

THE DNA “JIGSAW PUZZLE” STRUCTURE MODEL:
THE CASE STUDIES OF THE RICE AND YEAST GENOMES

A Thesis

by

YUN-HUA LIU

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE

December 2008

Major Subject: Plant Breeding

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ABSTRACT

The DNA “Jigsaw Puzzle” Structure Model: The Case Studies of the Rice and Yeast Genomes. (December 2008)

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How does DNA make the abundant and diverged life world? To address this question, a DNA “Jigsaw Puzzle” structure model was proposed and first tested by comprehensively analyzing the genome of the model dicot plant, *Arabidopsis thaliana*. However, it is unknown whether this model is held in other species. Here we report the studies of the DNA structure model using the monocot plant model species, rice (*Oryza sativa*), and the single-celled model species, yeast (*Saccharomyces cerevisiae*). Analyses of the genomes sequenced so far revealed that the genome of an organism consists of a limited number of sequence-specialized, so-called fundamental function elements. For a higher organism, these elements often include genes (GEN), retro-transposable elements (RTE), DNA transposable elements (DTE), simple sequence repeats (SSR) and low complex repeats (LCR). Datasets were developed for RTE, DTE, SSR, LCR and GEN as well as genes categorized into different function categories from the sequences of the rice and yeast genomes using appropriate window sizes. The datasets were subjected to statistical analyses to test the DNA “Jigsaw Puzzle” structure model in terms of the unambiguousness, correlation, uniqueness and selection of their genome-constituting element arrays. The analyses were conducted with a series of window sizes of the sequences at both the whole genome and individual chromosome levels, both including and excluding the centromeric regions. The results showed that all fundamental function elements of the genomes as well as the genes categorized into different function categories were arrayed in the genomes in an unambiguous manner resembling linear “Jigsaw Puzzles” at the whole genome and/or individual chromosome levels, no matter

whether the centromeric regions were included or excluded. The analyses revealed that arraying of the genomic elements was correlated significantly and uniquely for each chromosome and each species. This further confirmed the non-random arraying characteristic of the genomic elements for the DNA “Jigsaw Puzzle” structure model and suggested that the DNA “Jigsaw Puzzle” structure is unique for an organism, which has probably resulted from natural selection. These results unambiguously support the hypothesis of the DNA “Jigsaw Puzzle” structure model. Since the content, arraying and interaction pattern of the fundamental function elements were shown to be unique for each organism, variations of an organism in its DNA “Jigsaw Puzzle” array would lead to phenotypic variations, thus resulting in different organisms. Moreover, the fundamental function elements constituting a genome, as the four nucleotides (A, T, G and C) of DNA, could be arrayed into an infinite number of DNA molecules, thus giving different forms of organisms. Therefore, the DNA “Jigsaw Puzzle” structure model would provide a novel, but convincing explanation for the abundance, diversity and complexity of living organisms in the world.

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CHAPTER I

INTRODUCTION

There are probably trillions of organisms that differ in biology, morphology and complexity in the biosphere of the globe. The discoveries of DNA as the genetic materials of the organisms and its double helix structure in the last century have shed light to decipher the mystery of the organisms. However, it remains mysterious how the double helix DNA makes the abundant and diverged life world in terms of biology, morphology and complexity [1, 2]. Therefore, deciphering the underlying mechanisms of how DNA controls the abundance, diversity and complexity of the organisms has become an interesting subject in genetics and evolutionary biology.

Traditionally, it has been accepted widely that the abundance, diversity and complexity of the life world are attributed to the variation of genes. Nevertheless, the recent findings resulted from the large-scale genome-wide sequencing projects have cast a challenge on the traditional concepts and knowledge. It was found that the attributions of the organism complexity and diversity to variations of genes, including those in nucleotide sequence and gene number, are limited, even between diverged organisms. Consequently, the ruling role of gene variation in controlling organism's abundance, diversity and complexity is becoming doubtful. Therefore, several new hypotheses have been proposed recently to address the question about the abundance, diversity and complexity of organisms, in addition to the gene variation hypothesis. These include gene network and regulation, RNA alternative splicing, and the DNA "Jigsaw Puzzle" structure model.

The gene variation, including the numbers of genes and the variation in their nucleotide sequences, has been accepted widely to be responsible for the observed

This thesis follows the style of Genomics.

variations between diverged species. Nevertheless, the findings from recent genome-wide sequencing, annotation and comparative sequence analyses have questioned the role of gene variation in life abundance, diversity and complexity. It has been found that the numbers of genes are relatively consistent between diverged species while they are extremely different in genome size, biology, morphology and complexity. For instance, human has a genome size of about 3,300 Mb/1C, whereas the dicot plant model species, *Arabidopsis thaliana*, has a genome size of about 120 Mb/1C [3]. The genome size of the former is nearly 30-fold larger than that of the latter. In biology, morphology and complexity, there is no doubt that these two species are extremely different. However, both of them have approximately 26,000 genes. It is apparent that the variation of the number of genes could not well account for the abundance, diversity and complexity of organisms. At the gene nucleotide sequence level, it has also been found that diverged species share a similar set of genes. A pair of good examples in this regard is between human and chimpanzee. Although human and chimpanzee are dramatically diverged in biology, morphology and complexity, comparative analyses showed that their genes have a nearly 99% identity at the nucleotide sequence level [4]. The genome sequencing and annotation results have indicated that the gene variation itself, though it contributes to, at a significant level, does not provide a reasonable explanation for the abundance, diversity and complexity of organisms in the world.

Second, the abundance, diversity and complexity between diverged species were hypothesized to be attributed to gene network and regulation. In the other words, organisms differing in biology, morphology and complexity have different gene networks and regulation patterns. Nevertheless, the results of several studies did not support this hypothesis. Snel and his colleagues [5] studied the diversity of gene network and co-regulation between the lineages of eukaryotes and prokaryotes, and within each of the lineages. It was found that the gene co-regulation and network were highly conserved, not only within eukaryotic or prokaryotic organisms, but also between eukaryotic and prokaryotic organisms even though they were extremely

different in biology, complexity, morphology, and genome size. In the lineage of eukaryotes, over 76% of the gene co-regulation cases studied were found to be conserved between *Caenorhabditis elegans* and yeast (*Saccharomyces cerevisiae*) while they were estimated to be diverged 1.5 billion years ago. In the lineage of prokaryotes, 80% of the gene co-regulations examined was found to be conserved between *Escherichia coli* and *Bacillus subtilis*. These findings suggest that gene networks and co-regulations are conserved between diverged species, even though obvious variations exist among these species. However, such a degree of variation could not sufficiently account for the observed abundance and diversity of organisms in biology, complexity and morphology. The highly conserved gene co-regulations between diverged species may be of indication of house-keeping or ancestral functional genes rather than the diversity and complexity of organisms in genetics and evolution.

Third, RNA alternative splicing was proposed to make the abundant living forms that were different in biology, morphology and complexity in the world. RNA alternative splicing is a mechanism in which a single gene gives multiple transcripts based on which combination of exons incorporated into multiple matured mRNA transcripts, thus being translated into multiple proteins and further affecting phenotypes and complexity of organisms. It was found that a human gene, on average, contains between 10 and 15 exons and encodes three or more different proteins as a result of RNA alternative splicing [3]. Related species were proposed to have similar abilities of RNA alternative splicing that would yield similar gene products; whereas diverged species would have different alternative splicing abilities. Brett *et al.* [6] studied RNA alternative splicing by using the expressed sequence tags (ESTs) of genes and mRNAs derived from seven diverged species: human, mouse, rat, cow, fruit fly, worm, and *A. thaliana*. The result showed that there were no large differences observed in the proportion of genes that pursue RNA alternative splicing between the highly diverged species, classifying into mammals, insects, worms and plants, the variations being only 3 - 13%. Therefore, RNA alternative splicing may affect the gene products of the

same coding regions, but it may not significantly contribute to the abundance, diversity and complexity of the living organisms.

The hypotheses described above, including gene variation, gene network and co-regulation, RNA alternative splicing or their combinations, in spite of contributing to some degree, does not provide a convincing explanation of the abundance, diversity and complexity of living organisms observed in the world. Hence, Wu *et al.* [7] proposed the DNA “Jigsaw Puzzle” structure model. It was hypothesized that DNA is structured from a limited number of sequence-specialized fundamental function elements, including genes, DNA transposons, retrotransposons, simple repeats and low complex repeats, in a form resembling a linear “Jigsaw Puzzle”. The content, array and interaction of the fundamental function elements are responsible for the observed abundance, diversity and complexity of organisms. This is very similar to the manner in which how four nucleotides (A, T, G and C) make DNA molecules. Different arrays of the four nucleotides in DNA strands would result in different DNA molecules, thus giving different organisms.

In particular, the DNA “Jigsaw Puzzle” structure model [7] is specified by the following: (1) The elements or components constituting a DNA molecule must be arrayed in an unambiguous manner, as a linear “Jigsaw Puzzle”. Therefore, the array pattern is unique for a particular DNA molecule. (2) Distribution correlation exists between different elements constituting a DNA molecule and it is unique for a particular DNA molecule. (3) The array and distribution correlation of the elements are affected by chromosome rearrangement such as genetic recombination, nucleotide sequence translocation, inversion and insertions/deletions, and modified by nucleotide variations such as nucleotide substitutions. (4) Changing the content and/or order of the array would alter the activity level and/or mode of genes in the array, thus affecting phenotype. Therefore, phenotypic variations are largely attributed to the genomic element array and/or interactions. (5) The element array and distribution correlation of a DNA molecule are subjected to natural selection. The array that biologically provides advantageous fitness to the organism is selected and maintained in the population

whereas those having disadvantages to fitness such as deleterious ones are rapidly eliminated from the population by natural selection. Because the first and second points above are the most essential basis of the DNA “Jigsaw Puzzle” structure model, we had our focus on characteristics of the DNA structure model in this study.

The DNA “Jigsaw Puzzle” structure model was first tested by using the genome sequence of *A. thaliana*, which is the model species for molecular biology and genomics studies of dicot plants [7, 8]. It was found that the arraying, organization and interaction of the fundamental function elements constituting the *A. thaliana* genome support unambiguously for the hypothesis of DNA “Jigsaw Puzzle” model. Moreover, it was also shown that the arrays and interactions of the fundamental function elements were subjected to natural selection. However, it remains unknown whether the proposed model is held in other species.

In this study, we tested the DNA “Jigsaw Puzzle” structure model using the monocot plant model species, rice (*Oryza sativa*) and the single-celled, eukaryotic model species, yeast (*Saccharomyces cerevisiae*). Testing the arraying, organization and interactions of the fundamental function elements constituting the rice and yeast genomes would provide an additional line of evidence for the DNA “Jigsaw Puzzle” structure model.

Rice is one of the most important food crops in the world. Importantly, it is the model species of monocot plants in genomics and molecular biology research, and it represents an evolutionary lineage of the plant kingdom differing from *A. thaliana* previously studied by Wu and his colleagues [7]. Rice has a genome size of about 400 Mb/1C, distributed in 12 chromosomes. This number is more than three-fold larger than that of *A. thaliana*. It is the first crop plant whose genome has been completely sequenced [9] and annotated.

About 35% of the rice genome was found to be composed of transposable elements [10] and a total of 37,544 non-transposable elements were annotated while masking the pseudomolecules of the genome for repetitive sequences using the *ab*

initio gene finder FGENESH. The Institute for Genomic Research (TIGR) provides a rice genome sequence annotation of gene content in their database for community with a resource of the rice genome [11-12]. The rice genome sequences were processed with multiple *ab initio* gene finders, including FGENESH (<http://www.softberry.com>), Genemark.hmm (rice matrix; <http://opal.biology.gatech.edu/GeneMark/eukhmm.cgi>), Genscan (Arabidopsis matrix; <http://genes.mit.edu/GENSCAN.html>), Genscan (maize matrix; <http://genes.mit.edu/GENSCAN.html>), and GlimmerM (rice matrix; http://www.tigr.org/tdb/glimmERM/glmr_form.html). The output from the gene prediction programs and database searches were stored in *osa1*. Working models were generated using the FGENESH output, and putative identification for the genes was obtained from the most significant database match while models with no significant database match were labeled as hypothetical proteins. The database of TIGR is available through web-based interfaces, FTP downloads, and a Distributed Annotation System. Besides, more integrating genomic information about the rice genome is available at public web-based databases or on-line resources from different research groups.

Saccharomyces cerevisiae is an ideal eukaryotic microorganism for biological studies because of its small genome size (about 12 Mb/C), distributed in 16 chromosomes, and easy genetic manipulation [13]. Furthermore, because its genome is well-sequenced, well-annotated and well-characterized in functionality, it is suited for our research purposes. A database named the Yeast Genome Database of Munich Information Center for Protein Sequence (MIPS) was established for annotating the yeast genome. It is a primary source of the related or derived information and builds the repository for the European functional analysis projects. Moreover, the *Saccharomyces* Genome Database (SGD), which was set up for providing more powerful tools for comparison and integrating genomic information at a genome-wide scale, collects and organizes biological information about the genes and proteins of yeast from the scientific literature, and presents this information on individual Locus Pages for each

yeast gene through web-based databases [14]. The online resources and databases of yeast and rice provided platforms, resources and tools for this study.

In this study we analyzed the genome sequences of rice and yeast comprehensively to further test the DNA “Jigsaw Puzzle” structure model. The arraying, organization and interactions of the fundamental function components constituting the genomes were investigated. Furthermore, a sample of genes categorized into different function categories was selected to test their distribution and interaction patterns. This study provides not only a new line of evidence for the DNA “Jigsaw Puzzle” structure model, but also new knowledge about the rice and yeast genomes and new information for deeper understanding of the genomes.

CHAPTER II

MATERIALS AND METHODS

2.1 Data Extraction

Before exploring how the fundamental function elements, i.e., genes (GEN), retro-transposable elements (RTE), DNA transposable elements (DTE), simple sequence repeats (SSR) and/or low complex repeats (LCR), are structured into the rice or yeast genome, each of the elements was extracted along the DNA pseudomolecule of each chromosome of the genomes in an appropriate window size (see below). Moreover, we also collected the gene distribution data of a sample of function categories along each chromosome of the genomes using the window size.

2.1.1 Rice Data Extraction

We first downloaded the nucleotide sequences of the whole rice genome from the database of the International Rice Genome Sequencing Project (<http://rgp.dna.affrc.go.jp/IRGSP/>) released as Build 4.0 Pseudomolecules. Then, we segmented the genome sequences with a window size of 500 kb along each chromosome of the genome, as described by Wu *et al.* [7]. As a result, 46 – 88 segments were generated from each of the 12 rice chromosomes (Table 1). The segments of the sequences were scanned by the program RepeatMasker [15] to extract for the counts of RTE, DTE, SSR and LCR, respectively, in each window. RepeatMasker is a program that screens DNA sequences for interspersed repeats and low complexity sequences, and compares the query sequence against one or more files of sequences from target species in the RepeatMasker libraries. The sequences in the libraries provided within the RepeatMasker are consensus sequences derived from alignment of multiple copies of interspersed, satellite or low complex repeats. The count numbers of RTE, DTE, SSR and LCR in each 500 kb window along a chromosome were collected by this program.

The sequence comparisons in the program RepeatMasker were performed by WU-Blast (W. Gish, <http://blast.wustl.edu/>).

Although different types of repeat elements could be collected by the RepeatMasker, the numbers of genes and genes categorized into different functions in each window could not be done with it. So, we extracted the numbers of genes within each 500-kb segmented window from the rice genome annotation group of TIGR (<http://www.tigr.org/tdb/e2k1/osa1/>) with released Version 5.0. For the genes categorized into different functions along the rice genome, we used the Gene Ontology (GO) to classify gene function categories. The GO Consortium (<http://www.geneontology.org/>) was established to produce a structured, precisely defined, common and controlled vocabulary for describing the roles of genes and gene products in any organisms [16-21]. For this study, we randomly selected the genes categorized into 34 function categories from a total of 106 GO terms of rice from three main GO categories: molecular function, cellular component, and biological process (Table 2). The genes belonging to each of the selected function categories were extracted against their GO accession numbers in the TIGR's database in each 500-kb window along each chromosome of the genome. The genes with the same GO terms were categorized into the same function category.

2.1.2 Yeast Data Extraction

A similar procedure to that used in rice was employed to extract the datasets of the yeast genome. We downloaded the nucleotide sequences of the yeast genome from the Saccharomyces Genome Database (SGD) (<http://www.yeastgenome.org/>). The genome sequence was segmented using a 10-kb window size and subjected to analysis with the RepeatMasker to extract RTE, DTE, SSR and LCR in the yeast genome. The number of each element in 10 kb-window sizes was extracted by RepeatMasker against *S. cerevisiae*.

The numbers of genes were extracted in each 10-kb window along individual chromosomes from the SGD database. As used in the rice data extraction above, GO terms were employed to categorize the yeast genes by their products from the SGD database. Twenty gene categories that each had 33 or more gene counts in the entire yeast genome were selected for this study because small numbers of gene counts are not suited for distribution analysis by using statistical tools (Table 3). Genes with the same GO terms were categorized into the same function category.

To have a further insight into the rice and yeast genomes, we examined the density variations of each fundamental function element and gene function category among the 12 rice chromosomes and 16 yeast chromosomes by ANOVA. Fisher's LSD was used to test the mean density differences of each element or gene function category between different chromosomes.

2.2 Distribution independence test of genomic fundamental function elements and genes categorized into a function category in the rice and yeast genomes

The window size of sequence and centromeric regions were considered to be major factors that may influence the results of the genomic element distribution analysis [7]. Therefore, we first tested a series of window sizes to be used for statistical analyses. As defined by Wu *et al.* [7], an appropriate window size should provide (1) sufficient large values of variables that could properly reflect the distribution variation of each element along a chromosome, and (2) a sufficient number of variables that are suited for statistical analysis. Although the latter is not problematic for rice because its chromosome pseudomolecules have a size of 23 to 44 Mb, it may be of consideration for yeast because its chromosome pseudomolecules have only a size of 240 – 1,600 kb. To determine the appropriate window size for the rice dataset analysis of both fundamental function elements and genes with different functions using statistical tools, we tested the window sizes of 500 kb and 1000 kb [7]. To determine the appropriate window size for

the yeast dataset analysis of both fundamental function elements and genes with different functions using statistical tools, we tested the window sizes of 10 kb, 20 kb, 30 kb, 40 kb, 50 kb, 60 kb, 70 kb, 80 kb and 100 kb [7].

Previous studies showed that rice centromeres were abundant in repetitive sequences [22]. To estimate the potential influences of centromere-specific repeat elements on our analyses, we excluded the centromeric regions of all chromosomes, and then we tested the distributions of fundamental function elements against the random distribution model by the Chi-square Goodness-of-Fit test, as described by Wu *et al.* [7]. At both individual chromosome and whole genome levels, the results excluding centromeric regions were very similar to those including the centromeric regions, suggesting that the regional abundant repeat elements had no significant influences on our analyses of this study. This result was totally in agreement with those of Wu *et al.* [7] obtained in a similar analysis of the *A. thaliana* genome. Therefore, we analyzed the datasets of rice and yeast only at the whole genome and chromosome levels in this study.

To test whether each of the genomic fundamental function elements and the function categories of genes is distributed randomly or non-randomly along the whole genome and individual chromosomes, Chi-Square Goodness-of-Fit Test was conducted against the null hypothesis that each element is randomly distributed in the genome. The mean value of each element in the whole genome or individual chromosomes with the above window sizes was used as the expected value, and the actual number of each element in each window used as the observed value with the degree of freedom $n - 1$, where n represents the number of the sequence windows along the chromosome or the whole genome. Three levels of the two-tailed significance were established at $\alpha \leq 0.05$ (indicated by red color), 0.01 (indicated by green color) and 0.001(indicated by blue color).

2.3 Distribution correlation test of the genomic fundamental function elements and genes categorized into different function categories in the rice and yeast genomes

For such analyses, the phenomenon that a single gene has two or more functions is of significant consideration, in addition to the above window size and centromeric factors. Therefore, we first re-compiled the datasets of both the rice and yeast genomes pair-wisely by excluding the genes with both functions to prevent from being counted in both function categories of the pair under comparison. The Spearman's rank correlation coefficient (r_s) was then used to test the distribution correlation between the fundamental function elements and the genes categorized into different function categories. The results of such studies could provide not only an additional line of evidence for the DNA "Jigsaw Puzzle" structure model, but also useful information on the fundamental function element relationships and networks. The Spearman's rank correlation coefficient (r_s) between each pair of the elements or gene function categories was calculated by using the program SPSS 14.0 at the individual chromosome and whole genome levels. Three levels of the two-tailed significance were established at $\alpha \leq 0.05$ (indicated by red color), 0.01 (indicated by green color) and 0.001(indicated by blue color). Before calculating the Spearman's rank correlation coefficient, Q-Q plots were applied to test the distribution normality of each element.

The Spearman's rank correlation coefficient was also used to test the distribution correlation between each fundamental function element and genes categorized into each function category. The correlations were determined by the program SPSS 14.0 at the whole genome level for both rice and yeast. The two-tailed significance was established at three levels: $\alpha \leq 0.05$ (indicated by red color), 0.01 (indicated by green color) and 0.001 (indicated by blue color).

CHAPTER III

RESULTS

3.1 The constitution of the rice and yeast genomes

To determine the constitution of DNA contained in each chromosome of the rice and yeast genomes, we first looked for all related databases and literatures about the rice and yeast genomes. No genome-wide, comprehensively statistical dataset of any of the fundamental function elements was found for the rice or yeast genome. Hence, we explored the fundamental function elements and genes categorized into different functions via web-based public databases, annotation with the program RepeatMasker and GO classification.

3.1.1 The constitution of the rice genome

The genome sequence pseudomolecules of rice (*O. sativa* spp. *japonica*) consisted of a total of 372,077,801 base pairs [9]. We segmented the pseudomolecules sequences in 500-kb size into a total of 749 windows, with the numbers of segmented windows along each chromosome ranging from 46 to 88 (Table 1). The FASTA file of the segmented sequence in each window was analyzed with the program RepeatMasker against *O. sativa*. A total of 71,287 RTEs, 169,691 DTEs, 43,009 SSRs, and 48,632 LCRs were found. Further, the TIGR database showed there were a total of 41,836 genes (GENs) contained in the genome after the genes belonging to transposable elements were excluded. This result suggests that the rice genome is made of approximately 41,836 GENs, 71,287 RTEs, 169,691 DTEs, 43,009 SSRs, and 48,632 LCRs, being arrayed into 12 DNA molecules contained in the 12 chromosomes of the rice genome.

3.1.2 The constitution of the yeast genome

For the yeast genome analysis, we downloaded a total of 12,079,954 base pairs nucleotide sequence from the SGD. Analysis of the sequence using the program RepeatMasker found 524 RTEs, 1,187 SSRs and 1,288 LCRs, respectively (Table 4). Nevertheless, no DTE was identified in the sequence. The SGD showed that there were a total of 6,576 genes (GENs) contained in the genome after the genes categorized into transposable elements were excluded. This suggests that the yeast genome is made of 6,576 GENs, 524 RTEs, 1,187 SSRs and 1,288 LCRs, being arrayed into 16 DNA molecules contained in the 16 chromosomes of the yeast genome.

We compared the constitutions of the rice and yeast genomes with that of *A. thaliana* for which genome-wide statistical datasets were available for each element constituting the genome [7]. A significant difference among them was found to be the RTE/DTE ratio. Rice, yeast and *A. thaliana* represent monocot plants, single-celled eukaryotic organisms and dicot plants, respectively. The monocot rice has 2.38-fold more DTEs than RTEs whereas the dicot *A. thaliana* has 1.38-fold more DTEs than RTEs. For the single-celled yeast, there is no DTE in its genome while it contains 524 RTEs. Although further investigations are needed in the genomes of additional species, the difference in the genome constitution of the three species may represent a feature of monocot plants, dicot plants and lower-level eukaryotic organisms, respectively.

To further characterize the genomes of rice and yeast, we calculated the mean counts of each fundamental function element and the genes of each function category at the individual chromosome and whole genome levels in 500-kb windows for rice, and 60-kb windows for yeast. The differences in density of each element or gene function category between chromosomes were tested with ANOVA, followed by Fisher's LSD. For the rice genome, the densities of DTE and RTE of each chromosome were apparently larger than those of GEN, SSR and LCR, suggesting that the rice genome is more abundant in RTE and DTE than GEN, SSR and LCR (Table 1). In comparison between the 12 rice chromosomes, the densities of RTE in chromosomes 1, 2 and 3 were significantly lower than those of chromosomes 4 through 12 whereas the densities of

GEN in the three chromosomes were significantly higher than those of chromosomes 4 through 12 (Table 5). The density of DTE was the lowest in chromosome 4, being significantly lower than those of the rest of chromosomes. The SSR-most dense chromosomes were found to be chromosomes 2 and 3, whose SSR densities were significantly higher than those of chromosomes 4, 7, and 10 through 12. The density of LCR was the lowest in chromosome 4, which was significantly lower than those of chromosomes 1 through 6. For the genes categorized into different function categories, their densities varied significantly between chromosomes, even though no consistent pattern could be identified (Table 6).

For the yeast genome, significant differences were detected only in a limited number of chromosome pairs of its 16 chromosomes in densities of RTE and SSR, but not in the densities of LCR and GEN (Table 7). This suggests that although the densities of RTE and SSR are different between the yeast chromosomes, but those of GEN and LCR are alike among the chromosomes. For the genes categorized into different function categories, the similar results were obtained. No significant differences were detected between the yeast chromosomes in most of gene function categories while significant differences were detected between some chromosomes in some of the gene function categories (Table 7). In comparison with the rice genome, yeast chromosomes have a more uniform density of the fundamental function elements and genes with different functions.

3.2 Distribution independence test of fundamental function elements and genes categorized into a function category

3.2.1 Arraying of each genomic element in the rice genome

One of the predominant characteristics of the DNA “Jigsaw Puzzle” structure model [7] is that the fundamental function elements constituting a genome must be arrayed non-randomly, resembling a linear “Jigsaw Puzzle”. As shown above, the rice

genome consists of 12 chromosomal arrays of 41,836 GENs, 71,287 RTEs, 169,691 DTEs, 43,009 SSRs, and 48,632 LCRs. To test whether these elements are arrayed randomly or non-randomly in the genome and each chromosome, we tested their distribution along the whole genome and individual chromosomes by Chi-square Goodness-of-Fit Test. The null hypothesis was that each of the elements was distributed randomly. Since consistent results were obtained from the datasets of both windows (500- and 1000-kb) analyzed, the results only from the analysis of 500-kb windows are presented here.

The chi-square values of all five fundamental function elements, GEN, RTE, DTE, SSR and LCR, were significant at $\alpha \leq 0.001$ (Table 8) at the levels of both the whole genome and individual chromosomes from chromosome 1 through 12. The result rejected the null hypothesis, indicating that the fundamental function elements constituting the rice genome are arrayed non-randomly in the rice chromosomes and whole genome. This result strongly supports the DNA “Jigsaw Puzzle” structure model proposed by Wu *et al.* [7] in the dicot plant, *A. thaliana*, in which the DNA was shown to be structured from its fundamental function elements resembling a linear “Jigsaw Puzzle”.

Furthermore, we analyzed the distribution of the genes categorized into 34 function categories that were selected randomly to further verify the non-random distribution pattern of the rice genes in its chromosomes and whole genome using the same method as described above. The chi-square values of all gene function categories analyzed significantly ($\alpha \leq 0.001$) deviated from the null hypothesis at the whole genome level, except for the genes categorized into “Embryonic development” and “Chromatin binding” (Table 8). This result indicates that the genes categorized into a function category were also arrayed non-randomly in the rice genome. At the individual chromosome levels, although the distributions of the genes categorized into some function categories were not significantly deviated from the random distribution null hypothesis, the genes categorized into a vast majority of the 34 function categories were distributed non-randomly at a significance level of $\alpha \leq 0.001$ (Table

8). This indicates that the genes categorized into individual function categories are also arrayed non-randomly in the rice genome, further supporting the DNA “Jigsaw Puzzle” structure model.

3.2.2 Arraying of the genomic elements in the yeast genome

Similarly, we analyzed the distribution of each of the genomic fundamental function elements and genes categorized into 20 function categories using the Chi-square Goodness-of-Fit Test. For this experiment, we analyzed the sequence using 9 window sizes, including 10-, 20-, 30-, 40-, 50-, 60-, 70-, 80-, and 100-kb windows. It was found that the results were consistent from 60-kb through 100-kb windows (not shown); therefore, the window size of 60 kb was selected for the statistical analysis. At the whole-genome level, the distribution of all four fundamental function elements (DTE is absent in the yeast genome), GEN, RTE, SSR and LCR, were significantly ($\alpha \leq 0.001$) deviated from the random distribution null hypothesis. This supports the DNA “Jigsaw Puzzle” structure model. Nevertheless, at the individual chromosome levels, the distributions of these four fundamental function elements significantly deviated from the null hypothesis for some of the 16 yeast chromosomes, but not for others (Table 9). Of the four elements, the distributions of RTE and GEN were much more significantly deviated from the null hypothesis than those of SSR and LCR. Therefore, although the statistical significance level of the element distribution analysis at the individual chromosome level may be affected by the degrees of freedom or variables and the window sizes due to the small chromosome sizes of the yeast genome, the result supports the DNA “Jigsaw Puzzle” structure model.

For the genes categorized into different function categories, the distributions of the genes categorized into “DNA binding”, “Nucleus”, “Cytoplasm”, “Translation”, “Endocytosis” and “Response to drug” were arrayed non-randomly at a significance level of ≤ 0.05 at the whole genome level; however, those of others were not. Similar results were obtained at the individual chromosome levels, in which the distributions of

only some of the gene categories analyzed were arrayed non-randomly at a significance level of ≤ 0.05 .

3.3 Correlations of distribution between the genomic fundamental function elements and genes categorized into different function categories in the rice and yeast genomes

According to the DNA “Jigsaw Puzzle” structure model proposed by Wu *et al.* [7] in *A. thaliana*, distribution correlations exist between the fundamental function elements and gene function categories at the individual chromosome and whole genome levels, and the element distribution correlation pattern of each chromosome is unique, as they are arrayed non-randomly in the genome. The unique element distribution correlation pattern of each chromosome not only reflects the consequence of natural selection, but also may provide, at least in part, a basis of gene regulation and network. Therefore, to determine whether and what relationships exist in distribution between the genomic fundamental function elements, and genes categorized into different function categories, all possible pair-wise Spearman’s correlation coefficients and their significance levels were calculated for each pair of the elements at both the whole genome and individual chromosome levels of rice and yeast.

3.3.1 Correlations of distribution between fundamental function elements

3.3.1.1 The rice genome

Table 10 shows the distribution correlation coefficients and their significance levels of the five genomic fundamental function elements at both the whole genome and individual chromosome levels. The distributions of the elements were all shown to be correlated significantly, with $|r_s| = 0.215 \sim 0.879$, at both the whole genome and

individual chromosome levels, with exceptions for five pairs of the comparisons of two chromosomes (chromosomes 2 and 3). The distributions of LCR were positively correlated with those of DTE, SSR and GEN, respectively, but negatively with that of RTE. Interestingly, RTE was correlated negatively with DTE, and GEN was positively correlated with DTE, SSR and LCR in distribution. This result is just the opposite of those observed in the dicot *A. thaliana* genome [7]. It was also interesting that the GC content was positively correlated with the distribution of RTE and negatively correlated with the distribution of SSR and LCR, but no correlation was detected in the distribution between the GC content and GEN. This is also reverse of the results of the dicot *A. thaliana* genome [7]. Although further investigation is needed, these differences may suggest the uniqueness of the DNA “Jigsaw Puzzle” structures between the monocot and dicot plants.

3.3.1.2 The yeast genome

Table 11 shows the distribution correlation coefficients and their significance levels of the four yeast genomic fundamental function elements at the whole genome and individual chromosome levels. Significant distribution correlations were detected between LCR and SSR, GEN and RTE, GEN and SSR, and GEN and LCR, but not between RTE and LCR, and RTE and SSR. The correlation directions (positive or negative) of GEN with RTE, SSR and LCR were the same as those of rice, but the correlation direction of GEN with LCR was the opposite of that in *A. thaliana* [7]. In comparison with the GC content, the RTE and SSR both were correlated with the GC content significantly; however, the yeast correlation direction was the same as that of *A. thaliana* [7], but the opposite of that of rice. These suggest that the yeast genome is also unique in its DNA “Jigsaw Puzzle” structure.

At the individual chromosome level, a limited number of the pairs between GEN, RTE, SSR and LCR were detected to be correlated significantly in distribution; however, the significant correlations were strong, as indicated by the high value of $|r_{ij}|$,

with a range from 0.509 to 0.975. This result supports the existence of correlation in distribution among fundamental function elements and the uniqueness of the array pattern for each chromosome described in the DNA “Jigsaw Puzzle” structure model [7] even though the power of the statistical tools was found to be limited in such small sample numbers (n) and values of variables for each chromosome.

3.3.2 Correlations of distribution between genes with different functions

To further explore the uniqueness of the gene distribution along whole genome and individual chromosomes, we calculated the Spearman’s correlation coefficients and their significance levels pair-wisely between the genes categorized into 34 function categories for rice and 20 function categories for yeast. The information obtained from this experiment will also be useful for understanding the interactions and networks among the genes categorized into different function categories. For rice, the analysis was performed at both whole genome and individual chromosome levels, whereas for yeast it was conducted only at the whole genome level due to the insufficiency of the numbers of variables for statistical analysis for individual chromosomes.

3.3.2.1 The rice genome

Table 12 shows the distribution correlations and significance levels between the 34 gene function categories randomly selected from the datasets of the rice genes at the whole genome level. The arrays of most of the selected function category pairs were correlated with each other at a significance level of $\alpha \leq 0.001$, with the value of $|r_s|$ being up to 0.500. At the individual chromosome level, correlations were also detected in distribution among a number of the function category pairs compared. Although some of the function category pairs were correlated significantly between two or more chromosomes, no consistent correlation pattern was observed through all 12 chromosomes of the rice genome (Tables 13 – 24). These results support the

statement of the DNA “Jigsaw Puzzle” structure model that correlations exist among the elements constituting a genome and are unique for a DNA molecule.

3.3.2.2 The yeast genome

Table 25 shows the distribution correlations and significance levels between genes categorized different function categories at the whole-genome level. Although the statistical analysis may be affected by the limited number of genes in each function category, i.e., the values of variables, distribution correlations were detected between some of the function category pairs. Nevertheless, no distribution correlation was detected between most of the function category pairs by using the statistical tool.

3.3.3 Correlations of distribution between fundamental functional elements and genes with different functions

To dissect the distribution correlation of GEN with RTE, DTE, SSR and LCR in the genomes, we further analyzed the correlations between the fundamental function elements and genes categorized into each function category by calculating their Spearman’s correlation coefficients and significance levels pair-wisely. The analysis was performed for the rice genome at both whole-genome and individual chromosomes and for the yeast genome at the whole genome level due to its limited number of variables.

3.3.3.1 The rice genome

Table 26 shows the distribution correlations of the fundamental function elements with the genes categorized into each of 34 function categories at the whole genome level. The distributions of RTE were negatively correlated with the distributions of the genes belonging to all 34 function categories analyzed. In contrast, the distributions of DTE, SSR, LCR and GEN all had significantly positive

correlations with the arrays of genes belonging to the 34 function categories. Nevertheless, the degree of the significant correlation ($|r_s|$) varied by over 8 fold, ranging from 0.074 to 0.639. This suggests that the distributions of some of the gene function categories be more correlated with the arrays of RTE, DTE, SSR and LCR than those of others. There was no correlation detected between the GC content and the distributions of genes with different functions.

At the individual chromosome level, the numbers of significantly correlated fundamental function element/gene function category pairs were many fewer those at the whole genome level, but the degrees of the correlations were greatly increased, with a significant $|r_s|$ value ranging from 0.210 to 0.810 (Table 27). The distribution correlations of some of the fundamental function element/gene function category pairs were significant for all 12 chromosomes of the rice genome while those of others were significant only for some of the 12 chromosomes. For instance, the arrays of RTE were correlated significantly to the distributions of the genes involved in “Cellular component organization and biogenesis”, “Transcription”, “Transcription factor activity”, “Catalytic activity” and “Nucleus”, and the distribution correlations of SSR were correlated significantly with the distributions of genes categorized into “Response to stress” and “DNA binding” for all 12 rice chromosomes. Although the common distribution correlations existed across all chromosomes, the chromosome-specific correlations represented the majority of the correlations between the fundamental function elements and genes categorized into each function category. This result further supports the non-random arraying feature of the elements in the chromosomes and the uniqueness of the arrays for each chromosome. This observation may represent a consequence of natural selection.

3.3.3.2 The yeast genome

Table 28 shows the distribution correlations between fundamental function elements and genes with different functions detected in the yeast genome at the whole

genome level. Significant correlations were found between some pairs of SSR, LCR or GEN and genes with some functions, but not between RTE and the genes of the function categories. In the genome, the distributions of genes as a whole were significantly correlated with the distributions of genes categorized into “RNA binding”, “Translation”, “Protein amino acid phosphorylation”, “Ribosome biogenesis and assembly”, “Cytoplasm”, “Nucleus” and “Positive regulation of transcription from RNA polymerase II promoter”. This result suggests that arraying of the genes in the yeast genome be affected significantly by the genes categorized into the function categories. Furthermore, significant correlations were also observed between the arrays of SSR and the genes categorized into “Nucleus” and between LCR and the genes categorized into “Cytoplasm”. In other words, the genes categorized into “Nucleus” and “Cytoplasm” tends to reside at the regions where the SSR or LCR is more abundant in the yeast genome.

CHAPTER IV

DISCUSSION AND CONCLUSION

How does DNA as the genetic materials make the abundant and diverged life world? Wu *et al.* [7], for the first time, proposed the DNA “Jigsaw Puzzle” structure model to address this question and tested the model by comprehensively analyzing the genome of the dicot model plant species, *A. thaliana*. They proposed that the unique content, array and interaction of the fundamental function elements constituting a genome are responsible for the observed abundance, diversity and complexity of living organisms. As arraying of the four nucleotides in DNA strands, the fundamental function elements of DNA could be arrayed into an infinite number of DNA molecule “Jigsaw Puzzles” and thus genomes being responsible for an infinite number of organisms. This study has provided new, strong lines of evidence supporting the DNA “Jigsaw Puzzle” structure model using rice and yeast as experimental species, together with those of *A. thaliana*, making the model more universal in interpreting the abundance, diversity, and complexity of organisms in the world.

Rice is a monocot plant representing an evolutionary lineage of plants differing from that of the dicot *A. thaliana*. As discovered in the *A. thaliana* genome [7], the rice genome and chromosomes that each contains a single DNA molecule are made of non-random arrays of GEN, RTE, DTE, SSR and LCR, resembling a linear ‘Jigsaw Puzzle’. This finding is supported strongly by the following results. First, each of the fundamental function elements constituting the rice genome was found to be distributed in a non-random manner at both whole-genome and individual chromosome levels. Further dissection of the GEN element into different categories according to genes’ functions showed that genes with similar functions or categorized into the same function category was also arrayed in a non-random manner in the genome and individual chromosomes. Second, the elements constituting the rice

genome were significantly correlated in distribution in all cases tested, including those between different fundamental function elements, between genes with different functions, and between fundamental function elements and genes with different functions. The significant distribution correlations among the elements or genes further support the non-random arraying characteristic of the elements in the rice genome and chromosomes, and indicate that arraying of the elements has been subjected to natural selection. This may be of an indication, at least in part, of the elements or gene interactions and networks. Third, the distribution correlation patterns of the elements or genes for each chromosome were observed to be different from each other, suggesting that the element array of each chromosome is unique.

Yeast represents a single-celled organism. In comparison, it is much simpler in biology, morphology and complexity, and much smaller in genome size than the multiple-celled, higher-level species, rice and *A. thaliana*. Although the power of statistical tools used in this study did not seem sufficient for yeast analysis because of the small genome size (12 Mb/1C) and small chromosomes (240 – 1,600 kb) which could not give both sufficiently large sample sizes and sufficient number of variables for statistical analysis, the results similar to those of rice and *A. thaliana* were obtained for the yeast genome. All four fundamental function elements that constitute the yeast genome, GEN, RTE, SSR and LCR, were distributed in a manner that significantly deviated from the random distribution model at the whole genome level, though their distributions were not statistically significantly deviated from the random distribution model for some chromosomes. Significant distribution correlations were also observed between some of the elements or gene categories analyzed, in spite of being not between all.

The uniqueness of each DNA “Jigsaw Puzzle” has been further proven in this study. Although further investigation is needed to compare the DNA “Jigsaw Puzzles” contained in different chromosomes and organisms, element by element, the observed differences of the distribution correlation patterns of the elements or genes among different chromosomes of *A. thaliana* [7], rice and yeast (this study) and

among the three species support the uniqueness of DNA “Jigsaw Puzzle” structures for different chromosomes and different organisms. It was observed that *A. thaliana* [7], rice and yeast are different in genome constitution, with both the *A. thaliana* and rice genomes being more abundant in DTE than RTE, whereas the yeast genome having no DTE. However, the ratio of DTE/RTE of rice is 2.38, whereas that of *A. thaliana* is 1.38, the monocot rice being much more abundant in DTE than the dicot *A. thaliana*. These findings provide additional information about the uniqueness of the DNA “Jigsaw Puzzles” contained in each species. The uniqueness of each DNA “Jigsaw Puzzle” may be an indication of the consequences of natural selection for favor arrays of the fundamental function elements.

Further comparative analysis showed that conserved significant distribution correlations of the elements and gene function categories, including correlation direction, exist between rice and yeast, yeast and *A. thaliana* [7], and rice and *A. thaliana*, and among the three species. The examples of the conserved distribution correlations include those of RTE to GEN, and SSR to LCR among the three species, and the genes involved in “RNA binding” to “Plasma membrane” and the genes involved in “Nucleus” to “Translation” between rice and yeast. Moreover, it was also shown that the two plant species share more conserved significant distribution correlations of the elements and gene function categories than those between rice and yeast, yeast and *A. thaliana*, and among the three species. These results suggest, at least in part, that the DNA “Jigsaw Puzzle” structures contained in more related species share more similarities in the content, array and interaction of the elements as well as genes. This is in accordance with the general consequence of natural selection in view of that more similar species share more similarities in biology, morphology and complexity in the course of species evolution. Although additional studies are needed to determine the relationships between the DNA “Jigsaw Puzzles” structure and organism biology, the observed distribution correlations between the genome fundamental function elements and genes with different functions have provided new,

useful information of the genomic element or gene network for plant and animal breeding.

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APPENDIX A

Table 1
Mean densities of the fundamental function elements of individual rice chromosome with 500-kb windows

Chr*	N	RTE		DTE		SSR		LCR		GEN	
		Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation
1	88	75.568	35.289	239.557	50.118	59.727	18.755	69.102	15.947	61.614	13.885
2	72	79.167	37.406	236.417	51.808	64.236	17.145	69.764	16.163	60.931	12.490
3	73	73.027	45.644	242.918	53.246	63.110	15.363	70.740	15.937	63.274	14.079
4	71	106.366	57.563	197.521	60.512	49.239	18.820	58.282	19.044	51.746	18.174
5	60	96.967	50.943	217.933	71.043	59.017	16.721	65.633	19.299	55.733	17.558
6	63	97.460	46.872	237.270	65.602	59.032	18.351	67.032	16.658	55.556	14.770
7	60	100.383	46.649	226.433	64.126	54.183	18.155	62.633	19.621	55.650	16.981
8	57	105.860	48.163	225.561	65.815	57.175	16.715	61.316	17.587	51.930	15.303
9	47	100.170	47.487	222.745	75.606	57.447	21.175	64.213	21.339	52.191	19.151
10	46	112.500	52.509	223.587	71.162	55.022	21.441	63.696	21.529	53.413	15.822
11	57	107.561	40.518	227.561	54.000	52.982	14.871	62.772	14.328	52.772	13.681
12	55	109.545	41.805	211.618	52.233	54.618	21.211	59.745	15.428	48.600	14.867
Whole genome	749	95.176	47.562	226.557	61.696	57.422	18.551	64.929	17.977	55.856	16.057

* Chr: chromosome; N: number of 500-kb windows; RTE: Retro-transposable elements; DTE: DNA transposable elements; SSR: Simple repeats; LCR: Low complex repeats; and GEN: Genes

Table 2
Randomly selected functional categories of rice genes used in this study

	GO accession number of functional categories	Function Description	Abbreviation
<i>Biological Process</i>	0000003	Reproduction	RP
	0006118	Electron transport	ET
	0006350	Transcription	TC
	0006412	Translation	TL
	0006464	Protein modification process	PMP
	0006950	Response to stress	RTS
	0007049	Cell cycle	CC
	0007165	Signal transduction	ST
	0007275	Multicellular organismal development	MOD
	0008152	Metabolism	MT
	0008219	Cell death	CD
	0009056	Catabolic process	CP
	0009058	Biosynthesis process	BP
	0009790	Embryonic development	ED
	0009791	Post-embryonic process	PED
	0009908	Flower development	FD
	0015979	Photosynthesis	PS
	0016043	Cellular component organization and biogenesis	CCOB
	0016049	Cell growth	CG
	0030154	Cell differentiation	CDI
<i>Molecular Function</i>	0030528	Transcription regulator activity	TCRA
	0000166	Nucleotide binding	NTB
	0003676	Nucleic acid binding	NAB
	0003677	DNA binding	DNAB
	0003682	Chromatin binding	CHRB
	0003700	Transcription factor activity	TCFA
	0003723	RNA binding	RNAB
	0003824	Catalytic activity	CATA
	0004518	Nuclease activity	NUA
	0005215	Transporter activity	TPA
<i>Cellular Component</i>	0005515	Protein binding	PB
	0005618	Cell wall	CW
	0005634	Nucleus	NUS
	0005886	Plasma membrane	PM

Table 3
Functional categories of yeast with 33 or more genes used in this study

	GO accession number of functional categories	Function Description	Abbreviation
<i>Biological Process</i>	GO0000723	Telomere maintenance	TM
	GO0006364	rRNA processing	rRNAP
	GO0006412	Translation	TL
	GO0006468	Protein amino acid phosphorylation	PAAP
	GO0006950	Response to stress	RTS
	GO0006974	Response to DNA damage stimulus	RTDD
	GO0006888	ER to Golgi vesicle-mediated transport	EGT
	GO0006897	Endocytosis	EDCT
	GO0007047	Cell wall organization and biogenesis	CWOB
	GO0007165	Signal transduction	ST
	GO0042254	Ribosome biogenesis and assembly	RBA
	GO0042493	Response to drug	RTD
	GO0045944	Positive regulation of transcription from RNA polymerase II promoter	PRT
	<i>Molecular Function</i>	GO0003677	DNA binding
GO0003700		Transcription factor activity	TSFA
GO0003723		RNA binding	RNAB
GO0005515		Protein binding	PB
<i>Cellular Component</i>	GO0005634	Nucleus	NUS
	GO0005737	Cytoplasm	CPM
	GO0005886	Plasma membrane	PM

* The selected categories are the top 20 categories with most genes in the yeast whole genome.

Table 4
Mean densities of the fundamental function elements of individual yeast chromosomes with 60-kb windows

chr*	N	RTE		SSR		LCR		GEN	
		Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation
1	4	2.250	2.062	7.750	3.096	7.750	3.862	29.250	5.679
2	14	1.857	2.598	4.571	2.277	6.500	2.710	32.571	6.676
3	6	3.500	4.461	8.500	5.822	6.500	3.450	30.500	10.368
4	26	2.385	2.639	5.346	2.979	5.692	3.259	32.192	5.755
5	10	3.700	3.529	5.100	2.132	6.700	2.497	32.400	7.043
6	5	4.000	4.528	8.000	5.958	6.400	2.881	28.200	8.198
7	19	3.211	3.084	5.000	2.944	6.632	2.929	30.684	6.905
8	10	2.700	2.312	6.600	2.914	6.200	2.936	32.100	8.425
9	8	1.625	2.446	5.750	3.955	5.750	4.528	30.125	9.717
10	13	2.462	2.847	5.000	2.000	5.000	2.769	30.615	7.467
11	12	1.750	1.960	7.000	3.542	6.583	3.029	29.000	10.251
12	18	2.389	1.754	6.000	3.106	5.667	2.701	32.111	4.910
13	16	2.250	2.113	5.313	2.915	6.438	2.476	31.563	4.912
14	14	1.429	2.441	5.643	2.590	4.786	2.607	31.071	9.327
15	19	2.789	3.568	4.737	2.423	6.684	2.496	31.474	8.058
16	16	2.688	2.651	5.813	2.428	6.438	2.394	31.938	4.837
Whole genome	209	2.495	2.750	5.652	3.056	6.133	2.861	31.314	7.055

* Chr: chromosome; N: number of 60-kb windows; RTE: Retro-transposable elements; DTE: DNA transposable elements; SSR: Simple repeats; LCR: Low complex repeats; and GEN: Genes

Table 5
Mean density differences (Fisher's LSD) of fundamental function elements between the 12 chromosomes of the rice genome with 500-kb windows

A. RTE

y \ x	Oschr01	Oschr02	Oschr03	Oschr04	Oschr05	Oschr06	Oschr07	Oschr08	Oschr09	Oschr10	Oschr11	Oschr12
Oschr01												
Oschr02	-3.598											
Oschr03	2.541	6.139										
Oschr04	-30.798	-27.200	-33.339									
Oschr05	-21.398	-17.800	-23.939	9.400								
Oschr06	-21.892	-18.294	-24.433	8.906	-0.494							
Oschr07	-24.815	-21.217	-27.356	5.983	-3.417	-2.923						
Oschr08	-30.291	-26.693	-32.832	0.507	-8.893	-8.399	-5.476					
Oschr09	-24.602	-21.004	-27.143	6.196	-3.204	-2.710	0.213	5.689				
Oschr10	-36.932	-33.333	-39.473	-6.134	-15.533	-15.040	-12.117	-6.640	-12.330			
Oschr11	-31.993	-28.395	-34.534	-1.195	-10.595	-10.101	-7.178	-1.702	-7.391	4.939		
Oschr12	-33.977	-30.379	-36.518	-3.179	-12.579	-12.085	-9.162	-3.686	-9.375	2.955	-1.984	

C. SSR

y \ x	Oschr01	Oschr02	Oschr03	Oschr04	Oschr05	Oschr06	Oschr07	Oschr08	Oschr09	Oschr10	Oschr11	Oschr12
Oschr01												
Oschr02	-4.509											
Oschr03	-3.382	1.127										
Oschr04	10.488	14.997	13.870									
Oschr05	0.711	5.219	4.093	-9.777								
Oschr06	0.696	5.204	4.078	-9.792	-0.015							
Oschr07	5.544	10.053	8.926	-4.944	4.833	4.848						
Oschr08	2.552	7.061	5.934	-7.936	1.841	1.856	-2.992					
Oschr09	2.280	6.789	5.663	-8.207	1.570	1.585	-3.263	-0.271				
Oschr10	4.706	9.214	8.088	-5.782	3.995	4.010	-0.838	2.154	2.425			
Oschr11	6.745	11.254	10.127	-3.743	6.034	6.049	1.201	4.193	4.464	2.039		
Oschr12	5.109	9.618	8.491	-5.379	4.398	4.414	-0.435	2.557	2.829	0.404	-1.636	

E. GEN

y \ x	Oschr01	Oschr02	Oschr03	Oschr04	Oschr05	Oschr06	Oschr07	Oschr08	Oschr09	Oschr10	Oschr11	Oschr12
Oschr01												
Oschr02	0.683											
Oschr03	-1.660	-2.343										
Oschr04	9.867	9.184	11.527									
Oschr05	5.880	5.197	7.541	-3.987								
Oschr06	6.058	5.375	7.718	-3.809	0.178							
Oschr07	5.964	5.281	7.624	-3.904	0.083	-0.094						
Oschr08	9.684	9.001	11.344	-0.183	3.804	3.626	3.720					
Oschr09	9.422	8.739	11.082	-0.445	3.542	3.364	3.459	-0.262				
Oschr10	8.201	7.518	9.861	-1.667	2.320	2.143	2.237	-1.483	-1.222			
Oschr11	8.842	8.159	10.502	-1.025	2.961	2.784	2.878	-0.842	-0.580	0.641		
Oschr12	13.014	12.331	14.674	3.146	7.133	6.956	7.050	3.330	3.591	4.813	4.172	

B. DTE

y \ x	Oschr01	Oschr02	Oschr03	Oschr04	Oschr05	Oschr06	Oschr07	Oschr08	Oschr09	Oschr10	Oschr11	Oschr12
Oschr01												
Oschr02	3.140											
Oschr03	-3.361	-6.501										
Oschr04	42.036	38.896	45.397									
Oschr05	21.623	18.483	24.984	-20.412								
Oschr06	2.287	-0.853	5.648	-39.749	-19.337							
Oschr07	13.123	9.983	16.484	-28.912	-8.500	10.837						
Oschr08	13.995	10.855	17.356	-28.040	-7.628	11.708	0.872					
Oschr09	16.812	13.672	20.173	-25.224	-4.811	14.525	3.689	2.817				
Oschr10	15.970	12.830	19.331	-26.066	-5.654	13.683	2.846	1.974	-0.842			
Oschr11	11.995	8.855	15.356	-30.040	-9.628	9.708	-1.128	-2.000	-4.817	-3.974		
Oschr12	27.939	24.798	31.300	-14.097	6.315	25.652	14.815	13.943	11.126	11.969	15.943	

D. LCR

y \ x	Oschr01	Oschr02	Oschr03	Oschr04	Oschr05	Oschr06	Oschr07	Oschr08	Oschr09	Oschr10	Oschr11	Oschr12
Oschr01												
Oschr02	-0.662											
Oschr03	-1.637	-0.976										
Oschr04	10.821	11.482	12.458									
Oschr05	3.469	4.131	5.106	-7.352								
Oschr06	2.071	2.732	3.708	-8.750	-1.398							
Oschr07	6.469	7.131	8.106	-4.352	3.000	4.398						
Oschr08	7.786	8.448	9.424	-3.034	4.318	5.716	1.318					
Oschr09	4.890	5.551	6.527	-5.931	1.421	2.819	-1.579	-2.897				
Oschr10	5.407	6.068	7.044	-5.414	1.938	3.336	-1.062	-2.380	0.517			
Oschr11	6.330	6.992	7.968	-4.490	2.861	4.260	-0.139	-1.456	1.441	0.924		
Oschr12	9.357	10.018	10.994	-1.464	5.888	7.286	2.888	1.570	4.467	3.950	3.026	

Notes:

- (1) RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeat; LCR: Low complex repeat; and GEN: Gene.
- (2) The significance levels of the element mean density differences are indicated by highlighted colors, with blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.0$ and red for a significance level of $p \leq 0.05$, respectively.
- (3) The LSD values are the mean density differences of the element between row (x) and column (y). The positive value of LSD indicates that the mean density value of row (x) chromosome is larger than that of column (y) chromosome and vice versa.

Table 6
Mean density differences (Fisher's LSD) of genes categorized into each functional category between the 12 rice chromosomes with 500-kb windows

	MT	CC	TC	ET	RT	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
chr01 vs. chr02	0.893	-0.119	-0.027	-0.140	0.104	-0.057	0.350	-0.135	-0.282	0.110	0.018	0.061	-0.285	0.019	0.074	-0.201	-0.027	-0.242	-0.086	-0.301	-0.287	-0.088	0.189	0.280	0.030	0.010	-0.001	-0.063	-0.251	0.076	0.121	0.317	0.518	0.100
chr03	0.319	-0.019	-0.354	0.054	0.044	-0.153	1.268	-0.119	0.362	0.013	0.021	0.464	-0.302	-0.035	0.024	0.322	0.029	-0.532	-0.233	0.335	-0.384	-0.077	-0.452	0.658	-0.171	-0.239	0.041	-0.394	-0.451	0.092	0.984	0.743	0.467	-0.239
chr04	0.552	-0.010	0.831	0.237	0.235	0.478	0.744	1.186	0.268	0.082	0.028	0.238	0.083	0.074	0.099	0.304	0.000	0.591	-0.004	0.173	0.588	0.139	0.524	1.019	0.364	0.534	-0.002	0.052	0.686	0.087	0.756	0.541	-0.148	1.251
chr05	0.895	0.009	0.490	0.352	0.134	-0.040	1.164	0.395	0.988	0.068	0.012	0.327	0.717	0.052	0.069	0.333	0.023	0.174	0.053	0.202	0.336	-0.011	0.414	1.280	0.414	0.463	0.002	0.004	1.393	0.167	0.996	0.986	0.745	1.097
chr06	2.617	0.127	2.327	0.878	0.609	0.769	3.776	3.252	3.768	0.846	0.248	1.239	1.836	0.086	0.305	0.760	0.041	1.321	0.105	0.848	2.824	0.582	2.033	4.197	1.205	2.274	0.068	0.625	4.177	0.268	4.334	3.450	1.589	5.237
chr07	0.845	-0.074	0.857	-0.065	0.234	-0.140	1.347	1.412	0.505	0.352	0.112	0.344	-0.033	0.036	0.202	0.149	-0.043	0.391	0.020	0.352	0.802	0.089	0.848	0.814	0.114	0.680	0.035	-0.049	0.593	-0.016	0.730	0.720	-0.105	0.664
chr08	1.326	0.054	0.583	-0.037	0.363	0.294	2.346	1.256	1.634	0.138	0.067	0.354	0.657	0.050	0.089	0.352	0.004	0.538	0.066	0.383	0.602	0.176	0.608	2.372	0.364	0.479	0.033	0.047	1.141	0.126	1.395	1.597	0.831	2.451
chr09	1.514	-0.075	0.738	0.345	0.273	0.539	1.704	1.343	1.343	-0.145	0.061	0.265	0.470	0.038	0.161	0.583	-0.028	0.719	0.009	0.230	0.815	0.220	0.610	1.396	0.279	0.723	0.047	0.061	1.044	0.135	0.931	1.195	0.242	2.108
chr10	0.980	0.029	1.622	-0.084	-0.085	0.443	1.451	1.154	0.813	0.286	0.122	0.542	0.012	0.037	0.070	0.379	0.057	0.439	-0.081	0.146	1.559	0.425	0.789	0.885	0.190	1.025	0.068	-0.151	0.845	0.001	0.536	0.473	0.208	2.125
chr11	1.554	0.036	1.566	0.594	0.503	0.487	1.223	1.975	0.669	0.472	0.102	0.723	0.569	0.085	0.317	-0.473	0.039	0.837	0.119	-0.459	0.936	0.492	1.117	1.074	0.697	1.759	0.051	0.047	2.246	0.074	-0.306	1.018	0.322	3.048
chr12	1.391	0.014	1.148	0.505	0.348	0.325	2.182	1.464	1.741	0.668	0.132	0.968	1.316	0.066	0.261	0.348	0.057	0.645	0.082	0.448	1.239	0.391	0.670	1.845	0.818	1.248	0.050	0.257	1.848	0.139	1.934	2.205	0.868	2.618
chr02 vs. chr03	-0.573	0.100	-0.328	0.195	-0.059	-0.096	0.918	0.016	0.644	-0.096	0.004	0.403	-0.016	-0.054	-0.051	0.523	0.056	-0.290	-0.148	0.636	-0.097	0.012	-0.641	0.378	-0.201	-0.249	0.042	-0.331	-0.199	0.017	0.862	0.426	-0.051	-0.339
chr04	-0.340	0.109	0.858	0.377	0.131	0.535	0.394	1.321	0.549	-0.028	0.010	0.177	0.369	0.055	0.024	0.505	0.027	0.833	0.081	0.473	0.875	0.227	0.335	0.738	0.333	0.524	-0.001	0.115	0.937	0.011	0.634	0.224	-0.666	1.151
chr05	0.003	0.128	0.517	0.492	0.031	0.017	0.814	0.531	1.269	-0.042	-0.006	0.267	1.003	0.033	-0.006	0.533	0.050	0.417	0.139	0.503	0.622	0.078	0.225	1.000	0.383	0.453	0.003	0.068	1.644	0.092	0.875	0.669	0.228	0.997
chr06	1.724	0.246	2.353	1.018	0.506	0.825	3.427	3.387	4.050	0.736	0.230	1.179	2.121	0.067	0.230	0.960	0.067	1.563	0.190	1.149	3.111	0.671	1.843	3.917	1.175	2.264	0.069	0.688	4.429	0.192	4.212	3.133	1.071	5.137
chr07	-0.047	0.044	0.883	0.075	0.131	-0.083	0.997	1.547	0.786	0.242	0.094	0.283	0.253	0.017	0.128	0.350	-0.017	0.633	0.106	0.653	1.089	0.178	0.658	0.533	0.083	0.669	0.036	0.014	0.844	-0.092	0.608	0.403	-0.622	0.564
chr08	0.433	0.173	0.610	0.103	0.260	0.351	1.996	1.391	1.916	0.029	0.050	0.294	0.942	0.031	0.015	0.553	0.031	0.781	0.152	0.683	0.889	0.265	0.419	2.092	0.333	0.469	0.034	0.110	1.392	0.050	1.274	1.280	0.313	2.352
chr09	0.621	0.044	0.764	0.485	0.170	0.596	1.354	1.478	1.624	-0.254	0.044	0.204	0.756	0.020	0.086	0.784	-0.002	0.961	0.095	0.530	1.102	0.308	0.421	1.115	0.248	0.713	0.048	0.124	1.296	0.059	0.809	0.878	-0.275	2.009
chr10	0.088	0.147	1.649	0.056	-0.189	0.500	1.101	1.289	1.095	0.176	0.104	0.482	0.298	0.018	-0.005	0.580	0.083	0.681	0.005	0.446	1.845	0.513	0.600	0.605	0.159	1.015	0.069	-0.088	1.097	-0.074	0.415	0.156	-0.309	2.025
chr11	0.662	0.155	1.592	0.735	0.400	0.544	0.874	2.110	0.951	0.362	0.085	0.662	0.855	0.066	0.243	-0.272	0.066	1.079	0.205	-0.159	1.222	0.580	0.928	0.794	0.667	1.749	0.052	0.110	2.497	-0.002	-0.428	0.701	-0.196	2.948
chr12	0.498	0.132	1.174	0.645	0.244	0.382	1.832	1.599	2.022	0.558	0.114	0.908	1.601	0.047	0.187	0.548	0.083	0.888	0.168	0.748	1.525	0.479	0.481	1.565	0.788	1.238	0.051	0.320	2.099	0.063	1.813	1.888	0.351	2.518
chr03 vs. chr04	0.233	0.009	1.186	0.183	0.190	0.631	-0.524	1.305	-0.094	0.069	0.006	-0.226	0.385	0.109	0.075	-0.018	-0.029	1.123	0.229	-0.162	0.972	0.216	0.976	0.360	0.534	0.773	-0.043	0.446	1.137	-0.005	-0.228	-0.201	-0.615	1.490
chr05	0.576	0.028	0.844	0.297	0.090	0.113	-0.104	0.514	0.626	0.055	-0.009	-0.136	1.019	0.087	0.045	0.011	-0.006	0.707	0.287	-0.133	0.720	0.066	0.866	0.622	0.584	0.702	-0.039	0.398	1.844	0.075	0.013	0.244	0.279	1.336
chr06	2.297	0.146	2.681	0.823	0.565	0.921	2.509	3.371	3.406	0.833	0.226	0.776	2.137	0.121	0.281	0.437	0.012	1.853	0.338	0.513	3.209	0.659	2.484	3.539	1.376	2.513	0.027	1.019	4.628	0.176	3.350	2.707	1.122	5.476
chr07	0.526	-0.055	1.211	-0.120	0.190	0.013	0.079	1.531	0.142	0.338	0.091	-0.120	0.269	0.070	0.179	-0.173	-0.073	0.923	0.253	0.017	1.186	0.166	1.299	0.155	0.284	0.918	-0.006	0.345	1.044	-0.108	-0.254	-0.023	-0.571	0.903
chr08	1.007	0.073	0.937	-0.092	0.319	0.447	1.078	1.375	1.272	0.125	0.046	-0.109	0.958	0.084	0.066	0.030	-0.025	1.071	0.300	0.048	0.986	0.253	1.060	1.714	0.534	0.718	-0.008	0.441	1.591	0.034	0.412	0.854	0.364	2.690
chr09	1.194	-0.056	1.092	0.290	0.229	0.692	0.436	1.462	0.981	-0.158	0.040	-0.199	0.772	0.073	0.137	0.261	-0.058	1.251	0.242	-0.105	1.199	0.296	1.062	0.737	0.449	0.962	0.006	0.455	1.495	0.043	-0.053	0.452	-0.224	2.347
chr10	0.661	0.048	1.976	-0.138	-0.130	0.596	0.183	1.273	0.451	0.272	0.100	0.079	0.314	0.072	0.046	0.057	0.027	0.971	0.152	-0.189	1.943	0.501	1.241	0.227	0.360	1.264	0.027	0.243	1.296	-0.091	-0.448	-0.269	-0.258	2.364
chr11	1.235	0.055	1.920	0.540	0.459	0.640	-0.044	2.094	0.307	0.458	0.081	0.259	0.871	0.119	0.294	-0.795	0.010	1.369	0.352	-0.794	1.320	0.569	1.569	0.416	0.868	1.998	0.010	0.441	2.696	-0.019	-1.290	0.275	-0.145	3.287
chr12	1.071	0.033	1.502	0.450	0.303	0.478	0.914	1.583	1.379	0.655	0.110	0.505	1.617	0.101	0.238	0.026	0.027	1.178	0.315	0.113	1.623	0.467	1.122	1.187	0.989	1.487	0.009	0.651	2.298	0.046	0.950	1.462	0.401	2.857

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: P: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; R transport; TC: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynt RTS: Response to stress;

Table 6 (Continued)

	MT	CC	TC	ET	RT	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
chr04 vs. chr05	0.343	0.019	-0.341	0.114	-0.101	-0.519	0.420	-0.791	0.720	-0.014	-0.016	0.089	0.634	-0.022	-0.030	0.029	0.023	-0.417	0.058	0.030	-0.253	-0.150	-0.110	0.262	0.050	-0.071	0.004	-0.047	0.707	0.081	0.241	0.445	0.894	-0.154
chr06	2.064	0.137	1.495	0.641	0.375	0.290	3.032	2.066	3.500	0.764	0.220	1.001	1.752	0.012	0.206	0.456	0.040	0.730	0.109	0.676	2.236	0.443	1.508	3.178	0.841	1.740	0.070	0.574	3.491	0.181	3.578	2.909	1.737	3.986
chr07	0.293	-0.064	0.025	-0.302	-0.001	-0.619	0.603	0.226	0.237	0.269	0.084	0.106	-0.116	-0.038	0.104	-0.155	-0.044	-0.200	0.024	0.180	0.214	-0.050	0.323	-0.205	-0.250	0.146	0.037	-0.101	-0.093	-0.103	-0.026	0.178	0.044	-0.587
chr08	0.774	0.064	-0.248	-0.274	0.128	-0.184	1.602	0.070	1.366	0.056	0.040	0.117	0.574	-0.024	-0.010	0.048	0.004	-0.053	0.071	0.210	0.014	0.037	0.084	1.354	0.000	-0.055	0.035	-0.004	0.454	0.039	0.640	1.056	0.979	1.200
chr09	0.961	-0.065	-0.094	0.108	0.039	0.061	0.960	0.157	1.075	-0.227	0.034	0.027	0.387	-0.036	0.062	0.279	-0.029	0.128	0.013	0.057	0.227	0.081	0.086	0.377	-0.085	0.189	0.049	0.009	0.358	0.048	0.175	0.654	0.390	0.857
chr10	0.428	0.039	0.791	-0.321	-0.320	-0.035	0.707	-0.032	0.545	0.203	0.094	0.305	-0.071	-0.037	-0.029	0.075	0.056	-0.152	-0.077	-0.027	0.971	0.286	0.265	-0.133	-0.174	0.491	0.070	-0.202	0.159	-0.085	-0.220	-0.068	0.357	0.874
chr11	1.002	0.046	0.734	0.357	0.269	0.009	0.479	0.789	0.402	0.389	0.075	0.485	0.486	0.011	0.218	-0.777	0.039	0.246	0.123	-0.632	0.347	0.353	0.593	0.056	0.333	1.226	0.053	-0.004	1.560	-0.013	-1.062	0.477	0.470	1.797
chr12	0.838	0.024	0.316	0.267	0.113	-0.153	1.438	0.277	1.473	0.586	0.104	0.730	1.233	-0.008	0.163	0.044	0.056	0.055	0.086	0.275	0.650	0.252	0.146	0.827	0.455	0.714	0.052	0.205	1.162	0.052	1.178	1.663	1.016	1.367
chr05 vs. chr06	1.721	0.118	1.837	0.526	0.475	0.809	2.613	2.856	2.780	0.778	0.236	0.912	1.118	0.034	0.236	0.427	0.017	1.147	0.052	0.646	2.489	0.593	1.618	2.917	0.791	1.811	0.067	0.621	2.784	0.101	3.337	2.463	0.844	4.140
chr07	-0.050	-0.083	0.367	-0.417	0.100	-0.100	0.183	1.017	-0.483	0.283	0.100	0.017	-0.750	-0.017	0.133	-0.183	-0.067	0.217	-0.033	0.150	0.467	0.100	0.433	-0.467	-0.300	0.217	0.033	-0.054	-0.800	-0.183	-0.267	-0.267	-0.850	-0.433
chr08	0.431	0.045	0.093	-0.389	0.229	0.334	1.182	0.861	0.646	0.070	0.055	0.027	-0.061	-0.003	0.020	0.019	-0.019	0.364	0.013	0.181	0.267	0.187	0.194	1.092	-0.050	0.016	0.032	0.043	-0.253	-0.041	0.399	0.611	0.085	1.354
chr09	0.618	-0.084	0.248	-0.007	0.139	0.579	0.540	0.948	0.355	-0.213	0.049	-0.063	-0.247	-0.014	0.092	0.250	-0.052	0.544	-0.044	0.028	0.479	0.230	0.196	0.115	-0.135	0.260	0.045	0.056	-0.349	-0.032	-0.066	0.209	-0.503	1.011
chr10	0.085	0.020	1.132	-0.436	-0.220	0.483	0.287	0.759	-0.175	0.217	0.109	0.215	-0.705	-0.015	0.001	0.046	0.033	0.264	-0.134	-0.057	1.223	0.436	0.375	-0.395	-0.224	0.562	0.067	-0.155	-0.548	-0.166	-0.460	-0.513	-0.537	1.028
chr11	0.659	0.027	1.075	0.243	0.369	0.527	0.060	1.580	-0.318	0.404	0.090	0.396	-0.148	0.032	0.248	-0.805	0.016	0.662	0.066	-0.661	0.600	0.503	0.703	-0.206	0.283	1.296	0.049	0.043	0.853	-0.094	-1.303	0.032	-0.424	1.951
chr12	0.495	0.005	0.658	0.153	0.214	0.365	1.018	1.068	0.753	0.600	0.120	0.641	0.598	0.014	0.192	0.015	0.033	0.471	0.029	0.245	0.903	0.402	0.256	0.565	0.405	0.785	0.048	0.252	0.455	-0.029	0.938	1.218	0.123	1.521
chr06 vs. chr07	-1.771	-0.202	-1.470	-0.943	-0.375	-0.909	-2.429	-1.840	-3.263	-0.494	-0.136	-0.895	-1.868	-0.051	-0.102	-0.610	-0.084	-0.930	-0.085	-0.496	-2.022	-0.493	-1.185	-3.383	-1.091	-1.594	-0.033	-0.675	-3.584	-0.284	-3.604	-2.730	-1.694	-4.573
chr08	-1.291	-0.074	-1.744	-0.915	-0.246	-0.475	-1.430	-1.996	-2.134	-0.708	-0.180	-0.885	-1.179	-0.037	-0.216	-0.408	-0.037	-0.783	-0.038	-0.465	-2.222	-0.406	-1.424	-1.825	-0.841	-1.795	-0.035	-0.578	-3.037	-0.142	-2.938	-1.853	-0.759	-2.785
chr09	-1.103	-0.202	-1.589	-0.533	-0.336	-2.072	-1.908	-2.425	-0.991	-0.186	-0.975	-1.365	-0.048	-0.144	-0.177	-0.069	-0.602	-0.096	-0.618	-2.009	-0.363	-1.422	-2.801	-0.926	-1.551	-0.021	-0.565	-3.133	-0.133	-3.403	-2.255	-1.347	-3.128	
chr10	-1.637	-0.099	-0.705	-0.962	-0.695	-0.325	-2.326	-2.098	-2.955	-0.560	-0.126	-0.697	-1.823	-0.049	-0.235	-0.381	0.016	-0.882	-0.186	-0.703	-1.266	-0.157	-1.244	-3.312	-1.015	-1.249	0.000	-0.776	-3.332	-0.267	-3.797	-2.977	-1.381	-3.112
chr11	-1.063	-0.091	-0.761	-0.283	-0.106	-0.282	-2.553	-1.277	-3.099	-0.374	-0.145	-0.516	-1.266	-0.002	0.013	-1.232	-0.002	-0.485	0.014	-1.307	-1.889	-0.090	-0.916	-3.123	-0.508	-0.515	-0.018	-0.578	-1.931	-0.195	-4.640	-2.432	-1.267	-2.189
chr12	-1.226	-0.114	-1.179	-0.373	-0.262	-0.444	-1.595	-1.788	-2.027	-0.178	-0.116	-0.271	-0.520	-0.020	-0.043	-0.412	0.016	-0.676	-0.023	-0.401	-1.586	-0.191	-1.362	-2.352	-0.387	-1.026	-0.018	-0.369	-2.330	-0.130	-2.399	-1.245	-0.721	-2.618
chr07 vs. chr08	0.481	0.128	-0.274	0.028	0.129	0.434	0.999	-0.156	1.130	-0.213	-0.045	0.011	0.689	0.014	-0.113	0.203	0.047	0.147	0.046	0.031	-0.200	0.087	-0.239	1.559	0.250	-0.201	-0.002	0.096	0.547	0.142	0.666	0.877	0.935	1.788
chr09	0.668	-0.001	-0.119	0.410	0.039	0.679	0.357	-0.069	0.838	-0.496	-0.051	-0.079	0.503	0.003	-0.041	0.434	0.015	0.328	-0.011	-0.122	0.013	0.130	-0.237	0.582	0.165	0.044	0.012	0.110	0.451	0.151	0.201	0.475	0.347	1.445
chr10	0.135	0.103	0.765	-0.019	-0.320	0.583	0.104	-0.258	0.309	-0.066	0.009	0.199	0.045	0.001	-0.133	0.230	0.100	0.048	-0.101	-0.207	0.757	0.336	-0.059	0.072	0.076	0.346	0.033	-0.101	0.252	0.017	-0.193	-0.246	0.313	1.461
chr11	0.709	0.111	0.709	0.660	0.269	0.627	-0.124	0.563	0.165	0.120	-0.010	0.379	0.602	0.049	0.115	-0.622	0.082	0.446	0.099	-0.811	0.133	0.403	0.269	0.261	0.583	1.080	0.016	0.096	1.653	0.089	-1.036	0.298	0.426	2.384
chr12	0.545	0.088	0.291	0.570	0.114	0.465	0.835	0.052	1.236	0.317	0.020	0.624	1.348	0.030	0.059	0.198	0.100	0.255	0.062	0.095	0.436	0.302	-0.177	1.032	0.568	0.015	0.306	1.255	0.155	1.205	1.485	0.973	1.955	
chr08 vs. chr09	0.187	-0.129	0.155	0.382	-0.090	0.245	-0.642	0.087	-0.292	-0.283	-0.006	-0.090	-0.187	-0.011	0.072	0.231	-0.032	0.180	-0.057	-0.153	0.213	0.043	0.002	-0.977	-0.085	0.244	0.014	0.013	-0.096	0.009	-0.465	-0.402	-0.588	-0.343
chr10	-0.346	-0.025	1.039	-0.047	-0.449	0.149	-0.895	-0.102	-0.821	0.147	0.054	0.188	-0.645	-0.013	-0.019	0.027	0.053	-0.100	-0.147	-0.237	0.957	0.249	0.181	-1.487	-0.174	0.547	0.035	-0.198	-0.295	-0.125	-0.859	-1.124	-0.622	-0.327
chr11	0.228	-0.018	0.982	0.632	0.140	0.193	-1.123	0.719	-0.965	0.333	0.035	0.368	-0.088	0.035	0.228	-0.825	0.035	0.298	0.053	-0.842	0.333	0.316	0.509	-1.298	0.333	1.281	0.018	0.000	1.105	-0.053	-1.702	-0.579	-0.509	0.596
chr12	0.065	-0.040	0.565	0.542	-0.015	0.031	-0.164	0.208	0.107	0.530	0.064	0.614	0.659	0.016	0.172	-0.004	0.053	0.107	0.016	0.065	0.636	0.215	0.062	-0.527	0.455	0.769	0.017	0.210	0.707	0.012	0.539	0.608	0.038	0.167
chr09 vs. chr10	-0.533	0.104	0.884	-0.429	-0.359	-0.096	-0.253	-0.189	-0.530	0.430	0.060	0.278	-0.458	-0.001	-0.091	-0.204	0.085	-0.280	-0.090	-0.084	0.744	0.205	0.179	-0.510	-0.089	0.302								

Table 7
Mean density differences (Fisher's LSD) of fundamental function elements and genes categorized into each functional category between the 16 yeast chromosomes in a 60-kb window size

	RTE	SSR	LCR	GEN	TM	DNAB	TSFA	RANB	PB	NUS	CPM	PM	rRNAP	TL	PAAP	RTS	RTDD	EGT	EDCT	CWOB	ST	RBA	RTD	PRT
chr01 vs. chr02	0.393	3.179	1.250	-3.321	0.286	-0.179	-0.143	0.036	-0.464	-1.393	-2.786	-0.250	-0.107	-1.143	0.000	0.321	0.393	0.143	-1.000	-0.393	0.036	-0.214	0.607	0.321
chr01 vs. chr03	-1.250	-0.750	1.250	-1.250	-0.833	0.083	-0.167	-0.250	-0.083	-1.750	-1.000	-0.583	-0.417	-0.500	0.000	0.417	-0.083	0.333	-0.833	-0.583	0.083	0.000	1.083	0.750
chr01 vs. chr04	-0.135	2.404	2.058	-2.942	0.115	-0.327	-0.269	-0.481	-0.788	-2.712	-2.654	-0.365	-0.365	-1.038	0.000	0.058	0.327	0.115	-0.692	-0.212	0.019	-0.462	0.558	0.250
chr01 vs. chr05	-1.450	2.650	1.050	-3.150	0.800	-0.250	-0.300	-0.450	-0.350	-2.550	-2.400	-0.250	-0.050	-0.300	0.200	0.350	0.450	0.200	-1.700	-0.150	0.050	-0.300	0.850	0.550
chr01 vs. chr06	-1.750	-0.250	1.350	1.050	1.300	-0.150	-0.400	0.250	-0.550	-0.650	-1.200	-0.050	0.050	-0.300	-0.300	-0.050	0.550	0.100	-2.400	0.050	0.050	0.300	0.850	0.750
chr01 vs. chr07	-0.961	2.750	1.118	-1.434	0.026	0.092	-0.368	-0.382	-0.487	-1.987	-2.421	-0.303	-0.539	-0.868	-0.079	0.276	0.487	0.289	-0.684	-0.224	0.145	-0.184	0.566	0.487
chr01 vs. chr08	-0.450	1.150	1.550	-2.850	-0.100	0.050	-0.500	-0.750	-0.950	-0.850	-2.000	-0.350	-0.750	-0.900	-0.100	0.450	0.150	0.200	-0.700	-0.450	0.150	-0.700	0.850	0.550
chr01 vs. chr09	0.625	2.000	2.000	-0.875	0.875	-0.125	-0.250	-0.125	-0.375	-1.250	-1.750	-0.250	0.250	-0.375	-0.125	0.125	0.375	0.375	-0.500	-0.125	0.125	-0.375	-0.250	0.375
chr01 vs. chr10	-0.212	2.750	2.750	-1.365	0.654	-0.135	-0.231	-0.365	-1.058	-1.019	-2.154	-0.250	-0.058	-0.500	0.038	0.596	0.596	0.346	-1.077	-0.442	0.173	-0.654	0.635	0.673
chr01 vs. chr11	0.500	0.750	1.167	0.250	0.583	-0.083	-0.250	-0.083	-0.583	-0.500	-2.333	0.083	-0.083	-0.750	0.083	0.667	0.333	0.250	-0.583	-0.583	0.167	-0.750	0.833	0.250
chr01 vs. chr12	-0.139	1.750	2.083	-2.861	0.222	0.083	-0.333	-0.361	-0.528	-1.694	-2.444	-0.361	-0.528	-0.889	0.167	0.417	0.417	0.111	-0.833	-0.472	0.139	-0.556	0.750	0.417
chr01 vs. chr13	0.000	2.438	1.313	-2.313	0.000	-0.250	-0.375	-0.313	-0.813	-0.313	-3.125	0.125	-0.063	-1.000	0.188	0.375	0.563	-0.125	-0.875	-0.125	0.188	-0.125	0.938	0.375
chr01 vs. chr14	0.821	2.107	2.964	-1.821	0.786	-0.107	-0.214	-0.464	-0.536	-2.179	-3.071	-0.607	-0.536	-1.071	0.143	0.393	0.107	0.143	-0.429	-0.179	0.179	-0.929	0.750	0.393
chr01 vs. chr15	-0.539	3.013	1.066	-2.224	0.289	-0.118	-0.158	-0.382	-0.276	-1.776	-1.632	-0.566	-0.382	-0.395	-0.026	0.592	0.276	0.079	-0.947	-0.066	-0.013	-0.500	0.882	0.224
chr01 vs. chr16	-0.438	1.938	1.313	-2.688	0.250	-0.250	-0.188	-0.250	-0.625	-1.313	-2.688	-0.250	-0.500	-0.813	-0.063	0.500	0.500	0.313	-0.500	-0.125	0.000	-0.500	0.813	0.250
chr02 vs. chr03	-1.643	-3.929	0.000	2.071	-1.119	0.262	-0.024	-0.286	0.381	-0.357	1.786	-0.333	-0.310	0.643	0.000	0.095	-0.476	0.190	0.167	-0.190	0.048	0.214	0.476	0.429
chr02 vs. chr04	-0.527	-0.775	0.808	0.379	-0.170	-0.148	-0.126	-0.516	-0.324	-1.319	0.132	-0.115	-0.258	0.104	0.000	-0.264	-0.066	-0.027	0.308	0.181	-0.016	-0.247	-0.049	-0.071
chr02 vs. chr05	-1.843	-0.529	-0.200	0.171	0.514	-0.071	-0.157	-0.486	0.114	-1.157	0.386	0.000	0.057	0.843	0.200	0.029	0.057	0.057	-0.700	0.243	0.014	-0.086	0.243	0.229
chr02 vs. chr06	-2.143	-3.429	0.100	4.371	1.014	0.029	-0.257	0.214	-0.086	0.743	1.586	0.200	0.157	0.843	-0.300	-0.371	0.157	-0.043	-1.400	0.443	0.014	0.514	0.243	0.429
chr02 vs. chr07	-1.353	-0.429	-0.132	1.887	-0.259	0.271	-0.226	-0.417	-0.023	-0.594	0.365	-0.053	-0.432	0.274	-0.079	-0.045	0.094	0.147	0.316	0.169	0.109	0.030	-0.041	0.165
chr02 vs. chr08	-0.843	-0.209	0.300	0.471	-0.386	0.229	-0.357	-0.786	-0.486	0.543	0.786	-0.100	-0.643	0.243	-0.100	-0.129	-0.243	0.057	0.300	-0.057	0.114	-0.486	0.243	0.229
chr02 vs. chr09	0.232	-1.179	0.750	2.446	0.589	0.054	-0.107	-0.161	0.089	1.143	1.036	0.000	0.357	0.768	-0.125	-0.196	-0.018	0.232	0.500	0.268	0.089	-0.161	-0.857	0.054
chr02 vs. chr10	-0.604	-0.429	1.500	1.956	0.368	0.044	-0.088	-0.401	-0.593	0.374	0.632	0.000	0.049	0.643	0.038	0.275	0.203	0.203	-0.077	-0.049	0.137	-0.440	0.027	0.352
chr02 vs. chr11	0.107	-2.429	-0.083	3.571	0.298	0.095	-0.107	-0.119	-0.119	0.893	0.452	0.333	0.024	0.393	0.083	0.345	-0.060	0.107	0.417	-0.190	0.131	-0.536	0.226	-0.071
chr02 vs. chr12	-0.532	-1.429	0.833	0.460	-0.063	0.262	-0.190	-0.397	-0.063	-0.302	0.341	-0.111	-0.421	0.254	0.167	0.095	0.024	-0.032	0.167	-0.079	0.103	-0.341	0.143	0.095
chr02 vs. chr13	-0.393	-0.741	0.063	1.009	-0.286	-0.071	-0.232	-0.348	-0.348	1.080	-0.339	0.375	0.045	0.143	0.188	0.054	0.170	-0.268	0.125	0.268	0.152	0.089	0.330	0.054
chr02 vs. chr14	0.429	-1.071	1.714	1.500	0.500	0.071	-0.071	-0.500	-0.071	-0.786	-0.286	-0.357	-0.429	0.071	0.143	0.071	-0.286	0.000	0.571	0.214	0.143	-0.714	0.143	0.071
chr02 vs. chr15	-0.932	-0.165	-0.184	1.098	0.004	0.060	-0.015	-0.417	0.188	-0.383	1.154	-0.316	-0.274	0.748	-0.026	0.271	-0.117	-0.064	0.053	0.327	-0.049	-0.286	0.274	-0.098
chr02 vs. chr16	-0.830	-1.241	0.063	0.634	-0.036	-0.071	-0.045	-0.286	-0.161	0.080	0.098	0.000	-0.393	0.330	-0.063	0.179	0.107	0.170	0.500	0.268	-0.036	-0.286	0.205	-0.071
chr03 vs. chr04	1.115	3.154	0.808	-1.692	0.949	-0.410	-0.103	-0.231	-0.705	-0.962	-1.654	0.218	0.051	-0.538	0.000	-0.359	0.410	-0.218	0.141	0.372	-0.064	-0.462	-0.526	-0.500
chr03 vs. chr05	-0.200	3.400	-0.200	-1.900	1.633	-0.333	-0.133	-0.200	-0.267	-0.800	-1.400	0.333	0.367	0.200	0.200	-0.067	0.533	-0.133	-0.867	0.433	-0.033	-0.300	-0.233	-0.200
chr03 vs. chr06	-0.500	0.500	0.100	2.300	2.133	-0.233	-0.233	0.500	-0.467	1.100	-0.200	0.533	0.467	0.200	-0.300	-0.467	0.633	-0.233	-1.567	0.633	-0.033	0.300	-0.233	0.000
chr03 vs. chr07	0.289	3.500	-0.132	-0.184	0.860	0.009	-0.202	-0.132	-0.404	-0.237	-1.421	0.281	-0.123	-0.368	-0.079	-0.140	0.570	-0.044	0.149	0.360	0.061	-0.184	-0.518	-0.263
chr03 vs. chr08	0.800	1.900	0.300	-1.600	0.733	-0.033	-0.333	-0.500	-0.867	0.900	-1.000	0.233	-0.333	-0.400	-0.100	0.033	0.233	-0.133	0.133	0.133	0.067	-0.700	-0.233	-0.200
chr03 vs. chr09	1.875	2.750	0.750	0.375	1.708	-0.208	-0.083	0.125	-0.292	0.500	-0.750	0.333	0.667	0.125	-0.125	-0.292	0.458	0.042	0.333	0.458	0.042	-0.375	-1.333	-0.375
chr03 vs. chr10	1.038	3.500	1.500	-0.115	1.487	-0.218	-0.064	-0.115	-0.974	0.731	-1.154	0.333	0.359	0.000	0.038	0.179	0.679	0.013	-0.244	0.141	0.090	-0.654	-0.449	-0.077
chr03 vs. chr11	1.750	1.500	-0.083	1.500	1.417	-0.167	-0.083	0.167	-0.500	1.250	-1.333	0.667	0.333	-0.250	0.083	0.250	0.417	-0.083	0.250	0.000	0.083	-0.750	-0.250	-0.500
chr03 vs. chr12	1.111	2.500	0.833	-1.611	1.056	0.000	-0.167	-0.111	-0.444	0.056	-1.444	0.222	-0.111	-0.389	0.167	0.000	0.500	-0.222	0.000	0.111	0.056	-0.556	-0.333	-0.333
chr03 vs. chr13	1.250	3.188	0.063	-1.063	0.833	-0.333	-0.208	-0.063	-0.729	1.438	-2.125	0.708	0.354	-0.500	0.188	-0.042	0.646	-0.458	-0.042	0.458	0.104	-0.125	-0.146	-0.375
chr03 vs. chr14	2.071	2.857	1.714	-0.571	1.619	-0.190	-0.048	-0.214	-0.452	-0.429	-2.071	-0.024	-0.119	-0.571	0.143	-0.024	0.190	-0.190	0.405	0.405	0.095	-0.929	-0.333	-0.357
chr03 vs. chr15	0.711	3.763	-0.184	-0.974	1.123	-0.202	0.009	-0.132	-0.193	-0.026	-0.632	0.018	0.035	0.105	-0.026	0.175	0.360	-0.254	-0.114	0.518	-0.096	-0.500	-0.202	-0.526
chr03 vs. chr16	0.813	2.688	0.063	-1.438	1.083	-0.333	-0.021	0.000	-0.542	0.438	-1.688	0.333	-0.083	-0.313	-0.063	0.083	0.583	-0.021	0.333	0.458	-0.083	-0.500	-0.271	-0.500

Notes

Table 7 (Continued)

	RTE	SSR	LCR	GEN	TM	DNAB	TSFA	RANB	PB	NUS	CPM	PM	rRNAP	TL	PAAP	RTS	RTDD	EGT	EDCT	CWOB	ST	RBA	RTD	PRT
chr04 vs.																								
chr05	-1.315	0.246	-1.008	-0.208	0.685	0.077	-0.031	0.031	0.438	0.162	0.254	0.115	0.315	0.738	0.200	0.292	0.123	0.085	-1.008	0.062	0.031	0.162	0.292	0.300
chr06	-1.615	-2.654	-0.708	3.992	1.185	0.177	-0.131	0.731	0.238	2.062	1.454	0.315	0.415	0.738	-0.300	-0.108	0.223	-0.015	-1.708	0.262	0.031	0.762	0.292	0.500
chr07	-0.826	0.346	-0.939	1.508	-0.089	0.419	-0.099	0.099	0.302	0.725	0.233	0.063	-0.174	0.170	-0.079	0.219	0.160	0.174	0.008	-0.012	0.126	0.277	0.008	0.237
chr08	-0.315	-1.254	-0.508	0.092	-0.215	0.377	-0.231	-0.269	-0.162	1.862	0.654	0.015	-0.385	0.138	-0.100	0.392	-0.177	0.085	-0.008	-0.238	0.131	-0.238	0.292	0.300
chr09	0.760	-0.404	-0.058	2.067	0.760	0.202	0.019	0.356	0.413	1.462	0.904	0.115	0.615	0.663	-0.125	0.067	0.048	0.260	0.192	0.087	0.106	0.087	-0.808	0.125
chr10	-0.077	0.346	0.692	1.577	0.538	0.192	0.038	0.115	-0.269	1.692	0.500	0.115	0.308	0.538	0.038	0.538	0.269	0.231	-0.385	-0.231	0.154	-0.192	0.077	0.423
chr11	0.635	-1.654	-0.891	3.192	0.468	0.244	0.019	0.397	0.205	2.212	0.321	0.449	0.282	0.288	0.083	0.609	0.006	0.135	0.109	-0.372	0.147	-0.288	0.276	0.000
chr12	-0.004	-0.654	0.026	0.081	0.107	0.410	-0.064	0.120	0.261	1.017	0.209	0.004	-0.162	0.150	0.167	0.359	0.090	-0.004	-0.141	-0.261	0.120	-0.094	0.192	0.167
chr13	0.135	0.034	-0.745	0.630	-0.115	0.077	-0.106	0.168	-0.024	2.399	-0.471	0.490	0.303	0.038	0.188	0.317	0.236	-0.240	-0.183	0.087	0.168	0.337	0.380	0.125
chr14	0.956	-0.297	0.907	1.121	0.670	0.200	0.055	0.016	0.253	0.533	-0.418	-0.242	-0.170	-0.033	0.143	0.315	-0.220	0.264	0.033	0.033	0.159	-0.467	0.192	0.143
chr15	-0.405	0.609	-0.992	0.719	0.174	0.209	0.111	0.099	0.512	0.935	1.022	-0.200	-0.016	0.644	-0.026	0.534	-0.051	-0.036	-0.255	0.146	-0.032	-0.038	0.324	-0.026
chr16	-0.303	-0.466	-0.745	0.255	0.135	0.077	0.082	0.231	0.163	1.399	-0.034	0.115	-0.135	0.226	-0.063	0.442	0.173	0.197	0.192	0.087	-0.019	-0.038	0.255	0.000
chr05 vs.																								
chr06	-0.300	-2.900	0.300	4.200	0.500	0.100	-0.100	0.700	-0.200	1.900	1.200	0.200	0.100	0.000	-0.500	-0.400	0.100	-0.100	-0.700	0.200	0.000	0.600	0.000	0.200
chr07	0.489	0.100	0.068	1.716	-0.774	0.342	-0.068	0.068	-0.137	0.563	-0.021	-0.053	-0.489	-0.568	-0.279	-0.074	0.037	0.089	1.016	-0.074	0.095	0.116	-0.284	-0.063
chr08	1.000	-1.500	0.500	0.300	-0.900	0.300	-0.200	-0.300	-0.600	1.700	0.400	-0.100	-0.700	-0.600	-0.300	0.100	-0.300	0.000	1.000	-0.300	0.100	-0.400	0.000	0.000
chr09	2.075	-0.650	0.950	2.275	0.075	0.125	0.050	0.325	-0.025	1.300	0.650	0.000	0.300	-0.075	-0.325	-0.225	-0.075	0.175	1.200	0.025	0.075	-0.075	-1.100	-0.175
chr10	1.238	0.100	1.700	1.785	-0.146	0.115	0.069	0.085	-0.708	1.531	0.246	0.000	-0.008	-0.200	-0.162	0.246	0.146	0.146	0.623	-0.292	0.123	-0.354	-0.215	0.123
chr11	1.950	-1.900	0.117	3.400	-0.217	0.167	0.050	0.367	-0.233	2.050	0.067	0.333	-0.033	-0.450	-0.117	0.317	-0.117	0.050	1.117	-0.433	0.117	-0.450	-0.017	-0.300
chr12	1.311	-0.900	1.033	0.289	-0.578	0.333	-0.033	0.089	-0.178	0.856	-0.044	-0.111	-0.478	-0.589	-0.033	0.067	-0.033	-0.089	0.867	-0.322	0.089	-0.256	-0.100	-0.133
chr13	1.450	-0.213	0.263	0.837	-0.800	0.000	-0.075	0.138	-0.463	2.238	-0.725	0.375	-0.013	-0.700	-0.013	0.025	0.113	-0.325	0.825	0.025	0.138	0.175	0.088	-0.175
chr14	2.271	-0.543	1.914	1.329	-0.014	0.143	0.086	-0.014	-0.186	0.371	-0.671	-0.357	-0.486	-0.771	-0.057	0.043	-0.343	-0.057	1.271	-0.029	0.129	-0.629	-0.100	-0.157
chr15	0.911	0.363	0.016	0.926	-0.511	0.132	0.142	0.068	0.074	0.774	0.768	-0.316	-0.332	-0.095	-0.226	0.242	-0.174	-0.121	0.753	0.084	-0.063	-0.200	0.032	-0.326
chr16	1.013	-0.713	0.263	0.462	-0.550	0.000	0.113	0.200	-0.275	1.238	-0.288	0.000	-0.450	-0.513	-0.263	0.150	0.050	0.113	1.200	0.025	-0.050	-0.200	-0.038	-0.300
chr06 vs.																								
chr07	0.789	3.000	-0.232	-2.484	-1.274	0.242	0.032	-0.632	0.063	-1.337	-1.221	-0.253	-0.589	-0.568	0.221	0.326	-0.063	0.189	1.716	-0.274	0.095	-0.484	-0.284	-0.263
chr08	1.300	1.400	0.200	-3.900	-1.400	0.200	-0.100	-1.000	-0.400	-0.200	-0.800	-0.300	-0.800	-0.600	0.200	0.500	-0.400	0.100	1.700	-0.500	0.100	-1.000	0.000	-0.200
chr09	2.375	2.250	0.650	-1.925	-0.425	0.025	0.150	-0.375	0.175	-0.600	-0.550	-0.200	0.200	-0.075	0.175	0.175	-0.175	0.275	1.900	-0.175	0.075	-0.675	-1.100	-0.375
chr10	1.538	3.000	1.400	-2.415	-0.646	0.015	0.169	-0.615	-0.508	-0.369	-0.954	-0.200	-0.108	-0.200	0.338	0.646	0.046	0.246	1.323	-0.492	0.123	-0.954	-0.215	-0.077
chr11	2.250	1.000	-0.183	-0.800	-0.717	0.067	0.150	-0.333	-0.033	0.150	-1.133	0.133	-0.133	-0.450	0.383	0.717	-0.217	0.150	1.817	-0.633	0.117	-1.050	-0.017	-0.500
chr12	1.611	2.000	0.733	-3.911	-1.078	0.233	0.067	-0.611	0.022	-1.044	-1.244	-0.311	-0.578	-0.589	0.467	0.467	-0.133	0.011	1.567	-0.522	0.089	-0.856	-0.100	-0.333
chr13	1.750	2.688	-0.037	-3.363	-1.300	-0.100	0.025	-0.563	-0.263	0.338	-1.925	0.175	-0.113	-0.700	0.488	0.425	0.013	-0.225	1.525	-0.175	0.138	-0.425	0.088	-0.375
chr14	2.571	2.357	1.614	-2.871	-0.514	0.043	0.186	-0.714	0.014	-1.529	-1.871	-0.557	-0.586	-0.771	0.443	0.443	-0.443	0.043	1.971	-0.229	0.129	-1.229	-0.100	-0.357
chr15	1.211	3.263	-0.284	-3.274	-1.011	0.032	0.242	-0.632	0.274	-1.126	-0.432	-0.516	-0.432	-0.095	0.274	0.642	-0.274	-0.021	1.453	-0.116	-0.063	-0.800	0.032	-0.526
chr16	1.313	2.188	-0.037	-3.738	-1.050	-0.100	0.213	-0.500	-0.075	-0.663	-1.488	-0.200	-0.550	-0.513	0.238	0.550	-0.050	0.213	1.900	-0.175	-0.050	-0.800	-0.038	-0.500
chr07 vs.																								
chr08	0.511	-1.600	0.432	-1.416	-0.126	-0.042	-0.132	-0.368	-0.463	1.137	0.421	-0.047	-0.211	-0.032	-0.021	0.174	-0.337	-0.089	-0.016	-0.226	0.005	-0.516	0.284	0.063
chr09	1.586	-0.750	0.882	0.559	0.849	-0.217	0.118	0.257	0.112	0.737	0.671	0.053	0.789	0.493	-0.046	-0.151	-0.112	0.086	0.184	0.099	-0.020	-0.191	-0.816	-0.112
chr10	0.749	0.000	1.632	0.069	0.628	-0.227	0.138	0.016	-0.571	0.968	0.267	0.053	0.482	0.368	0.117	0.320	0.109	0.057	-0.393	-0.219	0.028	-0.470	0.069	0.186
chr11	1.461	-2.000	0.048	1.684	0.557	-0.175	0.118	0.298	-0.096	1.487	0.088	0.386	0.456	0.118	0.162	0.390	-0.154	-0.039	0.101	-0.360	0.022	-0.566	0.268	-0.237
chr12	0.822	-1.000	0.965	-1.427	0.196	-0.009	0.035	0.020	-0.041	0.292	-0.023	-0.058	0.012	-0.020	0.246	0.140	-0.070	-0.178	-0.149	-0.249	-0.006	-0.371	0.184	-0.070
chr13	0.961	-0.313	0.194	-0.878	-0.026	-0.342	-0.007	0.069	-0.326	1.674	-0.704	0.428	0.477	-0.132	0.266	0.099	0.076	-0.414	-0.191	0.099	0.043	0.059	0.372	-0.112
chr14	1.782	-0.643	1.846	-0.387	0.759	-0.199	0.154	-0.083	-0.049	-0.192	-0.650	-0.305	0.004	-0.203	0.222	0.117	-0.380	-0.147	0.256	0.045	0.034	-0.744	0.184	-0.094
chr15	0.421	0.263	-0.053	-0.789	0.263	-0.211	0.211	0.000	0.211	0.211	0.789	-0.263	0.158	0.474	0.053	0.316	-0.211	-0.211	-0.263	0.158	-0.158	-0.316	0.316	-0.263
chr16	0.523	-0.813	0.194	-1.253	0.224	-0.342	0.181	0.132	-0.138	0.674	-0.266	0.053	0.039	0.056	0.016	0.224	0.013	0.023	0.184	0.099	-0.145	-0.316	0.247	-0.237

Notes:

(1) RTE: Retro-transposable element; SSR: Simple repeats; LCR: Low complex repeats; GEN: Genes; TM: telomere maintenance; DNAB: DNA binding; TSFA: Transcription factor activity; RANB: RNA binding; PB: Protein binding; NUS: Nucleus; CPM: Cytoplasm; PM: Plasma membrane; rRNAP: rRNA processing; TL: Translation; PAAP: Protein amino acid phosphorylation; RTS: Response to stress; RTDD: Response to DNA damage stimulus; EGT: ER to Golgi vesicle-mediated transport; EDCT: Endocytosis; CWOB: Cell wall organization and biogenesis; ST: Signal transduction; RBA: Ribosome biogenesis and assembly; RTD: Response to drug; PRT: Positive regulation of transcription from RNA polymerase II promoter.

(2) Differently highlighting colors of the numbers indicate the significance levels of the gene or element mean density differences between chromosomes: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

(3) The LSD values are the mean density differences of the genes or elements between chromosomes in pair. The positive values of LSD indicate that the mean value of the former chromosome is larger than that of the latter one and vice versa.

Table 7 (Continued)

	RTE	SSR	LCR	GEN	TM	DNAB	TSFA	RANB	PB	NUS	CPM	PM	rRNAP	TL	PAAP	RTS	RTDD	EGT	EDCT	CWOB	ST	RBA	RTD	PRT
chr08 vs. chr09	1.075	0.850	0.450	1.975	0.975	-0.175	0.250	0.625	0.575	-0.400	0.250	0.100	1.000	0.525	-0.025	-0.325	0.225	0.175	0.200	0.325	-0.025	0.325	-1.100	-0.175
chr10	0.238	1.600	1.200	1.485	0.754	-0.185	0.269	0.385	-0.108	-0.169	-0.154	0.100	0.692	0.400	0.138	0.146	0.446	0.146	-0.377	0.008	0.023	0.046	-0.215	0.123
chr11	0.950	-0.400	-0.383	3.100	0.683	-0.133	0.250	0.667	0.367	0.350	-0.333	0.433	0.667	0.150	0.183	0.217	0.183	0.050	0.117	-0.133	0.017	-0.050	-0.017	-0.300
chr12	0.311	0.600	0.533	-0.011	0.322	0.033	0.167	0.389	0.422	-0.844	-0.444	-0.011	0.222	0.011	0.267	-0.033	0.267	-0.089	-0.133	-0.022	-0.011	0.144	-0.100	-0.133
chr13	0.450	1.288	-0.238	0.538	0.100	-0.300	0.125	0.438	0.138	0.538	-1.125	0.475	0.688	-0.100	0.288	-0.075	0.413	-0.325	-0.175	0.325	0.038	0.575	0.088	-0.175
chr14	1.271	0.957	1.414	1.029	0.886	-0.157	0.286	0.286	0.414	-1.329	-1.071	-0.257	0.214	-0.171	0.243	-0.057	-0.043	-0.057	0.271	0.271	0.029	-0.229	-0.100	-0.157
chr15	-0.089	1.863	-0.484	0.626	0.389	-0.168	0.342	0.368	0.674	-0.926	0.368	-0.216	0.368	0.505	0.074	0.142	0.126	-0.121	-0.247	0.384	-0.163	0.200	0.032	-0.326
chr16	0.013	0.788	-0.238	0.163	0.350	-0.300	0.313	0.500	0.325	-0.463	-0.688	0.100	0.250	0.087	0.038	0.050	0.350	0.113	0.200	0.325	-0.150	0.200	-0.038	-0.300
chr09 vs. chr10	-0.837	0.750	0.750	-0.490	-0.221	-0.010	0.019	-0.240	-0.683	0.231	-0.404	0.000	-0.308	-0.125	0.163	0.471	0.221	-0.029	-0.577	-0.317	0.048	-0.279	0.885	0.298
chr11	-0.125	-1.250	-0.833	1.125	-0.292	0.042	0.000	0.042	-0.208	0.750	-0.583	0.333	-0.333	-0.375	0.208	0.542	-0.042	-0.125	-0.083	-0.458	0.042	-0.375	1.083	-0.125
chr12	-0.764	-0.250	0.083	-1.986	-0.653	0.208	-0.083	-0.236	-0.153	-0.444	-0.694	-0.111	-0.778	-0.514	0.292	0.292	0.042	-0.264	-0.333	-0.347	0.014	-0.181	1.000	0.042
chr13	-0.625	0.438	-0.688	-1.438	-0.875	-0.125	-0.125	-0.188	-0.438	0.938	-1.375	0.375	-0.313	-0.625	0.313	0.250	0.188	-0.500	-0.375	0.000	0.063	0.250	1.188	0.000
chr14	0.196	0.107	0.964	-0.946	-0.089	0.018	0.036	-0.339	-0.161	-0.929	-1.321	-0.357	-0.786	-0.696	0.268	0.268	-0.268	-0.232	0.071	-0.054	0.054	-0.554	1.000	0.018
chr15	-1.164	1.013	-0.934	-1.349	-0.586	0.007	0.092	-0.257	0.099	-0.526	0.118	-0.316	-0.632	-0.020	0.099	0.467	-0.099	-0.296	-0.447	0.059	-0.138	-0.125	1.132	-0.151
chr16	-1.063	-0.063	-0.688	-1.813	-0.625	-0.125	0.063	-0.125	-0.250	-0.063	-0.938	0.000	-0.750	-0.438	0.063	0.375	0.125	-0.063	0.000	0.000	-0.125	-0.125	1.063	-0.125
chr10 vs. chr11	0.712	-2.000	-1.583	1.615	-0.071	0.051	-0.019	0.282	0.474	0.519	-0.179	0.333	-0.026	-0.250	0.045	0.071	-0.263	-0.096	0.494	-0.141	-0.006	-0.096	0.199	-0.423
chr12	0.073	-1.000	-0.667	-1.496	-0.432	0.218	-0.103	0.004	0.530	-0.675	-0.291	-0.111	-0.470	-0.389	0.128	-0.179	-0.179	-0.235	0.244	-0.030	-0.034	0.098	0.115	-0.256
chr13	0.212	-0.313	-1.438	-0.947	-0.654	-0.115	-0.144	0.053	0.245	0.707	-0.971	0.375	-0.005	-0.500	0.149	-0.221	-0.034	-0.471	0.202	0.317	0.014	0.529	0.303	-0.298
chr14	1.033	-0.643	0.214	-0.456	0.132	0.027	0.016	-0.099	0.522	-1.159	-0.918	-0.357	-0.478	-0.571	0.104	-0.203	-0.489	-0.203	0.648	0.264	0.005	-0.275	0.115	-0.280
chr15	-0.328	0.263	-1.684	-0.858	-0.364	0.016	0.073	-0.016	0.781	-0.757	0.522	-0.316	-0.324	0.105	-0.065	-0.004	-0.320	-0.267	0.130	0.377	-0.186	0.154	0.247	-0.449
chr16	-0.226	-0.813	-1.438	-1.322	-0.404	-0.115	0.043	0.115	0.433	-0.293	-0.534	0.000	-0.442	-0.313	-0.101	-0.096	-0.096	-0.034	0.577	0.317	-0.173	0.154	0.178	-0.423
chr11 vs. chr12	-0.639	1.000	0.917	-3.111	-0.361	0.167	-0.083	-0.278	0.056	-1.194	-0.111	-0.444	-0.444	-0.139	0.083	-0.250	0.083	-0.139	-0.250	0.111	-0.028	0.194	-0.083	0.167
chr13	-0.500	1.688	0.146	-2.563	-0.583	-0.167	-0.125	-0.229	-0.229	0.188	-0.792	0.042	0.021	-0.250	0.104	-0.292	0.229	-0.375	-0.292	0.458	0.021	0.625	0.104	0.125
chr14	0.321	1.357	1.798	-2.071	0.202	-0.024	0.036	-0.381	0.048	-1.679	-0.738	-0.690	-0.452	-0.321	0.060	-0.274	-0.226	-0.107	0.155	0.405	0.012	-0.179	-0.083	0.143
chr15	-1.039	2.263	-0.101	-2.474	-0.294	-0.035	0.092	-0.298	0.307	-1.276	0.702	-0.649	-0.298	0.355	-0.110	-0.075	-0.057	-0.171	-0.364	0.518	-0.180	0.250	0.048	-0.026
chr16	-0.938	1.188	0.146	-2.938	-0.333	-0.167	0.063	-0.167	-0.042	-0.813	-0.354	-0.333	-0.417	-0.063	-0.146	-0.167	0.167	0.063	0.083	0.458	-0.167	0.250	-0.021	0.000
chr12 vs. chr13	0.139	0.688	-0.771	0.549	-0.222	-0.333	-0.042	0.049	-0.285	1.382	-0.681	0.486	0.465	-0.111	0.021	-0.042	0.146	-0.236	-0.042	0.347	0.049	0.431	0.188	-0.042
chr14	0.960	0.357	0.881	1.040	0.563	-0.190	0.119	-0.103	-0.008	-0.484	-0.627	-0.246	-0.008	-0.183	-0.024	-0.024	-0.310	0.032	0.405	0.294	0.040	-0.373	0.000	-0.024
chr15	-0.401	1.263	-1.018	0.637	0.067	-0.202	0.175	-0.020	0.251	-0.082	0.813	-0.205	0.146	0.494	-0.193	0.175	-0.140	-0.032	-0.114	0.406	-0.152	0.056	0.132	-0.193
chr16	-0.299	0.188	-0.771	0.174	0.028	-0.333	0.146	0.111	-0.097	0.382	-0.243	0.111	0.028	0.076	-0.229	0.083	0.083	0.201	0.333	0.347	-0.139	0.056	0.063	-0.167
chr13 vs. chr14	0.821	-0.330	1.652	0.491	0.786	0.143	0.161	-0.152	0.277	-1.866	0.054	-0.732	-0.473	-0.071	-0.045	0.018	-0.455	0.268	0.446	-0.054	-0.009	-0.804	-0.188	0.018
chr15	-0.539	0.576	-0.247	0.089	0.289	0.132	0.217	-0.069	0.536	-1.464	1.493	-0.691	-0.319	0.605	-0.214	0.217	-0.286	0.204	-0.072	0.059	-0.201	-0.375	-0.056	-0.151
chr16	-0.438	-0.500	0.000	-0.375	0.250	0.000	0.188	0.063	0.188	-1.000	0.438	-0.375	-0.438	0.188	-0.250	0.125	-0.063	0.438	0.375	0.000	-0.188	-0.375	-0.125	-0.125
chr14 vs. chr15	-1.361	0.906	-1.898	-0.402	-0.496	-0.011	0.056	0.083	0.259	0.402	1.440	0.041	0.154	0.677	-0.169	0.199	0.169	-0.064	-0.519	0.113	-0.192	0.429	0.132	-0.169
chr16	-1.259	-0.170	-1.652	-0.866	-0.536	-0.143	0.027	0.214	-0.089	0.866	0.384	0.357	0.036	0.259	-0.205	0.107	0.393	0.170	-0.071	0.054	-0.179	0.429	0.063	-0.143
chr15 vs. chr16	0.102	-1.076	0.247	-0.464	-0.039	-0.132	-0.030	0.132	-0.349	0.464	-1.056	0.316	-0.118	-0.418	-0.036	-0.092	0.224	0.234	0.447	-0.059	0.013	0.000	-0.069	0.026

Notes:

(1) RTE: Retro-transposable element; SSR: Simple repeats; LCR: Low complex repeats; GEN: Genes; TM: telomere maintenance; DNAB: DNA binding; TSFA: Transcription factor activity; RANB: RNA binding; PB: Protein binding; NUS: Nucleus; CPM: Cytoplasm; PM: Plasma membrane; rRNAP: rRNA processing; TL: Translation; PAAP: Protein amino acid phosphorylation; RTS: Response to stress; RTDD: Response to DNA damage stimulus; EGT: ER to Golgi vesicle-mediated transport; EDCT: Endocytosis; CWOB: Cell wall organization and biogenesis; ST: Signal transduction; RBA: Ribosome biogenesis and assembly; RTD: Response to drug; PRT: Positive regulation of transcription from RNA polymerase II promoter.

(2) Differently highlighting colors of the numbers indicate the significance levels of the gene or element mean density differences between chromosomes: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

(3) The LSD values are the mean density differences of the genes or elements between chromosomes in pair. The positive values of LSD indicate that the mean value of the former chromosome is larger than that of the latter one and vice versa.

Table 8
Chi-square Goodness-of-Fit Test of arraying of the fundamental function elements and genes with different functions in the rice genome with 500-kb windows

	Mean of number counts and χ^2													
	Genome		chr1		chr2		chr03		chr04		chr05		chr06	
	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2
GC	43.606	35.470	43.780	1.920	43.330	2.310	43.690	1.640	44.270	2.370	43.950	2.790	43.600	1.790
GEN	55.856	3452.760	77.030	434.700	75.970	361.180	77.690	369.470	76.910	861.700	78.440	613.080	77.060	527.480
RTE	95.176	17778.500	76.280	1370.140	79.750	1237.330	73.430	2032.060	107.590	2106.150	96.750	1600.390	98.400	1350.850
DTE	226.557	12567.350	241.950	726.690	237.850	779.800	244.290	798.630	198.700	1258.510	220.050	1312.270	239.790	1021.040
SSR	57.422	4482.830	60.210	482.480	64.230	326.920	62.920	292.830	49.270	524.930	59.100	280.820	59.440	341.300
LCR	64.929	5052.990	69.720	275.040	70.010	261.320	71.100	248.100	58.730	415.500	66.220	320.360	67.600	236.120
MT	2.040	2026.810	3.045	429.000	2.113	113.200	2.694	134.180	2.514	123.130	2.153	149.510	0.435	71.960
CC	0.163	1449.670	0.159	99.015	0.282	179.040	0.181	70.200	0.171	69.750	0.153	63.230	0.032	46.000
TC	2.318	1748.410	3.080	177.660	3.099	129.340	3.411	102.050	2.200	213.960	2.580	103.410	0.726	59.480
ET	0.861	1595.030	1.080	145.000	1.225	233.130	1.028	127.140	0.843	92.090	0.729	79.660	0.194	91.430
RP	0.563	2307.770	0.782	215.670	0.690	97.930	0.736	100.980	0.557	129.810	0.661	93.110	0.177	73.630
TL	0.724	1080.370	0.954	83.850	1.014	80.720	1.097	89.680	0.457	93.200	0.983	100.780	0.177	62.360
PMP	2.989	3010.690	4.402	383.670	4.000	256.250	3.139	111.320	3.643	314.640	3.237	107.920	0.597	85.620
RTS	3.031	2224.660	4.080	232.000	4.183	153.200	4.139	150.490	2.829	238.540	3.678	125.510	0.806	79.360
ST	3.797	2610.220	4.747	362.840	4.972	223.580	4.319	113.170	4.471	204.750	3.763	119.880	0.952	98.050
MOD	0.840	1934.130	1.069	200.980	0.972	72.800	1.000	132.870	0.986	145.620	1.017	94.160	0.226	65.830
CD	0.224	910.920	0.287	98.920	0.282	86.740	0.274	82.120	0.271	87.970	0.288	69.980	0.048	59.020
CP	1.043	1663.560	1.494	152.700	1.437	117.790	0.986	90.020	1.257	167.160	1.169	178.990	0.242	47.120
BP	2.154	1721.510	2.540	194.220	2.831	224.010	2.819	114.470	2.471	159.230	1.847	114.850	0.710	91.620
ED	0.063	765.740	0.103	78.020	0.085	65.070	0.139	76.500	0.029	68.010	0.051	56.040	0.016	61.010
PED	0.222	1124.450	0.356	106.590	0.282	72.540	0.292	110.430	0.257	106.570	0.288	63.040	0.048	59.020
FD	0.746	2497.300	0.966	300.680	1.169	407.160	0.653	68.340	0.671	112.690	0.627	64.060	0.210	58.640
PS	0.045	891.240	0.057	82.010	0.085	65.070	0.028	70.020	0.057	101.030	0.034	57.030	0.016	61.010
CCOB	1.230	1288.590	1.598	134.810	1.831	123.540	2.125	114.020	0.986	97.090	1.424	100.030	0.274	81.610
CG	0.138	1489.530	0.138	133.030	0.225	206.070	0.375	167.930	0.143	88.070	0.085	77.660	0.032	60.020
CDI	0.916	2707.430	1.115	331.040	1.394	427.250	0.778	91.110	0.929	188.730	0.898	86.310	0.258	84.880
TCFA	2.928	1930.430	3.632	187.950	3.901	131.340	4.000	114.520	3.014	201.630	3.305	162.000	0.790	64.000
TCRA	0.601	1107.920	0.782	98.470	0.845	91.380	0.847	84.470	0.614	137.560	0.797	85.400	0.194	101.760
TPA	1.834	1480.270	2.414	175.060	2.155	117.730	2.819	94.390	1.843	188.260	2.000	67.160	0.355	60.790
NTB	3.615	2775.080	4.920	354.330	4.577	241.350	4.236	119.030	3.829	202.680	3.593	103.630	0.677	76.430
NAB	1.029	1837.390	1.379	157.220	1.338	67.200	1.556	106.360	0.971	106.030	0.949	95.830	0.161	52.080
DNAB	2.148	1693.770	2.851	134.740	2.845	116.580	3.083	249.680	2.286	157.300	2.356	114.420	0.548	62.790
CHRB	0.039	720.000	0.069	81.010	0.070	66.060	0.028	70.020	0.071	65.030	0.068	55.050	0.000	
RNAB	0.754	1813.380	0.793	126.590	0.859	92.910	1.194	97.340	0.743	109.900	0.780	62.320	0.161	64.480
CATA	4.175	2000.070	5.218	139.370	5.423	211.710	5.653	147.550	4.500	182.130	3.831	102.160	1.032	72.130
NUA	0.191	1004.070	0.287	96.860	0.211	56.180	0.194	68.420	0.200	56.100	0.119	52.090	0.016	61.010
PB	4.081	2860.760	5.138	377.870	4.958	213.320	4.111	89.790	4.329	216.870	4.119	128.620	0.758	76.060
CW	3.340	2639.220	4.437	234.830	4.056	268.860	3.653	137.060	3.814	251.060	3.424	118.240	0.952	87.540
PM	1.350	3193.330	1.816	316.240	1.282	107.960	1.319	91.980	1.957	297.820	1.068	71.720	0.210	58.640
NUS	4.804	2386.510	6.414	200.210	6.211	147.470	6.639	170.080	5.086	228.720	5.305	150.750	1.129	79.150

Notes:

(1) RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene; GC: GC content; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: Protein binding; CW: Cell wall; NUS: Nucleus; PM: Plasma membrane; ET: Electron transport; TC: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; ED: Embryonic development; PED: Post-embryonic process; FD: Flower development; PS: Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) Differently highlighted colors of the χ^2 values indicate their significance levels: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 8 (Continued)

	Mean of number counts and χ^2											
	chr07		chr08		chr09		chr10		chr11		chr12	
	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2
GC	43.502	1.630	43.385	1.950	43.659	2.370	43.569	1.930	42.866	1.530	43.421	11.820
GEN	77.017	538.070	75.054	569.570	75.630	491.130	53.422	214.920	75.020	515.730	74.520	655.960
RTE	101.542	1218.640	106.768	1193.850	102.170	944.450	114.022	1066.510	108.054	847.610	110.333	855.290
DTE	229.237	944.440	227.500	1017.500	227.590	937.750	225.489	983.370	227.964	714.190	211.352	697.270
SSR	54.746	334.770	57.107	292.410	58.700	295.270	54.844	387.400	52.714	238.220	54.074	450.020
LCR	63.356	329.970	61.857	266.260	65.610	256.520	64.200	317.800	62.911	181.930	59.537	216.060
MT	2.220	209.070	1.732	79.090	1.565	73.700	2.044	114.820	1.482	82.590	1.648	90.070
CC	0.237	306.380	0.107	106.070	0.239	113.780	0.133	39.100	0.107	58.200	0.148	46.150
TC	2.203	135.780	2.393	122.300	2.370	111.770	1.378	127.910	1.357	181.100	1.889	169.730
ET	1.153	118.110	1.107	167.560	0.739	79.660	1.156	96.870	0.482	99.960	0.556	60.360
RP	0.559	61.970	0.411	69.280	0.522	71.850	0.889	698.670	0.268	73.150	0.370	113.010
TL	1.085	108.320	0.661	64.810	0.413	60.900	0.511	84.990	0.464	95.040	0.611	47.440
PMP	3.034	423.180	2.036	140.510	2.717	194.120	2.956	80.490	3.179	331.050	2.111	114.930
RTS	2.644	122.610	2.750	149.850	2.761	128.420	2.844	332.140	2.000	128.320	2.500	150.400
ST	4.220	307.890	3.071	145.750	3.435	169.900	3.933	98.140	3.982	287.510	2.870	146.570
MOD	0.729	76.650	0.875	109.110	1.239	114.920	0.778	100.290	0.607	104.910	0.407	66.770
CD	0.186	69.520	0.232	60.370	0.239	68.460	0.178	70.880	0.179	83.820	0.167	69.170
CP	1.153	178.850	1.143	214.960	1.239	72.960	0.956	75.980	0.768	91.850	0.500	71.510
BP	2.576	140.980	1.911	85.210	2.109	79.930	2.467	103.910	1.982	120.950	1.185	97.440
ED	0.068	84.530	0.054	53.030	0.065	43.000	0.067	42.050	0.018	55.020	0.037	52.040
PED	0.153	76.280	0.268	100.900	0.196	77.890	0.289	142.990	0.036	54.030	0.093	92.290
FD	0.831	171.660	0.625	104.590	0.391	38.230	0.600	71.790	1.446	349.800	0.611	132.530
PS	0.102	112.040	0.054	53.030	0.087	42.000	0.000	0.018	55.020	0.000	0.000	0.000
CCOB	1.220	103.820	1.036	70.400	0.891	58.870	1.110	92.390	0.750	67.470	0.944	62.300
CG	0.119	52.040	0.054	81.220	0.130	86.000	0.222	107.170	0.018	55.020	0.056	51.060
CDI	0.763	106.070	0.714	61.510	0.891	130.680	0.978	71.280	1.589	429.050	0.610	154.780
TCFA	2.814	147.600	2.929	143.160	2.848	125.050	1.956	117.160	2.520	164.180	2.352	196.760
TCRA	0.678	71.320	0.554	92.600	0.565	66.010	0.333	80.230	0.286	61.260	0.389	156.820
TPA	1.576	88.400	1.714	139.350	1.826	63.900	1.511	123.500	1.286	116.250	1.648	134.360
NTB	4.085	334.200	2.518	136.020	3.543	155.130	3.933	209.250	3.821	294.850	2.889	127.530
NAB	1.271	135.520	0.982	55.100	1.109	85.220	1.200	596.900	0.607	89.190	0.519	49.560
DNAB	2.153	103.770	2.304	116.560	2.152	91.090	1.756	244.840	1.054	106.290	1.556	128.220
CHRB	0.034	57.010	0.036	54.020	0.022	45.000	0.000	0.018	55.020	0.019	53.020	0.000
RNAB	0.847	70.680	0.732	81.220	0.739	47.190	0.956	689.230	0.732	64.330	0.500	55.540
CATA	4.593	203.900	4.054	116.550	4.239	110.580	4.356	132.930	2.911	100.430	3.296	154.930
NUA	0.305	139.450	0.161	59.540	0.152	65.290	0.289	101.450	0.214	62.860	0.148	73.150
PB	4.407	293.960	3.679	166.100	4.239	150.210	4.578	254.110	5.429	288.130	3.037	148.790
CW	3.678	338.710	2.786	106.280	3.261	124.230	3.956	196.980	3.339	317.590	2.111	148.090
PM	1.932	533.660	0.964	174.420	1.587	140.650	1.578	62.020	1.482	299.650	0.944	128.880
NUS	5.729	256.710	3.911	138.750	4.348	183.280	4.156	125.470	3.250	126.700	3.667	161.200

Notes:

(1) RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene; GC: GC content; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: Protein binding; CW: Cell wall; NUS: Nucleus; PM: Plasma membrane; ET: Electron transport; TC: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; ED: Embryonic development; PED: Post-embryonic process; FD: Flower development; PS: Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) Differently highlighted colors of the χ^2 values indicate their significance levels: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 9
Chi-square Goodness-of-Fit Test of arraying of the fundamental function elements and genes with different functions in the yeast genome with 60-kb windows

	whole genome	df=209	Scchr01	df=3	Scchr02	df=13	Scchr03	df=5	Scchr04	df=25	Scchr05	df=9	Scchr06	df=4	Scchr07	df=18	Scchr08	df=9
	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2
GC	38.372	4.173	39.338	0.051	38.350	0.099	38.516	0.125	36.983	8.159	38.537	0.087	38.575	0.137	38.232	0.516	35.537	6.047
RTE	2.495	633.405	2.250	5.667	1.857	47.233	3.500	28.429	2.385	20.904	3.700	30.297	4.000	20.500	3.211	53.303	2.700	17.815
SSR	5.652	345.275	7.750	3.710	4.571	14.751	8.500	19.941	5.346	41.505	5.100	8.020	8.000	17.750	5.000	31.200	6.600	11.576
LCR	6.133	278.848	7.750	5.774	6.500	14.692	6.500	9.154	5.692	46.651	6.700	8.373	6.400	5.188	6.632	23.284	6.200	12.516
GEN	31.314	332.157	29.250	3.308	32.571	17.790	30.500	17.623	32.192	25.722	32.400	13.778	28.200	9.532	30.684	27.966	32.100	19.903
TM	1.200	233.000	1.500	7.333	1.214	23.359	2.333	6.573	1.385	17.439	0.700	8.714	0.200	4.000	1.474	11.355	1.600	6.500
DNAB	0.371	266.921	0.250	3.000	0.429	26.640	0.167	4.990	0.577	31.796	0.500	5.000	0.400	3.000	0.158	15.989	0.200	8.000
TSFA	0.267	206.242	0.000		0.143	11.988	0.167	5.002	0.269	19.017	0.300	7.000	0.400	3.000	0.368	17.446	0.500	5.000
RANB	0.571	198.648	0.250	3.000	0.214	11.015	0.500	3.000	0.731	37.094	0.700	5.857	0.000		0.632	19.653	1.000	8.000
PB	0.829	197.622	0.250	3.000	0.714	12.405	0.333	4.004	1.038	33.682	0.600	14.000	0.800	1.000	0.737	15.854	1.200	9.667
NUS	5.300	275.491	3.750	5.533	5.143	16.277	5.500	9.000	6.462	19.260	6.300	12.079	4.400	8.455	5.737	14.936	4.600	12.261
CPM	6.338	257.020	4.000	3.500	6.786	15.084	5.000	10.000	6.654	26.132	6.400	12.875	5.200	4.000	6.421	18.787	6.000	14.000
PM	1.038	228.993	0.750	3.667	1.000	20.000	1.333	8.502	1.115	23.904	1.000	10.000	0.800	6.000	1.053	17.993	1.100	13.545
rRNAP	0.557	215.107	0.250	3.000	0.357	9.004	0.667	1.999	0.615	19.763	0.300	7.000	0.200	4.000	0.789	16.677	1.000	12.000
TL	1.271	249.826	0.500	6.000	1.643	16.564	1.000	2.000	1.538	34.111	0.800	7.000	0.800	3.500	1.368	22.238	1.400	6.000
PAAP	0.476	202.481	0.500	6.000	0.500	15.000	0.500	7.000	0.500	25.000	0.300	13.667	0.800	8.500	0.579	11.453	0.600	7.333
RTS	0.386	201.443	0.750	3.000	0.429	12.654	0.333	4.004	0.692	28.234	0.400	6.000	0.800	3.500	0.474	9.993	0.300	7.000
RTDD	0.381	203.475	0.750	3.667	0.357	14.606	0.833	3.402	0.423	19.731	0.300	7.000	0.200	4.000	0.263	14.009	0.600	4.000
EGT	0.329	207.685	0.500	2.000	0.357	14.606	0.167	4.990	0.385	26.373	0.300	13.667	0.400	3.000	0.211	24.445	0.300	7.000
EDCT	0.819	301.739	0.000		1.000	16.000	0.833	3.400	0.692	25.342	1.700	3.588	2.400	31.333	0.684	8.926	0.700	5.857
CWOB	0.510	204.866	0.250	3.000	0.643	14.331	0.833	3.400	0.462	13.986	0.400	11.000	0.200	4.000	0.474	14.212	0.700	14.429
ST	0.157	189.894	0.250	3.000	0.214	11.009	0.167	4.990	0.231	19.980	0.200	18.000	0.200	4.000	0.105	17.043	0.100	9.000
RBA	0.929	213.055	0.500	6.000	0.714	12.405	0.500	3.000	0.962	17.631	0.800	7.000	0.200	4.000	0.684	14.774	1.200	8.000
RTD	0.552	257.109	1.250	5.400	0.643	11.220	0.167	4.990	0.692	34.015	0.400	6.000	0.400	3.000	0.684	20.621	0.400	6.000
PRT	0.362	222.365	0.750	3.667	0.429	12.654	0.000		0.500	29.000	0.200	8.000	0.000		0.263	14.006	0.200	18.000

Notes:

(1) RTE: Retro-transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene; TM: telomere maintenance; DNAB: DNA binding; TSFA: Transcription factor activity; RNAB: RNA binding; PB: Protein binding; NUS: Nucleus; CPM: Cytoplasm; PM: Plasma membrane; rRNAP: rRNA processing; TL: Translation; PAAP: Protein amino acid phosphorylation; RTS: Response to stress; RTDD: Response to DNA damage stimulus; EGT: ER to Golgi vesicle-mediated transport; EDCT: Endocytosis; CWOB: Cell wall organization and biogenesis; ST: Signal transduction; RBA: Ribosome biogenesis and assembly; RTD: Response to drug; PRT: Positive regulation of transcription from RNA polymerase II promoter.

(2) Differently highlighted colors of the χ^2 values indicate their significance levels: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 9 (Continued)

	Scchr09	df=7	Scchr10	df=12	Scchr11	df=11	Scchr12	df=17	Scchr13	df=15	Scchr14	df=13	Scchr15	df=18	Scchr16	df=15
	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2	Mean	χ^2
GC	38.905	0.178	36.401	8.095	38.088	0.097	37.785	3.970	37.490	4.421	38.795	0.279	37.673	5.050	38.105	0.121
RTE	1.625	25.769	2.462	39.492	1.750	24.143	2.389	21.883	2.250	29.778	1.429	54.183	2.789	82.161	2.688	39.226
SSR	5.750	19.043	5.000	9.600	7.000	19.714	6.000	27.333	5.313	23.988	5.643	15.455	4.737	22.311	5.813	15.214
LCR	5.750	24.957	5.000	18.400	6.583	15.329	5.667	21.881	6.438	14.281	4.786	18.463	6.684	16.772	6.438	13.348
GEN	30.125	21.938	30.615	21.855	29.000	39.862	32.111	12.761	31.563	11.467	31.071	36.398	31.474	37.133	31.938	10.988
TM	0.625	12.600	0.846	16.185	0.917	9.724	1.278	12.215	1.500	8.000	0.714	23.610	1.211	24.077	1.250	16.800
DNAB	0.375	5.000	0.385	13.186	0.333	26.026	0.167	26.946	0.500	24.000	0.357	14.606	0.368	28.319	0.500	16.000
TSFA	0.250	6.000	0.231	9.990	0.250	17.000	0.333	18.018	0.375	26.000	0.214	20.361	0.158	15.989	0.188	12.965
RANB	0.375	10.333	0.615	8.255	0.333	8.005	0.611	13.548	0.563	10.546	0.714	6.802	0.632	22.819	0.500	8.000
PB	0.625	3.000	1.308	8.234	0.833	6.803	0.778	11.711	1.063	15.935	0.786	18.270	0.526	12.808	0.875	8.857
NUS	5.000	12.400	4.769	17.678	4.250	12.765	5.444	14.410	4.063	66.685	5.929	20.059	5.526	17.506	5.063	8.480
CPM	5.750	3.391	6.154	22.374	6.333	14.001	6.444	25.830	7.125	14.000	7.071	22.759	5.632	25.288	6.688	13.073
PM	1.000	6.000	1.000	14.000	0.667	15.998	1.111	21.401	0.625	9.200	1.357	20.055	1.316	12.238	1.000	16.000
rRNAP	0.000		0.308	15.484	0.333	8.008	0.778	11.711	0.313	23.761	0.786	15.721	0.632	22.822	0.750	14.667
TL	0.875	10.143	1.000	26.000	1.250	22.600	1.389	21.798	1.500	12.000	1.571	13.640	0.895	22.111	1.313	11.757
PAAP	0.625	6.200	0.462	11.322	0.417	11.790	0.333	18.018	0.313	10.987	0.357	9.003	0.526	20.413	0.563	14.098
RTS	0.625	6.200	0.154	10.989	0.083	11.045	0.333	24.024	0.375	10.000	0.357	9.004	0.158	15.989	0.250	20.000
RTDD	0.375	5.000	0.154	10.995	0.417	16.588	0.333	18.018	0.188	12.965	0.643	17.440	0.474	22.651	0.250	12.000
EGT	0.125	7.000	0.154	10.989	0.250	17.000	0.389	26.421	0.625	9.200	0.357	9.003	0.421	15.752	0.188	12.965
EDCT	0.500	4.000	1.077	23.141	0.583	8.434	0.833	19.808	0.875	18.000	0.429	12.656	0.947	9.448	0.500	20.000
CWOB	0.375	5.000	0.692	6.892	0.833	9.204	0.722	27.162	0.375	10.000	0.429	12.656	0.316	25.651	0.375	15.333
ST	0.125	7.000	0.077	11.988	0.083	10.996	0.111	16.016	0.063	14.881	0.071	13.079	0.263	14.009	0.250	12.000
RBA	0.875	5.571	1.154	13.598	1.250	9.800	1.056	21.728	0.625	22.000	1.429	19.194	1.000	18.000	1.000	12.000
RTD	1.500	12.000	0.615	11.507	0.417	11.792	0.500	33.000	0.313	10.982	0.500	11.000	0.368	22.884	0.438	13.555
PRT	0.375	10.333	0.077	11.988	0.500	10.000	0.333	18.018	0.375	26.000	0.357	9.003	0.526	16.610	0.500	12.000

Notes:

(1) RTE: Retro-transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene; TM: telomere maintenance; DNAB: DNA binding; TSFA: Transcription factor activity; RNAB: RNA binding; PB: Protein binding; NUS: Nucleus; CPM: Cytoplasm; PM: Plasma membrane; rRNAP: rRNA processing; TL: Translation; PAAP: Protein amino acid phosphorylation; RTS: Response to stress; RTDD: Response to DNA damage stimulus; EGT: ER to Golgi vesicle-mediated transport; EDCT: Endocytosis; CWOB: Cell wall organization and biogenesis; ST: Signal transduction; RBA: Ribosome biogenesis and assembly; RTD: Response to drug; PRT: Positive regulation of transcription from RNA polymerase II promoter.

(2) Differently highlighted colors of the χ^2 values indicate their significance levels: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 10
Spearman's correlation coefficients of distribution between fundamental function elements of the rice genome with 500-kb windows

	whole genome						Oschr01						Oschr02						Oschr03					
	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC
RTE																								
DTE	-0.500						-0.303						-0.149						-0.045					
SSR	-0.695	0.584					-0.548	0.515					-0.586	0.429					-0.403	0.089				
LCR	-0.609	0.706	0.691				-0.438	0.551	0.628				-0.373	0.503	0.570				-0.375	0.497	0.557			
GEN	-0.788	0.452	0.670	0.624			-0.673	0.215	0.362	0.342			-0.824	0.054	0.535	0.402			-0.681	-0.147	0.400	0.262		
GC	0.099	-0.417	-0.223	-0.348	-0.023		0.110	-0.436	-0.359	-0.309	0.039		-0.031	-0.383	-0.310	-0.500	0.121		0.043	-0.600	-0.277	-0.493	0.181	
	Oschr04						Oschr05						Oschr06						Oschr07					
	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC
RTE																								
DTE	-0.634						-0.491						-0.479						-0.571					
SSR	-0.758	0.681					-0.750	0.434					-0.713	0.557					-0.665	0.674				
LCR	-0.664	0.844	0.758				-0.598	0.650	0.645				-0.659	0.686	0.750				-0.602	0.708	0.724			
GEN	-0.825	0.604	0.754	0.710			-0.879	0.469	0.727	0.672			-0.691	0.414	0.742	0.709			-0.717	0.598	0.777	0.758		
GC	0.106	-0.532	-0.203	-0.317	-0.068		0.188	-0.460	-0.251	-0.455	-0.133		0.368	-0.356	-0.259	-0.348	-0.155		0.067	-0.244	-0.099	-0.265	-0.052	
	Oschr08						Oschr09						Oschr10						Oschr11					
	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC	RTE	DTE	SSR	LCR	GEN	GC
RTE																								
DTE	-0.708						-0.632						-0.686						-0.572					
SSR	-0.795	0.602					-0.682	0.717					-0.876	0.645					-0.620	0.557				
LCR	-0.672	0.801	0.531				-0.625	0.847	0.798				-0.716	0.733	0.755				-0.589	0.638	0.469			
GEN	-0.749	0.651	0.713	0.665			-0.656	0.641	0.830	0.708			-0.772	0.631	0.727	0.781			-0.724	0.328	0.538	0.393		
GC	0.335	-0.454	-0.236	-0.527	-0.306		-0.037	-0.309	-0.098	-0.305	-0.021		0.259	-0.411	-0.164	-0.330	-0.135		0.269	-0.434	-0.076	-0.362	-0.039	
	Oschr12																							
	RTE	DTE	SSR	LCR	GEN	GC																		
RTE																								
DTE	-0.749																							
SSR	-0.711	0.788																						
LCR	-0.723	0.765	0.790																					
GEN	-0.877	0.742	0.793	0.738																				
GC	0.529	-0.631	-0.380	-0.468	-0.377																			

Notes:
(1) Oschr: *Oryza sativa* chromosome; GC: GC content; RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene.
(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the element pair under comparison whereas the negative (-) values of correlation coefficients indicate the negative correlation between the element pair under comparison. Differently highlighted colors indicate the significance levels of the distribution correlation between element pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 11
Spearman's correlation coefficients of distribution between the fundamental function elements of the yeast genome with 60-kb windows

	whole genome					Scchr01					Scchr02					Scchr03					Scchr04				
	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN
GC																									
RTE	-0.269					-0.632					0.164				-0.516						-0.516				
SSR	0.176	-0.013				0.800	-0.316				-0.253	0.102			0.319	-0.400					0.319	-0.400			
LCR	-0.083	0.093	0.240			0.200	-0.211	-0.400			-0.072	-0.233	-0.047		-0.145	0.832	0.000				-0.145	0.832	0.000		
GEN	0.026	-0.143	0.271	0.288		0.211	-0.889	-0.105	0.211		0.073	-0.399	0.213	0.543	0.754	0.062	0.294	0.441		0.754	0.062	0.294	0.441		
	Scchr05					Scchr06					Scchr07					Scchr08					Scchr09				
	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN
GC																									
RTE	-0.265					-0.600					-0.381				-0.393						-0.536				
SSR	0.068	-0.317				0.500	0.100				0.155	0.265			-0.061	0.311					0.762	-0.728			
LCR	0.177	-0.425	0.813			0.103	0.718	0.667			-0.147	-0.048	0.093		0.073	0.362	0.304				0.446	-0.207	0.386		
GEN	0.213	0.198	0.232	0.396		0.564	-0.051	0.975	0.526		0.125	0.019	0.740	0.203	-0.341	0.290	0.404	0.637		0.214	0.268	0.357	0.422		
	Scchr10					Scchr11					Scchr12					Scchr13					Scchr14				
	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN
GC																									
RTE	-0.495					0.425					-0.205				-0.708						-0.110				
SSR	0.440	-0.346				0.129	0.634				-0.302	-0.124			0.075	0.109					-0.023	-0.061			
LCR	0.448	0.040	0.539			0.306	0.254	0.005			-0.222	0.286	0.516		-0.438	0.280	0.268				0.099	-0.138	0.553		
GEN	0.503	-0.222	0.746	0.555		0.077	0.567	0.766	0.303		-0.239	-0.190	0.306	0.048	-0.364	-0.080	-0.122	0.173		0.153	-0.417	0.630	0.439		
	Scchr15					Scchr16																			
	GC	RTE	SSR	LCR	GEN	GC	RTE	SSR	LCR	GEN															
GC																									
RTE	-0.262					-0.062																			
SSR	0.589	0.278				0.184	-0.206																		
LCR	-0.130	0.182	0.247			-0.063	-0.509	-0.251																	
GEN	-0.218	-0.368	-0.161	0.136		-0.331	-0.356	-0.233	0.291																

Notes:
(1) Scchr: *Saccharomyces cerevisiae* chromosome; GC: GC content; RTE: Retro-transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene.
(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the element pair under comparison whereas the negative (-) values of correlation coefficients indicate the negative correlation between the element pair under comparison.
(3) Differently highlighted colors indicate the significance levels of the distribution correlation between element pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 12
Spearman's correlation coefficients of distribution between genes categorized into different functional categories in the whole rice genome with 500-kb windows

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA			
RP																																					
NTB	0.136																																				
NAB	0.171	0.260																																			
DNAB	0.142	0.301	0.335																																		
CHRB	0.024	0.030	0.056	0.142																																	
TCFA	0.126	0.332	0.253	0.187	0.112																																
RNAB	0.149	0.219	0.085	0.217	0.056	0.240																															
CATA	0.225	0.319	0.338	0.400	0.111	0.415	0.288																														
NUA	0.137	0.115	0.077	0.121	0.086	0.115	0.092	0.132																													
TPA	0.183	0.241	0.269	0.380	0.076	0.338	0.233	0.383	0.112																												
PB	0.176	0.332	0.264	0.315	--	0.335	0.275	0.331	0.157	0.296																											
CW	0.175	0.268	0.262	0.312	0.032	0.317	0.239	0.354	0.135	0.274	0.250																										
NUS	0.193	0.283	0.348	0.252	0.138	0.316	0.296	0.465	0.161	0.374	0.364	0.323																									
PM	0.054	0.118	0.134	0.189	-0.003	0.210	0.161	0.199	0.087	0.141	0.193	0.178	0.143																								
ET	0.107	0.141	0.186	0.221	0.054	0.197	0.124	0.184	0.062	0.240	0.132	0.157	0.245	0.079																							
TC	0.120	0.343	0.267	0.207	0.131	0.027	0.241	0.452	0.087	0.374	0.347	0.358	0.308	0.208	0.228																						
TL	0.130	0.214	0.187	0.266	0.036	0.246	0.167	0.286	0.120	0.204	0.222	0.198	0.254	0.113	0.126	0.271																					
PMP	0.176	0.277	0.264	0.292	0.091	0.309	0.235	0.316	0.129	0.265	0.245	0.230	0.197	0.229	0.143	0.329	0.214																				
RTS	0.119	0.245	0.332	0.337	0.085	0.332	0.278	0.423	0.123	0.339	0.302	0.330	0.363	0.193	0.201	0.411	0.273	0.257																			
CC	0.128	0.064	0.137	0.165	-0.055	0.123	0.112	0.087	0.030	0.108	0.081	0.048	0.095	0.049	0.102	0.157	0.049	0.046	0.187																		
ST	0.111	0.201	0.288	0.242	0.088	0.248	0.241	0.365	0.111	0.314	0.349	0.266	0.266	0.103	0.186	0.294	0.244	0.227	0.268	0.082																	
MOD	0.109	0.194	0.211	0.209	0.066	0.166	0.223	0.294	0.085	0.240	0.223	0.211	0.136	0.147	0.136	0.175	0.198	0.210	0.210	0.093	0.171																
MT	0.184	0.306	0.273	0.318	0.052	0.343	0.211	0.193	0.127	0.299	0.311	0.317	0.313	0.212	0.171	0.348	0.221	0.271	0.281	0.058	0.305	0.217															
CD	0.009	0.119	0.146	0.138	0.064	0.111	0.154	0.180	0.144	0.138	0.125	0.177	0.118	0.047	0.062	0.131	0.076	0.124	0.108	0.083	0.123	0.108	0.155														
CP	0.182	0.227	0.196	0.276	0.040	0.290	0.225	0.171	0.084	0.249	0.218	0.219	0.252	0.156	0.141	0.289	0.177	0.120	0.283	0.113	0.231	0.212	0.227	0.100													
BP	0.195	0.173	0.221	0.266	0.045	0.250	0.172	0.173	0.058	0.252	0.213	0.194	0.312	0.069	0.090	0.251	0.124	0.182	0.261	0.069	0.216	0.185	0.197	0.120	0.138												
ED	0.047	0.061	0.033	0.089	0.038	0.107	0.010	0.027	0.051	0.106	0.051	0.065	0.130	0.040	0.103	0.081	0.020	0.073	0.074	0.070	0.066	0.060	0.072	-0.002	0.095	0.078											
PED	0.114	0.104	0.179	0.126	0.062	0.160	0.088	0.141	0.013	0.149	0.109	0.146	0.099	0.046	0.098	0.181	0.114	0.133	0.173	0.045	0.111	0.086	0.165	0.063	0.122	0.084	0.088										
FD	0.080	0.102	0.187	0.066	0.052	0.062	0.188	0.188	0.172	0.177	0.149	0.179	0.169	0.133	0.094	0.070	0.092	0.090	0.104	0.017	0.073	0.124	0.199	0.067	0.154	0.131	-0.019	0.094									
PS	0.027	0.068	0.034	0.102	-0.007	0.062	0.085	0.089	0.008	0.061	0.106	0.051	0.112	0.065	0.011	0.057	0.054	0.065	0.063	0.044	0.083	0.062	0.065	0.130	0.110	0.079	-0.053	0.079	0.067								
CCOB	0.221	0.225	0.257	0.354	0.093	0.352	0.205	0.396	0.084	0.272	0.297	0.271	0.349	0.129	0.132	0.427	0.195	0.239	0.332	0.070	0.253	0.285	0.276	0.196	0.252	0.223	0.108	0.176	0.255	0.078							
CG	0.025	0.075	0.144	0.171	0.026	0.170	0.036	0.143	-0.036	0.135	0.093	0.081	0.133	0.069	0.075	0.166	0.078	0.074	0.145	0.049	0.110	0.136	0.085	0.028	0.063	0.090	0.053	0.090	0.002	-0.001	0.088						
CDI	0.103	0.079	0.160	0.117	-0.009	0.128	0.102	0.170	0.109	0.155	0.062	0.072	0.199	0.113	0.080	0.164	0.158	0.144	0.136	0.043	0.090	0.090	0.183	0.072	0.067	0.083	0.046	0.056	0.060	0.068	0.239	0.024					
TCRA	0.119	0.209	0.204	0.161	0.074	0.141	0.168	0.276	0.076	0.259	0.240	0.217	0.250	0.118	0.160	0.178	0.215	0.210	0.241	0.107	0.198	0.121	0.260	0.152	0.161	0.164	0.022	0.169	0.164	0.000	0.277	0.102	0.122				

Notes:
 (1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: cataly Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal deve Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.
 (2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene ca 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates
 (3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p < 0.001$, green for a significance level of $p < 0.01$, and red for a significance level of $p < 0.05$.

Table 13
Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 1 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA		
RP																																				
NTB	0.082																																			
NAB	-0.012	0.243																																		
DNAB	0.163	0.210	0.200																																	
CHRB	0.084	-0.032	-0.042	0.146																																
TCFA	-0.068	0.253	0.186	-0.012	0.062																															
RNAB	0.126	0.076	0.078	0.054	0.218	0.030																														
CATA	0.184	0.013	0.032	0.239	0.150	0.310	0.047																													
NUA	0.171	0.216	0.232	0.244	0.056	0.206	0.053	0.033																												
TPA	0.218	0.185	0.057	0.217	0.100	0.107	0.123	0.062	0.162																											
PB	0.042	0.135	0.220	0.242	--	0.189	0.182	0.040	0.241	0.140																										
CW	0.173	0.209	0.040	0.197	0.015	0.164	0.042	0.140	0.130	0.082	0.155																									
NUS	0.100	0.050	0.202	-0.011	0.104	-0.011	0.231	0.111	0.241	0.194	0.034	0.183																								
PM	-0.049	0.200	0.209	0.003	-0.037	0.024	0.081	-0.054	0.109	-0.023	0.119	0.158	0.181																							
ET	0.140	0.054	0.000	0.192	0.155	0.230	0.010	0.068	-0.062	0.214	0.043	0.076	0.113	0.024																						
TC	-0.031	0.309	0.094	-0.051	0.062	0.050	-0.011	0.240	0.142	0.142	0.221	0.194	0.149	0.095	0.133																					
TL	0.184	0.180	0.168	0.296	-0.120	0.290	0.023	0.083	0.130	-0.027	0.155	0.130	0.139	-0.015	-0.027	0.317																				
PMP	0.036	0.135	0.199	0.219	-0.008	0.166	0.043	-0.057	0.234	0.173	0.075	0.022	-0.003	0.153	0.020	0.249	0.132																			
RTS	0.027	-0.074	0.061	0.235	0.046	0.187	0.179	0.125	0.222	0.206	-0.010	0.027	0.096	-0.048	0.154	0.284	0.090	-0.095																		
CC	0.015	-0.071	0.008	0.166	-0.107	0.086	0.032	0.241	-0.052	0.070	-0.104	-0.063	0.015	0.088	0.364	0.148	0.171	-0.106	0.247																	
ST	0.091	0.043	0.142	0.245	0.143	0.224	0.041	0.084	0.260	0.176	0.255	0.191	0.190	0.036	0.149	0.267	0.148	0.101	0.110	0.026																
MOD	-0.091	0.034	0.023	0.016	-0.199	0.049	0.002	0.045	-0.005	0.021	-0.022	-0.018	0.047	-0.089	-0.057	0.041	0.240	-0.008	-0.054	0.020	-0.038															
MT	0.131	0.282	0.134	0.104	-0.098	0.165	-0.024	0.008	0.085	0.235	0.111	0.263	0.180	0.114	-0.044	0.296	0.151	0.108	0.117	0.069	0.208	-0.046														
CD	0.006	0.043	0.135	0.207	0.064	0.150	0.031	0.114	0.210	0.156	-0.083	0.004	0.087	-0.010	0.043	0.177	0.112	-0.001	0.094	0.148	0.033	-0.191	0.048													
CP	0.095	0.189	0.136	0.210	-0.060	0.233	-0.095	-0.057	0.056	0.254	0.089	0.021	0.210	0.110	0.123	0.319	0.124	0.055	0.027	0.078	0.242	0.033	0.122	0.064												
BP	0.227	0.037	0.053	0.264	0.194	0.223	0.124	0.066	-0.134	0.104	-0.007	0.050	0.014	-0.049	0.117	0.180	0.036	0.000	0.044	0.217	0.000	-0.095	-0.041	0.091	-0.022											
ED	0.095	0.017	-0.175	-0.015	-0.091	-0.125	-0.039	-0.028	-0.014	0.123	0.004	-0.113	0.021	-0.008	0.088	-0.138	0.017	0.091	0.077	0.079	0.066	-0.036	0.053	0.046	0.137	-0.006										
PED	-0.133	-0.130	0.000	0.100	-0.070	0.131	-0.168	0.038	-0.140	0.022	-0.098	-0.089	-0.034	-0.251	0.101	0.072	0.191	-0.123	-0.007	0.166	-0.070	0.204	0.067	-0.106	0.244	0.156	-0.006									
FD	0.179	0.057	0.169	0.107	0.079	0.087	0.067	0.211	0.264	0.112	0.010	-0.023	0.164	0.163	0.140	0.059	0.205	0.051	-0.070	0.013	0.077	-0.074	0.191	0.010	0.181	0.199	0.056	-0.035								
PS	0.096	0.029	0.048	0.018	-0.066	-0.045	0.158	0.072	-0.022	0.045	0.020	0.124	0.012	-0.089	0.002	-0.110	0.067	-0.033	-0.127	-0.097	0.037	-0.100	0.039	0.069	-0.053	-0.143	-0.083	-0.149	0.218							
CCOB	0.108	0.100	-0.037	0.046	0.087	0.247	-0.114	0.051	0.005	0.154	0.220	0.098	0.113	0.035	0.042	0.294	0.023	0.155	-0.035	-0.138	0.093	0.189	0.161	0.025	0.179	0.044	0.122	0.205	0.203	-0.116						
CG	-0.056	0.071	0.074	-0.005	-0.091	0.070	-0.001	0.134	-0.100	0.169	0.197	0.101	-0.058	0.113	0.082	0.102	0.087	0.032	0.045	0.101	-0.014	0.128	0.069	-0.039	-0.036	-0.031	0.007	0.080	-0.102	0.075	-0.054					
CDI	0.178	0.137	0.170	0.178	-0.083	0.192	0.033	0.049	0.160	0.058	-0.034	0.076	0.076	0.150	0.101	0.234	0.244	-0.004	0.041	-0.025	0.129	0.005	0.279	0.085	0.101	0.064	0.170	-0.071	0.031	0.108	0.314	0.009				
TCRA	0.049	0.101	0.103	0.047	0.132	0.119	0.147	0.049	0.020	0.127	0.240	0.120	0.166	0.021	0.062	0.070	0.211	0.037	0.295	0.057	0.103	-0.023	0.172	0.138	0.196	0.027	-0.019	0.104	0.081	-0.087	0.154	0.039	0.060			

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 14

Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 2 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA																
RP																																																		
NTB	0.247																																																	
NAB	-0.008	0.128																																																
DNAB	-0.050	0.144	0.113																																															
CHRB	-0.140	0.109	-0.063	0.150																																														
TCFA	0.077	0.219	0.097	0.193	0.154																																													
RNAB	0.065	0.164	0.034	0.047	-0.188	0.076																																												
CATA	0.280	0.166	0.285	0.252	-0.032	0.329	0.222																																											
NUA	-0.007	-0.048	0.003	-0.166	-0.006	-0.099	-0.044	-0.007																																										
TPA	-0.155	0.246	-0.070	0.311	0.148	0.256	0.005	0.060	-0.098																																									
PB	0.064	0.223	0.210	0.251	--	0.328	0.088	0.125	-0.164	0.216																																								
CW	0.148	0.287	0.109	0.247	0.005	0.277	0.080	0.160	-0.103	0.215	0.001																																							
NUS	0.060	0.133	0.237	0.092	0.145	0.296	0.072	0.345	-0.184	0.247	0.253	0.204																																						
PM	0.069	0.097	0.129	0.068	-0.026	0.128	0.115	0.105	-0.088	0.178	0.031	0.214	-0.092																																					
ET	0.317	0.107	0.300	0.196	-0.137	0.205	0.142	0.173	0.069	0.056	-0.039	0.093	0.314	-0.097																																				
TC	0.042	0.255	0.147	0.254	0.109	-0.067	0.046	0.358	-0.178	0.278	0.245	0.262	0.217	0.069	0.260																																			
TL	0.037	0.125	0.050	0.150	-0.032	-0.008	0.130	0.084	0.112	0.203	0.056	0.149	0.016	0.035	0.054	0.000																																		
PMP	0.186	0.158	0.297	0.195	0.229	0.226	0.217	0.227	-0.124	0.219	0.112	0.206	0.186	0.033	0.120	0.255	0.243																																	
RTS	0.050	0.184	0.239	0.156	0.036	0.231	0.191	0.352	0.030	0.055	0.175	0.128	0.140	0.264	0.211	0.229	0.216	0.174																																
CC	0.129	0.080	0.076	0.152	-0.122	0.114	0.016	0.025	-0.229	-0.094	0.098	-0.001	0.077	-0.007	-0.005	0.249	0.122	0.065	0.084																															
ST	0.099	0.134	0.362	0.145	0.013	0.229	0.218	0.303	-0.027	0.183	0.118	0.138	0.242	-0.040	0.105	0.287	0.076	0.241	0.123	0.048																														
MOD	0.176	0.198	0.217	-0.069	-0.080	-0.095	0.147	0.217	0.032	0.106	0.097	0.114	0.080	0.138	0.254	0.056	0.099	0.199	0.028	-0.030	0.201																													
MT	0.132	0.255	0.229	0.241	0.087	0.382	0.277	0.188	0.110	0.095	0.251	0.232	0.327	0.225	0.131	0.349	0.122	0.312	0.350	0.124	0.355	0.123																												
CD	0.163	0.215	0.224	0.210	0.105	0.125	0.210	0.343	-0.020	-0.017	0.162	0.226	0.190	0.073	0.146	0.215	0.056	0.158	0.097	0.022	0.197	0.140	0.201																											
CP	0.020	0.152	0.144	0.217	-0.037	0.230	0.177	0.087	-0.065	0.072	0.173	0.151	0.181	0.124	0.221	0.237	0.235	0.151	0.314	0.047	0.227	0.227	0.257	0.109																										
BP	0.208	0.051	0.237	0.172	-0.105	0.274	0.244	0.324	-0.003	0.101	0.129	0.075	0.353	-0.034	0.065	0.237	0.070	0.177	0.338	0.132	0.230	0.140	0.241	0.207	0.250																									
ED	--	-0.062	-0.128	0.000	-0.082	0.122	-0.146	-0.155	-0.031	-0.173	-0.177	0.040	-0.040	-0.170	0.241	0.105	-0.035	-0.096	-0.002	-0.007	-0.070	0.089	0.044	-0.020	0.075	-0.015																								
PED	0.129	0.058	0.181	-0.024	0.094	0.123	0.044	0.088	-0.130	0.016	0.189	0.129	0.117	0.027	0.148	-0.017	-0.185	0.110	0.195	-0.148	0.040	-0.106	0.077	0.082	0.023	0.042	0.227																							
FD	-0.010	0.138	0.174	0.089	0.055	0.115	0.102	0.308	-0.020	0.180	0.116	0.217	0.227	0.122	0.234	0.132	-0.060	0.073	-0.061	-0.105	0.070	0.248	0.329	0.036	0.214	0.110	-0.118	0.137																						
PS	-0.053	0.051	0.283	0.182	0.115	0.137	0.129	0.057	-0.031	0.001	0.164	0.027	0.244	0.079	-0.095	0.167	-0.197	0.191	0.148	0.147	0.174	0.092	0.196	0.301	0.225	0.198	-0.091	0.172	0.169																					
CCOB	0.063	0.237	0.001	0.259	0.081	0.219	0.118	0.158	-0.059	0.352	0.179	0.293	0.218	0.116	0.034	0.283	0.068	0.198	0.191	0.025	0.283	0.233	0.209	0.133	0.157	0.204	-0.177	-0.040	0.181	-0.019																				
CG	0.029	-0.099	-0.067	0.179	-0.103	0.306	-0.059	0.028	-0.193	0.080	-0.167	-0.074	0.079	-0.128	0.088	0.205	-0.048	-0.184	0.150	0.063	-0.052	0.030	-0.050	0.028	-0.003	0.137	0.032	0.062	-0.060	-0.114	0.064																			
CDI	-0.002	-0.031	0.188	0.070	0.030	0.133	0.042	0.132	-0.131	0.232	-0.019	0.096	0.252	0.082	0.094	0.124	0.083	0.051	-0.053	0.162	-0.058	0.012	0.136	-0.097	0.124	-0.067	-0.024	0.044	-0.028	0.061	0.162	-0.048																		
TCRA	-0.078	0.139	0.118	-0.083	0.048	0.020	-0.054	0.168	0.101	0.072	0.021	0.069	0.262	-0.042	0.021	0.074	0.215	0.086	0.188	0.022	0.156	0.088	0.258	0.162	0.175	-0.043	0.164	0.154	0.119	-0.010	0.090	-0.003	-0.049																	

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "-" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 15
Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 3 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA		
RP																																				
NTB	-0.077																																			
NAB	0.120	0.106																																		
DNAB	0.242	0.243	0.210																																	
CHRB	-0.018	-0.146	0.029	-0.111																																
TCFA	0.185	0.369	0.179	-0.059	0.042																															
RNAB	0.124	0.017	0.019	0.180	0.146	0.142																														
CATA	0.014	0.336	0.234	0.094	-0.002	0.253	0.317																													
NUA	0.108	0.122	0.025	0.121	0.138	0.158	0.040	0.151																												
TPA	0.246	0.146	0.119	0.094	-0.077	0.185	0.283	0.248	0.111																											
PB	0.140	0.291	0.124	0.241	--	0.339	0.202	0.344	0.209	0.137																										
CW	0.156	0.245	0.222	0.094	-0.147	0.260	0.308	0.476	0.131	0.269	0.160																									
NUS	0.213	-0.030	0.141	-0.009	0.052	0.340	0.212	0.311	0.263	0.187	0.156	0.287																								
PM	0.018	0.301	0.084	0.238	-0.211	0.268	0.103	0.240	0.102	0.129	0.315	0.152	0.085																							
ET	-0.102	-0.111	-0.026	-0.136	0.286	-0.090	0.199	0.142	0.181	0.099	0.071	-0.018	0.102	-0.140																						
TC	0.135	0.256	0.203	-0.002	0.052	-0.065	0.174	0.266	0.120	0.078	0.270	0.201	0.209	0.109	-0.046																					
TL	0.055	0.285	0.000	0.015	0.098	0.237	0.053	0.248	0.085	0.217	0.131	0.184	0.193	0.237	0.006	0.136																				
PMP	0.148	0.238	0.140	0.250	-0.125	0.413	0.267	0.398	0.116	0.204	0.244	0.174	0.312	0.222	0.022	0.330	0.257																			
RTS	0.032	0.190	0.224	0.141	-0.177	0.238	0.232	0.381	0.156	0.315	0.373	0.403	0.237	0.340	-0.257	0.107	0.349	0.304																		
CC	0.044	0.050	0.132	0.011	-0.074	-0.108	-0.002	-0.055	0.186	0.148	0.035	0.089	0.025	-0.018	0.088	-0.052	-0.176	-0.012	0.117																	
ST	0.270	-0.047	0.059	0.055	0.044	0.249	0.216	0.345	-0.008	0.429	0.128	0.126	0.154	0.117	-0.085	0.164	0.359	0.068	0.260	0.047																
MOD	0.047	0.182	-0.017	0.092	0.150	0.163	0.085	0.143	0.101	0.179	0.219	0.051	0.018	0.152	-0.180	0.051	-0.016	0.181	0.015	0.010	0.142															
MT	0.012	0.344	0.116	0.159	-0.020	0.338	0.239	0.305	0.253	0.149	0.286	0.446	0.140	0.373	-0.018	0.298	0.339	0.204	0.310	-0.074	0.159	0.289														
CD	-0.197	-0.115	-0.029	0.134	-0.088	0.084	0.138	-0.023	0.033	0.140	-0.095	-0.001	0.025	-0.187	-0.044	0.219	-0.009	0.004	-0.024	-0.151	-0.064	-0.053	-0.043													
CP	0.112	0.245	-0.115	-0.044	-0.076	0.270	0.173	0.153	0.171	0.277	0.204	0.203	0.037	0.272	-0.051	0.150	0.171	0.165	0.191	-0.109	0.107	0.333	0.106	-0.004												
BP	0.058	0.112	-0.038	0.091	0.071	0.009	0.154	0.201	-0.051	0.263	0.163	0.293	0.221	0.086	-0.054	0.024	0.205	0.148	0.229	-0.062	0.303	0.168	0.276	-0.017	0.057											
ED	--	0.048	0.204	0.115	0.189	0.220	0.050	0.108	0.281	0.159	0.190	0.179	0.164	0.118	0.194	0.111	-0.088	0.154	0.013	-0.057	0.156	0.161	0.081	-0.197	0.150	0.120										
PED	0.226	-0.054	0.000	0.118	-0.099	0.117	0.007	-0.015	0.028	-0.015	-0.138	0.019	-0.073	0.046	-0.262	0.209	0.172	0.101	0.171	-0.085	-0.052	-0.055	0.179	0.023	-0.208	-0.209	0.066									
FD	-0.065	0.119	-0.144	-0.082	-0.015	0.207	0.063	-0.111	0.027	0.144	0.107	0.243	0.207	0.072	-0.116	0.137	0.247	0.197	0.110	-0.059	0.192	0.060	0.035	0.062	0.248	0.109	-0.093	0.114								
PS	-0.149	0.108	-0.197	0.129	-0.028	0.095	0.081	-0.110	0.138	-0.069	0.095	-0.010	0.030	0.106	0.073	0.066	-0.084	0.042	-0.194	-0.074	0.006	0.006	-0.034	0.146	-0.137	-0.125	-0.063	0.081	-0.015							
CCOB	0.102	0.465	0.148	0.171	-0.110	0.269	0.364	0.313	0.222	0.074	0.418	0.277	0.230	0.391	-0.069	0.135	0.185	0.395	0.289	0.083	0.280	0.267	0.337	-0.054	0.387	0.076	0.255	0.028	0.174	0.079						
CG	0.057	0.105	0.136	0.115	-0.088	0.009	0.075	0.043	0.030	0.251	0.191	0.025	0.086	0.202	-0.082	-0.082	0.013	0.153	0.042	-0.026	0.099	-0.019	-0.141	-0.036	0.015	0.014	0.009	-0.031	-0.100	0.099	0.074					
CDI	0.007	0.026	-0.027	0.225	-0.157	0.207	-0.097	0.060	-0.171	0.050	0.087	0.236	0.361	0.093	0.009	0.116	0.088	0.178	0.151	0.181	0.069	0.000	0.213	0.151	-0.080	0.107	0.111	0.055	0.108	0.104	0.254	0.109				
TCRA	-0.024	0.054	-0.069	0.005	0.026	0.089	-0.123	0.090	-0.086	0.206	0.152	0.068	0.081	-0.096	-0.004	0.105	0.105	0.113	-0.117	0.036	-0.041	-0.063	0.163	0.063	-0.061	0.091	-0.099	0.138	0.055	0.077	0.016	0.011	0.251			

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHR: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene categories. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 16**Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 4 with 500-kb window**

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA	
RP																																			
NTB	0.165																																		
NAB	0.261	0.339																																	
DNAB	0.318	0.332	0.485																																
CHRB	-0.061	0.064	0.221	0.308																															
TCFA	0.276	0.182	0.330	0.279	0.196																														
RNAB	0.221	0.359	0.026	0.239	0.237	0.281																													
CATA	0.321	0.236	0.390	0.416	0.140	0.207	0.191																												
NUA	0.176	0.349	0.142	0.026	0.002	0.008	0.148	0.172																											
TPA	0.429	0.249	0.403	0.522	0.035	0.304	0.287	0.445	0.154																										
PB	0.225	0.206	0.437	0.336	--	0.130	0.346	0.352	0.342	0.327																									
CW	0.201	0.315	0.427	0.336	0.134	0.162	0.399	0.404	0.446	0.348	0.245																								
NUS	0.282	0.413	0.576	0.331	0.242	0.121	0.398	0.476	0.138	0.409	0.524	0.440																							
PM	0.143	0.158	0.288	0.123	0.108	0.028	0.391	0.066	0.283	-0.006	0.127	0.274	0.215																						
ET	0.112	0.240	0.345	0.220	-0.165	0.112	0.125	0.171	0.143	0.239	0.149	0.318	0.248	0.157																					
TC	0.238	0.326	0.406	0.223	0.289	-0.023	0.305	0.397	-0.003	0.413	0.367	0.339	0.279	0.153	0.295																				
TL	0.150	0.143	0.165	0.143	0.153	0.171	0.139	0.191	0.116	0.168	0.171	0.224	0.138	0.097	-0.035	0.285																			
PMP	0.218	0.119	0.435	0.289	0.233	0.081	0.435	0.249	0.339	0.197	0.218	0.293	0.209	0.381	0.242	0.260	0.181																		
RTS	0.254	0.242	0.555	0.391	0.324	0.379	0.311	0.425	0.272	0.491	0.373	0.408	0.414	0.128	0.303	0.460	0.349	0.334																	
CC	0.305	0.269	0.327	0.299	-0.118	0.292	0.104	0.048	-0.019	0.295	0.147	0.073	0.354	0.116	0.056	0.266	0.003	0.138	0.267																
ST	0.161	0.157	0.489	0.371	0.242	0.065	0.353	0.379	0.266	0.230	0.338	0.267	0.390	0.139	0.375	0.353	0.178	0.291	0.229	0.158															
MOD	0.402	0.188	0.412	0.277	0.358	0.182	0.455	0.303	0.243	0.382	0.285	0.269	0.246	0.175	0.214	0.183	0.219	0.279	0.354	0.128	0.163														
MT	0.293	0.219	0.308	0.214	0.155	0.197	0.285	0.081	0.264	0.205	0.285	0.177	0.112	-0.011	0.201	0.188	0.257	0.272	0.273	-0.093	0.223	0.300													
CD	0.100	0.272	0.322	0.257	0.115	0.104	0.412	0.191	0.075	0.265	0.123	0.342	0.141	0.135	0.141	0.190	0.240	0.193	0.274	0.193	0.162	0.349	0.200												
CP	0.381	0.119	0.213	0.325	0.086	0.345	0.353	0.123	0.219	0.275	0.156	0.263	0.205	0.046	0.170	0.305	0.111	0.029	0.440	0.160	0.244	0.280	0.284	0.211											
BP	0.091	-0.029	0.309	0.248	0.048	0.267	-0.032	-0.014	0.285	0.210	0.039	0.068	0.090	-0.122	0.048	0.113	0.071	0.062	0.213	0.084	0.172	0.268	0.180	-0.029	0.103										
ED	--	0.172	0.238	0.201	-0.047	0.185	0.253	-0.065	-0.084	0.289	0.071	0.008	0.219	0.135	-0.030	0.174	0.097	0.038	0.184	0.391	0.167	0.146	-0.040	0.351	-0.055	0.027									
PED	0.027	0.110	0.214	0.254	0.328	0.261	0.115	0.153	0.028	0.302	0.214	0.100	0.027	0.093	0.286	0.343	0.171	0.112	0.188	0.177	0.185	0.116	0.247	0.021	0.068	0.088	-0.080								
FD	0.196	0.186	0.446	0.090	0.060	0.053	0.277	0.376	0.345	0.347	0.214	0.168	0.132	0.167	0.196	0.089	0.136	0.103	0.325	0.096	0.211	0.427	0.280	-0.064	0.196	0.244	0.254	0.133							
PS	0.149	0.036	-0.037	0.139	-0.058	0.202	-0.074	0.179	-0.104	0.217	0.034	-0.001	0.194	-0.076	0.010	0.243	0.204	0.041	0.106	0.098	0.120	0.056	0.175	0.423	0.162	0.093	-0.036	0.242	0.139						
CCOB	0.502	0.020	0.479	0.628	0.317	0.418	0.313	0.508	-0.004	0.382	0.291	0.284	0.396	0.126	0.018	0.553	0.187	0.133	0.449	0.205	0.278	0.388	0.068	0.436	0.280	0.188	0.226	0.169	0.301	0.262					
CG	0.195	0.016	0.268	0.153	0.071	0.160	0.220	0.048	-0.068	0.139	0.027	0.156	0.180	0.075	0.117	0.157	0.035	0.056	0.170	0.131	0.134	0.250	0.167	0.366	0.020	-0.005	0.231	0.063	0.297	-0.075	0.184				
CDI	0.248	-0.033	0.237	0.072	-0.021	0.063	0.102	0.387	0.388	0.128	0.139	0.103	0.194	0.147	0.111	0.188	0.125	0.136	0.131	0.001	-0.040	0.184	0.213	0.095	0.167	-0.001	-0.136	0.162	0.072	0.127	0.190	0.048			
TCRA	0.330	0.054	0.373	0.167	0.196	0.045	0.234	0.239	0.047	0.174	0.191	0.173	0.154	0.039	0.252	0.217	0.091	0.105	0.260	0.169	0.107	0.228	0.097	0.200	0.077	0.163	0.155	0.225	0.365	-0.174	0.254	0.288	0.199		

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 17
Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 5 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA			
RP																																					
NTB	0.240																																				
NAB	0.028	0.306																																			
DNAB	0.126	0.360	0.396																																		
CHRB	0.187	0.142	-0.017	0.141																																	
TCFA	0.214	0.281	0.164	0.238	0.097																																
RNAB	-0.012	0.396	-0.030	0.178	0.128	0.218																															
CATA	0.184	0.423	0.175	0.445	0.164	0.428	0.329																														
NUA	0.144	0.180	-0.149	0.175	0.319	0.136	0.036	0.101																													
TPA	0.184	0.165	0.125	0.453	0.083	0.261	0.126	0.265	0.377																												
PB	0.273	0.287	0.191	0.234	--	0.204	0.356	0.247	0.121	0.151																											
CW	0.032	0.129	0.088	0.153	-0.068	0.276	0.110	0.220	0.002	0.117	0.220																										
NUS	0.316	0.252	0.191	0.397	0.225	0.362	0.225	0.521	0.160	0.221	0.327	0.182																									
PM	0.180	0.094	0.210	0.098	-0.041	0.216	0.341	0.135	0.049	0.109	0.151	-0.165	0.008																								
ET	-0.097	0.342	0.216	0.371	-0.073	0.313	0.223	0.187	0.010	0.108	0.220	0.200	0.220	0.264																							
TC	0.098	0.425	0.204	0.342	0.139	-0.124	0.212	0.474	0.167	0.290	0.249	0.259	0.327	0.179	0.414																						
TL	0.031	0.292	0.273	0.260	0.144	0.156	0.092	0.359	0.067	-0.021	0.303	0.146	0.284	0.127	0.315	0.136																					
PMP	0.319	0.216	0.190	0.427	0.188	0.377	0.318	0.384	0.033	0.247	0.152	0.188	0.217	0.158	0.368	0.446	0.297																				
RTS	0.088	0.339	0.334	0.443	0.150	0.403	0.201	0.474	-0.004	0.305	0.204	0.265	0.437	0.238	0.396	0.487	0.228	0.359																			
CC	0.195	0.080	0.297	0.096	0.088	0.061	0.127	0.025	0.008	0.069	0.056	-0.068	0.010	-0.058	0.093	0.180	0.064	0.121	0.185																		
ST	0.320	0.379	0.105	0.159	0.072	0.142	0.229	0.290	0.095	0.206	0.341	0.187	0.223	0.214	0.256	0.216	0.225	0.303	0.197	0.021																	
MOD	0.105	0.196	0.250	0.238	0.203	0.266	0.364	0.393	0.153	0.184	0.120	0.037	0.267	0.119	0.298	0.272	0.214	0.279	0.360	0.284	0.017																
MT	0.401	0.307	0.233	0.501	-0.065	0.445	0.325	0.379	-0.032	0.165	0.174	0.254	0.555	0.258	0.136	0.472	0.192	0.272	0.393	0.007	0.210	0.220															
CD	0.146	0.168	0.039	-0.047	0.157	-0.027	-0.009	0.159	0.273	0.235	0.188	0.127	-0.008	0.137	-0.039	0.026	-0.093	0.161	0.031	0.142	0.165	0.087	0.253														
CP	0.328	0.221	0.222	0.340	0.117	0.382	0.277	0.036	-0.091	0.088	0.112	0.280	0.221	0.081	0.273	0.323	0.296	0.059	0.319	0.406	0.129	0.370	0.308	0.060													
BP	0.326	0.186	0.083	0.202	0.071	0.329	0.213	0.224	-0.092	0.070	0.180	0.212	0.384	0.061	-0.073	0.274	0.126	0.291	0.363	0.127	0.125	0.334	0.330	0.065	0.258												
ED	--	0.120	-0.107	0.303	0.245	0.297	-0.105	0.130	0.155	0.153	0.007	0.049	0.326	-0.061	-0.192	0.275	-0.033	0.161	0.200	0.131	0.180	0.043	0.187	0.222	-0.057	0.136											
PED	0.192	0.187	0.183	0.082	0.003	0.162	0.303	0.290	0.033	0.135	-0.002	0.158	0.074	0.035	0.217	0.261	0.017	0.083	0.276	0.152	0.144	0.303	0.189	0.144	0.066	0.087	0.045										
FD	0.109	0.079	-0.076	-0.087	0.169	-0.049	0.020	0.125	0.330	0.235	0.012	-0.011	0.049	0.164	0.149	-0.027	-0.050	0.066	-0.060	0.053	-0.151	-0.024	0.115	0.326	0.040	0.030	0.049	0.171									
PS	-0.147	0.065	0.249	0.057	-0.050	0.238	0.262	0.225	-0.067	-0.132	-0.141	0.014	-0.022	0.034	0.242	0.100	0.282	0.065	0.105	0.196	-0.135	0.175	0.235	-0.102	0.295	0.253	-0.043	0.313	-0.012								
CCOB	0.280	0.176	0.014	0.283	0.110	0.255	-0.115	0.367	0.174	0.064	-0.048	0.089	0.205	-0.105	0.140	0.289	0.063	0.181	0.309	0.106	0.060	0.264	0.081	0.178	0.231	0.179	0.227	0.210	0.229	0.186							
CG	-0.101	-0.020	-0.066	-0.051	-0.071	-0.071	-0.159	-0.001	0.107	-0.005	-0.016	-0.049	-0.128	-0.165	-0.021	-0.025	0.149	-0.107	-0.026	-0.105	-0.038	0.055	-0.133	-0.147	-0.090	-0.126	-0.061	0.036	-0.021	-0.050	0.008						
CDI	-0.057	0.066	-0.062	-0.093	0.220	0.019	-0.087	0.092	0.047	0.012	-0.069	-0.218	-0.015	0.075	0.167	0.045	0.202	0.055	0.011	0.032	0.067	-0.093	-0.096	0.033	-0.095	-0.018	-0.007	-0.183	-0.066	0.093	0.187	-0.023					
TCRA	0.183	0.335	0.004	0.171	0.017	-0.004	0.178	0.342	0.149	0.359	0.238	0.119	0.198	0.146	0.127	0.014	0.118	0.345	0.241	0.192	0.269	0.168	0.331	0.318	0.136	0.337	0.200	0.394	0.264	-0.021	0.360	0.111	0.113				

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 18
Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 6 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA		
RP																																				
NTB	-0.009																																			
NAB	-0.135	0.257																																		
DNAB	-0.190	0.083	0.043																																	
CHRB	--	--	--	--																																
TCFA	0.007	0.290	-0.161	-0.050	--																															
RNAB	-0.125	0.349	-0.095	0.057	--	0.100																														
CATA	0.037	0.120	-0.068	0.030	--	0.271	-0.214																													
NUA	-0.052	0.185	-0.055	-0.107	--	0.068	0.305	0.033																												
TPA	0.271	0.069	0.117	-0.056	--	-0.004	0.086	-0.075	0.172																											
PB	-0.050	0.053	0.222	0.063	--	0.202	0.148	0.176	0.180	0.103																										
CW	-0.127	0.265	0.295	-0.091	--	0.077	0.232	0.042	0.147	0.277	0.056																									
NUS	-0.070	0.166	0.000	0.054	--	0.249	0.190	-0.053	0.183	0.057	-0.046	0.135																								
PM	0.132	0.150	0.224	0.157	--	0.136	0.178	-0.050	0.256	0.228	0.203	0.175	0.022																							
ET	0.076	0.108	-0.057	0.161	--	0.229	-0.043	0.027	-0.052	-0.186	0.147	-0.027	0.092	0.022																						
TC	0.087	0.334	0.011	-0.176	--	-0.005	0.189	0.116	0.076	-0.011	0.181	0.166	0.167	0.162	0.107																					
TL	-0.059	0.124	-0.072	0.020	--	-0.098	-0.019	0.107	-0.055	-0.207	0.066	0.127	-0.066	-0.062	0.196	0.086																				
PMP	-0.022	-0.032	0.042	0.136	--	0.348	0.206	0.148	0.204	0.042	-0.082	-0.084	0.090	-0.052	0.073	0.369	0.110																			
RTS	0.006	0.063	0.127	0.030	--	0.159	0.046	0.098	-0.118	0.064	0.072	-0.014	0.054	0.068	-0.082	0.281	0.101	0.088																		
CC	-0.074	0.135	0.169	0.237	--	0.181	0.435	-0.206	-0.023	-0.122	-0.025	-0.048	0.104	-0.088	0.176	0.193	-0.079	-0.134	0.068																	
ST	-0.237	0.079	-0.063	0.072	--	0.090	0.087	0.052	0.147	-0.087	-0.093	-0.083	0.016	-0.202	-0.028	0.081	0.209	-0.103	0.064	0.057																
MOD	-0.184	0.101	0.110	0.079	--	0.002	0.257	0.027	-0.061	-0.221	-0.078	-0.185	0.000	-0.118	0.162	-0.122	0.017	-0.016	-0.047	0.358	-0.207															
MT	-0.106	-0.002	-0.015	0.194	--	0.303	-0.005	0.094	0.158	-0.119	0.172	0.018	0.016	0.017	-0.047	0.156	0.103	0.056	-0.093	-0.122	-0.070	-0.018														
CD	--	-0.065	-0.097	--	--	--	-0.091	0.059	-0.028	0.000	-0.088	-0.009	--	0.078	-0.091	--	-0.097	0.010	--	-0.040	--	-0.108	-0.150													
CP	0.302	-0.159	-0.141	0.015	--	0.240	-0.123	0.157	-0.071	0.076	-0.023	-0.158	0.089	-0.084	0.094	0.062	-0.142	-0.157	0.149	-0.101	-0.195	0.003	0.089	0.225												
BP	0.055	-0.207	-0.157	-0.103	--	-0.114	-0.203	0.023	0.101	-0.083	-0.001	-0.206	-0.202	-0.008	-0.092	-0.163	0.062	-0.241	-0.041	-0.156	-0.225	-0.161	-0.117	0.055	-0.075											
ED	--	-0.102	-0.055	0.115	--	0.223	-0.052	0.152	-0.016	-0.086	-0.115	-0.120	0.018	-0.061	0.299	0.194	-0.055	-0.094	-0.118	-0.023	-0.117	--	0.158	-0.028	0.227	0.101										
PED	-0.091	-0.065	-0.097	-0.058	--	0.073	-0.091	--	-0.028	-0.151	-0.019	-0.212	-0.084	-0.108	0.142	-0.038	0.103	0.024	0.085	-0.040	-0.114	0.281	-0.082	-0.050	-0.065	-0.103	-0.028									
FD	-0.005	0.006	0.007	-0.102	--	0.061	0.026	0.172	0.256	0.102	-0.031	-0.006	0.179	0.282	0.022	0.079	-0.103	0.042	-0.117	-0.088	0.188	-0.117	0.048	--	0.009	-0.087	0.256	-0.108								
PS	-0.052	-0.102	-0.055	0.115	--	0.068	-0.052	--	-0.016	-0.086	-0.115	-0.120	0.018	-0.061	-0.052	0.076	-0.055	-0.094	--	-0.023	-0.117	-0.061	--	-0.028	--	--	-0.016	-0.028	-0.061							
CCOB	0.048	0.315	0.138	-0.042	--	-0.112	0.095	0.066	0.233	-0.064	0.289	0.226	0.012	0.153	0.101	0.036	0.161	0.148	-0.021	-0.092	0.083	-0.245	0.240	0.061	0.105	-0.056	-0.064	-0.113	0.144	-0.064						
CG	-0.074	0.236	-0.079	0.163	--	0.097	-0.074	-0.079	-0.023	-0.086	0.186	0.056	0.104	0.365	0.176	0.109	-0.079	0.229	-0.168	-0.033	0.183	-0.088	0.109	-0.040	-0.101	-0.006	-0.023	-0.040	-0.088	-0.023	-0.040	-0.088	-0.023	-0.061		
CDI	-0.197	-0.082	0.000	-0.095	--	0.008	0.269	0.025	0.245	0.051	-0.094	-0.075	0.154	0.038	-0.197	0.087	0.116	-0.076	-0.016	-0.087	-0.100	-0.045	0.003	-0.108	-0.180	-0.161	-0.061	0.072	-0.004	-0.061	0.225	0.131				
TCRA	-0.155	0.332	0.207	0.101	--	0.050	0.262	0.013	0.314	0.080	0.285	0.198	0.049	0.193	0.095	-0.006	0.115	0.343	0.252	0.189	0.102	0.049	0.140	-0.085	0.012	-0.120	-0.048	-0.085	0.042	-0.048	0.019	-0.069	0.157			

Notes:

- (1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.
- (2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates
- (3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 19
Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 7 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA				
RP																																						
NTB	0.079																																					
NAB	0.193	0.278																																				
DNAB	0.050	0.342	0.428																																			
CHRB	0.083	-0.095	0.000	-0.104																																		
TCFA	0.112	0.344	0.259	0.196	0.027																																	
RNAB	0.075	0.246	0.115	0.397	0.035	0.326																																
CATA	0.041	0.338	0.404	0.282	0.097	0.258	0.347																															
NUA	0.152	0.092	0.256	-0.003	0.195	-0.049	0.116	0.175																														
TPA	0.112	0.085	0.241	0.094	0.088	0.165	0.299	0.251	0.104																													
PB	0.280	0.349	0.204	0.389	--	0.366	0.326	0.427	0.014	0.200																												
CW	-0.016	0.145	0.284	0.474	0.035	0.335	0.230	0.260	0.080	0.182	0.296																											
NUS	0.147	0.364	0.457	0.336	0.092	0.226	0.389	0.368	0.110	0.156	0.485	0.325																										
PM	-0.117	-0.030	-0.173	0.120	-0.011	0.060	-0.027	0.091	-0.017	0.208	0.137	0.139	0.032																									
ET	0.014	0.185	0.311	0.030	0.057	-0.075	0.096	0.174	0.201	0.181	0.167	0.106	0.082	0.054																								
TC	0.047	0.280	0.365	0.218	0.061	-0.076	0.311	0.360	0.030	0.169	0.313	0.353	0.111	0.012	-0.045																							
TL	-0.016	0.082	0.089	0.275	0.006	0.150	0.045	0.333	0.129	0.180	0.158	0.233	0.160	0.099	0.179	0.172																						
PMP	0.094	0.326	0.280	0.291	-0.033	0.277	0.299	0.359	0.111	0.226	0.133	0.118	0.215	0.118	0.097	0.243	0.253																					
RTS	0.131	0.180	0.158	0.206	0.063	0.168	0.186	0.294	0.067	0.081	0.211	0.243	0.268	0.100	-0.088	0.297	0.150	0.140																				
CC	-0.028	0.097	0.045	0.224	-0.056	0.083	0.215	0.049	-0.118	0.206	0.185	0.062	0.067	0.110	0.135	0.023	0.049	0.180	0.094																			
ST	-0.006	0.236	0.135	0.289	-0.065	0.231	0.162	0.264	-0.007	0.408	0.519	0.066	0.124	0.167	0.152	0.292	0.303	0.057	0.109	0.170																		
MOD	-0.130	0.134	0.121	0.281	-0.151	0.051	0.173	0.214	-0.051	0.055	0.211	0.205	0.220	0.174	0.088	0.026	0.149	0.050	0.046	0.134	0.124																	
MT	0.164	0.252	0.219	0.128	0.080	-0.083	0.173	-0.004	0.213	0.197	0.263	0.105	0.247	0.150	0.105	0.000	-0.017	0.126	0.061	0.209	0.001	0.024																
CD	-0.081	0.176	0.017	0.042	-0.078	0.019	0.064	0.053	0.006	0.146	0.220	0.025	0.181	0.081	0.099	-0.062	-0.022	0.128	0.161	0.232	0.118	-0.070	0.080															
CP	0.202	0.288	0.179	0.310	-0.021	0.194	0.331	0.229	0.043	0.245	0.380	0.201	0.281	0.102	-0.054	0.289	0.095	0.225	0.205	0.089	0.274	-0.059	0.379	0.121														
BP	0.111	-0.006	0.096	0.198	-0.046	-0.090	0.138	0.189	-0.026	0.028	0.139	0.046	0.192	-0.242	-0.082	0.126	0.028	-0.077	0.091	0.004	-0.077	0.132	-0.148	0.142	0.040													
ED	--	-0.154	-0.131	-0.247	0.397	-0.009	-0.039	-0.243	0.138	0.040	0.004	-0.117	-0.080	-0.085	-0.132	-0.063	0.063	-0.084	0.141	-0.069	-0.053	-0.020	0.026	-0.096	-0.077	-0.222												
PED	0.234	0.066	0.272	0.013	-0.067	0.114	0.258	0.072	0.166	0.266	0.118	0.134	0.166	-0.040	-0.129	0.136	-0.099	0.119	0.002	-0.109	0.056	0.080	0.311	-0.017	0.442	0.220	-0.083											
FD	-0.013	0.341	0.357	0.319	-0.021	0.211	0.364	0.089	0.062	0.327	0.382	0.304	0.371	0.187	0.263	0.238	0.161	0.166	0.228	0.259	0.055	0.139	0.053	0.131	0.317	-0.092	-0.193	0.085										
PS	0.021	0.042	-0.105	0.159	-0.050	0.035	0.149	0.119	-0.104	0.256	0.159	0.212	0.263	0.235	-0.134	0.030	0.098	0.130	0.162	0.165	0.133	0.073	0.053	0.077	0.199	0.184	-0.061	0.101	0.032									
CCOB	0.262	0.107	0.325	0.382	0.025	0.212	0.304	0.478	0.013	0.120	0.107	0.247	0.335	-0.078	0.072	0.301	0.215	0.169	0.445	0.103	0.154	0.157	0.084	0.289	0.251	0.235	-0.056	-0.025	0.304	0.344								
CG	-0.021	0.139	0.173	0.181	-0.067	0.140	0.066	0.211	0.020	-0.122	0.063	0.164	0.159	-0.142	-0.152	0.211	-0.005	0.097	0.229	-0.109	0.105	0.240	0.046	-0.012	0.138	0.220	-0.083	0.355	0.228	0.107	0.137							
CDI	0.094	-0.107	0.250	0.153	-0.012	0.178	0.109	0.112	0.061	0.285	-0.102	0.027	0.320	0.131	0.219	0.223	0.268	0.007	0.099	0.131	-0.085	0.113	0.126	0.059	0.115	-0.121	0.046	0.102	0.107	0.030	0.151	0.057						
TCRA	0.046	0.363	0.323	0.141	-0.161	0.300	0.256	0.361	0.013	0.045	0.197	0.355	0.253	0.071	-0.029	0.195	0.149	0.342	0.345	0.162	0.308	0.127	0.301	0.034	0.322	0.019	-0.198	0.153	0.177	-0.075	0.195	0.135	0.028					

Notes:

- (1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHR: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.
- (2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene categories. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates
- (3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 20
Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 8 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA						
RP																																								
NTB	-0.044																																							
NAB	0.269	0.035																																						
DNAB	-0.021	0.145	0.181																																					
CHRB	0.052	-0.248	0.000	0.247																																				
TCFA	-0.006	0.152	0.206	0.158	0.150																																			
RNAB	0.206	0.024	-0.035	0.024	-0.161	0.196																																		
CATA	0.298	0.263	0.454	0.420	0.123	0.636	0.351																																	
NUA	0.161	0.058	0.015	0.316	0.192	0.383	0.113	0.270																																
TPA	0.024	0.023	0.403	0.369	-0.006	0.389	0.299	0.383	0.095																															
PB	-0.012	0.070	0.147	0.270	--	0.358	0.355	0.380	0.252	0.122																														
CW	-0.040	0.064	0.136	0.091	0.032	0.202	0.176	0.360	0.170	0.250	0.236																													
NUS	0.117	0.190	0.059	0.035	0.047	0.314	0.126	0.473	0.233	0.286	0.329	0.166																												
PM	-0.357	-0.181	-0.091	-0.077	-0.171	0.071	0.047	0.064	0.122	-0.109	-0.052	-0.102	-0.077																											
ET	0.126	0.109	0.162	0.340	0.189	0.460	0.170	0.286	0.088	0.327	0.113	0.221	0.337	0.127																										
TC	0.018	0.230	0.171	0.111	0.209	0.036	0.220	0.548	0.392	0.492	0.368	0.297	0.348	0.134	0.500																									
TL	0.003	0.116	0.117	-0.042	-0.168	-0.089	0.385	0.101	0.242	0.299	0.192	0.200	0.034	-0.029	0.037	-0.023																								
PMP	0.042	0.208	0.076	0.138	-0.089	0.260	0.134	0.308	0.269	-0.033	0.121	-0.009	0.055	0.086	0.128	0.311	0.073																							
RTS	0.018	0.070	0.293	0.247	-0.009	0.345	0.300	0.420	0.170	0.161	0.341	0.082	0.361	-0.015	0.186	0.350	0.118	0.213																						
CC	0.205	0.099	-0.005	0.177	-0.052	0.307	-0.059	0.120	0.080	-0.062	0.069	-0.175	0.151	0.010	-0.029	0.175	-0.242	0.090	0.120																					
ST	-0.126	0.178	0.302	-0.018	-0.053	0.202	0.274	0.305	0.167	0.163	0.373	0.209	0.212	-0.019	0.126	0.236	0.132	0.236	0.331	0.095																				
MOD	0.021	0.025	0.008	0.051	0.022	0.160	0.289	0.357	0.332	0.215	0.309	0.231	0.201	0.019	0.153	0.052	0.252	0.212	0.399	-0.013	0.243																			
MT	0.143	0.131	0.313	0.372	0.226	0.441	0.313	0.226	0.010	0.377	0.372	0.246	0.226	-0.045	0.307	0.430	0.156	0.078	0.224	0.256	0.314	0.327																		
CD	-0.149	0.183	0.165	0.230	0.139	0.235	0.202	0.284	0.210	0.028	0.285	0.110	0.190	-0.172	0.169	0.233	0.009	0.160	0.110	0.195	0.287	0.201	0.177																	
CP	0.106	-0.018	0.108	0.024	-0.161	0.118	0.276	0.138	0.049	0.093	0.252	0.018	0.185	0.073	0.001	0.103	-0.104	0.004	0.190	0.252	0.152	0.027	0.021	0.043																
BP	0.219	0.238	0.326	0.313	0.003	0.313	0.258	0.023	0.218	0.027	0.185	0.117	0.394	0.192	0.008	0.317	-0.122	0.192	0.277	0.021	0.075	0.140	0.137	0.114	0.160															
ED	--	-0.003	0.010	0.126	-0.045	0.039	-0.024	-0.056	-0.095	-0.017	-0.138	0.015	0.048	-0.094	-0.013	-0.019	-0.003	-0.034	-0.186	-0.065	-0.200	-0.204	-0.088	-0.115	-0.011	0.032														
PED	0.116	0.294	0.401	-0.137	-0.088	0.073	0.470	0.118	0.060	0.207	0.177	0.162	0.161	0.076	0.184	0.082	0.158	0.271	0.196	0.069	0.361	-0.118	0.123	0.112	0.066	0.132	0.087													
FD	-0.072	0.077	0.166	0.008	0.086	-0.085	0.217	0.169	0.132	0.078	0.226	0.035	-0.102	-0.113	0.031	-0.061	0.020	0.056	0.029	0.036	-0.051	0.147	0.286	-0.032	0.057	0.130	0.014	0.130												
PS	0.203	0.175	0.055	-0.012	-0.045	-0.089	0.152	0.006	0.159	-0.059	0.294	-0.172	0.150	0.005	-0.125	-0.075	0.247	0.063	0.132	-0.065	0.140	-0.016	-0.154	0.115	0.123	0.009	-0.056	0.087	0.014											
CCOB	0.049	0.099	0.352	0.226	0.037	0.278	0.227	0.413	0.148	0.255	0.226	0.215	0.214	-0.111	0.309	0.380	-0.007	0.026	0.111	-0.071	0.168	0.247	0.327	0.141	0.138	0.111	-0.091	0.224	0.216	0.242										
CG	-0.063	0.025	0.086	0.242	0.321	0.173	-0.125	0.040	-0.111	0.218	0.158	0.319	0.076	0.007	0.194	0.197	-0.128	0.049	0.097	-0.075	0.133	0.204	0.205	-0.134	-0.231	-0.043	-0.065	-0.126	0.111	-0.065	0.053									
CDI	0.115	0.057	0.082	-0.023	-0.184	0.060	0.097	0.113	0.157	0.061	-0.074	-0.047	0.055	0.080	0.075	0.144	0.130	0.089	0.124	0.011	0.134	0.133	0.028	0.256	-0.030	-0.028	-0.102	0.175	-0.013	0.094	0.184	0.144								
TCRA	-0.209	0.034	-0.033	0.028	0.017	0.095	0.163	0.252	0.203	0.381	0.359	0.133	0.082	0.222	0.349	0.142	0.140	0.026	-0.050	0.020	0.114	-0.037	0.194	0.121	-0.054	0.083	-0.182	-0.090	0.015	-0.047	0.245	0.087	0.065							

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison.

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 21

Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 9 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA				
RP																																						
NTB	-0.052																																					
NAB	0.026	0.182																																				
DNAB	0.022	0.192	0.520																																			
CHRB	-0.104	0.027	0.162	0.189																																		
TCFA	-0.209	0.178	0.196	0.156	0.105																																	
RNAB	-0.003	-0.005	-0.016	0.236	-0.142	0.208																																
CATA	0.167	0.143	0.101	0.335	0.170	0.186	0.223																															
NUA	0.328	-0.257	-0.248	-0.028	-0.051	-0.005	-0.017	0.029																														
TPA	-0.104	0.539	-0.028	0.189	0.217	0.252	0.039	0.296	-0.116																													
PB	-0.026	0.283	-0.033	0.093	--	0.191	0.006	0.214	-0.039	0.594																												
CW	0.313	0.058	0.140	0.321	0.049	0.273	0.071	0.447	0.125	0.352	0.158																											
NUS	-0.061	0.080	0.308	0.308	0.131	0.515	0.292	0.384	0.130	0.440	0.129	0.228																										
PM	0.075	0.154	-0.040	0.002	0.023	0.010	0.032	0.204	0.040	0.472	0.267	0.005	0.047																									
ET	0.029	0.355	0.150	0.247	0.203	0.092	-0.122	0.300	-0.098	0.325	0.274	0.353	0.322	0.267																								
TC	-0.181	0.168	0.286	0.208	0.167	0.173	0.191	0.216	-0.045	0.235	0.106	0.346	0.531	0.077	0.165																							
TL	-0.150	0.023	0.099	0.167	-0.100	0.158	0.160	0.328	-0.085	0.051	0.196	0.244	0.192	0.024	0.203	0.103																						
PMP	0.031	0.306	0.158	0.035	0.039	0.018	-0.042	0.242	-0.162	0.430	0.139	0.091	-0.010	0.024	0.317	-0.011	0.086																					
RTS	0.077	0.376	0.429	0.495	0.072	0.183	0.123	0.527	-0.145	0.236	0.272	0.584	0.301	0.309	0.523	0.255	0.280	0.256																				
CC	0.182	-0.036	-0.050	0.162	-0.062	-0.034	0.268	0.146	0.238	0.126	0.097	0.051	-0.048	0.044	0.136	-0.049	0.110	-0.110	0.210																			
ST	0.031	0.227	0.176	0.138	0.209	0.014	-0.134	0.291	-0.077	0.436	0.158	0.160	0.100	0.033	0.332	0.080	0.185	-0.028	0.357	-0.084																		
MOD	-0.020	0.420	0.265	0.321	0.151	0.100	0.110	0.602	-0.074	0.279	0.322	0.577	0.396	0.320	0.217	0.188	0.352	0.190	0.264	-0.066	0.496																	
MT	0.031	0.477	0.103	0.270	0.163	0.270	-0.125	0.167	-0.038	0.334	0.460	0.560	0.340	0.313	0.345	0.291	0.393	0.371	0.525	-0.045	0.584	0.524																
CD	-0.143	-0.243	0.053	0.127	-0.067	-0.041	-0.047	0.160	0.384	-0.281	-0.152	0.218	-0.038	-0.130	0.029	0.028	0.063	-0.342	0.042	0.108	-0.111	0.142	0.049															
CP	0.066	0.263	-0.013	0.271	0.234	0.318	0.293	0.337	0.057	0.375	0.285	0.267	0.377	0.117	0.181	0.186	0.177	0.246	0.217	0.110	0.190	0.122	0.321	-0.077														
BP	-0.004	0.418	0.175	0.328	0.172	0.081	0.002	0.232	-0.238	0.372	0.310	0.539	0.326	0.175	0.209	0.177	0.359	0.303	0.485	-0.006	0.380	0.571	0.433	0.029	0.163													
ED	--	0.279	0.038	0.134	-0.038	0.160	0.157	0.120	-0.090	0.187	0.230	0.260	0.207	0.269	0.296	0.138	0.083	0.281	0.283	0.369	0.292	0.096	0.248	-0.118	0.273	0.175												
PED	0.005	0.244	0.177	0.019	0.413	0.004	-0.121	-0.082	-0.132	-0.012	0.217	0.143	-0.002	0.270	0.021	0.043	-0.135	0.254	-0.036	-0.159	-0.004	-0.194	-0.121	-0.172	0.003	-0.044	0.150											
FD	0.183	-0.190	-0.015	0.180	-0.105	0.134	0.175	0.028	0.265	-0.004	0.033	0.260	0.101	-0.104	-0.162	0.024	0.012	-0.192	0.043	0.095	-0.096	0.022	-0.003	-0.135	0.072	-0.029	-0.186	-0.150										
PS	-0.027	0.145	-0.206	-0.046	-0.045	-0.146	-0.104	0.110	0.158	0.150	0.239	0.099	0.020	0.194	0.145	-0.121	-0.052	-0.040	0.014	0.082	0.134	0.159	-0.053	0.056	0.109	0.170	-0.080	-0.116	-0.064									
CCOB	0.216	0.148	0.339	0.585	0.240	0.551	0.195	0.464	-0.064	-0.078	0.206	0.356	0.609	0.033	0.261	0.616	0.068	0.114	0.461	0.037	0.342	0.382	0.284	0.200	0.401	0.265	0.132	0.188	0.334	-0.073								
CG	-0.074	0.208	0.143	0.037	0.472	0.162	-0.050	0.120	-0.105	--	0.179	0.072	0.066	0.148	0.204	0.147	0.097	0.100	0.134	0.077	0.096	0.158	0.240	-0.138	0.221	0.177	0.225	0.121	-0.217	-0.093	0.009							
CDI	0.041	0.329	0.159	0.200	0.109	0.089	0.133	0.115	-0.145	0.216	0.118	0.162	0.044	-0.017	0.017	0.046	0.181	0.259	0.235	-0.024	0.161	0.281	0.285	-0.078	0.203	0.422	0.275	0.168	0.018	-0.069	0.201	-0.024						
TCRA	0.067	0.063	0.281	0.283	0.155	0.114	0.144	0.258	0.080	0.188	0.137	0.312	0.362	0.064	0.316	0.221	0.222	-0.037	0.070	-0.037	0.153	0.259	0.176	0.205	0.081	0.293	0.019	0.134	0.187	0.054	0.496	-0.083	0.077					

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHR: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 22

Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 10 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA	
RP																																			
NTB	-0.126																																		
NAB	0.170	0.008																																	
DNAB	0.115	0.032	0.033																																
CHRB	--	--	--	--																															
TCFA	-0.046	0.063	-0.049	0.104	--																														
RNAB	0.130	0.089	0.109	-0.080	--	-0.047																													
CATA	0.217	0.144	0.386	0.437	--	0.426	0.279																												
NUA	0.030	-0.303	0.033	-0.020	--	0.039	-0.006	-0.162																											
TPA	-0.248	0.014	0.094	0.117	--	0.155	0.061	0.496	-0.037																										
PB	0.297	0.206	0.148	0.201	--	0.077	0.255	0.097	0.208	0.126																									
CW	0.034	0.158	0.190	0.245	--	0.132	0.170	0.316	-0.253	0.017	0.439																								
NUS	0.121	0.188	0.052	0.434	--	0.252	0.061	0.312	-0.148	0.131	0.309	0.335																							
PM	-0.070	-0.030	-0.121	0.117	--	0.029	-0.045	0.154	-0.314	0.060	0.243	0.100	-0.032																						
ET	-0.029	-0.055	-0.098	0.055	--	0.109	0.112	0.186	-0.096	0.304	0.031	0.016	-0.001	-0.064																					
TC	0.082	0.115	-0.092	0.200	--	0.158	-0.064	0.535	-0.120	0.131	0.188	0.272	0.328	0.235	0.113																				
TL	0.202	-0.065	-0.007	0.254	--	0.206	-0.230	0.266	-0.108	-0.134	-0.074	0.013	0.069	0.144	0.080	0.393																			
PMP	-0.075	0.032	0.086	-0.020	--	-0.018	-0.020	0.081	-0.156	0.098	-0.014	0.147	0.155	0.176	-0.077	0.035	-0.127																		
RTS	-0.051	0.421	0.211	0.078	--	0.106	0.340	0.237	-0.164	0.139	0.263	0.423	0.517	0.206	0.006	0.140	-0.056	0.262																	
CC	-0.049	0.007	0.422	-0.009	--	-0.080	0.225	0.187	0.374	0.281	0.100	0.103	0.149	-0.051	0.021	0.003	0.074	0.046	0.335																
ST	0.030	0.029	0.007	-0.008	--	0.042	0.095	0.278	-0.258	0.116	0.153	0.165	0.081	-0.044	0.194	0.172	0.059	-0.030	0.260	0.135															
MOD	0.156	0.242	0.264	0.339	--	0.438	0.113	0.328	-0.120	0.252	0.243	0.395	0.528	0.207	0.083	0.495	0.186	0.347	0.290	0.269	0.187														
MT	-0.172	0.139	0.322	0.259	--	0.368	0.033	-0.232	-0.093	0.296	0.070	0.146	0.289	-0.047	0.016	0.204	-0.105	0.039	-0.002	0.022	0.178	0.125													
CD	-0.161	-0.200	-0.044	0.095	--	0.113	-0.154	0.011	0.034	-0.077	0.037	-0.087	0.063	-0.181	-0.108	-0.007	-0.005	0.012	0.083	0.037	-0.087	0.156	0.128												
CP	0.001	0.090	0.334	0.181	--	0.390	0.172	0.045	0.055	0.226	-0.012	0.256	0.271	-0.051	0.135	0.272	0.054	0.189	0.201	0.195	0.269	0.431	0.286	0.183											
BP	0.028	-0.041	0.072	0.165	--	0.372	-0.023	-0.118	-0.057	0.263	-0.045	0.006	0.109	-0.128	0.373	0.334	0.268	-0.017	-0.133	0.143	0.126	0.103	0.030	0.087	0.282										
ED	--	-0.036	0.158	-0.014	--	-0.024	-0.016	0.012	0.117	0.003	0.191	0.080	-0.003	0.082	0.119	0.091	-0.083	-0.034	-0.007	0.159	0.091	0.000	-0.204	-0.102	0.140	0.226									
PED	0.036	-0.074	0.290	0.149	--	0.165	-0.191	0.190	0.138	0.047	-0.001	0.157	0.316	-0.073	0.109	0.249	0.259	0.081	0.097	0.210	0.064	0.051	0.197	0.194	0.204	0.111	0.122								
FD	0.093	0.013	0.226	-0.132	--	-0.065	0.195	0.241	-0.166	-0.071	0.299	0.266	0.169	-0.032	0.055	-0.149	-0.037	0.020	0.331	-0.173	0.188	0.183	0.285	0.084	0.147	0.089	-0.153	0.101							
PS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
CCOB	-0.084	0.078	0.159	0.124	--	0.115	0.021	0.263	0.041	0.062	0.173	0.051	0.248	0.014	0.068	0.256	0.007	-0.042	0.309	0.168	0.074	0.241	0.146	-0.026	0.146	0.150	0.194	0.389	0.201	--					
CG	-0.010	0.008	0.424	0.358	--	0.360	0.063	0.399	0.038	0.240	0.012	-0.159	0.241	0.055	0.131	0.393	0.285	0.109	0.238	0.495	0.253	0.368	0.282	0.099	0.303	0.339	0.196	0.280	-0.132	--	0.061				
CDI	0.160	0.089	0.141	-0.118	--	0.059	0.217	0.134	0.096	-0.035	0.037	-0.121	0.240	-0.098	0.048	-0.067	-0.072	0.245	0.326	0.039	0.130	0.148	0.100	-0.149	0.009	0.053	-0.007	-0.057	-0.068	--	0.281	-0.130			
TCRA	0.217	0.250	0.031	0.212	--	0.083	0.138	0.263	-0.112	0.091	0.086	0.253	0.205	-0.008	0.031	0.067	0.044	0.010	0.319	0.108	0.185	0.171	-0.018	-0.215	-0.001	0.137	0.045	-0.042	0.134	--	0.148	0.176	0.186		

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 23

Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 11 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA		
RP																																				
NTB	0.063																																			
NAB	0.261	0.030																																		
DNAB	0.146	0.057	0.222																																	
CHRB	-0.072	0.074	0.106	0.140																																
TCFA	0.389	0.168	0.107	0.122	0.078																															
RNAB	0.113	0.146	0.284	0.290	-0.117	0.153																														
CATA	0.218	0.017	0.397	0.260	0.033	0.280	0.333																													
NUA	0.082	0.023	0.086	0.239	-0.061	-0.007	0.165	0.036																												
TPA	0.031	-0.005	0.204	0.179	0.115	0.015	0.159	0.372	-0.026																											
PB	0.090	0.262	-0.014	0.041	--	0.034	0.105	0.040	0.018	0.066																										
CW	0.190	0.214	0.033	0.108	-0.008	0.224	0.227	-0.094	0.028	-0.068	0.147																									
NUS	0.166	0.118	0.287	0.025	0.012	0.123	0.279	0.291	0.072	0.175	0.145	0.100																								
PM	0.188	-0.034	0.024	0.151	0.141	0.185	0.028	0.029	0.097	-0.061	0.062	0.285	0.089																							
ET	0.052	-0.167	0.151	-0.004	-0.082	0.030	0.117	-0.039	-0.174	0.222	-0.264	-0.259	0.067	-0.211																						
TC	0.289	0.147	0.187	0.223	0.026	0.146	0.260	0.301	0.024	0.125	0.108	0.273	-0.091	0.100	0.044																					
TL	0.030	0.115	0.074	0.302	0.172	0.267	0.144	0.288	0.136	0.297	0.090	-0.053	0.255	-0.034	0.064	0.347																				
PMP	0.203	-0.044	-0.128	0.022	0.021	0.166	0.006	-0.033	0.018	0.044	0.224	0.142	0.049	0.162	-0.197	0.150	0.088																			
RTS	0.047	-0.315	0.052	0.194	-0.166	0.144	0.265	0.312	0.222	-0.014	-0.194	-0.092	-0.075	-0.221	0.153	0.308	0.169	-0.320																		
CC	0.314	-0.044	-0.024	0.255	-0.050	0.236	0.261	0.178	-0.012	-0.032	-0.065	0.169	0.048	-0.015	0.033	0.349	0.133	-0.071	0.262																	
ST	-0.021	-0.079	0.141	0.020	-0.053	-0.025	0.137	0.149	-0.016	0.069	0.130	0.254	-0.029	0.100	-0.047	0.021	-0.043	0.018	-0.198	-0.056																
MOD	0.141	-0.167	0.078	0.255	-0.092	-0.072	0.192	0.080	0.013	0.275	-0.039	0.023	0.047	-0.039	0.123	0.015	0.058	-0.066	0.129	0.208	-0.001															
MT	0.340	-0.214	0.141	0.087	-0.172	0.229	0.100	-0.061	-0.144	0.202	-0.088	-0.131	-0.118	0.009	0.175	0.153	0.047	-0.138	0.027	0.012	0.028	0.042														
CD	0.047	0.139	0.199	-0.069	-0.058	0.146	0.168	0.221	0.279	-0.053	0.212	0.342	0.189	0.307	-0.074	0.031	-0.067	0.217	0.055	0.126	0.194	0.271	0.149													
CP	0.023	-0.125	0.227	0.211	0.246	-0.100	0.167	-0.176	-0.026	0.028	-0.199	-0.182	-0.151	-0.055	0.128	0.162	0.080	-0.191	0.121	0.027	-0.091	0.073	-0.231	-0.104												
BP	0.067	-0.084	0.143	-0.129	-0.162	-0.113	0.113	-0.165	0.174	0.124	-0.031	-0.077	0.002	-0.160	-0.070	-0.041	-0.161	-0.075	0.135	-0.158	0.075	-0.066	0.153	0.150	-0.178											
ED	--	0.135	0.106	0.039	-0.018	0.219	0.076	0.119	-0.061	-0.141	0.220	-0.008	0.156	0.201	-0.082	-0.129	-0.086	0.136	-0.166	-0.050	0.082	-0.092	0.164	-0.058	-0.109	-0.162										
PED	-0.103	-0.205	0.000	0.072	-0.025	-0.079	-0.029	--	0.153	0.164	0.160	-0.009	-0.135	0.000	-0.117	-0.022	0.061	-0.260	--	-0.071	--	--	--	0.174	--	--	-0.025									
FD	-0.001	-0.076	-0.007	-0.020	-0.117	-0.226	0.107	-0.099	0.239	0.013	0.011	0.211	0.028	0.213	-0.176	-0.065	-0.227	-0.048	-0.303	-0.079	-0.032	0.084	-0.099	0.217	-0.159	0.116	-0.117	0.128								
PS	-0.072	-0.103	-0.106	0.140	-0.018	0.078	-0.117	-0.136	-0.061	-0.141	0.000	-0.103	-0.053	0.030	-0.082	0.099	-0.086	0.021	0.095	-0.050	-0.053	0.141	-0.025	-0.058	-0.109	-0.162	-0.018	-0.025	-0.117							
CCOB	0.268	0.147	0.092	0.156	-0.120	0.151	0.143	0.391	-0.061	0.212	0.308	0.057	0.272	0.208	0.059	0.313	0.171	0.196	-0.089	0.087	0.262	0.384	0.183	0.371	-0.189	0.061	0.182	0.187	0.250	-0.120						
CG	-0.072	--	0.106	0.140	1.000	0.078	-0.117	0.033	-0.061	--	--	-0.008	0.012	0.141	-0.082	0.026	0.172	0.021	-0.166	-0.050	-0.053	-0.092	-0.172	-0.058	0.246	-0.162	-0.018	-0.025	-0.117	-0.018	-0.120					
CDI	0.015	-0.089	-0.033	-0.070	-0.109	-0.086	0.058	-0.208	0.236	0.066	0.061	0.051	0.127	0.161	-0.252	-0.025	-0.077	0.214	-0.203	-0.225	-0.004	-0.075	-0.134	0.082	-0.302	0.204	-0.109	-0.156	-0.028	0.091	0.092	-0.109				
TCRA	0.220	0.169	0.092	0.210	-0.072	0.067	0.112	0.170	-0.131	0.162	0.195	-0.032	0.182	0.057	0.319	0.210	0.180	0.243	-0.035	0.187	0.200	0.106	0.235	0.029	0.102	-0.022	-0.072	-0.103	0.028	0.228	0.372	-0.072	0.076			

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "-" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 24

Spearman's correlation coefficients of distribution between genes categorized into different function categories in rice chromosome 12 with 500-kb window

	RP	NTB	NAB	DNAB	CHRB	TCFA	RNAB	CATA	NUA	TPA	PB	CW	NUS	PM	ET	TC	TL	PMP	RTS	CC	ST	MOD	MT	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCRA		
RP																																				
NTB	0.094																																			
NAB	0.306	0.255																																		
DNAB	0.049	0.216	0.118																																	
CHRB	-0.082	-0.213	-0.116	-0.151																																
TCFA	0.043	0.353	0.266	0.110	-0.158																															
RNAB	0.315	0.224	0.036	0.191	-0.108	0.304																														
CATA	0.066	0.171	0.118	0.197	0.009	0.161	0.133																													
NUA	0.042	0.052	0.104	0.166	-0.048	-0.057	0.254	0.113																												
TPA	0.233	0.127	0.421	0.478	-0.151	0.556	0.192	0.287	0.103																											
PB	0.106	0.355	0.344	0.307	--	0.484	0.278	0.199	-0.012	0.348																										
CW	0.181	0.084	0.304	0.297	-0.179	0.299	0.283	0.084	0.106	0.297	0.070																									
NUS	0.091	0.099	0.265	0.133	-0.134	0.248	0.274	0.285	0.119	0.534	0.203	0.078																								
PM	-0.027	0.032	0.050	0.295	-0.118	0.541	0.146	0.087	0.036	0.150	0.228	0.110	0.179																							
ET	0.087	-0.219	-0.059	0.086	0.225	-0.080	-0.207	0.064	0.008	0.089	-0.047	-0.193	0.020	-0.228																						
TC	0.083	0.390	0.254	0.152	-0.147	0.046	0.351	0.293	0.148	0.634	0.575	0.439	0.226	0.543	-0.028																					
TL	0.227	0.225	0.238	0.270	-0.123	0.249	0.419	0.223	0.164	0.176	0.307	0.091	0.241	0.113	-0.005	0.300																				
PMP	0.069	0.189	0.214	0.185	-0.179	0.312	0.288	0.225	0.046	0.182	0.416	0.090	-0.160	0.158	-0.156	0.416	0.102																			
RTS	0.200	0.316	0.330	0.165	-0.170	0.222	0.230	0.205	-0.033	0.273	0.396	0.352	0.179	0.169	0.005	0.457	-0.009	0.356																		
CC	0.062	-0.078	0.141	0.042	-0.056	0.053	-0.060	-0.235	0.015	-0.146	0.057	0.002	-0.106	-0.084	-0.098	0.103	0.011	0.003	-0.079																	
ST	-0.114	0.090	0.350	0.203	-0.196	0.384	0.318	0.226	-0.015	0.344	0.427	0.258	0.132	0.092	-0.154	0.447	0.248	0.146	0.395	-0.002																
MOD	0.143	0.154	0.155	0.028	0.183	0.020	0.083	0.054	-0.097	0.253	0.157	0.137	0.283	0.156	-0.166	0.041	0.049	0.267	0.117	-0.159	0.046															
MT	0.134	0.253	0.236	0.080	-0.186	0.176	0.142	0.112	0.065	0.322	0.300	0.355	0.160	0.165	0.063	0.293	0.041	0.414	0.328	-0.188	0.306	0.151														
CD	--	0.101	0.189	--	-0.052	--	0.392	0.040	0.050	0.327	0.118	0.214	--	0.066	0.016	--	0.209	0.032	--	-0.157	--	0.022	0.179													
CP	-0.022	0.292	0.116	0.156	-0.101	0.190	0.127	0.202	0.012	0.110	0.219	0.163	0.173	0.214	-0.112	0.129	0.290	0.095	0.177	-0.115	0.215	0.143	0.075	-0.075												
BP	0.427	0.089	0.314	0.317	0.027	0.334	0.173	0.290	0.033	0.441	0.274	-0.001	0.475	0.152	0.016	0.378	0.099	0.096	0.150	-0.071	0.070	0.076	0.114	0.269	-0.045											
ED	--	0.095	0.003	-0.006	-0.026	-0.082	-0.154	0.169	-0.068	0.035	-0.216	0.034	0.133	-0.028	0.084	-0.054	-0.119	-0.171	-0.093	-0.080	-0.279	0.189	0.038	-0.074	0.097	0.254										
PED	0.236	0.074	-0.063	0.062	-0.033	0.134	-0.049	-0.027	-0.084	0.116	-0.016	0.349	--	0.222	-0.190	0.108	-0.010	0.039	-0.016	0.120	0.015	0.219	0.011	0.175	0.056	-0.048	0.389									
FD	0.191	0.005	0.366	-0.155	-0.097	-0.224	0.346	-0.089	0.197	0.108	-0.035	0.154	-0.191	-0.044	-0.099	-0.019	0.121	-0.038	0.225	-0.010	-0.161	-0.204	0.157	-0.079	-0.053	0.002	-0.138	0.028								
PS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
CCOB	0.086	0.219	0.217	0.203	-0.141	0.278	0.226	0.265	0.098	0.385	0.412	0.288	0.263	0.165	-0.116	0.504	0.290	0.223	0.362	0.031	0.236	0.114	0.345	0.302	0.227	0.256	-0.201	0.086	0.097	--						
CG	0.016	-0.126	0.007	0.037	-0.033	0.238	-0.052	0.136	-0.084	-0.004	0.158	0.044	0.211	-0.121	-0.055	0.181	0.190	0.054	0.153	-0.099	0.151	0.054	0.131	0.140	0.119	0.043	-0.047	-0.058	-0.171	--	0.277					
CDI	0.204	0.016	0.297	0.182	-0.089	0.061	0.246	0.145	0.259	0.141	0.224	0.028	-0.048	-0.063	-0.039	0.234	0.246	0.174	0.224	0.016	0.181	0.012	0.300	0.106	0.134	0.008	-0.128	-0.007	0.398	--	0.230	-0.158				
TCRA	0.237	0.190	0.444	0.079	-0.071	0.098	0.241	0.119	0.236	0.400	0.259	0.149	0.314	0.339	0.076	0.252	0.167	0.192	0.316	0.153	0.283	-0.089	0.097	0.283	-0.010	0.304	-0.102	0.046	0.122	--	0.341	0.105	0.018			

Notes:

(1) RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: PCHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome or the whole genome after excluding the genes comparison. The signal "--" indicates

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 25
Spearman's correlation coefficients of distribution between the genes categorized into different function categories of the whole yeast genome with 60-kb windows

	TM	DNAB	TSFA	RNAB	PB	NUS	CPM	PM	rRNAP	TL	PAAP	RTS	RTDD	EGT	EDCT	CWOB	ST	RBA	RTD	PRT	
TM																					
DNAB	-0.052																				
TSFA	0.024	-0.020																			
RNAB	0.049	0.104	0.018																		
PB	-0.022	0.032	0.015	0.040																	
NUS	0.129	-0.014	-0.030	-0.023	-0.013																
CPM	0.108	-0.006	0.082	-0.034	0.055	-0.008															
PM	-0.059	-0.048	0.054	0.167	-0.060	0.045	-0.081														
rRNAP	0.206	0.034	0.032	0.003	-0.077	0.091	0.138	-0.003													
TL	0.187	-0.046	-0.035	0.076	0.008	0.182	0.164	-0.035	0.141												
PAAP	0.166	0.003	0.151	0.038	0.095	0.178	0.039	-0.013	0.040	0.046											
RTS	0.076	0.024	0.084	0.025	-0.011	-0.007	0.008	0.080	0.020	0.040	-0.036										
RTDD	-0.083	-0.067	0.174	0.060	0.040	0.046	-0.026	0.110	-0.001	-0.016	0.060	0.069									
EGT	0.044	-0.078	0.034	-0.039	-0.066	0.120	0.046	0.034	0.016	0.193	0.096	0.093	0.043								
EDCT	0.098	0.024	-0.060	0.096	0.014	-0.047	0.006	-0.061	-0.041	0.042	-0.007	0.049	-0.016	0.138							
CWOB	-0.040	0.026	-0.236	0.061	0.004	-0.108	0.019	0.001	0.016	0.177	-0.030	-0.071	-0.019	0.089	0.065						
ST	-0.072	0.115	-0.013	0.024	-0.119	0.111	-0.049	-0.028	-0.020	0.047	-0.093	-0.087	-0.066	0.001	-0.011	-0.028					
RBA	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
RTD	0.058	-0.027	0.135	-0.021	-0.005	-0.018	0.056	-0.012	-0.037	0.060	0.038	0.012	-0.037	0.153	0.037	0.027	0.071	--			
PRT	0.094	0.060	0.020	0.012	0.058	0.105	-0.063	-0.019	0.010	0.093	0.088	0.029	0.023	0.054	-0.030	-0.083	0.034	--	-0.013		

Notes:

(1) TM: telomere maintenance; DNAB: DNA binding; TSFA: Transcription factor activity; RNAB: RNA binding; PB: Protein binding; NUS: Nucleus; CPM: Cytoplasm; PM: Plasma membrane; rRNAP: rRNA processing; TL: Translation; PAAP: Protein amino acid phosphorylation; RTS: Response to stress; RTDD: Response to DNA damage stimulus; EGT: ER to Golgi vesicle-mediated transport; EDCT: Endocytosis; CWOB: Cell wall organization and biogenesis; ST: Signal transduction; RBA: Ribosome biogenesis and assembly; RTD: Response to drug; PRT: Positive regulation of transcription from RNA polymerase II promoter.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the gene category pair under comparison whereas the negative (-) values of correlation coefficients indicate the negative correlation between the gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the gene category pair had no genes along the chromosome after excluding the genes with both functions under comparison.

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 26
Spearman's correlation coefficients of distribution between fundamental function elements and genes with different functions in the whole rice genome with 500-kb windows

A.

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS
GC	0.013	-0.007	0.007	-0.019	0.026	-0.072	0.063	0.001	0.010	0.010	0.022	0.035	-0.009	0.035	0.047	-0.035	0.046
RTE	-0.431	-0.139	-0.621	-0.252	-0.311	-0.354	-0.397	-0.564	-0.463	-0.392	-0.281	-0.356	-0.316	-0.097	-0.245	-0.285	-0.129
DTE	0.209	0.032	0.339	0.183	0.190	0.139	0.171	0.303	0.263	0.176	0.186	0.224	0.233	0.044	0.114	0.202	0.035
SSR	0.311	0.112	0.517	0.196	0.241	0.295	0.282	0.474	0.355	0.337	0.201	0.287	0.228	0.064	0.243	0.230	0.089
LCR	0.286	0.109	0.384	0.198	0.247	0.208	0.248	0.398	0.282	0.247	0.193	0.303	0.266	0.090	0.174	0.213	0.061
GEN	0.462	0.150	0.582	0.299	0.298	0.361	0.460	0.566	0.505	0.382	0.242	0.394	0.367	0.123	0.232	0.270	0.151

B (continued)

	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	0.010	0.038	-0.033	-0.009	0.054	-0.036	0.027	0.050	0.026	0.062	-0.006	-0.042	-0.012	-0.035	0.038	0.038	0.038
RTE	-0.485	-0.107	-0.224	-0.575	-0.405	-0.441	-0.427	-0.388	-0.565	-0.141	-0.301	-0.519	-0.139	-0.444	-0.445	-0.237	-0.618
DTE	0.210	0.131	0.128	0.335	0.217	0.186	0.189	0.181	0.301	0.023	0.156	0.293	0.026	0.263	0.251	0.074	0.301
SSR	0.371	0.094	0.169	0.464	0.341	0.351	0.359	0.372	0.465	0.074	0.285	0.416	0.123	0.361	0.338	0.164	0.489
LCR	0.306	0.122	0.155	0.394	0.243	0.305	0.283	0.275	0.376	0.040	0.224	0.369	0.107	0.303	0.302	0.098	0.405
GEN	0.481	0.121	0.259	0.557	0.367	0.437	0.477	0.411	0.527	0.121	0.360	0.548	0.190	0.512	0.499	0.270	0.639

Notes:

(1) GC: GC content; RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeats; LCR: Low complex repeats; GEN: Gene; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; TCFA: Transcription factor activity; RNAB: RNA binding; CATA: catalytic activity; NUA: Nuclease activity; TPA: Transporter activity; PB: Protein binding; CW: Cell wall; NUS: Nucleus; PM: Plasma membrane; ET: Electron transport; TC: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MOD: Multicellular organismal development; MT: Metabolism; CD: Cell death; CP: Catabolic process; BP: Biosynthesis process; ED: Embryonic development; PED: Post-embryonic process; FD: Flower development; PS: Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the element/gene category pair under comparison whereas the negative (-) values of correlation coefficients indicate the negative correlation between the element/gene category pair under comparison.

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between element and gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 27**Spearman's correlation coefficients of distribution between the fundamental function elements and genes with different functions of rice individual chromosome with 500-kb windows***A. Rice chromosome 1*

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	0.110	0.075	0.082	0.138	0.073	-0.175	-0.012	-0.018	0.075	-0.033	0.039	0.059	0.016	-0.076	-0.132	-0.003	0.107	0.046	-0.062	-0.120	0.074	0.112	-0.032	-0.088	-0.107	-0.101	0.081	-0.033	0.020	-0.046	-0.014	-0.005	-0.086	0.095
RTE	-0.307	-0.047	-0.574	-0.190	-0.215	-0.340	-0.301	-0.382	-0.442	-0.125	-0.258	-0.250	-0.271	0.027	-0.174	-0.335	-0.034	-0.258	0.041	-0.278	-0.501	-0.386	-0.398	-0.385	-0.313	-0.532	-0.237	-0.113	-0.292	-0.274	-0.404	-0.288	-0.085	-0.474
DTE	0.056	0.012	0.242	0.142	0.210	0.265	0.232	0.307	0.291	0.097	0.118	0.235	0.131	0.183	0.150	0.245	-0.082	0.286	0.188	0.261	0.335	0.209	0.100	0.263	0.183	0.285	0.040	0.025	0.241	0.056	0.333	0.260	0.200	0.197
SSR	0.238	-0.013	0.493	0.103	0.074	0.239	0.339	0.347	0.353	0.213	0.095	0.233	0.107	0.027	0.193	0.211	-0.145	0.271	0.040	0.349	0.428	0.312	0.318	0.411	0.394	0.423	-0.078	0.098	0.184	0.279	0.314	0.235	0.179	0.412
LCR	0.160	0.155	0.298	0.044	0.038	0.232	0.210	0.274	0.169	0.165	0.025	0.324	0.169	0.041	0.292	0.055	-0.091	0.195	0.134	0.134	0.327	0.205	0.292	0.274	0.276	0.337	-0.053	0.094	0.276	0.162	0.267	0.209	0.010	0.319
GEN	0.455	0.060	0.521	0.189	0.195	0.359	0.433	0.371	0.535	0.156	0.112	0.214	0.201	-0.019	-0.009	0.314	0.197	0.274	0.082	0.384	0.483	0.337	0.345	0.551	0.330	0.504	0.178	0.226	0.306	0.232	0.535	0.516	0.231	0.514

B. Rice chromosome 2

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	0.058	0.077	0.083	0.051	0.085	-0.011	0.124	0.209	0.108	0.071	0.063	-0.038	0.029	-0.083	0.148	0.031	-0.016	0.013	-0.116	-0.113	-0.029	0.212	0.012	-0.012	0.164	0.083	0.158	-0.005	0.106	0.021	-0.048	0.024	0.005	0.091
RTE	-0.456	-0.138	-0.591	-0.213	-0.199	-0.302	-0.557	-0.490	-0.439	-0.236	-0.340	-0.369	-0.231	-0.117	-0.122	-0.267	-0.212	-0.432	0.018	-0.298	-0.577	-0.284	-0.351	-0.579	-0.254	-0.539	-0.167	-0.043	-0.346	0.175	-0.449	-0.505	-0.355	-0.677
DTE	0.185	-0.106	0.147	0.027	0.158	0.091	0.011	0.238	0.157	0.169	0.150	0.131	0.078	0.239	-0.008	0.088	0.064	0.091	0.127	-0.058	0.257	0.065	0.024	0.139	0.122	0.083	-0.029	0.080	0.209	-0.040	0.133	0.024	0.037	0.059
SSR	0.426	0.094	0.380	0.160	0.109	0.306	0.362	0.345	0.324	0.161	0.196	0.335	0.229	0.173	0.083	0.131	0.135	0.193	-0.044	0.177	0.451	0.282	0.117	0.382	0.295	0.233	0.096	0.378	-0.118	0.375	0.227	0.169	0.469	
LCR	0.199	-0.004	0.317	0.289	0.205	0.132	0.185	0.317	0.243	0.180	0.281	0.281	0.233	0.149	0.056	0.106	0.037	0.214	0.174	0.149	0.439	0.094	0.202	0.317	0.203	0.340	0.070	0.105	0.293	0.021	0.295	0.296	0.147	0.384
GEN	0.537	0.159	0.488	0.308	0.259	0.251	0.589	0.514	0.502	0.263	0.385	0.522	0.340	0.052	0.143	0.308	0.217	0.408	0.015	0.253	0.524	0.280	0.262	0.561	0.381	0.455	0.030	0.232	0.395	-0.088	0.444	0.504	0.300	0.703

C. Rice chromosome 3

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	0.166	-0.031	0.073	-0.029	-0.043	0.004	0.100	0.056	-0.074	0.117	0.043	0.072	0.135	0.079	0.210	0.019	0.185	0.015	-0.048	0.071	-0.009	0.087	-0.088	0.084	0.110	0.141	-0.052	0.000	0.132	0.155	0.066	0.038	0.003	0.019
RTE	-0.452	-0.117	-0.422	-0.170	-0.261	-0.283	-0.561	-0.540	-0.574	-0.346	-0.140	-0.342	-0.309	-0.154	-0.026	-0.245	-0.016	-0.460	0.096	-0.324	-0.482	-0.276	-0.404	-0.540	-0.139	-0.333	0.072	-0.239	-0.452	-0.238	-0.561	-0.422	-0.410	-0.629
DTE	-0.175	-0.058	0.108	0.072	-0.012	-0.122	-0.017	-0.016	-0.005	-0.308	0.114	-0.210	-0.155	-0.173	-0.143	-0.125	-0.179	-0.041	0.043	0.069	-0.002	-0.029	-0.107	-0.090	0.056	-0.021	-0.102	0.012	-0.069	-0.211	-0.045	0.044	-0.084	0.076
SSR	0.330	0.155	0.201	0.021	0.270	0.200	0.167	0.336	0.196	0.222	-0.093	0.106	0.120	0.106	-0.055	-0.069	-0.137	0.379	0.047	-0.038	0.217	0.219	0.249	0.344	0.194	0.306	-0.022	0.146	0.329	0.075	0.283	0.193	0.185	0.239
LCR	0.037	0.081	0.237	0.107	0.235	-0.014	0.187	0.128	0.073	0.061	0.124	0.058	-0.089	0.099	-0.145	0.145	-0.197	0.259	0.020	0.101	0.228	0.057	0.112	0.188	0.086	0.173	-0.110	0.188	0.075	-0.010	0.152	0.205	0.098	0.182
GEN	0.559	0.147	0.365	0.277	0.253	0.348	0.542	0.551	0.456	0.270	0.082	0.324	0.404	0.216	-0.063	0.244	0.032	0.506	0.025	0.247	0.441	0.198	0.460	0.531	0.308	0.293	0.016	0.491	0.634	0.370	0.634	0.549	0.338	0.600

D. Rice chromosome 4

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.175	0.153	0.027	-0.094	0.103	-0.349	0.068	0.130	-0.038	0.087	0.108	0.094	-0.071	-0.008	-0.042	-0.043	0.049	0.026	-0.002	-0.113	0.087	-0.019	0.093	0.023	0.095	0.030	0.060	0.038	-0.195	0.102	-0.022	0.120	0.160	0.104
RTE	-0.414	-0.163	-0.674	-0.332	-0.405	-0.424	-0.449	-0.744	-0.563	-0.594	-0.439	-0.440	-0.299	-0.123	-0.420	-0.457	-0.244	-0.634	-0.189	-0.353	-0.586	-0.443	-0.565	-0.469	-0.616	-0.678	-0.356	-0.440	-0.631	-0.181	-0.527	-0.561	-0.216	-0.658
DTE	0.471	0.059	0.405	0.411	0.310	0.379	0.226	0.398	0.370	0.306	0.139	0.379	0.287	0.060	0.346	0.308	0.063	0.326	0.169	0.211	0.410	0.378	0.297	0.219	0.347	0.365	0.074	0.331	0.547	0.104	0.326	0.242	0.046	0.392
SSR	0.413	0.229	0.537	0.281	0.397	0.413	0.369	0.642	0.386	0.480	0.318	0.297	0.229	0.143	0.389	0.362	0.076	0.421	0.120	0.240	0.493	0.350	0.508	0.418	0.578	0.554	0.239	0.478	0.534	0.175	0.476	0.393	0.133	0.580
LCR	0.540	0.130	0.472	0.316	0.462	0.359	0.254	0.512	0.431	0.352	0.342	0.442	0.324	0.183	0.267	0.401	0.145	0.384	0.178	0.186	0.552	0.365	0.379	0.272	0.414	0.417	0.060	0.377	0.530	0.087	0.308	0.232	0.006	0.444
GEN	0.430	0.238	0.619	0.363	0.474	0.329	0.514	0.782	0.599	0.566	0.423	0.491	0.337	0.137	0.419	0.471	0.249	0.588	0.100	0.335	0.566	0.281	0.585	0.470	0.592	0.666	0.271	0.468	0.672	0.238	0.596	0.536	0.246	0.678

Table 27 (Continued)

E. Rice chromosome 5

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.062	-0.275	-0.009	-0.094	-0.101	-0.159	-0.026	-0.155	0.073	-0.176	-0.006	-0.157	-0.141	0.166	-0.223	-0.003	-0.188	-0.071	0.177	0.032	-0.035	-0.155	-0.226	0.123	-0.073	-0.008	-0.062	-0.243	-0.225	-0.063	-0.084	-0.008	-0.002	-0.061
RTE	-0.608	-0.250	-0.725	-0.380	-0.481	-0.342	-0.564	-0.717	-0.516	-0.553	-0.402	-0.547	-0.416	-0.267	-0.416	-0.253	-0.206	-0.435	0.012	-0.079	-0.735	-0.482	-0.465	-0.519	-0.384	-0.704	-0.187	-0.375	-0.649	-0.213	-0.460	-0.326	-0.264	-0.720
DTE	0.399	0.026	0.338	0.340	0.297	0.031	0.262	0.373	0.238	0.371	0.232	0.384	0.419	-0.020	0.214	0.065	0.158	0.147	-0.002	-0.159	0.418	0.176	0.270	0.090	0.037	0.244	0.100	0.130	0.432	0.004	0.261	0.224	0.148	0.329
SSR	0.564	0.049	0.603	0.354	0.411	0.263	0.497	0.602	0.535	0.449	0.443	0.327	0.363	0.139	0.544	0.358	0.118	0.385	-0.095	0.086	0.534	0.446	0.351	0.515	0.326	0.521	0.224	0.317	0.668	0.259	0.405	0.312	0.355	0.670
LCR	0.444	0.084	0.394	0.405	0.452	0.163	0.346	0.601	0.393	0.360	0.284	0.244	0.419	0.239	0.300	0.237	0.064	0.250	-0.018	0.033	0.426	0.241	0.441	0.267	0.171	0.456	0.224	0.186	0.579	0.171	0.355	0.242	0.215	0.483
GEN	0.664	0.154	0.674	0.417	0.486	0.397	0.675	0.745	0.617	0.475	0.347	0.556	0.520	0.347	0.430	0.250	0.161	0.530	-0.033	0.084	0.727	0.469	0.409	0.637	0.324	0.666	0.214	0.347	0.728	0.229	0.528	0.447	0.292	0.810

F. Rice chromosome 6

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.104	-0.010	-0.057	-0.028	-0.167	0.013	0.124	-0.059	-0.120	0.214	-0.053	0.092	-0.351	0.014	0.176	-0.210	-0.133	-0.120	0.107	-0.057	0.134	0.053	-0.063	-0.040	0.020	-0.024	--	-0.044	-0.178	-0.112	-0.109	0.069	-0.061	0.008
RTE	-0.338	-0.139	-0.288	0.037	-0.112	-0.065	-0.162	-0.230	-0.295	-0.103	-0.156	-0.066	-0.136	0.066	-0.002	-0.262	-0.175	-0.261	-0.045	-0.150	-0.332	-0.080	-0.204	-0.305	-0.139	-0.216	--	-0.367	-0.357	-0.199	-0.210	-0.257	-0.209	-0.406
DTE	0.225	-0.002	0.099	0.024	0.105	0.001	0.119	0.250	0.372	0.087	0.230	0.168	0.339	-0.035	-0.109	0.283	0.161	0.091	0.107	0.121	0.253	0.150	0.019	0.086	-0.190	0.150	--	0.055	0.317	-0.010	0.121	0.102	-0.031	0.145
SSR	0.207	0.137	0.171	0.041	0.184	0.108	0.105	0.363	0.286	0.251	0.178	0.113	0.084	-0.147	0.146	0.137	0.143	0.224	0.040	-0.006	0.194	0.118	0.158	0.207	0.155	0.251	--	0.189	0.349	0.000	0.184	0.247	0.044	0.222
LCR	0.278	0.005	0.154	-0.008	0.158	0.119	0.282	0.325	0.386	0.075	0.119	0.117	0.155	-0.077	-0.055	0.347	0.087	0.230	-0.130	0.170	0.300	0.256	0.218	0.289	0.049	0.086	--	0.241	0.394	0.210	0.338	0.354	0.136	0.290
GEN	0.311	0.224	0.330	0.128	0.081	0.079	0.196	0.359	0.344	0.328	0.039	-0.032	0.136	0.007	0.107	0.114	0.059	0.196	-0.057	0.099	0.439	0.354	0.148	0.305	0.196	0.265	--	0.343	0.284	0.217	0.296	0.299	0.195	0.358

G. Rice chromosome 7

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.044	-0.050	-0.013	-0.266	0.037	-0.098	0.095	-0.091	-0.088	-0.004	0.014	0.108	0.120	-0.099	0.158	-0.190	0.327	0.045	-0.001	0.059	0.072	0.047	-0.167	-0.001	-0.080	0.012	-0.150	-0.005	-0.129	-0.294	0.037	0.094	-0.031	0.151
RTE	-0.320	-0.109	-0.453	-0.247	-0.079	-0.480	-0.509	-0.452	-0.505	-0.225	-0.031	-0.320	-0.224	0.080	-0.157	-0.313	-0.157	-0.380	-0.180	-0.224	-0.390	-0.491	-0.329	-0.511	-0.412	-0.544	0.013	-0.463	-0.660	-0.075	-0.585	-0.548	-0.155	-0.629
DTE	0.312	0.194	0.283	0.281	0.027	0.174	0.450	0.261	0.456	0.115	0.183	0.271	0.372	-0.215	0.040	0.384	0.137	0.297	0.286	0.262	0.260	0.182	0.380	0.474	0.238	0.357	-0.110	0.329	0.388	0.114	0.514	0.404	0.215	0.432
SSR	0.253	0.070	0.547	0.231	0.231	0.301	0.499	0.493	0.435	0.180	0.154	0.359	0.186	-0.089	0.278	0.562	0.271	0.504	0.270	0.401	0.449	0.287	0.381	0.532	0.553	0.539	-0.005	0.644	0.477	0.212	0.490	0.463	0.099	0.652
LCR	0.333	0.063	0.367	0.327	0.059	0.292	0.426	0.317	0.339	0.116	-0.017	0.325	0.229	-0.069	0.155	0.397	0.154	0.331	0.195	0.274	0.285	0.243	0.451	0.472	0.436	0.397	0.046	0.481	0.412	0.368	0.471	0.458	0.149	0.509
GEN	0.426	0.174	0.487	0.324	0.119	0.386	0.613	0.402	0.548	0.298	-0.010	0.432	0.143	-0.069	0.216	0.476	0.270	0.415	0.180	0.469	0.423	0.397	0.436	0.577	0.486	0.478	0.046	0.437	0.597	0.277	0.643	0.653	0.292	0.732

H. Rice chromosome 8

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.203	-0.163	-0.336	-0.119	0.115	-0.166	-0.288	-0.309	-0.220	-0.271	-0.253	-0.212	-0.245	0.267	-0.149	-0.186	0.062	-0.077	0.134	-0.113	-0.425	-0.068	-0.067	-0.206	-0.084	-0.253	-0.046	-0.006	-0.289	-0.322	-0.338	-0.163	0.031	-0.322
RTE	-0.585	-0.060	-0.746	-0.355	-0.316	-0.211	-0.252	-0.647	-0.472	-0.495	-0.302	-0.299	-0.436	0.177	-0.300	-0.307	-0.048	-0.605	-0.067	-0.111	-0.671	-0.398	-0.454	-0.229	-0.521	-0.568	-0.148	-0.426	-0.663	-0.265	-0.537	-0.339	-0.064	-0.688
DTE	0.499	0.131	0.614	0.225	0.154	0.028	0.211	0.578	0.371	0.371	0.275	0.455	0.565	-0.069	0.263	0.313	0.041	0.307	-0.058	0.007	0.599	0.307	0.226	0.181	0.365	0.517	0.206	0.373	0.543	0.281	0.471	0.265	0.029	0.549
SSR	0.543	0.019	0.636	0.326	0.199	0.261	0.258	0.584	0.524	0.470	0.320	0.311	0.337	-0.184	0.311	0.361	0.117	0.484	0.094	0.143	0.577	0.344	0.535	0.307	0.547	0.552	0.096	0.476	0.579	0.320	0.516	0.377	0.075	0.656
LCR	0.619	0.200	0.546	0.263	0.189	0.099	0.230	0.558	0.289	0.233	0.336	0.374	0.574	-0.048	0.258	0.337	0.098	0.338	-0.165	0.052	0.572	0.182	0.222	0.291	0.394	0.564	0.084	0.306	0.547	0.234	0.380	0.207	-0.017	0.476
GEN	0.508	0.115	0.586	0.348	0.143	0.237	0.387	0.474	0.466	0.299	0.173	0.454	0.455	-0.005	0.333	0.123	0.158	0.477	-0.021	0.142	0.554	0.313	0.450	0.415	0.434	0.488	0.000	0.391	0.632	0.218	0.574	0.417	0.186	0.685

Notes:

(1) GC: GC content; RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeats; LCR: Low complex repeats; GEN: Gene; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; Low complex repeats; GEN: Gene; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; PB: Protein binding; CW: Cell wall; NUS: Nucleus; PM: Plasma membrane; ET: Electron transport; TC: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MO: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; ED: Embryonic development; PED: Post-embryonic process; FD: Flower development; PS: Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the element/gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome after excluding the genes with two or more functions.

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between element and gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 27 (Continued)*I. Rice chromosome 9*

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	0.076	0.014	0.077	0.047	0.022	0.019	0.031	0.080	0.060	-0.068	0.034	-0.138	-0.037	0.083	0.142	0.133	-0.045	0.223	0.056	0.008	0.092	-0.026	0.030	0.096	0.195	0.160	0.174	-0.067	-0.094	0.062	-0.002	0.016	0.038	0.099
RTE	-0.375	-0.033	-0.537	-0.384	-0.220	-0.234	-0.211	-0.568	-0.383	-0.551	-0.316	-0.253	-0.468	-0.180	0.038	-0.148	-0.028	-0.527	-0.051	-0.261	-0.509	-0.544	-0.240	-0.261	-0.318	-0.530	-0.087	-0.147	-0.471	-0.055	-0.253	-0.650	-0.163	-0.620
DTE	0.356	0.047	0.458	0.224	0.165	0.233	0.159	0.457	0.399	0.446	0.410	0.321	0.555	0.125	-0.080	0.180	-0.003	0.381	0.049	0.399	0.485	0.461	0.232	0.211	0.251	0.482	0.179	0.103	0.446	-0.019	0.226	0.513	0.018	0.510
SSR	0.453	0.089	0.679	0.413	-0.011	0.414	0.231	0.546	0.508	0.589	0.256	0.439	0.552	0.196	0.024	0.203	0.205	0.489	0.144	0.276	0.689	0.562	0.386	0.346	0.236	0.666	0.190	0.185	0.475	0.022	0.411	0.624	0.260	0.681
LCR	0.437	0.136	0.450	0.283	0.161	0.355	0.253	0.543	0.370	0.477	0.260	0.524	0.603	0.196	0.006	0.226	0.093	0.485	0.061	0.405	0.494	0.417	0.328	0.288	0.224	0.550	0.076	0.156	0.584	0.030	0.324	0.603	0.133	0.513
GEN	0.665	0.098	0.597	0.477	0.078	0.378	0.477	0.699	0.662	0.684	0.210	0.572	0.633	0.218	0.069	0.223	0.112	0.644	0.174	0.412	0.589	0.458	0.525	0.565	0.270	0.655	0.185	0.137	0.600	-0.082	0.549	0.732	0.334	0.750

J. Rice chromosome 10

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.099	0.017	0.025	0.096	-0.201	-0.146	-0.089	-0.072	-0.025	0.035	0.083	0.044	0.153	0.070	-0.023	-0.170	--	-0.123	0.109	-0.205	0.026	0.079	-0.155	-0.165	0.111	-0.041	--	-0.209	-0.074	-0.103	-0.157	-0.131	-0.098	-0.236
RTE	-0.376	-0.302	-0.626	-0.207	-0.359	-0.246	-0.056	-0.505	-0.271	-0.600	-0.107	-0.415	-0.349	-0.086	-0.470	-0.196	--	-0.414	-0.339	-0.050	-0.573	-0.348	-0.413	-0.261	-0.315	-0.596	--	-0.215	-0.659	-0.153	-0.410	-0.256	-0.041	-0.619
DTE	0.216	0.090	0.455	0.204	0.440	0.127	0.164	0.298	0.366	0.367	0.133	0.329	0.202	0.179	0.252	0.275	--	0.200	0.246	0.154	0.409	0.164	0.260	0.213	0.249	0.498	--	0.248	0.532	0.116	0.509	0.348	0.011	0.530
SSR	0.330	0.226	0.588	0.110	0.395	0.222	0.135	0.496	0.331	0.545	0.208	0.395	0.236	0.007	0.476	0.208	--	0.376	0.251	0.054	0.428	0.256	0.269	0.256	0.385	0.567	--	0.178	0.624	-0.010	0.367	0.289	0.075	0.638
LCR	0.209	0.212	0.366	0.067	0.434	0.162	0.296	0.431	0.409	0.453	0.210	0.373	0.192	0.043	0.432	0.247	--	0.331	0.230	0.207	0.363	0.221	0.179	0.248	0.298	0.360	--	0.088	0.482	0.225	0.441	0.299	0.034	0.551
GEN	0.230	0.399	0.568	0.214	0.388	0.138	0.226	0.465	0.360	0.556	0.221	0.381	0.343	0.166	0.381	0.258	--	0.338	0.380	0.185	0.455	0.308	0.178	0.301	0.334	0.524	--	0.192	0.595	0.245	0.562	0.404	0.103	0.544

K. Rice chromosome 11

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.117	0.041	-0.090	-0.323	0.066	0.145	0.249	-0.128	0.039	-0.171	0.032	0.092	-0.215	0.158	-0.133	0.091	-0.227	0.051	0.195	0.020	-0.021	-0.101	-0.045	0.234	0.107	0.010	0.195	0.130	-0.126	0.050	0.130	0.119	0.211	0.198
RTE	-0.209	-0.161	-0.511	-0.224	-0.212	-0.322	-0.305	-0.238	-0.249	-0.327	-0.214	-0.072	-0.046	0.049	0.035	-0.061	-0.203	-0.322	-0.057	-0.163	-0.488	-0.286	-0.370	-0.342	-0.313	-0.360	-0.057	-0.341	-0.311	-0.100	-0.273	-0.286	-0.203	-0.469
DTE	0.075	0.011	0.267	0.211	-0.051	-0.048	0.169	-0.027	0.140	0.059	0.028	0.162	0.018	-0.179	0.032	0.213	0.073	-0.086	0.024	0.131	0.155	0.136	0.053	0.241	-0.049	0.241	0.024	0.033	-0.009	0.009	0.142	0.269	0.114	0.078
SSR	-0.096	0.167	0.387	0.174	0.026	0.179	0.107	0.299	0.119	0.189	0.103	0.140	-0.016	-0.126	-0.029	0.141	0.203	0.104	-0.004	0.062	0.221	0.215	0.158	0.277	0.284	0.350	-0.004	0.453	0.175	0.164	0.183	0.257	0.104	0.237
LCR	0.061	-0.024	0.204	0.196	-0.028	-0.047	0.090	0.128	-0.035	0.255	-0.112	0.190	0.005	-0.118	-0.046	-0.052	0.228	0.048	0.163	0.014	0.155	0.133	0.237	0.125	0.099	0.179	0.163	0.111	0.097	-0.065	0.034	0.043	-0.042	0.095
GEN	0.208	0.154	0.511	0.198	0.148	0.437	0.188	0.414	0.240	0.202	0.255	0.209	0.173	0.053	0.023	-0.033	-0.093	0.473	0.138	-0.053	0.508	0.258	0.225	0.361	0.397	0.395	0.138	0.408	0.507	0.170	0.290	0.198	0.223	0.464

L. Rice chromosome 12

	MT	CC	TC	ET	RP	TL	PMP	RTS	ST	MOD	CD	CP	BP	ED	PED	FD	PS	CCOB	CG	CDI	TCFA	TCRA	TPA	NTB	NAB	DNAB	CHRB	RNAB	CATA	NUA	PB	CW	PM	NUS
GC	-0.249	-0.110	-0.409	-0.034	-0.137	-0.166	-0.131	-0.148	-0.217	-0.093	-0.252	0.068	-0.139	-0.086	-0.153	-0.178	--	-0.274	-0.071	-0.125	-0.404	-0.147	-0.311	-0.113	-0.228	-0.301	0.043	0.152	-0.113	0.188	-0.259	-0.273	-0.225	-0.198
RTE	-0.465	-0.068	-0.746	-0.101	-0.301	-0.388	-0.475	-0.534	-0.620	-0.151	-0.377	-0.312	-0.362	0.101	-0.177	-0.241	--	-0.576	-0.177	-0.317	-0.676	-0.398	-0.609	-0.445	-0.451	-0.612	0.206	-0.273	-0.422	-0.008	-0.641	-0.475	-0.398	-0.617
DTE	0.326	0.198	0.630	-0.012	0.373	0.224	0.331	0.516	0.489	0.184	0.402	0.149	0.302	-0.018	0.258	0.346	--	0.422	0.217	0.247	0.574	0.416	0.454	0.406	0.509	0.446	-0.077	0.092	0.265	-0.039	0.558	0.487	0.323	0.418
SSR	0.165	0.193	0.689	0.081	0.400	0.366	0.316	0.412	0.489	0.181	0.351	0.293	0.423	0.018	0.293	0.188	--	0.470	0.156	0.182	0.663	0.480	0.553	0.495	0.512	0.597	-0.060	0.279	0.356	0.080	0.605	0.520	0.394	0.537
LCR	0.266	0.167	0.594	-0.141	0.362	0.346	0.391	0.511	0.514	0.114	0.409	0.279	0.341	0.000	0.253	0.298	--	0.563	0.189	0.226	0.604	0.361	0.445	0.593	0.471	0.489	-0.116	0.348	0.227	-0.051	0.600	0.569	0.395	0.590
GEN	0.468	0.039	0.778	0.134	0.426	0.409	0.456	0.592	0.579	0.227	0.432	0.294	0.511	-0.018	0.241	0.244	--	0.602	0.199	0.327	0.699	0.468	0.656	0.462	0.476	0.571	-0.051	0.382	0.546	0.124	0.610	0.495	0.383	0.682

Notes:

(1) GC: GC content; RTE: Retro-transposable element; DTE: DNA transposable element; SSR: Simple repeats; LCR: Low complex repeats; GEN: Gene; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: DNA binding; CHRB: Chromatin binding; Low complex repeats; GEN: Gene; RP: Reproduction; NTB: Nucleotide binding; NAB: Nucleic acid binding; DNAB: D Transporter activity; PB: Protein binding; CW: Cell wall; NUS: Nucleus; PM: Plasma membrane; ET: Electron transport; TC: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal transduction; MO: Transcription; TL: Translation; PMP: Protein modification process; RTS: Response to stress; CC: Cell cycle; ST: Signal ED: Embryonic development; PED: Post-embryonic process; FD: Flower development; PS: Photosynthesis; CCOB: Cellular component organization and biogenesis; CG: Cell growth; CDI: Cell differentiation; TCRA: Transcription regulator activity.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the element/gene category pair under co element/gene category pair under comparison. The signal "--" indicates that the correlation coefficient could not be calculated because one of the functional category pair had no genes along the chromosome after excluding the genes with two or more functions.

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between element and gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

Table 28
Spearman's correlation coefficients of distribution in the whole yeast genome with 60-kb windows

A.

	TM	DNAB	TSFA	RNAB	PB	NUS	CPM	PM	rRNAP	TL
GC	-0.269	-0.179	-0.006	-0.097	-0.035	-0.207	-0.100	-0.026	-0.106	-0.142
RTE	0.072	0.096	-0.065	0.134	0.012	0.012	-0.034	0.052	0.132	-0.100
SSR	0.056	0.007	0.064	0.077	0.104	0.139	0.123	0.124	-0.063	0.149
LCR	0.195	-0.002	0.017	0.118	0.069	0.083	0.206	0.169	0.044	0.125
GEN	0.259	0.015	0.174	0.164	0.125	0.407	0.496	0.011	0.150	0.391

B (Continued)

	PAAP	RTS	RTDD	EGT	EDCT	CWOB	ST	RBA	RTD	PRT
GC	-0.059	0.000	-0.013	-0.033	0.034	0.006	0.021	-0.140	-0.059	0.013
RTE	-0.028	-0.028	0.000	0.000	0.109	0.064	-0.022	-0.034	-0.012	-0.094
SSR	-0.012	-0.017	0.091	0.151	0.066	-0.080	-0.040	0.017	0.017	0.025
LCR	0.107	-0.064	0.037	0.163	0.149	0.041	0.169	0.092	-0.035	0.146
GEN	0.201	0.154	0.106	0.098	0.184	0.084	-0.003	0.279	0.051	0.211

Notes:

(1) GC: GC content; RTE: Retro-transposable element; SSR: Simple repeat; LCR: Low complex repeat; GEN: Gene; TM: telomere maintenance; DNAB: DNA binding; TSFA: Transcription factor activity; RNAB: RNA binding; PB: Protein binding; NUS: Nucleus; CPM: Cytoplasm; PM: Plasma membrane; rRNAP: rRNA processing; TL: Translation; PAAP: Protein amino acid phosphorylation; RTS: Response to stress; RTDD: Response to DNA damage stimulus; EGT: ER to Golgi vesicle-mediated transport; EDCT: Endocytosis; CWOB: Cell wall organization and biogenesis; ST: Signal transduction; RBA: Ribosome biogenesis and assembly; RTD: Response to drug; PRT: Positive regulation of transcription from RNA polymerase II promoter.

(2) The values of the correlation coefficient indicate the degree of correlation, ranging from 0.000 for no correlation to 1.000 for complete correlation. The positive values of correlation coefficients indicate the positive correlation between the element/gene category pair under comparison whereas the negative (-) values of correlation coefficients indicate the negative correlation between the element/gene category pair under comparison.

(3) Differently highlighted colors indicate the significance levels of the distribution correlation between gene category pairs: blue for a significance level of $p \leq 0.001$, green for a significance level of $p \leq 0.01$, and red for a significance level of $p \leq 0.05$.

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