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**Genome-wide analysis and expression characteristics of small auxin-up RNA (*SAUR*) genes in moso bamboo
(*Phyllostachys edulis*)**

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Draft

Abstract: Moso bamboo (*Phyllostachys edulis*) is well-known for its rapid shoot growth. Auxin exerts pleiotropic effects on plant growth. The small auxin-up RNA (*SAUR*) genes are early auxin-responsive genes involved in plant growth. In total, 38 *SAUR* genes were identified in *P. edulis* (*PheSAUR*). A comprehensive overview of the *PheSAUR* gene family is presented, including the gene structures, phylogeny and subcellular location predictions. A transcriptome analysis indicated that 37 (except *PheSAUR18*) of the *PheSAUR* genes were expressed during shoot growth process and the *PheSAUR* genes were differentially expressed. Furthermore, quantitative real-time PCR analysis indicated that all of the *PheSAUR* genes could be induced in different tissues of seedlings and that 37 (except *PheSAUR41*) of the *PheSAUR* genes were up-regulated after indole-3-acetic acid (IAA) treatment. These results reveal a comprehensive overview of the *PheSAUR* gene family and may pave the way for deciphering their functions during bamboo development.

Keywords: *Phyllostachys edulis*; PheSAUR; shoot growth; IAA; qRT-PCR

Introduction

Moso bamboo (*Phyllostachys edulis*) is a large woody bamboo in Asia, and the most economically important bamboo in China. Under suitable conditions, the shoots can grow from 0 to 20 meters in less than 3 months (Peng et al. 2010; Peng et al. 2013a). Mountains of lumber are produced in the process. However, research was focused on the growth mode and shoot anatomical structures (Murphy and Alvin 1992; Lin et al. 2002). Thus, what actually happens to moso bamboo during its rapid growth process and what regulates the internal mechanisms? These questions are attracting scientific interest.

The plant hormone exerts a pleiotropic effect on various aspects of plant growth and development, including cell elongation, cell division, differentiation, root initiation, apical dominance and tropic responses. Auxin mediates these effects at the molecular level by altering the expression levels of numerous genes (Abel and Theologis 1996; Hagen and Guilfoyle 2002). One of the vital auxin-responsive families is the small auxin-up RNA (*SAUR*) gene family. *SAUR* genes have been identified in mung bean (Yamamoto et al. 1992), pea (Guilfoyle et al. 1993), tomato (Zurek et al. 1994), *Arabidopsis* (Gil et al. 1994), apple (Watillon et al. 1998), radish (Ann et al. 1998), maize (Yang and Poovaiah 2000), rice (Jain et al. 2006b), moss (Rensing et al. 2008), sorghum (Wang et al. 2010), potato, tobacco, pepper, petunia (Wu et al. 2012), cotton (Yang et al. 2012), litchi (Kuang et al. 2012), peach (Tatsuki et al. 2013), poplar (Wang et al. 2014) and citrus (Xie et al. 2015). Until now, no *SAUR* gene had been reported in *P. edulis* (*PheSAUR*).

SAUR can be induced by the application of exogenous auxin. These auxin-induced genes then control downstream genes. Most of the biological functions of *SAUR* genes are focused on hypocotyl growth stem elongation and altering auxin transport. Recently, the biological mechanism of the *SAUR* genes was demonstrated in promoting cell expansion in *Arabidopsis*. *SAUR19* subfamily (AT5G18010, AT5G18020, AT5G18030, AT5G18050, AT5G18060 and AT5G18080) proteins could provide a mechanistic link between auxin and plasma membrane H⁺-ATPases in *Arabidopsis* (Spartz et al.

2014; Ren and Gray 2015). The SAUR19 protein (AT5G18010) also interacts with the PP2C-D subfamily of the type 2C protein phosphatases and negatively regulates plasma membrane H⁺-ATPase activity (Spartz et al. 2014). SAUR76, 77 and 78 (AT5G20820, AT1G17345 and AT1G72430) were identified as associating with the ethylene receptors ethylene response2 and ethylene insensitive. These proteins could be induced by auxin and ethylene (Li et al. 2015). However, the overexpression of *SAUR39* (LOC_Os09g37330) in rice showed lower shoot and root growth, altered shoot morphology, smaller vascular tissues, and lower yields (Kant et al. 2009). *AtSAUR36* (AT2G45210) had been reported to be involved in the promotion of leaf senescence in *Arabidopsis* (Hou et al. 2013).

The *SAUR* gene family contains numerous auxin-response genes in different species, including 81 *SAURs* (with 2 pseudogenes) in *Arabidopsis* (Hagen and Guilfoyle 2002), 58 *SAURs* (with 2 pseudogenes) in rice (Jain et al. 2006), 18 *SAURs* in moss (Rensing et al. 2008), 71 *SAURs* in *sorghum* (Wang et al. 2010), 134 *SAURs* in potato, 99 *SAURs* in tomato (Wu et al. 2012), 79 *SAURs* in maize (Chen et al. 2014) and 70 *SAURs* in citrus (Xie et al. 2015). These reports also reported their main functions in these species. The most prevalently demonstrated function of the *SAUR* genes is in promoting plant growth. *P. edulis* is a bamboo with rapid shoot growth, which is its most significant characteristic. *SAUR* genes may play the same functions in bamboo.

The fast growing speed in moso bamboo is uncommon in plant species. However, the mechanism of rapid growth is still obscure in bamboo. Transcriptome analysis of moso bamboo shoots would provide important information in revealing the mechanism on the whole side (Peng et al. 2013b). But the detailed genes involved in the growing process are still not clear. *SAUR* gene family is one of the important gene families in auxin signaling and was never reported in bamboo. Identification of *PheSAUR* genes in moso bamboo is necessary for revealing the mechanism of rapid growing. Here, a genome-wide analysis of the *PheSAUR* genes could provide detailed information on the most numerous early auxin-responsive gene family.

Materials and Methods

Searching for *P. edulis* SAUR family genes

Bamboo genome database (<http://www.bamboogdb.org/>) resources were used for the identification of putative SAURs in bamboo (Zhao et al. 2014). The coding sequences and amino acid sequences of *Arabidopsis* and rice SAUR genes and proteins were downloaded from The *Arabidopsis* Information Resource (<https://www.arabidopsis.org/>) and Genome Annotation Project Database (<http://rice.plantbiology.msu.edu/>) (Lamesch et al. 2012; Kawahara et al. 2013). BLAST search algorithms BLASTP and BLASTN were used to identify putative *PheSAURs* in bamboo using *Arabidopsis* (*AtSAUR*), rice SAUR (*OsSAUR*) coding and protein sequences as queries. Pfam 02519 in the Pfam database (<http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>) was used to confirm each predicted *PheSAUR* protein (with cut off e-value of e^{-5}) sequence (Marchler-Bauer et al. 2014).

Phylogenetic analysis of *PheSAUR* genes

A multiple sequence alignment analysis was conducted using the ClustalX (version 2.1) program with default parameters (Larkin et al. 2007). The phylogenetic analysis was carried out using the neighbor-joining method, and the unrooted tree was displayed using the Mega6.0 program (Tamura et al. 2013). Bootstrap values (above 50%) from 1000 replicates are indicated at each node.

Structure and sequence analysis of *PheSAUR* genes

All of the *P. edulis* genome and coding sequences were obtained from the bamboo genome database. The Gene Structure Display Server (<http://gsds1.cbi.pku.edu.cn/index.php>) was used to analyze the gene structures (Guo et al. 2007).

The 1,500 bp of genomic sequences upstream of the 5' untranslated regions (UTR) of each gene were downloaded for an

upstream element searching. Plant CARE (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>), a database of plant *cis*-acting regulatory DNA elements, was used to identify auxin-responsive elements (Lescot et al. 2002). The downstream (DST) elements were searched manually for the presence of conserved nucleotides in the 3'UTR of each *PheSAUR* retrieved from the bamboo genome database. The conserved consensus motifs in PheSAUR, OsSAUR and AtSAUR proteins were searched by MEME (<http://meme-suite.org/>) (Bailey et al. 2006). IMEter v2.0 (<http://korflab.ucdavis.edu/cgi-bin/web-imeter2.pl>) was used to calculate the intron-mediated enhancement (IME) signals in introns (Parra et al. 2011). CELLO v2.5 Server (<http://cello.life.nctu.edu.tw/>) was used to predict the probable protein localization for candidate PheSAURs (Yu et al. 2004).

The top internodes of *P. edulis* shoots and culms at different heights

The top internodes of *P. edulis* shoots and culms at 0.1, 1, 3, 6, 9, 12, 15 (control) meters were collected in Anhui Province, China, where is a natural distribution area. Eight different heights of shoots and the culm after leaf expansion were selected in accordance with the developmental stages of *P. edulis*. Subsequently, each sample was cut from the tissue located in the basal part of the internodes, and finally collected. These materials were used for the transcriptome analysis of *PheSAUR* genes.

Seedlings of *P. edulis* used for qRT-PCR

P. edulis seedlings were grown in vermiculite in a growth chamber (26°C for 16 h light/18°C for 8 h dark) for 2 months. For the auxin treatment, IAA was dissolved with dimethyl sulphoxide (DMSO) and then made as IAA solution. 1 mM IAA was irrigated into vermiculite. The leaves, stems and roots of these seedlings were collected at 0, 1, 3 and 5 hours after IAA treatment. These materials were promptly transferred into liquid nitrogen for quantitative real-time PCR (qRT-PCR). Three independent biological replicates were made.

RNA isolation, transcriptome sequencing and relative expression level analysis of *PheSAUR* genes

Total RNA was extracted using the TRIzol reagent (Invitrogen, USA). The quality and quantity of purified RNA was initially assessed on an agarose gel using a NanoDrop 8000 spectrophotometer (NanoDrop, Thermo Scientific, Germany), and then the integrity of RNA samples was further evaluated using an Agilent 2100 Bioanalyzer (Agilent Technologies, USA).

Top internodes of shoots from 8 different heights (0.1m, 0.5m, 1m, 3m, 6m, 9m, 12m and control (15m)) of moso bamboos were collected. The RNA-seq libraries of 8 different samples for transcriptome sequencing were constructed according to the Illumina kit instructions (Illumina, San Diego, CA, USA). The library was sequenced to generate 101-nt paired-end reads using Illumina HiSeq™2000 at MacroGen in Shenzhen, China. RNA-seq with a quality score of Phred $\geq$ 20 were indexed, trimmed, and aligned. Clean reads were aligned to the moso bamboo genome. Cufflinks was used to measure the relative abundance of transcripts by FPKM method (Fragments Per Kilobase of exon model per Million mapped reads). The FPKM values were used to analyze the relative expression levels of *PheSAUR* genes in shoot growth.

For qRT-PCR, Primer 3 web (version4.0.0, <http://primer3.ut.ee/>) was used to design the specific primers based on the *SAURs* 3' untranslated regions and coding sequences (Untergasser et al. 2012). The primers of all the *PheSAUR* genes used for were listed (Table S3). Tonoplast intrinsic protein 41 gene (*TIP41*) was used as a control (Fan et al. 2013). The qRT-PCR reactions were carried out with the Light Cycler480 System (Roche, USA) using the SYBR Premix EX Taq™ kit (Roche, USA). The following amplification reactions were performed for qRT-PCR: 95°C for 10 seconds, 60°C for 10 seconds, and 72°C for 20 seconds. The experiments were repeated 3 times with independent cDNA samples. The expression levels of *PheSAUR* genes are presented using fold change values transformed to log₂ format compared to controls. Data were analyzed using Roche manager software and the relative figures were plotted by Sigma Plot 10.0.

Results

SAUR family members in *P. edulis*

SAUR is a large gene family that contains over 70 members in *Arabidopsis thaliana* and 58 members in *Oryza sativa*. The *P. edulis SAUR* family sequences were obtained by searching annotations in the Bamboo Genome Database. A total of 44 sequences were obtained. Finally, proteins of all the 44 genes were confirmed by a Pfam search for the presence of an auxin-inducible signature conserved in coding sequences or amino acid sequences. A total of 38 *PheSAUR* genes were obtained. The length of amino acid sequences ranged from 83 to 1148. *PheSAUR* proteins possess a predicted molecular mass ranging from 8.88 to 128.04 kDa and theoretical isoelectric point (pI) ranging from 5.47 to 11.91 (**Table 1**).

Phylogenetic relationships of *PheSAUR* genes

To explore the evolutionary expansion of *PheSAURs* in the bamboo genome, an unrooted tree was constructed from an alignment of their full-length protein sequences. This analysis revealed that all of the *PheSAURs* grouped broadly into four clusters, containing 16, 15, 3 and 4 members respectively, with well-supported bootstrap values (**Fig. 1**). Among the 38 *PheSAURs*, 15 sister pairs were formed, 8 (*PheSAUR9* and *PheSAUR42*, *PheSAUR11* and *PheSAUR13*, *PheSAUR19* and *PheSAUR24*, *PheSAUR1* and *PheSAUR37*, *PheSAUR41* and *PheSAUR44*, *PheSAUR5* and *PheSAUR23*, *PheSAUR7* and *PheSAUR8*, and *PheSAUR31* and *PheSAUR36*) of which had very strong bootstrap support (95%). These results suggest that the expansion of *PheSAUR* genes through gene duplications was probably. The duplications of *PheSAUR* genes may be explained as maintaining a proper relationship with other interacting proteins (Jain et al. 2006a; Remington et al. 2004).

To examine the phylogenetic relationship of *PheSAUR*, *OsSAUR* and *AtSAUR* proteins, an unrooted tree was constructed from an alignment of their full-length protein sequences (**Fig. 2**). The bamboo *PheSAUR* proteins were clustered distinctly

into 5 groups along with OsSAURs and AtSAURs. In addition, this analysis revealed that most OsSAURs and PheSAURs clustered in species-specific distinct clades. This result indicates that most *OsSAURs* and *PheSAURs* expanded in a species-specific manner.

Structure and sequence analysis of *PheSAUR* genes

Gene structures of the *PheSAURs* were showed in **Fig. 1**. Six of these genes contain introns, and 2 of them possess more introns (2 introns in *PheSAUR37* and 18 introns in *PheSAUR42*). Eight *PheSAUR* CDS were not complete. The lengths of untranslated regions (UTR) were showed (**Table S1**).

We calculated the intron-mediated enhancement (IME) signals in 6 *PheSAUR* genes containing introns using IMETER v2.0, which calculates whether an intron is likely to enhance gene expression. Our results showed that introns of 3 *PheSAUR* genes (*PheSAUR1*, *PheSAUR43* and *PheSAUR32*) had high scores (**Table 1**). By using CELLO v2.5 Server, it was found that 21 and 20 *PheSAUR* proteins possess signal sequences for targeting the nucleus and mitochondria. Some other members were predicted to localize to cytoplasmic and plasma membrane.

To understand the biological functions of the *PheSAURs*, an investigation of the 1,500 bp upstream sequences in *PheSAURs*, which represents their promoter region, using plantCARE and a manual search revealed the presence of a few to several putative auxin-responsive elements in most of them (**Table 1**). Some putative auxin-responsive *cis*-elements were identified in the promoter regions of the *SAUR* genes in bamboo, suggesting that these *SAURs* might be involved in the auxin signal-transduction pathway.

The sequence ATAGAT (or a variation only at the first nucleotide position) and GTA regions were simultaneously identified in 20 *PheSAUR* genes in their 3'UTR (**Table S2**), and were perceived as the binding sites of downstream (DST) elements. The DST elements could induce *SAUR* mRNA instability. Hence, the expression levels of *PheSAUR* genes could

be regulated at the mRNA level.

Previous studies proved that most of SAUR proteins contain a conserved SAUR-specific domain (SSD) of approximately 60 residues in the central region (Park et al. 2007). Here, the conserved motif distributions in PheSAUR, OsSAUR and AtSAUR proteins were analyzed using MEME tool. Three extremely conservative motifs (motifs I-III) were simultaneously found in 157 or more proteins out of all the 172 tested SAUR proteins (Fig. S1).

***PheSAUR* gene expression levels at internodes of shoots at different heights**

To gain insight into the functions and expression levels of *PheSAURs* in different growth and developmental processes, transcriptome sequencing data from the developing top internodes of bamboo shoots were used to analyze *PheSAURs* (Fig. 3). According to transcriptome sequencing data, one gene was not expressed during the shoot growth process and the Fragments Per Kilobase of exon model per Million mapped reads (FPKM) data for most of the genes were lower than 5 during this process (Table S4). *PheSAUR18* was not expressed during this process. Some genes were differentially expressed. In the period of cell division (0.5-1 m), some *PheSAUR* genes (*PheSAUR15*, *PheSAUR20*, *PheSAUR21*, *PheSAUR22* and *PheSAUR29*) were specifically expressed. In the fast growing period (3–9 m) in moso bamboo shoots, numerous *PheSAUR* genes (*PheSAUR2*, *PheSAUR7*, *PheSAUR8*, *PheSAUR23*, *PheSAUR25*, *PheSAUR26*, *PheSAUR34* and *PheSAUR35*) were particularly expressed.

Expression characterization of *PheSAUR* genes in seedlings and after IAA treatment

The expression profiles of all of the *PheSAUR* genes were experimentally verified using quantitative real-time PCR (qRT-PCR) analysis (Fig. 4 and Fig. 5). Most of the *PheSAUR* genes were activated within 1 h in at least one organ following the IAA treatment, although to varying degrees (Fig. 4). Of the 38 *PheSAUR* genes, 36 (except *PheSAUR9* and

PheSAUR41) were activated after the IAA treatment in at least one organ. Four genes (*PheSAUR5*, *PheSAUR15*, *PheSAUR31* and *PheSAUR36*) *PheSAUR* genes were specifically up regulated in the leaves after IAA treatment.

Expression levels of three organs from *P. edulis* seedlings were also showed (**Fig. 5**). All of the genes were expressed in leaves, stems and roots. However, some *PheSAURs* showed organ-/tissue-specific expression patterns in bamboo. *PheSAUR2*, *PheSAUR15*, *PheSAUR20*, *PheSAUR28* and *PheSAUR35* were specifically expressed in stems. *PheSAUR4*, *PheSAUR6*, *PheSAUR9*, *PheSAUR17*, *PheSAUR26*, *PheSAUR37* and *PheSAUR44* were mainly expressed in leaves. *PheSAUR18* and *PheSAUR36* exhibited higher expression levels in roots than in the other organs.

Discussion

SAUR gene structure and intron functions

Previous researchers have identified and annotated some *SAUR* genes in *Arabidopsis*, rice, *Physcomitrella*, *sorghum* and *Solanaceae* (Hagen and Guilfoyle 2002; Jain et al. 2006b; Rensing et al. 2008; Wang et al. 2010; Wu et al. 2012). In this study, we identified 38 *SAUR* genes in moso bamboo. All of the members were predicted to encode *SAUR* domains. Interestingly, most of the *PheSAURs* are intronless (**Table 1**). This phenomenon also exists in the *SAUR* genes of other species (Jain et al. 2006b; Rensing et al. 2008; Wang et al. 2010; Wu et al. 2012). Potential function of introns, such as a signal for mRNA export, and alternative splicing-based exon shuffling has been revealed (Fedorova and Fedorov 2003; Roy and Gilbert 2006). In addition, many introns also have the ability to promote gene expression through a process termed IME (Mascarenhas et al. 1990). The *PheSAUR* genes with high scored IME implying that these introns are expected to enhance expression. Many studies have indicated that introns may play an important role in genetic evolution and have potential functions (Fedorova and Fedorov 2003; Lecharny et al. 2003; Roy and Gilbert 2006).

Evolution of *PheSAUR* genes

Moso bamboo has 24 pairs of chromosomes, twice that of rice. However, rice contains at least 20 more *SAUR* genes (58) than moso bamboo (38). It is not clear when these species differentiate. However, *PheSAUR* genes could be divided into several models according to relative expression levels, which meant redundancy not only in moso bamboo, but also in the evolutionary history of the *SAUR* gene family. Interestingly, the coding sequence of *PheSAUR42* was 3,447 bp, which is unusually long for the *SAUR* family.

Regulation of *PheSAUR* genes

Gene expression can be regulated during DNA transcription and RNA processing or at the mature RNA and protein translation levels. The *SAUR* gene family is particular because of the DST elements. The DST element in the 3' UTR could contribute to the instability of *SAUR* mRNA. Hence, there is a particular regulatory process for *SAUR* gene expression at the mRNA level (Newman et al. 1993). The exact consensus DST element of ATAGAT (or a variation only at the first nucleotide position) and GTA regions were identified in 20 *PheSAUR* genes. The DST elements could be identified in 12 *OsSAUR* gene family sub-groups. The ratio of genes containing DST elements in *P. edulis* was more than twice that in *Oryza sativa*. The presence of a DST element in the downstream region of *OsSAURs* may be responsible for the instability of their mRNAs and thereby regulate their expression. Partial mRNAs encoded by *SAUR* genes were highly unstable because of the DST elements in their 3'UTRs (Newman et al. 1993; Sullivan et al. 1996; Jain et al. 2006b), which is thought to be a common regulatory mechanism in the *SAUR* gene family. The SAUR proteins (SAUR19 subfamily) in *Arabidopsis* were proved to be highly unstable. However, the addition of an N-terminal (GFP or strep) tag and a C-terminal (GFP or GUS) tag increased the stability of SAUR19 subfamily proteins and SAUR63, respectively (Chae et al. 2012; Spartz et al. 2012).

Expression levels of *PheSAUR* genes

PheSAUR15, *PheSAUR20*, *PheSAUR21*, *PheSAUR22* and *PheSAUR29*, which were specially expressed at 0.5-1 m, may be involved in cell division in shoot growth. *PheSAUR* genes (*PheSAUR2*, *PheSAUR7*, *PheSAUR8*, *PheSAUR23*, *PheSAUR25*, *PheSAUR26*, *PheSAUR34* and *PheSAUR35*), which were particularly expressed at 3-9 m, suggest that they may play important roles in promoting shoot elongation.

According to qRT-PCR, 7 (*PheSAUR4*, *PheSAUR6*, *PheSAUR9*, *PheSAUR13*, *PheSAUR17*, *PheSAUR26*, *PheSAUR37*), 5 (*PheSAUR2*, *PheSAUR15*, *PheSAUR20*, *PheSAUR28* and *PheSAUR35*) and 2 (*PheSAUR11*, *PheSAUR18*) *PheSAUR* genes showed leaf-, stem- and root-specific expression, respectively, which indicates that these genes may play significant roles in different organs. Most of the genes were up-regulated in leaves and roots indicating that leaves and roots were the more important growing parts of *P. edulis* seedlings. More auxin may be produced in the leaves and roots to maintain plant growth in seedlings. As determined by qRT-PCR, most of the *PheSAUR* genes were up-regulated from 0 to 5 hours, implying that these genes were more likely to play critical roles in regulating IAA responses in leaves and roots. Specifically up regulated *PheSAUR* genes (*PheSAUR5*, *PheSAUR15*, *PheSAUR31* and *PheSAUR36*) in leaf may be involved in the developments of leaf in *P. edulis* seedlings. *PheSAUR27* may be involved in growth of stem. No root specifically up regulated *PheSAUR* genes were detected and most genes (except *PheSAUR5*, *PheSAUR15*, *PheSAUR16*, *PheSAUR27*, *PheSAUR31*, *PheSAUR36* and *PheSAUR41*) were up regulated in root. These genes may be involved in the growth of root.

Putative functions of *PheSAUR* genes

Due to the important character of fast growing, growing mechanism of moso bamboo was urgently needed to study. The *SAUR* gene family is one of the early auxin-responsive gene families and encodes short-lived proteins. It may play important

roles in plant cell elongation. Recently, the functions of *SAUR* genes have become an important research topic. The putative functions of *SAUR* genes depend largely on the distribution of the proteins these genes encode. The subcellular locations of *SAUR* proteins were studied in recent years. Most of the proteins could be observed in the nucleus, cytoplasm or plasma membrane. The expression levels of most of the genes were up-regulated after auxin treatment (Kant et al. 2009; Chae et al. 2012; Spartz et al. 2012; Kong et al. 2013; Markakis et al. 2013; Li et al. 2015). Most studies demonstrated that *SAUR* proteins could promote cell elongation. The functions of *SAUR* genes were demonstrated in the process of cell elongation (Spartz et al. 2014). In our study, most *PheSAUR* genes were up-regulated after IAA treatment. Hence, *PheSAUR* genes may play similar roles in *P. edulis*.

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Fig. 1. Phylogenetic tree and gene structure of *PheSAUR* genes. A, Neighbor-joining method and MEGA 6.0 software were used for phylogenetic analysis of *PheSAUR*s with their amino acid sequences. A showed the relationship of all the 38 *PheSAUR* genes. All the *PheSAUR* genes could be divided into 4 subgroups. Bootstrap value (above 50%) supports from 1000 replicates are indicated at each branch. B, Gene structures of all the *PheSAUR* genes were showed. The green color parts represent exons and the black lines represent introns.

Fig. 2. Phylogenetic relationship of *PheSAUR*, *AtSAUR* and *OsSAUR* proteins. Neighbor-joining method and MEGA 6.0 software were used for phylogenetic analysis of SAUR proteins from *Phyllostachys edulis* (*PheSAUR*), *Arabidopsis thaliana* (*AtSAUR*) and *Oryza sativa* (*OsSAUR*). In total, 38 *PheSAUR*, 55 *OsSAUR* and 79 *AtSAUR* proteins were analyzed and could be divided into 5 subgroups. *PheSAUR*, *AtSAUR* and *OsSAUR* proteins were highlighted in Red circles, blue triangles and green boxes respectively. Bootstrap value (above 50%) supports from 1000 replicates are indicated at each branch.

Fig. 3. Heat map of the FPKM values of *PheSAUR* genes. Top internodes were collected at the heights of 0.1, 0.5, 1, 3, 6, 9, 12 and 15 meters (control). Fragments Per Kilobase of exon model per Million mapped reads (FPKM) was used to build the heat map. The color scale is shown at the right of the heat map.

Fig. 4. Heat map of the real-time quantitative PCR (qRT-PCR) analysis results of *PheSAUR* genes in leaves, stems and roots under IAA treatments. Leaf, stem and root were used for analysis and the materials were collected at 0, 1, 3 and 5 hours. The expression levels of *PheSAUR* genes are presented using fold change values transformed to log2 format compared to controls. Expression levels of leave, stems and roots at 0 h were unified to 1. The color scale is shown at the right of the heat map.

Fig. 5. Relative expression levels of *PheSAURs* in leaves, stems and roots in *P. edulis* seedlings. Leaves, stems and roots in *P. edulis* seedlings were collected and quantitative real-time PCR was used for analysis.

Fig. S1. Conserved consensus motifs identified in PheSAUR, OsSAUR and AtSAUR proteins. Five conserved consensus motifs in PheSAUR, OsSAUR and AtSAUR proteins (172 proteins) were found by MEME. The symbol heights represent the relative frequency of each residue. The numbers of sites and e-value for each motif are also shown.

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Table 1 Overview of *PheSAUR* genes in moso bamboo

Name	Gene ID	length	MW/kDa	PI	Intro number/IMeter v2.0 scores	CELLO localization	Auxin-responsive elements
<i>PheSAUR1</i>	PH01000001G1450	257	27.08	9.33	1/18.9	Plasma Membrane(1.253)/ Chloroplast(1.219)/ Mitochondrial(1.026)	no
<i>PheSAUR2</i>	PH01000003G0680	110	12.55	11.86	0	Nuclear(2.479)	no
<i>PheSAUR4</i>	PH01000052G0130	178	19.68	5.47	1/9.17	Cytoplasmic(2.045)	no
<i>PheSAUR5</i>	PH01000057G0880	144	15.66	9.20	0	Mitochondrial(1.799)	no
<i>PheSAUR6</i>	PH01000084G0620	163	17.86	9.05	0	Nuclear(2.902)	no
<i>PheSAUR7</i>	PH01000105G0420	141	14.88	8.55	0	Nuclear(1.735)/ Chloroplast(1.416)	yes
<i>PheSAUR8</i>	PH01000110G0260	133	14.35	8.54	0	Nuclear(1.315)/ Mitochondrial(1.250)/ Chloroplast(1.179)	no
<i>PheSAUR9</i>	PH01000164G1020	126	13.85	7.89	0	Nuclear(2.049)	yes
<i>PheSAUR11</i>	PH01000300G0250	116	12.01	9.02	0	Mitochondrial(1.356)/ Chloroplast(1.075)	no

<i>PheSAUR12</i>	PH01000300G0310	94	10.02	6.28	0	Cytoplasmic(1.751)	yes
<i>PheSAUR13</i>	PH01000338G0730	116	11.96	9.16	0	Mitochondrial(1.263)	no
<i>PheSAUR14</i>	PH01000402G1010	83	8.88	8.55	0	Chloroplast(1.875)	no
<i>PheSAUR15</i>	PH01000407G0060	120	12.98	8.59	0	Nuclear(1.812)	no
						Mitochondrial(1.481)/	
<i>PheSAUR16</i>	PH01000548G0100	121	13.91	8.80	0	Cytoplasmic(1.388)/	yes
						Nuclear(1.033)	
						Nuclear(1.382)/	
<i>PheSAUR17</i>	PH01001308G0070	116	13.03	9.26	0	Mitochondrial(1.205)/	no
						Cytoplasmic(1.062)	
						Nuclear(1.691)/	
<i>PheSAUR18</i>	PH01001346G0370	160	17.49	8.75	0		yes
						Cytoplasmic(1.220)	
						Mitochondrial(1.498)/	
<i>PheSAUR19</i>	PH01001542G0200	109	11.79	9.22	0		no
						Nuclear(1.036)	
<i>PheSAUR20</i>	PH01001832G0020	154	17.28	8.81	0	Mitochondrial(1.312)	no
<i>PheSAUR21</i>	PH01001866G0310	144	16.04	8.83	0	Nuclear(1.641)/	yes
<i>PheSAUR22</i>	PH01002017G0200	154	17.23	11.91	0	Nuclear(3.237)	no
						Mitochondrial(1.489)/	
<i>PheSAUR23</i>	PH01002025G0060	147	16.54	9.96	0		yes
						Nuclear(1.474)/	
<i>PheSAUR24</i>	PH01002316G0030	179	18.70	9.33	0	Nuclear(1.534)/	yes

<i>PheSAUR25</i>	PH01002921G0180	125	13.75	6.10	0		no
<i>PheSAUR26</i>	PH01002921G0190	140	15.50	8.92	0	Mitochondrial(1.700)	yes
<i>PheSAUR27</i>	PH01002921G0250	145	16.28	7.64	0	Mitochondrial(1.237)	yes
<i>PheSAUR28</i>	PH01003140G0110	102	11.02	7.77	0	Mitochondrial(2.099)	yes
<i>PheSAUR29</i>	PH01003399G0150	113	12.15	9.62	0	Cytoplasmic(1.762)/ Mitochondrial(1.269)	no
<i>PheSAUR31</i>	PH01003710G0040	155	16.01	8.52	0	Mitochondrial(1.280)/ Chloroplast(1.088)	no
<i>PheSAUR32</i>	PH01004171G0020	129	14.51	5.91	1/21.5	Cytoplasmic(1.772)	no
<i>PheSAUR34</i>	PH01004534G0100	147	15.67	8.24	0	Chloroplast(2.619)	yes
<i>PheSAUR35</i>	PH01004534G0130	134	14.95	6.81	0	/Nuclear(1.331) Mitochondrial(1.560)/	no
<i>PheSAUR36</i>	PH01006019G0010	138	15.10	6.37	0	Nuclear(1.267)/ Cytoplasmic(1.110)	yes
<i>PheSAUR37</i>	PH01006114G0030	246	27.20	11.05	2/17.12	Mitochondrial(2.541) Nuclear(1.494)/	yes
<i>PheSAUR38</i>	PH01015485G0020	95	10.68	7.62	0	Chloroplast(1.042)/ Cytoplasmic(1.039)	yes
<i>PheSAUR41</i>	PH01000012G1930	109	12.22	7.23	0	Mitochondrial(1.365)/	yes

						Nuclear(1.195)	
<i>PheSAUR42</i>	PH01000114G0400	1148	128.04	6.59	18/13.39	Nuclear(2.750)	no
						Plasma	
<i>PheSAUR43</i>	PH01000345G0270	171	19.44	7.17	1/23.69	Membrane(1.236)/	yes
						Mitochondrial(1.108)	
						Nuclear(1.350)/	
<i>PheSAUR44</i>	PH01002861G0060	112	12.54	6.37	0	Cytoplasmic(1.190)/	no
						Mitochondrial(1.114)	

Note: length represent the amino acid sequences of PheSAUR proteins.

MW (molecular weight) represents the predicted weights of PheSAUR proteins.

PI represents the predicted isoelectric point of PheSAUR proteins.

Fig. 1. Phylogenetic tree and gene structure of PheSAUR genes. A, Neighbor-joining method and MEGA 6.0 software were used for phylogenetic analysis of PheSAURs with their amino acid sequences. A showed the relationship of all the 38 PheSAUR genes. All the PheSAUR genes could be divided into 4 subgroups. Bootstrap value (above 50%) supports from 1000 replicates are indicated at each branch. B, Gene structures of all the PheSAUR genes were showed. The green color parts represent exons and the black lines represent introns.

Fig. 1
112x147mm (300 x 300 DPI)

Fig. 2. Phylogenetic relationship of PheSAUR, AtSAUR and OsSAUR proteins. Neighbor-joining method and MEGA 6.0 software were used for phylogenetic analysis of SAUR proteins from *Phyllostachys edulis* (PheSAUR), *Arabidopsis thaliana* (AtSAUR) and *Oryza sativa* (OsSAUR). In total, 38 PheSAUR, 55 OsSAUR and 79 AtSAUR proteins were analyzed and could be divided into 5 subgroups. PheSAUR, AtSAUR and OsSAUR proteins were highlighted in Red circles, blue triangles and green boxes respectively. Bootstrap value (above 50%) supports from 1000 replicates are indicated at each branch.

Fig. 2
86x87mm (300 x 300 DPI)

Fig. 3. Heat map of the FPKM values of PheSAUR genes. Top internodes were collected at the heights of 0.1, 0.5, 1, 3, 6, 9, 12 and 15 meters (control). Fragments Per Kilobase of exon model per Million mapped reads (FPKM) was used to build the heat map. The color scale is shown at the right of the heat map.

Fig. 3

131x201mm (300 x 300 DPI)

Fig. 4. Heat map of the real-time quantitative PCR (qRT-PCR) analysis results of PheSAUR genes in leaves, stems and roots under IAA treatments. Leaf, stem and root were used for analysis and the materials were collected at 0, 1, 3 and 5 hours. The expression levels of PheSAUR genes are presented using fold change values transformed to log2 format compared to controls. Expression levels of leaf, stems and roots at 0 h were unified to 1. The color scale is shown at the right of the heat map.

Fig. 4
141x233mm (300 x 300 DPI)

Fig. 5. Relative expression levels of PheSAURs in leaves, stems and roots in *P. edulis* seedlings. Leaves, stems and roots in *P. edulis* seedlings were collected and quantitative real-time PCR was used for analysis.

Fig. 5

56x37mm (600 x 600 DPI)

62x45mm (600 x 600 DPI)

Table S1 The length of upstream and downstream untranslated regions

Name	Gene ID	length of upstream	length of downstream
		UTR (bp)	UTR (bp)
<i>PheSAUR1</i>	PH01000001G1450	141	614
<i>PheSAUR2</i>	PH01000003G0680	112	207
<i>PheSAUR4</i>	PH01000052G0130	1276	835
<i>PheSAUR5</i>	PH01000057G0880	133	411
<i>PheSAUR6</i>	PH01000084G0620	81	242
<i>PheSAUR7</i>	PH01000105G0420	108	381
<i>PheSAUR8</i>	PH01000110G0260	223	749
<i>PheSAUR9</i>	PH01000164G1020	333	508
<i>PheSAUR11</i>	PH01000300G0250	95	457
<i>PheSAUR12</i>	PH01000300G0310	121	887
<i>PheSAUR13</i>	PH01000338G0730	102	865
<i>PheSAUR14</i>	PH01000402G1010	112	79
<i>PheSAUR15</i>	PH01000407G0060	104	107
<i>PheSAUR16</i>	PH01000548G0100	90	476
<i>PheSAUR17</i>	PH01001308G0070	151	898
<i>PheSAUR18</i>	PH01001346G0370	480	861
<i>PheSAUR19</i>	PH01001542G0200	127	915
<i>PheSAUR20</i>	PH01001832G0020	78	172

<i>PheSAUR21</i>	PH01001866G0310	78	1658
<i>PheSAUR22</i>	PH01002017G0200	69	57
<i>PheSAUR23</i>	PH01002025G0060	105	208
<i>PheSAUR24</i>	PH01002316G0030	270	417
<i>PheSAUR25</i>	PH01002921G0180	166	473
<i>PheSAUR26</i>	PH01002921G0190	428	466
<i>PheSAUR27</i>	PH01002921G0250	67	84
<i>PheSAUR28</i>	PH01003140G0110	79	378
<i>PheSAUR29</i>	PH01003399G0150	1687	642
<i>PheSAUR31</i>	PH01003710G0040	102	736
<i>PheSAUR32</i>	PH01004171G0020	137	533
<i>PheSAUR34</i>	PH01004534G0100	109	157
<i>PheSAUR35</i>	PH01004534G0130	151	659
<i>PheSAUR36</i>	PH01006019G0010	97	368
<i>PheSAUR37</i>	PH01006114G0030	568	44
<i>PheSAUR38</i>	PH01015485G0020	195	132
<i>PheSAUR41</i>	PH01000012G1930	315	977
<i>PheSAUR42</i>	PH01000114G0400	625	295
<i>PheSAUR43</i>	PH01000345G0270	3291	397
<i>PheSAUR44</i>	PH01002861G0060	334	323

Table S2 The numbers of DST elements in downstream untranslated region

Name	Gene ID	Number of motif ATAGAT (or a variation only at the first nucleotide position)	Number of motif GTA
<i>PheSAUR1</i>	PH01000001G1450	2	5
<i>PheSAUR2</i>	PH01000003G0680	0	3
<i>PheSAUR4</i>	PH01000052G0130	1	15
<i>PheSAUR5</i>	PH01000057G0880	0	3
<i>PheSAUR6</i>	PH01000084G0620	0	1
<i>PheSAUR7</i>	PH01000105G0420	1	5
<i>PheSAUR8</i>	PH01000110G0260	2	13
<i>PheSAUR9</i>	PH01000164G1020	2	10
<i>PheSAUR11</i>	PH01000300G0250	2	10
<i>PheSAUR12</i>	PH01000300G0310	0	15
<i>PheSAUR13</i>	PH01000338G0730	1	10
<i>PheSAUR14</i>	PH01000402G1010	0	4
<i>PheSAUR15</i>	PH01000407G0060	0	2
<i>PheSAUR16</i>	PH01000548G0100	1	8
<i>PheSAUR17</i>	PH01001308G0070	1	14
<i>PheSAUR18</i>	PH01001346G0370	0	11
<i>PheSAUR19</i>	PH01001542G0200	1	20

<i>PheSAUR20</i>	PH01001832G0020	0	2
<i>PheSAUR21</i>	PH01001866G0310	6	35
<i>PheSAUR22</i>	PH01002017G0200	0	0
<i>PheSAUR23</i>	PH01002025G0060	0	3
<i>PheSAUR24</i>	PH01002316G0030	1	5
<i>PheSAUR25</i>	PH01002921G0180	3	10
<i>PheSAUR26</i>	PH01002921G0190	2	5
<i>PheSAUR27</i>	PH01002921G0250	1	4
<i>PheSAUR28</i>	PH01003140G0110	0	6
<i>PheSAUR29</i>	PH01003399G0150	0	3
<i>PheSAUR31</i>	PH01003710G0040	0	13
<i>PheSAUR32</i>	PH01004171G0020	1	8
<i>PheSAUR34</i>	PH01004534G0100	0	4
<i>PheSAUR35</i>	PH01004534G0130	0	5
<i>PheSAUR36</i>	PH01006019G0010	1	7
<i>PheSAUR37</i>	PH01006114G0030	0	0
<i>PheSAUR38</i>	PH01015485G0020	0	2
<i>PheSAUR41</i>	PH01000012G1930	2	6
<i>PheSAUR42</i>	PH01000114G0400	1	2
<i>PheSAUR43</i>	PH01000345G0270	0	7
<i>PheSAUR44</i>	PH01002861G0060	1	3

Table S3 Primers of *PheSAUR* genes used for qRT-PCR analysis

Name	Gene ID	Forward (F)/Reverse (R)	sequence
<i>PheSAUR1</i>	PH01000001G1450	F	CAACAATGGTGGATTCGTGG
		R	CACGGACAGGGAGAGTAAAA
<i>PheSAUR2</i>	PH01000003G0680	F	TGATGTGGTAGTACTATTGGGTT
		R	TGTGATGAGATGAGAACAGATCA
<i>PheSAUR4</i>	PH01000052G0130	F	AAATGAGGCTAAGTTAAACGGAG
		R	AAGGTGTCCAAAGCATCATAAAA
<i>PheSAUR5</i>	PH01000057G0880	F	GTGAAGTGAGATGGCTGAGA
		R	GGATTGACAAGGGAAGGGA
<i>PheSAUR6</i>	PH01000084G0620	F	CGGTTTAGAATTTACTCTACTGCC
		R	GTTGCATTACCCAATCCAGATC
<i>PheSAUR7</i>	PH01000105G0420	F	TCGACCGCTGATTAATACGA
		R	CCATGTTTCATATGTGTGCGT
<i>PheSAUR8</i>	PH01000110G0260	F	TAACCTGCTTTGAGTTCGATTG
		R	ATCATCAGCAACTCCATCGATA
<i>PheSAUR9</i>	PH01000164G1020	F	AGAGCTTCTGTTCTCCTTCAG
		R	CATGCCCCAAAATTCCAGAA
<i>PheSAUR11</i>	PH01000300G0250	F	GCTTAGTGTCTCCGATCCTG

		R	ACTGAGTAGAGCACAACACA
		F	CAAGCCTTACAAGCTTTACATGA
<i>PheSAUR12</i>	PH01000300G0310	R	GTTGAAGGAGGAGAGGGTATTAT
		F	TTCAGCCTCGACAAGCTTAT
<i>PheSAUR13</i>	PH01000338G0730	R	GTCCCAAATGTCTCGCAAAA
		F	GTGCCCCAAAGTTGTAGCTA
<i>PheSAUR14</i>	PH01000402G1010	R	ACATGCTACACAAATCAAAGCA
		F	GCCGCCCCGTACACTATTTA
<i>PheSAUR15</i>	PH01000407G0060	R	AAATCAATGAATCGAACAAATAGCC
		F	TTGTCTTGCCCCTTTGTTTC
<i>PheSAUR16</i>	PH01000548G0100	R	AAAGCTCATCAATCGCAAAC
		F	TCAAGTTGCACCAGTACAGT
<i>PheSAUR17</i>	PH01001308G0070	R	TTCTGATCCTGTGTATGGGC
		F	TTCATCGTTGTTCCATTAGTCTG
<i>PheSAUR18</i>	PH01001346G0370	R	GCCACCATTATTCATAGTTCACA
		F	TTTATCAGTTCAACACACACACA
<i>PheSAUR19</i>	PH01001542G0200	R	GCAATGCAACAAAAGAAAGTAGA
		F	AGTAGCTGTTTCTAGCTTCTGA
<i>PheSAUR20</i>	PH01001832G0020	R	TTCTTCCATTTCCTGTATCCCA
		F	TCCTCGACCTTTTCTTGCTTA
<i>PheSAUR21</i>	PH01001866G0310	R	ATACCCTTGAAGCCAATACGT
<i>PheSAUR22</i>	PH01002017G0200	F	CGAAGATTTATCGATCCAGCTTG

		R	GTCTCCTCCATCTCCTCCTC
<i>PheSAUR23</i>	PH01002025G0060	F	ACATAGGTCATTTAGCAGGCT
		R	CTGGTGTCTGGTAGTAACGT
<i>PheSAUR24</i>	PH01002316G0030	F	ACTTGTTCTTCTTTTCCTAGGGA
		R	ACTAGCAATTTCTCCTCATTTCAC
<i>PheSAUR25</i>	PH01002921G0180	F	GGAACGTATGCCACTCTTATTTT
		R	GGTCGTTACAGTACTTCACATTT
<i>PheSAUR26</i>	PH01002921G0190	F	AAAATGTGCATAAGTGAAAGAACC
		R	TATACTGACAAATAAAACCGGCTT
<i>PheSAUR27</i>	PH01002921G0250	F	GGTCTTAGCCAATCACTACCTATA
		R	CACATTACATCACATGAAGATTACC
<i>PheSAUR28</i>	PH01003140G0110	F	TTGTCCTCAGATGATTGCCT
		R	CAGTACACATGAGAGCACGA
<i>PheSAUR29</i>	PH01003399G0150	F	TTGTTTGATAAGAGGAAATGCGTA
		R	GGTGAAAGAGAGAAGAAAATGCTA
<i>PheSAUR31</i>	PH01003710G0040	F	GGGCGAGTGAGTAATTTAAATGA
		R	CGGTAATGACACTGTTAATCTCC
<i>PheSAUR32</i>	PH01004171G0020	F	GTGAGATGCAAACAACGACA
		R	GACAACCCAATCACCACAAC
<i>PheSAUR34</i>	PH01004534G0100	F	TTGCCGTGTACTCTTTGTGT
		R	CCACCTTCCTTGATTGCTTG
<i>PheSAUR35</i>	PH01004534G0130	F	CAGAGTTTTGCCCTGTTTGT

		R	CTGGCGTGCTAACATTTTCAT
<i>PheSAUR36</i>	PH01006019G0010	F	CATGGGTTCGATTTGCTTAAGAT
		R	AGCGATTAGAGAGAATTAACAGC
<i>PheSAUR37</i>	PH01006114G0030	F	TCAAGAGGGAAAGAGGAGGA
		R	TCAAAGGTCTCCGCTTTCTT
<i>PheSAUR38</i>	PH01015485G0020	F	GGAATCGAGAAGGAGTAAGCA
		R	CCCCTGGCTCCATCTCAT
<i>PheSAUR41</i>	PH01000012G1930	F	TAGGGTCGGTTAAGCAGTTC
		R	CTCACCACAGACCAATCGTA
<i>PheSAUR42</i>	PH01000114G0400	F	TGGTGTGTTGATTGATCCAAATC
		R	ATGTCAGTTTCAGAGTCCTTACA
<i>PheSAUR43</i>	PH01000345G0270	F	CCTACAAGGTATTCATCGATTTC
		R	TGAGGGTTGTTTTTCATGCTAATT
<i>PheSAUR44</i>	PH01002861G0060	F	TCGAGGTGTTAATTTCTTGCT
		R	AACGAGAGAACAGATGACGA

Table S4 Transcriptome FPKM value of *PheSAUR* genes at 8 different heights of shoots and culms

Name	Gene ID	0.1 m	0.5 m	1 m	3 m	6 m	9 m	12 m	CK (15 m)
<i>PheSAUR1</i>	PH01000001G1450	0.238399	0	0.040608	0.531424	0.091154	0.165218	0.209561	0.783899
<i>PheSAUR2</i>	PH01000003G0680	0	0.339284	0.207312	1.00812	0	0	0	0
<i>PheSAUR4</i>	PH01000052G0130	0.25989	1.32177	1.46806	0.416624	0.972593	1.76392	1.95883	0
<i>PheSAUR5</i>	PH01000057G0880	8.69593	8.22589	9.06753	0.577953	3.2346	1.29457	3.68508	0.117531
<i>PheSAUR6</i>	PH01000084G0620	1.5099	0.29722	0.365117	0.808685	0	0	0.240336	0
<i>PheSAUR7</i>	PH01000105G0420	0	0.063198	0.057461	0	0	9.33936	0.069771	4.46281
<i>PheSAUR8</i>	PH01000110G0260	0	0	0	0	0	4.59367	0.112032	1.74821
<i>PheSAUR9</i>	PH01000164G1020	0.25783	0	0	0	0	0.053235	0.050309	0
<i>PheSAUR11</i>	PH01000300G0250	1.2787	1.86998	1.03571	3.09127	4.85629	2.07223	0.698749	16.4721
<i>PheSAUR12</i>	PH01000300G0310	0	0	0	0.063421	0.064841	0.077262	0.072608	0.431536
<i>PheSAUR13</i>	PH01000338G0730	1.08455	1.69019	1.83147	0.297877	1.39191	0.506291	0.204044	1.84008
<i>PheSAUR14</i>	PH01000402G1010	0.452957	0.684589	0.15558	0.508328	0.886649	55.3061	6.01933	70.5448
<i>PheSAUR15</i>	PH01000407G0060	0	0.870805	1.72627	0.128695	0.131402	0.319152	0.308355	0.19651
<i>PheSAUR16</i>	PH01000548G0100	5.27703	4.00668	4.58403	7.77211	4.10484	5.18857	4.91773	4.37797
<i>PheSAUR17</i>	PH01001308G0070	0.519692	1.31016	1.03549	1.70057	0.514573	20.182	3.05086	32.776
<i>PheSAUR18</i>	PH01001346G0370	0	0	0	0	0	0	0	0
<i>PheSAUR19</i>	PH01001542G0200	2.2913	2.94281	4.76682	2.52187	5.88824	2.6819	1.27398	16.5764
<i>PheSAUR20</i>	PH01001832G0020	1.04974	1.34607	2.97842	0.222484	0.226025	1.09861	0.514694	0

<i>PheSAUR21</i>	PH01001866G0310	0.530307	1.01901	3.63868	0.026443	0.079263	2.17467	0.634594	0.691474
<i>PheSAUR22</i>	PH01002017G0200	1.02654	9.02713	17.5585	2.55931	1.52753	2.68893	3.85556	0
<i>PheSAUR23</i>	PH01002025G0060	0.113015	1.09779	0.058723	0.382449	6.32658	3.72098	4.46079	0.94316
<i>PheSAUR24</i>	PH01002316G0030	4.97948	1.38178	2.83484	1.87975	1.51126	3.14987	1.27049	8.15745
<i>PheSAUR25</i>	PH01002921G0180	0.695561	1.93473	2.21018	4.48449	2.35552	1.40366	2.40372	1.73979
<i>PheSAUR26</i>	PH01002921G0190	0.695561	1.93473	2.21018	4.48449	2.35552	1.40366	2.40372	1.73979
<i>PheSAUR27</i>	PH01002921G0250	0.155847	0.065795	0	0.259294	0.259493	0.15859	0.075319	0.0802286
<i>PheSAUR28</i>	PH01003140G0110	16.5349	2.25868	1.08377	3.68308	1.04483	3.59899	4.96179	1.23799
<i>PheSAUR29</i>	PH01003399G0150	0	0	0.023756	0	0	0	0	0
<i>PheSAUR31</i>	PH01003710G0040	4.7955	7.86176	7.0024	9.42338	3.45954	1.89812	3.00291	0
<i>PheSAUR32</i>	PH01004171G0020	19.6366	11.4953	14.7051	0.253392	0.817853	1.74777	1.29828	0
<i>PheSAUR34</i>	PH01004534G0100	0	0.088368	0.245363	0.088087	0	0.435946	0.103436	0.117665
<i>PheSAUR35</i>	PH01004534G0130	0.771403	0.732269	1.81377	0.252667	0.671263	3.89851	1.91514	2.45801
<i>PheSAUR36</i>	PH01006019G0010	0.191732	2.746	2.88193	3.40668	0.43985	5.13804	6.60921	6.0851
<i>PheSAUR37</i>	PH01006114G0030	0.215018	0.182631	0.260692	0.634877	0.357897	1.22155	1.07533	1.39094
<i>PheSAUR38</i>	PH01015485G0020	0	0.178194	0.165622	0.442405	0.35375	0.546556	0.922929	0.905248
<i>PheSAUR41</i>	PH01000012G1930	0.327422	0.229035	0.168075	0	0.358984	6.00615	1.52938	101.464
<i>PheSAUR42</i>	PH01000114G0400	11.5764	13.3291	8.58859	16.6493	10.4563	16.0201	10.6155	13.8312
<i>PheSAUR43</i>	PH01000345G0270	0.070862	0.157456	0.216617	0	0.07949	7.74348	0.184518	47.6931
<i>PheSAUR44</i>	PH01002861G0060	1.9647	2.425	2.09428	1.34111	1.93485	2.36954	1.35545	0.676737