	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25289897	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25289903	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25289961	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25290013	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25290014	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42720
25302492	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25303224	A	G	synonymous_variant	LOW	LOC_Os04g42750
25303243	A	C	missense_variant	MODERATE	LOC_Os04g42750
25303261	T	A	missense_variant	MODERATE	LOC_Os04g42750
25303289	C	T	missense_variant	MODERATE	LOC_Os04g42750
25303292	G	A	stop_gained	HIGH	LOC_Os04g42750
25303308	A	G	synonymous_variant	LOW	LOC_Os04g42750
25303385	G	A	missense_variant	MODERATE	LOC_Os04g42750
25303413	G	A	synonymous_variant	LOW	LOC_Os04g42750
25303424	A	G	missense_variant	MODERATE	LOC_Os04g42750
25303472	C	T	missense_variant	MODERATE	LOC_Os04g42750
25303567	T	C	missense_variant	MODERATE	LOC_Os04g42750

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25303571	C	T	missense_variant	MODERATE	LOC_Os04g42750
25303595	T	C	missense_variant	MODERATE	LOC_Os04g42750
25303636	A	G	missense_variant	MODERATE	LOC_Os04g42750
25303640	A	G	missense_variant	MODERATE	LOC_Os04g42750
25303665	C	T	synonymous_variant	LOW	LOC_Os04g42750
25303700	C	T	missense_variant	MODERATE	LOC_Os04g42750
25303825	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25303880	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25303903	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25303974	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25304004	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25304012	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25304166	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25304171	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g42760
25343527	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g42784
25343550	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g42784
25343615	A	G	splice_region_variant&intron_variant	LOW	LOC_Os04g42810
25343621	T	C	missense_variant&splice_region_variant	MODERATE	LOC_Os04g42810
25343702	A	C	missense_variant	MODERATE	LOC_Os04g42810
25343806	C	T	missense_variant	MODERATE	LOC_Os04g42810
25366650	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42850
25403706	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g42940
25403714	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g42940
25403780	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g42940
25403872	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g42940
25417401	A	G	missense_variant	MODERATE	LOC_Os04g42960
25417407	C	A	missense_variant	MODERATE	LOC_Os04g42960
25417417	C	T	synonymous_variant	LOW	LOC_Os04g42960
25417458	A	G	missense_variant	MODERATE	LOC_Os04g42960
25451083	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43010
25452015	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43020
25505621	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43070
25505759	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43070
25505766	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g43070
25520176	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43090
25524110	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43130
25524152	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43130
25524248	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43130
25558031	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g43164
25558037	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43164
25558066	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43164
25558151	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43164
25560956	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43170

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25587501	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43230
25587545	T	C	missense_variant	MODERATE	LOC_Os04g43250
25587591	C	T	synonymous_variant	LOW	LOC_Os04g43250
25591415	G	A	synonymous_variant	LOW	LOC_Os04g43260
25591461	G	T	missense_variant	MODERATE	LOC_Os04g43260
25591466	A	G	synonymous_variant	LOW	LOC_Os04g43260
25591472	T	A	synonymous_variant	LOW	LOC_Os04g43260
25591517	C	T	synonymous_variant	LOW	LOC_Os04g43260
25591528	C	T	missense_variant	MODERATE	LOC_Os04g43260
25591536	A	G	missense_variant	MODERATE	LOC_Os04g43260
25591541	C	T	synonymous_variant	LOW	LOC_Os04g43260
25591555	A	C	missense_variant	MODERATE	LOC_Os04g43260
25591558	T	C	missense_variant	MODERATE	LOC_Os04g43260
25591592	A	G	synonymous_variant	LOW	LOC_Os04g43260
25592805	T	C	synonymous_variant	LOW	LOC_Os04g43260
25617600	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43300
25617656	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43300
25617672	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43300
25645722	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43360
25649910	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43370
25653267	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25653559	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25653703	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25653918	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25654166	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25654180	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25654209	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g43380
25670160	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670171	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670206	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670277	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670305	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670345	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670435	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670763	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670803	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670830	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670914	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670929	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670934	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670946	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670963	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25670992	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25671004	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25671120	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43400

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25671132	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25671148	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43400
25676003	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43400
25677085	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43400
25677093	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43400
25677158	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43400
25677262	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g43400
25690262	T	C	intron_variant	MODIFIER	LOC_Os04g43410
25690275	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25690299	G	A	intron_variant	MODIFIER	LOC_Os04g43410
25690328	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25690412	G	A	intron_variant	MODIFIER	LOC_Os04g43410
25690855	T	C	intron_variant	MODIFIER	LOC_Os04g43410
25690960	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25690992	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25691007	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25691032	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25691108	G	A	intron_variant	MODIFIER	LOC_Os04g43410
25691154	G	A	intron_variant	MODIFIER	LOC_Os04g43410
25691187	T	C	intron_variant	MODIFIER	LOC_Os04g43410
25691188	A	G	intron_variant	MODIFIER	LOC_Os04g43410
25691216	C	A	intron_variant	MODIFIER	LOC_Os04g43410
25691269	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25691341	G	A	intron_variant	MODIFIER	LOC_Os04g43410
25691372	G	C	intron_variant	MODIFIER	LOC_Os04g43410
25691374	T	C	intron_variant	MODIFIER	LOC_Os04g43410
25691412	A	G	intron_variant	MODIFIER	LOC_Os04g43410
25691418	A	G	intron_variant	MODIFIER	LOC_Os04g43410
25691437	G	A	intron_variant	MODIFIER	LOC_Os04g43410
25691447	C	T	intron_variant	MODIFIER	LOC_Os04g43410
25691471	T	C	intron_variant	MODIFIER	LOC_Os04g43410
25694765	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43410
25694788	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43410
25726119	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726166	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726172	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726218	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726233	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726262	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726280	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726290	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726297	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726303	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726315	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726330	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43480

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25726371	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726379	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726384	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25726403	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43480
25735819	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43490
25740954	A	T	synonymous_variant	LOW	LOC_Os04g43500
25756678	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756726	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756758	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756774	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756799	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756801	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756833	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756862	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756913	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756923	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756944	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756958	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25756989	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757000	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757005	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757011	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757058	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757070	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757075	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757108	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757122	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757170	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757174	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757271	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757283	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757289	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757299	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757313	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757343	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757376	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757396	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757419	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757425	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757442	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757450	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757469	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757499	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757506	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757518	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25757525	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757531	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757538	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757562	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757605	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757609	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757651	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757659	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757663	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25757671	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g43550
25781790	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43570
25794686	A	G	synonymous_variant	LOW	LOC_Os04g43590
25794713	A	G	synonymous_variant	LOW	LOC_Os04g43590
25794908	T	G	synonymous_variant	LOW	LOC_Os04g43590
25795034	A	C	missense_variant	MODERATE	LOC_Os04g43590
25797085	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g43600
25798363	G	T	synonymous_variant	LOW	LOC_Os04g43590
25798373	A	G	synonymous_variant	LOW	LOC_Os04g43590
25798428	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g43590
25800729	C	T	synonymous_variant	LOW	LOC_Os04g43600
25801877	T	C	missense_variant	MODERATE	LOC_Os04g43600
25815199	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g43630
25815246	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g43630
25815274	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g43630
25873210	G	A	synonymous_variant	LOW	LOC_Os04g43720
25892307	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43730
25911143	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911264	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911351	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911371	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911378	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911404	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911517	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911676	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911789	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911793	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911852	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911903	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911924	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911946	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911948	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25911959	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912014	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912176	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912212	G	A	missense_variant	MODERATE	LOC_Os04g43770

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25912248	G	A	splice_region_variant&intron_variant	LOW	LOC_Os04g43770
25912408	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912468	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912538	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912585	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912608	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912647	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912732	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912788	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25912917	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913098	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913118	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913127	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913138	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913142	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913157	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913204	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913282	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913328	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913335	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913386	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913391	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913448	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913509	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913605	A	T	splice_region_variant&intron_variant	LOW	LOC_Os04g43770
25913698	G	A	missense_variant	MODERATE	LOC_Os04g43770
25913709	C	T	splice_acceptor_variant&intron_variant	HIGH	LOC_Os04g43770
25913805	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913811	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913835	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913937	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25913994	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914039	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914049	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914081	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914114	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914120	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914183	G	A	synonymous_variant	LOW	LOC_Os04g43770
25914232	C	T	missense_variant	MODERATE	LOC_Os04g43770
25914243	A	G	synonymous_variant	LOW	LOC_Os04g43770
25914254	A	T	missense_variant	MODERATE	LOC_Os04g43770
25914310	G	T	missense_variant	MODERATE	LOC_Os04g43770
25914325	A	G	missense_variant	MODERATE	LOC_Os04g43770

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25914438	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914477	C	T	missense_variant	MODERATE	LOC_Os04g43770
25914539	C	T	missense_variant	MODERATE	LOC_Os04g43770
25914544	T	C	synonymous_variant	LOW	LOC_Os04g43770
25914566	G	A	splice_region_variant&intron_variant	LOW	LOC_Os04g43770
25914573	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914627	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914671	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914721	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25914744	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43760
25915002	C	T	missense_variant	MODERATE	LOC_Os04g43770
25915013	A	G	missense_variant	MODERATE	LOC_Os04g43770
25915019	C	T	missense_variant	MODERATE	LOC_Os04g43770
25915046	A	G	missense_variant	MODERATE	LOC_Os04g43770
25915057	A	G	synonymous_variant	LOW	LOC_Os04g43770
25915061	C	T	missense_variant	MODERATE	LOC_Os04g43770
25915085	A	G	start_lost	HIGH	LOC_Os04g43770
25915108	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915128	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915130	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915145	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915175	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915179	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915221	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915288	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915342	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915370	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25915384	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43770
25920672	C	T	missense_variant	MODERATE	LOC_Os04g43780
25920694	T	C	synonymous_variant	LOW	LOC_Os04g43780
25920734	A	G	missense_variant	MODERATE	LOC_Os04g43780
25920773	G	A	missense_variant	MODERATE	LOC_Os04g43780
25920815	G	A	missense_variant	MODERATE	LOC_Os04g43780
25920834	T	C	missense_variant	MODERATE	LOC_Os04g43780
25920864	T	C	missense_variant	MODERATE	LOC_Os04g43780
25920882	G	A	missense_variant	MODERATE	LOC_Os04g43780
25920927	C	T	missense_variant	MODERATE	LOC_Os04g43780
25921010	G	A	missense_variant	MODERATE	LOC_Os04g43780
25921024	A	G	synonymous_variant	LOW	LOC_Os04g43780
25921048	C	A	missense_variant	MODERATE	LOC_Os04g43780
25921054	A	G	synonymous_variant	LOW	LOC_Os04g43780
25921594	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25921723	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25921892	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43780

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
25922112	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25924075	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25924118	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25924133	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25924157	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g43780
25965696	G	A	missense_variant	MODERATE	LOC_Os04g43850
25973067	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43850
25989355	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43870
25989465	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43870
25990345	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g43870
25997587	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g43900
26008027	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43900
26008055	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g43900
26012120	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43910
26012123	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g43910
26044895	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g43922
26044960	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43922
26044984	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43922
26051721	G	A	missense_variant	MODERATE	LOC_Os04g43940
26051726	G	A	synonymous_variant	LOW	LOC_Os04g43940
26053199	T	C	missense_variant	MODERATE	LOC_Os04g43950
26053377	A	G	synonymous_variant	LOW	LOC_Os04g43950
26053410	T	C	synonymous_variant	LOW	LOC_Os04g43950
26053520	T	C	missense_variant	MODERATE	LOC_Os04g43950
26053971	C	T	synonymous_variant	LOW	LOC_Os04g43950
26054100	T	C	synonymous_variant	LOW	LOC_Os04g43950
26054136	T	C	synonymous_variant	LOW	LOC_Os04g43950
26054521	C	G	missense_variant	MODERATE	LOC_Os04g43950
26054576	A	T	missense_variant	MODERATE	LOC_Os04g43950
26056686	G	A	synonymous_variant	LOW	LOC_Os04g43950
26058986	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g43960
26059073	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g43960
26064858	G	A	stop_gained	HIGH	LOC_Os04g43980
26066940	A	C	synonymous_variant	LOW	LOC_Os04g43980
26069078	G	A	synonymous_variant	LOW	LOC_Os04g43980
26069127	T	A	missense_variant	MODERATE	LOC_Os04g43980
26069130	C	T	missense_variant	MODERATE	LOC_Os04g43980
26083389	G	A	missense_variant	MODERATE	LOC_Os04g44000
26083474	T	G	missense_variant	MODERATE	LOC_Os04g44000
26083599	A	G	missense_variant	MODERATE	LOC_Os04g44000
26083726	T	C	missense_variant	MODERATE	LOC_Os04g44000
26084027	A	G	missense_variant	MODERATE	LOC_Os04g44000
26088931	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44030
26089051	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44030
26089142	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44030

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26106375	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44080
26106388	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g44080
26106472	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44080
26106483	T	C	start_lost	HIGH	LOC_Os04g44080
26106555	G	A	splice_region_variant&intron_variant	LOW	LOC_Os04g44080
26107128	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g44090
26107165	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44090
26107171	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44090
26107183	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g44090
26107256	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44090
26121221	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g44140
26122525	A	G	synonymous_variant	LOW	LOC_Os04g44140
26161539	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g44180
26217169	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44250
26217198	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44250
26217210	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g44250
26217240	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44250
26246107	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g44320
26246191	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44320
26268864	C	T	synonymous_variant	LOW	LOC_Os04g44370
26269062	C	G	missense_variant	MODERATE	LOC_Os04g44370
26269125	G	T	missense_variant	MODERATE	LOC_Os04g44370
26269166	C	T	synonymous_variant	LOW	LOC_Os04g44370
26269337	C	T	synonymous_variant	LOW	LOC_Os04g44370
26269451	G	A	synonymous_variant	LOW	LOC_Os04g44370
26269475	C	T	synonymous_variant	LOW	LOC_Os04g44370
26270285	C	T	synonymous_variant	LOW	LOC_Os04g44370
26270369	G	T	synonymous_variant	LOW	LOC_Os04g44370
26270389	A	C	missense_variant	MODERATE	LOC_Os04g44370
26270409	C	T	missense_variant	MODERATE	LOC_Os04g44370
26270696	C	T	synonymous_variant	LOW	LOC_Os04g44370
26270700	C	T	missense_variant	MODERATE	LOC_Os04g44370
26273088	G	C	synonymous_variant	LOW	LOC_Os04g44370
26273105	C	T	missense_variant	MODERATE	LOC_Os04g44370
26273134	G	A	missense_variant	MODERATE	LOC_Os04g44370
26274046	A	G	missense_variant	MODERATE	LOC_Os04g44370
26274110	T	A	missense_variant	MODERATE	LOC_Os04g44370
26275989	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44370
26276086	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44370
26276106	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44370
26276139	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44370
26294276	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44410
26298569	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g44420
26298574	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26322567	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322573	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322594	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322635	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322655	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322675	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322700	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322702	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322800	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322842	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322875	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322904	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322933	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26322970	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26323036	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26323048	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26323141	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44480
26327626	A	G	synonymous_variant	LOW	LOC_Os04g44480
26327853	C	T	missense_variant	MODERATE	LOC_Os04g44480
26327868	C	T	missense_variant	MODERATE	LOC_Os04g44480
26328507	C	T	missense_variant	MODERATE	LOC_Os04g44480
26334873	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g44480
26335181	C	T	missense_variant	MODERATE	LOC_Os04g44490
26336046	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g44480
26336065	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g44480
26336089	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g44480
26336170	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g44480
26340760	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g44490
26410303	C	T	stop_gained	HIGH	LOC_Os04g44630
26413091	C	T	missense_variant	MODERATE	LOC_Os04g44640
26413648	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g44630
26417996	G	A	intron_variant	MODIFIER	LOC_Os04g44640
26418086	A	G	intron_variant	MODIFIER	LOC_Os04g44640
26418311	C	T	intron_variant	MODIFIER	LOC_Os04g44640
26419339	G	A	intron_variant	MODIFIER	LOC_Os04g44640
26419475	G	T	intron_variant	MODIFIER	LOC_Os04g44640
26464808	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g44690
26464922	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g44690
26500268	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44740
26500327	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g44740
26500347	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g44740
26500369	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g44740
26500383	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44740
26500437	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g44740
26607171	G	A	stop_gained	HIGH	LOC_Os04g44970

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26657584	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45050
26657709	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45050
26688799	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45130
26689036	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45130
26722058	A	G	missense_variant	MODERATE	LOC_Os04g45220
26722078	G	C	synonymous_variant	LOW	LOC_Os04g45220
26722111	G	A	synonymous_variant	LOW	LOC_Os04g45220
26722124	A	G	missense_variant	MODERATE	LOC_Os04g45220
26722312	C	T	synonymous_variant	LOW	LOC_Os04g45220
26722534	G	A	synonymous_variant	LOW	LOC_Os04g45220
26722556	G	T	missense_variant	MODERATE	LOC_Os04g45220
26722618	C	T	start_lost	HIGH	LOC_Os04g45220
26722777	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45200
26723028	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45200
26723035	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45200
26775344	C	T	missense_variant	MODERATE	LOC_Os04g45300
26775409	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775438	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775485	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775497	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775506	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775539	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775542	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775570	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775634	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775652	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775691	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775699	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775739	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775754	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775767	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775802	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775839	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26775997	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776043	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776077	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776114	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776132	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776203	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776209	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26776703	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45300
26788471	A	T	stop_gained	HIGH	LOC_Os04g45320
26790931	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26790993	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26791056	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45320

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26793165	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26793187	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26793191	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26793204	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26793257	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26794011	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45320
26827030	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45370
26827160	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45370
26836211	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26836223	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26836291	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26836337	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26836345	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26836381	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26836434	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g45370
26839154	G	A	stop_gained	HIGH	LOC_Os04g45380
26839186	G	A	missense_variant	MODERATE	LOC_Os04g45380
26839188	G	A	synonymous_variant	LOW	LOC_Os04g45380
26839197	A	G	synonymous_variant	LOW	LOC_Os04g45380
26839278	T	C	synonymous_variant	LOW	LOC_Os04g45380
26839302	A	G	synonymous_variant	LOW	LOC_Os04g45380
26839320	T	A	missense_variant	MODERATE	LOC_Os04g45380
26839331	C	T	missense_variant	MODERATE	LOC_Os04g45380
26839349	T	C	missense_variant	MODERATE	LOC_Os04g45380
26839412	C	T	missense_variant	MODERATE	LOC_Os04g45380
26839477	A	G	missense_variant	MODERATE	LOC_Os04g45380
26839498	G	A	missense_variant	MODERATE	LOC_Os04g45380
26839532	G	A	stop_gained	HIGH	LOC_Os04g45380
26839569	C	T	synonymous_variant	LOW	LOC_Os04g45380
26839881	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26839896	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26839904	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26839911	C	T	splice_region_variant&intron_variant	LOW	LOC_Os04g45380
26839933	C	T	missense_variant	MODERATE	LOC_Os04g45380
26839952	G	A	missense_variant	MODERATE	LOC_Os04g45380
26839962	C	T	synonymous_variant	LOW	LOC_Os04g45380
26840012	G	A	missense_variant	MODERATE	LOC_Os04g45380
26840026	T	C	missense_variant	MODERATE	LOC_Os04g45380
26840063	G	T	missense_variant	MODERATE	LOC_Os04g45380
26840112	C	T	synonymous_variant	LOW	LOC_Os04g45380
26840133	A	G	synonymous_variant	LOW	LOC_Os04g45380
26840134	C	T	missense_variant	MODERATE	LOC_Os04g45380
26840147	G	A	missense_variant	MODERATE	LOC_Os04g45380
26840179	C	T	missense_variant	MODERATE	LOC_Os04g45380

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26840910	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26841085	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26841146	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26841155	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g45390
26844619	G	T	missense_variant	MODERATE	LOC_Os04g45390
26844704	T	C	missense_variant	MODERATE	LOC_Os04g45390
26844725	G	A	stop_gained	HIGH	LOC_Os04g45390
26845006	G	A	missense_variant	MODERATE	LOC_Os04g45390
26845021	G	T	missense_variant	MODERATE	LOC_Os04g45390
26845130	A	T	missense_variant	MODERATE	LOC_Os04g45390
26845198	G	A	missense_variant	MODERATE	LOC_Os04g45390
26845208	A	G	missense_variant	MODERATE	LOC_Os04g45390
26846260	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45380
26860254	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860310	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860342	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860415	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860431	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860443	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860518	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860535	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26860657	T	C	missense_variant	MODERATE	LOC_Os04g45410
26861501	A	C	synonymous_variant	LOW	LOC_Os04g45420
26861525	C	T	synonymous_variant	LOW	LOC_Os04g45420
26861536	T	G	missense_variant	MODERATE	LOC_Os04g45420
26861541	G	A	missense_variant	MODERATE	LOC_Os04g45420
26861550	G	C	missense_variant	MODERATE	LOC_Os04g45420
26861555	T	C	synonymous_variant	LOW	LOC_Os04g45420
26861580	G	A	missense_variant	MODERATE	LOC_Os04g45420
26861628	G	A	missense_variant	MODERATE	LOC_Os04g45420
26861670	A	G	missense_variant	MODERATE	LOC_Os04g45420
26861688	G	A	missense_variant	MODERATE	LOC_Os04g45420
26861691	T	A	missense_variant	MODERATE	LOC_Os04g45420
26861738	T	C	synonymous_variant	LOW	LOC_Os04g45420
26861760	C	T	splice_acceptor_variant&intron_variant	HIGH	LOC_Os04g45420
26861843	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26861852	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26861952	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26861954	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26861967	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26861999	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862001	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862040	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862053	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26862125	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862141	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862144	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862182	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862190	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862249	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862276	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862303	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862311	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862390	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862404	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862480	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45400
26862581	G	T	synonymous_variant	LOW	LOC_Os04g45420
26862633	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862675	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862683	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862700	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862771	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862837	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862850	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862917	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26862938	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26863079	T	G	missense_variant	MODERATE	LOC_Os04g45420
26863083	G	A	missense_variant	MODERATE	LOC_Os04g45420
26863156	C	T	missense_variant	MODERATE	LOC_Os04g45420
26863157	A	G	synonymous_variant	LOW	LOC_Os04g45420
26863289	A	G	synonymous_variant	LOW	LOC_Os04g45420
26863307	G	A	synonymous_variant	LOW	LOC_Os04g45420
26863324	C	G	missense_variant	MODERATE	LOC_Os04g45420
26863343	C	T	splice_region_variant&intron_variant	LOW	LOC_Os04g45420
26863390	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26863405	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26863422	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26863452	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26863476	G	A	missense_variant&splice_region_variant	MODERATE	LOC_Os04g45420
26863533	T	C	missense_variant	MODERATE	LOC_Os04g45420
26863625	A	G	synonymous_variant	LOW	LOC_Os04g45420
26863690	T	C	missense_variant	MODERATE	LOC_Os04g45420
26863707	C	T	missense_variant	MODERATE	LOC_Os04g45420
26864011	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26864031	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26864131	C	T	synonymous_variant	LOW	LOC_Os04g45420
26864191	A	G	synonymous_variant	LOW	LOC_Os04g45420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26864207	T	A	missense_variant	MODERATE	LOC_Os04g45420
26864229	T	C	missense_variant	MODERATE	LOC_Os04g45420
26864238	T	C	missense_variant	MODERATE	LOC_Os04g45420
26864283	A	G	missense_variant	MODERATE	LOC_Os04g45420
26864314	G	A	synonymous_variant	LOW	LOC_Os04g45420
26864366	A	G	missense_variant	MODERATE	LOC_Os04g45420
26864385	G	A	stop_gained	HIGH	LOC_Os04g45420
26864460	T	C	missense_variant	MODERATE	LOC_Os04g45420
26864470	G	A	synonymous_variant	LOW	LOC_Os04g45420
26864697	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45410
26864801	T	C	synonymous_variant	LOW	LOC_Os04g45420
26864803	G	A	missense_variant	MODERATE	LOC_Os04g45420
26865160	C	T	missense_variant	MODERATE	LOC_Os04g45420
26865257	C	G	missense_variant	MODERATE	LOC_Os04g45420
26865301	C	A	missense_variant	MODERATE	LOC_Os04g45420
26865312	G	T	missense_variant	MODERATE	LOC_Os04g45420
26865331	T	C	missense_variant	MODERATE	LOC_Os04g45420
26865355	G	C	missense_variant	MODERATE	LOC_Os04g45420
26865402	C	T	missense_variant	MODERATE	LOC_Os04g45420
26865511	G	A	stop_gained	HIGH	LOC_Os04g45420
26865524	C	T	synonymous_variant	LOW	LOC_Os04g45420
26865586	C	T	missense_variant	MODERATE	LOC_Os04g45420
26865591	C	T	missense_variant	MODERATE	LOC_Os04g45420
26865600	A	T	missense_variant	MODERATE	LOC_Os04g45420
26865618	T	C	missense_variant	MODERATE	LOC_Os04g45420
26865725	G	A	synonymous_variant	LOW	LOC_Os04g45420
26865838	G	A	stop_gained	HIGH	LOC_Os04g45420
26865867	G	A	missense_variant	MODERATE	LOC_Os04g45420
26865887	A	C	synonymous_variant	LOW	LOC_Os04g45420
26865899	G	A	synonymous_variant	LOW	LOC_Os04g45420
26865924	T	C	missense_variant	MODERATE	LOC_Os04g45420
26865929	G	A	synonymous_variant	LOW	LOC_Os04g45420
26865958	C	T	missense_variant	MODERATE	LOC_Os04g45420
26865977	C	T	synonymous_variant	LOW	LOC_Os04g45420
26865983	A	G	synonymous_variant	LOW	LOC_Os04g45420
26866016	C	T	stop_gained	HIGH	LOC_Os04g45420
26866028	A	G	synonymous_variant	LOW	LOC_Os04g45420
26866037	T	C	splice_acceptor_variant&intron_variant	HIGH	LOC_Os04g45420
26866047	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866057	A	T	intron_variant	MODIFIER	LOC_Os04g45420
26866063	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866088	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866115	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866130	T	C	intron_variant	MODIFIER	LOC_Os04g45420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26866178	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26866188	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866215	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866224	C	G	intron_variant	MODIFIER	LOC_Os04g45420
26866228	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866239	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26866270	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866283	C	G	intron_variant	MODIFIER	LOC_Os04g45420
26866285	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866298	A	G	splice_donor_variant&intron_variant	HIGH	LOC_Os04g45420
26866320	T	C	missense_variant	MODERATE	LOC_Os04g45420
26866356	G	T	stop_gained	HIGH	LOC_Os04g45420
26866360	G	T	synonymous_variant	LOW	LOC_Os04g45420
26866386	G	A	missense_variant	MODERATE	LOC_Os04g45420
26866397	C	T	splice_acceptor_variant&intron_variant	HIGH	LOC_Os04g45420
26866445	G	T	intron_variant	MODIFIER	LOC_Os04g45420
26866473	T	G	intron_variant	MODIFIER	LOC_Os04g45420
26866482	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26866512	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866526	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866527	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866541	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866543	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866559	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866587	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26866600	T	G	intron_variant	MODIFIER	LOC_Os04g45420
26866603	G	T	intron_variant	MODIFIER	LOC_Os04g45420
26866620	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866625	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26866633	T	C	intron_variant	MODIFIER	LOC_Os04g45420
26866646	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26866654	A	G	intron_variant	MODIFIER	LOC_Os04g45420
26866718	T	C	synonymous_variant	LOW	LOC_Os04g45420
26866726	T	C	missense_variant	MODERATE	LOC_Os04g45420
26866760	A	G	synonymous_variant	LOW	LOC_Os04g45420
26866881	G	T	missense_variant	MODERATE	LOC_Os04g45420
26866889	A	G	synonymous_variant	LOW	LOC_Os04g45420
26866998	G	A	missense_variant	MODERATE	LOC_Os04g45420
26867006	G	A	synonymous_variant	LOW	LOC_Os04g45420
26867050	T	C	missense_variant	MODERATE	LOC_Os04g45420
26867134	C	T	missense_variant	MODERATE	LOC_Os04g45420
26867138	T	G	synonymous_variant	LOW	LOC_Os04g45420
26867159	A	G	synonymous_variant	LOW	LOC_Os04g45420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26867192	G	A	synonymous_variant	LOW	LOC_Os04g45420
26867393	G	A	synonymous_variant	LOW	LOC_Os04g45420
26867420	A	G	synonymous_variant	LOW	LOC_Os04g45420
26867437	T	C	missense_variant	MODERATE	LOC_Os04g45420
26867440	T	C	missense_variant	MODERATE	LOC_Os04g45420
26867448	G	T	missense_variant	MODERATE	LOC_Os04g45420
26867465	T	A	synonymous_variant	LOW	LOC_Os04g45420
26867484	A	G	missense_variant	MODERATE	LOC_Os04g45420
26867546	C	A	synonymous_variant	LOW	LOC_Os04g45420
26867571	C	T	missense_variant	MODERATE	LOC_Os04g45420
26867583	G	A	missense_variant	MODERATE	LOC_Os04g45420
26867615	G	T	synonymous_variant	LOW	LOC_Os04g45420
26867638	C	T	missense_variant	MODERATE	LOC_Os04g45420
26867646	G	C	missense_variant	MODERATE	LOC_Os04g45420
26867651	G	A	synonymous_variant	LOW	LOC_Os04g45420
26867659	T	C	missense_variant	MODERATE	LOC_Os04g45420
26867663	C	G	synonymous_variant	LOW	LOC_Os04g45420
26867675	C	T	synonymous_variant	LOW	LOC_Os04g45420
26867723	G	T	synonymous_variant	LOW	LOC_Os04g45420
26867769	T	C	missense_variant	MODERATE	LOC_Os04g45420
26867787	A	G	missense_variant	MODERATE	LOC_Os04g45420
26867836	T	C	missense_variant	MODERATE	LOC_Os04g45420
26867907	G	A	missense_variant	MODERATE	LOC_Os04g45420
26867911	G	A	missense_variant	MODERATE	LOC_Os04g45420
26868005	G	A	synonymous_variant	LOW	LOC_Os04g45420
26868007	T	C	missense_variant	MODERATE	LOC_Os04g45420
26868033	G	A	missense_variant	MODERATE	LOC_Os04g45420
26868110	C	T	synonymous_variant	LOW	LOC_Os04g45420
26868128	T	C	synonymous_variant	LOW	LOC_Os04g45420
26868131	C	T	missense_variant	MODERATE	LOC_Os04g45420
26868342	T	A	intron_variant	MODIFIER	LOC_Os04g45420
26868359	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26868375	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26868376	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26868420	C	T	intron_variant	MODIFIER	LOC_Os04g45420
26868428	A	G	splice_donor_variant&intron_variant	HIGH	LOC_Os04g45420
26868441	T	C	missense_variant	MODERATE	LOC_Os04g45420
26868455	G	C	synonymous_variant	LOW	LOC_Os04g45420
26868497	C	T	synonymous_variant	LOW	LOC_Os04g45420
26868508	C	A	missense_variant	MODERATE	LOC_Os04g45420
26868541	C	T	missense_variant	MODERATE	LOC_Os04g45420
26868583	C	A	missense_variant	MODERATE	LOC_Os04g45420
26868659	A	G	synonymous_variant	LOW	LOC_Os04g45420
26868707	A	G	synonymous_variant	LOW	LOC_Os04g45420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26868775	C	T	missense_variant	MODERATE	LOC_Os04g45420
26868800	A	G	synonymous_variant	LOW	LOC_Os04g45420
26868818	G	A	synonymous_variant	LOW	LOC_Os04g45420
26868836	T	A	missense_variant	MODERATE	LOC_Os04g45420
26868862	C	T	missense_variant	MODERATE	LOC_Os04g45420
26868892	G	A	missense_variant	MODERATE	LOC_Os04g45420
26868915	C	T	missense_variant	MODERATE	LOC_Os04g45420
26868919	T	C	missense_variant	MODERATE	LOC_Os04g45420
26868988	G	A	missense_variant	MODERATE	LOC_Os04g45420
26868992	G	A	synonymous_variant	LOW	LOC_Os04g45420
26869010	G	A	synonymous_variant	LOW	LOC_Os04g45420
26869027	C	T	missense_variant	MODERATE	LOC_Os04g45420
26869069	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869102	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869159	C	A	stop_gained	HIGH	LOC_Os04g45420
26869167	C	G	missense_variant	MODERATE	LOC_Os04g45420
26869174	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869203	C	T	missense_variant	MODERATE	LOC_Os04g45420
26869250	G	A	synonymous_variant	LOW	LOC_Os04g45420
26869269	G	A	intron_variant	MODIFIER	LOC_Os04g45420
26869371	G	A	missense_variant	MODERATE	LOC_Os04g45420
26869445	G	A	synonymous_variant	LOW	LOC_Os04g45420
26869454	C	T	synonymous_variant	LOW	LOC_Os04g45420
26869533	G	A	missense_variant	MODERATE	LOC_Os04g45420
26869535	G	A	synonymous_variant	LOW	LOC_Os04g45420
26869560	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869581	A	G	missense_variant	MODERATE	LOC_Os04g45420
26869634	G	A	synonymous_variant	LOW	LOC_Os04g45420
26869640	C	T	synonymous_variant	LOW	LOC_Os04g45420
26869648	G	C	missense_variant	MODERATE	LOC_Os04g45420
26869652	T	C	synonymous_variant	LOW	LOC_Os04g45420
26869671	A	G	missense_variant	MODERATE	LOC_Os04g45420
26869711	C	G	missense_variant	MODERATE	LOC_Os04g45420
26869754	T	C	synonymous_variant	LOW	LOC_Os04g45420
26869794	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869796	A	C	synonymous_variant	LOW	LOC_Os04g45420
26869839	C	T	missense_variant	MODERATE	LOC_Os04g45420
26869877	A	T	missense_variant	MODERATE	LOC_Os04g45420
26869923	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869951	T	C	missense_variant	MODERATE	LOC_Os04g45420
26869953	A	G	missense_variant	MODERATE	LOC_Os04g45420
26869972	C	T	missense_variant	MODERATE	LOC_Os04g45420
26869981	A	G	splice_region_variant&intron_variant	LOW	LOC_Os04g45420
26869988	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g45430

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26869992	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g45430
26870030	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45430
26870065	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g45430
26870087	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45430
26870119	G	A	missense_variant	MODERATE	LOC_Os04g45420
26870186	T	C	missense_variant	MODERATE	LOC_Os04g45420
26870211	T	C	synonymous_variant	LOW	LOC_Os04g45420
26870235	A	G	synonymous_variant	LOW	LOC_Os04g45420
26870253	T	A	missense_variant	MODERATE	LOC_Os04g45420
26870264	C	T	missense_variant	MODERATE	LOC_Os04g45420
26870291	A	T	missense_variant	MODERATE	LOC_Os04g45420
26870297	T	G	missense_variant	MODERATE	LOC_Os04g45420
26870345	C	T	missense_variant	MODERATE	LOC_Os04g45420
26870410	A	G	missense_variant	MODERATE	LOC_Os04g45420
26870431	G	A	missense_variant	MODERATE	LOC_Os04g45420
26870465	G	A	stop_gained	HIGH	LOC_Os04g45420
26870496	A	G	synonymous_variant	LOW	LOC_Os04g45420
26870502	C	T	synonymous_variant	LOW	LOC_Os04g45420
26870555	A	G	synonymous_variant	LOW	LOC_Os04g45420
26870572	C	T	missense_variant	MODERATE	LOC_Os04g45420
26870600	G	C	missense_variant	MODERATE	LOC_Os04g45420
26870678	G	T	missense_variant	MODERATE	LOC_Os04g45420
26870713	C	T	missense_variant	MODERATE	LOC_Os04g45420
26870721	G	A	synonymous_variant	LOW	LOC_Os04g45420
26870725	C	T	missense_variant	MODERATE	LOC_Os04g45420
26870736	C	T	synonymous_variant	LOW	LOC_Os04g45420
26870758	G	T	missense_variant	MODERATE	LOC_Os04g45420
26870814	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45430
26870866	C	T	missense_variant	MODERATE	LOC_Os04g45420
26870895	C	T	synonymous_variant	LOW	LOC_Os04g45420
26870898	C	A	synonymous_variant	LOW	LOC_Os04g45420
26870906	T	C	missense_variant	MODERATE	LOC_Os04g45420
26870916	C	T	synonymous_variant	LOW	LOC_Os04g45420
26870945	G	A	missense_variant	MODERATE	LOC_Os04g45420
26870959	T	C	missense_variant	MODERATE	LOC_Os04g45420
26870974	A	G	missense_variant	MODERATE	LOC_Os04g45420
26870996	G	T	missense_variant	MODERATE	LOC_Os04g45420
26871045	C	T	synonymous_variant	LOW	LOC_Os04g45420
26871080	G	A	missense_variant	MODERATE	LOC_Os04g45420
26871184	T	C	missense_variant	MODERATE	LOC_Os04g45420
26871241	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871306	T	C	synonymous_variant	LOW	LOC_Os04g45420
26871320	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871353	T	C	missense_variant	MODERATE	LOC_Os04g45420
26871363	A	G	synonymous_variant	LOW	LOC_Os04g45420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26871448	T	C	missense_variant	MODERATE	LOC_Os04g45420
26871486	C	T	synonymous_variant	LOW	LOC_Os04g45420
26871493	C	T	missense_variant	MODERATE	LOC_Os04g45420
26871533	C	T	missense_variant	MODERATE	LOC_Os04g45420
26871566	G	A	stop_gained	HIGH	LOC_Os04g45420
26871572	T	C	missense_variant	MODERATE	LOC_Os04g45420
26871585	C	A	synonymous_variant	LOW	LOC_Os04g45420
26871602	G	A	stop_gained	HIGH	LOC_Os04g45420
26871614	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871679	T	C	missense_variant	MODERATE	LOC_Os04g45420
26871712	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871718	C	T	missense_variant	MODERATE	LOC_Os04g45420
26871763	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871770	G	A	missense_variant	MODERATE	LOC_Os04g45420
26871791	C	T	missense_variant	MODERATE	LOC_Os04g45420
26871803	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871816	T	C	synonymous_variant	LOW	LOC_Os04g45420
26871823	C	T	missense_variant	MODERATE	LOC_Os04g45420
26871836	C	T	missense_variant	MODERATE	LOC_Os04g45420
26871856	A	T	missense_variant	MODERATE	LOC_Os04g45420
26871892	A	G	missense_variant	MODERATE	LOC_Os04g45420
26871914	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26871969	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26871977	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26871982	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26871989	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872002	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872021	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872031	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872033	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872069	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872082	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872115	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872132	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872150	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872178	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872206	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872209	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872230	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872238	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872262	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872309	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872411	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872425	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872434	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26872460	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872461	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872486	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872518	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872547	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872561	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872587	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872610	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872617	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872630	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872638	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872671	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872686	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872715	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872721	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872731	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872743	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872757	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872769	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872783	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872794	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872835	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872847	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26872932	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873053	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873098	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873131	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873141	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873148	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873176	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873192	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873195	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873231	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873303	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873306	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873336	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873376	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873408	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873439	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873465	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873466	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873530	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26873551	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45420
26878492	G	A	synonymous_variant	LOW	LOC_Os04g45430

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26888489	T	C	splice_region_variant&intron_variant	LOW	LOC_Os04g45440
26888531	C	T	synonymous_variant	LOW	LOC_Os04g45440
26888688	G	A	missense_variant	MODERATE	LOC_Os04g45440
26888692	T	C	missense_variant	MODERATE	LOC_Os04g45440
26888753	G	A	synonymous_variant	LOW	LOC_Os04g45440
26888921	A	T	synonymous_variant	LOW	LOC_Os04g45440
26890630	C	T	missense_variant	MODERATE	LOC_Os04g45440
26890634	C	T	synonymous_variant	LOW	LOC_Os04g45440
26897190	G	A	missense_variant	MODERATE	LOC_Os04g45450
26897218	C	T	missense_variant	MODERATE	LOC_Os04g45450
26897234	T	C	synonymous_variant	LOW	LOC_Os04g45450
26897257	A	C	missense_variant	MODERATE	LOC_Os04g45450
26897260	C	T	missense_variant	MODERATE	LOC_Os04g45450
26897277	C	T	missense_variant	MODERATE	LOC_Os04g45450
26897281	G	A	missense_variant	MODERATE	LOC_Os04g45450
26897384	T	A	missense_variant	MODERATE	LOC_Os04g45450
26897388	G	A	missense_variant	MODERATE	LOC_Os04g45450
26897400	A	G	missense_variant	MODERATE	LOC_Os04g45450
26897459	C	T	stop_gained	HIGH	LOC_Os04g45450
26897524	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897530	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897539	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897548	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897566	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897584	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897588	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897608	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897621	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897627	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897644	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897762	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897827	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26897830	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26898111	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26898119	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26898144	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45450
26910859	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26910974	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26911033	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26911064	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26911076	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26911089	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26911270	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26911563	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45470

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
26911577	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45470
26929018	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45510
26940648	C	A	synonymous_variant	LOW	LOC_Os04g45540
26942605	C	T	synonymous_variant	LOW	LOC_Os04g45540
26942658	T	C	missense_variant	MODERATE	LOC_Os04g45540
26942677	T	C	synonymous_variant	LOW	LOC_Os04g45540
26944812	C	T	synonymous_variant	LOW	LOC_Os04g45540
26947682	T	C	missense_variant	MODERATE	LOC_Os04g45550
26947715	G	A	missense_variant	MODERATE	LOC_Os04g45550
26947784	C	A	missense_variant	MODERATE	LOC_Os04g45550
26947812	A	G	missense_variant	MODERATE	LOC_Os04g45550
26947837	C	T	synonymous_variant	LOW	LOC_Os04g45550
26947930	A	G	synonymous_variant	LOW	LOC_Os04g45550
26947948	T	C	synonymous_variant	LOW	LOC_Os04g45550
26947962	G	A	missense_variant	MODERATE	LOC_Os04g45550
26947972	G	A	synonymous_variant	LOW	LOC_Os04g45550
26948035	A	G	synonymous_variant	LOW	LOC_Os04g45550
26948040	C	T	missense_variant	MODERATE	LOC_Os04g45550
26948081	C	T	missense_variant	MODERATE	LOC_Os04g45550
26948107	C	T	synonymous_variant	LOW	LOC_Os04g45550
26948108	C	T	missense_variant	MODERATE	LOC_Os04g45550
26948286	C	T	missense_variant	MODERATE	LOC_Os04g45550
26948414	G	A	missense_variant	MODERATE	LOC_Os04g45550
26948422	A	C	synonymous_variant	LOW	LOC_Os04g45550
26948451	G	A	missense_variant	MODERATE	LOC_Os04g45550
26948497	G	A	synonymous_variant	LOW	LOC_Os04g45550
26948553	C	T	missense_variant	MODERATE	LOC_Os04g45550
26948572	C	T	synonymous_variant	LOW	LOC_Os04g45550
27006272	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006481	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006573	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006693	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006713	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006757	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006943	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006986	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27006998	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45650
27040763	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27040767	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27040782	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27040866	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27042938	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27043001	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27043028	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27043031	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45710

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27043057	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27043090	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45710
27049263	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049287	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049289	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049299	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049302	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049376	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049385	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049388	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27049446	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27050219	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27050280	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27050327	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27050351	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27050483	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27050539	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051022	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051029	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051068	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051239	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051258	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051279	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051282	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27051316	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45720
27054628	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27054634	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27054640	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27054717	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27054723	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27054764	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27054952	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27055020	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27055036	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27055089	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27055099	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27055105	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45730
27084612	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45750
27084614	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45750
27084637	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45750
27084656	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45750
27085043	G	A	start_lost	HIGH	LOC_Os04g45760
27085049	C	T	synonymous_variant	LOW	LOC_Os04g45760
27085178	A	G	synonymous_variant	LOW	LOC_Os04g45760
27085182	T	C	synonymous_variant	LOW	LOC_Os04g45760

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27085217	A	G	missense_variant	MODERATE	LOC_Os04g45760
27085251	T	G	missense_variant	MODERATE	LOC_Os04g45760
27085314	G	A	missense_variant	MODERATE	LOC_Os04g45760
27085637	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085670	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085714	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085754	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085778	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085781	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085796	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085800	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085813	A	C	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085823	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085835	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085875	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085896	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27085952	A	G	synonymous_variant	LOW	LOC_Os04g45760
27085955	T	C	synonymous_variant	LOW	LOC_Os04g45760
27086006	G	A	synonymous_variant	LOW	LOC_Os04g45760
27086027	T	A	synonymous_variant	LOW	LOC_Os04g45760
27086063	C	T	synonymous_variant	LOW	LOC_Os04g45760
27086096	T	C	synonymous_variant	LOW	LOC_Os04g45760
27086116	C	T	missense_variant	MODERATE	LOC_Os04g45760
27086157	A	G	missense_variant	MODERATE	LOC_Os04g45760
27086204	T	C	synonymous_variant	LOW	LOC_Os04g45760
27086208	G	A	missense_variant	MODERATE	LOC_Os04g45760
27086345	A	G	synonymous_variant	LOW	LOC_Os04g45760
27086402	A	G	synonymous_variant	LOW	LOC_Os04g45760
27087325	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087331	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087358	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087361	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087377	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087394	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087424	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087446	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27087455	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45770
27090891	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45760
27121546	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g45810
27121652	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45810
27121666	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g45810
27121884	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g45810
27142141	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45834
27144268	C	T	3_prime_UTR_variant	MODIFIER	LOC_Os04g45834
27144344	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45850

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27144370	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g45850
27162388	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45860
27162432	T	C	missense_variant	MODERATE	LOC_Os04g45870
27162476	T	C	synonymous_variant	LOW	LOC_Os04g45870
27169448	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169460	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169466	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169484	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169502	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169525	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169560	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169606	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169635	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169653	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169691	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169706	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169743	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169745	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169777	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169843	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169847	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169890	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169908	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169918	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27169922	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171154	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171183	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171199	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171216	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171226	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171251	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171258	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171288	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171292	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171332	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171377	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171419	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171432	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171458	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171470	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171510	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171567	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171636	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171727	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171754	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g45890

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27171857	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27171931	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45890
27172124	C	T	synonymous_variant	LOW	LOC_Os04g45890
27172176	C	T	missense_variant	MODERATE	LOC_Os04g45890
27172193	C	A	missense_variant	MODERATE	LOC_Os04g45890
27172362	T	C	missense_variant	MODERATE	LOC_Os04g45890
27172367	A	G	synonymous_variant	LOW	LOC_Os04g45890
27172383	G	T	missense_variant	MODERATE	LOC_Os04g45890
27172427	C	A	missense_variant	MODERATE	LOC_Os04g45890
27172430	C	G	missense_variant	MODERATE	LOC_Os04g45890
27172447	C	G	missense_variant	MODERATE	LOC_Os04g45890
27172454	G	C	synonymous_variant	LOW	LOC_Os04g45890
27172484	A	G	synonymous_variant	LOW	LOC_Os04g45890
27172532	A	C	missense_variant	MODERATE	LOC_Os04g45890
27172574	T	C	synonymous_variant	LOW	LOC_Os04g45890
27172586	A	G	synonymous_variant	LOW	LOC_Os04g45890
27172597	T	G	missense_variant	MODERATE	LOC_Os04g45890
27172601	A	G	synonymous_variant	LOW	LOC_Os04g45890
27172630	T	A	missense_variant	MODERATE	LOC_Os04g45890
27172693	C	T	missense_variant	MODERATE	LOC_Os04g45890
27172716	G	A	missense_variant	MODERATE	LOC_Os04g45890
27172748	A	T	synonymous_variant	LOW	LOC_Os04g45890
27172756	T	C	missense_variant	MODERATE	LOC_Os04g45890
27172910	G	A	intron_variant	MODIFIER	LOC_Os04g45890
27172976	C	A	intron_variant	MODIFIER	LOC_Os04g45890
27177978	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g45890
27178057	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g45890
27178116	A	T	upstream_gene_variant	MODIFIER	LOC_Os04g45890
27179474	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g45900
27179485	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g45900
27179504	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g45900
27179638	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g45900
27268601	A	C	missense_variant	MODERATE	LOC_Os04g46030
27368874	A	G	missense_variant	MODERATE	LOC_Os04g46210
27368881	G	A	missense_variant	MODERATE	LOC_Os04g46210
27368990	C	T	synonymous_variant	LOW	LOC_Os04g46210
27369673	G	A	missense_variant	MODERATE	LOC_Os04g46210
27369699	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46210
27369727	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46210
27369793	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46210
27369811	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g46210
27385083	G	A	intergenic_region	MODIFIER	LOC_Os04g46220-LOC_Os04g46240
27385091	T	C	intergenic_region	MODIFIER	LOC_Os04g46220-LOC_Os04g46240

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27385171	A	G	intergenic_region	MODIFIER	LOC_Os04g46220-LOC_Os04g46240
27386214	C	G	intergenic_region	MODIFIER	LOC_Os04g46220-LOC_Os04g46240
27393839	G	C	upstream_gene_variant	MODIFIER	LOC_Os04g46240
27393869	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46240
27401783	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46240
27401803	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46240
27401806	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g46240
27402667	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g46240
27402720	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46240
27438508	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46300
27438683	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46300
27438741	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46300
27438772	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46300
27439367	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46300
27440444	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46310
27530355	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46430
27530365	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46430
27578538	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46490
27580517	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46490
27580527	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46490
27580567	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46490
27593704	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46520
27620865	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27620978	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27620982	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621130	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621153	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621160	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621173	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621186	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621258	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621268	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621283	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621288	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621341	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621346	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621352	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27621446	A	T	downstream_gene_variant	MODIFIER	LOC_Os04g46580
27625332	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g46600
27648103	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648123	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648140	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648156	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46639

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27648188	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648258	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648270	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648311	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648335	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648360	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27648363	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46639
27669071	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g46670
27669084	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46670
27669326	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g46670
27681442	A	G	missense_variant	MODERATE	LOC_Os04g46690
27683721	A	T	missense_variant	MODERATE	LOC_Os04g46690
27683747	A	G	splice_region_variant&intron_variant	LOW	LOC_Os04g46690
27684984	C	T	missense_variant	MODERATE	LOC_Os04g46690
27685111	T	C	synonymous_variant	LOW	LOC_Os04g46690
27704762	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46730
27704790	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g46730
27715987	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716012	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716345	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716374	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716376	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716431	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716442	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716468	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716478	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716486	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716511	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716514	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716522	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716527	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716536	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716540	T	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716558	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716572	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716588	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716624	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716641	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716644	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716659	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716679	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716705	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716739	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46750
27716751	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46750

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27729976	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g46750
27730000	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46750
27730011	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46750
27730250	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730323	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730342	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730356	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730437	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730450	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730521	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730526	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730548	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730690	G	A	missense_variant	MODERATE	LOC_Os04g46770
27730776	G	C	missense_variant	MODERATE	LOC_Os04g46770
27730788	G	A	synonymous_variant	LOW	LOC_Os04g46770
27730811	G	A	stop_gained	HIGH	LOC_Os04g46770
27730827	C	A	synonymous_variant	LOW	LOC_Os04g46770
27730929	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27730958	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731009	C	G	missense_variant	MODERATE	LOC_Os04g46770
27731189	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731199	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731229	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731253	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731282	T	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731300	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731348	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27731352	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46760
27738318	A	T	missense_variant	MODERATE	LOC_Os04g46800
27738330	C	T	missense_variant	MODERATE	LOC_Os04g46800
27738382	T	C	synonymous_variant	LOW	LOC_Os04g46800
27738421	T	C	synonymous_variant	LOW	LOC_Os04g46800
27738432	T	C	missense_variant	MODERATE	LOC_Os04g46800
27738460	C	T	synonymous_variant	LOW	LOC_Os04g46800
27738479	A	T	missense_variant	MODERATE	LOC_Os04g46800
27738482	C	T	missense_variant	MODERATE	LOC_Os04g46800
27747144	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747151	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747168	G	T	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747170	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747244	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747281	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747439	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27747540	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g46820
27774144	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46870

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27774177	C	G	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774224	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774249	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774251	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774268	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774270	G	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774300	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774313	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774326	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774335	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774346	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774350	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774366	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774386	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774400	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774406	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774432	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774435	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774451	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774456	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774463	G	A	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774469	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774476	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27774506	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g46870
27878857	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27878883	C	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27878888	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27878922	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27878938	G	C	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879073	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879075	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879099	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879114	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879126	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879140	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879178	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879204	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879205	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879258	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879367	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879382	A	C	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879417	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879549	T	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879613	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879635	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g47040

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27879679	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879717	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879740	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879848	C	T	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27879863	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27880045	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27880091	C	A	downstream_gene_variant	MODIFIER	LOC_Os04g47040
27896478	G	A	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909729	G	A	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909770	A	G	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909795	G	A	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909827	C	T	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909852	T	C	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909876	G	A	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909893	C	T	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909912	A	T	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27909919	C	T	intergenic_region	MODIFIER	LOC_Os04g47040-LOC_Os04g47059
27919179	A	C	intron_variant	MODIFIER	LOC_Os04g47059
27919213	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27919636	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27919770	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27919776	G	T	intron_variant	MODIFIER	LOC_Os04g47059
27919806	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27919889	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27919947	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27919982	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27920090	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27920096	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27920160	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27920178	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27920388	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27920531	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27920688	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27920695	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27920795	T	A	intron_variant	MODIFIER	LOC_Os04g47059
27920961	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27921518	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27921765	A	G	intron_variant	MODIFIER	LOC_Os04g47059

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
27921787	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27921931	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27921965	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27922053	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922126	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27922320	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922339	A	T	intron_variant	MODIFIER	LOC_Os04g47059
27922340	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27922352	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922509	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27922536	G	T	intron_variant	MODIFIER	LOC_Os04g47059
27922546	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27922563	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27922582	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922599	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27922652	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922657	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922682	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27922706	A	C	intron_variant	MODIFIER	LOC_Os04g47059
27922758	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27922783	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27922791	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27922814	C	T	intron_variant	MODIFIER	LOC_Os04g47059
27922858	A	G	intron_variant	MODIFIER	LOC_Os04g47059
27924266	G	A	intron_variant	MODIFIER	LOC_Os04g47059
27924355	A	C	intron_variant	MODIFIER	LOC_Os04g47059
27929292	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27929354	T	C	intron_variant	MODIFIER	LOC_Os04g47059
27930669	T	G	intron_variant	MODIFIER	LOC_Os04g47059
27934683	T	A	intron_variant	MODIFIER	LOC_Os04g47059
27941819	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g47059
27967201	T	C	synonymous_variant	LOW	LOC_Os04g47100
27977337	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977581	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977615	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977747	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977770	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977781	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977819	T	C	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977924	A	G	downstream_gene_variant	MODIFIER	LOC_Os04g47110
27977974	G	A	downstream_gene_variant	MODIFIER	LOC_Os04g47110
28028397	T	C	synonymous_variant	LOW	LOC_Os04g47190
28033996	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28034012	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28034083	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g47190

Candidate region (bp)	Nipponbare	CP	Variant type	Effect	LOC_ID
28034099	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28034987	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28035110	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28035139	C	A	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28035181	T	C	upstream_gene_variant	MODIFIER	LOC_Os04g47190
28040770	C	T	upstream_gene_variant	MODIFIER	LOC_Os04g47210
28059741	T	G	upstream_gene_variant	MODIFIER	LOC_Os04g47240
28059842	A	G	upstream_gene_variant	MODIFIER	LOC_Os04g47240