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Title: Young Genes out of the Male: an Insight from Evolutionary Age Analysis of the Pollen Transcriptome

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Running title: Young Genes out of the Pollen

Short Summary: Cui et al., observed a number of young genes in both rice and *Arabidopsis thaliana* using a phylostratigraphic approach and further transcriptome age analysis revealed that a phylogenetically younger transcriptome is expressed in pollen grains compared with other plant tissues. The young transcriptomes of the male reproductive cells with dramatic complexity and diversity contained a higher ratio of anti-sense and inter-genic transcripts which supports that pollen grains serve as an “innovation incubator” for the birth of new genes

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Abstract

The birth of new genes in genomes is an important evolutionary event. Several studies reveal that new genes in animals tend to be preferentially expressed in male reproductive tissues such as testis (Betrán et al., 2002; Begun et al., 2007; Dubruille et al., 2012), and thus an “out of the testis” hypothesis for the emergence of new genes has been proposed (Vinckenbosch et al., 2006; Kaessmann, 2010). However, such phenomena have not been examined in plant species. Here, by employing a phylostratigraphic method we dated the origin of protein coding genes in rice and *Arabidopsis thaliana* and observed a number of young genes in both species. These young genes tend to encode short extracellular proteins, which may be involved in rapid evolving processes, such as: reproductive barriers, species specification and anti-microbial processes. Further analysis of transcriptome age indexes across different tissues revealed that male reproductive cells express a phylogenetically younger transcriptome than other plant tissues. Compared to sporophytic tissues, the young transcriptomes of the male gametophyte displayed greater complexity and diversity, which included a higher ratio of anti-sense and inter-genic transcripts, reflecting pervasive transcription state that facilitated the emergence of new genes. Here, we propose that pollen may act as an “innovation incubator” for the birth of *de novo* genes. With cases of male-biased expression of young genes reported in animals, the “new genes out of the male” model revealed a common evolutionary force that drives reproductive barriers, species specification and the upgrading of defensive mechanisms against pathogens.

Keywords: pollen, evolution, young genes, transcriptome

Introduction

The birth of new genes in genomes during evolution has been considered a major driving force for functional and phenotypic innovation. In the 1970s, it was proposed that duplication of genes and genomes is the main source for creating novel genes and that all new genes arise from existing genes (Ohno, 1970). Furthermore, it has been argued that new genes are most likely derived from random changes based on old ones, which was called the “tinker model” (Jacob, 1977). Such models have been widely accepted and molecular mechanisms in support have been identified over the years, such as whole genome duplication, chromosome segmental duplication, gene fusion, exon shuffling and transposable element domestication (Long et al., 2003). However, recent discoveries of *de novo* originated young genes tell another story. Lineage specific genes and orphan genes which lack homologues in other lineages were found in many species, for example, in fruit fly (Begun et al., 2007; Zhou et al., 2008; Chen et al., 2010), human (Wu et al., 2011; Xie et al., 2012), mouse (Murphy and McLysaght, 2012), yeast (Carvunis et al., 2012), rice (Xiao et al., 2009) and *Arabidopsis thaliana* (Silveira et al., 2013). Systematic investigation of *de novo* genes suggested that emergence of genes from non-genic regions in genomes is rather frequent and there may be a progressive process for *de novo* emergence of genes from non-genic sequences to proto-genes and finally functional genes (Neme and Tautz, 2013). The current knowledge about *de novo* genes is quite limited due to the lack of sequence similarities with well-characterized proteins, hindering their function annotation and analysis. Thus, *de novo* genes remain mysteries in the genome, especially with respect to the evolutionary forces which have contributed to their emergence, the reasons related to their selection and fixation during evolution, as well as their functional roles in both plants and animals.

In this study, we dated the origin of protein coding genes in *Arabidopsis thaliana* and rice. We found a number of recently evolved young genes in the rice and *Arabidopsis* genomes. Young genes tend to encode small proteins of simple structures which share common features with *de novo* genes (Neme and Tautz, 2013). Annotations of those genes suggested their involvement in defense and reproduction processes. Further transcriptome age index analysis revealed one particular group of tissues associated with high expression of young genes: the plant male gametophyte. Besides the younger transcriptome age than other tissues, the transcriptome of pollen also displayed greater complexity and diversity with a higher ratio of anti-sense and inter-genic transcripts. Finally, we summarize an evolutionary model to explain the emergence of new genes out of male reproductive cells based on our discoveries.

Results

Phylostratigraphic Profiles of Rice and *Arabidopsis* Genes

To determine the evolutionary age of protein-coding genes and to differentiate between old and young genes in rice and *Arabidopsis*, we adopted a BLAST-based phylostratigraphic approach (Tomislav Domazet-Loso, Josip Brajkovic, 2007). Each gene was assigned to a phylostratum (PS), representing the oldest phylogenetic node to which the gene can be traced (see Methods, Tables S1 and S2). The phylostratigraphic approach does not discriminate orthologs and paralogs, but can trace the origin of founder genes, which first emerged and formed the basis of new gene lineages or families (Tomislav Domazet-Loso, Josip Brajkovic, 2007). Ages of additional genes in the same gene lineage that have arisen through duplication or other mechanisms are all mapped to the founder genes. To avoid bias resulting from interspersed repetitive sequences in the genome, TE-related (TE, transposable element) genes were excluded from the subsequent analysis. To increase the reliability of the phylostratigraphic analysis, both protein and CDS sequences were used in the BLAST step (Tomislav Domazet-Loso, Josip Brajkovic, 2007). Figure 1A and B show the resulting distribution of the 40,457 rice non-TE related protein-coding genes and 27,365 *Arabidopsis* non-TE related protein-coding genes across 13 PS. PS1-2 contains the oldest genes with homologous sequences in prokaryotes and eukaryotic ancestors and PS3 contains old genes with homologous sequences in algae. PS13 encompasses the youngest genes restricted to the considered species (SSOG, species-specific orphan genes) and PS11-12 includes the genes that are only present in the closely related species and are named TSOG (Taxon-specific orphan genes). Here, for comparison and simplicity, we define all genes from PS1-PS3 as old and those from PS11-PS13 as young. As a result, in rice, ~43% of the protein-coding genes are old and ~19% are deemed young. In *Arabidopsis*, old genes comprise ~53% of the total protein-coding genes and only ~8.6% of protein-coding genes are young. Overall, rice has more young genes (478 SSOG, 1.18%; 7,367 TSOG, 18.21%) than *Arabidopsis* (861 SSOG, 3.14%; 1,492 TSOG, 5.45%), which is consistent with previous studies based on the analysis of EST and gene families (Vandepoele and Peer, 2005; Guo, 2013). Notably, the SSOG may be redefined as TSOG in the future as more closely related genomes are released. The peaks in PS (Figure 1A and B) mirror major events in evolutionary history; for instance, PS5 coincides with the emergence of embryos, while PS8 may be associated with the emergence of angiosperms.

Young Genes Evolved Simpler Structure

Here, we investigated the genomic features of old (PS1-PS13) and young (PS11-PS13) genes and observed that the young genes from both rice and the *Arabidopsis* are shorter and possess fewer exons compared with those of old genes (Figure 1C). In addition, young genes were predicted to encode small proteins lacking InterPro domain annotations, in contrast to the old genes (Figure 1C). Permutation tests confirmed that these observations are statistically significant at level 0.001. These findings are consistent with previous observations that young genes generally have simple

exon/intron structures, encoding short proteins with simple structures (Carvunis et al., 2012; Neme and Tautz, 2013; Ding et al., 2012) and that young protein coding genes may evolve longer and more complex gene structures through progressively gaining U1 sites (U1 snRNP recognition sites) and losing PAS (poly-A sites) at the 5' end during evolution (Almada et al., 2013). Moreover, we observed that young genes in both rice and *Arabidopsis* are not enriched in chromosome block duplication regions of chromosomes (Figure S1), implying that these young genes in rice and *Arabidopsis* were less likely generated through block duplication.

Functional Characterization of Young Genes

To analyze the functions of young genes, we performed gene set enrichment analysis (GSEA), whereby genes were classified based on TAIR10 (Lamesch et al., 2012) and MSU6.1 (Ouyang et al., 2007) annotation into those with known and unknown function (See Methods). Altogether 83% and 96% old genes of rice and *Arabidopsis* respectively, have been functionally characterized. In contrast, only 3% and 33% of rice and *Arabidopsis* young genes, respectively, are functionally annotated (Figure 1D). Further, gene ontology (GO) enrichment analysis in *Arabidopsis* and rice revealed that the set of old genes is mostly enriched for biological process GO terms related to processes in primary metabolism (Figure 2A and S2A), while young genes are likely associated with defense (Figure 2B and S2B). In addition, according to GO cellular localization, proteins encoded by old genes tend to be localized in the cytosol, organelle and nuclei (Figure 2C and S2C), while proteins encoded by young genes are likely localized in endomembrane system, extracellular regions or anchored to membrane (Figure 2D and S2D).

The fewer functional annotations of young genes pertain to plant defense and male reproduction (Table S3-4). For instance, young genes were found to encode pollen self-incompatibility proteins, pollen allergens, Lipid Transfer Protein (LTP) family proteins, glycine-rich proteins, proline-rich proteins, SCR (SCARECROW) proteins, RALF (Rapid Alkalinization Factor) family proteins and defensin-like proteins (Tables S3 and S4). Some LTP proteins were shown to transport sporopollenin precursors from tapetal cells to the microspore surface and are essential for successful pollen adhesion and tube guidance (Guan et al., 2012). Glycine-rich proteins and proline-rich proteins are known as pollen wall proteins (Goldberg et al., 1993). Pollen-specific RALF proteins were reported to regulate pollen tube elongation in tomato (Covey et al., 2010). SCR proteins are pollen coat proteins and are determinants of male self-incompatibility required for species specification (Higashiyama, 2010). Defensin belongs to a group of cationic peptides that exhibit broad spectrum antimicrobial activity (Silverstein et al., 2007). It is interesting that defensins from both animals and plants contribute not only as innate immunity defense components, but also in male reproduction. Bin1b is a rat defensin protein with functions in antimicrobe and sperm maturation, storage and

protection (Li et al., 2001). *AtLURE1* encodes a *Arabidopsis* specific defensin functioning as diffusible pollen tube attractant (Takeuchi and Higashiyama, 2012). Therefore, old genes play a key role in fundamental intracellular processes and have evolved relatively complex exon/intron structures. However, most young genes belong to *de novo* originated genes encoding short extracellular proteins that may be involved in rapidly evolving processes such as the formation of reproductive barriers, species specification and anti-microbial processes.

The Transcriptomes of Pollen are Evolutionarily Young

With the age of each gene determined, the evolutionary transcriptome age of a certain tissue can be quantified by the transcriptome age index (TAI, the weighted sum of PS ranks of genes by their expression levels) methods, which have successfully revealed molecular hourglass signatures of embryo development in both animals (Domazet-Lošo and Tautz, 2010) and plants (Quint et al., 2012). Higher TAI indicates younger transcriptome age, while lower TAI reflects a more ancient transcriptome. Here, we use TAI to determine which of the plant tissues express the youngest transcriptome. To conduct TAI computation, we compiled a compendium of microarray data that covers a wide range of tissues/organs from publically available datasets (Table S5). Microarray samples of tissues/organs were classified into 18 tissue groups for rice (covering pollen, sperm, root, anther, leaf, ovary, stigma, etc.; see Table S5 for a complete list) and 22 for *Arabidopsis* (covering pollen, stamen, root, sepal, petal, fruit, leaf, stem flower, etc.; see Table S5 for a complete list). Since it is known that retrogenes are up-regulated in pollen (Abdelsamad and Pecinka, 2014), to rule out the possible bias caused by retrogenes, we removed 95 reported rice retrogenes (Sakai et al., 2011) and 241 reported *Arabidopsis* retrogenes (Abdelsamad and Pecinka, 2014) from the phylostrata rank data sets in the TAI computation.

In rice tissues, the TAI values ranged from 4.55 (stigma/ovary) to 5.16 (germinating pollen) (Figure 3A), and *Arabidopsis* TAI values ranged from 3.39 (vegetative apex) to 3.55 (sperm) (Figure 3B) in tissues. In both rice and *Arabidopsis*, the highest TAI value was observed in the transcriptomes of male reproductive cells (pollen and sperm), suggesting that pollen expresses the evolutionarily youngest transcriptome among all tissues. In rice, an evident increase of TAI was observed from the unicellular pollen stage to the pollen germination stage (Figure 3A), suggesting that, the transcriptome progressively becomes evolutionarily younger during the maturation of pollen grains. A similar trend was observed in *Arabidopsis*, except that TAI of bi-cellular pollen was lower than that of unicellular pollen. In higher plants, mature pollen contains two sperm cells and a vegetative cell (VC). In rice, the TAI of sperm cells ranked between bi-cellular pollen, and tri-cellular pollen, while in *Arabidopsis* the TAI of the sperm displayed the highest TAI followed by germinating pollen grains. In agreement with the annotation of young genes,

the largest TAI value observed in germinated pollen grains and sperm, implies the involvement of young genes in pollen-tube development and fertilization. In addition, we observed that apart from the male reproductive tissues, roots displayed relatively high TAI values in both rice and *Arabidopsis*. As plant roots interact with soil microbes, they may have evolved young genes, such as secreted small peptide-encoding genes, which play a role in root-microbe interactions. For example, a large family of defensin-like proteins were found to be expressed in *Medicago* root nodules (Nallu et al., 2013). It has been previously shown that many genes in stamen and pollen transcriptome were expressed at higher or lower ends compared with other tissues (Wang et al., 2010). The high TAI in pollen grains may be due to the up-regulation of young genes and/or down-regulation of old genes. In support of this hypothesis, we observed a major transcriptomic shift between male gametes and sporophytic tissues, lower expression levels of genes in the three most ancient phylostrata (PS1-3) and high expression of genes in the three most recent phylostrata (PS11-13) in pollen (Figure 3 C-D).

The TAI method employs phylostrata rank data, which is based on the emergence of founder genes and cannot distinguish between orthologs and paralogs. To exclude possible bias of the phylostratigraphic method, we used two alternative methods to confirm our findings. Firstly, we adopted a sequence divergence based method to determine which tissue displayed highest level of transcriptome divergence. The same transcriptome datasets of rice and *Arabidopsis* were used to determine the transcriptome divergence index (TDI) (Quint et al., 2012). TDI is the weighted mean of K_a/K_s ratios of ortholog genes by their expression levels (see Methods). TDI reflects the level of selective pressure on the transcriptomes, which is one major force to drive evolution. Again, higher TDI values were observed in pollen and sperm compared with other tissues in both rice and *Arabidopsis*, indicating more divergent transcriptome and less selective pressure in plant male reproductive cells (Figure 4 A-B). Emergence of young genes can be further validated by the comparison of syntenic regions of closely related species, although some may be missed due to lack of synteny. Next, we investigated the expression pattern of the young genes which were supported by syntenic evidence. Using the anchor point genes (genes from the same gene family located in a colinear segment) from PLAZA database (Proost et al., 2009), a total of 1,495 young genes (PS12-13) in rice were observed to be anchor point genes in *Oryza sativa*, *Brachypodium distachyon* and *Zea mays* (Table S6). In addition, 176 young genes in *Arabidopsis* were identified to anchor point genes in *A. thaliana*, *A. lyrata*, *Theobroma cacao* (Table S7). We calculated the relative expression level of those validated young genes and a male-biased pattern was evident in both species (Figure 4 C-D).

Next, we tested whether the observed younger evolutionary age of the male germ transcriptome could arise purely by chance. We developed a randomization process as a control. We measured the differences of average TAI values between male gametophyte samples and the remaining tissues (D_{TAI}), and tested the significance of D_{TAI} by shuffling the evolutionary ranks of genes. The randomization process was repeated 10,000 times, generating a null distribution of D_{TAI} . For data based on phylostrata ranks, D_{TAI} value was 0.32 for rice, 0.083 for *Arabidopsis*, larger than the maxima of the D_{TAI} based on shuffled data (Figure S3

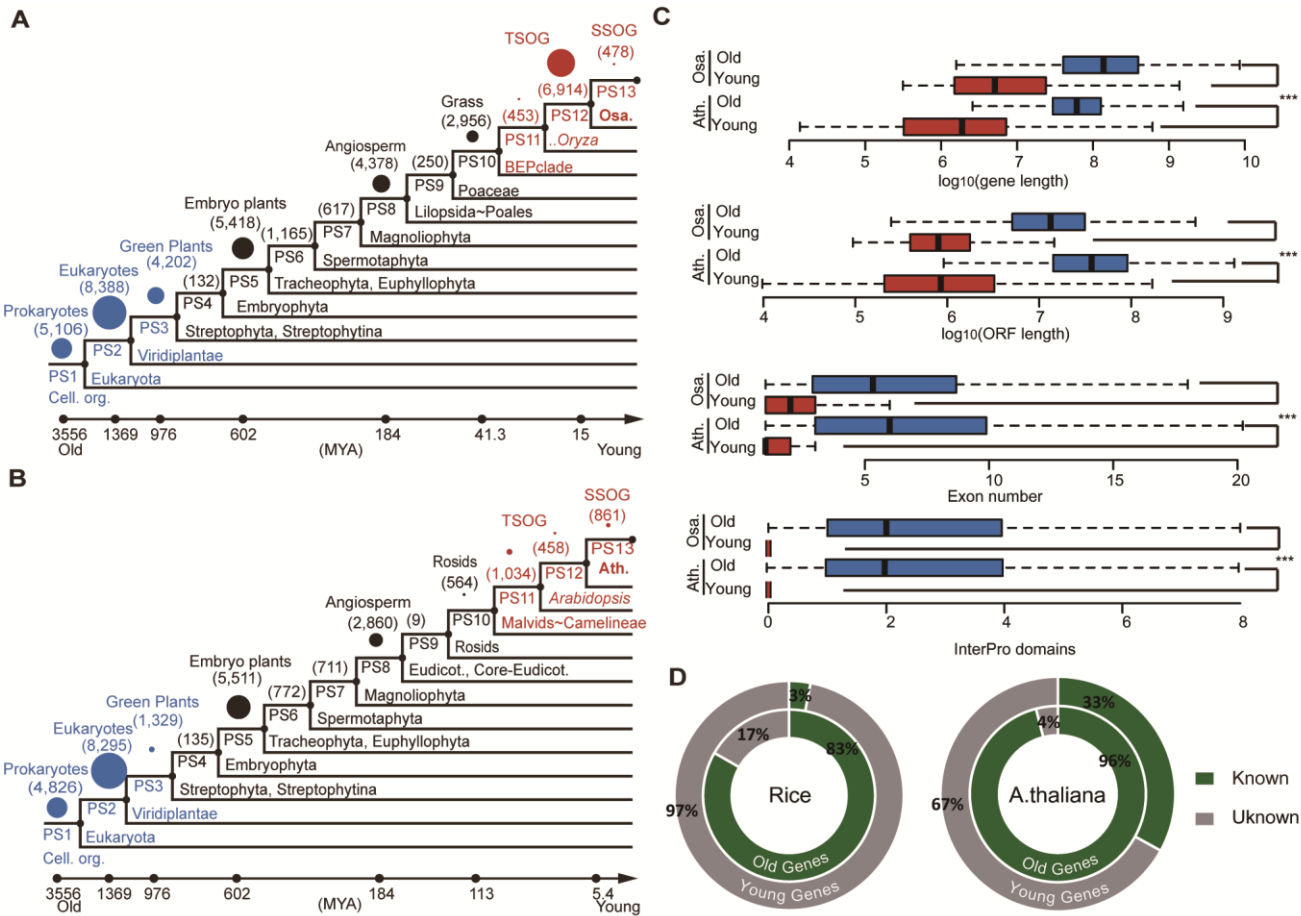


Figure 1. Phylostratigraphic profiles and general features of rice and *Arabidopsis* genes. Numbers in parentheses show the number of genes in each phylostratum (PS1-PS13). The numbers of genes in major phylostrata are proportional to the size of the filled circles. Here, we define old genes as genes from PS1-PS3 (blue) and new genes as those from PS11-PS13 (red). **(A)** Phylostratigraphic profile of rice genes. **(B)** Phylostratigraphic profile of *Arabidopsis* genes. **(C)** Gene features of new genes and old genes. The observed differences of gene features between new genes and old gene are significant at the 0.001 level (permutation test) **(D)** Percentage of genes with/without known function annotations in new genes (red) and old genes (blue). Abbreviations: PS: phylostratum. Cell.org: cellular organism; TSG: taxon-specific orphan genes; SSG: species-specific gene; Osa: *Oryza sativa*. Ath: *Arabidopsis thaliana*.), thus

ensuring statistical significance at level of 0.0001. We conclude that the observation of the young pollen transcriptome in this study is robust.

Transcriptome Age Index Correlates with Transcriptome Complexity

According to *de novo* gene emergence model, there should be a continuum ranging from non-genic sequences to protein-coding genes, in which intermediate products exist, such as intergenic transcripts, long non-coding RNAs

(lncRNA) and proto-genes observed in yeast (Carvunis et al., 2012). Therefore, we hypothesized that evolutionarily young transcriptomes should display complexity because of the presence of the intermediates during the evolutionary process of functional genes. Redundant probes of Affymetrix rice genome array can be remapped to inter-genic and anti-sense of current gene models. We used rice as an example and conducted probe redefinition to obtain expression values of inter-genic and anti-sense transcripts (See Methods). Interestingly, across different tissues, TAI (the weighted sum of phylostrata ranks of genes by their expression levels) values were slightly negatively correlated with absolute average expression levels of genic probe sets, but were strongly correlated with antisense and inter-genic probe sets (Figure 5A). Such observation supported that evolutionarily young transcriptomes displayed a high level of non-genic transcripts, including anti-sense transcripts, inter-genic transcripts, transposons and retrotransposons. The average absolute expression levels of genic regions were slightly lower in male germ cells than other tissues, while levels of antisense and intergenic probe sets were much higher in male germ cells than in the remaining tissues. We quantified the association between the TAI values across different tissues and the gene expression by using the Pearson correlation coefficient. Old genes were predominantly positively correlated with the TAI vector, while young genes and transposable-elements related genes were mostly negatively correlated (Figure 4B). These observations suggest that transposable element activity is an important factor shaping the evolutionary age of the transcriptome, but TE-related loci and young genes are both up-regulated in pollen

Discussion

The male reproductive organ as a major source new genes has been extensively studied in animals. The first reported new genes, *jingwei* in *Drosophila* (Long and Langley, 1993) and *Pkg2* in mammals (McCarrey and Thomas, 1987), were found specifically expressed in testes. Several cases of male-biased expression of young genes have been reported in *Drosophila* (Nurminsky et al., 1998; Levine et al., 2006; Begun et al., 2007). Recently, the testis were found to express a complex transcriptome with higher levels of inter-genic transcripts and young lncRNAs (Soumillon et al., 2013). Recently, genomic studies revealed that new genes evolved male-biased expression in mammals (Emerson et al., 2004; Zhang, Vibranovski, Landback, et al., 2010) and drosophila (Betrán et al., 2002; Zhang, Vibranovski, Krinsky, et al., 2010). An “out of testis model” was proposed whereby new genes may initially be expressed in testis and later evolve more diverse expression patterns (Vinckenbosch et al., 2006). In this study, we provide evidence of pollen-biased expression of young genes cells in both monocot and dicot plants, which leads to a possible common mechanism to drive the emergence of young genes in male reproductive tissues.

Several hypotheses have been put forward to explain this phenomenon: In animal species, gene trafficking has been considered a contributing factor; for instance, in *D. melanogaster*, many of the novel autosome genes are derived from X-linked parental genes and display male-biased expression (Long et al., 2013). However, this scenario cannot account for rice and *Arabidopsis*, which lack sex chromosomes. Another hypothesis is associated with control of expression by epigenetics and chromatin state. In both mammals and plants, male germ cells express a specific histone H3 variant (Sano and Tanaka, 2005). Human testis-specific histone H3T was reported less stable than the conventional H3.1 histone (Tachiwana et al., 2010). Special chromatin state of meiotic and post-meiotic male gamete cells may widely exist in non-coding genomic regions. Gaining a rather simple promoter element could be sufficient to drive expression in such a permissive chromatin state. In addition, transposable elements are more likely inserted into actively transcribed regions with open chromatin in the germline (McVicker and Green, 2010). Transposable element movements bring sequence changes to open chromatin regions which may also aid the birth of de novo genes. Ahmed and Ales reported pollen-specific activation of 216 novel retrogenes in *Arabidopsis*, which supports the hypothesis of special chromatin states favoring the creation of new genes (Abdelsamad and Pecinka, 2014).

Here we speculate that, to make new genes or genetic changes inheritable, the molecular mechanisms creating them may occur in germ cells. Notably, in many species, male cells transmit more mutations than the female to the offspring due to more germ-cell divisions (Li et al., 2002; Whittle and Johnston, 2003). We further hypothesize that male-biased expression of new genes and male-biased mutation may be driven by the same evolutionary forces: male gamete competition (Figure 6). For species in which the male reproductive organ produces far more gametes than females, the presence of male gamete competition allows male gametophyte cells to tolerate higher mutation rates or gene birth than female germ cells. Female gametes are fewer in number and require more resources in production. As a result, the cost of genetic mutation/innovation in female germ cells is high and, thus, the genome in female cells should be tightly controlled. Male gamete competition reduces the chance of transferring harmful genetic changes to the offspring and can function as a selective process for adaptive new genes (Figure 6). It will be interesting to investigate the relationship between the sex-biased expression of young genes and different mating modes of species in the future. Our model suggests that in species in which the female can produce a large quantity of egg cells, male-biased expression pattern may not be observed, which can be tested in the future. In summary, in both higher plants and animals, a circle of emergence and selection of young genes may exist in male gametophyte cells that provides not only a driving force for species specification but also continuous raw materials for upgrading of plant defensive strategies against microorganisms.

Methods

Phylostratigraphy. The phylostratigraphic analysis in rice (*Oryza sativa japonica*) and *Arabidopsis* was performed according to procedures described in previous studies (Quint et al., 2012; Domazet-Lošo and Tautz, 2010). In this study, the phylogeny data for rice and *Arabidopsis* was obtained from the NCBI taxonomy database. A reference protein and CDS sequence database was constructed, which consisted of protein sequences from NCBI nr database (2011-Mar-1) and protein/CDS sequences from 44 completely sequenced plant genomes in Plaza v2.5 (Proost et al., 2009) and Ensembl Plants (Kersey et al., 2010). Our reference database provided exhaustive coverage over protein/CDS sequences across a wide range of organisms. To avoid the bias resulted from interspersed repetitive sequences in the genome, we excluded TE-related gene models from the analysis (Type I TE: Ty3-gypsy subclass, Ty1-copia subclass, LINE subclass, SINE subclass, centromere-specific retrotransposon, and other unclassified retrotransposons; Type II TE: CACTA,En/Spm sub-class, Mutator sub-class, Pong sub-class, Ac/Ds sub-class, Mariner sub-class, RIPER7, MuDR and other unclassified transposons). In total, 40,457 non-TE protein sequences of rice loci (MSU 6.1) and 27,365 non-TE *Arabidopsis* protein coding genes (TAIR10) were blasted against the reference database by BLASTp using an E-value cut-off of $<10^{-3}$, which were previously reported to provide an optimal compromise between sensitivity and accuracy (Albà and Castresana, 2007). The same cutoff was used for BLASTn against CDS reference database. The evolutionary age of a protein-coding gene was assigned to the most distant (ancient) phylostratum, in which detectable similarity of any proteins could be found.

Statistical analysis of gene features and annotations

Functional annotations, general features and genomic location of rice and *Arabidopsis* genes were obtained from MSU Rice Genome Project (Ouyang et al., 2007) and TAIR (Lamesch et al., 2012), respectively. Comparison of features between young genes and old genes was tested by permutation test of phylostratigraphic ranks of genes and corresponding features. Function annotation was firstly classified into two groups. Genes that were given a null annotation (“unknown protein”, “hypothetical protein” or “expressed protein”) were grouped to “unknown”; otherwise, they are referred to as “known”. The significance of observed number of known and unknown genes in old genes and young genes was tested by Chi-square test. For detailed function enrichment analysis of new genes, we selected annotation terms which occurred more than 10 times and calculated the enrichment against all genes with functional annotations in the genome. Function terms with enrichment greater than 1 were tested by Fisher’s exact test. GO enrichment analysis was conducted on DAVID website (Huang et al., 2009).

Microarray dataset preparation and data analysis

Transcriptome datasets were obtained from published Affymetrix microarray datasets in the GEO (Barrett et al., 2009) and ArrayExpress (Parkinson et al., 2007) databases, which were further classified into tissue groups (Table S5). For rice, 137 microarray samples from four data series (GEO accessions: GSE14304 (Fujita et al., 2010), GSE17002 (Russell et al., 2012), GSE27988 (Wei et al., 2010), GSE29212 (Peng et al., 2012)) were obtained and classified into 18 groups of tissues. For *Arabidopsis*, 244 microarray samples from seven data series (GEO accessions: GSE5630, GSE5631, GSE5632, GSE5633, GSE5634 (Schmid et al., 2005); GSE6162 (Honys and Twell, 2004); GSE17343 (Qin et al., 2009); ArrayExpress accession: E-ATMX-35 (Borges et al., 2008)) were obtained and classified into 22 tissue groups. To map microarray probes to current gene model, we created customized microarray probe set definition files (CDF files). The procedure was as follows: 1) probe sequences were BLASTed against target gene sequences; 2) probes that perfectly matched to a single gene were selected; 3) probes matched to the reverse complement strand of a gene model were grouped into the anti-sense probe sets; 4) probes were grouped into probe sets, each representing a single gene and having at least three uniquely mapped probes. The probe-gene mapping information was processed by a customized Perl script to generate a CDF file. Following this procedure, we built two custom CDF files for rice and *Arabidopsis*. The custom CDF file for rice contained 35,202 probe sets that were matched to genes and 2,439 probe sets that were matched to the antisense strand of genes. Custom CDF file for *Arabidopsis* contained 20,392 probe sets matched to *Arabidopsis* genes and 70 probe sets matched to the antisense strand of genes. For each organism, microarray samples from individual studies were combined and normalized by RMAExpress(Irizarry, 2003) using custom CDF files with default settings. Probe set expression levels in a certain tissue group was computed as the arithmetic mean of expression levels of the probe set in all samples within the tissue group.

TAI calculation and statistical analysis

The TAI method was developed by Domazet-Lošo et al (Domazet-Lošo and Tautz, 2010). TAI of sample s is defined as the weighted mean of phylostratum rank ps_i of gene i by the expression value e_{is} in transcriptome of sample s ,

$$TAI_s = \frac{\sum_{i=1}^n ps_i \cdot e_{is}}{\sum_{i=1}^n e_{is}},$$

where n is the total number of genes in the analysis. High TAI indicates that the transcriptome is evolutionarily young, while low TAI value suggests the transcriptome is evolutionarily ancient.

We defined D_{TAI} as average TAI values from m male germ sample minus average TAI values from o other samples, as follows:

$$D_{TAI} = \frac{\sum_{i=1}^m TAI_i}{m} - \frac{\sum_{j=1}^o TAI_j}{o}.$$

The significance of observed D_{TAI} based on real data was determined by permutation test. We randomly shuffled the phylostratum rank of genes in the study 10,000 times and a null distribution of D_{TAI} was computed. No permuted D_{TAI} was larger than the real ones, and guaranteeing P -values less than 0.0001.

K_a/K_s ratios and TDI calculation.

K_a/K_s ratios for *O.sativa* vs *O.glaberrima* (Ensembl plants, AGI 1.1.20) (Wang et al., 2014) and *A.thaliana* vs. *A.lyrata* (Plaza2.5) were calculated using gKaKs (Zhang et al., 2013). gKaKs used BLAT and bl2seq to align CDS to genome and then used KaKs_calculator to compute K_a/K_s ratios. For the computation of K_a/K_s ratios, we used MS (Model-selected) methods. TDI was defined as the weighted mean of K_a/K_s ratios of gene i by the expression value e_{is} in the transcriptome of sample s

$$TDI_s = \frac{\sum_{i=1}^n \left(\frac{K_{ai}}{K_{si}} \right) \cdot e_{is}}{\sum_{i=1}^n e_{is}},$$

where n was the total number of genes in the analysis. High TDI indicated that the transcriptome is more divergent, while low TDI value represents a more conserved transcriptome.

Validation of young genes by syntenic evidence

Anchor point genes of closely related species were downloaded from the PLAZA database (Proost et al., 2009). Anchor point genes are genes from the same gene family located in a colinear segment. As for *A. thaliana*, anchor point genes in *A. lyrata* and *T. cacao* were used to screen young genes in PS13 with syntenic evidence. As for *O.sativa*, anchor point genes in *B. distachyon* and *Z. mays* were used to screen young genes in PS12-13 with syntenic evidence. For each young gene identified using phylostratigraphy, we first checked if it lacked anchor point counterparts in the genomes of the two closely related species selected. Next, we determined the nearest upstream and downstream genes (within three-gene distance) that have anchor point counterparts in the genomes of two closely related species among the selected. If the counterpart anchor genes were close (within five-gene distance) in the genomes of the two closely related species, we selected the young gene as supported by syntenic evidence.

Relative expression levels for phylostrata

Relative expression levels were computed using methods described in (Domazet-Lošo and Tautz, 2010). The mean relative expression level e_{ij} of phylostratum j and tissues group i were computed as the arithmetic mean of expression level of all genes in phylostratum j . Then e_{ij} was normalized according to the following equation, in which e_{jmin}/e_{jmax} was the minimum/maximum mean expression level of phylostratum j across all tissue groups:

$$f_{js} = \frac{e_{ij} - e_{jmin}}{e_{jmax} - e_{jmin}}.$$

The transformation scales the relative expression level f_{js} , for phylostratum j in tissue group s , between 0 and 1.

Expression levels of antisense and inter-genic transcripts

The Affymetrix Rice Genome Array (GPL2025) had off target probes that matched the antisense strand of genes as well as inter-genic regions. Expression levels of the antisense probe set were obtained by using a custom CDF file as described above. For detection of inter-genic transcripts, probe sequences were BLASTed against the gene models and inter-genic sequences of the rice genome (MSU 6.1). The same rules describe above was used to create CDF file covering 7,436 probe sets that match to inter-genic regions.

Correlation between TAI values and gene expression vector

TAI values across all tissue groups-groups were defined as a vector: tai . Likewise, the i th gene expression profile across all tissue-groups x_i is also a vector. The correlation between the TAI vector tai and the i th gene expression profile was measured by Pearson Correlation Coefficient (PCC):

$$PCC_i = \frac{x_i \cdot tai}{\|x_i\| \|tai\|}.$$

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Ministry of Science and Technology, China (2013CB126902 and 2011CB100101); the 863 High-Tech Project, Ministry of Science and Technology, China (2011AA10A101 and 2012AA10A302).

Figure Legends

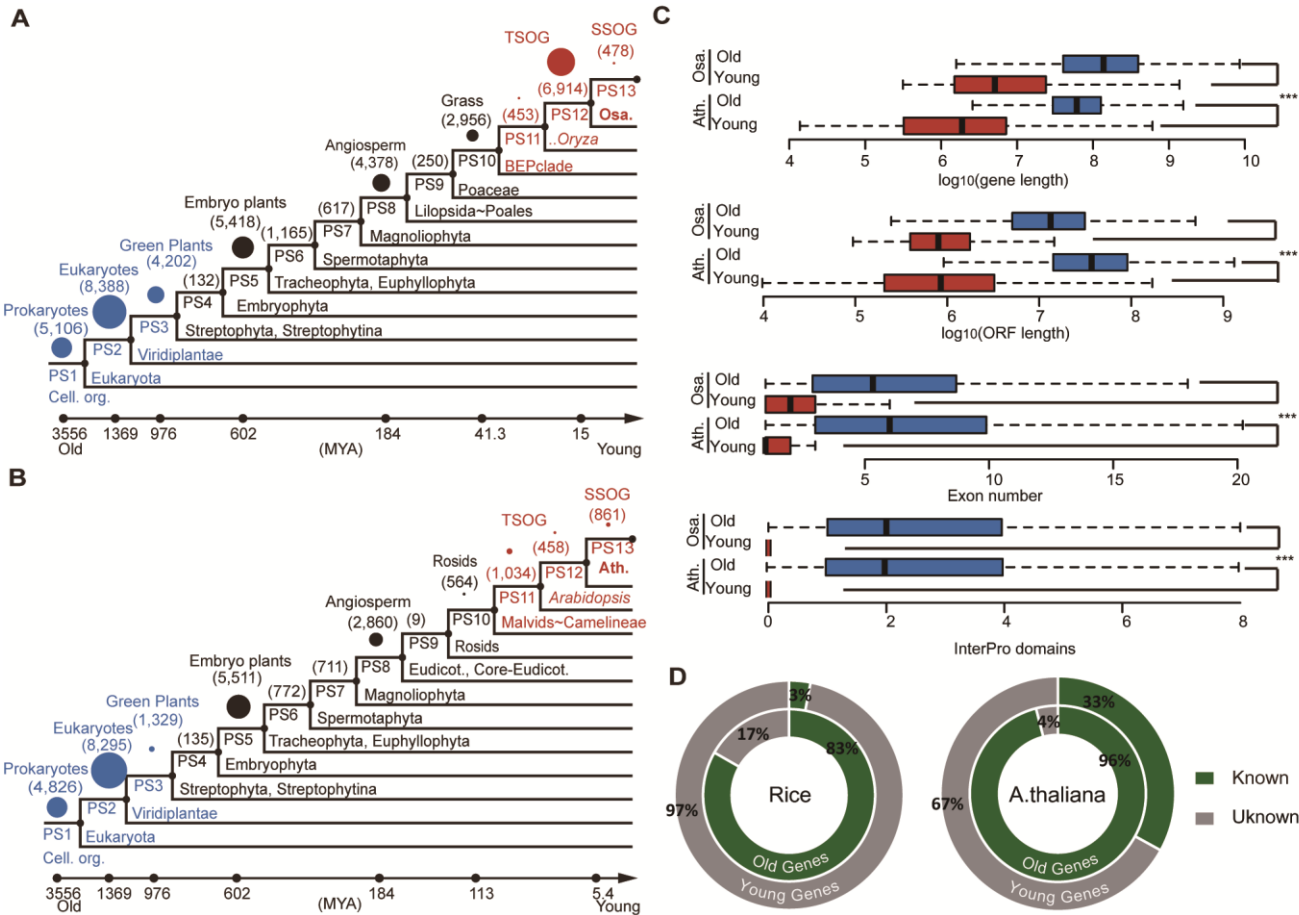


Figure. 1. Phylostratigraphic profiles and general features of rice and *Arabidopsis* genes. Numbers in parentheses show the number of genes in each phylostratum (PS1-PS13). The numbers of genes in major phylostrata are proportional to the size of the filled circles. Here, we define old genes as genes from PS1-PS3 (blue) and new genes as those from PS11-PS13 (red). **(A)** Phylostratigraphic profile of rice genes. **(B)** Phylostratigraphic profile of *Arabidopsis* genes. **(C)** Gene features of new genes and old genes. The observed differences of gene features between new genes and old gene are significant at the 0.001 level (permutation test) **(D)** Percentage of genes with/without known function annotations in new genes (red) and old genes (blue). Abbreviations: PS: phylostratum. Cell.org: cellular organism; TSG: taxon-specific orphan genes; SSG: species-specific gene; Osa: *Oryza sativa*. Ath: *Arabidopsis thaliana*.

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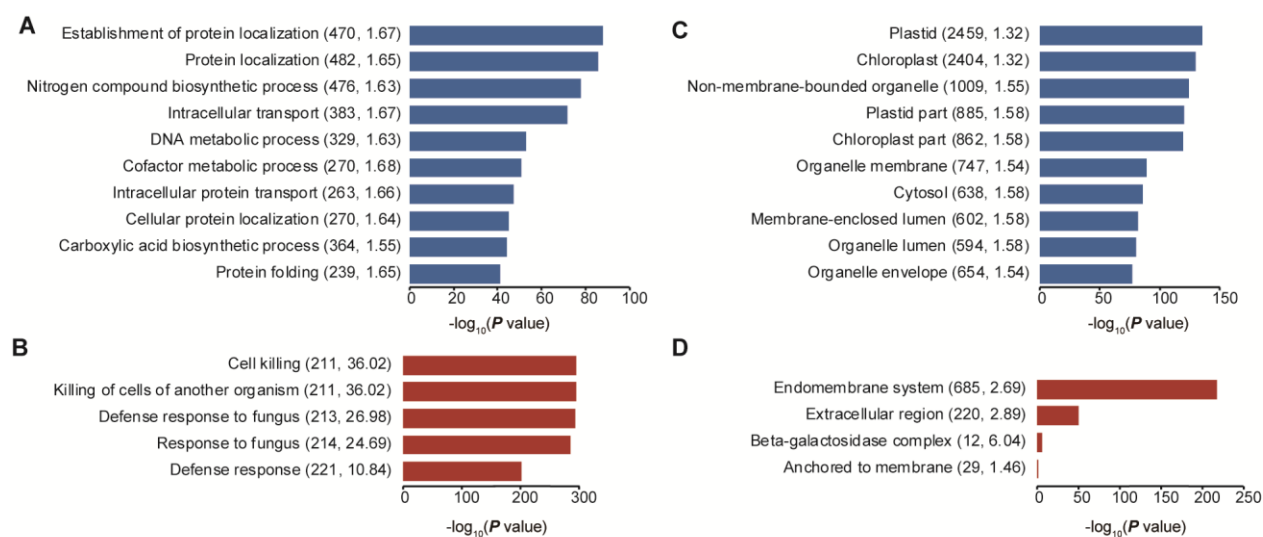


Figure. 2 Gene Ontology enrichment for old genes and young genes in Arabidopsis. (A). The top 10 most significant biological process GO terms of old genes; (B). Significant biological process GO terms of young genes; (C). The top 10 most significant cellular component GO terms of old genes; (D). Significant cellular component GO terms of young genes. Number of query genes in each GO term and their enrichment against all genes in the same GO term are shown in parentheses.

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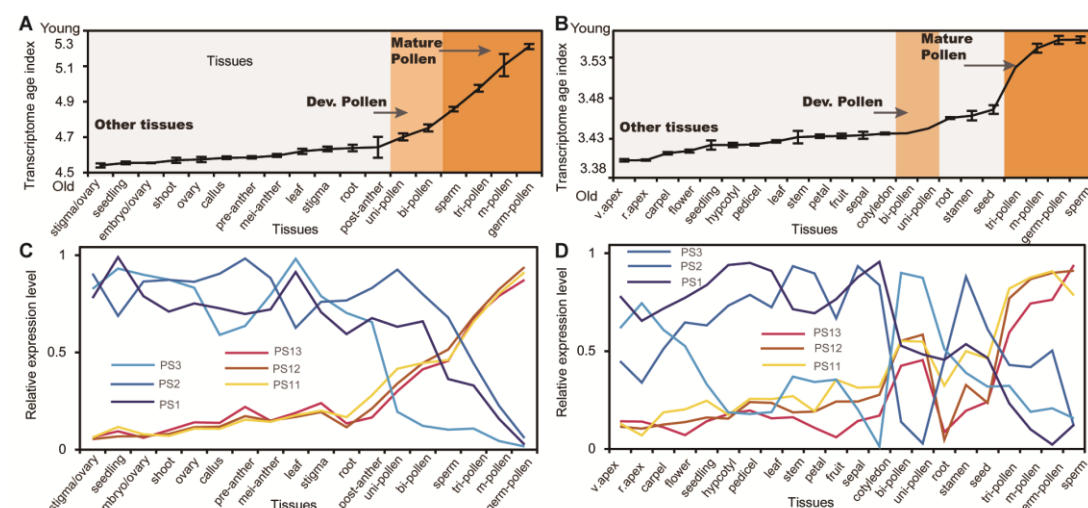


Figure. 3. Transcriptome age index (TAI) profiles across different groups of tissues. (A-B) The TAI profiles across 18 tissue groups in rice (A) and 22 tissues groups in *A. thaliana* (B). The observed patterns of TAI are significant ($P < 0.0001$), tested by permutation test. (C-D) Relative expression values of the old genes (PS1-3) and young genes (PS11-13) across different tissues in rice (C) and *A. thaliana* (D). Abbreviations: pre-anther denotes anther before meiosis, mei-anther, anther at meiotic stage; uni-pollen, pollen at unicellular stage; bi-pollen, pollen at bicellular stage; tri-pollen, pollen at tricellular stage; m-pollen, mature pollen; germ-pollen, germinating pollen; v-apex, vegetative shoot apex; while r-apex denotes reproductive shoot apex.

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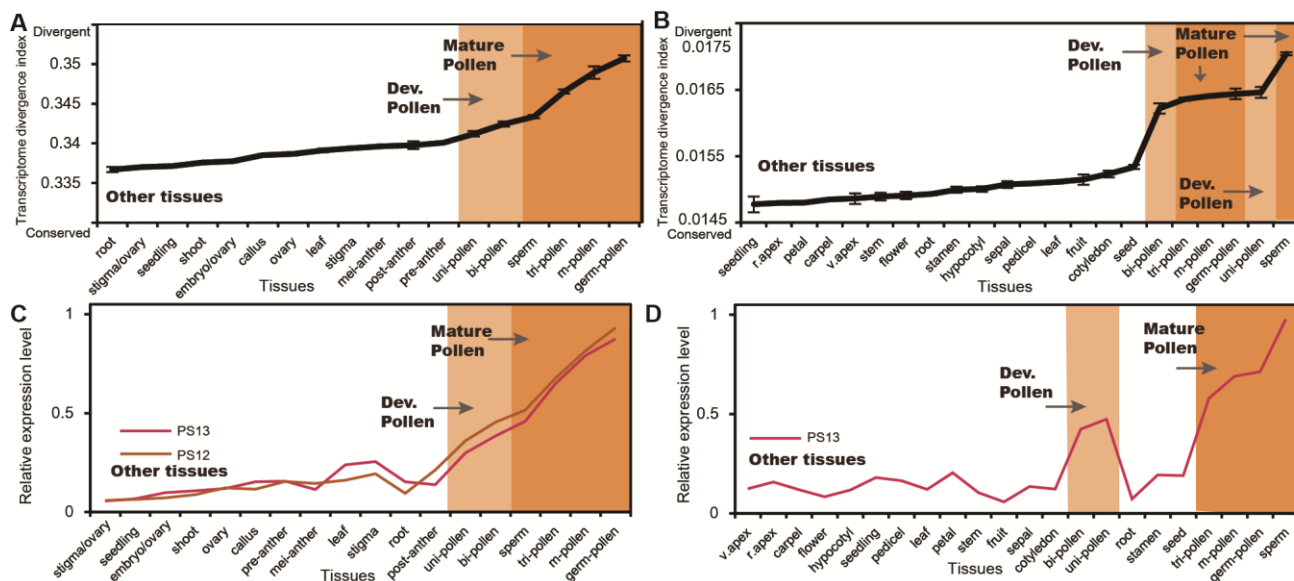


Figure. 4. Transcriptome divergence index (TDI) profiles across different tissues. (A). Rice. (B). Arabidopsis. The orange areas highlight data for the male germ cell and male gametophyte. Higher TDI value indicates more divergent transcriptome. (C-D) Relative expression values of young genes with syntenic evidence across different tissues in rice (C) and *A. thaliana* (D). Abbreviations: pre-anther, anther before meiosis; mei-anther, anther at meiotic stage; uni-pollen, pollen at unicellular stage; bi-pollen, pollen at bicellular stage; tri-pollen, pollen at tricellular stage; m-pollen, the mature pollen grain stage; germ-pollen, germinating pollen; v-apex, vegetative shoot apex; r-apex, reproductive shoot apex.

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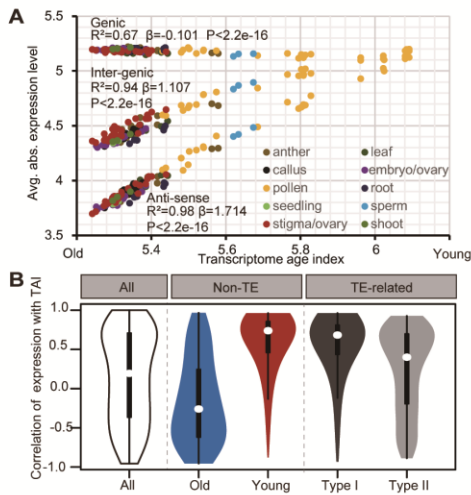


Figure 5. Correlation between TAI and expression patterns of different groups of transcripts. (A) Scatter plot of transcriptome age index versus average absolute expression values of probes across different tissues. Colors indicate classification of tissues in groups. Genic probes match genes; Inter-genic probes match inter-genic regions; anti-sense probes match anti-sense strand of genes. TAI is slightly negatively correlated with absolute average expression levels of genic probe sets ($\beta=-0.101$, $R^2=0.67$, $P\text{-value}<2.2e-16$), but strongly correlated with anti-sense ($\beta=1.714$, $R^2=0.98$, $P\text{-value}<2.2e-16$) and inter-genic probe sets ($\beta=1.107$, $R^2=0.94$, $P\text{-value}<2.2e-16$) (B). Violin-plot showing the distribution of correlation coefficients between TAI and expression level of different groups of genes. Abbreviations: All, all genes on the microarray; Old: old genes (PS1=3); Young: young genes (PS11-13); TE, transposable element; Type I, retrotransposons; Type II, DNA transposons.

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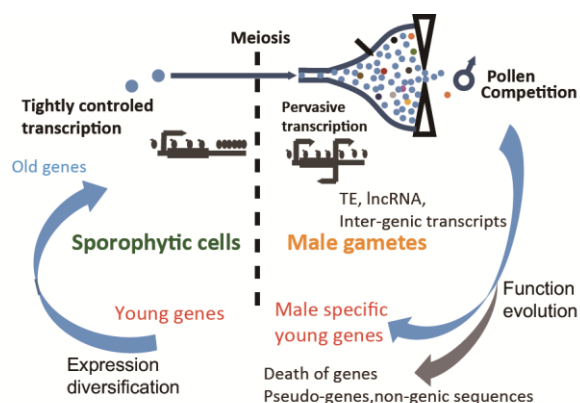


Figure. 6. The “out of male” model for emergence of new genes. The special chromatin state of non-coding regions in post meiotic male gametes facilitates promiscuous transcription, which in turn provides raw material for the emergence of new genes. Young genes tend to be firstly expressed in male gametes. Male gamete competition acts as a pilot trial or proving ground for the function of new genes, eliminating gametes that carry harmful genetic changes and fixing changes with neutral or beneficial effects. In the longer term some young genes may gain regulatory elements of promoters and expression in sporophytic tissues.

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Supplementary Materials:

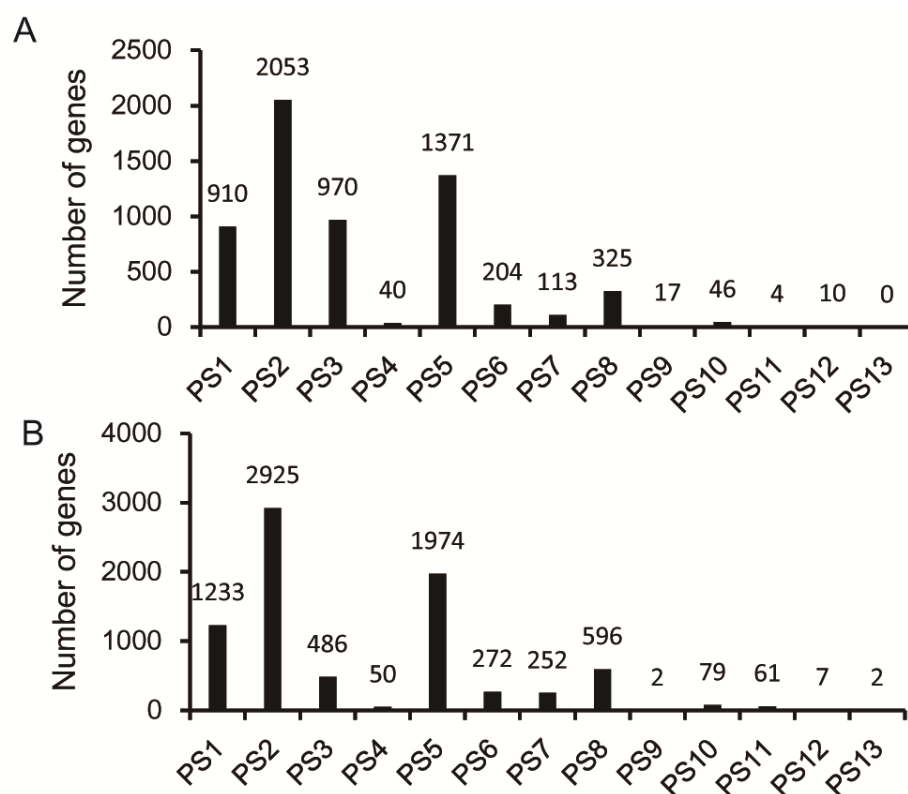


Figure. S1. Phylostratigraphic distribution of genes located in chromosome segmental duplication region. (A).

rice; **(B).***Arabidopsis*. The P-value of the observed patterns is less than 0.001 tested by permutation test.

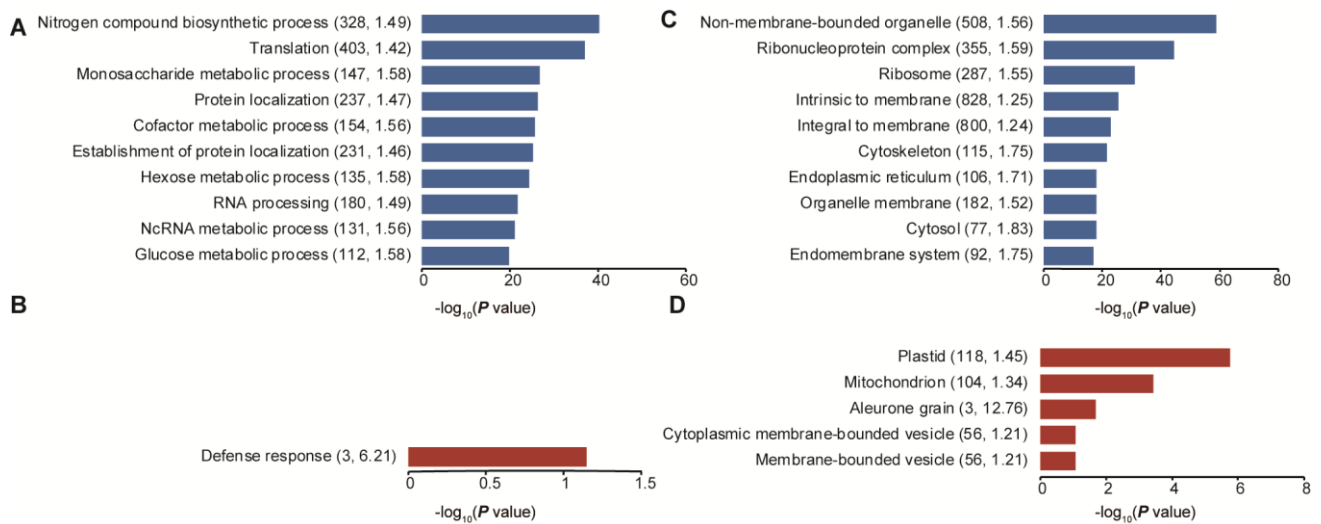


Figure. S2 Gene Ontology enrichment for old genes and young genes in rice. (A) Top 10 most significant biological process GO terms of old genes. **(B)** Significant biological process GO terms of young genes. **(C)** Top 10 most significant cellular component GO terms of old genes; **(D).** Significant cellular component GO terms of young genes. Numbers in the brackets show the count of query genes found in each GO terms and their enrichment against all genes in the same GO terms.

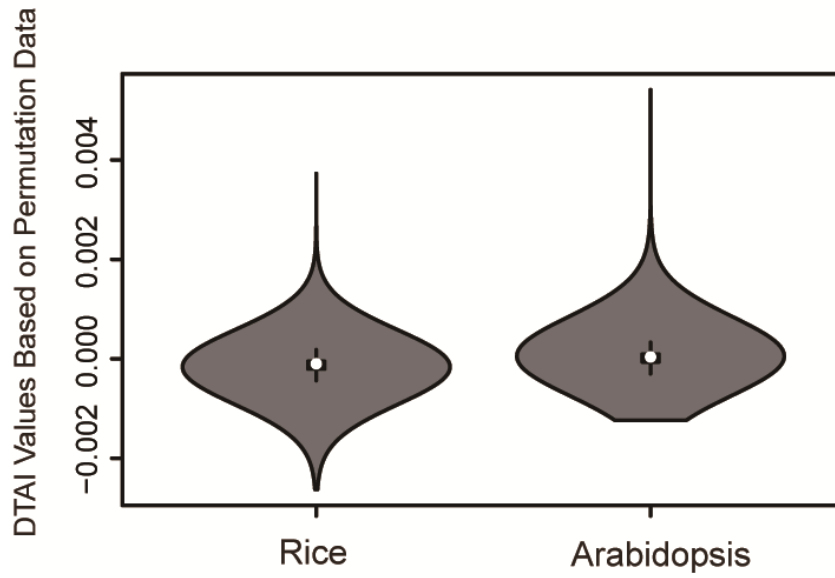


Figure. S3. Violin-plot of D_{TAI} values based on 10000 permuted evolutionary rank data. D_{TAI} stands for the differences of average TAI values between male gametophyte samples and other tissues. D_{TAI} values based on real phylostrata data is 0.32 in rice, 0.083 in *Arabidopsis*, both of which are far larger than the maxima of D_{TAI} values based on shuffled data.

Table S1. Data sets used in the BLAST searches for construction of phylostratigraphic map in *Oryza sativa*.

PS	Phylostratum	NCBI nr protein sequences	44 Genomes included in the reference database
PS13	<i>Oryza sativa</i>	223,975	<i>Oryza sativa japonica</i> (MSU 6.1)(26)
PS12	Ehrhartoideae, Oryzeae, <i>Oryza</i>	3,385	<i>Oryza barthii</i> , <i>Oryza brachyantha</i> , <i>Oryza glaberrima</i> , <i>Oryza glumaepatula</i> , <i>Oryza meridionalis</i> , <i>Oryza nivara</i> , <i>Oryza punctata</i> , <i>Oryza rufipogon</i> , <i>Leersia perrieri</i> , (Ensembl Plants)
PS11	BEP clade	88,476	<i>Brachypodium distachyon</i> (Plaza 2.5)(25)
PS10	Poaceae	155,495	<i>Aegilops tauschii</i> , <i>Hordeum vulgare</i> , <i>Triticum aestivum</i> , <i>Triticum urartu</i> (Ensembl Plants)
PS9	Liliopsida, commelinid, Poales	27,334	<i>Zea mays</i> , <i>Sorghum bicolor</i> (Plaza 2.5), <i>Setaria italic</i> (Ensembl Plants)
PS8	Magnoliophyta	953,250	<i>Musa acuminata</i> (Ensembl Plants)
PS7	Spermatophyta	23,952	<i>Arabidopsis thaliana</i> (TAIR 10)(27), <i>Arabidopsis lyrata</i> , <i>Carica papaya</i> , <i>Theobroma cacao</i> , <i>Vitis vinifera</i> , <i>Populus trichocarpa</i> , <i>Ricinus communis</i> , <i>Manihot esculenta</i> , <i>Fragaria vesca</i> , <i>Malus domestica</i> , <i>Glycine max</i> , <i>Medicago truncatula</i> , <i>Lotus japonicus</i> (Plaza 2.5), <i>Amborella trichopoda</i> , <i>Brassica oleracea</i> , <i>Brassica rapa</i> , <i>Prunus persica</i> , <i>Solanum lycopersicum</i> (Ensembl Plants)
PS6	Tracheophyta, Euphyllophyta	59,511	<i>Selaginella moellendorffii</i> (Plaza 2.5)
PS5	Embryophyta	75,337	<i>Physcomitrella patens</i> (Plaza 2.5)
PS4	Streptophyta, Streptophytina	2,120	
PS3	Viridiplantae	131,117	<i>Ostreococcus lucimarinus</i> , <i>Ostreococcus tauri</i> , <i>Micromonas</i> sp. RCC299, <i>Volvox carteri</i> , <i>Chlamydomonas reinhardtii</i> (Plaza 2.5)
PS2	Eukaryota	4,341,039	
PS1	cellular organisms	8,051,821	

Table S2. Data sets used in the BLAST searches for construction of phylostratigraphic map in *Arabidopsis thaliana*.

PS	Phylostratum	NCBI nr protein sequences	44 Genomes included in the reference database
PS13	<i>Arabidopsis thaliana</i>	90,857	<i>Arabidopsis thaliana</i> (TAIR 10)
PS12	<i>Arabidopsis</i>	67,687	<i>Arabidopsis lyrata</i> (Plaza 2.5)
PS11	Malvids Brassicales, Brassicaceae, Camelineae	81,706	<i>Theobroma cacao</i> (Plaza 2.5), <i>Carica papaya</i> (Plaza 2.5), <i>Brassica rapa</i> , <i>Brassica oleracea</i> (Ensembl Plants)
PS10	Rosids	632,500	<i>Lotus japonicus</i> , <i>Medicago truncatula</i> , <i>Glycine max</i> , <i>Malus domestica</i> , <i>Fragaria vesca</i> , <i>Manihot esculenta</i> , <i>Ricinus communis</i> , <i>Populus trichocarpa</i> (Plaza 2.5) <i>Solanum lycopersicum</i> , <i>Prunus persica</i> (Ensembl Plants)
PS9	Eudicotyledons, CoreEudicotyledons	74,309	
PS8	Magnoliophyta	504,856	<i>Oryza sativa</i> (MSU 6.1), <i>Brachypodium distachyon</i> , <i>Sorghum bicolor</i> , <i>Zea mays</i> (Plaza 2.5), <i>Oryza barthii</i> , <i>Oryza brachyantha</i> , <i>Oryza glaberrima</i> , <i>Oryza glumaepatula</i> , <i>Oryza meridionalis</i> , <i>Oryza nivara</i> , <i>Oryza punctata</i> , <i>Oryza rufipogon</i> , <i>Leersia perrieri</i> , <i>Aegilops tauschii</i> , <i>Hordeum vulgare</i> , <i>Triticum aestivum</i> , <i>Triticum urartu</i> , <i>Setaria italic</i> , <i>Musa acuminata</i> , <i>Amborella trichopoda</i> (Ensembl Plants)
PS7	Spermatophyta	23,952	
PS6	Tracheophyta, Euphyllophyta	59,511	<i>Selaginella moellendorffii</i> (Plaza 2.5)
PS5	Embryophyta	B b 7,5337	<i>Physcomitrella patens</i> (Plaza 2.5)
PS4	Streptophyta, Streptophytina	2,120	
PS3	Viridiplantae	131,117	<i>Ostreococcus lucimarinus</i> , <i>Ostreococcus tauri</i> , <i>Micromonas</i> sp. RCC299, <i>Volvox carteri</i> , <i>Chlamydomonas reinhardtii</i> (Plaza 2.5)
PS2	Eukaryota	4,341,039	
PS1	cellular organisms	8,051,821	

Table S3. Enriched functional annotations of young genes from PS11-PS13 in rice.

Annotations	Count in Young Genes	Count in Genome	Coverage	Enrichment	P-value
Defensin-like DEFL family	29	59	49.2%	31.55	p-value < 2.2E-16
Glycine-rich protein	28	57	49.1%	31.53	p-value < 2.2E-16
Prolamin precursor	26	28	92.9%	59.59	p-value < 2.2E-16
Latency associated nuclear antigen	25	25	100.0%	64.18	p-value < 2.2E-16
RALF family protein	21	41	51.2%	32.87	p-value < 2.2E-16
LTP family protein precursor	18	164	11.0%	7.04	8.96E-10
Pollen related protein	18	104	17.3%	11.11	p-value < 2.2E-16
LigA, putative	17	26	65.4%	41.96	p-value < 2.2E-16
Thionin family protein	12	82	14.6%	9.39	5.82E-12
Maternally expressed gene	10	11	90.9%	58.34	p-value < 2.2E-16

Table S4. Enriched functional annotations of young genes from PS11-PS13 in *Arabidopsis thaliana*.

Annotations	Count in Young Genes	Count in Genome	Coverage	Enrichment	P-Value
defensin-like protein	78	115	67.8%	20.57	< 2.2E-16
S locus-related pollen glycoprotein	33	58	56.9%	17.26	< 2.2E-16
glycine-rich protein	45	107	42.1%	12.75	< 2.2E-16
Plant thionin family protein	42	48	87.5%	26.54	< 2.2E-16
lipoprotein	37	105	35.2%	10.69	< 2.2E-16
SCR-like protein	22	27	81.5%	24.71	< 2.2E-16
ECA1 gametogenesis related family protein	17	58	29.3%	8.89	2.18E-10
hydroxyproline-rich glycoprotein	15	130	11.5%	3.50	6.45E-06
Cystatin/monellin superfamily protein	11	25	44.0%	13.34	1.08E-08
Cysteine-rich protein	11	21	52.4%	15.89	2.61E-09
arabinogalactan protein	13	42	31.0%	9.39	2.04E-08
Beta-galactosidase related protein	14	20	70.0%	21.23	9.76E-13
CLAVATA3/ESR-RELATED	12	31	38.7%	11.74	7.39E-09

Table S5. Microarray datasets used in the transcriptome age index calculation for rice and *Arabidopsis*.

Species	Datasets ID	Sample ID	Tissues	Tissue groups
Rice	GSE14304	GSM351427	anther at archesporial cells forming stage	pre-meiotic anther
Rice	GSE14304	GSM351428	anther at archesporial cells forming stage	pre-meiotic anther
Rice	GSE14304	GSM351429	anther at archesporial cells forming stage	pre-meiotic anther
Rice	GSE14304	GSM351430	anther at pre-meiotic s/g2 stage	pre-meiotic anther
Rice	GSE14304	GSM351431	anther at pre-meiotic s/g3 stage	pre-meiotic anther
Rice	GSE14304	GSM351432	anther at pre-meiotic s/g4 stage	pre-meiotic anther
Rice	GSE14304	GSM351433	anther at meiotic leptotene stage	meiotic anther
Rice	GSE14304	GSM351434	anther at meiotic leptotene stage	meiotic anther
Rice	GSE14304	GSM351435	anther at meiotic leptotene stage	meiotic anther
Rice	GSE14304	GSM351436	anther at meiotic leptotene stage	meiotic anther
Rice	GSE14304	GSM351437	anther at meiotic zygotene-pachytene stage	meiotic anther
Rice	GSE14304	GSM351438	anther at meiotic zygotene-pachytene stage	meiotic anther
Rice	GSE14304	GSM351439	anther at meiotic zygotene-pachytene stage	meiotic anther
Rice	GSE14304	GSM351440	anther at meiotic diplotene-tetrad stage	meiotic anther
Rice	GSE14304	GSM351441	anther at meiotic diplotene-tetrad stage	meiotic anther
Rice	GSE14304	GSM351442	anther at meiotic diplotene-tetrad stage	meiotic anther
Rice	GSE14304	GSM351443	anther at meiotic diplotene-tetrad stage	meiotic anther
Rice	GSE14304	GSM351444	anther at uni-nucleated gametophyte stage	post meiotic anther

Rice	GSE14304	GSM351445	anther at uni-nucleated gametophyte stage	post meiotic anther
Rice	GSE14304	GSM351446	anther at uni-nucleated gametophyte stage	post meiotic anther
Rice	GSE14304	GSM351447	anther at bi-cellular gametophyte stage	post meiotic anther
Rice	GSE14304	GSM351448	anther at bi-cellular gametophyte stage	post meiotic anther
Rice	GSE14304	GSM351449	anther at bi-cellular gametophyte stage	post meiotic anther
Rice	GSE14304	GSM351450	anther at tri-cellular mature pollen stage	post meiotic anther
Rice	GSE14304	GSM351451	anther at tri-cellular mature pollen stage	post meiotic anther
Rice	GSE14304	GSM351452	anther at tri-cellular mature pollen stage	post meiotic anther
Rice	GSE14304	GSM357614	unpollinated stigma	stigma
Rice	GSE14304	GSM357615	unpollinated stigma	stigma
Rice	GSE14304	GSM357616	unpollinated stigma	stigma
Rice	GSE14304	GSM357617	unpollinated ovary	ovary
Rice	GSE14304	GSM357618	unpollinated ovary	ovary
Rice	GSE14304	GSM357619	unpollinated ovary	ovary
Rice	GSE14304	GSM357620	pollinating stigma	stigma
Rice	GSE14304	GSM357621	pollinating stigma	stigma
Rice	GSE14304	GSM357622	pollinating ovary bottom	ovary
Rice	GSE14304	GSM357623	pollinating ovary bottom	ovary
Rice	GSE14304	GSM357624	pollinating ovary bottom	ovary
Rice	GSE14304	GSM357625	stigma and ovary 15-25 min after pollination	stigma and ovary
Rice	GSE14304	GSM357626	stigma and ovary 15-25 min after pollination	stigma and ovary
Rice	GSE14304	GSM357627	stigma and ovary 15-25 min after pollination	stigma and ovary
Rice	GSE14304	GSM357628	stigma and ovary 40-50 min after pollination	stigma and ovary
Rice	GSE14304	GSM357629	stigma and ovary 40-50 min after pollination	stigma and ovary

Rice	GSE14304	GSM357630	stigma and ovary 40-50 min after pollination	stigma and ovary
Rice	GSE14304	GSM357631	stigma and ovary 5-7 hrs after pollination	stigma and ovary
Rice	GSE14304	GSM357632	stigma and ovary 5-8 hrs after pollination	stigma and ovary
Rice	GSE14304	GSM357633	stigma and ovary 5-9 hrs after pollination	stigma and ovary
Rice	GSE14304	GSM357636	unpollinated ovary top	ovary
Rice	GSE14304	GSM357637	unpollinated ovary top	ovary
Rice	GSE14304	GSM357638	unpollinated ovary top	ovary
Rice	GSE14304	GSM357639	1 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357640	1 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357641	1 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357642	2 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357643	2 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357644	2 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357645	3 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357646	3 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357647	3 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357648	4 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357649	4 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357650	4 dap embryo sac bottom	embryo and ovary
Rice	GSE14304	GSM357651	unpollinated ovary	ovary
Rice	GSE14304	GSM357652	unpollinated ovary	ovary
Rice	GSE14304	GSM357653	unpollinated ovary	ovary
Rice	GSE14304	GSM357654	1 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357655	1 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357656	2 dap embryo sac top	embryo and ovary

Rice	GSE14304	GSM357657	2 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357658	3 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357659	3 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357660	4 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357661	4 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357662	4 dap embryo sac top	embryo and ovary
Rice	GSE14304	GSM357664	growing callus	callus
Rice	GSE14304	GSM357665	growing callus	callus
Rice	GSE14304	GSM357666	growing callus	callus
Rice	GSE14304	GSM357667	regenerating callus 2 days	callus
Rice	GSE14304	GSM357668	regenerating callus 2 days	callus
Rice	GSE14304	GSM357669	regenerating callus 2 days	callus
Rice	GSE14304	GSM357670	regenerating callus 4 days	callus
Rice	GSE14304	GSM357671	regenerating callus 4 days	callus
Rice	GSE14304	GSM357672	regenerating callus 4 days	callus
Rice	GSE14304	GSM357673	regenerating callus 6 days	callus
Rice	GSE14304	GSM357674	regenerating callus 6 days	callus
Rice	GSE14304	GSM357675	regenerating callus 6 days	callus
Rice	GSE14304	GSM357676	regenerating callus 8 days	callus
Rice	GSE14304	GSM357677	regenerating callus 8 days	callus
Rice	GSE14304	GSM357678	regenerating callus 8 days	callus
Rice	GSE14304	GSM357679	root	root
Rice	GSE14304	GSM357680	root	root
Rice	GSE14304	GSM357681	root	root
Rice	GSE14304	GSM357682	shoot	shoot
Rice	GSE14304	GSM357683	shoot	shoot
Rice	GSE14304	GSM357684	shoot	shoot
Rice	GSE14304	GSM357685	young leaf	leaf
Rice	GSE14304	GSM357686	young leaf	leaf
Rice	GSE14304	GSM357687	young leaf	leaf

Rice	GSE14304	GSM357688	young leaf	leaf
Rice	GSE17002	GSM425463	seedling	seedling
Rice	GSE17002	GSM425464	seedling	seedling
Rice	GSE17002	GSM425465	seedling	seedling
Rice	GSE17002	GSM425466	anthesis pollen	mature pollen
Rice	GSE17002	GSM425467	anthesis pollen	mature pollen
Rice	GSE17002	GSM425468	anthesis pollen	mature pollen
Rice	GSE17002	GSM425469	sperm at anthesis	sperm cell
Rice	GSE17002	GSM425470	sperm at anthesis	sperm cell
Rice	GSE17002	GSM425471	sperm at anthesis	sperm cell
Rice	GSE27988	GSM692527	cultured plant callus	callus
Rice	GSE27988	GSM692528	cultured plant callus	callus
Rice	GSE27988	GSM692529	cultured plant callus	callus
Rice	GSE27988	GSM692530	leaf	leaf
Rice	GSE27988	GSM692531	leaf	leaf
Rice	GSE27988	GSM692532	leaf	leaf
Rice	GSE27988	GSM692533	root	root
Rice	GSE27988	GSM692534	root	root
Rice	GSE27988	GSM692535	root	root
Rice	GSE27988	GSM692536	uninucleate microspore	uninucleate microspore
Rice	GSE27988	GSM692537	uninucleate microspore	uninucleate microspore
Rice	GSE27988	GSM692538	uninucleate microspore	uninucleate microspore
Rice	GSE27988	GSM692539	bicellular pollen	bi-cellular pollen
Rice	GSE27988	GSM692540	bicellular pollen	bi-cellular pollen
Rice	GSE27988	GSM692541	bicellular pollen	bi-cellular pollen
Rice	GSE27988	GSM692542	tricellular pollen	tri-cellular pollen
Rice	GSE27988	GSM692543	tricellular pollen	tri-cellular pollen
Rice	GSE27988	GSM692544	tricellular pollen	tri-cellular pollen
Rice	GSE27988	GSM692545	mature pollen	mature pollen
Rice	GSE27988	GSM692546	mature pollen	mature pollen
Rice	GSE27988	GSM692547	mature pollen	mature pollen
Rice	GSE27988	GSM692548	germinated pollen	germinated pollen
Rice	GSE27988	GSM692549	germinated pollen	germinated pollen
Rice	GSE27988	GSM692550	germinated pollen	germinated pollen
Rice	GSE29212	GSM720598	uninucleate microspore	uninucleate microspore
Rice	GSE29212	GSM720599	uninucleate microspore	uninucleate microspore
Rice	GSE29212	GSM720600	bicellular pollen	bicellular pollen
Rice	GSE29212	GSM720601	bicellular pollen	bicellular pollen
Rice	GSE29212	GSM720602	tricellular pollen	tricellular pollen
Rice	GSE29212	GSM720603	tricellular pollen	tricellular pollen
A.thalina	GSE5632	GSM131576	flower	flower
A.thalina	GSE5632	GSM131577	flower	flower
A.thalina	GSE5632	GSM131578	flower	flower
A.thalina	GSE5632	GSM131579	flower	flower
A.thalina	GSE5632	GSM131580	flower	flower

A.thalina	GSE5632	GSM131581	flower	flower
A.thalina	GSE5632	GSM131582	flower	flower
A.thalina	GSE5632	GSM131583	flower	flower
A.thalina	GSE5632	GSM131584	flower	flower
A.thalina	GSE5632	GSM131585	sepal	sepal
A.thalina	GSE5632	GSM131586	sepal	sepal
A.thalina	GSE5632	GSM131587	sepal	sepal
A.thalina	GSE5632	GSM131588	petal	petal
A.thalina	GSE5632	GSM131589	petal	petal
A.thalina	GSE5632	GSM131590	petal	petal
A.thalina	GSE5632	GSM131591	stamen	stamen
A.thalina	GSE5632	GSM131592	stamen	stamen
A.thalina	GSE5632	GSM131593	stamen	stamen
A.thalina	GSE5632	GSM131594	carpel	carpel
A.thalina	GSE5632	GSM131595	carpel	carpel
A.thalina	GSE5632	GSM131596	carpel	carpel
A.thalina	GSE5632	GSM131597	flower	flower
A.thalina	GSE5632	GSM131598	flower	flower
A.thalina	GSE5632	GSM131599	flower	flower
A.thalina	GSE5632	GSM131600	pedicel	pedicel
A.thalina	GSE5632	GSM131601	pedicel	pedicel
A.thalina	GSE5632	GSM131602	pedicel	pedicel
A.thalina	GSE5632	GSM131603	sepal	sepal
A.thalina	GSE5632	GSM131604	sepal	sepal
A.thalina	GSE5632	GSM131605	sepal	sepal
A.thalina	GSE5632	GSM131606	petal	petal
A.thalina	GSE5632	GSM131607	petal	petal
A.thalina	GSE5632	GSM131608	petal	petal
A.thalina	GSE5632	GSM131609	stamen	stamen
A.thalina	GSE5632	GSM131610	stamen	stamen
A.thalina	GSE5632	GSM131611	stamen	stamen
A.thalina	GSE5632	GSM131612	carpel	carpel
A.thalina	GSE5632	GSM131613	carpel	carpel
A.thalina	GSE5632	GSM131614	carpel	carpel
A.thalina	GSE5632	GSM131615	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131616	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131617	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131618	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131619	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131620	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131621	mutant equivalent flower equivalent	flower

A.thalina	GSE5632	GSM131622	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131623	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131624	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131625	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131626	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131627	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131628	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131629	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131630	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131631	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131632	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131633	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131634	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131635	mutant equivalent flower equivalent	flower
A.thalina	GSE5632	GSM131636	pollen	mature pollen
A.thalina	GSE5632	GSM131637	pollen	mature pollen
A.thalina	GSE5632	GSM131638	pollen	mature pollen
A.thalina	GSE5632	GSM131639	flower	flower
A.thalina	GSE5632	GSM131640	flower	flower
A.thalina	GSE5632	GSM131641	flower	flower
A.thalina	GSE5630	GSM131495	cotyledon	cotyledon
A.thalina	GSE5630	GSM131496	cotyledon	cotyledon
A.thalina	GSE5630	GSM131497	cotyledon	cotyledon
A.thalina	GSE5630	GSM131498	leaf	leaf
A.thalina	GSE5630	GSM131499	leaf	leaf
A.thalina	GSE5630	GSM131500	leaf	leaf
A.thalina	GSE5630	GSM131501	rosette leaf	leaf
A.thalina	GSE5630	GSM131502	rosette leaf	leaf
A.thalina	GSE5630	GSM131503	rosette leaf	leaf
A.thalina	GSE5630	GSM131504	rosette leaf	leaf
A.thalina	GSE5630	GSM131505	rosette leaf	leaf
A.thalina	GSE5630	GSM131506	rosette leaf	leaf

A.thalina	GSE5630	GSM131507	rosette leaf	leaf
A.thalina	GSE5630	GSM131508	rosette leaf	leaf
A.thalina	GSE5630	GSM131509	rosette leaf	leaf
A.thalina	GSE5630	GSM131510	rosette leaf	leaf
A.thalina	GSE5630	GSM131511	rosette leaf	leaf
A.thalina	GSE5630	GSM131512	rosette leaf	leaf
A.thalina	GSE5630	GSM131513	rosette leaf	leaf
A.thalina	GSE5630	GSM131514	rosette leaf	leaf
A.thalina	GSE5630	GSM131515	rosette leaf	leaf
A.thalina	GSE5630	GSM131516	rosette leaf	leaf
A.thalina	GSE5630	GSM131517	rosette leaf	leaf
A.thalina	GSE5630	GSM131518	rosette leaf	leaf
A.thalina	GSE5630	GSM131519	rosette leaf	leaf
A.thalina	GSE5630	GSM131520	rosette leaf	leaf
A.thalina	GSE5630	GSM131521	rosette leaf	leaf
A.thalina	GSE5630	GSM131522	rosette leaf	leaf
A.thalina	GSE5630	GSM131523	rosette leaf	leaf
A.thalina	GSE5630	GSM131524	rosette leaf	leaf
A.thalina	GSE5630	GSM131525	rosette leaf	leaf
A.thalina	GSE5630	GSM131526	rosette leaf	leaf
A.thalina	GSE5630	GSM131527	rosette leaf	leaf
A.thalina	GSE5630	GSM131528	leaf	leaf
A.thalina	GSE5630	GSM131529	leaf	leaf
A.thalina	GSE5630	GSM131530	leaf	leaf
A.thalina	GSE5630	GSM131531	leaf	leaf
A.thalina	GSE5630	GSM131532	leaf	leaf
A.thalina	GSE5630	GSM131533	leaf	leaf
A.thalina	GSE5630	GSM131534	leaf	leaf
A.thalina	GSE5630	GSM131535	leaf	leaf
A.thalina	GSE5630	GSM131536	leaf	leaf
A.thalina	GSE5630	GSM131537	leaf	leaf
A.thalina	GSE5630	GSM131538	leaf	leaf
A.thalina	GSE5630	GSM131539	leaf	leaf
A.thalina	GSE5630	GSM131540	cauline leaf	leaf
A.thalina	GSE5630	GSM131541	cauline leaf	leaf
A.thalina	GSE5630	GSM131542	cauline leaf	leaf
A.thalina	GSE5630	GSM131543	rosette leaf	leaf
A.thalina	GSE5630	GSM131544	rosette leaf	leaf
A.thalina	GSE5630	GSM131545	rosette leaf	leaf
A.thalina	GSE5630	GSM131546	rosette leaf	leaf
A.thalina	GSE5630	GSM131547	rosette leaf	leaf
A.thalina	GSE5630	GSM131548	rosette leaf	leaf
A.thalina	GSE5630	GSM131549	rosette leaf	leaf
A.thalina	GSE5630	GSM131550	rosette leaf	leaf
A.thalina	GSE5630	GSM131551	rosette leaf	leaf
A.thalina	GSE5630	GSM131552	leaf	leaf
A.thalina	GSE5630	GSM131553	leaf	leaf
A.thalina	GSE5630	GSM131554	leaf	leaf

A.thalina	GSE5634	GSM131685	fruit	fruit
A.thalina	GSE5634	GSM131686	fruit	fruit
A.thalina	GSE5634	GSM131687	fruit	fruit
A.thalina	GSE5634	GSM131688	fruit	fruit
A.thalina	GSE5634	GSM131689	fruit	fruit
A.thalina	GSE5634	GSM131690	fruit	fruit
A.thalina	GSE5634	GSM131691	fruit	fruit
A.thalina	GSE5634	GSM131692	fruit	fruit
A.thalina	GSE5634	GSM131693	fruit	fruit
A.thalina	GSE5634	GSM131694	seed	seed
A.thalina	GSE5634	GSM131695	seed	seed
A.thalina	GSE5634	GSM131696	seed	seed
A.thalina	GSE5634	GSM131697	seed	seed
A.thalina	GSE5634	GSM131698	seed	seed
A.thalina	GSE5634	GSM131699	seed	seed
A.thalina	GSE5634	GSM131700	seed	seed
A.thalina	GSE5634	GSM131701	seed	seed
A.thalina	GSE5634	GSM131702	seed	seed
A.thalina	GSE5634	GSM131703	seed	seed
A.thalina	GSE5634	GSM131704	seed	seed
A.thalina	GSE5634	GSM131705	seed	seed
A.thalina	GSE5634	GSM131706	seed	seed
A.thalina	GSE5634	GSM131707	seed	seed
A.thalina	GSE5634	GSM131708	seed	seed
A.thalina	GSE5633	GSM131643	hypocotyl	hypocotyl
A.thalina	GSE5633	GSM131644	hypocotyl	hypocotyl
A.thalina	GSE5633	GSM131645	hypocotyl	hypocotyl
A.thalina	GSE5633	GSM131646	vegetative shoot apex, leaf	vegetative shoot apex
A.thalina	GSE5633	GSM131647	vegetative shoot apex, leaf	vegetative shoot apex
A.thalina	GSE5633	GSM131648	vegetative shoot apex, leaf	vegetative shoot apex
A.thalina	GSE5633	GSM131649	vegetative shoot apex	vegetative shoot apex
A.thalina	GSE5633	GSM131650	vegetative shoot apex	vegetative shoot apex
A.thalina	GSE5633	GSM131651	vegetative shoot apex	vegetative shoot apex
A.thalina	GSE5633	GSM131652	shoot apex	vegetative shoot apex
A.thalina	GSE5633	GSM131653	shoot apex	vegetative shoot apex
A.thalina	GSE5633	GSM131654	shoot apex	vegetative shoot apex
A.thalina	GSE5633	GSM131655	stem	stem
A.thalina	GSE5633	GSM131656	stem	stem
A.thalina	GSE5633	GSM131657	stem	stem
A.thalina	GSE5633	GSM131658	stem node	stem
A.thalina	GSE5633	GSM131659	stem node	stem
A.thalina	GSE5633	GSM131660	stem node	stem

[illegible]

A.thalina	GSE5631	GSM131558	root	root
A.thalina	GSE5631	GSM131559	root	root
A.thalina	GSE5631	GSM131560	root	root
A.thalina	GSE5631	GSM131561	root	root
A.thalina	GSE5631	GSM131562	root	root
A.thalina	GSE5631	GSM131563	root	root
A.thalina	GSE5631	GSM131564	root	root
A.thalina	GSE5631	GSM131565	root	root
A.thalina	GSE5631	GSM131566	root	root
A.thalina	GSE5631	GSM131567	root	root
A.thalina	GSE5631	GSM131568	root	root
A.thalina	GSE5631	GSM131569	root	root
A.thalina	GSE5631	GSM131570	root	root
A.thalina	GSE5631	GSM131571	root	root
A.thalina	GSE5631	GSM131572	root	root
A.thalina	GSE5631	GSM131573	root	root
A.thalina	GSE5631	GSM131574	root	root
A.thalina	GSE5631	GSM131575	root	root
A.thalina	GSE6162	<u>GSM142734</u>	DH001_ATH1_A1-UNM1	uninucleate microspore
A.thalina	GSE6162	<u>GSM142735</u>	DH001_ATH1_A2-BCP1	bicellular pollen
A.thalina	GSE6162	<u>GSM142736</u>	DH001_ATH1_A3-TCP1	tricellular pollen
A.thalina	GSE6162	<u>GSM142737</u>	DH001_ATH1_A4-UNM2	uninucleate microspore
A.thalina	GSE6162	<u>GSM142738</u>	DH001_ATH1_A5-BCP2	bicellular pollen
A.thalina	GSE6162	<u>GSM142739</u>	DH001_ATH1_A6-TCP2	tricellular pollen
A.thalina	GSE6162	<u>GSM142740</u>	DH001_ATH1_A7-MPG1	mature pollen
A.thalina	GSE17343	<u>GSM433634</u>	Dry pollen, biological rep1	mature pollen
A.thalina	GSE17343	<u>GSM433635</u>	Dry pollen, biological rep2	tmature pollen
A.thalina	GSE17343	<u>GSM433636</u>	Dry pollen, biological rep3	mature pollen
A.thalina	GSE17343	<u>GSM433637</u>	Dry pollen, biological rep4	mature pollen
A.thalina	GSE17343	<u>GSM433638</u>	0.5PT, biological rep1	germinated pollen
A.thalina	GSE17343	<u>GSM433639</u>	0.5PT, biological rep2	germinated pollen
A.thalina	GSE17343	<u>GSM433640</u>	0.5PT, biological rep3	germinated pollen
A.thalina	GSE17343	<u>GSM433641</u>	0.5hPT, biological rep4	germinated pollen
A.thalina	GSE17343	<u>GSM433642</u>	4hPT, biological rep1	germinated pollen
A.thalina	GSE17343	<u>GSM433643</u>	4hPT, biological rep2	germinated pollen

A.thalina	GSE17343	<u>GSM433644</u>	4hPT, biological rep3	germinated pollen
A.thalina	GSE17343	<u>GSM433645</u>	4hPT, biological rep4	germinated pollen
A.thalina	GSE17343	<u>GSM433646</u>	SIVPT, biological rep1	germinated pollen
A.thalina	GSE17343	<u>GSM433647</u>	SIVPT, biological rep2	germinated pollen
A.thalina	GSE17343	<u>GSM433648</u>	SIVPT, biological rep3	germinated pollen
A.thalina	E-ATMX-35	Seedling Rep 1	Seedling Rep 1	seedling
A.thalina	E-ATMX-35	Seedling Rep 2	Seedling Rep 2	seedling
A.thalina	E-ATMX-35	Seedling Rep 3	Seedling Rep 3	seedling
A.thalina	E-ATMX-35	Pollen Rep 1	Pollen Rep 1	mature pollen
A.thalina	E-ATMX-35	Pollen Rep 2	Pollen Rep 2	mature pollen
A.thalina	E-ATMX-35	Pollen Rep 3	Pollen Rep 3	mature pollen
A.thalina	E-ATMX-35	Sperm Rep 1	Sperm Rep 1	sperm
A.thalina	E-ATMX-35	Sperm Rep 2	Sperm Rep 2	sperm
A.thalina	E-ATMX-35	Sperm Rep 3	Sperm Rep 3	sperm

Table S6. List of 1,495 young genes (PS12-13) supported by syntenic evidence in rice.

Rice Gene	PS	Flanking anchor gene pairs in <i>B. distachyon</i>	Flanking anchor gene pairs in <i>Z. mays</i>
LOC_Os01g01730	12	LOC_Os01g01720-BD2g00660. . LOC_Os01g01740-BD2g00670	LOC_Os01g01720-ZM03g07290. . LOC_Os01g01740-ZM03g07280
LOC_Os01g01880	12	LOC_Os01g01870-BD2g00740. . LOC_Os01g01890-BD2g00750	LOC_Os01g01870-ZM03g07200. . LOC_Os01g01890-ZM03g07190
LOC_Os01g02490	12	LOC_Os01g02440-BD2g01170. . LOC_Os01g02560-BD2g01130	LOC_Os01g02440-ZM08g02400. . LOC_Os01g02560-ZM08g02360
LOC_Os01g02850	12	LOC_Os01g02840-BD2g01320. . LOC_Os01g02860-BD2g01330	LOC_Os01g02840-ZM08g02460. . LOC_Os01g02880-ZM08g02480
LOC_Os01g02990	12	LOC_Os01g02940-BD2g01480. . LOC_Os01g03020-BD2g01504	LOC_Os01g02940-ZM08g02530. . LOC_Os01g03020-ZM08g02570
LOC_Os01g03770	12	LOC_Os01g03760-BD2g02000. . LOC_Os01g03820-BD2g02010	LOC_Os01g03760-ZM03g06240. . LOC_Os01g03820-ZM03g06230
LOC_Os01g03810	12	LOC_Os01g03760-BD2g02000. . LOC_Os01g03820-BD2g02010	LOC_Os01g03760-ZM03g06240. . LOC_Os01g03820-ZM03g06230
LOC_Os01g03960	12	LOC_Os01g03950-BD2g02070. . LOC_Os01g03980-BD2g02080	LOC_Os01g03950-ZM03g06140. . LOC_Os01g03980-ZM03g06130
LOC_Os01g03989	12	LOC_Os01g03980-BD2g02080. . LOC_Os01g04010-BD2g02090	LOC_Os01g03980-ZM08g02960. . LOC_Os01g04010-ZM08g02990
LOC_Os01g04000	12	LOC_Os01g03980-BD2g02080. . LOC_Os01g04010-BD2g02090	LOC_Os01g03980-ZM08g02960. . LOC_Os01g04010-ZM08g02990
LOC_Os01g04005	13	LOC_Os01g03980-BD2g02080. . LOC_Os01g04010-BD2g02090	LOC_Os01g03980-ZM08g02960. . LOC_Os01g04010-ZM08g02990
LOC_Os01g04250	12	LOC_Os01g04230-BD2g02290. . LOC_Os01g04260-BD2g02297	LOC_Os01g04230-ZM03g05920. . LOC_Os01g04260-ZM03g05900
LOC_Os01g04270	12	LOC_Os01g04260-BD2g02297. . LOC_Os01g04280-BD2g02310	LOC_Os01g04260-ZM03g05900. . LOC_Os01g04280-ZM03g05890
LOC_Os01g04610	12	LOC_Os01g04580-BD2g02537. . LOC_Os01g04630-BD2g02560	LOC_Os01g04590-ZM03g05560. . LOC_Os01g04630-ZM03g05550
LOC_Os01g04830	12	LOC_Os01g04814-BD2g02730. . LOC_Os01g04860-BD2g02740	LOC_Os01g04814-ZM08g03360. . LOC_Os01g04870-ZM08g03370
LOC_Os01g05770	12	LOC_Os01g05720-BD2g03320. . LOC_Os01g05790-BD2g03340	LOC_Os01g05720-ZM08g03600. . LOC_Os01g05790-ZM08g03610
LOC_Os01g06570	12	LOC_Os01g06560-BD2g00210. . LOC_Os01g06580-BD2g00220	LOC_Os01g06560-ZM03g04460. . LOC_Os01g06580-ZM03g04450
LOC_Os01g07364	12	LOC_Os01g07360-BD2g04170. . LOC_Os01g07370-BD2g04180	LOC_Os01g07360-ZM03g03980. . LOC_Os01g07370-ZM03g03970
LOC_Os01g07460	12	LOC_Os01g07420-BD2g04230. . LOC_Os01g07480-BD2g04270	LOC_Os01g07450-ZM03g03880. . LOC_Os01g07480-ZM03g03840
LOC_Os01g07470	12	LOC_Os01g07420-BD2g04230. . LOC_Os01g07480-BD2g04270	LOC_Os01g07450-ZM03g03880. . LOC_Os01g07480-ZM03g03840
LOC_Os01g07900	12	LOC_Os01g07890-BD2g04597. . LOC_Os01g07910-BD2g04610	LOC_Os01g07890-ZM03g03490. . LOC_Os01g07910-ZM03g03480
LOC_Os01g08240	12	LOC_Os01g08220-BD2g04840. . LOC_Os01g08270-BD2g04860	LOC_Os01g08220-ZM03g03290. . LOC_Os01g08270-ZM03g03260
LOC_Os01g08390	12	LOC_Os01g08380-BD2g04990. . LOC_Os01g08400-BD2g05000	LOC_Os01g08380-ZM03g03130. . LOC_Os01g08400-ZM03g03120
LOC_Os01g08980	12	LOC_Os01g08970-BD2g05430. . LOC_Os01g09000-BD2g05460	LOC_Os01g08970-ZM08g05180. . LOC_Os01g09000-ZM08g05170
LOC_Os01g09680	12	LOC_Os01g09670-BD2g05770. . LOC_Os01g09700-BD2g05790	LOC_Os01g09670-ZM03g02150. . LOC_Os01g09700-ZM03g02140
LOC_Os01g09690	12	LOC_Os01g09670-BD2g05770. . LOC_Os01g09700-BD2g05790	LOC_Os01g09670-ZM03g02150. . LOC_Os01g09700-ZM03g02140
LOC_Os01g09710	12	LOC_Os01g09700-BD2g05790. . LOC_Os01g09740-BD2g05808	LOC_Os01g09700-ZM03g02140. . LOC_Os01g09720-ZM03g02120
LOC_Os01g09970	12	LOC_Os01g09890-BD2g05940. . LOC_Os01g10010-BD2g05960	LOC_Os01g09890-ZM08g05210. . LOC_Os01g09990-ZM08g05240
LOC_Os01g10030	13	LOC_Os01g10020-BD2g05970. . LOC_Os01g10040-BD2g05980	LOC_Os01g10020-ZM03g01930. . LOC_Os01g10040-ZM03g01920
LOC_Os01g10160	12	LOC_Os01g10150-BD2g06060. . LOC_Os01g10180-BD2g06090	LOC_Os01g10150-ZM08g05300. . LOC_Os01g10180-ZM08g05320
LOC_Os01g10170	12	LOC_Os01g10150-BD2g06060. . LOC_Os01g10180-BD2g06090	LOC_Os01g10150-ZM08g05300. . LOC_Os01g10180-ZM08g05320
LOC_Os01g10650	12	LOC_Os01g10630-BD2g06410. . LOC_Os01g10680-BD2g06420	LOC_Os01g10630-ZM03g01830. . LOC_Os01g10680-ZM03g01860
LOC_Os01g10660	12	LOC_Os01g10630-BD2g06410. . LOC_Os01g10680-BD2g06420	LOC_Os01g10630-ZM03g01830. . LOC_Os01g10680-ZM03g01860
LOC_Os01g10670	12	LOC_Os01g10630-BD2g06410. . LOC_Os01g10680-BD2g06420	LOC_Os01g10630-ZM03g01830. . LOC_Os01g10680-ZM03g01860
LOC_Os01g10860	12	LOC_Os01g10850-BD2g06497. . LOC_Os01g10870-BD2g06530	LOC_Os01g10840-ZM08g05520. . LOC_Os01g10870-ZM08g05550
LOC_Os01g11170	12	LOC_Os01g11160-BD2g06700. . LOC_Os01g11210-BD2g06710	LOC_Os01g11160-ZM03g01400. . LOC_Os01g11210-ZM03g01390
LOC_Os01g11190	12	LOC_Os01g11160-BD2g06700. . LOC_Os01g11210-BD2g06710	LOC_Os01g11160-ZM03g01400. . LOC_Os01g11210-ZM03g01390
LOC_Os01g11360	12	LOC_Os01g11350-BD2g06790. . LOC_Os01g11370-BD2g06800	LOC_Os01g11350-ZM03g01330. . LOC_Os01g11370-ZM03g01310
LOC_Os01g11870	12	LOC_Os01g11850-BD2g07020. . LOC_Os01g11880-BD2g07040	LOC_Os01g11860-ZM04g11800. . LOC_Os01g11880-ZM04g11790
LOC_Os01g12010	12	LOC_Os01g12000-BD2g07130. . LOC_Os01g12020-BD2g07140	LOC_Os01g12000-ZM08g05950. . LOC_Os01g12020-ZM08g05960
LOC_Os01g13380	12	LOC_Os01g13340-BD2g08000. . LOC_Os01g13390-BD2g08030	LOC_Os01g13340-ZM03g00430. . LOC_Os01g13404-ZM03g00400
LOC_Os01g13510	12	LOC_Os01g13490-BD2g08110. . LOC_Os01g13520-BD2g08120	LOC_Os01g13490-ZM03g00360. . LOC_Os01g13520-ZM03g00350
LOC_Os01g14514	12	LOC_Os01g14510-BD2g08660. . LOC_Os01g14520-BD2g08670	LOC_Os01g14430-ZM08g06630. . LOC_Os01g14540-ZM08g06640
LOC_Os01g15330	12	LOC_Os01g15320-BD2g09300. . LOC_Os01g15340-BD2g09320	LOC_Os01g15320-ZM08g01150. . LOC_Os01g15340-ZM08g01140
LOC_Os01g15560	12	LOC_Os01g15550-BD2g09460. . LOC_Os01g15580-BD2g09480	LOC_Os01g15550-ZM03g08630. . LOC_Os01g15600-ZM03g08640
LOC_Os01g15590	12	LOC_Os01g15580-BD2g09480. . LOC_Os01g15600-BD2g09470	LOC_Os01g15550-ZM03g08630. . LOC_Os01g15600-ZM03g08640
LOC_Os01g16060	12	LOC_Os01g16040-BD2g09790. . LOC_Os01g16080-BD2g09800	LOC_Os01g16040-ZM03g08970. . LOC_Os01g16080-ZM03g08950
LOC_Os01g16070	12	LOC_Os01g16040-BD2g09790. . LOC_Os01g16080-BD2g09800	LOC_Os01g16040-ZM03g08970. . LOC_Os01g16080-ZM03g08950
LOC_Os01g17410	13	LOC_Os01g17402-BD2g10890. . LOC_Os01g17430-BD2g10910	LOC_Os01g17402-ZM08g00360. . LOC_Os01g17430-ZM08g00340
LOC_Os01g18250	12	LOC_Os01g18240-BD2g11080. . LOC_Os01g18280-BD2g11090	LOC_Os01g18240-ZM03g10140. . LOC_Os01g18280-ZM03g10150
LOC_Os01g18410	12	LOC_Os01g18400-BD2g11140. . LOC_Os01g18450-BD2g11160	LOC_Os01g18400-ZM08g00200. . LOC_Os01g18450-ZM08g00170
LOC_Os01g18460	12	LOC_Os01g18450-BD2g11160. . LOC_Os01g18584-BD2g11170	LOC_Os01g18450-ZM08g00170. . LOC_Os01g18530-ZM08g00150
LOC_Os01g18780	12	LOC_Os01g18670-BD2g11210. . LOC_Os01g18800-BD2g11220	LOC_Os01g18670-ZM03g10370. . LOC_Os01g18800-ZM03g10400

LOC_Os01g19180	12	LOC_Os01g19170-BD2g11380. . LOC_Os01g19220-BD2g11410	LOC_Os01g19170-ZM08g06900. . LOC_Os01g19220-ZM08g06920
LOC_Os01g19780	12	LOC_Os01g19770-BD2g11567. . LOC_Os01g19800-BD2g11577	LOC_Os01g19770-ZM03g10780. . LOC_Os01g19800-ZM03g10790
LOC_Os01g19980	12	LOC_Os01g19970-BD2g11676. . LOC_Os01g19990-BD2g11690	LOC_Os01g19970-ZM03g10850. . LOC_Os01g19990-ZM03g10860
LOC_Os01g20010	12	LOC_Os01g19990-BD2g11690. . LOC_Os01g20030-BD2g11707	LOC_Os01g19990-ZM03g10860. . LOC_Os01g20030-ZM03g10880
LOC_Os01g20020	13	LOC_Os01g19990-BD2g11690. . LOC_Os01g20030-BD2g11707	LOC_Os01g19990-ZM03g10860. . LOC_Os01g20030-ZM03g10880
LOC_Os01g20920	12	LOC_Os01g20910-BD2g11820. . LOC_Os01g20940-BD2g11830	LOC_Os01g20910-ZM03g11000. . LOC_Os01g20930-ZM03g11020
LOC_Os01g21100	12	LOC_Os01g21070-BD2g11870. . LOC_Os01g21120-BD2g11890	LOC_Os01g21070-ZM08g07190. . LOC_Os01g21120-ZM08g07220
LOC_Os01g21800	12	LOC_Os01g21630-BD2g12047. . LOC_Os01g21820-BD2g12067	LOC_Os01g21630-ZM03g11340. . LOC_Os01g21820-ZM03g11330
LOC_Os01g21950	12	LOC_Os01g21940-BD2g12110. . LOC_Os01g21960-BD2g12120	LOC_Os01g21940-ZM03g11370. . LOC_Os01g21960-ZM03g11390
LOC_Os01g21980	12	LOC_Os01g21970-BD2g12130. . LOC_Os01g21990-BD2g12140	LOC_Os01g21970-ZM03g11440. . LOC_Os01g21990-ZM03g11450
LOC_Os01g22000	12	LOC_Os01g21990-BD2g12140. . LOC_Os01g22010-BD2g12160	LOC_Os01g21990-ZM03g11450. . LOC_Os01g22010-ZM03g11460
LOC_Os01g22650	12	LOC_Os01g22640-BD2g12370. . LOC_Os01g22660-BD2g12340	LOC_Os01g22640-ZM03g11680. . LOC_Os01g22660-ZM03g11690
LOC_Os01g22930	12	LOC_Os01g22900-BD2g12427. . LOC_Os01g22954-BD2g12460	LOC_Os01g22900-ZM08g07720. . LOC_Os01g22954-ZM08g07730
LOC_Os01g26090	12	LOC_Os01g26039-BD2g12850. . LOC_Os01g26120-BD2g12830	LOC_Os01g26039-ZM03g12300. . LOC_Os01g26120-ZM03g12270
LOC_Os01g26110	12	LOC_Os01g26039-BD2g12850. . LOC_Os01g26120-BD2g12830	LOC_Os01g26039-ZM03g12300. . LOC_Os01g26120-ZM03g12270
LOC_Os01g36330	12	LOC_Os01g36240-BD2g40590. . LOC_Os01g36390-BD2g40600	LOC_Os01g36240-ZM08g09130. . LOC_Os01g36390-ZM08g09140
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LOC_Os11g19450	12	LOC_Os11g19340-BD4g20220. . LOC_Os11g19460-BD4g20190	LOC_Os11g19340-ZM04g04580. . LOC_Os11g19460-ZM04g04570
LOC_Os11g19454	12	LOC_Os11g19340-BD4g20220. . LOC_Os11g19460-BD4g20190	LOC_Os11g19340-ZM04g04580. . LOC_Os11g19460-ZM04g04570
LOC_Os11g26900	12	LOC_Os11g26890-BD4g19497. . LOC_Os11g26910-BD4g19510	LOC_Os11g26890-ZM04g05190. . LOC_Os11g26910-ZM04g05180
LOC_Os11g29820	12	LOC_Os11g29810-BD4g19000. . LOC_Os11g29840-BD4g19040	LOC_Os11g29810-ZM04g04790. . LOC_Os11g29840-ZM04g04780
LOC_Os11g29830	12	LOC_Os11g29810-BD4g19000. . LOC_Os11g29840-BD4g19040	LOC_Os11g29810-ZM04g04790. . LOC_Os11g29840-ZM04g04780
LOC_Os11g29860	12	LOC_Os11g29850-BD4g19047. . LOC_Os11g29870-BD4g19060	LOC_Os11g29850-ZM02g42280. . LOC_Os11g29870-ZM02g42290
LOC_Os11g30520	12	LOC_Os11g30500-BD4g18820. . LOC_Os11g30560-BD4g18800	LOC_Os11g30500-ZM02g42380. . LOC_Os11g30560-ZM02g42420
LOC_Os11g31600	12	LOC_Os11g31590-BD4g18260. . LOC_Os11g31620-BD4g18220	LOC_Os11g31590-ZM02g42530. . LOC_Os11g31620-ZM02g42510
LOC_Os11g31715	12	LOC_Os11g31650-BD4g18197. . LOC_Os11g31640-BD4g18210	LOC_Os11g31650-ZM04g05420. . LOC_Os11g31640-ZM04g05410
LOC_Os11g32130	12	LOC_Os11g32110-BD4g17410. . LOC_Os11g32160-BD4g17390	LOC_Os11g32110-ZM04g05650. . LOC_Os11g32160-ZM04g05660
LOC_Os11g32730	13	LOC_Os11g32650-BD4g17230. . LOC_Os11g32750-BD4g17217	LOC_Os11g32720-ZM04g30610. . LOC_Os11g32750-ZM04g30600
LOC_Os11g34100	12	LOC_Os11g34080-BD4g16940. . LOC_Os11g34120-BD4g16900	LOC_Os11g34080-ZM04g30390. . LOC_Os11g34120-ZM04g30360
LOC_Os11g35720	12	LOC_Os11g35710-BD3g22802. . LOC_Os11g35710-BD3g22786	LOC_Os11g35710-ZM05g19320. . LOC_Os11g35710-ZM05g19290
LOC_Os11g36130	12	LOC_Os11g36090-BD4g24457. . LOC_Os11g36140-BD4g24430	LOC_Os11g36090-ZM08g03670. . LOC_Os11g36140-ZM08g03660
LOC_Os11g37250	12	LOC_Os11g37230-BD4g15190. . LOC_Os11g37260-BD4g15200	LOC_Os11g37230-ZM04g32810. . LOC_Os11g37260-ZM04g32800
LOC_Os11g37530	12	LOC_Os11g37520-BD4g15130. . LOC_Os11g37540-BD4g15117	LOC_Os11g37520-ZM02g43780. . LOC_Os11g37540-ZM02g43790
LOC_Os11g37810	12	LOC_Os11g37780-BD4g44603. . LOC_Os11g37850-BD4g44575	LOC_Os11g37780-ZM02g23350. . LOC_Os11g37850-ZM02g23340
LOC_Os11g41920	12	LOC_Os11g41910-BD4g12180. . LOC_Os11g41900-BD4g12190	LOC_Os11g41910-ZM02g44880. . LOC_Os11g41900-ZM02g44870
LOC_Os11g43540	12	LOC_Os11g43520-BD4g11320. . LOC_Os11g43590-BD4g11310	LOC_Os11g43520-ZM04g01220. . LOC_Os11g43590-ZM04g01210
LOC_Os11g43570	13	LOC_Os11g43520-BD4g11320. . LOC_Os11g43590-BD4g11310	LOC_Os11g43520-ZM04g01220. . LOC_Os11g43590-ZM04g01210
LOC_Os12g01720	12	LOC_Os12g01700-BD1g65110. . LOC_Os12g01730-BD1g65100	LOC_Os12g01700-ZM01g12640. . LOC_Os12g01730-ZM01g12650
LOC_Os12g02140	12	LOC_Os12g02130-BD4g25620. . LOC_Os12g02150-BD4g25630	LOC_Os12g02130-ZM10g01480. . LOC_Os12g02150-ZM10g01470
LOC_Os12g03140	12	LOC_Os12g03130-BD4g43950. . LOC_Os12g03150-BD4g43937	LOC_Os12g03130-ZM10g00670. . LOC_Os12g03150-ZM10g00660
LOC_Os12g03220	12	LOC_Os12g03190-BD4g43920. . LOC_Os12g03260-BD4g43900	LOC_Os12g03190-ZM10g00620. . LOC_Os12g03260-ZM10g00610
LOC_Os12g04710	12	LOC_Os12g04700-BD1g62057. . LOC_Os12g04700-BD1g62037	LOC_Os12g04700-ZM01g15840. . LOC_Os12g04700-ZM01g15820
LOC_Os12g06120	12	LOC_Os12g06100-BD4g42110. . LOC_Os12g06130-BD4g42100	LOC_Os12g06100-ZM10g02130. . LOC_Os12g06130-ZM10g02140
LOC_Os12g06790	12	LOC_Os12g06780-BD4g41800. . LOC_Os12g06800-BD4g41790	LOC_Os12g06780-ZM10g02610. . LOC_Os12g06800-ZM10g02600
LOC_Os12g06940	12	LOC_Os12g06910-BD4g41717. . LOC_Os12g06980-BD4g41697	LOC_Os12g06910-ZM03g19470. . LOC_Os12g06980-ZM03g19450
LOC_Os12g06950	12	LOC_Os12g06910-BD4g41717. . LOC_Os12g06980-BD4g41697	LOC_Os12g06910-ZM03g19470. . LOC_Os12g06980-ZM03g19450
LOC_Os12g07070	12	LOC_Os12g07060-BD4g41597. . LOC_Os12g07110-BD4g41590	LOC_Os12g07060-ZM10g02730. . LOC_Os12g07110-ZM10g02740
LOC_Os12g07460	12	LOC_Os12g07450-BD4g41400. . LOC_Os12g07480-BD4g41430	LOC_Os12g07450-ZM03g19260. . LOC_Os12g07480-ZM03g19290
LOC_Os12g07470	12	LOC_Os12g07450-BD4g41400. . LOC_Os12g07480-BD4g41430	LOC_Os12g07450-ZM03g19260. . LOC_Os12g07480-ZM03g19290
LOC_Os12g08120	12	LOC_Os12g08090-BD4g41040. . LOC_Os12g08130-BD4g41030	LOC_Os12g08090-ZM10g03190. . LOC_Os12g08130-ZM10g03150
LOC_Os12g08710	12	LOC_Os12g08700-BD4g40850. . LOC_Os12g08720-BD4g40810	LOC_Os12g08700-ZM03g18760. . LOC_Os12g08720-ZM03g18790
LOC_Os12g08750	12	LOC_Os12g08740-BD4g40790. . LOC_Os12g08770-BD4g40780	LOC_Os12g08740-ZM10g03950. . LOC_Os12g08770-ZM10g03960

LOC_Os12g08970	13	LOC_Os12g08920-BD4g40680. . LOC_Os12g09000-BD4g40670	LOC_Os12g08920-ZM06g03410. . LOC_Os12g08980-ZM06g03370
LOC_Os12g09340	12	LOC_Os12g09320-BD4g41040. . LOC_Os12g09320-BD4g41030	LOC_Os12g09320-ZM10g03190. . LOC_Os12g09320-ZM10g03150
LOC_Os12g09360	12	LOC_Os12g09320-BD4g41040. . LOC_Os12g09320-BD4g41030	LOC_Os12g09320-ZM10g03190. . LOC_Os12g09320-ZM10g03150
LOC_Os12g09370	12	LOC_Os12g09320-BD4g41040. . LOC_Os12g09320-BD4g41030	LOC_Os12g09320-ZM10g03190. . LOC_Os12g09320-ZM10g03150
LOC_Os12g09380	12	LOC_Os12g09320-BD4g41040. . LOC_Os12g09320-BD4g41030	LOC_Os12g09320-ZM10g03190. . LOC_Os12g09320-ZM10g03150
LOC_Os12g10290	12	LOC_Os12g10200-BD4g40410. . LOC_Os12g10320-BD4g40400	LOC_Os12g10200-ZM10g05620. . LOC_Os12g10320-ZM10g05630
LOC_Os12g12220	12	LOC_Os12g12170-BD4g40100. . LOC_Os12g12260-BD4g40090	LOC_Os12g12170-ZM10g05820. . LOC_Os12g12260-ZM10g05840
LOC_Os12g12230	12	LOC_Os12g12170-BD4g40100. . LOC_Os12g12260-BD4g40090	LOC_Os12g12170-ZM10g05820. . LOC_Os12g12260-ZM10g05840
LOC_Os12g12250	12	LOC_Os12g12170-BD4g40100. . LOC_Os12g12260-BD4g40090	LOC_Os12g12170-ZM10g05820. . LOC_Os12g12260-ZM10g05840
LOC_Os12g13740	12	LOC_Os12g13720-BD2g43150. . LOC_Os12g13720-BD2g43120	LOC_Os12g13720-ZM08g23510. . LOC_Os12g13720-ZM08g23500
LOC_Os12g18790	12	LOC_Os12g18770-BD4g39060. . LOC_Os12g18860-BD4g39050	LOC_Os12g18770-ZM01g26090. . LOC_Os12g18860-ZM01g26060
LOC_Os12g18810	12	LOC_Os12g18770-BD4g39060. . LOC_Os12g18860-BD4g39050	LOC_Os12g18770-ZM01g26090. . LOC_Os12g18860-ZM01g26060
LOC_Os12g18850	12	LOC_Os12g18770-BD4g39060. . LOC_Os12g18860-BD4g39050	LOC_Os12g18770-ZM01g26090. . LOC_Os12g18860-ZM01g26060
LOC_Os12g19110	12	LOC_Os12g19090-BD5g13670. . LOC_Os12g19180-BD5g13680	LOC_Os12g19090-ZM02g12100. . LOC_Os12g19180-ZM02g12080
LOC_Os12g19170	12	LOC_Os12g19090-BD5g13670. . LOC_Os12g19180-BD5g13680	LOC_Os12g19090-ZM02g12100. . LOC_Os12g19180-ZM02g12080
LOC_Os12g28760	12	LOC_Os12g28750-BD4g07590. . LOC_Os12g28770-BD4g07580	LOC_Os12g28750-ZM10g03750. . LOC_Os12g28770-ZM10g03730
LOC_Os12g29050	12	LOC_Os12g28770-BD4g07580. . LOC_Os12g29220-BD4g07570	LOC_Os12g28770-ZM10g03730. . LOC_Os12g29220-ZM10g03740
LOC_Os12g29160	12	LOC_Os12g28770-BD4g07580. . LOC_Os12g29220-BD4g07570	LOC_Os12g28770-ZM10g03730. . LOC_Os12g29220-ZM10g03740
LOC_Os12g29180	13	LOC_Os12g28770-BD4g07580. . LOC_Os12g29220-BD4g07570	LOC_Os12g28770-ZM10g03730. . LOC_Os12g29220-ZM10g03740
LOC_Os12g29510	12	LOC_Os12g29500-BD4g07490. . LOC_Os12g29520-BD4g07470	LOC_Os12g29500-ZM03g15010. . LOC_Os12g29520-ZM03g15020
LOC_Os12g29540	12	LOC_Os12g29520-BD4g07470. . LOC_Os12g29550-BD4g07450	LOC_Os12g29520-ZM10g03600. . LOC_Os12g29550-ZM10g03590
LOC_Os12g30160	13	LOC_Os12g30150-BD1g06300. . LOC_Os12g30150-BD1g06270	LOC_Os12g30150-ZM05g02930. . LOC_Os12g30150-ZM05g02900
LOC_Os12g30170	12	LOC_Os12g30150-BD1g06300. . LOC_Os12g30150-BD1g06270	LOC_Os12g30150-ZM05g02930. . LOC_Os12g30150-ZM05g02900
LOC_Os12g30314	12	LOC_Os12g30150-BD1g06300. . LOC_Os12g30150-BD1g06270	LOC_Os12g30150-ZM05g02930. . LOC_Os12g30150-ZM05g02900
LOC_Os12g30330	12	LOC_Os12g30150-BD1g06300. . LOC_Os12g30150-BD1g06270	LOC_Os12g30150-ZM05g02930. . LOC_Os12g30150-ZM05g02900
LOC_Os12g30380	13	LOC_Os12g30150-BD1g06300. . LOC_Os12g30150-BD1g06270	LOC_Os12g30150-ZM05g02930. . LOC_Os12g30150-ZM05g02900
LOC_Os12g35050	12	LOC_Os12g35040-BD4g05830. . LOC_Os12g35060-BD4g05817	LOC_Os12g35040-ZM10g05060. . LOC_Os12g35060-ZM10g05070
LOC_Os12g35590	12	LOC_Os12g35580-BD4g05560. . LOC_Os12g35610-BD4g05540	LOC_Os12g35580-ZM10g04930. . LOC_Os12g35610-ZM10g04920
LOC_Os12g36130	13	LOC_Os12g36110-BD4g05360. . LOC_Os12g36170-BD4g05317	LOC_Os12g36110-ZM10g04850. . LOC_Os12g36170-ZM10g04820
LOC_Os12g36160	12	LOC_Os12g36110-BD4g05360. . LOC_Os12g36170-BD4g05317	LOC_Os12g36110-ZM10g04850. . LOC_Os12g36170-ZM10g04820
LOC_Os12g36735	12	LOC_Os12g36670-BD4g05157. . LOC_Os12g36750-BD4g05130	LOC_Os12g36670-ZM10g04720. . LOC_Os12g36740-ZM10g04710
LOC_Os12g36820	12	LOC_Os12g36810-BD4g05050. . LOC_Os12g36830-BD4g05040	LOC_Os12g36810-ZM10g04660. . LOC_Os12g36830-ZM10g04650
LOC_Os12g36960	12	LOC_Os12g36950-BD4g04870. . LOC_Os12g37060-BD4g04850	LOC_Os12g36950-ZM03g17420. . LOC_Os12g37060-ZM03g17390
LOC_Os12g36970	12	LOC_Os12g36950-BD4g04870. . LOC_Os12g37060-BD4g04850	LOC_Os12g36950-ZM03g17420. . LOC_Os12g37060-ZM03g17390
LOC_Os12g37800	12	LOC_Os12g37780-BD4g04440. . LOC_Os12g37840-BD4g04420	LOC_Os12g37780-ZM01g26450. . LOC_Os12g37840-ZM01g26480
LOC_Os12g38470	12	LOC_Os12g38460-BD4g03890. . LOC_Os12g38490-BD4g03867	LOC_Os12g38460-ZM01g27080. . LOC_Os12g38480-ZM01g27090
LOC_Os12g38520	12	LOC_Os12g38490-BD4g03867. . LOC_Os12g38570-BD4g03847	LOC_Os12g38490-ZM03g16750. . LOC_Os12g38570-ZM03g16740
LOC_Os12g38950	12	LOC_Os12g38930-BD4g03670. . LOC_Os12g38960-BD4g03630	LOC_Os12g38930-ZM03g16600. . LOC_Os12g38960-ZM03g16590
LOC_Os12g40380	12	LOC_Os12g40360-BD4g02860. . LOC_Os12g40419-BD4g02850	LOC_Os12g40340-ZM01g28450. . LOC_Os12g40419-ZM01g28470
LOC_Os12g40850	12	LOC_Os12g40840-BD4g02630. . LOC_Os12g40860-BD4g02620	LOC_Os12g40840-ZM03g16000. . LOC_Os12g40860-ZM03g16010
LOC_Os12g42590	12	LOC_Os12g42570-BD4g01320. . LOC_Os12g42600-BD4g01310	LOC_Os12g42570-ZM03g13590. . LOC_Os12g42600-ZM03g13620
LOC_Os12g43564	12	LOC_Os12g43560-BD4g00980. . LOC_Os12g43580-BD4g00967	LOC_Os12g43560-ZM01g30360. . LOC_Os12g43580-ZM01g30340

Table S7. List of 176 young genes (PS13) supported by syntenic evidence in Arabidopsis.

Ath gene	PS	Flanking anchor gene pairs in <i>A. lyrata</i>	Flanking anchor gene pairs in <i>T. cacao</i>
AT1G04501	13	AT1G04500-AL1G03870. . AT1G04510-AL1G03880	AT1G04500-TC04G026230. . AT1G04510-TC04G026240
AT1G04684	13	AT1G04680-AL1G04120. . AT1G04690-AL1G04130	AT1G04680-TC04G021780. . AT1G04690-TC04G021750
AT1G08032	13	AT1G08030-AL1G07630. . AT1G08035-AL1G07640	AT1G08030-TC09G033530. . AT1G08040-TC09G033560
AT1G10652	13	AT1G10650-AL1G10670. . AT1G10657-AL1G10680	AT1G10650-TC02G024010. . AT1G10657-TC02G024030
AT1G12411	13	AT1G12410-AL1G12770. . AT1G12420-AL1G12780	AT1G12410-TC03G026060. . AT1G12420-TC03G026080
AT1G26921	13	AT1G26920-AL1G26540. . AT1G26930-AL1G26530	AT1G26920-TC02G033620. . AT1G26940-TC02G033600
AT1G27565	13	AT1G27540-AL1G28690. . AT1G27580-AL1G28680	AT1G27530-TC08G006530. . AT1G27590-TC08G006560
AT1G28281	13	AT1G28280-AL1G29450. . AT1G28290-AL1G29460	AT1G28280-TC06G015670. . AT1G28290-TC06G015680
AT1G28304	13	AT1G28300-AL1G29470. . AT1G28305-AL1G29490	AT1G28300-TC06G015590. . AT1G28310-TC06G015560
AT1G28307	13	AT1G28305-AL1G29490. . AT1G28310-AL1G29500	AT1G28300-TC06G015590. . AT1G28310-TC06G015560
AT1G31772	13	AT1G31770-AL1G32950. . AT1G31780-AL1G32960	AT1G31770-TC03G030790. . AT1G31780-TC03G030780
AT1G32225	13	AT1G32220-AL1G33460. . AT1G32230-AL1G33490	AT1G32220-TC03G029960. . AT1G32230-TC03G029940
AT1G32975	13	AT1G32970-AL1G34330. . AT1G32990-AL1G34340	AT1G32970-TC03G022580. . AT1G32990-TC03G022540
AT1G47660	13	AT1G47655-AL1G41040. . AT1G47670-AL1G41060	AT1G47655-TC08G001210. . AT1G47670-TC08G001200
AT1G51823	13	AT1G51820-AL5G14780. . AT1G51830-AL5G14770	AT1G51820-TC06G007100. . AT1G51830-TC06G007080
AT1G52905	13	AT1G52900-AL1G47920. . AT1G52910-AL1G47940	AT1G52900-TC07G006670. . AT1G52910-TC07G006640
AT1G53039	13	AT1G53035-AL1G48100. . AT1G53040-AL1G48110	AT1G53035-TC00G024350. . AT1G53040-TC00G024340
AT1G53785	13	AT1G53780-AL1G40110. . AT1G53790-AL1G40120	AT1G53780-TC06G010870. . AT1G53800-TC06G010830
AT1G55615	13	AT1G55610-AL1G50240. . AT1G55620-AL1G50250	AT1G55610-TC07G000200. . AT1G55620-TC07G000180
AT1G58235	13	AT1G58230-AL2G07580. . AT1G58242-AL2G07610	AT1G58230-TC08G006100. . AT1G58250-TC08G006140
AT1G59535	13	AT1G59530-AL2G06880. . AT1G59540-AL2G06870	AT1G59530-TC08G007120. . AT1G59540-TC08G007110
AT1G59885	13	AT1G59870-AL2G06250. . AT1G59890-AL2G06240	AT1G59870-TC00G062170. . AT1G59890-TC00G062130
AT1G64142	13	AT1G64140-AL2G00910. . AT1G64150-AL2G00890	AT1G64140-TC03G028250. . AT1G64150-TC03G028260
AT1G67875	13	AT1G67870-AL2G15970. . AT1G67880-AL2G15980	AT1G67856-TC02G024970. . AT1G67880-TC02G024950
AT1G70209	13	AT1G70200-AL2G18610. . AT1G70210-AL2G18620	AT1G70200-TC00G074850. . AT1G70210-TC00G074890
AT1G77746	13	AT1G77740-AL2G26700. . AT1G77750-AL2G26710	AT1G77740-TC08G010020. . AT1G77750-TC08G009990
AT2G02023	13	AT2G02020-AL5G01180. . AT2G02030-AL5G01160	AT2G02020-TC09G030370. . AT2G02040-TC09G030360
AT2G02026	13	AT2G02020-AL5G01180. . AT2G02030-AL5G01160	AT2G02020-TC09G030370. . AT2G02040-TC09G030360
AT2G05803	13	AT2G05790-AL3G31250. . AT2G05810-AL3G31270	AT2G05790-TC01G017650. . AT2G05810-TC01G017670
AT2G06095	13	AT2G06090-AL3G31660. . AT2G06200-AL3G31670	AT2G06050-TC09G007090. . AT2G06210-TC09G007120
AT2G13363	13	AT2G13360-AL3G33150. . AT2G13370-AL3G33160	AT2G13360-TC09G023620. . AT2G13370-TC09G023630
AT2G16668	13	AT2G16660-AL3G37210. . AT2G16700-AL3G37220	AT2G16660-TC02G005170. . AT2G16700-TC02G005140
AT2G17960	13	AT2G17950-AL3G38760. . AT2G17970-AL3G38770	AT2G17950-TC01G001780. . AT2G17970-TC01G001790
AT2G18270	13	AT2G18260-AL3G39330. . AT2G18280-AL3G39340	AT2G18250-TC01G003010. . AT2G18280-TC01G003050
AT2G18610	13	AT2G18600-AL3G39760. . AT2G18620-AL3G39770	AT2G18600-TC01G003720. . AT2G18630-TC01G003750
AT2G20150	13	AT2G20142-AL3G35880. . AT2G20160-AL3G35840	AT2G20140-TC00G026220. . AT2G20180-TC00G026240
AT2G22088	13	AT2G22070-AL4G01310. . AT2G22090-AL4G01330	AT2G22070-TC01G009790. . AT2G22090-TC01G009750
AT2G22241	13	AT2G22240-AL4G01700. . AT2G22250-AL4G01710	AT2G22240-TC01G009380. . AT2G22250-TC01G009420
AT2G22820	13	AT2G22810-AL7G02840. . AT2G22830-AL7G02850	AT2G22810-TC08G006930. . AT2G22830-TC08G006960
AT2G28401	13	AT2G28400-AL4G11580. . AT2G28410-AL4G11560	AT2G28390-TC09G033440. . AT2G28410-TC09G033400
AT2G29654	13	AT2G29650-AL4G14180. . AT2G29660-AL4G14190	AT2G29650-TC09G030210. . AT2G29660-TC09G030200
AT2G29679	13	AT2G29670-AL4G14220. . AT2G29680-AL4G14230	AT2G29670-TC09G030170. . AT2G29680-TC09G030160
AT2G31005	13	AT2G30990-AL4G15760. . AT2G31010-AL4G15770	AT2G30990-TC01G013820. . AT2G31010-TC01G013810
AT2G34185	13	AT2G34180-AL4G19410. . AT2G34190-AL4G19420	AT2G34180-TC06G014180. . AT2G34190-TC06G014150
AT2G34186	13	AT2G34180-AL4G19410. . AT2G34190-AL4G19420	AT2G34180-TC06G014180. . AT2G34190-TC06G014150
AT2G36571	13	AT2G36570-AL4G22040. . AT2G36580-AL4G22050	AT2G36570-TC05G008010. . AT2G36580-TC05G007990
AT2G36632	13	AT2G36630-AL4G22100. . AT2G36640-AL4G22110	AT2G36630-TC05G007920. . AT2G36640-TC05G007880
AT2G36881	13	AT2G36880-AL4G22380. . AT2G36885-AL4G22400	AT2G36880-TC05G007120. . AT2G36885-TC05G007090
AT2G36916	13	AT2G36910-AL4G22460. . AT2G36920-AL4G22480	AT2G36910-TC05G007070. . AT2G36930-TC05G007060
AT2G38350	13	AT2G38340-AL4G24680. . AT2G38360-AL4G24690	AT2G38340-TC05G001640. . AT2G38360-TC05G001610
AT2G40004	13	AT2G40000-AL4G26640. . AT2G40010-AL4G26680	AT2G40000-TC10G001870. . AT2G40010-TC10G001880
AT2G40711	13	AT2G40700-AL4G27600. . AT2G40720-AL4G27610	AT2G40700-TC00G061430. . AT2G40720-TC00G061420
AT2G43871	13	AT2G43870-AL4G31500. . AT2G43880-AL4G31510	AT2G43870-TC05G000120. . AT2G43890-TC05G000100
AT2G45412	13	AT2G45410-AL6G41470. . AT2G45420-AL6G41460	AT2G45410-TC01G037490. . AT2G45420-TC01G037470

AT2G45434	13	AT2G45430-AL4G33340. . AT2G45440-AL4G33350	AT2G45430-TC01G037430. . AT2G45440-TC01G037410
AT2G46308	13	AT2G46300-AL4G34320. . AT2G46310-AL4G34330	AT2G46300-TC01G034900. . AT2G46320-TC01G034860
AT2G46662	13	AT2G46660-AL5G32810. . AT2G46680-AL5G32820	AT2G46660-TC01G034020. . AT2G46680-TC01G033980
AT3G04721	13	AT3G04720-AL3G04430. . AT3G04730-AL3G04440	AT3G04720-TC05G027320. . AT3G04730-TC05G027350
AT3G04732	13	AT3G04730-AL3G04440. . AT3G04735-AL3G04450	AT3G04730-TC05G027350. . AT3G04740-TC05G027370
AT3G05193	13	AT3G05190-AL3G05030. . AT3G05200-AL3G05040	AT3G05190-TC05G029740. . AT3G05200-TC05G029710
AT3G05602	13	AT3G05600-AL3G05530. . AT3G05610-AL3G05540	AT3G05600-TC05G030460. . AT3G05610-TC05G030480
AT3G06142	13	AT3G06140-AL3G06190. . AT3G06150-AL3G06200	AT3G06140-TC04G022910. . AT3G06145-TC04G022880
AT3G07273	13	AT3G07270-AL3G07650. . AT3G07290-AL3G07680	AT3G07270-TC01G021170. . AT3G07290-TC01G021130
AT3G08762	13	AT3G08760-AL3G08840. . AT3G08770-AL3G08850	AT3G08760-TC04G016330. . AT3G08770-TC04G016380
AT3G09863	13	AT3G09860-AL3G10070. . AT3G09870-AL3G10080	AT3G09860-TC05G006810. . AT3G09870-TC05G006850
AT3G13403	13	AT3G13400-AL3G13920. . AT3G13410-AL3G13930	AT3G13400-TC09G020250. . AT3G13410-TC09G020190
AT3G13404	13	AT3G13400-AL3G13920. . AT3G13410-AL3G13930	AT3G13400-TC09G020250. . AT3G13410-TC09G020190
AT3G13857	13	AT3G13850-AL3G14550. . AT3G13860-AL3G14560	AT3G13850-TC06G008890. . AT3G13860-TC06G008910
AT3G15111	13	AT3G15110-AL3G15900. . AT3G15115-AL3G15910	AT3G15110-TC07G008850. . AT3G15120-TC07G008810
AT3G15251	13	AT3G15250-AL3G16060. . AT3G15260-AL3G16070	AT3G15220-TC07G008450. . AT3G15260-TC07G008420
AT3G16117	13	AT3G16110-AL1G47170. . AT3G16120-AL1G47160	AT3G16110-TC06G008460. . AT3G16120-TC06G008430
AT3G17845	13	AT3G17840-AL3G19290. . AT3G17850-AL3G19300	AT3G17840-TC03G006900. . AT3G17850-TC03G006880
AT3G18779	13	AT3G18773-AL3G20360. . AT3G18780-AL3G20380	AT3G18770-TC01G010940. . AT3G18780-TC01G010900
AT3G19055	13	AT3G19050-AL3G20610. . AT3G19080-AL3G20620	AT3G19050-TC02G008310. . AT3G19080-TC02G008350
AT3G19274	13	AT3G19270-AL3G20820. . AT3G19280-AL3G20830	AT3G19270-TC02G008770. . AT3G19280-TC02G008800
AT3G22436	13	AT3G22430-AL3G24800. . AT3G22440-AL3G24810	AT3G22430-TC04G023760. . AT3G22440-TC04G023770
AT3G22723	13	AT3G22720-AL3G25060. . AT3G22730-AL3G25070	AT3G22690-TC04G024140. . AT3G22740-TC04G024150
AT3G22968	13	AT3G22961-AL3G25330. . AT3G22970-AL3G25350	AT3G22960-TC00G092370. . AT3G22970-TC00G092360
AT3G24516	13	AT3G24515-AL3G27950. . AT3G24520-AL3G27960	AT3G24515-TC09G009860. . AT3G24520-TC09G009830
AT3G25221	13	AT3G25220-AL8G11530. . AT3G25230-AL8G11510	AT3G25220-TC01G021040. . AT3G25230-TC01G021030
AT3G27968	13	AT3G27960-AL5G07180. . AT3G27970-AL5G07200	AT3G27960-TC04G000920. . AT3G27970-TC04G000910
AT3G28170	13	AT3G28150-AL5G07340. . AT3G28180-AL5G07360	AT3G28150-TC04G000450. . AT3G28180-TC04G000420
AT3G29195	13	AT3G29185-AL5G08730. . AT3G29200-AL5G08750	AT3G29185-TC04G009730. . AT3G29200-TC04G009770
AT3G30160	13	AT3G29970-AL5G09460. . AT3G30180-AL5G09490	AT3G29970-TC00G011650. . AT3G30180-TC00G011680
AT3G43153	13	AT3G43120-AL6G21090. . AT3G43190-AL6G21110	AT3G43120-TC09G006380. . AT3G43190-TC09G006370
AT3G43160	13	AT3G43120-AL6G21090. . AT3G43190-AL6G21110	AT3G43120-TC09G006380. . AT3G43190-TC09G006370
AT3G43402	13	AT3G43300-AL5G10950. . AT3G43430-AL5G10960	AT3G43300-TC09G006060. . AT3G43430-TC09G006040
AT3G43420	13	AT3G43300-AL5G10950. . AT3G43430-AL5G10960	AT3G43300-TC09G006060. . AT3G43430-TC09G006040
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AT3G49051	13	AT3G49050-AL5G17970. . AT3G49055-AL5G17980	AT3G49050-TC03G020360. . AT3G49055-TC03G020320
AT3G49230	13	AT3G49220-AL5G18310. . AT3G49240-AL5G18340	AT3G49220-TC03G020960. . AT3G49240-TC03G020920
AT3G49551	13	AT3G49550-AL5G18750. . AT3G49560-AL5G18760	AT3G49550-TC03G022100. . AT3G49560-TC03G022140
AT3G49744	13	AT3G49740-AL5G19070. . AT3G49750-AL5G19080	AT3G49740-TC01G006970. . AT3G49750-TC01G006930
AT3G50540	13	AT3G50530-AL5G20030. . AT3G50560-AL5G20050	AT3G50530-TC01G004660. . AT3G50560-TC01G004680
AT3G50550	13	AT3G50530-AL5G20030. . AT3G50560-AL5G20050	AT3G50530-TC01G004660. . AT3G50560-TC01G004680
AT3G50682	13	AT3G50670-AL5G20170. . AT3G50685-AL5G20190	AT3G50670-TC01G003360. . AT3G50685-TC01G003400
AT3G50764	13	AT3G50760-AL5G20340. . AT3G50770-AL5G20350	AT3G50760-TC01G003810. . AT3G50770-TC01G003830
AT3G51057	13	AT3G51050-AL5G20690. . AT3G51060-AL5G20700	AT3G51050-TC01G002340. . AT3G51060-TC01G002320
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AT3G57072	13	AT3G57070-AL5G27450. . AT3G57080-AL5G27470	AT3G57070-TC05G015550. . AT3G57080-TC05G015540
AT3G58540	13	AT3G58530-AL5G29120. . AT3G58550-AL5G29130	AT3G58530-TC05G020560. . AT3G58560-TC05G020590
AT3G60286	13	AT3G60280-AL5G30910. . AT3G60290-AL5G30920	AT3G60280-TC01G039350. . AT3G60300-TC01G039310
AT3G61763	13	AT3G61760-AL5G32680. . AT3G61770-AL5G32690	AT3G61760-TC01G034410. . AT3G61770-TC01G034400
AT3G62907	13	AT3G62900-AL5G33980. . AT3G62910-AL5G34000	AT3G62900-TC01G029870. . AT3G62910-TC01G029830
AT4G00342	13	AT4G00340-AL6G41330. . AT4G00350-AL6G41320	AT4G00340-TC01G035740. . AT4G00350-TC01G035730
AT4G01328	13	AT4G01320-AL6G40270. . AT4G01330-AL6G40260	AT4G01320-TC01G035490. . AT4G01330-TC01G035500
AT4G01671	13	AT4G01670-AL6G39880. . AT4G01680-AL6G39860	AT4G01660-TC01G033100. . AT4G01680-TC01G033070
AT4G02325	13	AT4G02320-AL6G39110. . AT4G02330-AL6G39080	AT4G02320-TC01G030870. . AT4G02330-TC01G030860

AT4G02489	13	AT4G02485-AL6G38870. . AT4G02500-AL6G38860	AT4G02485-TC01G030300. . AT4G02500-TC01G030290
AT4G03113	13	AT4G03110-AL6G38170. . AT4G03115-AL6G38160	AT4G03110-TC01G029380. . AT4G03115-TC01G029390
AT4G04078	13	AT4G04040-AL6G36110. . AT4G04080-AL6G36130	AT4G04040-TC06G019880. . AT4G04180-TC06G019860
AT4G06639	13	AT4G06634-AL6G29660. . AT4G06676-AL6G29690	AT4G06634-TC00G050000. . AT4G06676-TC00G050040
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AT4G10596	13	AT4G10595-AL6G33010. . AT4G10600-AL6G33020	AT4G10590-TC03G022660. . AT4G10610-TC03G022680
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AT4G12380	13	AT4G12370-AL6G35630. . AT4G12390-AL6G35650	AT4G12350-TC03G025710. . AT4G12390-TC03G025670
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AT4G21216	13	AT4G21215-AL7G21470. . AT4G21220-AL7G21460	AT4G21215-TC06G018590. . AT4G21220-TC06G018560
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AT4G31136	13	AT4G31130-AL7G10440. . AT4G31140-AL7G10430	AT4G31130-TC09G000160. . AT4G31140-TC09G000150
AT4G31280	13	AT4G31270-AL7G10320. . AT4G31290-AL7G10310	AT4G31270-TC09G000240. . AT4G31290-TC09G000250
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AT5G02811	13	AT5G02810-AL6G01910. . AT5G02820-AL6G01920	AT5G02810-TC05G005720. . AT5G02820-TC05G005750
AT5G04238	13	AT5G04230-AL6G03560. . AT5G04240-AL6G03570	AT5G04230-TC10G005730. . AT5G04240-TC10G005770
AT5G04386	13	AT5G04370-AL6G03710. . AT5G04390-AL6G03720	AT5G04360-TC10G006910. . AT5G04390-TC10G006940
AT5G05598	13	AT5G05590-AL6G05190. . AT5G05600-AL6G05200	AT5G05590-TC10G001370. . AT5G05600-TC10G001390
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AT5G17847	13	AT5G17840-AL6G17770. . AT5G17850-AL6G17780	AT5G17840-TC00G020110. . AT5G17850-TC00G020100
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AT5G23989	13	AT5G23980-AL6G23810. . AT5G23990-AL6G23800	AT5G23980-TC03G020030. . AT5G23990-TC03G020020
AT5G24250	13	AT5G24240-AL6G24170. . AT5G24260-AL6G24190	AT5G24240-TC03G020950. . AT5G24260-TC03G020940
AT5G27170	13	AT5G27150-AL6G28290. . AT5G27200-AL6G28280	AT5G27150-TC05G024620. . AT5G27200-TC05G024590
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AT5G64343	13	AT5G64340-AL8G31030. . AT5G64350-AL8G31040	AT5G64330-TC02G010860. . AT5G64350-TC02G010820
AT5G65533	13	AT5G65530-AL8G32360. . AT5G65540-AL8G32370	AT5G65530-TC01G007910. . AT5G65540-TC01G007900

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