Melatonin confers cadmium tolerance by modulating critical heavy metal transporters in radish plants

Running title: Melatonin enhances Cd tolerance in radish

Liang Xu¹, Fei Zhang¹, Mingjia Tang¹, Yan Wang¹, Junhui Dong¹, Jiali Ying¹, Yinglong Chen², Bing Hu³, Cui Li¹, Liwang Liu^{1*}

¹National Key Laboratory of Crop Genetics and Germplasm Enhancement, Key Laboratory of Horticultural Crop Biology and Genetic Improvement (East China) of MOAR, College of Horticulture, Nanjing Agricultural University, Nanjing 210095, P.R.China

²School of Earth and Environment, and The UWA's Institute of Agriculture, The University of Western Australia, Perth, WA 6009, Australia

³College of Life Science, Nanjing Agricultural University, Nanjing 210095, P.R.China

Corresponding author:

Prof. Liwang Liu, Ph.D

Institution: National Key Laboratory of Crop Genetics and Germplasm Enhancement,

College of Horticulture, Nanjing Agricultural University, P.R.China

Phone: +86-25-84395563

Fax: +86-25-84395266

E-mail: nauliulw@njau.edu.cn

Abstract

Cadmium (Cd) is an environmental pollutant that causes health hazard to living organisms. Melatonin (MT) has emerged as a ubiquitous pleiotropic molecule capable of coordinating heavy metal (HM) stresses in plants. However, it remains unclear how melatonin mediates Cd uptake and accumulation at transcriptional and/or posttranscriptional level in radish. Herein, the activities of five key antioxidant enzymes were increased, while root and shoot Cd content were dramatically decreased by melatonin. A combined small RNA and transcriptome sequencing analysis showed that 14 differentially expressed microRNAs (DEMs) and 966 differentially expressed genes (DEGs) were shared between Cd and Cd+MT conditions. In all, 18 and 8 correlated miRNA-DEG pairs were identified in Con vs. Cd and Con vs. Cd+MT comparison, respectively. Several DEGs encoding YSL (yellow stripe 1-like), HMA (heavy metal ATPases) and ABC (ATP-binding cassette) transporters were involved in Cd chelation and sequestration in radish. Root exposure to Cd²⁺ induced excess reactive oxygen species (ROS) and some specific signaling molecules including CaMs, CDPKs and MAPKs, which consequently trigger several metal-binding peptides and metal transporter genes to establish redox homeostasis and eliminate Cd toxicity in radish plants. Notably, transgenic analysis revealed that over-expression of RsMT1 gene could enhance Cd tolerance of tobacco plants, indicating that the exogenous melatonin confers Cd tolerance might attribute to melatonin-mediated up-regulation of *RsMT1* gene in radish plants. These results could contribute to clarify molecular basis of melatonin-mediated Cd stress response in radish, and pave the way for high-efficient genetically engineering low-Cd-content cultivars in radish breeding programs.

KEYWORDS

Cadmium stress, melatonin, *Raphanus sativus*, miRNAs, transcriptome, *RsMT1* gene, regulatory network

1. INTRODUCTION

Soil contamination with heavy metals (HMs) from natural, agricultural and industrial sources has become a worldwide agricultural and environmental issue.¹ Cadmium (Cd) is a widespread non-essential trace metal that poses hazardous impact on living organisms. Plant exposure to excess Cd²⁺ could trigger a range of serious morphological, physiological and metabolic disruptions, e.g. photosynthesis and transpiration inhibition, carbohydrate metabolism disruption, protein degradation and lipid peroxidation.^{2,3} Cd can accumulate in human body by environmental and dietary ingestion, leading to a variety of health hazards such as bladder, kidney damage and lung cancer.⁴ How to reduce Cd content in edible plant organs and achieve effective control of Cd into the food chain are pivotal for crop improvement and human health.

Comprehensive molecular characterization of the genes, proteins and metabolites involved in hormone signaling and regulatory pathways conferring HM stress response is a fundamental step for genetically engineering low-Cd-content edible crops. Several metal transporters such as zinc-iron permease (ZIP), ATP-binding cassette (ABC), natural resistance-associated macrophage protein (Nramp) and P₁B-ATPases were participated in cellular Cd uptake, accumulation and translocation within plants.^{5,6} MicroRNA (miRNA), a class of endogenous noncoding small RNAs, can modulate its target mRNAs at the transcriptional and post-transcriptional levels via mRNA cleavage or translational inhibition. Recent transgenic studies demonstrated that the miRNA-guided gene regulation played vital regulatory roles in plant response to a range of HM stresses.^{7,8,9} In rice, overexpression of miR166 improved Cd sensitivity and tolerance, and reduced Cd root-to-shoot translocation and accumulation in grains through regulation of its HD-Zip target genes.¹⁰

Phytohormones, a diverse group of signaling molecules, were considered as key endogenous regulators in positive modulation of physiological and molecular responses to the HM stresses.^{11,12} Clarification of the molecular mechanisms underlying hormonal homoeostasis and their stress signaling network are vital for genetic improvement of plant tolerance to HMs. Melatonin (N-acetyl-5-methoxytryptamine) is a ubiquitous signal molecule with numerous cellular and

Page 5 of 152

physiological functions in animals and plant kingdoms.^{13,14} Many studies revealed the vital regulatory roles of melatonin in regulating biological processes of plant growth, development and environmental stress responses.^{15,16,17} In recent years, melatonin acted as bio-stimulator for enhancing tolerance against biotic and/or abiotic stresses such as heat, cold, drought, salinity and heavy metal had been extensively characterized in some plant species.¹⁸⁻²³ Current studies demonstrating the melatonin-mediated network of Cd stress response are mainly focused on the physiological and cellular level.²⁴⁻²⁶ A recent study indicated that exogenous melatonin conferred Cd tolerance through counterbalancing the hydrogen peroxide homeostasis in wheat.²⁷ However, little information is available on genome-wide characterization of melatonin-induced differentially regulated genes and miRNAs under Cd stress, resulting in the molecular mechanism of melatonin-mediated Cd stress response remains elusive in plants, especially in root vegetable crops.

Radish (Raphanus sativus L.), an important economical root vegetable crop of Brassicaceae family, is highly sensitive to various HM stresses. Considering substantial natural variation of root Cd uptake and accumulation was found among different radish genotypes, it's imperative to develop genetically engineered low-Cd-content radish cultivars.²⁸ Although several root Cd-responsive miRNAs and genes had been characterized in our previous studies,^{29,30} no systematical research focusing on melatonin-mediated network of Cd stress response was reported in radish. In this study, based on assaying melatonin-induced dynamic changes of Cd content and activities of several antioxidant enzymes, we aimed to assess global miRNAome and transcriptome changes and identify melatonin-induced miRNAs and metal transporter genes under Cd stress in radish. Expression profiles of a few Cd-responsive miRNAs and genes were confirmed by RT-qPCR analysis. Furthermore, a schematic regulatory network of melatonin-mediated Cd uptake and accumulation was proposed in radish. These findings would not only facilitate clarifying molecular mechanism underlying melatonin-mediated Cd uptake and accumulation in radish, but also provide useful basis for establishing optional strategies to achieve genetically engineering low-Cd-content radish cultivars.

2. MATERIALS AND METHODS

2.1 Plant materials and growth conditions

After surface-sterilization, the radish seeds of advanced inbred line 'NAU-RG' were germinated at 25°C in an incubator. Germinated seeds were planted and cultivated in a growth chamber with a photoperiod cycle of 14h/25°C light and 10h/18°C dark for three weeks. Then, the seedlings with uniform size were transplanted into a container containing half-strength Hoagland nutrient solution.²⁸ One week later, the seedlings were treated with 50 μ M CdCl₂ for 24 h. Thereafter, the foliar portions of radish plants were sprayed with 10, 25, 50, 100 and 200 μ M melatonin. Seedlings grown in Cd-free nutrient solution were employed as controls. Three replicates were used for each treatment with three plants for each replicate. Roots and shoots were harvested and immersed in liquid nitrogen and stored at -80°C for further use.

2.2 Determination of antioxidant enzyme and Cd content

To isolate the antioxidant enzyme, 0.1 g of powdered fresh root and shoot sample was suspended in potassium phosphate buffer (50 mM, pH 7.0) consisted of 0.1 mM EDTA and 1% polyvinylpyrrolidone (w/v). After the fully-vortexed homogenate centrifuged at 12,000×g for 15 min at 4 °C , the supernatant was collected for the determination of enzymatic activity. The activities of glutathione reductase (GR), superoxide dismutase (SOD), peroxidase (POD), ascorbate peroxidase (APX) and catalase (CAT) enzymes were measured according to the previous studies.^{31,32} For Cd content determination, the root and shoot samples were oven-dried at 85 °C to constant weight, respectively. Then, 0.5 g of homogenized powdered sample were digested in an HNO₃ and HClO₄ mixture (v/v = 3:1) at 180 °C for 6 h. The Cd contents were measured using an Inductively Coupled Plasma-Optical Emission Spectrometer (ICP-OES, Thermo Fisher iCAP 7400).

2.3 cDNA library preparation and Illumina sequencing

Total RNA was extracted from Cd-free (Control), Cd-treated (Cd) and Cd+MT-treated (Cd+MT) radish roots with Trizol reagent (Invitrogen, USA), and two biological replicates were set for each condition. Six cDNA libraries were prepared

 using Illumina Paired End Sample Prep Kit (Illumina, USA) according to the manufacturer's recommendations. Six small RNA libraries were generated according to the instruction of NEBNext[®] Multiplex Small RNA Library Prep Set for Illumina[®] (NEB, USA). Both mRNA-seq and sRNA-seq libraries were sequenced using the Illumina HiSeq 2500 platform.

2.4 Genome mapping and differential expression analysis

Clean reads from mRNA and sRNA sequencing were obtained by filtering raw reads with the adaptor sequences, contaminants and low-quality reads. sRNA reads matching the non-coding RNA (rRNA, tRNA, snRNA, and snoRNA) were removed. The clean reads were mapped to the radish reference genome ³³ using Bowtie ³⁴ and Tophat 2 ³⁵ programs, with no mismatch (for sRNA reads) and two mismatches (for mRNA reads) allowed. Gene expression levels of the mRNA and sRNA reads were calculated using fragments per kilobase of transcript per million fragments mapped (FPKM) and transcripts per million reads (TPM) approach, respectively. Using the DESeq2 analysis³⁶, only the genes satisfy fold change > 2 and adjusted *p* (padj) < 0.05 were considered as DEGs. For known miRNA identification, the mapped unique sRNA reads with length of 20-24 nt were aligned against with known miRNA sequence in miRBase 22.0. Then, the novel miRNAs were screened from the remaining unmatched sRNA reads using miREvo ³⁷ and mirdeep2 software.³⁸ Differentially expressed miRNAs (DEMs) were determined with fold change > 1 and adjusted *p* (padj) < 0.05 with the DESeq2 approach.³⁶

2.5 miRNA target prediction and function annotation

Prediction of miRNA target gene was carried out using the psRobot_tar in psRobot scripts in psRobot (omicslab.genetics.ac.cn/psRobot).³⁹ To allocate genes to functional categories and predict their biological functions, GO functional classification (http://www.geneontology.org) and KEGG pathway (http://www.genome.jp/kegg/) analysis were performed using GOseq ⁴⁰ and KOBAS software (KOBAS, Surrey, UK), respectively. The GO terms and KEGG pathway were defined as significantly enriched with the condition of corrected *p* value < 0.05.

2.6 Quantitative real-time PCR analysis

Total RNA and sRNA were isolated from radish roots using Trizol reagent (Invitrogen) following the manufacturer's instructions. The PCR was carried out with a SYBR Primix Ex Taq kit (TaKaRa), and the reaction was conducted on ROCHE LightCycler 480 instruments followed the reported protocols.³⁰ Each sample was assayed in triplicate with the *RsActin* gene used as the internal standard. Relative expression level was calculated with the $2^{-\Delta\Delta C_T}$ formula.⁴¹ Statistical significance was determined with Duncan's multiple comparison test at the *p*<0.05 level. The specific RT-qPCR primers were listed in Supplementary Table S1.

2.7 Genetic transformation and generation of transgenic tobacco plants

To generate constructs for RsMT1 overexpression (OE-RsMT1) lines, the full-length of RsMT1 coding region was amplified with RsMT1-EcoR I-F/RsMT1-BamH I-R and then transferred into the pCAMBIA2301 vector containing the cauliflower mosaic virus 35S promoter and nos terminator sequences. Thereafter, the recombinant binary plasmid was introduced into tobacco (*Nicotiana benthamiana*) plants using Agrobacterium tumefaciens strain GV3101 via leaf disc transformation. Transgenic T0 plants were regenerated on Murashige and Skoog (MS) agar medium containing 100 mg/L kanamycin. Positive plants were further self-fertilized twice to generate the third generation lines (T3). Semi-quantitative RT-PCR analysis was carried out in OE-RsMT1 and wild-type (WT) plants with the *NtActin* gene used as internal reference. Root length and Cd content were measured for OE-RsMT1 and WT plants, respectively. Three biological replicates were performed for each genotype, and three plants per genotype were measured for each replicate.

3. RESULTS

3.1 Melatonin-induced changes of Cd content and antioxidant activities

To investigate the changes of Cd content and antioxidant systems responding to melatonin (MT) under cadmium stress, the activities of several key antioxidant enzymes were assayed at 24 h after root treatment with Cd (50μ M), or Cd (50μ M)+MT (0, 10, 25, 50, 100 and 200 μ M). As shown in Figure 1A, the root and shoot Cd content were significantly decreased by different concentration of melatonin treatments, both of which reached to the minimum level at the 50μ M melatonin. Moreover, the activities of five key antioxidant enzymes consisted of GR, SOD, POD, CAT and APX were significantly increased under Cd stress, among which further increased by different melatonin concentration and reached to the highest level at the 50μ M melatonin (Figure 1B-F), indicating that the increased activities of antioxidant system by MT could contribute to the alleviation of Cd-induced oxidative stress in radish, and the concentration of 50μ M melatonin is the most effective for alleviating root Cd stress in radish. Thus, the transcriptional and post-transcriptional changes of the Cd-treated and Cd+ 50μ M MT treated root in radish were further investigated.

3.2 Identification of melatonin-induced differentially expressed genes

To investigate the MT-induced transcriptional changes in Cd-exposed taproot, six cDNA libraries were constructed from Control, Cd and Cd+MT treated roots with two biological replicates for each library. After the removal of low-quality reads as well as those containing adapter and poly-N, more than 26 M clean paired-end (PE) reads were generated from each library (Table S2), among which 63.47%-65.0% were uniquely mapped to the radish reference genome sequences (Table S3). For each library, the R² of sequencing data from two biological replicates was larger than 0.93, indicating the gene expression profiles were highly reproducible among replicates (Figure S1). Differential analysis showed that a total of 2249 (1185 up- and 1064 down-regulated), 1462 (812 up- and 650 down-regulated) and 306 (181 up- and 125 down-regulated) genes were differentially expressed in Con vs. Cd, Con vs. Cd+MT and Cd vs. Cd+MT comparison, respectively (Figure 2A). In all, 17 DEGs were

overlapped among these three comparisons, while 966 DEGs were shared between Con vs. Cd and Con vs. Cd+MT comparison (Figure 2B). As expected, the majority of DEGs exhibited similar up- or down-regulated expression patterns in Con vs. Cd and Con vs. Cd+MT comparison (Figure 2C, D), while a proportion of genes were specially induced under the Cd+MT condition (Figure 2E).

3.3 Functional annotation of DEGs

 GO enrichment analysis showed that the carbohydrate metabolic process, microtubule-based movement and microtubule-based process in biological process category as well as the hydrolase activity-acting on glycosyl bonds, hydrolase activity-hydrolyzing O-glycosyl compounds and transferase activity-transferring glycosyl groups in molecular function category were the most significantly enriched GO items under both Cd and Cd+MT conditions (Figure 3A, Table S4). However, several GO items were only uniquely enriched under one condition. For example, the cellular carbohydrate metabolic process and lipid modification in biological process category as well as copper ion binding and glucosyltransferase activity in molecular function category were unique terms under Cd condition, while those of cellulose metabolic process and glucan biosynthetic process in biological process category as well as chitin binding in molecular function category were uniquely enriched under Cd+MT condition. These results indicated that several different biological processes were specifically induced under the Cd and/or Cd+MT conditions in radish roots.

To further characterize the molecular interactions among the DEGs, a total of nine KEGG terms were significantly enriched under both Cd and Cd+MT conditions with corrected p < 0.05 (Figure 3B, Supplementary Table S4). Interestingly, several pathways including glucosinolate biosynthesis, cysteine and methionine metabolism, flavonoid biosynthesis and glutathione metabolism were more highly enriched under Cd+MT conditions, indicating that several DEGs involved in these specific biological processes might play critical roles in melatonin-mediated Cd uptake and accumulation in radish. However, no GO and KEGG terms were significantly enriched in the Cd vs. Cd+MT comparison, which partially due to the fact that only few DGEs were identified to get the enriched terms in this comparison.

3.4 Critical DEGs encoding heavy metal transporters

As metal transporters playing vital roles in Cd uptake, accumulation and transport process, a total of 37 DEGs encoding heavy metal transporters were identified, which were further classified into seven clusters (I–VII) based on their expression patterns under the Cd and Cd+MT conditions (Figure 4A, Table S6). The cluster I and II consisted of significantly up-regulated genes under both Cd and Cd+MT conditions, and the fold changes of six genes in cluster I were higher under Cd+MT conditions, while 11 genes in cluster II had lower fold changes under Cd+MT conditions. In contrast, the cluster III and IV consisted of significantly down-regulated genes under both Cd and Cd+MT conditions, and the three genes in cluster III had higher fold changes under Cd+MT conditions, while seven genes in cluster IV had lower fold changes under Cd+MT conditions. In addition, the two genes in cluster V exhibited up-regulated expression only under Cd condition, while five and three genes in cluster VI and VII were up- and down-regulated under only Cd+MT conditions, respectively. As compared with the Cd condition, some up- or down-regulated genes under Cd+MT conditions might act as vital regulatory factors in melatonin-mediated Cd uptake and accumulation in radish.

3.5 Identification of known and novel miRNAs under Cd stress in radish

To identify the root post-transcriptional changes under Cd and Cd+MT conditions, a total of six sRNA libraries (two replicates for each condition) were constructed from radish roots under Con, Cd and Cd+MT condition, respectively. After filtering out low-quality tags and adaptor contaminations, more than 12 M clean reads were acquired from each sRNA library (Supplementary Table 7). The number of unique reads ranging from 18 to 30 nt were varied from 2,641,514 to 3,407,898, among which 55.87~61.09% unique reads were mapped to the radish genome reference sequences (Supplementary Table S8). All the six libraries exhibited similar size distributions, with reads of 21 nt being predominant, followed by the reads of 22 and 24 nt (Supplementary Figure S2). As expected, a high correlation coeffcient over 0.938 was observed between two replicates (Supplementary Figure S1B), suggesting the sRNA expression profile was highly reproducible among replicates.

Based on searching against miRBase 22.0 database with no mismatch, a total of 88 known miRNAs belonging to 37 miRNA families were identified, among which the number of member for each family ranged from 1 to 6 (Supplementary Table S9). The majority of them were expressed in all six sRNA libraries, whereas a proportion of them showed specific expression pattern under a few special conditions. In detail, miR166e-5p, miR390a-3p and miR399f were specially expressed under the Cd condition, while the miR156j, miR157c-3p, miR172d-5p and miR2111a-3p were only induced under the Cd+MT condition. Moreover, 33 novel miRNAs were identified from all six sRNA libraries with length ranging from 19 to 24 nt. Among them, 30 novel miRNAs were enriched in all three conditions, whereas two miRNAs (miRn26 and miRn32) and two (miRn5 and miRn33) novel miRNAs were induced and repressed under the Cd+MT condition, respectively (Supplementary Table S10).

3.6 Melatonin-induced DEMs and their target genes in radish

Differential expression analysis showed that a total of 30 (12 up- and 18 down-regulated), and 22 (12 up- and 10 down-regulated) and 17 (11 up- and 6 down-regulated) DEMs were identified in Con vs. Cd, Con vs. Cd+MT and Cd vs. Cd+MT comparison, respectively (Figure 4B; Supplementary Table S11). In all, 14 DEMs were shared between the Cd and Cd+MT condition, while 16 and 8 DEMs were specially expressed under Cd and Cd+MT condition, respectively. As expected, several DEMs belonging to a certain miRNA family exhibited similar expression patterns. For instance, two DEMs (miR166a-3p and miR166g-3p) of miR166 family were significantly up-regulated under Cd+MT condition, while two other DEMs (miR169f-3p and miR169g-3p) of miR169 family were significantly down-regulated under both Cd and Cd+MT condition, indicating that different members of a certain miRNA family might have similar functions and play conserved roles in the regulatory network of melatonin mitigating Cd stress.

In total, 1833 target genes were identified for the 88 known miRNAs (Supplementary Table S12). Interestingly, a proportion of miRNAs target to more than one transcription factor (TF) genes, while several different miRNAs target to the same TF gene. For instance, miR156a-5p was the regulator of both WRKY19

(Rsa1.0 02846.1 g00003.1) and Squamosa promoter-binding-like protein 5 (Rsa1.0 01148.1 g00009.1) genes, whereas miR156j and miR157d regulate the expression of CDPK3 (Rsa1.0 02356.1 g00006.1) gene. Notably, a few metal transporter genes were targeted by several DEMs. In detail, miR156j targets YSL7 (Rsa1.0 01882.1 g00002.1) and three ABC gene transporter gene (Rsa1.0 06163.1 g00001.1, Rsa1.0 05020.1 g00001.1 and Rsa1.0 00387.1 g00026.1), while miR319c targets the BOR1 (Rsa1.0 01583.1 g00006.1 and Rsa1.0 02070.1 g00011.1) and BOR4 (Rsa1.0 00703.1 g00002.1) genes. However, only 14 targets were identified for one novel miRNA, which might be partially attributed to the fact that some novel miRNAs targeted the genes by inhibiting translation rather than by mRNA digestion.

3.7 miRNA-mRNA interaction and RT-qPCR validation

To dissect the potential relationship between miRNAs and their target genes, the differentially expressed miRNA-target pairs were identified by comparing sRNA and transcriptome sequencing data. As expected, both negative and positive correlations in expression patterns were detected between the DEMs and their target genes. In detail, there were 18 (8 negatively and 10 positively) correlated miRNA-mRNA pairs in the Con vs. Cd comparison, whereas 8 (2 negatively and 6 positively) correlated miRNA-mRNA pairs were found in the Con vs. Cd+MT comparison, respectively (Supplementary Table S13). Most of these differentially expressed targets encoded various transcription factors and metal transporters. As shown in Figure 5A, the miR396b-5p exhibited opposite expression patterns with its target gene BGLU4, whereas the remaining three miRNAs showed positive expression patterns with their corresponding target genes. Also, the expression profiles of two miRNAs and their target genes from RT-qPCR analysis fitted well with that from transcriptome data (Figure 5B). To investigate the dynamic expression patterns of DEGs under Cd stress in radish, a total of eight DEGs were selected for RT-qPCR assays. Six out of eight genes (AEC, ERNP, GCN1, GSTU13, MRP10 and PDR12) were up-regulated under Cd or Cd+MT condition, whereas the other two genes (HMT and BGLU44) were down-regulated under both Cd and Cd+MT condition (Figure 6). The results indicated that the expression patterns of these DEGs shared coincidental expression tendency with the transcriptome data.

3.8 Over-expression of RsMT1 gene enhance Cd tolerance in tobacco plants

Based on the expression profiles from transcriptome sequencing, further functional characterization of a significantly up-regulated gene, RsMT1, was carried out using the transgenic analysis in tobacco plants. To test the difference of Cd tolerance, the sterilized seeds of wild-type and OE-RsMT1 plants were germinated on one-half-strength MS medium for three days and then the seedlings were transferred to 1/2 MS media with 5.0 mM CdCl₂ for one week. As shown in Figure 7a, the root of OE-RsMT1 plants exhibited continuing elongation, whereas the growth of wild-type seedlings was inhibited. The average root length of OE-RsMT1 plants is two folds longer than that of WT seedlings (Figure 7b). Similarly, the plant height of four-week-old OE-RsMT1 plants was much higher than that of the WT lines under 20 µM CdCl₂ treatment (Figure 7c). Semi-quantitative RT-PCR analysis showed that the *RsMT1* gene exhibited high expression level in OE-RsMT1 plants, whereas there was almost no expression were observed in the WT plants (Figure 7d). Moreover, the Cd content in OE-RsMT1 tobacco plants was significantly higher than that in WT lines (p < 0.01; Figure 7e), indicating that the over-expression of *RsMT1* gene could promote chelation of Cd²⁺ and enhance Cd tolerance of tobacco plants. Collectively, it could be suggested that the exogenous melatonin can confer Cd tolerance might partially attribute to melatonin-mediated up-regulation of RsMT1 gene in radish plants.

4. DISCUSSION

Cd is one of the most widespread heavy-metal pollutants that poses environmental health concern to living organisms. Recently, the melatonin-mediated Cd stress has becoming to be a candidate promising approach to efficiently manage Cd accumulation and reduce Cd risks.^{8,26,42} Although melatonin-mediated Cd-induced morphological and physiological changes had been addressed in some plant species,²⁴⁻²⁶ the molecular basis of melatonin-mediated Cd uptake and accumulation at the transcriptional and post-transcriptional levels remain largely unexplored in root vegetable crops. In the current study, the melatonin- mediated miRNAome and transcriptome changes under Cd stress were systematically investigated in radish.

4.1 Melatonin-induced regulation of signal transduction networks

Phytohormones are essential plant growth regulators playing vital roles in development and various environmental stress responses. Plant exposure of HMs could induce increased biosynthesis of various phytohormones to enhance HM tolerance via hormone signaling cross-talk. Previous studies indicated that the auxin could be involved in plant responses to metal stresses via modulating auxin stability, transport, and redistribution.^{5,25} In this study, two DEGs encoding auxin-responsive protein (IAA2 and IAA15) were up-regulated under both Cd and Cd+MT conditions, whereas two DEGs encoding ethylene insensitive 3-like protein (EIL3) were induced under Cd+MT condition (Table S14), indicating that positive regulation of several specific biosynthetic and catabolic genes of auxin and ethylene might contribute to the effective melatonin alleviation on Cd toxicity in radish roots.

On coping with HM stress, plants evolved coordinated signal transduction networks to positively regulate their normal growth, development and metabolism processes. A myriad of calcium sensing proteins such as Calmodulins (CaMs), CaM like proteins (CMLs), calmodulin domain protein kinases (CPKs) and calcium-dependent protein kinases (CDPKs) were identified to be acted as major Ca²⁺ signaling sensors in HM-mediated signal transduction pathways in plants.²⁷ In this study, several DEGs encoding CDPK9, CRK39, CML11, CML27 and CML37 were significantly

up-regulated under Cd+MT condition, whereas four DEGs encoding CRK8 were markedly down-regulated under both Cd and Cd+MT conditions (Table S14). It was evidenced that the CDPK could work together with MAPK for stress signals transmission to deal with HM stress.^{5,43} Two up-regulated genes encoded MAPKK4 and MAPK19, and four down-regulated genes encoding four MAPKs (MAPKK6, MAPK13, MAPK17 and MAPK21) were found under both Cd and Cd+MT conditions, reflecting the involvement of cross-talk between CDPKs and MAPKs in mediating Cd stress were repressed under the melatonin treatment. These results emphasize the complexity of interactions between calcium and MAPK signaling and their downstream signaling transduction pathways under Cd treatment in radish plants.

4.2 Melatonin activated antioxidase systems to alleviate Cd stress

HM-induced excessive generation of reactive oxygen species (ROS) is one of the most important factors inhibiting plant growth and development.^{8,27} In recent years, increasing evidences revealed that melatonin can activate antioxidant systems to mediate ROS scavenge and counterbalance redox homeostasis under abiotic stresses in plants.^{44,45} In this study, exogenous melatonin treatment further increased the SOD, POD, APX and GR activities under Cd stress, which was in consistent with previous studies in wheat, apple and cucumber.^{27,46,47} Four out of seven DEGs encoding PODs (e.g. POD45 and POD56) were significantly up-regulated under both Cd and Cd+MT conditions (Table S14), which might partially contribute to the increased activities of several antioxidant enzymes in Cd-treated radish roots.

In plants, the GST-mediated ROS scavenging represents a critical detoxification process implicated in biotic/abiotic stress response.^{1,32} The GSTs can not only accelerate the efflux of HM-induced ROS and maintain intracellular redox balance, but also conjugate the glutathione (GSH) with metal ion into low- or non-toxic complexes to reduce the HM toxicity.⁴⁸ Overexpression of GSTs in rice and soybean resulted in increased metal binding capacity and enhanced cellular defense against oxidative stress.⁴⁹ Notably, the miR158a-3p positively regulates the GSTU13 gene in this study, indicating its crucial role in metal binding capacity and redox balancing.

Moreover, four DEGs encoding GSTs were markedly up-regulated under Cd treatment, among which the expression were further increased under Cd+MT condition (Table S14), which provided evidence that the exogenous melatonin can activate specific antioxidant systems, and consequently regulate a series of functional genes associated with redox and antioxidant properties to alleviate Cd-induced oxidative stress in radish roots.

4.3 Metal transporters are responsible for melatonin-mediated Cd homeostasis

Many metal transporters are responsible for root HM uptake and shoot translocation in plants.^{50,51} Several studies indicated that the yellow stripe 1-like (YSL) and heavy metal ATPases (HMA) proteins are important transporters playing vital roles in root Cd uptake, transport and homeostasis in plants.^{52,53} Specially, the HMA2 and HMA4 transporters are involved in Zn/Cd uptake and root-to-shoot translocation in several plant species including Arabidopsis, rice, wheat and barley.⁵⁴⁻⁵⁶ In this study, the miR156j-targeting YSL7 gene was significantly up-regulated under both the Cd and Cd+MT conditions, while the other DEG encoding YSL2 exhibited up-regulated pattern only under the Cd conditions. Moreover, one DEG encoding HMA2 was significantly down-regulated under both Cd and Cd+MT conditions (Figure 4A), whereas another DEG encoding HMA4 was markedly up-regulated under Cd and Cd+MT conditions. It is worthwhile to mention that the fold changes of both YSLs and HMAs were relatively lower under Cd+MT condition than Cd condition, indicating that the melatonin might reduce the Cd accumulation through repressing the expression of some specific metal transporter genes and consequently preventing the Cd-chelates to enter the radish root cells. The ATP-binding cassette (ABC) transporters are key membrane proteins implicated in uptake and transport of a number of heavy metals.^{5,57} Increasing number of studies revealed the relevance of ABC transporters in the biological process of mediating PC-Cd or glutathione (GSH)-Cd complex transport into vacuole in plants.⁵⁸ In this study, miR156j and miR162a target to the ABCA2 gene, while miR172c targets to the ABCG6 gene (Table S12). Moreover, four DEGs (ABCG40, ABCB21, ABCC14 and ABCF1) encoding ABC transporter genes were significantly up-regulated under both Cd and

Cd+MT conditions, whereas two other ABC transporter genes (ABCG25 and ABCG39) were induced under Cd+MT condition (Figure 4A), which demonstrated the complex roles of DEMs and their target ABC genes involved in melatonin-mediated regulatory network of Cd stress response. Further functional characterization of these metal transporter genes could contribute to reveal the molecular mechanism underlying melatonin-mediated Cd uptake and accumulation in radish.

4.4 Melatonin-mediated regulatory network of Cd uptake and accumulation

To clarify the critical melatonin-mediated process of Cd stress response in radish, a schematic molecular regulatory network of Cd uptake and accumulation was proposed based on melatonin-induced DEGs and DEMs in this study (Figure 8). Cd enters the radish root cell and induces some HM stress responsive signals, which were transmitted to the nucleus through several specific signaling molecules such as CaMs, CDPKs and MAPKs.⁵⁹ Consequently, some specific metal-binding peptides and Cd-responsive genes were activated to enable positive adaptive response to Cd stress. In brief, the MT1 and PCS (phytochelatin synthase) gene was up-regulated to chelate and sequester Cd-PCS HMV into the vacuole. Moreover, several metal transporters (e.g. YSLs, ABCs and HMAs) were activated or repressed to transport Cd²⁺ out of the root cell. In addition, melatonin-induced increased activities of some critical antioxidant enzymes (e.g. GR, SOD, POD, APX and CAT) contributed to scavenge Cd-induced ROS and maintain redox balance in radish root cells. Collectively, the positive regulation of melatonin-mediated coordinated regulatory network provided essential energy and nutrient supply for alleviating Cd toxicity and establishes redox homeostasis in radish plants.

In summary, the genome-wide characterization of melatonin mediated Cd-induced miRNAome and transcriptome changes was firstly investigated in radish roots. Several candidate DEGs encoding the YSL, HMA and ABC transporters were key participants involved in melatonin-mediated regulatory networks of Cd uptake and accumulation in radish. It was firstly evidenced that the exogenous melatonin could confer Cd tolerance, which might attribute to melatonin-mediated up-regulation

of *RsMT1* gene in radish plants. Further characterization of biological roles for these metal transporter genes would be useful for better understanding of melatonin-mediated processes associated with Cd homeostasis and detoxification in radish roots. The outcomes of this study would facilitate unraveling molecular mechanism underlying melatonin-mediated Cd uptake and accumulation in plants, and provide fundamental basis for efficient genetic management of Cd accumulation in radish and other root vegetable crops.

to pee per perez

ACKNOWLEDGEMENTS

This work was supported by grants from the National Natural Science Foundation of China (31601766), China Postdoctoral Science Foundation (2016T90472, 2015M570458), Jiangsu Planned Projects for Postdoctoral Research Funds (1402021B) and Key Technology R&D Program of Jiangsu Province (BE2016379).

CONFLICT OF INTEREST

The authors have no competing financial interests to declare.

References

- 1. Clemens S, Aarts MGM, Thomine S, Verbruggen N. Plant science: the key to preventing slow cadmium poisoning. *Trends Plant Sci.* 2013;18:92-99.
- 2. DalCorso G, Manaraa A, Furinia A. An overview of heavy metal challenge in plants: from roots to shoots. *Metallomics*. 2013;5:1117-1132.
- 3. Ismael MA, Elyamine AM, Moussa MG, Cai M, Zhao XH, Hu CX. Cadmium in plants: uptake, toxicity, and its interactions with selenium fertilizers. *Metallomics*. 2019;11:255.
- Cui J, Liu T, Li Y, Li F. Selenium reduces cadmium uptake into rice suspension cells by regulating the expression of lignin synthesis and cadmium-related genes. *Sci. Total Environ*. 2018;644:602-610.
- 5. Jalmi SK, Bhagat PK, Verma D, et al. Traversing the links between heavy metal stress and plant signaling. *Front Plant Sci.* 2018;9:12.
- 6. Singh S, Parihar P, Singh R, Singh VP, Prasad SM. Heavy metal tolerance in plants: role of transcriptomics, proteomics, metabolomics, and ionomics. *Front Plant Sci.* 2016;6:1143.
- 7. Gupta OP, Sharma P, Gupta RK, Sharma I. MicroRNA mediated regulation of metal toxicity in plants: present status and future perspectives. *Plant Mol Biol.* 2014;84:1-18.
- 8. Gu Q, Chen Z, Yu X, et al. Melatonin confers plant tolerance against cadmium stress via the decrease of cadmium accumulation and reestablishment of microRNA-mediated redox homeostasis. *Plant Sci.* 2017;261:28-37.
- 9. Ding Y, Wang Y, Jiang Z, et al. MicroRNA268 overexpression affects rice seedling growth under cadmium stress. *J Agric Food Chem*. 2017;65:5860-5867.
- 10. Ding Y, Gong S, Wang Y, et al. MicroRNA166 modulates cadmium tolerance and accumulation in rice. *Plant Physiol*. 2018; 7:1691-1703.
- 11. Ni J, Wang QJ, Shah FA, et al. Exogenous melatonin confers cadmium tolerance by counterbalancing the hydrogen peroxide homeostasis in wheat seedlings. *Molecules*. 2018;23:799.
- 12. Lee HY, Back K. Cadmium disrupts subcellular organelles, including chloroplasts, resulting in melatonin induction in plants. *Molecules*. **2017**; 22:1791.
- 13. Debnath B, Hussain M, Irshad M, et al. Exogenous melatonin mitigates acid rain stress to tomato plants through modulation of leaf ultrastructure, photosynthesis and antioxidant potential. *Molecules*. 2018;23:388.
- 14. Cai SY, Zhang Y, Xu YP, et al. *HsfA1a* upregulates melatonin biosynthesis to confer cadmium tolerance in tomato plants. *J Pineal Res.* 2017;62:e12387.
- 15. Qi ZY, Wang KX, Yan MY, et al. Melatonin alleviates high temperature-induced pollen abortion in *Solanum lycopersicum*. *Molecules*. 2018;23:386.
- Byeon Y, Back K. Melatonin synthesis in rice seedlings *in vivo* is enhanced at high temperatures and under dark conditions due to increased serotonin N-acetyltransferase and N-acetylserotonin methyltransferase activities. *J. Pineal Res.* 2014;56:189-195.
- 17. Arnao MB, Hernandez-Ruiz J. Function of melatonin in plants: a review, J. Pineal Res.

2015;59:133-150.

- 18. Xu W, Cai SY, Zhang Y, et al. Melatonin enhances thermotolerance by promoting cellular protein protection in tomato plants. *J Pineal Res.* 2016;61:457-469.
- Liang D, Gao F, Ni Z, et al. Melatonin improves heat tolerance in kiwifruit seedlings through promoting antioxidant enzymatic activity and glutathione S-transferase transcription. *Molecules*. 2018;23:584.
- Bałabusta M, Katarzyna S, Posmyk MM. Exogenous melatonin improves antioxidant defense in cucumber seeds (*Cucumis sativus* L.) germinated under chilling stress. *Front Plant Sci.* 2016;7:575.
- 21. Li X, Wei JP, Scott ER, et al. Exogenous melatonin alleviates cold stress by promoting antioxidant defense and redox homeostasis in *Camellia sinensis* L. *Molecules*. 2018;23:165.
- 22. Cui G, Zhao X, Liu S, Sun F, Chao Z, Xi Y. Benificial effects of melatonin in overcoming drought stress in wheat seedlings. *Plant Phyiol Biochem.* 2017;18:138.
- 23. Liang C, Zheng G, Li W, et al. Melatonin delays leaf senescence and enhances salt stress tolerance in rice. *J Pineal Res.* 2015;59:91-101.
- 24. Li MQ, Hasan MK, Li CX, et al. Melatonin mediates selenium-induced tolerance to cadmium stress in tomato plants. *J Pineal Res.* 2016;61:291-302.
- Lee K, Back K. Overexpression of rice Serotonin N-acetyltransferase 1 in transgenic rice plants confers resistance to cadmium and senescence and increases grain yield. J Pineal Res. 2017;62: e12392.
- 26. Cai SY, Zhang Y, Xu YP, et al. HsfA1a upregulates melatonin biosynthesis to confer cadmium tolerance in tomato plants. *J Pineal Res.* 2017; 62: e12387.
- 27. Ni J, Wang Q, Shah FA, et al. Exogenous melatonin confers cadmium tolerance by counterbalancing the hydrogen peroxide homeostasis in wheat seedlings. *Molecules*. 2018;23:799.
- Xu L, Wang LJ, Gong YQ, et al. Genetic linkage map construction and QTL mapping of cadmium accumulation in radish (*Raphanus sativus* L.). *Theor Appl Genet*. 2012;125:659-670.
- Xu L, Wang Y, Zhai LL, et al. Genome-wide identification and characterization of cadmium-responsive microRNAs and their target genes in radish (*Raphanus sativus* L.) roots. *J Exp Bot* 2013;64:4271–4287.
- 30. Xu L, Wang Y, Liu W, et al. *De novo* sequencing of root transcriptome reveals complex cadmium-responsive regulatory networks in radish (*Raphanus sativus* L.). *Plant Sci.* 2015;236:313-323.
- 31. Hasan MK, Ahammed GJ, Yin L, et al. Melatonin mitigates cadmium phytotoxicity through modulation of phytochelatins biosynthesis, vacuolar sequestration, and antioxidant potential in *Solanum lycopersicum* L. *Front Plant Sci.* 2015;6:601.
- 32. Qi ZY, Wang KX, Yan MY, et al. Melatonin alleviates high temperature-induced pollen abortion in *Solanum lycopersicum*. *Molecules*. 2018; 23: 386.

2	
2	
4	
5	
6	
7	
8	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	
19	
20	
21	
22	
25	
24	
25	
20	
28	
29	
30	
31	
32	
33	
34	
35	
36	
37	
38	
39	
40	
41	
42	
43	
44	
45	
46	
4/ 10	
4ð 70	
49 50	
50	
57	
53	
54	
55	
56	
57	
58	
59	
60	

- 33. Jeong YM, Kim N, Ahn BO, et al. Elucidating the triplicated ancestral genome structure of radish based on chromosome-level comparison with the *Brassica* genomes. *Theor Appl Genet*. 2016;129:1357-1372.
- 34. Langmead B, Salzberg S. Fast gapped-read alignment with Bowtie 2. *Nature Methods*. 2012;9:357-359.
- 35. Kim D, Pertea G, Trapnell C, Pimentel H, Ryan Kelley R, Salzberg SL. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol.* 2013;14:R36.
- 36. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol.* 2014;15:550.
- 37. Wen M, Shen Y, Shi S, Tang T. MiREvo: An Integrative microRNA evolutionary analysis platform for next-generation sequencing experiments. *BMC Bioinformatics*. 2012;13:140.
- Friedlander MR, Mackowiak SD, Li N, Chen W, Rajewsky N. MiRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. *Nucleic Acids Res.* 2011;40:37-52.
- 39. Wu HJ, Ma YK, Chen T, Wang M, Wang XJ. PsRobot: A web-based plant small RNA meta-analysis toolbox. *Nucleic Acids Res.* 2012;40:W22–W28.
- 40. Young MD, Wakefield MJ, Smyth GK, Oshlack A. Gene ontology analysis for RNA-seq: accounting for selection bias. *Genome Biol.* 2010; 11:R14.
- 41. Livak, K.J. and Schmittgen, T.D. (2001) Analysis of relative gene expression data using real-time quantitative PCR and the $2^{-\Delta\Delta CT}$ method. *Methods*. 2001;25:402-408.
- 42. Kaya C, Okant M, Ugurlar F, Alyemeni MN, Ashraf M, Ahmad P. Melatonin-mediated nitric oxide improves tolerance to cadmium toxicity by reducing oxidative stress in wheat plants. *Chemosphere*. 2019;225:627-638.
- Opdenakker K, Remans T, Vangronsveld J, Cuypers A. Mitogen-Activated Protein (MAP) kinases in plant metal stress: regulation and responses in comparison to other biotic and abiotic stresses. *Int J Mol Sci.* 2012;13:7828–7853.
- 44. Sharif R, Xie C, Zhang HQ, et al. Melatonin and is effects on plant systems. *Molecules*. 2018,23:2352.
- 45. Byeon Y, Lee HY, Hwang OJ, Lee HJ, Lee K, Back K. Coordinated regulation of melatonin synthesis and degradation genes in rice leaves in response to cadmium treatment. *J Pineal Res.* 2015;58:470.
- 46. Wei Z, Gao T, Liang B, Zhao Q, Ma F, Li C. Effects of exogenous melatonin on methyl viologen-mediated oxidative stress in apple leaf. *Int J Mol Sci.* 2018;19:316.
- 47. Zhang HJ, Zhang N, Yang RC, et al. Melatonin promotes seed germination under high salinity by regulating antioxidant systems, ABA and GA4 interaction in cucumber (*Cucumis sativus* L.). *J Pineal Res.* 2014;57:269-279.
- 48. Ahsan N, Nakamura T, Komatsu S. Differential responses of microsomal proteins and metabolites in two contrasting cadmium (Cd)-accumulating soybean cultivars under Cd

stress. Amino Acids. 2012;42:17-327.

- 49. Bozzi AT, Zimanyi CM, Nicoludis JM, Lee BK, Zhang CH, Gaudet R. Structures in multiple conformations reveal distinct transition metal and proton pathways in an Nramp transporter. *eLife*. 2019;8:e41124.
- 50. Ehrnstorfer IA, Manatschal C, Arnold FM, Laederach J, Dutzler R. Structural and mechanistic basis of proton-coupled metal ion transport in the SLC11/NRAMP family. *Nat Commun.* 2017;8:14033.
- Feng S, Tan J, Zhang Y, et al. Isolation and characterization of a novel cadmium-regulated Yellow Stripe-Like transporter (SnYSL3) in *Solanum nigrum. Plant Cell Rep.* 2017;36:281-296.
- 52. Liedschulte V, Laparra H, Battey JND, et al. Impairing both *HMA4* homeologs is required for cadmium reduction in tobacco. *Plant Cell Environ*. 2017;40:364-377.
- Yan J, Wang P, Wang P, et al. A loss-of function allele of *OsHMA3* associated with high cadmium accumulation in shoots and grain of *Japonica* rice cultivars. *Plant Cell Environ*. 2016;39:1941-1954.
- 54. Satoh-Nagasawa N, Mori M, Nakazawa N, et al. Mutations in rice (*Oryza sativa*) heavy metal ATPase 2 (*OsHMA2*) restrict the translocation of zinc and cadmium. *Plant Cell Physiol*. 2012;53:213-224.
- 55. Yamaji N, Xia JX, Mitani-Ueno N, Yokosho K, Ma JF. Preferential delivery of zinc to developing tissues in rice is mediated by P-type heavy metal ATPase OsHMA2. *Plant Physiol.* 2013;162:927-939.
- 56. Hwang JU, Song WY, Hong D, et al. Plant ABC transporters enable many unique aspects of a terrestrial plant's lifestyle. *Mol Plant*. 2016;9:338-355.
- 57. Mandal SK, Adhikari R, Sharma A, Chandravanshi M, Gogoi P, Kanaujia SP. Designating ligand specificities to metal uptake ABC transporters in *Thermus thermophilus* HB8. *Metallomics*. 2019;11:597-612.
- Xu L, Wang Y, Zhang F, et al. Dissecting root proteome changes reveals new insight into cadmium stress response in radish (*Raphanus sativus* L.). *Plant Cell Physiol*. 2017;58:1901-1913.

Figure legends

FIGURE 1 Melatonin-induced changes of Cd content (A) and the activity of key antioxidant enzyme's activity (B~F) under Cd stress. Data are means \pm SE of three biological replicates. Columns with different letters indicate significant differences at P < 0.01 according to Duncan's multiple range test. MT, melatonin; SOD, superoxide dismutase; POD, peroxidase; APX, ascorbate peroxidase; CAT, catalase; GR, Glutathione reductase. Con, control; ND, None-detected.

FIGURE 2 Summary of DEGs from three comparisons. (A) Number of significantly up-regulated (red bar) and down-regulated (blue bar) genes. (B) Venn diagrams of DEGs. (C)~(E) Heat map of up-regulated (C), down-regulated (D) and non-responsive (E) genes from Con vs. Cd comparison and their corresponding expression profiles from the other two comparisons. The log_2 (FC) value in blue and red color indicate low and high expression level, respectively.

FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the GO biological process and molecular function terms as well as metabolic pathways significantly enriched in DEGs (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S5.

FIGURE 4 Heat map of DEGs encoding metal transporters (A) as well as known and novel DEMs (B). The cluster I~VII in (A) was classified based on the log₂ (FC) values from three comparisons. The detailed information is shown in Table S6.

FIGURE 5 Expression pattern of DEMs and their target genes under Cd stress with/without melatonin treatment. A, Differential expression data from RNA-Seq. B, Expression data of target genes from RT-qPCR analysis. Data are mean \pm SE from three biological replicates. Columns with different letters indicate significant differences at P < 0.01 according to Duncan's multiple range test. Grey box represents the gene expression is not changed significantly.

FIGURE 6 RT-qPCR expression profiles of DEGs (A) and DEMs (B) under Cd stress with/without melatonin treatment. Data are mean \pm SE from three biological replicates. Columns with different letters indicate significant differences at p < 0.01 according to Duncan's multiple range test.

FIGURE 7 Overexpression of *RsMT1* gene leads into enhanced Cd tolerance of tobacco plants. (a) Phenotypes of OE-RsMT1 and WT plants under Cd stress. Three-day-old plants were transferred to 1/2 MS medium with 5.0μ M CdCl₂. Photographs were taken one week after the transfer. (b) Root length of OE-RsMT1 and WT plants as described in (a). (c) Phenotypes of four-week-old OE-RsMT1 and WT plants. (d) Expression profile of the RsMT1 gene in OE-RsMT1 and WT plants

as described in (c). (e) Cd content of OE-RsMT1 and WT plants as described in (c). Data are presented as means \pm SE. ** means p<0.01 significant level.

FIGURE 8 Proposed schematic model for the melatonin-mediated Cd uptake and accumulation in radish. CaM, calmodulin; CML, calmodulin-like protein; CDPK, calcium-dependent protein kinase; GR, glutathione reductase; SOD, superoxide dismutase; POD, peroxidase; CAT, catalase; APX, ascorbate peroxidase; PCS, phytochelatin synthase; MT, metallothionein; YSL2, yellow stripe-like transporter 2; YSL7, yellow stripe-like transporter 7; ZIP12, zinc iron permease 12. CAX4, vacuolar cation/proton exchanger 4; HMA2, heavy metal atpase 2; HMA4, heavy metal atpase 4.

Supporting Information

Figure S1 Heatmap of correlation coefficient between two replicates for each mRNA (A) and sRNA (B) library. White and red represents the low and high correlation, respectively.

Figure S2 Length distribution of sRNA among six libraries.

Table S1 Primers used for RT-qPCR analysis in this study.

Table S2 Summary of data statistics of mRNA libraries.

Table S3 Mapping of RNA-seq reads to the radish genome sequence.

Table S4 The enriched GO categories for the DEGs.

Table S5 The enriched KEGG terms for the DEGs.

Table S6 Identification of DEGs encoding heavy metal transporters.

Table S7 Summary of data statistics of six sRNA libraries.

Table S8 Summary of sRNAs ranging from 18 to 30 nt in six sRNA libraries.

Table S9 Identification and expression of known miRNAs in six sRNA libraries.

Table S10 Identification and expression of novel miRNAs in six sRNA libraries.

Table S11 Identification of differential expressed miRNAs among three comparisons.

Table S12 Identification of target genes for the known and novel miRNAs.

Table S13 Differentially expressed miRNAs and their target genes derived from **RNA-Seq.**

Table S14 Identification of DEGs involved in ROS scavenging and signaling transduction.



FIGURE 1 Melatonin-induced changes of Cd content (A) and the activity of key antioxidant enzyme's activity (B~F) under Cd stress. Data are means ± SE of three biological replicates. Columns with different letters indicate significant differences at P < 0.01 according to Duncan's multiple range test. MT, melatonin; SOD, superoxide dismutase; POD, peroxidase; APX, ascorbate peroxidase; CAT, catalase; GR, Glutathione reductase. Con, control; ND, None-detected.

Journal of Pineal Research

Con vs. Cd Con vs. Cd+MT

448

Convs. Cd+MT

Cd vs. Cd+MT

6

4

2

0

-2

-4

-6

48

949

17

150

Cd vs. Cd+MT

Con vs. Cd

Ε

В

1192

91

Up-regulated Down-regulated

Cd vs. Cd+MT

Con VS. Cd Con VS. Cd VS. Cd+NMT Cd VS. Cd+NMT

5

0

10

D

Con vs. Cd+MT

5

0

-5



expression level, respectively.

59 60

Converte de la contraction process magnética de la contraction		Α		, ^b ;	CATENT		C	9 (CO+MT CO+MT
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process of main metabolic process of the state o		Con	Co	CG	J. V.S.	con'	Cou	, Cç	⁷ 12.
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Carbohydrate metabolic process				Heme binding
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic pathways significantly enriched in gathered and table of process and molecular function terms as well as metabolic process.					Oxidation-reduction process	\vdash	_	⊢	Carbohydrate binding Hydrolase activity Biol. Mol.
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values)					Movement of cell or subcellular component			\vdash	Dioxygenase activity process function
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic process of licesanine-outlaining compared tradbolic process.					Microtubule-based process				Chitinase activity 12 6 0 6 12
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic process.					Single-organism process				- Copper ion binding -log (adj. p)
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic process.					Microtubule-based movement	-	_	<u> </u>	Chucosyltransferase activity
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic process.			-		Pyrimidine nucleotide biosynthetic process		_		Oxidoreductase activity on a sulfur group of donors
Cellular carbohydrate metabolic processArninoglycan metabolic processDyrindine - outsining compound metabolic processOrganonitrogen compound catabolic processOrganic acid metabolic processOrganonitrogen metabolic processOrganonitrogen metabolic processOrganonitrogen polysocharid metabolic processOrganonitrogen metabolic processOrganonitrogen compound catabolic processOrganonitrogen polysocharid metabolic processOrganonitrogen metabolic processOrganonitrogen metabolic processOrganonitrogen polysocharid metabolic processOrganonitrogen polysocharid processOrganonitrogen polysocharid processOrganonitrogen polysocharid processOrganonitr					Carbohydrate derivative catabolic process				Drug transporter activity
Cytoskeleton roganization Aninogiycan metabolic process Lipid modification Pyrimidine -ucleotide metabolic process Organization catabolic process Organization complex transferase activity Profile complex transferase Catabolic process Organization Organization or process Organization or process Organization or process Organization or process Organization or biogenesis Glutamine finally amino acti metabolic process Glutamine metabolic process Glutamine metabolic process Glutamine metabolic process Glutamine metabolic process Glutamine metabolic process Strife Category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic protests Premyteroparal biosynthesis Premyteroparal biosynthesis Profile process and molecular function terms as well as metabolic protests Profile process and molecular function terms as well as metabolic protests Profile process and molecular function terms as well as metabolic protests Profile process and molecular function terms as well as metabolic protests Profile process and molecular function terms as well as metabolic protests Profile process and molecular function terms as well as metabolic protests Profile procests an	Į				Cellular carbohydrate metabolic process				Drug transmembrane transporter activity
Animological metabolic process Lipid modification Prynindler-contability compound metabolic process Organonitrogen compound catabolic process Organication is biological process Organication is biological process Organication acid metabolic process Organication acid process Organication acid metabolic process Organication process Organication organication or biogenesis Organication process Organication pro			_		Cytoskeleton organization			<u> </u>	
Image: statistic statisti	-		_		Pyrimidine nucleotide metabolic process		_	\vdash	Xylogiucan:xylogiucosyl transferase activity
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic pathways significantly enriched in galaxies of estabolics process.					Lipid modification		_		Cofactor binding
Organointogen compound catabolic process Organointogen compound catabolic process Organic acid metabolic process <td></td> <td></td> <td></td> <td></td> <td>Pyrimidine-containing compound metabolic process</td> <td></td> <td></td> <td></td> <td>Iron ion binding</td>					Pyrimidine-containing compound metabolic process				Iron ion binding
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic process.			_		Organonitrogen compound catabolic process			\vdash	UDP-glucosyltransferase activity
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents the biological process and molecular function terms as well as metabolic protess (dugusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S4	-		_		Carboxylic acid metabolic process		_	<u> </u>	Iubulin binding
Organic acid metabolic process Lipid glycosylation Gellular amino acid metabolic process Microtubule cytoskeleton organization Glycosylation Gellulase biosynthetic process Beta-glucan metabolic process Gellular amino acid metabolic process Gellulase biosynthetic process Gellulase biosynthetic process Gellular amino biosynthetic process Gellular amino acid metabolic process Gellular protechrid metabolic process Glucan biosynthetic process Glutar metabolic pr			-		Aminoglycan catabolic process			\vdash	Catalytic activity
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S4					Organic acid metabolic process				Protein complex binding
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic protess (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S4					Lipid glycosylation				Microtubule motor activity
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in formation is shown in Table S4 and Table S			_		Cellular amino acid metabolic process			\vdash	Oxidoreductase activity, incorpor. or reduction of mol. oxygen
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S	-		_		Microtubule cytoskeleton organization			⊢	Hydrolase activity, acting on glycosyl bonds
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S4	·				Cellulose biosynthetic process		_	\vdash	Transferase activity, transferring glycosyl compounds
Beta-glucan biosynthetic process Beta-glucan metabolic process Chilin metabolic process Cell wall macromolecule catabolic process Cell wall macromolecule metabolic process Cell wall optication for process Cell wall organization or biogenesis Glucan metabolic process Cell wall organization or biogenesis Glutamine metabolic process Cell wall organization or biogenesis Glutamine metabolic process Cell wall organization or biogenesis Glutamine metabolic process FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) repre					Cellulose metabolic process				Cytoskeletal protein binding
Beta-glucan metabolic process Chitin metabolic process Drug transmembrane transport Cell wall macromolecule catabolic process Cell wall macromolecule metabolic process Cell wall gucan metabolic process Cell wall gucan metabolic process Glucosinolate biosynthesis Glucosinine - containing compound catabolic process Glutamine metabolic process Glucosinol category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S4					Beta-glucan biosynthetic process				Motor activity
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Beta-glucan metabolic process		_	\vdash	Microtubule binding
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Chitin metabolic process			L	
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Drug transmembrane transport	D			MT of
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Cell wall macromolecule catabolic process	D	С	9 ($d^{+}N'$
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Cellular polysaccharide metabolic process	- 00	1S.	VS.	49.0 I I I I I I I I I I I I I I I I I I I
Figure 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Cell wall macromolecule metabolic process	Co.	Cor	CC	0 1 2 3
Cysteline and metholine metabolism Cysteline and metholine metabolism Cysteline and metholine metabolism Glucan metabolic process Gluconsmine-containing compound catabolic process Cell wall organization or biogenesis Glucanine metabolic process Phenylpropanoid biosynthesis Glucanine metabolic process Phenylpropanoid biosynthesis Silosynthesis of secondary metabolites Phenylpropanoid biosynthesis FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S1	-		_		Polysaccharide metabolic process				Glucosinolate biosynthesis
Figure 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Cellular glucan metabolic process				Cysteine and methionine metabolism
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Glucan metabolic process				Flavonoid biosynthesis
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Amino sugar catabolic process				Glutathione metabolism
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Chitin catabolic process				Phenylalanine metabolism
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Cell wall organization or biogenesis				Tyrosine metabolism
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S					Glutamine metabolic process			<u> </u>	Biosynthesis of secondary metabolites
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S									
FIGURE 3 Functional category enrichment of DEGs from three comparisons. (A) and (B) represents th biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S									
biological process and molecular function terms as well as metabolic pathways significantly enriched in (adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S		inct	ior	ر ا در	category enrichment of DEGs	from	th	roc	(A) and (B) represents the
(adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S		unct	101				un		
(adjusted p values < 0.05), respectively. The detailed information is shown in Table S4 and Table S	biological pro	ces	s a	nd	molecular function terms as v	vell a	s n	net	abolic pathways significantly enriched in
	(adjusted	рv	alu	les	< 0.05), respectively. The de	tailed	1 in	for	rmation is shown in Table S4 and Table S
	(dajastea	Ρ.	are	100	(0.05), respectively. The de	canec			

Journal of Pineal Research



FIGURE 4 Heat map of DEGs encoding metal transporters (A) as well as known and novel DEMs (B). The cluster I~VII in (A) was classified based on the log2 (FC) values from three comparisons. The detailed information is shown in Table S6.

В

2.0

1.5

1.0

0.5

miR857

miR164a

65-

-

а

b

RsPXM16

ab

RsNAC3

а

b

а

Cd+MT







FIGURE 6 RT-qPCR expression profiles of DEGs (A) and DEMs (B) under Cd stress with/without melatonin treatment. Data are mean \pm SE from three biological replicates. Columns with different letters indicate significant differences at p < 0.01 according to Duncan's multiple range test.



FIGURE 7 Overexpression of RsMT1 gene leads into enhanced Cd tolerance of tobacco plants. (a) Phenotypes of OE-RsMT1 and WT plants under Cd stress. Three-day-old plants were transferred to 1/2 MS medium with 5.0µM CdCl2. Photographs were taken one week after the transfer. (b) Root length of OE-RsMT1 and WT plants as described in (a). (c) Phenotypes of four-week-old OE-RsMT1 and WT plants. (d) Expression profile of the RsMT1 gene in OE-RsMT1 and WT plants as described in (c). (e) Cd content of OE-RsMT1 and WT plants as described in (c). Data are presented as means ± SE. ** means p<0.01 significant level.



FIGURE 8 Proposed schematic model for the melatonin-mediated Cd uptake and accumulation in radish. CaM, calmodulin; CML, calmodulin-like protein; CDPK, calcium-dependent protein kinase; GR, glutathione reductase; SOD, superoxide dismutase; POD, peroxidase; CAT, catalase; APX, ascorbate peroxidase; PCS, phytochelatin synthase; MT, metallothionein; YSL2, yellow stripe-like transporter 2; YSL7, yellow stripe-like transporter 7; ZIP12, zinc iron permease 12. CAX4, vacuolar cation/proton exchanger 4; HMA2, heavy metal atpase 2; HMA4, heavy metal atpase 4.



Figure S1 Heatmap of correlation coefficient between two replicates for each mRNA (A) and sRNA (B) library. White and red represents the low and high correlation, respectively.


Table S1 Primers used for RT-qPCR analysis in this study.

Gene	Primer	Sequence
$D_{\alpha}MAC2$	F	GGATTACGAGGTATCAAGAA
KSNAC3	R	CAGGTAGTGGCTTATGAG
$D_{c}DVM16$	F	TGTCCAGTCTTCAGTTAAG
KSF AMITO	R	TCAGTTCTTCCTTCTTCAG
Rs AFC	F	GTACAATGTTGGACAAGAC
<i>NSALC</i>	R	ACAGTGAGAGCAAGAATG
<i>R</i> <i>c</i> F <i>R N P</i>	F	AGAGGTAGTTGAAGAAGAAG
KSEKIVI	R	AATGAGACACGAAGGTAG
$R_{s}CCN1$	F	CGTATCCTTGTTGTGGTA
NSOCIVI	R	CTTCATCTGGTTCTCTTCA
R _c CSTU13	F	TCACTCAACATCGTTCAG
KSUS1015	R	AGAAGGAAGGATAGAAGGA
$D_{\alpha}HMT$	F	CCATCTTCTTCCTCTATCG
INSTITUT I	R	CTGTTGTTGTTGCTCTTC
$D_{c}MDD10$	F	GTCCACTCATCAGTTCAA
KSIMIKI 10	R	AAGCATCATATCGGAGAG
	F	AGTAACGAGACAGAAGAAC
KSI DK12	R	CAAGGACATCCATCAGAG
D _c D _C III//	F	CTCATAACTCCACCATACC
KSDGLU44	R	GTTGCCATAATGTTCCTTC
miR164a	—	UGGAGAAGCAGGGCACGUGCA
miR857	—	UUUUGUAUGUUGAAGGUGUAU
RsMT1-EcoR I	F	CGGAATTCCAGCAAATAAAGGCATCAA
RsMT1-BamH I	R	CGGGATCCCTTTTCCCCCAGTTTTTC

Table S2 Summary of data statistics of mRNA libraries.

	Sample name	CK_1	CK_2	Cd100_1
	Raw reads	28077892	28309276	27798076
	Adaptor	45799 (0.16%)	71299 (0.25%)	75855 (0.27%)
	Containing N	323606 (1.15%)	325637 (1.15%)	321208 (1.56%)
	Low quality reads	502622 (1.79%)	522756 (1.85%)	289604 (1.04%)
`	Clean reads	26333838(93.79%)	26469892 (93.50%)	26424742 (95.06%)
)	Clean_Q20 (%)	94.76	94.69	95.67
2	Clean_Q30 (%)	88.49	88.43	90.06
3	GC content (%)	47.04	46.74	46.7

Cd100_2	Cd_50MT1	Cd_50MT2
27543336	28329070	30456458
56784 (0.21%)	52361 (0.18%)	84616 (0.28 %)
318261 (1.16%)	326757 (1.15%)	347242 (1.14%)
273935 (0.99%)	406256 (1.43%)	376856 (1.24 %)
26245376 (95.29%)	26758322 (94.46%)	28839030 (94.69 %)
95.78	95.16	95.49
90.26	89.19	89.81
46.64	46.81	46.79

 Table S3 Mapping of RNA-seq reads to the radish genome sequence.

2	Table S3 Mapping of	RNA-seq reads to the ra	dish genome sequenc	e.
3	Sample name	CK_1	CK_2	Cd100_1
4 5	Total reads	26333838	26469892	26424742
5 6	Total mapped	17002374 (64.56%)	16921713 (63.93%)	17247699 (65.27%)
7	Multiple mapped	131993 (0.5%)	121414 (0.46%)	128474 (0.49%)
8	Uniquely mapped	16870381 (64.06%)	16800299 (63.47%)	17119225 (64.78%)
9 10	Reads map to '+'	8424346 (31.99%)	8380453 (31.66%)	8548193 (32.35%)
11	Reads map to '-'	8446035 (32.07%)	8419846 (31.81%)	8571032 (32.44%)

for per period

4
5
6
7
8
0
9 10
10
11
12
13
14
15
16
17
18
19
20
21
27
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
30
10
40
41
42
43
44
45
46
47
48
49
50
51

3	Cd100 2	Cd 50MT1	Cd 50MT2	
4	26245376	26758322	28839030	
5	17308479 (65.95%)	17346360 (64.83%)	18889152 (65.5%)	
7	129651 (0.49%)	132339 (0.49%)	143302 (0.5%)	
8	17178828 (65.45%)	17214021 (64.33%)	18745850 (65%)	
9	8577378 (32.68%)	8596914 (32.13%)	9360241 (32.46%)	
10 11	8601450 (32.77%)	8617107 (32.2%)	9385609 (32.54%)	
12				
13				
14 15				
16				
17				
18				
19 20				
21				
22				
23				
24 25				
26				
27				
28 20				
30				
31				
32				
33 34				
35				
36				
37				
30 39				
40				
41				
42 43				
44				
45				
46 47				
48				
49				
50				
51 52				
52				
54				
55				
56 57				

2 3	Table S4 The Cd vs. Con	enriched GO categor	ies for the DEGs.		
4	GO accession	Term type	Description	DEG item	Bg item
5	 GO:0005975	Biological process	carbohydrate metabolic process	179	2346
6 7	GO:0007017	Biological process	microtubule-based process	42	360
8	GO:0044710	Biological process	single-organism metabolic process	419	8562
9	GO:0044699	Biological process	single-organism process	691	15307
10	GO:0006928	Biological process	movement of cell or subcellular component	35	346
11	GO:0007018	Biological process	microtubule-based movement	23	168
13	GO:0044723	Biological process	single-organism carbohydrate metabolic process	88	1293
14	GO:0055114	Biological process	oxidation-reduction process	185	3379
15 16	GO:0006073	Biological process	cellular glucan metabolic process	21	189
10	GO:0044042	Biological process	glucan metabolic process	21	189
18	GO:1901565	Biological process	organonitrogen compound catabolic process	21	195
19	GO:0019752	Biological process	carboxylic acid metabolic process	92	1530
20	GO:0043436	Biological process	oxoacid metabolic process	92	1531
22	GO:0030259	Biological process	lipid glycosylation	13	80
23	GO:0006082	Biological process	organic acid metabolic process	92	1536
24	GO:0006026	Biological process	aminoglycan catabolic process	9	44
25	GO:0070085	Biological process	glycosylation	23	229
20	GO:0000226	Biological process	microtubule cytoskeleton organization	19	180
28	GO:0071554	Biological process	cell wall organization or biogenesis	27	302
29	GO:0006520	Biological process	cellular amino acid metabolic process	65	1046
30	GO:0006022	Biological process	aminoglycan metabolic process	10	67
32	GO:0006220	Biological process	pyrimidine nucleotide metabolic process	10	69
33	GO:0030258	Biological process	lipid modification	14	121
34	GO:0006541	Biological process	glutamine metabolic process	9	56
35 36	GO:1901564	Biological process	organonitrogen compound metabolic process	188	3915
37	GO:0072527	Biological process	pyrimidine-containing compound metabolic proces	14	127
38	GO:0006032	Biological process	chitin catabolic process	7	37
39	GO:0046348	Biological process	amino sugar catabolic process	7	37
40 41	GO:1901072	Biological process	glucosamine-containing compound catabolic proce	7	37
42	GO:1901136	Biological process	carbohydrate derivative catabolic process	12	104
43	GO:0044262	Biological process	cellular carbohydrate metabolic process	53	821
44	GO:0007010	Biological process	cytoskeleton organization	32	448
45 46	GO:0006221	Biological process	pyrimidine nucleotide biosynthetic process	9	64
47	GO:0016798	Molecular function	hydrolase activity, acting on glycosyl bonds	104	1093
48	GO:0004553	Molecular function	hydrolase activity, hydrolyzing O-glycosyl compou	97	1038
49 50	GO:0016757	Molecular function	transferase activity, transferring glycosyl groups	90	957
51	GO:0008017	Molecular function	microtubule binding	35	248
52	GO:0015631	Molecular function	tubulin binding	35	264
53	GO:0016758	Molecular function	transferase activity, transferring hexosyl groups	64	691
54	GO:0003824	Molecular function	catalytic activity	987	22363
55 56	GO:0032403	Molecular function	protein complex binding	40	377
57	GO:0003777	Molecular function	microtubule motor activity	23	159
58	GO:0008092	Molecular function	cytoskeletal protein binding	50	625
59 60	GO:0003774	Molecular function	motor activity	30	288
00	GO:0016705	Molecular function	oxidoreductase activity, acting on paired donors, w	63	837

1					
2	GO:0016491	Molecular function	oxidoreductase activity	193	3622
3	GO:0030246	Molecular function	carbohydrate binding	35	365
4	GO:0016787	Molecular function	hydrolase activity	404	8556
5	GO:0005506	Molecular function	iron ion binding	46	625
7	GO:0020037	Molecular function	heme binding	47	690
8	GO:0030170	Molecular function	pyridoxal phosphate binding	20	211
9	GO:0035251	Molecular function	UDP-glucosyltransferase activity	12	91
10 11	GO:0048037	Molecular function	cofactor binding	71	1169
12	GO:0046906	Molecular function	tetrapyrrole binding	48	723
13	GO:0046527	Molecular function	glucosyltransferase activity	12	94
14	GO:0004568	Molecular function	chitinase activity	7	37
15 16	GO:0005507	Molecular function	copper ion binding	21	242
10	GO:0051213	Molecular function	dioxygenase activity	25	310
18	00.0001210				010
19	Cd+MT vs. C	on			
20	GO accession	Term type	Description	DEG item	Bg item
21	GO:0005975	Biological process	carbohydrate metabolic process		2346
23	GO:0007018	Biological process	microtubule-based movement	20	168
24	GO:0007017	Biological process	microtubule-based process	30	360
25 26	GO:0044699	Biological process	single-organism process	474	15307
20 27	GO:0006073	Biological process	cellular glucan metabolic process	18	189
28	GO:0044042	Biological process	glucan metabolic process	18	189
29	GO:0071554	Biological process	cell wall organization or biogenesis	23	302
30 21	GO:0006541	Biological process	glutamine metabolic process	9	56
31	GO:0044710	Biological process	single-organism metabolic process	278	8562
33	GO:0055114	Biological process	oxidation-reduction process	125	3379
34	GO:0030244	Biological process	cellulose biosynthetic process	10	87
35 36	GO:0006928	Biological process	movement of cell or subcellular component	22	346
37	GO:0030243	Biological process	cellulose metabolic process	10	92
38	GO:0051274	Biological process	beta-glucan biosynthetic process	11	109
39	GO:0051273	Biological process	beta-glucan metabolic process	11	114
40 41	GO:0006030	Biological process	chitin metabolic process	7	46
42	GO:1901071	Biological process	glucosamine-containing compound metabolic proce	7	46
43	GO:0009250	Biological process	glucan biosynthetic process	11	119
44	GO:0016998	Biological process	cell wall macromolecule catabolic process	8	64
45 46	GO:0006032	Biological process	chitin catabolic process	6	37
47	GO:0046348	Biological process	amino sugar catabolic process	6	37
48	GO:1901072	Biological process	glucosamine-containing compound catabolic proce	6	37
49 50	GO:0006855	Biological process	drug transmembrane transport	12	138
50 51	GO:0015893	Biological process	drug transport	12	138
52	GO:0042493	Biological process	response to drug	12	140
53	GO:0044036	Biological process	cell wall macromolecule metabolic process	8	69
54 55	GO:0009064	Biological process	glutamine family amino acid metabolic process	10	109
55 56	GO:0005976	Biological process	polysaccharide metabolic process	35	701
57	GO:0044264	Biological process	cellular polysaccharide metabolic process	33	649
58	GO:0016798	Molecular function	hydrolase activity, acting on glycosyl bonds	78	1093
59 60	GO:0004553	Molecular function	hydrolase activity, hydrolyzing O-glycosyl compou	73	1038
00	GO:0016757	Molecular function	transferase activity, transferring glycosyl groups	66	957

1 ว	GO:0016758	Molecular function	transferase activity transferring hexosyl groups	51	691
3	GO:0003824	Molecular function	catalytic activity	676	22363
4	GO:0003777	Molecular function	microtubule motor activity	20	159
5	GO:0016705	Molecular function	oxidoreductase activity, acting on paired donors, w	51	837
7	GO:0008017	Molecular function	microtubule binding	24	248
8	GO:0015631	Molecular function	tubulin binding	24	264
9	GO:0003774	Molecular function	motor activity	25	288
10	GO:0016787	Molecular function	hydrolase activity	287	8556
12	GO:0032403	Molecular function	protein complex binding	29	377
13	GO:0016491	Molecular function	oxidoreductase activity	136	3622
14 15	GO:0020037	Molecular function	heme binding	39	690
16	GO:0046906	Molecular function	tetrapyrrole binding	39	723
17	GO:0030170	Molecular function	pyridoxal phosphate binding	17	211
18	GO:0016706	Molecular function	oxidoreductase activity, acting on paired donors, w	18	240
19 20	GO:0030246	Molecular function	carbohydrate binding	24	365
20	GO:0016671	Molecular function	oxidoreductase activity, acting on a sulfur group of	6	40
22	GO:0004568	Molecular function	chitinase activity	6	37
23	GO:0008061	Molecular function	chitin binding	6	37
24	GO:0016762	Molecular function	xyloglucan:xyloglucosyl transferase activity	7	52
26	GO:0015238	Molecular function	drug transmembrane transporter activity	12	143
27	GO:0090484	Molecular function	drug transporter activity	12	143
28	GO:0048037	Molecular function	cofactor binding	50	1169
29 30	GO:0035251	Molecular function	UDP-glucosyltransferase activity	9	91
31					

Cd+MT vs. Cd

GO_accession	Term_type	Description	DEG_item Bg_item
No enriched G	O categories at padj	<0.05.	

Ruicz

Journal of Pineal Research

2	
3	
1	
-	
5	
6	
7	
8	
a	
10	
10	
11	
12	
13	
11	
14	
15	
16	
17	
18	
10	
17	
20	
21	
22	
23	
21	
24	
25	
26	
27	
28	
20	
29	
30	
31	
32	
33	
34	
25	
22	
36	
37	
38	
39	
10	
тU 1	
41	
42	
43	
44	
45	
16	
40	
47	
48	
49	
50	
51	
51	
52	
53	
54	
55	
56	
57	
50	
JQ	
59	

p-value	Corrected_p-value
9.95E-18	4.42E-14
1.13E-10	8.32E-08
2.72E-08	1.10E-05
5.61E-08	2.07E-05
1.17E-07	3.70E-05
1.48E-07	4.37E-05
4.60E-07	0.00012765
5.96E-07	0.00015565
1.31E-05	0.0023329
1.31E-05	0.0023329
2.25E-05	0.0038336
2.41E-05	0.0039266
2.48E-05	0.0039266
2.68E-05	0.0040913
2.77E-05	0.0040913
2.99E-05	0.0042728
6.14E-05	0.0084988
6.46E-05	0.0084988
8.08E-05	0.010241
0.00012267	0.015119
0.00024654	0.026045
0.00025451	0.026262
0.00030422	0.029999
0.00032557	0.030735
0.00036586	0.033776
0.00039178	0.033776
0.00041027	0.033776
0.00041027	0.033776
0.00041027	0.033776
0.00051632	0.041653
0.00056376	0.043884
0.00057642	0.044096
0.00064889	0.048798
2 90F-17	6 43F-14
2.90E-17	0.+3E-14 1 72E-12
7 16E-14	7 9/E-11
7.10E-14	3 22E-08
1 80E 10	1 1/F 07
A 71E 10	2 61E 07
4./1E-10	2.01E-07 8 66E 07
1./0E-09	0.00E-0/
1.05E-08	4.0/E-00
0.18E-08	2.11E-03
6.93E-07	0.0001/0//
1.04E-06	0.00023699
1.07E-06	0.00023699

2	1.73E-06	0.00036462
3	3.10E-06	0.00062447
4	7.17E-06	0.0013828
5	6.51E-05	0.0084988
7	0.00021036	0.024145
8	0.00021223	0.024145
9	0.00022541	0.025004
10	0.00023456	0.025383
12	0.00030425	0 029999
13	0.00032073	0.030735
14	0.00041027	0.033776
15	0.00041106	0.033776
16 17	0.00053182	0.033170
18	0.00033102	0.012137
19		
20	n value	Corrected n value
21	$\frac{p-value}{6.0040E}$ 11	
22	0.9949E-11	7.7391E-06
24	1.43/3E-08	7.3189E-00
25	1.4846E-08	/.3189E-06
26	1.0634E-07	0.000037767
27	1.8583E-06	0.00045806
28 29	1.8583E-06	0.00045806
30	7.1049E-06	0.0015762
31	0.00001505	0.0030353
32	0.000017875	0.0034484
33	0.000028518	0.0048667
35	0.000041492	0.006575
36	0.000059461	0.0087943
37	0.000073024	0.010452
38	0.00007978	0.011062
39 40	0.00012654	0.016514
41	0.00016578	0.019819
42	0.00016578	0.019819
43	0.00016973	0.019819
44	0.00027112	0.029089
45	0.00028846	0.029089
47	0.00028846	0.029089
48	0.00028846	0.029089
49	0.00033663	0.03247
50 51	0.00033663	0.03247
52	0.00037765	0.033513
53	0.00045925	0.038447
54	0.00050639	0.041609
55 56	0.00051932	0.041895
57	0.00060002	0 047541
58	6 1753E-16	2.74E-12
59	1 2171E-14	2.712.12 2.7001E-11
60	3 8108F-12	5 6362F-09
	2.01000 12	

1.73E-06

0.00036462

9.9928E-11	8.8676E-08
1.8105E-09	1.3388E-06
6.6094E-09	4.1894E-06
3.0486E-08	0.000013527
3.7296E-08	0.000015044
1.1065E-07	0.000037767
1.5675E-07	0.00004968
2.6832E-07	0.00007937
3.1114E-07	0.000086283
3.7449E-06	0.00087452
7.8207E-06	0.0016524
0.000020773	0.0038403
0.000035698	0.0058663
0.000056478	0.0086411
0.000085401	0.011483
0.00028466	0.029089
0.00028846	0.029089
0.00036116	0.033513
0.00037409	0.033513
0.00045234	0.038447
0.00045234	0.038447
0.00061462	0.047843
0.0006332	0.048439
o-value	Corrected_p-value

p-value	Corrected_p-value

Cd vs. Con

Term	ID	Input number	Background numbe	p-value
Cysteine and methionine metabolism	ko00270	27	99	0.0005873
Glucosinolate biosynthesis	ko00966	10	19	0.00077705
Tyrosine metabolism	ko00350	15	40	0.0007415

Cd+MT vs. Con

Ca+IVI I vs. Con				
Term	ID	Input number	Background number	p-value
Glucosinolate biosynthesis	ko00966	10	19	1.5923E-05
Glutathione metabolism	ko00480	21	93	3.7356E-05
Phenylalanine metabolism	ko00360	23	114	7.4214E-05
Flavonoid biosynthesis	ko00941	9	21	0.00014621
Cysteine and methionine metabolism	ko00270	20	99	0.0002115
Ubiquinone and other terpenoid-quinone	ko00130	10	32	0.00050821
Biosynthesis of secondary metabolites	ko01110	100	995	0.00303746
Phenylpropanoid biosynthesis	ko00940	23	154	0.00296965
Cd+MT vs. Cd				
Term	ID	Input number	Background number	p-value
No enriched KEGG terms at padj <0.05.				

Cd+MT vs. Cd

Term	ID	Input number	Background numberp-value
No enriched KEGG terms at padj <0.05.			

3
4
5
6
7
, 0
0
9
10
11
12
13
14
15
16
17
10
10
19
20
21
22
23
24
25
26
20
27
28
29
30
31
32
33
34
35
36
20
3/
38
39
40
41
42
43
44
45
16
-10 17
4/ 40
48
49
50
51
52
53
54
55
56
50
5/
20

1 2

Corrected p-value	Hyperlink
0.029528014	http://www.genome.jp/kegg-bin/show_pathway?ko00270
0.029528014	http://www.genome.jp/kegg-bin/show_pathway?ko00966
0.029528014	http://www.genome.jp/kegg-bin/show_pathway?ko00350
Corrected p-value	Hyperlink
0.001608182	http://www.genome.jp/kegg-bin/show_pathway?ko00966
0.001886482	http://www.genome.jp/kegg-bin/show_pathway?ko00480
0.002498552	http://www.genome.jp/kegg-bin/show_pathway?ko00360
0.003691892	http://www.genome.jp/kegg-bin/show_pathway?ko00941
0.004272371	http://www.genome.jp/kegg-bin/show_pathway?ko00270
0.008554861	http://www.genome.jp/kegg-bin/show_pathway?ko00130
0.038347882	http://www.genome.jp/kegg-bin/show_pathway?ko01110
0.038347882	http://www.genome.ip/kegg-bin/show_pathway?ko00940

Corrected p-value Hyperlink

Per Periev

 Table S6 Identification of DEGs encoding heavy metal transporters.

Cluster name	Gene name	log ₂ (Cd/Con)	log ₂ (Cd+MT/Con)	log ₂ (Cd+MT/Cd)
	ABCG40	5.54	7.54	1.99
	РНТ3	4.62	5.87	1.23
	LHT7	1.85	3.80	1.95
Cluster I	CAX4	1.82	4.96	3.15
	ABCB21	1.31	2.57	1.25
	MTPA2	1.15	1.60	0.44
	ATX1	6.93	4.46	-2.48
	STP6	6.06	4.65	-1.43
	ALMT2	5.98	4.32	-1.67
	MT2A	5.25	3.66	-1.60
	PHT1-4	4.76	2.99	-1.78
Cluster II	SWEET11	4.52	2.55	-1.98
	ABCC14	4.27	1.42	-2.87
	ABCF1	3.94	1.63	-2.32
	ZIP12	3.78	2.51	-1.28
	YSL7	2.02	1.95	-0.07
	HMA4	1.60	1.45	-0.20
	OPT4	-1.44	-1.90	-0.45
Cluster III	NPF	-1.58	-2.82	-1.26
	NRT2.1	-2.06	-3.66	-1.61
	HMA2	-2.19	-1.25	0.88
	SULTR3;2	-3.60	-2.51	1.08
	GTR2	-3.70	-2.01	1.68
Cluster IV	MSL9	-4.06	-1.05	3.00
	SULTR3	-4.10	-1.78	2.31
	VGT1	-5.85	-3.89	1.95
	HIPP21	-6.66	-4.77	1.88
Cluster V	MFS12	1.75	0.81	-0.99
Cluster v	YSL2	1.71	0.65	-1.12
Cluster VI	IGMT4	0.93	4.17	3.23
	UTR2	0.67	2.07	1.39
	PHO1-3	0.47	2.21	1.74
	PLT5	0.24	2.10	1.85
	ABCG25	0.29	1.69	1.39
	ABCG39	-0.19	-1.60	-1.41
Cluster VII	VITH2	-0.68	-3.04	-2.36
	USO1	0.33	-5.34	-5.68

Annotation	
ABC transporter G family member 40	
Phosphate transporter 3	
LYS/HIS transporter 7	
CAX4, Vacuolar cation/proton exchanger 4	
ABC transporter B family member 21	
MTPA2; metal tolerance protein A2	
Copper transport protein ATX1	
Sugar transport protein 6	
Aluminum-activated malate transporter 2	
Metallothionein 2A	
Inorganic phosphate transporter 1-4	
Bidirectional sugar transporter SWEET11	\neg
ABC transporter C family member 14	\neg
ABC transporter E family member 1	
Zine transporter 12	
Metal nicotianamine transporter VSL7	_
Putative cadmium/zing transporting $\Delta TPase HM \Delta A$	
OPT/ ARATH Oligonantida transportar /	_
Nitrata/nentida transportar family (NDE) gapas	_
Nitrate/peptide transporter 2 1	_
Codmium/ring transporting ATDaga UMA2	
Sulfate transporter 2.2	
Chaosin slate transmerter 2	_
Glucosinolate transporter-2	
Selfete transmenter 2	
Surface transporter 3	Y ,
vacuolar glucose transporter 1	
Heavy metal transport/detoxification domain-containing prote	in 12
MFS12_Major facilitator superfamily domain-containing prot	$\frac{12}{3}$
Metal-nicotianamine transporter YSL2	_
Indole glucosinolate O-methyltransferase 4	
UDP-galactose transporter 2	
Phosphate transporter PHO1-3	_
Polyol transporter 5	
ABC transporter G family member 25	
ABC transporter G family member 39	

 Table S7 Summary of data statistics of six sRNA libraries.

3	Sample	total_reads	N% > 10%	low quality	5'_adapter_contaminants	3_adapter_null or insert_nul
4 5	Con_1	14720732	0	24808	15709	482285
5 6	Con_2	14932432	1	23966	14656	406298
7	Cd_1	13138302	0	20540	17799	374048
8	Cd_2	14372733	0	19978	13313	490116
9	Cd+MT_1	13053468	0	20645	11489	429586
10 11	Cd+MT_2	12562421	0	20509	15324	362287

for per period

1	
2	
3	
1	
4	
S	
6	
7	
8	
9	
1	0
1	1
1	2
1	3
1	ر ۸
1	+
1	5 7
1	6
1	7
1	8
1	9
2	0
2	1
2	2
2	2
2	ر ۸
2	4
2	5
2	6
2	7
2	8
2	9
3	0
3	1
2	ว
2	2 2
2	د ۸
3	4
3	5
3	6
3	7
3	8
3	9
4	0
4	1
4	2
4	2
1	ر ۸
4	4
4	د د
4	6

with ployA/T/G/Cclean reads4579414152136 (96.14%)4045614447055 (96.75%)4024412685671 (96.55%)3884813810478 (96.09%)3112312560625 (96.22%)3681412127487 (96.54%)

for per peries

Table S8 Summary of sRNAs ranging from 18 to 30 nt in six sRNA libraries.

			<u> </u>		
3	Sample	Clean reads	Unique reads	Mapped reads	Mapped unique reads
4 5	Con_1	11627933	3258353	6164702 (53.02%)	1990581 (61.09%)
5 6	Con_2	11423108	3053611	6400559 (56.03%)	1831473 (59.98%)
7	Cd_1	9607208	3133142	6201167 (64.55%)	1806479 (57.66%)
8	Cd_2	10163274	3407898	7016378 (69.04%)	1983600 (58.21%)
9	Cd+MT_1	9768533	2643509	5214240 (53.38%)	1511942 (57.19%)
10	Cd+MT_2	9720930	2641514	4784395 (49.22%)	1475782 (55.87%)

to per peries

2	Table S9 Identif	ication and expression of known miRNAs in six	sRNA libra	ries.	
3	Name	Sequence	Length	Con_1	Con_2
4	miR156a-3p	GCUCACUGCUCUUUCUGUCAGA	22	4.0	10.0
5	miR156a-5p	UGACAGAAGAGAGUGAGCAC	20	168.0	161.0
7	miR156c-3p	GCUCACUGCUCUAUCUGUCAGA	22	27.0	29.0
8	miR156f-3p	GCUCACUCUCUAUCCGUCACC	21	1.0	0.0
9	miR156g	CGACAGAAGAGAGUGAGCAC	20	1.0	0.0
10	miR156i	UGACAGAAGAGAGAGAGAGCAC	20	0.0	0.0
12	miR157a-3p	GCUCUCUAGCCUUCUGUCAUC	21	18.0	19.0
13	miR157a-5p	LIUGACAGAAGAUAGAGAGCAC	21	18.0	25.0
14	miR157c-3p	GCUCUCUAUACUUCUGUCACC	21	0.0	0.0
15	miR157d		20	1.0	0.0
16 17	miR158a-3n		20	17124.0	30442.0
18	miR158b		20	97.0	158.0
19	miR1500		20	53050.0	65800.0
20	miR159a		21	11025.0	12718.0
21	miR1590-5p		21	2712.0	2462.0
22 23	miR160a 2n		21	2/13.0	10.0
24	miR160a-5p		21	215.0	10.0
25	miR160a-5p		21	315.0	292.0
26	miR160c-3p		21	3.0	0.0
2/	miR162a-3p		21	7281.0	9183.0
20	miR162a-5p	UGGAGGCAGCGGUUCAUCGAUC	22	50.0	21.0
30	miR164a	UGGAGAAGCAGGGCACGUGCA	21	4213.0	5382.0
31	miR164c-3p	CACGUGUUCUACUACUCCAAC	21	270.0	386.0
32	miR164c-5p	UGGAGAAGCAGGGCACGUGCG	21	1471.0	1914.0
33 34	miR165a-3p	UCGGACCAGGCUUCAUCCCCC	21	875.0	922.0
35	miR165a-5p	GGAAUGUUGUCUGGAUCGAGG	21	63.0	17.0
36	miR166a-3p	UCGGACCAGGCUUCAUUCCCC	21	9404.0	10922.0
37	miR166a-5p	GGACUGUUGUCUGGCUCGAGG	21	122.0	53.0
38	miR166e-5p	GGAAUGUUGUCUGGCACGAGG	21	0.0	0.0
39 40	miR167a-3p	GAUCAUGUUCGCAGUUUCACC	21	134.0	52.0
41	miR167a-5p	UGAAGCUGCCAGCAUGAUCUA	21	485.0	243.0
42	miR167c-3p	UAGGUCAUGCUGGUAGUUUCACC	23	23.0	33.0
43	miR167c-5p	UAAGCUGCCAGCAUGAUCUUG	21	69.0	56.0
44 45	miR167d	UGAAGCUGCCAGCAUGAUCUGG	22	235.0	147.0
46	miR168a-3p	CCCGCCUUGCAUCAACUGAAU	21	668.0	359.0
47	miR168a-5p	UCGCUUGGUGCAGGUCGGGAA	21	1060.0	924.0
48	miR169a-5p	CAGCCAAGGAUGACUUGCCGA	21	1.0	4.0
49 50	miR169b-3p	GGCAAGUUGUCCUUCGGCUACA	22	27.0	13.0
51	miR169b-5p	CAGCCAAGGAUGACUUGCCGG	21	8.0	6.0
52	miR169d	UGAGCCAAGGAUGACUUGCCG	21	1.0	1.0
53	miR169f-3p	GCAAGUUGACCUUGGCUCUGC	21	41.0	18.0
54	miR169g-3p	UCCGGCAAGUUGACCUUGGCU	21	121.0	79.0
56	miR170-3p	UGAUUGAGCCGUGUCAAUAUC	21	0.0	0.0
57	miR170-5p	UAUUGGCCUGGUUCACUCAGA	21	1.0	1.0
58	miR171a-3p	UGAUUGAGCCGCGCCAAUAUC	21	18.0	13.0
59 60	miR171b-3p	UUGAGCCGUGCCAAUAUCACG	21	1.0	1.0
00	miR171b-5p	AGAUAUUAGUGCGGUUCAAUC	21	1.0	0.0
	- T		1		

			,	
miR172a	AGAAUCUUGAUGAUGCUGCAU	21	157.0	239.0
miR172b-5p	GCAGCACCAUUAAGAUUCAC	20	52.0	16.0
miR172c	AGAAUCUUGAUGAUGCUGCAG	21	540.0	580.0
miR172d-5p	GCAACAUCUUCAAGAUUCAGA	21	0.0	0.0
miR172e-3p	GGAAUCUUGAUGAUGCUGCAU	21	502.0	602.0
miR2111a-3p	GUCCUCGGGAUGCGGAUUACC	21	0.0	0.0
miR2111a-5p	UAAUCUGCAUCCUGAGGUUUA	21	3.0	1.0
miR319a	UUGGACUGAAGGGAGCUCCCU	21	79232.0	105659.0
miR319c	UUGGACUGAAGGGAGCUCCUU	21	13526.0	18031.0
miR390a-3p	CGCUAUCCAUCCUGAGUUUCA	21	0.0	0.0
miR390a-5p	AAGCUCAGGAGGGAUAGCGCC	21	547.0	522.0
miR390b-3p	CGCUAUCCAUCCUGAGUUCC	20	1.0	0.0
miR391-5p	UUCGCAGGAGAGAUAGCGCCA	21	54.0	69.0
miR393a-5p	UCCAAAGGGAUCGCAUUGAUCC	22	0.0	2.0
miR394a	UUGGCAUUCUGUCCACCUCC	20	2736.0	3861.0
miR395a	CUGAAGUGUUUGGGGGAACUC	21	155.0	93.0
miR395b	CUGAAGUGUUUGGGGGGGACUC	21	70.0	50.0
miR396a-3p	GUUCAAUAAAGCUGUGGGAAG	21	2859.0	1815.0
miR396a-5p	UUCCACAGCUUUCUUGAACUG	21	11403.0	10241.0
miR396b-3p	GCUCAAGAAAGCUGUGGGAAA	21	162.0	110.0
miR396b-5p	UUCCACAGCUUUCUUGAACUU	21	6287.0	6229.0
miR397a	UCAUUGAGUGCAGCGUUGAUG	21	55.0	66.0
miR 398a-3p	UGUGUUCUCAGGUCACCCCUU	21	483.0	446.0
miR 398b-3p	UGUGUUCUCAGGUCACCCCUG	21	7021.0	7132.0
miR 398b-5p		21	0.0	1.0
miR 399h		21	33.0	39.0
miR 399f		21	0.0	0.0
miR400		21	8.0	8.0
miR403-3n		21	1514.0	1626.0
miR403-5p		21	0.0	0.0
miR408-3n		21	4940.0	6355.0
miR/08-5p		21	2891.0	3100.0
miR 5630a	GCUAAGAGCGGUUCUGAUGGA	21	2071.0	1.0
miR5658		21	0.0	1.0
miP 8171		21	0.0	0.0
miD 9175		21	1.0	141.0
$\frac{1111R8173}{1112}$		20	141.0	275.0
miR824-3p		21	437.0	3/3.0
miR824-5p		21	128.0	/9.0
miK82/		21	1.0	1.0
m1K857		21	8.0	10.0
miK858a		21	15.0	50.0
m1K858b	UUCGUUGUCUGUUCGACCUUG	21	2.0	1.0

Cd_1	Cd_2	Cd+MT_1	Cd+MT_2
20.0	10.0	28.0	24.0
142.0	173.0	277.0	187.0
34.0	39.0	106.0	62.0
0.0	0.0	0.0	0.0
0.0	0.0	2.0	4.0
1.0	0.0	1.0	0.0
75.0	65.0	38.0	65.0
25.0	33.0	24.0	38.0
0.0	0.0	0.0	2.0
0.0	0.0	2.0	0.0
49639.0	54216.0	29506.0	25093.0
273.0	274.0	176.0	155.0
57035.0	74927.0	46344.0	45549.0
12097.0	15662.0	7079.0	8119.0
3351.0	4493.0	2555.0	2233.0
1.0	1.0	2.0	4.0
240.0	321.0	374.0	283.0
0.0	0.0	0.0	1.0
11403.0	9582.0	6150.0	7142.0
19.0	23.0	20.0	31.0
8867.0	11268.0	7428.0	5691.0
393.0	249.0	257.0	414.0
2864.0	4002.0	2193.0	1655.0
1208.0	1575.0	1320.0	918.0
15.0	15.0	13.0	25.0
13181.0	21875.0	11885.0	8370.0
5.0	11.0	30.0	62.0
1.0	1.0	0.0	0.0
6.0	16.0	60.0	47.0
319.0	455.0	455.0	324.0
210.0	275.0	182.0	65.0
281.0	465.0	269.0	109.0
158.0	175.0	185.0	166.0
137.0	444.0	317.0	256.0
646.0	1015.0	890.0	781.0
0.0	1.0	0.0	1.0
3.0	4.0	9.0	8.0
2.0	2.0	3.0	1.0
0.0	0.0	0.0	0.0
1.0	2.0	3.0	1.0
2.0	6.0	9.0	6.0
0.0	2.0	0.0	0.0
0.0	0.0	0.0	0.0
4.0	7.0	25.0	14.0
1.0	4.0	1.0	9.0

1					
2	240.0	251.0	86.0	120.0	
3	3.0	11.0	9.0	7.0	
4	967.0	1122.0	318.0	378.0	
5	0.0	0.0	1.0	0.0	
6	1250.0	0.0	248.0	386.0	
/ Q	1239.0	933.0	240.0	380.0	
0 0	0.0	0.0	0.0	1.0	
10	1.0	2.0	0.0	5.0	
11	80384.0	135518.0	67006.0	72840.0	
12	14235.0	24959.0	8945.0	7652.0	
13	1.0	1.0	0.0	0.0	
14	256.0	406.0	135.0	208.0	
15	0.0	0.0	1.0	0.0	
16	84.0	120.0	84.0	0.0	
17 18	04.0	120.0	04.0	93.0	
19	2.0	1.0	2.0	0.0	
20	3246.0	2982.0	3001.0	3991.0	
21	78.0	69.0	125.0	176.0	
22	9.0	16.0	36.0	66.0	
23	190.0	318.0	396.0	485.0	
24	9903.0	15220.0	8442.0	9771.0	
25	33.0	38.0	49.0	58.0	
26	14400.0	12275.0	5071.0	9062.0	
27	14490.0	12273.0	30/1.0	8902.0	0
20	111.0	66.0	194.0	114.0	
30	295.0	232.0	505.0	551.0	\mathbf{N}
31	6451.0	3679.0	10577.0	16509.0	
32	0.0	0.0	0.0	1.0	
33	8.0	9.0	8.0	21.0	
34	1.0	0.0	0.0	0.0	
35	1.0	6.0	5.0	3.0	
30	2976.0	1865.0	1526.0	2205.0	6.
38	2770.0	1805.0	1320.0	2205.0	
39	1.0	0.0	15217.0	0.0	\sim
40	4932.0	5606.0	15317.0	/822.0	
41	2127.0	4895.0	3298.0	1938.0	
42	1.0	0.0	0.0	0.0	
43	1.0	1.0	0.0	2.0	
44	0.0	0.0	0.0	0.0	
45 46	55.0	161.0	58.0	95.0	
47	333.0	631.0	496.0	342.0	
48	71.0	50.0	202 0	120.0	
49	/1.0	50.0	203.0	130.0	
50	3.0	4.0	2.0	2.0	
51	36.0	28.0	111.0	87.0	
52	173.0	168.0	61.0	180.0	
53	1.0	3.0	3.0	4.0	
54					,

Table Sty Identification and expression of novel mixings in six sking indrafies.

Name Sequence Length Con_1 Con_2 Cd_1 Cd_2 miRn1 UUGGACUGAAGGAGCUCCCU 21 218.0 278.0 206.0 423.0 miRn10 CCUGCCUUCCAUCAACUGAAU 21 307.0 240.0 403.0 430.0 miRn11 UGGGACAUUGGAACUGUGAGU 21 322.0 97.0 23.0 58.0 miRn12 GCAUCAUCAUCAAGAUUCAGA 21 322.0 97.0 23.0 58.0 miRn13 UCGCUUGGUCAAGUUCAAUUAUG 19 76.0 117.0 139.0 67.0 miRn14 UCAACGUUGACUUGCCUUGU 21 141.0 83.0 2.0 5.0 miRn15 GCAAGUUGCAUUCCCUUGUGAACCU 24 4.0 8.0 8.0 16.0 miRn17 AAGGCAUCUCCAUUGGAUCUAUGGAUU 21 47.0 13.0 9.0 20.0 miRn18 MUGUGGGCCCCAUGACUCAUUGAUU 21 47.0 13.0 9.0 20.0 1.0 3.0 1.0 4.0 3.0 miRn17 </th <th>2</th> <th>Table S10</th> <th>Identification and expression of novel miRN</th> <th>As in six :</th> <th>sRNA libra</th> <th>ries.</th> <th></th> <th></th>	2	Table S10	Identification and expression of novel miRN	As in six :	sRNA libra	ries.		
miRn1 UUGGACUGAAGGGAGCUCCCU 21 218.0 278.0 206.0 423.0 miRn10 CCUGCCUUCCAUCAACUGAAU 21 307.0 240.0 403.0 430.0 miRn11 UGGGACAUUGGAACUGUGAGU 21 307.0 240.0 403.0 430.0 miRn12 GCAUCAUCAUCAUCAAGAUUCAGA 21 322.0 97.0 23.0 58.0 miRn13 UCGCUUGGUGCAGGUCGGAC 21 134.0 125.0 118.0 168.0 miRn14 UCAACGUUGAACUUGGUCUGU 21 141.0 83.0 2.0 5.0 miRn15 GCAAGUUGAACUUGGCUCUGU 21 141.0 83.0 2.0 5.0 miRn17 AAGGCAUCUCCCUACGUAGC 21 3.0 1.0 6.0 47.0 miRn19 UGUGGGCCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn20 CCAACUUGUUCCCCUACCACACGUG 21 3.0 1.0 4.0 3.0 miRn21 MAGGACAACAUUACUCUUCCUCCCACACCA 22 3.0 12	3	Name	Sequence	Length	Con_1	Con_2	Cd_1	Cd_2
miRn10 CCUGCCUUCCAUCAACUGAAU 21 307.0 240.0 403.0 430.0 miRn11 UGGGACAUUGGAACUGUGAGU 21 5.0 10.0 8.0 29.0 miRn12 GCAUCAUCAUCAAGAUUCAGA 21 322.0 97.0 23.0 58.0 miRn13 UGCCUUGGUGCAGGUCGAGU 21 134.0 125.0 118.0 168.0 miRn14 UCAACGUUGGCUCAAUUAUG 19 76.0 117.0 139.0 67.0 miRn15 GCAAGUUGAACUUGGCUCAGU 21 141.0 83.0 2.0 5.0 miRn16 ACGGUAUCUCCCCUACGUAGCU 21 141.0 83.0 2.0 5.0 miRn17 AAGGACAUCUCAUCUGUGAACCU 24 4.0 8.0 8.0 16.0 miRn19 UGUGGGCCCCACUGACAUGGU 21 152.0 182.0 182.0 182.0 miRn20 CCAACUUGUUAUGCACCACCACA 22 3.0 1.0 4.0 3.0 miRn21 AAGGACAUAGAAAUAGAACUUACUA 21 15.0 5.0 <td>4</td> <td>miRn1</td> <td>UUGGACUGAAGGGAGCUCCCU</td> <td>21</td> <td>218.0</td> <td>278.0</td> <td>206.0</td> <td>423.0</td>	4	miRn1	UUGGACUGAAGGGAGCUCCCU	21	218.0	278.0	206.0	423.0
miRn11 UGGGACAUUGGAACUGUGAGU 21 5.0 10.0 8.0 29.0 miRn12 GCAUCAUCAUCAUCAAGAUUCAGA 21 322.0 97.0 23.0 58.0 miRn13 UCGCUUGGUGCAGGUCGGGAC 21 134.0 125.0 118.0 168.0 miRn13 UCACGUUGGUCAAUUAUG 19 76.0 117.0 139.0 67.0 miRn15 GCAAGUUGAACUUGCCUCUGU 21 141.0 83.0 2.0 5.0 miRn16 ACGGUAUCUCCCCUACGUAGC 21 3.0 1.0 6.0 47.0 miRn17 AAGAGCAUCUCACUUGAUUGGAUU 21 47.0 27.0 13.0 9.0 miRn19 UGUGGGCCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn20 CCAACUUGUUCCCCCACCACCA 22 3.0 12.0 1842.0 184.2 miRn21 AAGUGAAUGUUAUUGUAGAAUGUQ 24 1.0 9.0 20.0 1.0 3.0 1.0 4.0 3.0 miRn21 AAGUGAAUGUUUU	5	miRn10	CCUGCCUUCCAUCAACUGAAU	21	307.0	240.0	403.0	430.0
miRn12 GCAUCAUCAUCAAGAUUCAGA 21 322.0 97.0 23.0 58.0 miRn13 UCGCUUGGUGCAGGUCGGGAC 21 134.0 125.0 118.0 168.0 miRn14 UCAACGUUGGCUCAAUUAUG 19 76.0 117.0 139.0 67.0 11 miRn15 GCAAGUUGACUUGGCUCAGU 21 141.0 83.0 2.0 5.0 12 miRn16 ACGGUAUCUCCCUCAUCGUAGC 21 3.0 1.0 6.0 47.0 14 miRn17 AAGAGCAUCUCCAUUGGAUU 21 47.0 27.0 13.0 9.0 16 miRn18 AUCAUGGGCCCACAUGGAAUGAAUUAAUU 21 528.0 6970.0 1821.0 1842.0 17 miRn20 CCAACUUGUUCCCCCACCACA 22 3.0 1.0 4.0 3.0 18 miRn21 AAGUGAAUGUAAUUGUAGAAUGUG 24 1.0 9.0 20.0 19 miRn21 AAGUGACUAUCCAUUCGAUU 21 3.0 1.0 4.0 3.0 <t< td=""><td>7</td><td>miRn11</td><td>UGGGACAUUGGAACUGUGAGU</td><td>21</td><td>5.0</td><td>10.0</td><td>8.0</td><td>29.0</td></t<>	7	miRn11	UGGGACAUUGGAACUGUGAGU	21	5.0	10.0	8.0	29.0
9 miRn13 UCGCUUGGUGCAGGUCGGGAC 21 134.0 125.0 118.0 168.0 11 miRn14 UCAACGUUGGCUCAAUUAUG 19 76.0 117.0 139.0 67.0 12 miRn15 GCAAGUUGAACUUGGCUCUGU 21 141.0 83.0 2.0 5.0 13 miRn16 ACGGUAUCUCCCUCAGUAGC 21 3.0 1.0 6.0 47.0 14 miRn17 AAGAGCAUCUCCAUUGGAACCU 24 4.0 8.0 8.0 16.0 15 miRn18 AUCAUGCGAUCUCAUUGGAUCU 21 47.0 27.0 13.0 9.0 16 miRn18 AUCAUGCGAUCACAGUG 21 3.0 6.0 1.0 5.0 17 miRn20 GCACAGUAGAAACAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 18 miRn21 AAGUGAAUGUUAUUGUAGAAUGU 24 1.0 9.0 10.0 4.0 3.0 11 MiRn23 AAGGACUACCAUAUAGAUUGUCUCU 24 6.0 <td>8</td> <td>miRn12</td> <td>GCAUCAUCAUCAAGAUUCAGA</td> <td>21</td> <td>322.0</td> <td>97.0</td> <td>23.0</td> <td>58.0</td>	8	miRn12	GCAUCAUCAUCAAGAUUCAGA	21	322.0	97.0	23.0	58.0
miRn14 UCAACGUUGGCUCAAUUAUG 19 76.0 117.0 139.0 67.0 miRn15 GCAAGUUGAACUUGGCUCUGU 21 141.0 83.0 2.0 5.0 miRn16 ACGGUAUCUCCCUCCUACUAGC 21 3.0 1.0 6.0 47.0 miRn17 AAGAGCAUCUCCAUCUGUGAACCU 24 4.0 8.0 8.0 16.0 miRn18 AUCAUGCGAUCUCCAUUGGAUU 21 47.0 27.0 13.0 9.0 miRn19 UGUGGGCCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn2 GGACGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 20.0 miRn22 AUCAUGCAUUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 miRn23 AAGGACUACCAUAUUGGAACG 23 3.0 2.0 1.0 3.0 miRn24 UUAUAGGAUCUCUUUCUGAUU 21 5.0 5.0 4.0 2.0<	9	miRn13	UCGCUUGGUGCAGGUCGGGAC	21	134.0	125.0	118.0	168.0
miRn15 GCAAGUUGAACUUGGCUCUGU 21 141.0 83.0 2.0 5.0 miRn16 ACGGUAUCUCCCCUACGUAGC 21 3.0 1.0 6.0 47.0 miRn17 AAGAGCAUCUCCAUCUGUGAACCU 24 4.0 8.0 8.0 16.0 miRn18 AUCAUGCGAUCUCAUUGGAUU 21 47.0 27.0 13.0 9.0 miRn19 UGGGGCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn19 UGGGGCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn2 GGACGAGAAGAAUAGAAUGUA 21 15258.0 6970.0 1821.0 1842.0 miRn2 MCAACUGCUAUCCCCUACCACACA 22 3.0 12.0 9.0 20.0 miRn21 AAGGAAUGUUAUUGUAGAAUGUQ 24 1.0 9.0 10.0 4.0 miRn23 AAGGACUACCAAUAAUCUUUCUCUU 24 6.0 11.0 6.0 6.0 miRn24 UUUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 <td>10 11</td> <td>miRn14</td> <td>UCAACGUUGGCUCAAUUAUG</td> <td>19</td> <td>76.0</td> <td>117.0</td> <td>139.0</td> <td>67.0</td>	10 11	miRn14	UCAACGUUGGCUCAAUUAUG	19	76.0	117.0	139.0	67.0
miRn16 ACGGUAUCUCCCCUACGUAGC 21 3.0 1.0 6.0 47.0 miRn17 AAGAGCAUCUCCAUCUGUGAACCU 24 4.0 8.0 8.0 16.0 miRn18 AUCAUGCGAUCUCAUUGGAUU 21 47.0 27.0 13.0 9.0 miRn19 UGUGGGCCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn2 GGACGAGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 miRn2 GGACGACACCUUGUUCCCCACCACCA 22 3.0 1.2.0 9.0 20.0 miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 21 miRn21 AAGGACUACCAAUAAUCUUGCUCU 24 6.0 11.0 6.0 6.0 22 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 23 miRn24 UUAUAGAGUAAACAUAUUCU 22 48.0 94.0 68.0 224.0 miRn24 UUCAUGCCUAACAACAACAUACC	12	miRn15	GCAAGUUGAACUUGGCUCUGU	21	141.0	83.0	2.0	5.0
14 miRn17 miRn17 AAGAGCAUCUCAUCUGUGAACCU 24 4.0 8.0 8.0 16.0 miRn18 AUCAUGCGAUCUCAUUGGAUU 21 47.0 27.0 13.0 9.0 miRn19 UGUGGGCCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn2 GGACGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 miRn2 GGACGAGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 miRn2 GGACGAGAGAGUUCCCCACCACCA 22 3.0 1.2.0 9.0 20.0 miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 miRn22 AAGGACUACCAAUAAUCUUGGAUUG 21 3.0 1.0 4.0 3.0 miRn23 AAGGACUACAAAACAUAUUGGAACG 23 3.0 2.0 1.0 3.0 miRn24 UUAUAGAGUAUAACAAACAUAUC 22 48.0 94.0 68.0 224.0 miRn25 AAACUGCCUUACAAGAUUAAUGCUC 21	13	miRn16	ACGGUAUCUCCCCUACGUAGC	21	3.0	1.0	6.0	47.0
mikn18 AUCAUGCGAUCUCAUUGGAUU 21 47.0 27.0 13.0 9.0 mikn19 UGUGGGCCCCACUGACAGUG 21 3.0 6.0 1.0 5.0 mikn2 GGACGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 mikn20 CCAACUUGUUCCCCCACCACCA 22 3.0 12.0 9.0 20.0 mikn21 AAGUGAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 mikn22 AUCAUGCUAUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 mikn23 AAGGACUACCAAUAUUGGAUU 21 3.0 1.0 4.0 3.0 mikn24 UUAUAGAGUAAACUAUUGGAUCU 24 6.0 11.0 6.0 6.0 mikn25 AAACUGCUAACAAAACUAUC 22 48.0 94.0 68.0 224.0 mikn26 UGCAGCAUCAUCACAAGAUUCCC 21 0.0 0.0 5.0 2.0 mikn27 CAAAGAGGUCGAUUGAUUCCCUCUCCCA 21 17232.0 9024.0	14	miRn17	AAGAGCAUCUCCAUCUGUGAACCU	24	4.0	8.0	8.0	16.0
miRn19 UGUGGGCCCCACUGACACGUG 21 3.0 6.0 1.0 5.0 miRn2 GGACGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 miRn20 CCAACUUGUUCCCCCACCACCA 22 3.0 12.0 9.0 20.0 miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 miRn22 AUCAUGCUAUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 miRn23 AAGGACUACCAAUAAUCUUGCUCU 24 6.0 11.0 6.0 6.0 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 miRn24 UUAUAGAGUAACAAUAUC 22 48.0 94.0 68.0 224.0 miRn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 miRn29 UCUUGCCGUGAUUUAUGAUACCCU 22 5577.0 6741.0 96	15 16	miRn18	AUCAUGCGAUCUCAUUGGAUU	21	47.0	27.0	13.0	9.0
miRn2 GGACGAGAAGAAUAGAACUUA 21 15258.0 6970.0 1821.0 1842.0 miRn20 CCAACUUGUUCCCCCACCACCA 22 3.0 12.0 9.0 20.0 miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 miRn22 AUCAUGCUAUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 miRn23 AAGGACUACCAAUAAUCUUGGAUC 24 6.0 11.0 6.0 6.0 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 miRn25 AAACUGCCUAAACAAACAUAUC 22 48.0 94.0 68.0 224.0 miRn26 UGCAGCAUCAUCAUCAGAUUCCC 21 0.0 0.0 5.0 2.0 miRn27 CAAAGAGGUCGAUUGAUUGCU 21 5.0 5.0 4.0 2.0 miRn28 AGUUCUAUUCUUCUCGGUCCA 21 17232.0 9024.0 2910.0 3054.0 miRn30 UGUGACUUGAAGGAACUCCU 22 5577.0 6741.0	17	miRn19	UGUGGGCCCCACUGACACGUG	21	3.0	6.0	1.0	5.0
19 miRn20 CCAACUUGUUCCCCCACCACCA 22 3.0 12.0 9.0 20.0 20 miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 22 miRn22 AUCAUGCUAUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 23 miRn23 AAGGACUACCAAUAAUCUUGCUCU 24 6.0 11.0 6.0 6.0 24 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 25 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 26 miRn24 UUAUAGAGUCAACAAACAUAUC 22 48.0 94.0 68.0 224.0 27 miRn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 0.0 28 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 17232.0 9024.0 2910.0 3054.0 31 miRn28 AGUUCUAUCUCUCCGUCCA 22 5577.0	18	miRn2	GGACGAGAAGAAUAGAACUUA	21	15258.0	6970.0	1821.0	1842.0
miRn21 AAGUGAAUGUUAUUGUAGAAUGUG 24 1.0 9.0 10.0 4.0 miRn22 AUCAUGCUAUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 miRn23 AAGGACUACCAAUAAUCUUGCUCU 24 6.0 11.0 6.0 6.0 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 miRn25 AAACUGCCUAAACAAACAUAUC 22 48.0 94.0 68.0 224.0 miRn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 miRn29 UCUUGCCGUGAUUUAUGAUGCU 21 17232.0 9024.0 2910.0 3054.0 miRn31 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 miRn31 UUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0	19 20	miRn20	CCAACUUGUUCCCCCACCACCA	22	3.0	12.0	9.0	20.0
mikn22 AUCAUGCUAUCCCUUUCGAUU 21 3.0 1.0 4.0 3.0 mikn23 AAGGACUACCAAUAAUCUUGCUCU 24 6.0 11.0 6.0 6.0 mikn23 AAGGACUACCAAUAAUCUUGGALCG 23 3.0 2.0 1.0 3.0 mikn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 mikn25 AAACUGCCUAAACAAACAUAUC 22 48.0 94.0 68.0 224.0 mikn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 mikn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 mikn28 AGUUCUAUUCUUCUGGUCCCA 21 17232.0 9024.0 2910.0 3054.0 mikn30 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 mikn31 UUAUAGAGUAAACUAUUGGAGC 22 5.0 2.0 7.0 4.0 mikn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0	20 21	miRn21	AAGUGAAUGUUAUUGUAGAAUGUG	24	1.0	9.0	10.0	4.0
23 miRn23 AAGGACUACCAAUAAUCUUGCUCU 24 6.0 11.0 6.0 6.0 24 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 26 miRn25 AAACUGCCUAAACAAACAUAUC 22 48.0 94.0 68.0 224.0 27 miRn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 28 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 29 miRn28 AGUUCUAUUCUUCUCGUCCCA 21 17232.0 9024.0 2910.0 3054.0 31 miRn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 32 miRn30 UGUGACUUGUGCUUUAGUAUUA 22 5.0 2.0 7.0 4.0 34 miRn31 UUAUAGAGUAAACUAUUGGACC 22 54.0 46.0 44.0 39.0 36 miRn31 UUGGACAAGGAAACACAUG 21 1.0 1.0	22	miRn22	AUCAUGCUAUCCCUUUCGAUU	21	3.0	1.0	4.0	3.0
24 miRn24 UUAUAGAGUAAACUAUUGGAACG 23 3.0 2.0 1.0 3.0 26 miRn25 AAACUGCCUAAACAAACAUAUC 22 48.0 94.0 68.0 224.0 27 miRn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 28 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 29 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 30 miRn28 AGUUCUAUUCUUCUGGUCCCA 21 17232.0 9024.0 2910.0 3054.0 31 miRn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 32 miRn30 UGUGACUUGAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 33 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 5.0 2.0 7.0 4.0 34 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 4	23	miRn23	AAGGACUACCAAUAAUCUUGCUCU	24	6.0	11.0	6.0	6.0
mikn25 AAACUGCCUAAACAAACAUAUC 22 48.0 94.0 68.0 224.0 mikn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 mikn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 mikn28 AGUUCUAUUCUUCUCGUCCCA 21 17232.0 9024.0 2910.0 3054.0 mikn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 mikn3 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 mikn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 mikn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 mikn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 mikn33 UGCCAAAGGAAGAACAAUG 22 0.0 0.0 2.0 0.0 mikn33 UGCCAAAGGAAGAACACAUG 21 1.0 1.0 <t< td=""><td>24 25</td><td>miRn24</td><td>UUAUAGAGUAAACUAUUGGAACG</td><td>23</td><td>3.0</td><td>2.0</td><td>1.0</td><td>3.0</td></t<>	24 25	miRn24	UUAUAGAGUAAACUAUUGGAACG	23	3.0	2.0	1.0	3.0
miRn26 UGCAGCAUCAUCAAGAUUCCC 21 0.0 0.0 5.0 2.0 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 miRn28 AGUUCUAUUCUUCUCGUCCCA 21 17232.0 9024.0 2910.0 3054.0 miRn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 miRn3 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 miRn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 0.0 0.0 0.0 miRn4 GGGUCGAUAUGAGAACACAUG 21 1.0 0.0 0	25 26	miRn25	AAACUGCCUAAACAAACAUAUC	22	48.0	94.0	68.0	224.0
28 miRn27 CAAAGAGGUCGAUUGAAUGCU 21 5.0 5.0 4.0 2.0 29 miRn28 AGUUCUAUUCUUCUCGUCCCA 21 17232.0 9024.0 2910.0 3054.0 31 miRn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 32 miRn3 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 33 miRn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 34 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 36 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 0.0 0.0 2.0 0.0 37 miRn31 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 38 miRn4 GGGUCGAUAUGAGAACACAUG 21 1.0 0.0 0.0 40 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0	27	miRn26	UGCAGCAUCAUCAAGAUUCCC	21	0.0	0.0	5.0	2.0
29 miRn28 AGUUCUAUUCUUCUCGUCCCA 21 17232.0 9024.0 2910.0 3054.0 31 miRn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 32 miRn3 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 33 miRn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 34 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 36 miRn31 UUAUAGAGGAAAACUAUUGGAGC 22 0.0 0.0 2.0 0.0 37 miRn32 AGAUGGACAAUAGAAGAACAUG 21 1.0 1.0 0.0 0.0 38 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 39 miRn4 GGGUCGAUAUGAGAACACAUG 21 1.0 0.0 0.0 0.0 40 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 <td>28</td> <td>miRn27</td> <td>CAAAGAGGUCGAUUGAAUGCU</td> <td>21</td> <td>5.0</td> <td>5.0</td> <td>4.0</td> <td>2.0</td>	28	miRn27	CAAAGAGGUCGAUUGAAUGCU	21	5.0	5.0	4.0	2.0
miRn29 UCUUGCCGUGAUUUAUGAAUGC 22 648.0 517.0 52.0 100.0 100.0 miRn3 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 miRn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 36 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 37 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 38 miRn4 GGGUCGAUAUGAGAACACAUG 21 6438.0 5878.0 1349.0 10688.0 39 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0 0.0 40 miRn6 UUAAGUGUCUGUAUGUAUGGGC 22 1677.0 2144.0 3163.0 3152.0	29	miRn28	AGUUCUAUUCUUCUCGUCCCA	21	17232.0	9024.0	2910.0	3054.0
miRn3 UUGGACUGAAGGGAACUCCCU 22 5577.0 6741.0 9662.0 8238.0 miRn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 6438.0 5878.0 1349.0 1068.0 miRn4 GGGUCGAUAUGAGAACACAUG 21 1.0 0.0 0.0 0.0 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0 0.0 miRn6 UUAAGUGUCUGUAUGUAUGAGAC 22 1677.0 2144.0 3163.0 3152.0 miRn7 UUUUUCAUGAGAAGUAGUUGC 22 260.0 752.0 617.0 622.0 miRn8 UGGAGAAGCAGGGGCACGUGC 20 55.0 67.0	30	miRn29	UCUUGCCGUGAUUUAUGAAUGC	22	648.0	517.0	52.0	100.0
33 miRn30 UGUGACUUGUGCUUUAGUAUA 22 5.0 2.0 7.0 4.0 34 miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 36 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 37 miRn33 UGCCAAAGGAAGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 38 miRn4 GGGUCGAUAUGAGAACACAUG 21 6438.0 5878.0 1349.0 1068.0 39 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0 0.0 40 miRn6 UUAAGUGUCUGUAUGUAUGGGC 22 1677.0 2144.0 3163.0 3152.0 41 miRn6 UUUUUCAUGAGAAGUAGGGC 22 260.0 752.0 617.0 622.0 42 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 </td <td>32</td> <td>miRn3</td> <td>UUGGACUGAAGGGAACUCCCU</td> <td>22</td> <td>5577.0</td> <td>6741.0</td> <td>9662.0</td> <td>8238.0</td>	32	miRn3	UUGGACUGAAGGGAACUCCCU	22	5577.0	6741.0	9662.0	8238.0
miRn31 UUAUAGAGUAAACUAUUGGAGC 22 54.0 46.0 44.0 39.0 39.0 miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 37 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 38 miRn4 GGGUCGAUAUGAGAACACAUG 21 6438.0 5878.0 1349.0 1068.0 39 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0 0.0 40 miRn6 UUAAGUGUCUGUAUGUAUGGGC 22 1677.0 2144.0 3163.0 3152.0 41 miRn7 UUUUUCAUGAGAAGUAGAUUUG 22 260.0 752.0 617.0 622.0 43 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	33	miRn30	UGUGACUUGUGCUUUAGUAUA	22	5.0	2.0	7.0	4.0
miRn32 AGAUGGACAAUAGAAGAACAUG 22 0.0 0.0 2.0 0.0 0.0 0.0 2.0 0.0 <td>34 25</td> <td>miRn31</td> <td>UUAUAGAGUAAACUAUUGGAGC</td> <td>22</td> <td>54.0</td> <td>46.0</td> <td>44.0</td> <td>39.0</td>	34 25	miRn31	UUAUAGAGUAAACUAUUGGAGC	22	54.0	46.0	44.0	39.0
37 miRn33 UGCCAAAGGAGAGUUGCCCUU 21 1.0 1.0 0.0 0.0 38 miRn4 GGGUCGAUAUGAGAACACAUG 21 6438.0 5878.0 1349.0 1068.0 39 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0 0.0 40 miRn6 UUAAGUGUCUGUAUGUAUGGACC 21 1.0 0.0 0.0 0.0 41 miRn6 UUAAGUGUCUGUAUGUAUGGGC 22 1677.0 2144.0 3163.0 3152.0 42 miRn7 UUUUUCAUGAGAAGUAGAUUUG 22 260.0 752.0 617.0 622.0 43 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	36	miRn32	AGAUGGACAAUAGAAGAACAUG	22	0.0	0.0	2.0	0.0
38 miRn4 GGGUCGAUAUGAGAACACAUG 21 6438.0 5878.0 1349.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 1068.0 10068.0	37	miRn33	UGCCAAAGGAGAGUUGCCCUU	21	1.0	1.0	0.0	0.0
39 miRn5 UUCCACAGCUUUCUUGAACUG 21 1.0 0.0 0.0 0.0 40 miRn6 UUAAGUGUCUGUAUGUAUGGGC 22 1677.0 2144.0 3163.0 3152.0 42 miRn7 UUUUUCAUGAGAAGUAGAUUUG 22 260.0 752.0 617.0 622.0 43 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	38	miRn4	GGGUCGAUAUGAGAACACAUG	21	6438.0	5878.0	1349.0	1068.0
miRn6 UUAAGUGUCUGUAUGUAUGGGC 22 1677.0 2144.0 3163.0 3152.0 42 miRn7 UUUUUCAUGAGAAGUAGAUUUG 22 260.0 752.0 617.0 622.0 43 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	39	miRn5	UUCCACAGCUUUCUUGAACUG	21	1.0	0.0	0.0	0.0
42 miRn7 UUUUUCAUGAGAAGUAGAUUUG 22 260.0 752.0 617.0 622.0 43 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	40	miRn6	UUAAGUGUCUGUAUGUAUGGGC	22	1677.0	2144.0	3163.0	3152.0
43 miRn8 UGGAGAAGCAGGGCACGUGC 20 55.0 67.0 171.0 188.0 44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	42	miRn7	UUUUUCAUGAGAAGUAGAUUUG	22	260.0	752.0	617.0	622.0
44 miRn9 AAGCUCAGGAGGGAUAGCGCC 21 3.0 2.0 0.0 1.0	43	miRn8	UGGAGAAGCAGGGCACGUGC	20	55.0	67.0	171.0	188.0
	44 45	miRn9	AAGCUCAGGAGGGAUAGCGCC	21	3.0	2.0	0.0	1.0

Journal of Pineal Research

1
ו ר
2
3
4
5
6
7
, o
0
9
10
11
12
13
14
15
16
17
17
18
19
20
21
22
23
24
27
25
26
27
28
29
30
31
32
22
27
24
35
36
37
38
39
40
41
12
42
45
44
45
46
47
48
49
50
51
51
52
53
54
55

<u>d+MT_1</u>	Cd+MT_2	Hairpin.pos
309.0	166.0	Rsa1.0_02734.1:1253212848:+
196.0	292.0	Rsa1.0_00091.1:100173100491:-
5.0	10.0	Rsa1.0_01260.1:1066610983:+
5.0	27.0	Rsa1.0_02040.1:435750:+
129.0	99.0	Rsa1.0_04538.1:1578916106:-
184.0	172.0	Rsa1.0_00123.1:201603201920:-
30.0	21.0	Rsa1.0_00108.1:468042468359:-
4.0	7.0	Rsa1.0_04552.1:86969013:-
8.0	3.0	Rsa1.0_00693.1:160537160857:-
14.0	21.0	Rsa1.0_00847.1:3725837575:+
2.0	1.0	Rsa1.0_03744.1:74307748:-
9553.0	8385.0	Rsa1.0_21880.1:473790:+
0.0	4.0	Rsa1.0_11906.1:42674585:+
5.0	5.0	Rsa1.0_01069.1:59536274:-
1.0	5.0	Rsa1.0_05713.1:1205512373:-
0.0	5.0	Rsa1.0_01695.1:1621916540:+
2.0	4.0	Rsa1.0_34995.1:77394:-
110.0	89.0	Rsa1.0_00110.1:3486335182:+
3.0	1.0	Rsa1.0_00715.1:1218312500:-
1.0	1.0	Rsa1.0_11206.1:198515:-
10881.0	9303.0	Rsa1.0_21880.1:474789:-
14.0	80.0	Rsa1.0_00022.1:182718183035:+
1289.0	3975.0	Rsa1.0_00994.1:152493152810:-
1.0	3.0	Rsa1.0_06717.1:22012519:-
33.0	70.0	Rsa1.0_01029.1:122559122877:+
11.0	6.0	Rsa1.0_02345.1:1262512943:+
0.0	1.0	Rsa1.0_01801.1:3317833495:+
2837.0	2752.0	Rsa1.0_00088.1:8494085258:+
0.0	0.0	Rsa1.0_01001.1:43724689:-
2131.0	2682.0	Rsa1.0_36295.1:164482:+
1542.0	940.0	Rsa1.0_01312.1:3422534544:-
107.0	93.0	Rsa1.0_00164.1:3528135597:+
0.0	0.0	Rsa1.0_01154.1:1725017566:-

1
2
3
4
5
s c
0
/
8
9
10
11
12
13
14
15
16
17
17 10
10
19
20
21
22
23
24
25
26
27
28
20
29
30
31
32
33
34
35
36
37
38
39
10
40
41 42
42
43
44
45
46
47
48
49
50
51
52
52
22
54
55
56
57
58

gag	cuuucuucgguccacucauagaauaauaugugagauuuaauugacucucgacucauucau
ucg	cuuggugcaggucgggaacugauuggcugacaccgccacgugaauuuucacgguuggcuugugagcagggaucggauccugccuucc
ugg	gacauuggaacugugaguuucagaacgauauaaaagaucauggauacaguaaagagauuuaacucaaaugaggcuaguauaucuaugg
gca	ucaucaucaagauucagaaaucauauucucugauggguucuucguucg
ucg	cuuggugcaggucgggacuaauucgcugacacagccacguggcucuuuuccuuauugguuugugagcagggauuggaucccgccuug
uca	uugagugcagcguugaugauuaacuucuuauucauugucgaauggauuaaagcaauuuacaucaacguuggcucaauuaug
uga	Igccaaggaugacuugccgauuuucaccaacuagucuaaaauuugauuaugguguucggcaaguugaacuuggcucugu
uuc	gcaggagagauagcgccaucaccuaucuucugauagucuagcugauggugaugacgguaucuccccuacguagc
aag	адсаисиссаисидидаассисаиддддаддиииассаааааааииииииии
ucc	aaagggaucgcauugauccaaauuaagcugaauuauuccccaauaguuauucuuuuccucaaucguaagauguaaagaagacgacuug
auu	uuucagugggacccacauucaagaaaaaacucaacagauuucguuucuuccuaagacgaccuuuagcuuggguuugacaaucuggug
gga	icgagaagaauagaacuuauucuuaacacauuuguauuuacaaaucucgugagaguaaguucuauucuucucguuccg
gug	guggugguucaagcugauguaggcucaaaacgauauagaagguguucacuugauguaugu
aag	ugaauguuauuguagaauguguauuuuuuuuuuuaucauucuaaauacacauucuacaauaacacucacuug
ucc	aaagggaucgcauugauccuaaguaaggugaauucucccuauuauuuucuuaauuauuggcaaagaaaucccaaaaauuugcuuggu
aga	gcaucauuauugguaguccuuaggauuagguccuuaauauacauauauguauauguauauaua
cuc	uaauguucacuuuauaauaauuacucuauaauagaguggauuauaaaauaauguuaccuuuccauuccagauuuugaguaaaacaa
aaa	cugccuaaacaaacauaucaaugaaucauauugugagauuacauauuauugucuccuauuuaaagcaguuauuuaacacaauuaauu
ugc	agcaucaucaagauucccaagaggcgauaaucaaaggaaaccacaucucuugugaaucuuaaugaugcagcauc
uau	uuauagucgaccuuuccuccgguuacugggggugcaaagaggucgauugaaugcu
gaa	cgagaagaauagaacuuacucucacgagauuuguaaauacaaauguguuaagaauaaguucuauucuucucguccca
gaa	cauaagagcggcguugagauuaggccauggucuugccgugauuuaugaaugc
aga	guuuccuuaaguccauucacauguugugauuugauccaauuagcuccagacucauucau
uau	ugaagcacaagccaugugucagaauuugauggccgugugacuugugcuuuaguaua
uuc	aaugguuuaaucuauaauagaguuacucuauuuuuauggagaaaauagaguaaaacuauuauuucauuccaaauauagagugaaaaaa
aga	uggacaauagaagaacauguuccuaucaucaaauuuaauguauucaacgaaugauuggaacauguuauucucuugucuaacuaa
ggg	aaauucaacuuuggcaaagaaacuauaaucagugagcuacacaacauguugcucacaaguuugagguugagucuuugccaaaggagag
ggg	guegauaugagaacaeaugueeagueaaeggeuguaaugaegeeaegueauuagaaeaaaueuueeuuueeauguguueueaggueaee
uuc	cacagcuuucuugaacugcaaccuucuucagauuaguuuuuauucucguauauaua
uua	agugucuguauguaugggcugaguaggcacaaucacaucauuaucaaaugugaauuggggauuuuaccuccuccacccauaccauaca
aau	cgccucucaugaaaaaguuaugugaaagcaucuaaacgaaaauguuacauaugaguaugcaagaauaaaauacauucaagauuuuugg
ugg	agaagcagggcacgugcacuacuaacucaucucuuagcccacaaauauacacacucuccccaaaugcauguauaagauagau
aag	cucaggagggauagcgccaucaugaucacucacaucgauauuuuuggcgcuguccauccugaguuuc

1 2 3 4 5 6 7 8 9 10 11 12 13	
14 15 16	;ugugaacccccauuaguuucacuaauggggaugcucua
17 18 19 20 21 22	ıgggccccacugacacgug
23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40	gcucu
41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60	g

Table S11 Identification of differential expressed miRNAs among three comparisions

miDNA	Cd vs. Con		Cd+MT vs. Con			Cd+MT vs.		
IIIIKINA	log ₂ (FC)	p-value	padj	log ₂ (FC)	p-value	padj	log ₂ (FC)	p-value
miR156a-3p		—	_	1.5292	6.98E-03	0.035294	_	—
miR156c-3p		—		1.5019	1.07E-03	0.008848	_	—
miR157a-3p	1.6885	0.000522	0.002608	1.3531	0.005313	0.03223	_	_
miR158a-3p	1.0073	0.009775	0.030327		_		_	_
miR158b	0.98082	0.016058	0.045497					
miR160a-3p	-2.3599	0.002176	0.008042		_	_	_	_
miR164a	0.93873	0.008021	0.026221					
miR164c-5p	0.8825	0.013307	0.039004		_	_	_	_
miR166a-5p	-3.1158	2.90E-08	2.74E-07		_	_	1.9794	4.02E-05
miR167a-3p	-2.8181	4.99E-07	4.24E-06		_	_	1.9138	2.26E-05
miR167c-3p	2.8203	2.03E-11	3.46E-10	1.9304	7.72E-05	0.001004		
miR167c-5p	2.3012	1.02E-08	1.45E-07	1.5314	0.000731	0.006648	_	
miR169b-3p	-2.0702	0.002102	0.008042		_		_	_
miR169f-3p	-3.2664	3.05E-06	2.16E-05	-2.4129	7.59E-05	0.001004	_	_
miR169g-3p	-4.0743	9.81E-13	2.44E-11	-2.933	2.88E-09	8.75E-08	_	_
miR172a		—			_		-1.0199	0.005819
miR172b-5p	-2.016	0.001626	0.006582	-1.4312	0.011853	0.04903	_	_
miR172c		_	-	_	_	_	-1.3389	7.17E-05
miR172e-3p		_	_ (_	_	-1.4914	0.000162
miR319c		_	_	\mathbf{O} –	_	_	-0.99209	0.003335
miR390a-5p		_	_	-1.3656	0.000254	0.002571		_
miR395b	-2.1303	3.55E-05	0.000189	_			1.6878	0.00023
miR396a-3p	-3.1272	1.19E-14	1.01E-12	-2.06	2.23E-08	5.07E-07		_
niR396b-3p	-1.8776	2.53E-05	0.000154	-1.059	0.010499	0.045494		_
miR396b-5p	0.98777	0.00999	0.030327		_			_
miR397a				1.3319	0.001817	0.012716		
miR398b-3p		_	_	0.99034	0.005744	0.032514	1.1971	0.004579
miR399b	-1.8885	0.000653	0.002775			_		_
miR408-3p		_	_	1.0765	0.007655	0.036665	1.0552	0.006036
miR824-5p			_		_		1.2637	0.002174
miR857	1.5394	0.007104	0.024155	3.0215	2.84E-10	2.59E-08	1.4251	0.00047
miR858a	2.1258	1.74E-05	0.000114	1.625	0.001556	0.011803		_
miRn16	2.5025	0.000644	0.002775			_		_
miRn18	-1.5764	0.005297	0.01876					
miRn20							-1.4974	0.006556
miRn28	-2.0762	1.09E-06	8.39E-06		_		1.6585	7.37E-07
miRn29	-2.8819	1.15E-12	2.44E-11	-2.9356	1.37E-09	6.22E-08		
miRn3					_	_	-1.348	0.002793
miRn32			_	2.0316	0.002024	0.013153		_
miRn4	-2.2535	1.21E-08	1.47E-07	-0.91179	0.008065	0.036695	1.1118	0.002329
miRn7				1.2465	0.006074	0.032514		
miRn8	1.3912	0.000601	0.002775					_
miRn12	-2.2534	3.02E-05	0.000171	-2.8278	8.72E-08	1.59E-06		
miRn2	-2.4869	2.48E-08	2.64E-07				2.1311	2.69E-10
'D 17	4 2 2 2 5	7 705 14	2 21E 12	1 60/	0.000189	0.002146	2 0334	6 80E 05

NT-4 !! !!	
Note: "—"	means no significant difference was found in this comparision. log ₂ (FC): log ₂ (fold ch

2	
3	
4	
5	
6	
7	
, 0	
0	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	
19	
20	
21	
22	
23	
24	
25	
26	
27	
28	
29	
30	
31	
37	
22	
27 2√	
54 25	
22	
20	
3/	
38	
39	
40	
41	
42	
43	
44	
45	
46	
47	
48	
49	
50	
51	
52	
53	
54	
55	
56	
57	
58	
59	
60	

Cd

padj	
—	
—	
0.001166	
0.0008/5	
0.043763	
0.043703	
0.001386	
0.002692	
0.029755	
0.003335	
_	
0.037944	
0.043763	
0.024563	
0.006061	
0.044/34	
4.2/E-03	
0.027001	
0.027001	
0.024563	
3.12E-08	

0.001386

to per peries

2	Table S12 Identification of target	genes for the known and nove	
3	miRNA	Target gene ID	
4	miR156a-3p	Rsa1.0 00667.1 g00013.1	
5	miR156a-5p	Rsa1.0_00316.1_g00008.1	
0 7	miR156a-5p	Rsa1 0 04852 1 g00005 1	
8	miR156a-5n	Rsa1 0 00894 1 000014 1	
9	miR156a 5p	$\frac{1100}{10000000000000000000000000000000$	
10	miR(150a-5p	$Rsa1.0_000/2.1_g00002.1$	
11	miR156a-5p	Rsa1.0_00943.1_g00007.1	
12	miR156a-5p	Rsa1.0_01020.1_g00007.1	
13 14	m1R156a-5p	Rsa1.0_01068.1_g00001.1	
15	miR156a-5p	Rsa1.0_01022.1_g00011.1	
16	miR156a-5p	Rsa1.0_02675.1_g00008.1	
17	miR156a-5p	Rsa1.0_08717.1_g00001.1	
18	miR156a-5p	Rsa1.0_07943.1_g00001.1	
19	miR156a-5p	Rsa1.0_01256.1_g00004.1	
20	miR156a-5p	Rsa1.0 01104.1 g00029.1	
22	miR156a-5p	Rsa1.0 02413.1 g00008.1	
23	miR156a-5p	Rsa1.0 10928.1 g00001.1	
24	miR156a-5p	Rsa1 0 02931 1 g00002 1	
25	miR156a-5p	Rsa1 0, 00003 1, g00030 1	
26 27	miR156a 5p	$R_{sa1.0} 00005.1 g000050.1$	
28	miR156a-5p	$R_{sa1.0}_{-02400.1}_{-0000011}$	
29	miR150a-5p	Rsa1.0_02/13.1_g00001.1	
30	miR136a-3p,miR136g	Rsa1.0_03451.1_g00003.1	
31	miR156a-5p,miR156g	Rsa1.0_02846.1_g00003.1	
32	m1R156a-5p,m1R156g	Rsa1.0_00071.1_g00047.1	
33 34	miR156a-5p,miR156g	Rsa1.0_08401.1_g00001.1	
35	miR156a-5p,miR156g	Rsa1.0_00870.1_g00006.1	
36	miR156a-5p,miR156g	Rsa1.0_04892.1_g00002.1	
37	miR156a-5p,miR156g	Rsa1.0_00078.1_g00028.1	
38	miR156a-5p,miR156g	Rsa1.0_04399.1_g00001.1	
39 40	miR156a-5p,miR156g	Rsa1.0_11699.1_g00001.1	
41	miR156a-5p,miR156g	Rsa1.0_03385.1_g00003.1	
42	miR156a-5p,miR156g	Rsa1.0 09711.1 g00001.1	
43	miR156a-5p,miR156g	Rsa1.0 06163.1 g00001.1	
44	miR156a-5p.miR156g	Rsa1.0 00018.1 g00013.1	
45 46	miR156a-5p.miR156g	 Rsa1.0_01145.1_g00010.1	
47	miR156a-5p miR156g	Rsa1 0 00294 1 g00023 1	
48	miR156a-5n miR156g	Rsa1.0_00106.1_g00018.1	
49	miR156a-5p,miR156g	$R_{sa1.0} 00000.1 g00010.1$	
50	miR156a-5p,miR156g	$\frac{\text{Rsa}1.0_00964.1_g00002.1}{\text{Rsa}1.0_00064.1_g00002.1}$	
51	miR150a-5p,miR150g	Rsa1.0_09004.1_g00002.1	
52 53	miR156a-5p,miR156g	Rsa1.0_03959.1_g00003.1	
54	mik156a-5p,mik156j,mik156g	Ksa1.0_01148.1_g00009.1	
55	miR156a-5p,miR15/a-5p,miR157	Ksa1.0_04/86.1_g00004.1	
56	m1R156a-5p,m1R157d,m1R156j	Rsa1.0_00092.1_g00050.1	
5/ 58	miR156a-5p,miR157d,miR156j	Rsa1.0_00043.1_g00002.1	
59	miR156a-5p,miR157d,miR156j,n	Rsa1.0_00001.1_g00030.1	
60	miR156a-5p,miR157d,miR156j,n	Rsa1.0_00011.1_g00004.1	
	miR156a-5p,miR158b,miR158a-3	Rsa1.0_00620.1_g00003.1	

2 miR1566-3p Rsa1.0 00665.1 g00005.1 3 miR156c-3p Rsa1.0 00668.1 g00001.1 5 miR156c-3p Rsa1.0 0303.0.1 g00001.1 6 miR156c-3p Rsa1.0 0303.0.1 g00001.1 7 miR156c-3p Rsa1.0 20060.1 g00001.1 9 miR156f-3p Rsa1.0 20065.1 g00001.1 10 miR156f-3p Rsa1.0 20065.1 g00001.1 11 miR156f-3p Rsa1.0 00457.1 g00001.1 12 miR156g Rsa1.0 00246.1 g00007.1 13 miR156g Rsa1.0 00246.1 g00007.1 14 miR156g Rsa1.0 00246.1 g00007.1 15 miR156g Rsa1.0 00246.1 g00017.1 16 miR156g Rsa1.0 00252.1 g00017.1 17 miR156g Rsa1.0 00052.1 g00006.1 17 miR156g Rsa1.0	1			
3 miR156c-3p Rsa1.0 200868.1 g00005.1 5 miR156c-3p Rsa1.0 20300.1 g00001.1 6 miR156f-3p Rsa1.0 20085.1 g00001.1 7 miR156f-3p Rsa1.0 20060.1 g00001.1 7 miR156f-3p Rsa1.0 20085.1 g00010.1 7 miR156f-3p Rsa1.0 20085.1 g0001.1 7 miR156g Rsa1.0 00451.1 g00001.1 7 miR156g Rsa1.0 00451.1 g00007.1 7 miR156g Rsa1.0 00451.1 g00007.1 7 miR156g Rsa1.0 00426.1 g00007.1 7 miR156g Rsa1.0 00426.1 g00007.1 7 miR156g Rsa1.0 00246.1 g00007.1 7 miR156g Rsa1.0 00246.1 g00007.1 7 miR156g Rsa1.0 00236.1 g00007.1 7 miR156g Rsa1.0 0016.1 g00007.1 7 miR156g Rsa1.0 00130.1	2	miR156a-5p,miR5658	Rsa1.0_00656.1_g00015.1	
4 miR156c-3p Rsa1.0 0306.1 g00001.1 6 miR156c-3p Rsa1.0 0300.1 g00001.1 7 miR156c-3p Rsa1.0 07495.1 g00001.1 8 miR156c-3p Rsa1.0 00719.1 g00001.1 11 miR156c-3p Rsa1.0 00657.1 g00017.1 12 miR156c-3p Rsa1.0 00246.1 g00001.1 13 miR156g Rsa1.0 00246.1 g00001.1 14 miR156g Rsa1.0 00246.1 g00001.1 15 miR156g Rsa1.0 00236.1 g00001.1 16 miR156g Rsa1.0 00236.1 g00001.1 17 miR156g Rsa1.0 00372.1 g0001.1 18 miR156g Rsa1.0 0016.1 g00006.1 19 miR156g Rsa1.0 0016.1 g00006.1 19 miR156g Rsa1.0 0016.1 g00001.1 19 miR156g Rsa1.0	3	miR156c-3p	Rsa1.0_00868.1_g00005.1	
6 miR156c-3p Rsa1.0 03030.1 g00003.1 7 miR156c-3p Rsa1.0 07191.g00005.1 9 miR156c-3p Rsa1.0 20060.1 g00005.1 9 miR156c-3p Rsa1.0 20060.1 g00005.1 10 miR156c-3p,miR5658 Rsa1.0 00657.1 g00017.1 11 miR156g Rsa1.0 00246.1 g00007.1 12 miR156g Rsa1.0 00246.1 g00007.1 13 miR156g Rsa1.0 00246.1 g00007.1 14 miR156g Rsa1.0 00246.1 g00007.1 15 miR156g Rsa1.0 00246.1 g00007.1 16 miR156g Rsa1.0 00481.1 g00017.1 17 miR156g Rsa1.0 00481.1 g00017.1 18 miR156g Rsa1.0 00481.1 g00017.1 18 miR156g Rsa1.0 00372.1 g00015.1 19 miR156g Rsa1.0 00372.1<	4	miR156c-3p	Rsa1.0_30652.1_g00001.1	
miR156f-3p Rsa1.0 17495.1 g00001.1 miR156f-3p Rsa1.0 000719.1 g00005.1 miR156f-3p Rsa1.0 00657.1 g0001.1 miR156f-3p,miR5658 Rsa1.0 00457.1 g00017.1 miR156g Rsa1.0 00426.1 g00007.1 miR156g Rsa1.0 00246.1 g00007.1 miR156g Rsa1.0 00236.1 g00007.1 miR156g Rsa1.0 00236.1 g00007.1 miR156g Rsa1.0 00372.1 g00015.1 miR156g Rsa1.0 00160.1 g00022.1 miR156g Rsa1.0 00163.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0148.1 g00001.1 miR156g,miR156a-5p Rsa1.0 0148.1 g0000	6	miR156c-3p	Rsa1.0_03030.1_g00003.1	
8 miR156f-3p Rsa1.0 00719.1 g00005.1 10 miR156f-3p Rsa1.0 20060.1 g00001.1 11 miR156f-3p,miR5658 Rsa1.0 00657.1 g00017.1 13 miR156g Rsa1.0 00249.1 g00007.1 14 miR156g Rsa1.0 00240.1 g0007.1 15 miR156g Rsa1.0 00240.1 g00007.1 16 miR156g Rsa1.0 00240.1 g00006.1 17 miR156g Rsa1.0 00264.1 g00007.1 18 miR156g Rsa1.0 00048.1 g00007.1 18 miR156g Rsa1.0 00372.1 g00005.1 19 miR156g Rsa1.0 00137.1 g00021.1 111 miR156g Rsa1.0 00137.1 g00007.1 111 miR156g Rsa1.0 00136.1 g00002.1 111 miR156g Rsa1.0 00136.1 g00002.1 111 miR156g,miR156a-5p Rs	7	miR156f-3p	Rsa1.0_17495.1_g00001.1	
miR156f-3p Rsa1.0 20060.1 g0001.1 miR156f-3p,miR5658 Rsa1.0 00857.1 g00017.1 miR156g Rsa1.0 00249.1 g00002.1 miR156g Rsa1.0 00240.1 g00007.1 miR156g Rsa1.0 00246.1 g00007.1 miR156g Rsa1.0 00236.1 g00007.1 miR156g Rsa1.0 00236.1 g00007.1 miR156g Rsa1.0 00236.1 g00006.1 miR156g Rsa1.0 00522.1 g00017.1 miR156g Rsa1.0 00072.1 g00005.1 miR156g Rsa1.0 00073.1 g00005.1 miR156g Rsa1.0 00073.1 g00002.1 miR156g,miR156a-5p Rsa1.0 00072.1 g0002.1 miR156g,miR156a-5p Rsa1.0 00378.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0130.1 g0002.1 miR156g,miR156a-5p Rsa1.0 0130.1 g0002.1 miR156g,miR156a-5p Rsa1.0 0130.1<	8	miR156f-3p	Rsa1.0_00719.1_g00005.1	
miR156f-3p Rsa1.0 00851.1 g0001.1 miR156g Rsa1.0 00457.1 g0002.1 miR156g Rsa1.0 00249.1 g00007.1 miR156g Rsa1.0 00249.1 g00007.1 miR156g Rsa1.0 00246.1 g00007.1 miR156g Rsa1.0 00236.1 g00006.1 miR156g Rsa1.0 00522.1 g00017.1 miR156g Rsa1.0 000522.1 g00017.1 miR156g Rsa1.0 000522.1 g00015.1 miR156g Rsa1.0 00006.1 g00005.1 miR156g Rsa1.0 000372.1 g00001.1 miR156g Rsa1.0 00130.1 g00021.1 miR156g,miR156a-5p Rsa1.0 00137.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0148.1 g00002.1 miR156g,miR156a-5p Rsa1.0 01305.1 g00002.1 miR156g,miR156a-5p Rsa1.0 01305.1 g00002.1 miR156g,miR156a-5p Rsa1.0 01305.1	9 10	miR156f-3p	Rsa1.0_20060.1_g00001.1	
miR156f-3p,miR5658 Rsa1.0 00657.1 g00017.1 miR156g Rsa1.0 00249.1_g00017.1 miR156g Rsa1.0 00249.1_g00007.1 miR156g Rsa1.0 00246.1_g00007.1 miR156g Rsa1.0 00236.1_g00006.1 miR156g Rsa1.0 00522.1_g00013.1 miR156g Rsa1.0 000648.1_g00006.1 miR156g Rsa1.0 00061.1_g00006.1 miR156g Rsa1.0 00160.1_g00005.1 miR156g Rsa1.0 000062.1_g00028.1 miR156g,miR156a-5p Rsa1.0 000021.1 miR156g,miR156a-5p Rsa1.0 0130.1_g00021.1 miR156g,miR156a-5p Rsa1.0 0148.1_g00003.1 miR156g,miR156a-5p Rsa1.0 0148.1_g00002.1 miR156g,miR156a-5p Rsa1.0 0130.1_g0002.1 miR156g,miR156a-5p Rsa1.0 01303.1_g00002.1 miR156g,miR156a-5p Rsa1.0 01303.1_g00004.1 miR156g,miR156a-5p Rsa1.0 01305.1_g00003.1 miR156g,miR156a-5p Rsa1.0 001012.1_g00003.1	11	miR156f-3p	Rsa1.0_00851.1_g00010.1	
miR156g Rsa1.0 04511.1 g00002.1 miR156g Rsa1.0 00249.1 g00017.1 miR156g Rsa1.0 00246.1 g00007.1 miR156g Rsa1.0 002246.1 g00007.1 miR156g Rsa1.0 00236.1 g00006.1 miR156g Rsa1.0 00232.1 g00017.1 miR156g Rsa1.0 00052.1 g00006.1 miR156g Rsa1.0 00071.1 g00059.1 miR156g Rsa1.0 00016.1 g000051.1 miR156g,miR156a-5p Rsa1.0 00016.1 g00021.1 miR156g,miR156a-5p Rsa1.0 00130.1 g0002.1 miR156g,miR156a-5p Rsa1.0 00148.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0148.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0148.1 g00002.1 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01907.1 g00007.1 miR156g,miR156a-5p Rsa1.0<	12	miR156f-3p,miR5658	Rsa1.0_00657.1_g00017.1	
14 miR156g Rsa1.0 00249.1 g00007.1 16 miR156g Rsa1.0 00246.1 g00007.1 17 miR156g Rsa1.0 107474.1 g00001.1 18 miR156g Rsa1.0 00236.1 g00006.1 19 miR156g Rsa1.0 00232.1 g00006.1 20 miR156g Rsa1.0 00372.1 g00006.1 21 miR156g Rsa1.0 00130.1 g00021.1 22 miR156g Rsa1.0 00130.1 g00021.1 23 miR156g,miR156a-5p Rsa1.0 00130.1 g00002.1 24 miR156g,miR156a-5p Rsa1.0 004369.1 g00002.1 25 miR156g,miR156a-5p Rsa1.0 01305.1 g00002.1 26 miR156g,miR156a-5p Rsa1.0 01305.1 g00002.1 27 miR156g,miR156a-5p Rsa1.0 01305.1 g00002.1 28 miR156g,miR156a-5p Rsa1.0 01305.1 g00002.1 29 miR156g,miR156a-5p Rsa1.0 00454.1 g00003.1 3	13	miR156g	Rsa1.0_04511.1_g00002.1	
miR156g Rsa1.0_00246.1_g00007.1 miR156g Rsa1.0_17474.1_g00001.1 miR156g Rsa1.0_00236.1_g00006.1 miR156g Rsa1.0_00522.1_g00013.1 miR156g Rsa1.0_0052.1_g0006.1 miR156g Rsa1.0_0016.1_g00005.1 miR156g Rsa1.0_000372.1_g00015.1 miR156g,miR156a-5p Rsa1.0_00062.1_g00028.1 miR156g,miR156a-5p Rsa1.0_00062.1_g00028.1 miR156g,miR156a-5p Rsa1.0_0130.1_g00021.1 miR156g,miR156a-5p Rsa1.0_0130.1_g00021.1 miR156g,miR156a-5p Rsa1.0_0130.1_g0002.1 miR156g,miR156a-5p Rsa1.0_0130.1_g00004.1 miR156g,miR156a-5p Rsa1.0_0130.1_g00004.1 miR156g,miR156a-5p Rsa1.0_0130.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01075.1_g00006.1 miR156g,miR156a-5p Rsa1.0_00075.1_g00007.1 miR156g,miR156a-5p Rsa1.0_00071.1_g00002.1 miR156g,miR156a-5p Rsa1.0_00071.1_g00003.1 miR156g,miR156a-5p Rsa1.0_00071.1_g00007.1 miR156g,miR156a-5p Rsa1.0_00071.1_g00007.1 miR156g,miR156a-5p Rsa1.0_00071.1_g00007.1 <	14 15	miR156g	Rsa1.0_00249.1_g00017.1	
miR156g Rsa1.0_17474.1_g00001.1 miR156g Rsa1.0_00236.1_g00006.1 miR156g Rsa1.0_00522.1_g00017.1 miR156g Rsa1.0_00522.1_g00013.1 miR156g Rsa1.0_0016.1_g00006.1 miR156g Rsa1.0_0017.1_g00015.1 miR156g Rsa1.0_0017.1_g00015.1 miR156g Rsa1.0_0013.1_g00021.1 miR156g,miR156a-5p Rsa1.0_00062.1_g00002.1 miR156g,miR156a-5p Rsa1.0_01436.1_g00002.1 miR156g,miR156a-5p Rsa1.0_0130.1_g0002.1 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01302.1_g00002.1 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01302.1_g00003.1 miR156g,miR156a-5p Rsa1.0_00990.1_g00001.1 miR156g,miR156a-5p Rsa1.0_00990.1_g00001.1 miR156g,miR156a-5p Rsa1.0_00975.1_g00005.1 miR156g,miR156a-5p Rsa1.0_00075.1_g00005.1 miR156g,miR156a-5p Rsa1.0_0045.1_g00003.1 miR156g,miR156a-5p Rsa1.0_0045.1_g00003.1 miR156g,miR156a-5p,RiR156j Rsa1.0_00075.1_g00007.1 <t< td=""><td>15</td><td>miR156g</td><td>Rsa1.0_00246.1_g00007.1</td><td></td></t<>	15	miR156g	Rsa1.0_00246.1_g00007.1	
miR156g Rsa1.0 00236.1 g0006.1 miR156g Rsa1.0 00648.1 g00017.1 miR156g Rsa1.0 00522.1 g00013.1 miR156g Rsa1.0 00522.1 g00013.1 miR156g Rsa1.0 00016.1 g00059.1 miR156g Rsa1.0 00103.1 g00021.1 miR156g,miR156a-5p Rsa1.0 00130.1 g00021.1 miR156g,miR156a-5p Rsa1.0 00378.1 g00003.1 miR156g,miR156a-5p Rsa1.0 01436.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0136.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0136.1 g00002.1 miR156g,miR156a-5p Rsa1.0 01383.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01502.1 g00001.1 miR156g,miR156a-5p Rsa1.0 01502.1 g00001.1 miR156g,miR156a-5p Rsa1.0 001001.1 g00001.1 miR156g,miR156a-5p Rsa1.0 00075.1 g00001.1 miR156g,miR	17	miR156g	Rsa1.0_17474.1_g00001.1	
miR156g Rsa1.0 00648.1 g00017.1 miR156g Rsa1.0 00522.1 g00013.1 miR156g Rsa1.0 01806.1 g00006.1 miR156g Rsa1.0 00016.1 g00059.1 miR156g Rsa1.0 000372.1 g00015.1 miR156g,miR156a-5p Rsa1.0 000372.1 g00021.1 miR156g,miR156a-5p Rsa1.0 00062.1 g00022.1 miR156g,miR156a-5p Rsa1.0 00130.1 g00002.1 miR156g,miR156a-5p Rsa1.0 0148.1 g00003.1 miR156g,miR156a-5p Rsa1.0 01983.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01502.1 g00004.1 miR156g,miR156a-5p Rsa1.0 01502.1 g00001.1 miR156g,miR156a-5p Rsa1.0 001502.1 g00001.1	18	miR156g	Rsa1.0_00236.1_g00006.1	
20 miR156g Rsa1.0_00522.1_g00013.1 21 miR156g Rsa1.0_01806.1_g00006.1 22 miR156g Rsa1.0_00130.1_g00021.1 23 miR156g,miR156a-5p Rsa1.0_00130.1_g00021.1 24 miR156g,miR156a-5p Rsa1.0_008378.1_g00001.1 25 miR156g,miR156a-5p Rsa1.0_00372.1_g00021.1 26 miR156g,miR156a-5p Rsa1.0_00378.1_g00003.1 27 miR156g,miR156a-5p Rsa1.0_01305.1_g00002.1 28 miR156g,miR156a-5p Rsa1.0_01305.1_g00002.1 29 miR156g,miR156a-5p Rsa1.0_01305.1_g00002.1 30 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 31 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01000.1_g00001.1 35 miR156g,miR156a-5p Rsa1.0_01000.1_g00001.1 36 miR156g,miR156a-5p Rsa1.0_00090.1_g00012.1 37 miR156g,miR156a-5p Rsa1.0_00090.1_g00001.1 38 miR156g,miR156a-5p Rsa1.0_00090.1_g00001.1 39 miR156g,miR156a-5p Rsa1.0_00075.1_g00000.1 40 miR156g,miR156a-5p Rsa1.0_00012.1_	19	miR156g	Rsa1.0 00648.1 g00017.1	
miR156g Rsa1.0_01806.1_g00006.1 miR156g Rsa1.0_00016.1_g00059.1 miR156g Rsa1.0_00372.1_g00015.1 miR156g,miR156a-5p Rsa1.0_00062.1_g00021.1 miR156g,miR156a-5p Rsa1.0_0130.1_g00021.1 miR156g,miR156a-5p Rsa1.0_0148.1_g00003.1 miR156g,miR156a-5p Rsa1.0_0148.1_g00002.1 miR156g,miR156a-5p Rsa1.0_0128.1_g00002.1 miR156g,miR156a-5p Rsa1.0_0128.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 miR156g,miR156a-5p Rsa1.0_01201.1_g00001.1 miR156g,miR156a-5p Rsa1.0_01000000.1 miR156g,miR156a-5p Rsa1.0_000000.1 miR156g,miR156a-5p Rsa1.0_000000.1 miR156g,miR156a-5p Rsa1.0_000001.1 miR156g,miR156a-5p Rsa1.0_000001.1 miR156g,miR156a-5p Rsa1.0_000001.1 miR156g,miR156a-5p,miR156j Rsa1.0_00001.1 miR156g,miR156a-5p,miR156j Rsa1.0_00001.1 miR156g,miR156a-5p,miR156j Rsa1.0_00001.1 miR156g,miR156a-5p,miR156j Rsa1.0_00001.1 <t< td=""><td>20 21</td><td>miR156g</td><td>Rsa1.0 00522.1 g00013.1</td><td></td></t<>	20 21	miR156g	Rsa1.0 00522.1 g00013.1	
23 miR156g Rsa1.0_00016.1_g00059.1 24 miR156g Rsa1.0_00372.1_g00015.1 25 miR156g,miR156a-5p Rsa1.0_00062.1_g00021.1 26 miR156g,miR156a-5p Rsa1.0_008378.1_g00001.1 27 miR156g,miR156a-5p Rsa1.0_01148.1_g00003.1 28 miR156g,miR156a-5p Rsa1.0_0148.1_g00002.1 29 miR156g,miR156a-5p Rsa1.0_0130.1_g00024.1 31 miR156g,miR156a-5p Rsa1.0_01983.1_g00004.1 33 miR156g,miR156a-5p Rsa1.0_01930.5_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01900.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_01900.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_01900.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_000990.1_g00012.1 37 miR156g,miR156a-5p Rsa1.0_00000.1_g00001.1 38 miR156g,miR156a-5p Rsa1.0_000000.1_g00001.1 39 miR156g,miR156a-5p Rsa1.0_00000.1_g00003.1 34 miR156g,miR156a-5p Rsa1.0_000001.1_g00002.1 34 miR156g,miR156a-5p Rsa1.0_00001.1_g00002.1 34 miR156g,miR156a-5p,miR156j	22	miR156g	Rsa1.0 01806.1 g00006.1	
24 miR156g Rsa1.0 00372.1 g00015.1 25 miR156g,miR156a-5p Rsa1.0 00130.1 g00021.1 26 miR156g,miR156a-5p Rsa1.0 00062.1 g00021.1 27 miR156g,miR156a-5p Rsa1.0 00062.1 g00021.1 28 miR156g,miR156a-5p Rsa1.0 00130.1 g00001.1 29 miR156g,miR156a-5p Rsa1.0 001305.1 g00002.1 30 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 31 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 32 miR156g,miR156a-5p Rsa1.0 01305.1 g00004.1 34 miR156g,miR156a-5p Rsa1.0 01305.1 g00003.1 35 miR156g,miR156a-5p Rsa1.0 00001.1 g00001.1 36 miR156g,miR156a-5p Rsa1.0 00071.1 g00001.1 37 miR156g,miR156a-5p Rsa1.0 00075.1 g00005.1 38 miR156g,miR156a-5p Rsa1.0 00075.1 g00003.1 40 miR156g,miR156a-5p,miR156j Rsa1.	23	miR156g	Rsa1.0 00016.1 g00059.1	
25 miR156g,miR156a-5p Rsa1.0_00130.1_g00021.1 27 miR156g,miR156a-5p Rsa1.0_00062.1_g00028.1 28 miR156g,miR156a-5p Rsa1.0_00378.1_g00001.1 29 miR156g,miR156a-5p Rsa1.0_0148.1_g00003.1 30 miR156g,miR156a-5p Rsa1.0_00201.1_g00024.1 31 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_01001.1_g00001.1 37 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 38 miR156g,miR156a-5p Rsa1.0_00990.1_g00001.1 39 miR156g,miR156a-5p Rsa1.0_0007.1_g00000.1 41 miR156g,miR156a-5p Rsa1.0_0007.1_g00000.1 42 miR156g,miR156a-5p Rsa1.0_0007.1_g00002.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1_g00002.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1_g00002.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1_g00002.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1_g00002.1 47	24	miR156g	Rsa1.0 00372.1 g00015.1	
miR156g,miR156a-5p Rsa1.0 00062.1 g00028.1 miR156g,miR156a-5p Rsa1.0 08378.1 g00001.1 miR156g,miR156a-5p Rsa1.0 01148.1 g00002.1 miR156g,miR156a-5p Rsa1.0 04369.1 g00024.1 miR156g,miR156a-5p Rsa1.0 01983.1 g0004.1 miR156g,miR156a-5p Rsa1.0 01983.1 g0004.1 miR156g,miR156a-5p Rsa1.0 01983.1 g0004.1 miR156g,miR156a-5p Rsa1.0 01305.1 g0004.1 miR156g,miR156a-5p Rsa1.0 01903.1 g0004.1 miR156g,miR156a-5p Rsa1.0 02106.1 g00003.1 miR156g,miR156a-5p Rsa1.0 00090.1 g00012.1 miR156g,miR156a-5p Rsa1.0 00075.1 g00001.1 miR156g,miR156a-5p Rsa1.0 00075.1 g00007.1 miR156g,miR156a-5p,miR156j Rsa1.0 00071.1 g00002.1 miR156g,miR156a-5p,miR156j Rsa1.0 00012.1 g00004.1 miR156g,miR156a-5p,miR156j Rsa1.0 00012.1 g00004.1 miR156g,miR156a-5p,miR156j Rs	25 26	miR156g,miR156a-5p	Rsa1.0 00130.1 g00021.1	
28 miR156g,miR156a-5p Rsa1.0_08378.1_g00001.1 29 miR156g,miR156a-5p Rsa1.0_01148.1_g00003.1 30 miR156g,miR156a-5p Rsa1.0_04369.1_g00002.1 31 miR156g,miR156a-5p Rsa1.0_01983.1_g00004.1 32 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 33 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 37 miR156g,miR156a-5p Rsa1.0_0075.1_g00003.1 38 miR156g,miR156a-5p Rsa1.0_00075.1_g00007.1 39 miR156g,miR156a-5p Rsa1.0_00075.1_g00007.1 40 miR156g,miR156a-5p,miR156j Rsa1.0_00045.1_g00003.1 41 miR156g,miR156a-5p,miR156j Rsa1.0_00045.1_g00004.1 42 miR156g,miR156a-5p,miR156j Rsa1.0_00045.1_g00007.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_00045.1_g00007.1 44 miR156g,miR156a-5p,miR157a-Rsa1.0_00380.1_g00004.1 miR156g,miR156a-5p,miR157a-Rsa	27	miR156g,miR156a-5p	Rsa1.0 00062.1 g00028.1	
29 miR156g,miR156a-5p Rsa1.0_01148.1_g00003.1 30 miR156g,miR156a-5p Rsa1.0_04369.1_g00002.1 31 miR156g,miR156a-5p Rsa1.0_00201.1_g00024.1 32 miR156g,miR156a-5p Rsa1.0_01983.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_0105.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_0106.1_g00003.1 37 miR156g,miR156a-5p Rsa1.0_0090.1_g00012.1 38 miR156g,miR156a-5p Rsa1.0_0075.1_g00005.1 39 miR156g,miR156a-5p Rsa1.0_0097.1_g00007.1 40 miR156g,miR156a-5p Rsa1.0_0097.1_g00007.1 41 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1_g00003.1 42 miR156g,miR156a-5p,miR156j Rsa1.0_0003.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_0002.1_g00003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_0003.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_0007.1 48 miR156g,miR156a-5p,	28	miR156g,miR156a-5p	Rsa1.0 08378.1 g00001.1	
30 miR156g,miR156a-5p Rsa1.0_04369.1_g00002.1 31 miR156g,miR156a-5p Rsa1.0_01201.1_g00024.1 33 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 36 miR156g,miR156a-5p Rsa1.0_01000.1 37 miR156g,miR156a-5p Rsa1.0_00090.1_g00012.1 38 miR156g,miR156a-5p Rsa1.0_00064.1_g00001.1 39 miR156g,miR156a-5p Rsa1.0_00064.1_g00001.1 40 miR156g,miR156a-5p Rsa1.0_00075.1_g00001.1 41 miR156g,miR156a-5p Rsa1.0_00071.1_g00007.1 42 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00003.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00002.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00002.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00002.1 47 miR156g,miR156a-5p,miR157a-Rsa1.0_00071.1_g00002.1 miR156g,miR156j,miR156a-5p,Rsa1.0_00071.1_g00002.1 50 miR156g,miR156j,miR156a-5p,Rsa1.0_000	29	miR156g,miR156a-5p	Rsa1.0 01148.1 g00003.1	
1 1 1 1 32 miR156g,miR156a-5p Rsa1.0_00201.1_g00024.1 33 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01502.1_g00006.1 36 miR156g,miR156a-5p Rsa1.0_02106.1_g00003.1 36 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 37 miR156g,miR156a-5p Rsa1.0_007110.1_g00001.1 38 miR156g,miR156a-5p Rsa1.0_000664.1_g00008.1 40 miR156g,miR156a-5p Rsa1.0_00075.1_g00005.1 41 miR156g,miR156a-5p Rsa1.0_00045.4.1_g00003.1 42 miR156g,miR156a-5p,miR156j Rsa1.0_00045.4.1_g00003.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00043.1_g00004.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00043.1_g00006.1 48 miR156g,miR156a-5p,miR157a-5 Rsa1.0_00043.1_g00001.1 50 miR156g,miR156a-5p,miR156a-5p,m Rsa1.0_00043.1_g00001.1 miR156g,miR156a	30 31	miR156g,miR156a-5p	Rsa1.0 04369.1 g00002.1	
33 miR156g,miR156a-5p Rsa1.0_01983.1_g00004.1 34 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_01502.1_g00006.1 36 miR156g,miR156a-5p Rsa1.0_02106.1_g00003.1 37 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 38 miR156g,miR156a-5p Rsa1.0_000664.1_g00008.1 40 miR156g,miR156a-5p Rsa1.0_00075.1_g00005.1 41 miR156g,miR156a-5p Rsa1.0_001997.1_g00007.1 42 miR156g,miR156a-5p, Rsa1.0_001997.1_g00007.1 43 miR156g,miR156a-5p, miR156j Rsa1.0_00012.1_g0003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00026.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00075.1_g00006.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00026.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_000435.1_g00006.1 48 miR156g,miR156a-5p,miR156a-5p, Rsa1.0_00043.1_g00009.1 50 miR156g,miR156a-5p, Rsa1.0_00043.1_g00009.1 51 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g0001.1 52 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g0001.1 53 miR156g,miR156j,mi	32	miR156g,miR156a-5p	Rsa1.0 00201.1 g00024.1	
34 miR156g,miR156a-5p Rsa1.0_01305.1_g00004.1 35 miR156g,miR156a-5p Rsa1.0_01502.1_g00006.1 36 miR156g,miR156a-5p Rsa1.0_02106.1_g00003.1 37 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 39 miR156g,miR156a-5p Rsa1.0_007110.1_g00001.1 40 miR156g,miR156a-5p Rsa1.0_0075.1_g00008.1 41 miR156g,miR156a-5p Rsa1.0_00775.1_g00005.1 42 miR156g,miR156a-5p Rsa1.0_0077.1_g00007.1 43 miR156g,miR156a-5p, mRs1.0_0075.1_g00003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00075.1_g00003.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00003.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00003.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 48 miR156g,miR156a-5p,miR157a- Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR157a- Rsa1.0_000435.1_g00007.1 50 miR156g,miR156a-5p,Rsa1.0_000435.1_g00007.1 miR156g,miR156j,miR156a-5p,Rsa1.0_00340.1_g00001.1 51 miR156g,miR156j,miR156a-5p,Rsa1.0_00340.1_g00001.1 miR156g,miR156j,miR156a-5p,Rsa1.0_00340.1_g00001.1 <td< td=""><td>33</td><td>miR156g.miR156a-5p</td><td>Rsa1.0 01983.1 g00004.1</td><td></td></td<>	33	miR156g.miR156a-5p	Rsa1.0 01983.1 g00004.1	
35 miR156g,miR156a-5p Rsa1.0_01502.1_g00006.1 37 miR156g,miR156a-5p Rsa1.0_02106.1_g00003.1 38 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 39 miR156g,miR156a-5p Rsa1.0_00664.1_g00008.1 40 miR156g,miR156a-5p Rsa1.0_00064.1_g00005.1 41 miR156g,miR156a-5p Rsa1.0_00075.1_g00007.1 42 miR156g,miR156a-5p Rsa1.0_000454.1_g00003.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_000454.1_g00003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00006.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_000435.1_g00006.1 48 miR156g,miR156a-5p,miR157a-4 Rsa1.0_00043.1_g00006.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_00043.1_g00006.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00043.1_g00001.1 52 miR156g,miR156j,miR156a-5p, Rsa1.0_000340.1_g00014.1 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g00014.1 53 miR156g,miR156j,miR157a-5p,miR157d, Rsa1.0_00351.1_g00001.1 miR156g,miR157a-5p,miR157d, Rsa	34	miR156g.miR156a-5p	Rsa1.0 01305.1 g00004.1	
37 miR156g,miR156a-5p Rsa1.0_02106.1_g00003.1 38 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 39 miR156g,miR156a-5p Rsa1.0_00664.1_g00008.1 40 miR156g,miR156a-5p Rsa1.0_0075.1_g00005.1 41 miR156g,miR156a-5p Rsa1.0_0075.1_g00007.1 42 miR156g,miR156a-5p Rsa1.0_00454.1_g00003.1 43 miR156g,miR156a-5p, miR156j Rsa1.0_00075.1_g00007.1 44 miR156g,miR156a-5p, miR156j Rsa1.0_000454.1_g00003.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 48 miR156g,miR156a-5p,miR156j Rsa1.0_000435.1_g00007.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_000435.1_g00007.1 51 miR156g,miR156j,miR156a-5p, Rsa1.0_00245.1_g00001.1 52 miR156g,miR156j,miR156a-5p, Rsa1.0_00245.1_g00001.1 53 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g00014.1 54 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 55 miR156g,miR157a-5p,miR157d,Rsa1.0_23904.1_g00001.1 56	35 36	miR156g.miR156a-5p	Rsa1.0 01502.1 g00006.1	
38 miR156g,miR156a-5p Rsa1.0_00990.1_g00012.1 39 miR156g,miR156a-5p Rsa1.0_07110.1_g00001.1 40 miR156g,miR156a-5p Rsa1.0_00664.1_g00008.1 41 miR156g,miR156a-5p Rsa1.0_00075.1_g00007.1 42 miR156g,miR156a-5p Rsa1.0_00454.1_g00003.1 43 miR156g,miR156a-5p,miR156j Rsa1.0_00454.1_g00003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_0071.1_g00026.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00435.1_g00006.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00435.1_g00007.1 48 miR156g,miR156a-5p,Rsa1.0_00435.1_g00007.1 50 miR156g,miR156a-5p,Rsa1.0_00435.1_g00007.1 51 miR156g,miR156j,miR156a-5p,Rsa1.0_00340.1_g00062.1 53 miR156g,miR156j,miR156a-5p,Rsa1.0_00340.1_g0001.1 54 miR156g,miR156j,miR156a-5p,Rsa1.0_00340.1_g00014.1 55 miR156g,miR157a-5p,miR157d,Rsa1.0_00351.1_g00013.1 56 miR156g,miR157a-5p,miR157d,Rsa1.0_0351.1_g0001.1 56 miR156g,miR157a-5p,miR157d,Rsa1.0_23904.1_g00001.1 56 miR156g,miR157a-5p,miR157d,Rsa1.0_23904.1_g00001.1 <td>37</td> <td>miR156g.miR156a-5p</td> <td>Rsa1.0 02106.1 g00003.1</td> <td>•</td>	37	miR156g.miR156a-5p	Rsa1.0 02106.1 g00003.1	•
39 miR156g,miR156a-5p Rsa1.0_07110.1_g00001.1 41 miR156g,miR156a-5p Rsa1.0_00664.1_g00008.1 42 miR156g,miR156a-5p Rsa1.0_0075.1_g00005.1 43 miR156g,miR156a-5p Rsa1.0_01997.1_g00007.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00454.1_g00003.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00003.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00003.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00004.1 48 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR157a-7_Rsa1.0_00158.1_g00007.1 50 miR156g,miR156a-5p,miR157a-7_Rsa1.0_00435.1_g00007.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00435.1_g00007.1 52 miR156g,miR156j,miR156a-5p Rsa1.0_00043.1_g00009.1 53 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 miR156g,miR156j,miR157a-5p,niRa1.0_00374.1_g00009.1 54 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	38	miR156g,miR156a-5p	Rsa1.0 00990.1 g00012.1	
40 miR156g,miR156a-5p Rsa1.0_00664.1_g00008.1 41 miR156g,miR156a-5p Rsa1.0_00075.1_g00005.1 42 miR156g,miR156a-5p Rsa1.0_00975.1_g00007.1 43 miR156g,miR156a-5p Rsa1.0_00454.1_g00003.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00004.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g000026.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 48 miR156g,miR156a-5p,miR157a- Rsa1.0_000435.1_g00007.1 49 miR156g,miR156a-5p,miR157a- Rsa1.0_00948.1_g00009.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_000435.1_g00007.1 51 miR156g,miR156j,miR156a-5p, Rsa1.0_00948.1_g00009.1 53 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g0001.1 54 miR156g,miR156j,miR156a-5p, Rsa1.0_00374.1_g00001.1 55 miR156g,miR157a-5p,miR157d,r Rsa1.0_00374.1_g00009.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_0351.1_g00013.1 57 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	39	miR156g,miR156a-5p	Rsa1.0 07110.1 g00001.1	
42 miR156g,miR156a-5p Rsa1.0_00075.1_g00005.1 43 miR156g,miR156a-5p Rsa1.0_01997.1_g00007.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00454.1_g00003.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00032.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00032.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 48 miR156g,miR156a-5p,miR157a- Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR157a- Rsa1.0_00435.1_g00006.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 51 miR156g,miR156j,miR156a-5p, Rsa1.0_002545.1_g00001.1 52 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g00062.1 54 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g00014.1 55 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 57 miR156g,miR157a-5p,miR157d,r Rsa1.0_0351.1_g00013.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	40 41	miR156g.miR156a-5p	 Rsa1.0_00664.1_g00008.1	4
43 miR156g,miR156a-5p Rsa1.0_01997.1_g00007.1 44 miR156g,miR156a-5p,miR156j Rsa1.0_00454.1_g00003.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00004.1 48 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR157a-4 Rsa1.0_00158.1_g00006.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_00435.1_g00007.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 52 miR156g,miR156j,miR156a-5p, Rsa1.0_000401.1_g00062.1 53 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g0001.1 54 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g00014.1 55 miR156g,miR156j,miR157d,rini Rsa1.0_00374.1_g00009.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	42	miR156g.miR156a-5p	Rsa1.0 00075.1 g00005.1	
44 miR156g,miR156a-5p,miR156j Rsa1.0_00454.1_g00003.1 45 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_03890.1_g00004.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 48 miR156g,miR156a-5p,miR157a-3 Rsa1.0_00158.1_g00006.1 49 miR156g,miR156j,miR156a-5p Rsa1.0_00435.1_g00007.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 52 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 53 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g0001.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_00374.1_g00009.1 55 miR156g,miR156j,miR157d,r Rsa1.0_00374.1_g00001.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	43	miR156g.miR156a-5p	Rsa1.0 01997.1 g00007.1	
45 miR156g,miR156a-5p,miR156j Rsa1.0_00012.1_g00032.1 46 miR156g,miR156a-5p,miR156j Rsa1.0_03890.1_g00004.1 47 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 48 miR156g,miR156a-5p,miR156j Rsa1.0_00158.1_g00006.1 49 miR156g,miR156j,miR156a-5p Rsa1.0_00435.1_g00006.1 50 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00007.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 53 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 55 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 56 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1	44	miR156g.miR156a-5p.miR156j	Rsa1.0 00454.1 g00003.1	
47 miR156g,miR156a-5p,miR156j Rsa1.0_03890.1_g00004.1 48 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR157a- Rsa1.0_00158.1_g00006.1 50 miR156g,miR156j Rsa1.0_00435.1_g00007.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00435.1_g00007.1 52 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 53 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 55 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 56 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	45 46	miR156g,miR156a-5p,miR156j	Rsa1.0 00012.1 g00032.1	
48 miR156g,miR156a-5p,miR156j Rsa1.0_00071.1_g00026.1 49 miR156g,miR156a-5p,miR157a-\$ Rsa1.0_00158.1_g00006.1 50 miR156g,miR156j Rsa1.0_00435.1_g00007.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 52 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 53 miR156g,miR156j,miR156a-5p, Rsa1.0_002545.1_g00001.1 54 miR156g,miR156j,miR156a-5p, Rsa1.0_00340.1_g00014.1 55 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 56 miR156g,miR156j,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	47	miR156g,miR156a-5p,miR156j	Rsa1.0 03890.1 g00004.1	
49 miR156g,miR156a-5p,miR157a-3 Rsa1.0_00158.1_g00006.1 51 miR156g,miR156j Rsa1.0_00435.1_g00007.1 52 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 53 miR156g,miR156j,miR156a-5p Rsa1.0_0001.1_g00062.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 56 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 56 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	48	miR156g.miR156a-5p.miR156i	Rsa1.0 00071.1 g00026.1	
50 miR156g,miR156j Rsa1.0_00435.1_g00007.1 51 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 52 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 53 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 55 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	49	miR156g.miR156a-5p.miR157a-5	Rsa1.0 00158.1 g00006.1	
51 miR150g,miR150j name_or 10011_g0000911 52 miR156g,miR156j,miR156a-5p Rsa1.0_00948.1_g00009.1 53 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 56 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 57 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	50 51	miR156g miR156i	Rsa1 0 00435 1 g00007 1	
53 miR156g,miR156j,miR156a-5p Rsa1.0_00001.1_g00062.1 54 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 55 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 56 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	52	miR156g.miR156i.miR156a-5p	Rsa1.0 00948.1 g00009.1	
54 miR156g,miR156j,miR156a-5p,n Rsa1.0_02545.1_g00001.1 55 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 56 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	53	miR156g.miR156i.miR156a-5p	Rsa1.0 00001.1 g00062.1	
55 miR156g,miR156j,miR156a-5p,n Rsa1.0_00340.1_g00014.1 56 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 57 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	54	miR156g.miR156i.miR156a-5p.n	Rsa1.0 02545.1 g00001.1	
57 miR156g,miR156j,miR157d,miR Rsa1.0_00374.1_g00009.1 58 miR156g,miR157a-5p,miR157d,r Rsa1.0_00351.1_g00013.1 59 miR156g,miR157a-5p,miR157d,r Rsa1.0_23904.1_g00001.1 60 miR156g,miR157a-5p,miR157d,r Rsa1.0_41914.1_g00001.1	55 56	miR156g.miR156i miR156a-5n n	Rsa1.0 00340 1 g00014 1	
58 59 60 miR156g,miR157a-5p,miR157d,rRsa1.0_00351.1_g00013.1 miR156g,miR157a-5p,miR157d,rRsa1.0_23904.1_g00001.1 miR156g,miR157a-5p,miR157d,rRsa1.0_41914.1_g00001.1	57	miR156g.miR156i miR157d miR	Rsa1.0 00374 1 g00009 1	
59 60 miR156g,miR157a-5p,miR157d,rRsa1.0_23904.1_g00001.1 miR156g,miR157a-5p,miR157d,rRsa1.0_41914.1_g00001.1	58	miR156g miR157a-5p miR157d r	Rsa1 0 00351 1 000013 1	
miR156g,miR157a-5p,miR157d,rRsa1.0 41914.1 g00001.1	59	miR156g.miR157a-5p.miR157d.r	Rsa1.0 23904 1 g00001 1	
	UO	miR156g,miR157a-5p.miR157d.r	Rsa1.0 41914.1 g00001.1	

1			
2	m1R156g,m1R157d,m1R156a-5p,r	Rsa1.0_05583.1_g00003.1	
3	miR156g,miR157d,miR157a-5p,r	Rsa1.0_06065.1_g00002.1	
5	miR156g,miR157d,miR157a-5p,r	Rsa1.0_00158.1_g00005.1	
6	miR156j	Rsa1.0_02527.1_g00005.1	
7	miR156j	Rsa1.0_11225.1_g00001.1	
8	miR156j	Rsa1.0_00376.1_g00011.1	
9 10	miR156j	Rsa1.0_02415.1_g00003.1	
11	miR156j	Rsa1.0_00033.1_g00032.1	
12	miR156j	Rsa1.0_02848.1_g00006.1	
13	miR156j	Rsa1.0_01123.1_g00003.1	
14 15	miR156j	Rsa1.0_00017.1_g00030.1	
15	miR156j	Rsa1.0_00316.1_g00006.1	
17	miR156j	Rsa1.0 00117.1 g00019.1	
18	miR156j	Rsa1.0 00020.1 g00049.1	
19	miR156j	Rsa1.0 00003.1 g00022.1	
20	miR156i	Rsa1.0 00005.1 g00032.1	
21	miR156i	Rsa1.0 02162.1 g00005.1	
23	miR156i	Rsa1.0_00458.1_g00001.1	
24	miR156i	Rsa1 0 03015 1 000005 1	
25	miR156i	Rsa1.0_01164.1_g00003.1	
26 27	miR156j	Rsa1.0_01380.1_g00003.1	
28	miR156j	Rsa1.0_01560.1_g00005.1	
29	miR150j	$R_{sa1.0}_{0.0009:1}g00001.1$	
30	miR150j	Rsa1.0_01809.1_g00002.1	
31	miR130j	Rsa1.0_03911.1_g00003.1	
32 33	miR156j	Rsa1.0_04/12.1_g00001.1	
34	miR156j	Rsa1.0_00841.1_g00005.1	
35	miR156j	Rsa1.0_04298.1_g00002.1	
36	miR156j	Rsa1.0_00100.1_g00045.1	
3/	miR156j	Rsa1.0_00531.1_g00009.1	
39	miR156j	Rsa1.0_04628.1_g00002.1	
40	miR156j	Rsa1.0_03717.1_g00002.1	
41	miR156j	Rsa1.0_00315.1_g00010.1	
42	miR156j	Rsa1.0_00659.1_g00011.1	
43 44	miR156j	Rsa1.0_01882.1_g00002.1	
45	miR156j	Rsa1.0_00094.1_g00029.1	
46	miR156j	Rsa1.0_00278.1_g00011.1	
47	miR156j	Rsa1.0_02158.1_g00001.1	
48	miR156j	Rsa1.0_00097.1_g00013.1	
49 50	miR156j	Rsa1.0_02071.1_g00003.1	
51	miR156j	Rsa1.0_01878.1_g00005.1	
52	miR156j	Rsa1.0_00630.1_g00003.1	
53	miR156j	Rsa1.0_00019.1_g00025.1	
54 55	miR156j	Rsa1.0_02798.1_g00001.1	
56	miR156j	Rsa1.0 69883.1 g00001.1	
57	miR156j	Rsa1.0 00360.1 g00003.1	
58	miR156j	Rsa1.0 00037.1 g00025.1	
59 60	miR156j	Rsa1.0 02096.1 g00001.1	
00	miR156j	Rsa1.0 10213.1 g00001.1	

1			1
2	miR156j	Rsa1.0_08779.1_g00002.1	
3	miR156j	Rsa1.0_05127.1_g00001.1	
4	miR156j	Rsa1.0_17331.1_g00001.1	
6	miR156j	Rsa1.0_00418.1_g00018.1	
7	miR156j	Rsa1.0_00090.1_g00021.1	
8	miR156j	Rsa1.0 00946.1 g00009.1	
9	miR156j	Rsa1.0 52244.1 g00001.1	
10 11	miR156j	Rsa1.0 00512.1 g00018.1	
12	miR156i	Rsa1 0 07884 1 g00001 1	
13	miR156i	Rsa1 0, 05090 1, g00002 1	
14	miR156i	Rsa1.0_04674.1_g00003.1	
15	miR156i	Rsa1.0_00714.1_g00006.1	
16 17	miR156j	$R_{sa1.0}_{00714.1}_{0000041}$	
17	miR156j	1100000000000000000000000000000000000	
19	miR150j	$R_{sa1.0}_{-40555.1}g00001.1$	
20	miR150j	$R_{sa1.0}_{00004.1}_{0000001}$	
21	miR130j	Rsa1.0_01143.1_g00009.1	
22	iniR156j	Rsa1.0_13284.1_g00001.1	
23	miR156j	Rsa1.0_01460.1_g00007.1	
25	m1R156j	Rsa1.0_00540.1_g00004.1	
26	miR156j	Rsa1.0_00063.1_g00030.1	
27	miR156j	Rsa1.0_15165.1_g00001.1	
28 29	miR156j	Rsa1.0_01634.1_g00002.1	
30	miR156j	Rsa1.0_00179.1_g00039.1	
31	miR156j	Rsa1.0_00075.1_g00017.1	
32	miR156j	Rsa1.0_08854.1_g00001.1	
33	miR156j	Rsa1.0_15456.1_g00001.1	
34 35	miR156j	Rsa1.0_02792.1_g00003.1	
36	miR156j	Rsa1.0_13471.1_g00003.1	
37	miR156j	Rsa1.0_02206.1_g00007.1	
38	miR156j	Rsa1.0_14126.1_g00001.1	
39 40	miR156j	Rsa1.0_00729.1_g00013.1	
41	miR156j	Rsa1.0_00802.1_g00006.1	9
42	miR156j	Rsa1.0_00014.1_g00012.1	
43	miR156j	Rsa1.0 00211.1 g00035.1	
44 45	miR156j	Rsa1.0 21595.1 g00001.1	
45	miR156j	Rsa1.0 05909.1 g00001.1	
47	miR156j	Rsa1.0 02888.1 g00006.1	
48	miR156i	Rsa1.0 08349.1 g00002.1	
49	miR156i	Rsa1.0 01799.1 g00004.1	
50 51	miR156i	Rsa1 0 04236 1 g00002 1	
52	miR156i	Rsa1 0 00125 1 g00022 1	
53	miR156i	Rsa1.0_19592.1_g00001.1	
54	miR156i	Rsa1 0 01339 1 000007 1	
55 56	miR156i	Rsa1 0 62252 1 000001 1	
57	miR156i	Rsa1 0 16338 1 m00001 1	
58	miR156j	$\frac{1.521.0}{1.0250.1} = \frac{1000001.1}{200001.1}$	
59	miR156i	$\frac{1.5a1.0}{8.5a1.0} = 0.01403.1 = \frac{200010.1}{600010.1}$	
60	miD 156i	$R_{aa1.0} 00132.1 g00010.1$	
	mmx150j	1\sa1.0_00301.1_g00014.1	

1			
2	miR156j	Rsa1.0_01151.1_g00005.1	
3	miR156j	Rsa1.0_01978.1_g00002.1	
4 5	miR156j	Rsa1.0_08195.1_g00001.1	
6	miR156j	Rsa1.0_01562.1_g00007.1	
7	miR156j	Rsa1.0_00005.1_g00028.1	
8	miR156j	Rsa1.0_00320.1_g00014.1	
9	miR156j	Rsa1.0 29085.1 g00001.1	
10 11	miR156j	Rsa1.0 05020.1 g00001.1	
12	miR156j	Rsa1.0 01282.1 g00012.1	
13	miR156j	Rsa1.0 00387.1 g00026.1	
14	miR156j	Rsa1.0 01326.1 g00005.1	
15	miR156i	Rsa1.0 01155.1 g00008.1	
10	miR156i	Rsa1 0 02557 1 g00001 1	
18	miR156i	Rsa1 0 01370 1 g00001 1	
19	miR156i	Rsa1 0 14043 1 g00001 1	
20	miR156i	Rsa1.0_01845_1_g00006_1	
21	miR156j	Rsa1.0_01624_1_g00008_1	
22	miR156j	Rsa1.0_01024.1_g00003.1	
24	miR156j	Rsa1.0_00111_1_g00009_1	
25	miR156j	$R_{sa1.0}_{00111.1}_{000009.1}$	
26 27	miR150j	Rsa1.0_00398.1_g00012.1	
27 28	miR130j	Rsa1.0_02/31.1_g00004.1	
29	miR156j	Rsa1.0_02021.1_g00006.1	
30	miR156j	Rsa1.0_00353.1_g00010.1	
31	miR156j	Rsa1.0_01190.1_g00006.1	
32	miR156j	Rsa1.0_03304.1_g00004.1	
33 34	miR156j	Rsa1.0_00399.1_g00017.1	
35	miR156j	Rsa1.0_05345.1_g00001.1	
36	miR156j	Rsa1.0_00060.1_g00030.1	
37	miR156j	Rsa1.0_00713.1_g00017.1	
38 39	miR156j	Rsa1.0_13865.1_g00001.1	
40	miR156j	Rsa1.0_06645.1_g00002.1	
41	miR156j	Rsa1.0_01699.1_g00004.1	
42	miR156j	Rsa1.0_00082.1_g00007.1	
43 44	miR156j	Rsa1.0_01415.1_g00003.1	
44	miR156j	Rsa1.0_03309.1_g00004.1	
46	miR156j	Rsa1.0_00168.1_g00001.1	
47	miR156j	Rsa1.0_00471.1_g00003.1	
48	miR156j	Rsa1.0_03255.1_g00002.1	
49 50	miR156j	Rsa1.0_02019.1_g00005.1	
51	miR156j	Rsa1.0 00285.1 g00020.1	
52	miR156j	Rsa1.0 02604.1 g00001.1	
53	miR156j	Rsa1.0 02267.1 g00008.1	
54 55	miR156j	Rsa1.0 00878.1 g00026.1	
55 56	miR156j	Rsa1.0 00039.1 g00014.1	
57	miR156i	Rsa1.0 02001.1 g00009.1	
58	miR156i	Rsa1.0 00544 1 g00004 1	
59	miR156i	Rsa1 0 00131 1 900011 1	
00	miR156i	Rsa1 0 10397 1 000001 1	

1			
2	miR156j	Rsa1.0_00056.1_g00046.1	
3	miR156j	Rsa1.0_01002.1_g00001.1	
4	miR156j	Rsa1.0_00383.1_g00036.1	
5	miR156j	Rsa1.0_02663.1_g00001.1	
7	miR156j	Rsa1.0_06030.1_g00002.1	
8	miR156j	Rsa1.0 05565.1 g00002.1	
9	miR156j	Rsa1.0 03606.1 g00003.1	
10	miR156j	Rsa1.0 02750.1 g00007.1	
11	miR156i	Rsa1 0 01292 1 g00006 1	
13	miR156i	Rsa1 0 00209 1 g00007 1	
14	miR156i	Rsa1 0 02324 1 g00004 1	
15	miR156i	Rsa1 0 06821 1 g00001 1	
10 17	miR156i	Rsa1 0 04497 1 g00003 1	
18	miR156i	Rsa1.0_08142.1_g00001.1	
19	miR156i	Rsa1.0_00/36.1_g00007.1	
20	miR156j	$\frac{1}{2} \frac{1}{2} \frac{1}$	
21	miR150j	$R_{sa1.0}_{04124.1}g00003.1$	
22	miR150j	$R_{sa1.0}_{00005} = 0000000000000000000000000000000$	
24	miR150j	Rsa1.0_00093.1_g00002.1	
25	miR130j	Rsa1.0_00323.1_g00007.1	
26	miR156j	Rsa1.0_22056.1_g00001.1	
27	miR156j	Rsa1.0_00287.1_g00009.1	
20	miR156j	Rsa1.0_03125.1_g00004.1	
30	miR156j	Rsa1.0_01214.1_g00014.1	
31	miR156j	Rsa1.0_01327.1_g00002.1	
32	miR156j	Rsa1.0_03640.1_g00003.1	
33 34	miR156j	Rsa1.0_00302.1_g00010.1	
35	miR156j	Rsa1.0_00915.1_g00001.1	
36	miR156j	Rsa1.0_00108.1_g00037.1	
37	miR156j	Rsa1.0_00706.1_g00011.1	
38	miR156j	Rsa1.0_00049.1_g00020.1	
40	miR156j	Rsa1.0_02431.1_g00008.1	
41	miR156j	Rsa1.0_62747.1_g00001.1	
42	miR156j	Rsa1.0_05702.1_g00002.1	
43	miR156j	Rsa1.0_00017.1_g00151.1	
44	miR156j	Rsa1.0_01937.1_g00010.1	
46	miR156j	Rsa1.0_00069.1_g00037.1	
47	miR156j	Rsa1.0_00060.1_g00057.1	
48	miR156j	Rsa1.0_02554.1_g00001.1	
49 50	miR156j	Rsa1.0_00070.1_g00012.1	
51	miR156j	Rsa1.0_07657.1_g00001.1	
52	miR156j	Rsa1.0 00737.1 g00015.1	
53	miR156j	Rsa1.0 00639.1 g00014.1	
54 55	miR156j	Rsa1.0 00972.1 g00005.1	
56	miR156j	Rsa1.0 01018.1 g00009.1	
57	miR156j	Rsa1.0 01609.1 g00002.1	
58	miR156j	Rsa1.0 02812.1 g00005.1	
59 60	miR156j	Rsa1.0 00617.1 g00002.1	
00	miR156j	Rsa1.0 00928.1 g00005.1	
	<u> </u>		
1			
----------	------------------------------	-----------------------------	--
2	miR156j	Rsa1.0_00018.1_g00035.1	
3	miR156j	Rsa1.0_01067.1_g00001.1	
4 5	miR156j	Rsa1.0_00105.1_g00026.1	
6	miR156j	Rsa1.0_00196.1_g00018.1	
7	miR156j	Rsa1.0_00124.1_g00033.1	
8	miR156j	Rsa1.0_00262.1_g00012.1	
9 10	miR156j	Rsa1.0_00221.1_g00002.1	
11	miR156j	Rsa1.0_00568.1_g00001.1	
12	miR156j	Rsa1.0_00082.1_g00003.1	
13	miR156j	Rsa1.0_00170.1_g00026.1	
14 15	miR156j	Rsa1.0_01144.1_g00005.1	
16	miR156j	Rsa1.0_00226.1_g00014.1	
17	miR156j	Rsa1.0_00127.1_g00035.1	
18	miR156j	Rsa1.0_00668.1_g00002.1	
19 20	miR156j	Rsa1.0_03239.1_g00001.1	
20	miR156j	Rsa1.0_01073.1_g00004.1	
22	miR156j	Rsa1.0_03235.1_g00006.1	
23	miR156j,miR156a-5p	Rsa1.0_00293.1_g00040.1	
24	miR156j,miR156a-5p,miR156g	Rsa1.0_02584.1_g00008.1	
25 26	miR156j,miR156a-5p,miR157a-5	Rsa1.0 00237.1 g00024.1	
27	miR156j,miR156a-5p,miR157a-5	Rsa1.0 00793.1 g00003.1	
28	miR156j,miR156a-5p,miR157d,n	Rsa1.0 03583.1 g00002.1	
29	miR156j,miR156a-5p,miR157d,n	Rsa1.0 00469.1 g00014.1	
30 31	miR156j,miR156a-5p,miR157d,n	Rsa1.0 00986.1 g00007.1	
32	miR156j,miR156a-5p,miR157d,n	Rsa1.0 04786.1 g00005.1	
33	miR156j,miR156a-5p,miR157d,n	Rsa1.0 04683.1 g00002.1	
34	miR156j,miR156g	Rsa1.0 00565.1 g00011.1	
35 36	miR156j,miR156g	Rsa1.0 00237.1 g00041.1	
37	miR156j,miR157a-5p,miR157d	Rsa1.0 05244.1 g00002.1	
38	miR156j,miR157a-5p,miR157d,n	Rsa1.0 00138.1 g00022.1	
39	miR156j,miR157d	Rsa1.0 02356.1 g00006.1	
40 41	miR156i.miR157d	 Rsa1.0_04695.1_g00003.1	
42	miR156i.miR157d	Rsa1.0 01150.1 g00004.1	
43	miR156j,miR157d	Rsa1.0 02553.1 g00001.1	
44	miR156i.miR157d	 Rsa1.0_00567.1_g00010.1	
45 46	miR156j.miR157d.miR156a-5p.n	Rsa1.0 05648.1 g00002.1	
47	miR156j.miR157d.miR157a-5p.n	 Rsa1.0_00829.1_g00019.1	
48	miR156i.miR167c-5p.miR167a-5	 Rsa1.0_00548.1_g00007.1	
49	miR156i.miR393a-5p	Rsa1.0_03774.1_g00002.1	
50 51	miR156i.miR5658	Rsa1.0 00638.1 g00003.1	
52	miR156i.miR5658	Rsa1.0_00556.1_g00022.1	
53	miR156j.miR5658.miR157d	Rsa1.0 02071.1 g00002.1	
54	miR157a-3p	Rsa1.0 00173.1 g00033.1	
55 56	miR157a-3p	Rsa1.0 01249.1 g00005.1	
57	miR157a-3p	Rsa1.0 02186.1 g00004.1	
58	miR157a-3p	Rsa1.0 01084 1 g00007 1	
59	miR157a-3p	Rsa1.0 01338 1 g00010 1	
00	miR157a-3p	Rsa1.0 03247.1 g00003.1	
	- · · · - r		

1		r	1
2	miR157a-3p	Rsa1.0_00960.1_g00004.1	
3	miR157a-3p	Rsa1.0_01083.1_g00002.1	
4	miR157a-3p,miR857	Rsa1.0_05206.1_g00004.1	
5	miR157a-5p	Rsa1.0 04128.1 g00002.1	
7	miR157a-5p	Rsa1.0 00190.1 g00049.1	
8	miR157a-5p	Rsa1.0 02923.1 g00003.1	
9	miR157a-5p.miR156i	Rsa1.0 16217.1 g00001.1	
10	miR157a-5p.miR157d	Rsa1.0 00832.1 g00003.1	
11	miR157a-5n miR157d	Rsa1 0, 04527 1, g00007 1	
13	miR157a-5p miR157d	Rsa1.0_00326.1_g00027.1	
14	$miR157a_{5}n miR157d$	Rsa1.0_05/68.1_g00003.1	
15	miR157a-5p,miR157d $miP157a-5p,miP157d$	$R_{sa1.0}_{0.000000000000000000000000000000000$	
16	miR157a-5p,miR157d	1000000000000000000000000000000000000	
17	miR157a-5p,miR157d	$Rsa1.0_00790.1_{g00004.1}$	
19	miR13/a-3p,mR13/d	Rsa1.0_00033.1_g00004.1	
20	miR15/a-5p,miR15/d,miR156a-5	Rsa1.0_04235.1_g00002.1	
21	miR15/a-5p,miR15/d,miR156a-	Rsa1.0_01094.1_g00010.1	
22	miR15/a-5p,miR15/d,miR156a-3	Rsa1.0_04683.1_g00003.1	
23	miR15/a-5p,miR15/d,miR156a-5	Rsa1.0_00/22.1_g00009.1	
25	miR15/a-5p,miR15/d,miR156a-5	Rsa1.0_00026.1_g00007.1	
26	miR157a-5p,miR157d,miR156j	Rsa1.0_00660.1_g00005.1	
27	miR157a-5p,miR157d,miR156j	Rsa1.0_05719.1_g00002.1	
28 29	miR157c-3p	Rsa1.0_13653.1_g00001.1	
30	miR157c-3p	Rsa1.0_02281.1_g00005.1	
31	miR157c-3p	Rsa1.0_01443.1_g00003.1	
32	miR157c-3p	Rsa1.0_00038.1_g00033.1	
33	miR157c-3p	Rsa1.0_03415.1_g00005.1	
35	miR157c-3p	Rsa1.0_04916.1_g00001.1	
36	miR157c-3p	Rsa1.0_07517.1_g00001.1	
37	miR157c-3p	Rsa1.0_01804.1_g00001.1	
38	miR157c-3p	Rsa1.0_02318.1_g00001.1	
39 40	miR157c-3p	Rsa1.0_00339.1_g00006.1	
41	miR157c-3p	Rsa1.0_02667.1_g00005.1	9
42	miR157c-3p	Rsa1.0_08242.1_g00002.1	
43	miR157c-3p	Rsa1.0_05224.1_g00001.1	
44 45	miR157c-3p	Rsa1.0_00234.1_g00012.1	
46	miR157c-3p	Rsa1.0_03018.1_g00002.1	
47	miR157c-3p	Rsa1.0 03189.1 g00003.1	
48	miR157c-3p,miR8175	Rsa1.0 00984.1 g00004.1	
49	miR157d	Rsa1.0 00087.1 g00056.1	
50	miR157d	Rsa1.0 03992.1 g00004.1	
52	miR157d	Rsa1.0 04073.1 g00003.1	
53	miR157d	Rsa1.0 00752.1 g00002.1	
54	miR157d	Rsa1.0 01352.1 g00004.1	
55 56	miR157d	Rsa1 0 00284 1 g00002 1	
57	miR157d	Rsa1 0 02346 1 000002 1	
58	miR157d	Rsa1 0 00651 1 000018 1	
59	miR157d	Rsa1 0 02405 1 000005 1	
60	miR157d	Rsa1 0 01232 1 000003 1	
		1.5	1

1			
2	miR157d	Rsa1.0_01674.1_g00006.1	
3	miR157d	Rsa1.0_00394.1_g00002.1	
4	miR157d	Rsa1.0_02541.1_g00004.1	
6	miR157d	Rsa1.0_00811.1_g00007.1	
7	miR157d	Rsa1.0_04279.1_g00002.1	
8	miR157d	Rsa1.0_00179.1_g00010.1	
9	miR157d	Rsa1.0 01645.1 g00005.1	
10 11	miR157d	Rsa1.0 17001.1 g00001.1	
12	miR157d	Rsa1.0 12678.1 g00001.1	
13	miR157d	Rsa1.0 07376.1 g00001.1	
14	miR157d	Rsa1.0 11656.1 g00001.1	
15 16	miR157d	Rsa1.0 00940.1 g00002.1	
10	miR157d,miR156a-5p,miR156j,n	Rsa1.0 00349.1 g00013.1	
18	miR157d.miR157a-5p	 Rsa1.0_00722.1_g00017.1	
19	miR157d miR157a-5p	Rsa1 0 06750 1 g00001 1	
20	miR157d miR157a-5p	Rsa1 0 04028 1 g00003 1	
21	miR157d miR157a-5n miR156a-	Rsa1 0 00294 1 000025 1	
23	miR157d miR157a-5n miR156a-	Rsa1 0 04403 1 g00002 1	
24	miR157d, $miR157a$ -5p, $miR156i$	Rsa1.0_00876.1_g00002.1	
25	miR157d, $miR157a-5p$, $miR156j$	$\frac{1}{2} \frac{1}{2} \frac{1}$	
26 27	miR157d,miR157a-5p,miR150j	$R_{sa1.0}_{-02198.1}_{-g00006.1}$	
27	miR15/d,IIIK15/a-5p,IIIK150j	Rsa1.0_02725.1_g00000.1	
29	miR138a-3p	Rsa1.0_02838.1_g00003.1	
30	miR138a-3p	Rsa1.0_03019.1_g00002.1	
31	miR158a-3p	Rsa1.0_00/84.1_g00005.1	
32	miR158a-3p	Rsa1.0_00059.1_g00013.1	
34	m1R158a-3p	Rsa1.0_05353.1_g00001.1	
35	miR158a-3p	Rsa1.0_22303.1_g00001.1	
36	miR158a-3p	Rsa1.0_01086.1_g00002.1	
37	miR158a-3p	Rsa1.0_02069.1_g00002.1	
38 30	miR158a-3p	Rsa1.0_01285.1_g00007.1	
40	miR158a-3p	Rsa1.0_02683.1_g00001.1	
41	miR158a-3p	Rsa1.0_00668.1_g00006.1	
42	miR158a-3p	Rsa1.0_01389.1_g00008.1	
43	miR158a-3p	Rsa1.0_03554.1_g00002.1	
44	miR158a-3p	Rsa1.0_02387.1_g00004.1	
46	miR158a-3p	Rsa1.0_03157.1_g00002.1	
47	miR158a-3p,miR158b	Rsa1.0_01308.1_g00009.1	
48	miR158a-3p,miR158b	Rsa1.0 09853.1 g00001.1	
49 50	miR158a-3p,miR158b	Rsa1.0 18616.1 g00001.1	
50	miR158a-3p,miR158b	Rsa1.0 00018.1 g00064.1	
52	miR158a-3p,miR158b	Rsa1.0 03991.1 g00002.1	
53	miR158a-3p,miR158b	Rsa1.0 00008.1 g00043.1	
54 55	miR158a-3p,miR158b	Rsa1.0 00853.1 g00007.1	
55 56	miR158a-3p.miR158b	Rsa1.0 00273.1 g00039.1	
57	miR158a-3p miR170-5p	Rsa1.0 04448 1 g00004 1	
58	miR158b	Rsa1 0 01405 1 900014 1	
59	miR158b	Rsa1 0 05086 1 g00002 1	
60	miR158b	Rsa1 0 04092 1 000002 1	

1			l
2	miR158b	Rsa1.0_00204.1_g00023.1	l .
3	miR158b	Rsa1.0_24716.1_g00001.1	
4 5	miR158b,miR158a-3p	Rsa1.0_01077.1_g00014.1	
6	miR158b,miR158a-3p	Rsa1.0_16565.1_g00001.1	
7	miR158b,miR158a-3p	Rsa1.0_07407.1_g00002.1	
8	miR158b,miR158a-3p	Rsa1.0_01467.1_g00008.1	
9 10	miR158b,miR158a-3p	Rsa1.0_07590.1_g00001.1	
10	miR158b,miR158a-3p	Rsa1.0_34975.1_g00001.1	l .
12	miR158b,miR158a-3p	Rsa1.0_00433.1_g00014.1	
13	miR158b,miR158a-3p	Rsa1.0_02124.1_g00002.1	
14	miR158b,miR158a-3p	Rsa1.0 01209.1 g00003.1	
15 16	miR159a	Rsa1.0 11027.1 g00002.1	
10	miR159a	Rsa1.0 04428.1 g00004.1	
18	miR159a	Rsa1.0 00133.1 g00019.1	
19	miR159a	 Rsa1.0_01556.1_g00005.1	
20	miR159a	Rsa1 0 04138 1 g00005 1	
21 22	miR159a miR159b-3n miR159c	Rsa1 0 00982 1 g00005 1	
23	miR 159a miR 159b-3p miR 159c	Rsa1 0 09089 1 000001 1	
24	miR 159a miR 159b-3p miR 159c	Rsa1 0 03293 1 000003 1	
25	miR159a miR159b-3p miR159c	Rsa1.0_04154.1_g00002.1	
26 27	miR(15)a,miR(15)b-5p,miR(15)c	$R_{sa1.0}_{-04134.1}_{-g00001.1}$	
27	miR159a,miR159c,miR159c-3p	$R_{sa1.0}_{0.04041} = g_{0000011}$	
29	miR159a, miR159c, miR159c-3p	Rsa1.0_00404.1_g00009.1	
30	miR159a, miR159c, miR159c-3p	Rsa1.0_00840.1_g00012.1	
31	miR159a,miR159c,miR159b-3p	Rsa1.0_23994.1_g00001.1	
32 33	¹ miR159a,miR159c,miR159b-3p	Rsa1.0_00207.1_g00028.1	
34	miR159a,miR159c,miR319c,miR	Rsa1.0_06447.1_g00002.1	l I
35	m1R159b-3p	Rsa1.0_00092.1_g00058.1	
36	m1R159b-3p	Rsa1.0_22548.1_g00001.1	
3/	m1R159b-3p	Rsa1.0_00190.1_g00053.1	
30 39	miR159b-3p	Rsa1.0_07916.1_g00002.1	
40	miR159b-3p,miR159a	Rsa1.0_00002.1_g00074.1	
41	miR159b-3p,miR159c	Rsa1.0_09080.1_g00001.1	
42	miR159b-3p,miR159c	Rsa1.0_04267.1_g00001.1	
43 44	miR159b-3p,miR159c,miR159a	Rsa1.0_02516.1_g00003.1	l
45	miR159b-3p,miR159c,miR159a	Rsa1.0_02581.1_g00006.1	
46	miR159b-3p,miR159c,miR159a	Rsa1.0_01027.1_g00010.1	
47	miR159b-3p,miR159c,miR159a	Rsa1.0_01249.1_g00010.1	
48 40	miR159b-3p,miR319c,miR159c,r	Rsa1.0_01813.1_g00006.1	
49 50	miR159b-3p,miR319c,miR159c,r	Rsa1.0_01000.1_g00006.1	l l
51	miR159b-3p,miR319c,miR159c,r	Rsa1.0_01308.1_g00007.1	
52	miR159b-3p,miR5658,miR159c,r	Rsa1.0_04131.1_g00003.1	
53	miR159c	Rsa1.0_00955.1_g00004.1	l .
54 55	miR159c,miR159a	Rsa1.0 08538.1 g00001.1	l .
55	miR159c,miR159b-3p.miR159a	Rsa1.0 06290.1 g00002.1	
57	miR159c,miR159b-3p.miR159a	Rsa1.0 00154.1 g00027.1	
58	miR160a-3p	Rsa1.0 00646.1 g00014.1	
59 60	miR160a-3p	Rsa1.0 00897.1 g00008.1	
00	miR160a-3p	Rsa1.0 00187.1 g00026.1	
	1		

I	· · · · · · · · · · · · · · · · · · ·		
2	miR160a-5p	Rsa1.0_00381.1_g00005.1	
3	miR160a-5p	Rsa1.0_00119.1_g00039.1	
4	miR160a-5p	Rsa1.0_00897.1_g00011.1	
5 6	miR160a-5p	Rsa1.0 00124.1 g00036.1	
7	miR160a-5p	Rsa1.0 02992.1 g00004.1	
8	miR160a-5p.miR156i	Rsa1.0_03073.1_g00005.1	
9	miR160c-3n	Rsa1 0 09283 1 g00002 1	
10	miR160c-3n	Rsa1 0 05041 1 g00001 1	
11	miR160c-3n	Rsa1.0_01283.1_g00006.1	
12	miR160c-5p	$R_{sa1.0}_{01283.1}$ g00000.1	
14	miR100c-3p	$Rsa1.0_03095.1_g00005.1$	
15	inik 102a-3p	Rsa1.0_00079.1_g00033.1	
16	miR162a-3p	Rsa1.0_09923.1_g00001.1	
17	miR162a-3p	Rsa1.0_08//9.1_g00004.1	
18 19	m1R162a-5p,m1R162a-3p	Rsa1.0_00058.1_g00021.1	
20	miR164a	Rsa1.0_00611.1_g00008.1	
21	miR164a	Rsa1.0_00305.1_g00014.1	
22	miR164a	Rsa1.0_08720.1_g00002.1	
23	miR164a	Rsa1.0_00381.1_g00015.1	
24 25	miR164a,miR164c-5p,miR172d-5	Rsa1.0_00568.1_g00009.1	
26	miR164a,novel_35,miR164c-5p	Rsa1.0_07738.1_g00002.1	
27	miR164a,novel 35,miR164c-5p	Rsa1.0 01302.1 g00005.1	
28	miR164a,novel 35,miR164c-5p	Rsa1.0 00541.1 g00022.1	
29	miR164a,novel 35,miR164c-5p	Rsa1.0 00278.1 g00019.1	
30 31	miR164c-3p	Rsa1.0 04657.1 g00001.1	
32	miR164c-3p	Rsa1.0 00379.1 g00011.1	
33	miR164c-5p	Rsa1 0 00014 1 g00019 1	
34	miR164c-5p	Rsa1 0 00842 1 g00011 1	
35	miR164c-5p	Rsa1 0 00251 1 g00024 1	
37	miR164c-5p	Rsa1 0, 00605 1, g00016 1	
38	miR164c-5n miR164a	Rsa1.0_00253.1_g00028.1	
39	miR164c-5n miR164a	Rsa1.0_00387.1_g00024.1	
40	miR164c 5n miR164a	1100000000000000000000000000000000000	
41 42	miR164a 5n miP164a noval 25	$R_{sa1.0}_{00004.1}_{00002.1}$	
43	$miR164c-5p,miR164a,movel_55$	$R_{sa1.0}_{001/0.1}g00021.1$	
44	IIIR104c-3p,IIIR104a,II0vel_33	Rsa1.0_00492.1_g00003.1	
45	miR164c-5p,miR164a,novel_35	Rsa1.0_00314.1_g00012.1	
46	miR164c-5p,novel_35,miR164a	Rsa1.0_06642.1_g00002.1	
47 48	miR164c-5p,novel_35,miR164a	Rsa1.0_00466.1_g00002.1	
49	miR165a-3p	Rsa1.0_05218.1_g00004.1	
50	miR165a-3p	Rsa1.0_01115.1_g00008.1	
51	miR165a-5p	Rsa1.0_00662.1_g00018.1	
52	miR165a-5p	Rsa1.0_02004.1_g00001.1	
55 54	miR165a-5p	Rsa1.0_01828.1_g00006.1	
55	miR165a-5p	Rsa1.0_00556.1_g00038.1	
56	miR165a-5p	Rsa1.0_03962.1_g00004.1	
57	miR165a-5p	Rsa1.0_26999.1_g00001.1	
58	miR165a-5p	Rsa1.0_00207.1_g00021.1	
59 60	miR165a-5p	Rsa1.0_00234.1_g00019.1	
	miR166a-3p	Rsa1.0_00733.1_g00006.1	

1			
2	miR166a-3p	Rsa1.0_00085.1_g00017.1	1
3	miR166a-3p	Rsa1.0_02161.1_g00003.1	l
4	miR166a-3p	Rsa1.0_07052.1_g00001.1	1
6	miR166a-3p	Rsa1.0_01043.1_g00006.1	1
7	miR166a-3p	Rsa1.0_11222.1_g00001.1	1
8	miR166a-5p	Rsa1.0 06046.1 g00002.1	1
9	miR166e-5p	Rsa1.0 00622.1 g00011.1	1
10	miR166e-5p	Rsa1.0 06029.1 g00001.1	1
12	miR166e-5p	 Rsa1.0_04440.1_g00001.1	1
13	miR166e-5p	Rsa1.0 01946.1 g00002.1	
14	miR166e-5p	Rsa1 0 00698 1 g00003 1	
15	miR166e-5p	Rsa1 0 00230 1 g00011 1	
16 17	miR166e-5p	Rsa1 0 03322 1 000004 1	
18	miR166e-5p miR165a-5p	Rsa1 0 00977 1 000003 1	
19	miR167a-3n	Rsa1.0_00380.1_g000018.1	
20	miR167a-3n	Rsa1.0_00064_1_g00028_1	
21	miR167a-3p	$\frac{\text{Rsa1.0}_{00004.1}}{\text{Rsa1.0}_{00004.1}} = \frac{1}{200023.1}$	
22	miR167a-3p	1000000000000000000000000000000000000	
24	miR167a-5p	1000000000000000000000000000000000000	
25	miR167a - 5p $miR167a - 5p$	Rsa1.0_03078.1_g00004.1	
26	miR10/a-3p,miR10/c-3p	Rsa1.0_01882.1_g00004.1	
27 28	miR16/a-5p,miR16/c-5p	Rsa1.0_01113.1_g00009.1	
29	miR16/c-5p	Rsa1.0_00329.1_g00008.1	
30	miR16/c-5p	Rsa1.0_05490.1_g00001.1	
31	miR16/c-5p	Rsa1.0_01823.1_g00002.1	
32	miR16/c-5p	Rsa1.0_00519.1_g00011.1	
33 34	miR167c-5p,miR5658	Rsa1.0_03113.1_g00003.1	
35	miR168a-3p	Rsa1.0_02173.1_g00002.1	
36	miR168a-5p	Rsa1.0_02946.1_g00003.1	
37	miR168a-5p	Rsa1.0_02490.1_g00004.1	
38 39	miR169a-5p	Rsa1.0_00029.1_g00024.1	
40	miR169a-5p	Rsa1.0_02937.1_g00005.1	
41	miR169a-5p	Rsa1.0_02655.1_g00005.1	
42	miR169a-5p	Rsa1.0_01797.1_g00006.1	
43 44	miR169a-5p	Rsa1.0_00506.1_g00002.1	
45	miR169a-5p,miR169b-5p,miR169	Rsa1.0_02406.1_g00004.1	
46	miR169a-5p,miR169b-5p,miR169	Rsa1.0_00694.1_g00010.1	
47	miR169b-5p	Rsa1.0_00032.1_g00024.1	
48	miR169b-5p	Rsa1.0_00977.1_g00014.1	l l
49 50	miR169b-5p	Rsa1.0_14221.1_g00002.1	l .
51	miR169b-5p	Rsa1.0_01811.1_g00005.1	
52	miR169b-5p,miR169a-5p	Rsa1.0_00429.1_g00001.1	
53	miR169b-5p,miR169a-5p	Rsa1.0_00083.1_g00034.1	
54 55	miR169b-5p,miR169a-5p	Rsa1.0_00509.1_g00014.1	
56	miR169b-5p,miR169a-5p,miR169	Rsa1.0_01436.1_g00005.1	
57	miR169b-5p,miR169a-5p,miR169	Rsa1.0_00046.1_g00029.1	
58	miR169b-5p,miR169d,miR396b-	Rsa1.0_00518.1_g00006.1	
59 60	miR169d	Rsa1.0_03544.1_g00001.1	
	miR169d	Rsa1.0_00306.1_g00012.1	

2	miR169d,miR169a-5p,miR169b-	Rsa1.0 01855.1 g00009.1	
3	miR169d.miR169b-5p	Rsa1.0 09683.1 g00001.1	
4	miR169d miR169b-5p miR169a-	Rsa1 0 00553 1 g00014 1	
5	miR169d miR169b-5p miR169a-	Rsa1 0 00307 1 g00009 1	
6 7	miR 169d miR 169b-5p miR 169a-	Rsa1 0, 00060 1, g00008 1	
8	miR169d, $miR169b$ -5p, $miR169a$ -	Rsa1.0_00046.1_g00028.1	
9	miR160d miR160b 5p miR160a	$R_{sa1.0} = 00040.1 = g00020.1$	
10	miR169d, $miR169b$ -5p, $miR169a$ -	$\frac{Rsa1.0}{00000000000000000000000000000000000$	
11	miR109d,miR1090-5p,miR109a-	$Rsa1.0_00010.1_g00003.1$	
12	IIIIK1091-3p	Rsa1.0_03010.1_g00003.1	
14	miR169f-3p	Rsa1.0_00337.1_g00007.1	
15	miR169f-3p	Rsa1.0_03111.1_g00002.1	
16	miR169f-3p	Rsa1.0_00278.1_g00013.1	
17	miR169f-3p	Rsa1.0_05059.1_g00001.1	
18 19	miR169f-3p,miR169b-5p,miR169	Rsa1.0_03674.1_g00004.1	
20	miR169g-3p	Rsa1.0_01499.1_g00003.1	
21	miR169g-3p	Rsa1.0_00576.1_g00024.1	
22	miR170-3p	Rsa1.0_01434.1_g00006.1	
23	miR170-3p	Rsa1.0_06840.1_g00002.1	
24	miR170-3p	Rsa1.0_00058.1_g00028.1	
25 26	miR170-3p,miR171b-3p	Rsa1.0_00152.1_g00017.1	
27	miR170-5p	Rsa1.0 62908.1 g00001.1	
28	miR170-5p	Rsa1.0 00734.1 g00004.1	
29	miR171a-3p	Rsa1.0 03527.1 g00004.1	
30 21	miR171a-3p	Rsa1.0_00474.1_g00005.1	
32	miR171a-3p	Rsa1 0 00081 1 g00022 1	
33	miR171a-3n miR170-3n miR1711	Rsa1 0, 01373 1, 000003 1	
34	miR171a-3p miR170-3p miR1711	Rsa1.0_02830.1_g00004.1	
35	miR171b-3n	$\frac{1}{2} \frac{1}{2} \frac{1}$	
30 37	miR1710-5p	$R_{sol} = 0.000371 \pm 0.000201$	
38	miR(1710-5p) miR(171h 2p miR(170 2p miR(171))	1000000000000000000000000000000000000	
39	miR171b-3p,miR170-3p,miR171	Rsa1.0_03244.1_g00001.1	
40		Rsa1.0_01094.1_g00004.1	
41	miR1/10-3p,miR1/1a-3p,miR1/	Rsa1.0_00693.1_g00004.1	
42 43	miR1/16-5p	Rsa1.0_06227.1_g00001.1	
44	miR1/1b-5p	Rsa1.0_01811.1_g00010.1	
45	miR171b-5p	Rsa1.0_00024.1_g00015.1	
46	miR171b-5p	Rsa1.0_00352.1_g00007.1	
47	miR171b-5p	Rsa1.0_00621.1_g00005.1	
48 49	miR171b-5p	Rsa1.0_02860.1_g00004.1	
50	miR172a	Rsa1.0_00767.1_g00007.1	
51	miR172a	Rsa1.0_00008.1_g00021.1	
52	miR172a	Rsa1.0_00071.1_g00046.1	
53	miR172a	Rsa1.0_04207.1_g00003.1	
54 55	miR172a	Rsa1.0_00887.1_g00003.1	
56	miR172a	Rsa1.0_02358.1_g00002.1	
57	miR172a,miR172c,miR172e-3p	Rsa1.0 01717.1 g00004.1	
58	miR172a,miR172c,miR172e-3p	Rsa1.0 01237.1 g00007.1	
59 60	miR172a,miR172e-3p	Rsa1.0 10548.1 g00001.1	
00	miR172a,miR172e-3p,miR172c	Rsa1.0_00099.1_g00005.1	

1			1
2	miR172a,miR5658,miR172e-3p	Rsa1.0_00483.1_g00005.1	1
3	miR172b-5p	Rsa1.0_02092.1_g00009.1	1
4	miR172b-5p	Rsa1.0_04890.1_g00001.1	1
5	miR172b-5p	Rsa1.0 27165.1 g00001.1	1
7	miR172b-5p	Rsa1.0 00546.1 g00002.1	1
8	miR172b-5p	Rsa1.0 00289.1 g00002.1	1
9	miR172b-5p	Rsa1 0 00599 1 g00016 1	l
10	miB172h-5n	Rsa1 0, 09807 1, g00001 1	1
 12	miR172b_5p	$\frac{1660110}{2} = 0.0000000000000000000000000000000000$	1
12	miR(1720-5p)	$P_{col} = 0.05636 \pm 0.00002 \pm 0.00002 \pm 0.000002 \pm 0.0000000000$	1
14	miR1720-5p	1000000000000000000000000000000000000	1
15	miR1/20-5p	$Rsa1.0_00728.1_g00011.1$	1
16	miR1/20-5p	Rsa1.0_03448.1_g00004.1	1
1/	miR1/20-5p	Rsa1.0_1/189.1_g00001.1	1
10	miR1/2b-5p	Rsa1.0_05518.1_g00001.1	1
20	miR172b-5p	Rsa1.0_00038.1_g00052.1	l
21	miR172b-5p	Rsa1.0_00763.1_g00004.1	1
22	miR172b-5p	Rsa1.0_01685.1_g00010.1	l
23	miR172b-5p	Rsa1.0_04225.1_g00001.1	l
24 25	miR172b-5p	Rsa1.0_00754.1_g00001.1	1
26	miR172b-5p,miR164a,miR164c-5	Rsa1.0_00003.1_g00029.1	1
27	miR172c	Rsa1.0 02754.1 g00005.1	1
28	miR172c	Rsa1.0 25366.1 g00001.1	1
29	miR172c	Rsa1.0 00218.1 g00024.1	1
30 31	miR172c	Rsa1.0 00018.1 g00066.1	
32	miR172c,miR172a	Rsa1.0 00576.1 g00016.1	
33	miR172c,miR172b-5p,miR172e-3	Rsa1.0 00285.1 g00011.1	
34	miR172c.miR172e-3p.miR172a	Rsa1.0 04622.1 g00002.1	
35 36	miR172c.miR172e-3p.miR172a.n	Rsa1.0 04013.1 g00001.1	
37	miR172d-5p	Rsa1.0 01634.1 g00010.1	•
38	miR172d-5p	Rsa1.0 00340.1 g00015.1	
39	miR172d-5p	Rsa1.0 01742.1 g00005.1	
40 41	miR172d-5p	Rsa1 0 01868 1 g00004 1	4
42	miR172d-5p	Rsa1 0 01785 1 g00002 1	
43	miR172d-5p	Rsa1 0 01419 1 g00007 1	
44	miR172d-5p	Rsa1 0 34341 1 g00001 1	
45	miR172d-5p	Rsa1 0 02149 1 000004 1	1
40	miR172d-5p	Rsa1.0_21756.1_g00001.1	
48	miR172d-5p	Rsa1.0_06648.1_g00003.1	
49	miR172d-5p	$\frac{1100}{200000000000000000000000000000000$	
50	miR172d-5p	$\frac{11000024551}{200004.1}$	1
51 52	miR172d-5p	$R_{sa1.0}_{-04744.1}_{-g000011}$	l
53	miR1/2d-5p	$R_{sa1.0}_{13347.1}g00001.1$	l
54	miN1/20-3p $miD172d.5r$	1000000000000000000000000000000000000	
55	miki/2a-5p	Ksa1.0_01774.1_000004.1	
56 57	miK1/2d-5p	Ksa1.0_01//4.1_g00003.1	
57 58	miR1/2d-5p	Ksa1.0_02827.1_g00003.1	
59	miR1/2d-5p	Ksa1.0_02733.1_g00001.1	
60	miR172d-5p	Rsa1.0_00368.1_g00001.1	
	m1R172d-5p	Ksa1.0_00105.1_g00019.1	

2	miR172d-5p	Rsa1.0_00359.1_g00004.1	
3	miR172d-5p	Rsa1.0 00496.1 g00003.1	
4	miR172d-5p	Rsa1.0 00426.1 g00011.1	
5	miR172e-3p	Rsa1.0 01092.1 g00002.1	
7	miR172e-3p	 Rsa1.0_00319.1_g00019.1	
8	miR172e-3p	Rsa1.0 01109.1 g00008.1	
9	miR172e-3n	Rsa1 0 02149 1 g00003 1	
10	miR172e-3n	Rsa1 0 00159 1 000043 1	
 12	miR172e-3p miR172a	Rsa1 0 04939 1 g00001 1	
12	miR(172e-3p,miR(172a)) miR(172e-3p,miR(172a))	$\frac{1}{2} \frac{1}{2} \frac{1}$	
14	miR(172e-3p,miR(172e,miR(172a)) miR(172e-3p,miR(172e,miR(172a))	$\frac{R_{sa1.0} - 00524.1}{R_{sa1.0} - 000242} + \frac{1}{\sigma} \frac{\sigma}{\sigma} \frac{\sigma}{\sigma}$	
15	miR(1/2c-5p,miR(1/2c,miR(1/2a)))	$\frac{1}{2} \frac{1}{2} \frac{1}$	
16 17	miR172e-3p,miR172e,miR172a miR172a, 2p,miR172a,miR172a	$\frac{1}{2} \frac{1}{2} \frac{1}$	
17 18	miR1/2e-3p,miR1/2c,miR1/2a miR172a, 2p,miR172a,miR172a	Rsa1.0_00201.1_g00027.1	
19	miR1/2e-3p,miR1/2c,miR1/2a	Rsa1.0_00021.1_g00004.1	
20	miR2111a-3p	Rsa1.0_00156.1_g00014.1	
21	miR2111a-5p	Rsa1.0_00300.1_g00021.1	
22	miR2111a-5p	Rsa1.0_00252.1_g00018.1	
23 24	miR319a	Rsa1.0_12335.1_g00001.1	
25	miR319a	Rsa1.0_02059.1_g00003.1	
26	miR319a,miR159c,miR159b-3p,r	Rsa1.0_01523.1_g00007.1	
27	miR319a,miR159c,miR319c	Rsa1.0_01779.1_g00003.1	
28	miR319a,miR319c	Rsa1.0_01271.1_g00009.1	
29 30	miR319a,miR396b-5p,miR396a-5	Rsa1.0_24799.1_g00001.1	
31	miR319c	Rsa1.0_25214.1_g00001.1	
32	miR319c	Rsa1.0_00466.1_g00013.1	
33	miR319c	Rsa1.0_20996.1_g00001.1	
34	miR319c	Rsa1.0 00377.1 g00011.1	
35 36	miR319c	Rsa1.0 00703.1 g00002.1	
37	miR319c	Rsa1.0 01583.1 g00006.1	
38	miR319c	Rsa1.0 02070.1 g00011.1	
39	miR319c	Rsa1.0 03198.1 g00001.1	
40 41	miR319c	Rsa1.0 06859.1 g00002.1	
42	miR319c	Rsa1.0 00793.1 g00010.1	
43	miR319c miR159c miR319a	Rsa1 0 06149 1 g00004 1	
44	miR319c miR159c miR319a	Rsa1 0 12766 1 g00001 1	
45 46	miR 319c miR 159c miR 319a	Rsa1 0 04329 1 000001 1	
40 47	miR 319c miR 319a	Rsa1.0_13515.1_g00001.1	
48	miR319c miR319a	$\frac{13310}{200000000000000000000000000000000000$	
49	miR319c miR319a	$\frac{R_{sa1.0} - 00540.1}{R_{sa1.0} - 10084.1} = \frac{200017.1}{r_{sa1.0} - 10084.1}$	
50	miR319c,miR319a miP310c miP310c	$\frac{10004.1}{200001.1}$	
51	miR319c, miR319a	Rsa1.0_03100.1_g00001.1	
53	miR3190,miR319a	$R_{a1.0} 00/80.1 g00008.1$	
54	miD200a 2m:D2001 2	$Rsa1.0_00352.1_g00015.1$	
55	mik390a-3p,mik390b-3p	Ksa1.0_150/2.1_g00001.1	
56	m1K390a-5p	Ksa1.0_01281.1_g00013.1	
57 58	m1R390a-5p	Ksa1.0_03430.1_g00005.1	
59	m1R390a-5p	Rsa1.0_00002.1_g00063.1	
60	m1R390a-5p	Rsa1.0_07699.1_g00003.1	
	miR390a-5p	Rsa1.0_00157.1_g00044.1	

1			
2	miR390a-5p	Rsa1.0_00556.1_g00023.1	
3	miR390a-5p	Rsa1.0_00001.1_g00002.1	
4	miR390a-5p	Rsa1.0_00009.1_g00011.1	
6	miR390b-3p,miR390a-3p	Rsa1.0_00398.1_g00019.1	
7	miR391-5p	Rsa1.0 00412.1 g00008.1	
8	miR391-5p	Rsa1.0 06930.1 g00001.1	
9	miR391-5p	Rsa1.0 00124.1 g00026.1	
10	miR393a-5p	Rsa1.0 00031.1 g00028.1	
12	miR393a-5p	Rsa1 0 00332 1 g00003 1	
13	miR 393a-5p	Rsa1 0 00330 1 g00013 1	
14	miR 393a-5p	Rsa1 0 02710 1 g00004 1	
15	miR 393a-5n	Rsa1.0_00002.1_g00071.1	
16 17	miR393a-5p	Rsa1.0_00417.1_g00019.1	
18	miR393a-5p	$\frac{1}{10000000000000000000000000000000000$	
19	miR393a-5p	$\frac{1}{2} \frac{1}{2} \frac{1}$	
20	miR2020.5n	$\frac{1}{10000000000000000000000000000000000$	
21	miR393a-5p	Rsa1.0_02127.1_g000001.1	
22	miR393a-5p	Rsa1.0_00202.1_g000005.1	
24	mik393a-5p	Rsa1.0_00020.1_g00021.1	
25	miR394a	Rsa1.0_04167.1_g00002.1	
26	m1R394a	Rsa1.0_01455.1_g00006.1	
27 20	miR394a	Rsa1.0_00299.1_g00005.1	
20 29	miR394a	Rsa1.0_02830.1_g00002.1	
30	miR394a	Rsa1.0_00460.1_g00009.1	
31	miR394a	Rsa1.0_05076.1_g00007.1	
32	miR395a	Rsa1.0_70604.1_g00001.1	
33 34	miR395a	Rsa1.0_08869.1_g00002.1	
35	miR395a	Rsa1.0_05783.1_g00001.1	
36	miR395a	Rsa1.0_07396.1_g00002.1	
37	miR395a	Rsa1.0_01569.1_g00004.1	
38	miR395a	Rsa1.0_03819.1_g00003.1	
39 40	miR395a	Rsa1.0_00033.1_g00053.1	
41	miR395a	Rsa1.0_00886.1_g00015.1	
42	miR395a	Rsa1.0_13934.1_g00001.1	
43	miR395a,miR395b	Rsa1.0_04988.1_g00002.1	
44 45	miR395a,miR395b	Rsa1.0_00468.1_g00009.1	
46	miR395b	Rsa1.0_01740.1_g00002.1	
47	miR395b	Rsa1.0_01776.1_g00006.1	
48	miR395b	Rsa1.0 02280.1 g00005.1	
49 50	miR395b	Rsa1.0 00184.1 g00005.1	
51	miR395b	Rsa1.0 00789.1 g00002.1	
52	miR395b	Rsa1.0 14196.1 g00001.1	
53	miR395b	Rsa1.0 02838.1 g00001.1	
54 57	miR395b	Rsa1.0 08670.1 g00002.1	
55 56	miR395b	Rsa1.0 01131 1 g00002 1	
57	miR 395b miR 395a	Rsa1 0 00493 1 g00009 1	
58	miR 395b miR 395a	Rsa1 0 00057 1 g00018 1	
59	miR 395b miR 395a	Rsa1 0 01524 1 g00007 1	
00	miR396a-3p	Rsa1.0 05599.1 g00005.1	

1			
2	miR396a-3p	Rsa1.0_00187.1_g00013.1	
3	miR396a-5p	Rsa1.0_00559.1_g00015.1	
4	miR396a-5p	Rsa1.0_01430.1_g00005.1	
5	miR396a-5p	Rsa1.0_05819.1_g00002.1	
7	miR396a-5p	Rsa1.0 00037.1 g00016.1	
8	miR396a-5p	Rsa1.0 07051.1 g00001.1	
9	miR396a-5p	Rsa1.0 05986.1 g00002.1	
10	miR396a-5p	 Rsa1.0_71688.1_g00001.1	
11	miR 396a-5n	Rsa1 0 01351 1 g00002 1	
13	$miR 396a_5n$	Rsa1.0_01986.1_g00002.1	
14	miR396a-5p	$\frac{1100}{10000000000000000000000000000000$	
15	miR390a-5p	$R_{sa1.0}_{-00949.1}_{-g000021}$	
16	miR390a-5p	Rsa1.0_03079.1_g00003.1	
17 18	mik396a-5p	Rsa1.0_00356.1_g00039.1	
19	miR396a-5p	Rsa1.0_03832.1_g00002.1	
20	miR396a-5p	Rsa1.0_19817.1_g00001.1	
21	m1R396a-5p	Rsa1.0_03174.1_g00004.1	
22	miR396a-5p	Rsa1.0_12795.1_g00002.1	
23	miR396a-5p	Rsa1.0_01084.1_g00006.1	
24	miR396a-5p	Rsa1.0_00675.1_g00001.1	
26	miR396a-5p	Rsa1.0_08879.1_g00001.1	
27	miR396a-5p	Rsa1.0_02988.1_g00003.1	
28	miR396a-5p	Rsa1.0_07592.1_g00002.1	
29	miR396a-5p	Rsa1.0_00019.1_g00045.1	
30 31	miR396a-5p	Rsa1.0 05235.1 g00001.1	
32	miR396a-5p	Rsa1.0 07559.1 g00001.1	
33	miR396a-5p	Rsa1.0 00531.1 g00013.1	
34	miR396a-5p	Rsa1.0 01368.1 g00005.1	
35 36	miR396a-5p	Rsa1.0 03268.1 g00002.1	
37	miR396a-5p	Rsa1 0 04164 1 g00003 1	
38	miR 396a-5p	Rsa1 0 10285 1 g00001 1	
39	miR 396a-5n miR 396h-5n	Rsa1 0 00320 1 g00017 1	
40	miR 396a-5n miR 396b-5n	Rsa1.0_02616.1_g00004.1	
41	$miR396a_{5},miR396b_{5},miR39b_{5},miR30b_{5},miR30b_{5},miR30b_{5},miR3b$	Rsa1.0_02610.1_g000001.1	
43	miR396a-5p,miR396b-5p	$\frac{1.5a_{1.0}}{2.5a_{1.0}} = \frac{1.5a_{1.0}}{2.5a_{1.0}} = $	
44	miR396a-5p,miR396b-5p	$R_{sa1.0} = 00040.1 = g000091.1$	
45	miR390a-5p,miR3900-5p	$R_{sa1.0}_{00575.1}g00008.1$	
46 47	miR390a-5p,miR3900-5p	$Rsa1.0_14703.1_g00001.1$	
48	inik390a-3p,inik3900-3p	Rsa1.0_00032.1_g00031.1	
49	miR396a-5p,miR396b-5p	Rsa1.0_09034.1_g00001.1	
50	miR396a-5p,miR5658,miR396b-3	Rsa1.0_03276.1_g00003.1	
51	m1R396b-3p	Rsa1.0_00017.1_g00146.1	
52 53	m1R396b-5p	Rsa1.0_01509.1_g00001.1	
54	m1R396b-5p	Rsa1.0_01415.1_g00004.1	
55	miR396b-5p	Rsa1.0_05908.1_g00002.1	
56	miR396b-5p	Rsa1.0_19380.1_g00001.1	
57	miR396b-5p	Rsa1.0_00407.1_g00011.1	
эө 59	miR396b-5p	Rsa1.0_00002.1_g00030.1	
60	miR396b-5p	Rsa1.0_02919.1_g00002.1	
	miR396b-5p	Rsa1.0_01228.1_g00007.1	

1			
2	miR396b-5p	Rsa1.0_03034.1_g00003.1	
3	miR396b-5p	Rsa1.0_00090.1_g00011.1	
4 5	miR396b-5p	Rsa1.0_06561.1_g00002.1	
6	miR396b-5p	Rsa1.0_00024.1_g00022.1	
7	miR396b-5p	Rsa1.0_07720.1_g00002.1	
8	miR396b-5p	Rsa1.0_30464.1_g00001.1	
9 10	miR396b-5p	Rsa1.0_03358.1_g00003.1	
10	miR396b-5p	Rsa1.0_01896.1_g00003.1	
12	miR396b-5p	Rsa1.0_02870.1_g00004.1	
13	miR396b-5p	Rsa1.0_08220.1_g00002.1	
14	miR396b-5p	Rsa1.0 00394.1 g00027.1	
15 16	miR396b-5p	Rsa1.0 04355.1 g00001.1	
17	miR396b-5p,miR156f-3p	Rsa1.0 37312.1 g00001.1	
18	miR396b-5p,miR156f-3p	Rsa1.0 01523.1 g00008.1	
19	miR396b-5p.miR396a-5p	Rsa1.0 02734.1 g00002.1	
20	miR396b-5p.miR396a-5p	Rsa1.0 01481.1 g00010.1	
21	miR396b-5p.miR396a-5p	Rsa1.0 00707.1 g00001.1	
23	miR 396b-5p miR 396a-5p	Rsa1.0 01359.1 g00007.1	
24	miR 396b-5p miR 396a-5p	Rsa1 0 06427 1 g00002 1	
25	miR 396b-5p miR 396a-5p	Rsa1 0 00159 1 g00036 1	
20 27	miR 396b-5n miR 396a-5n	Rsa1.0_00107.1_g00067.1	
28	miR 396b-5n miR 396a-5n	Rsa1.0_00982.1_g00001.1	
29	miR 396b-5n miR 396a-5n	Rsa1 0 01882 1 g00001 1	
30	miR396b-5p, $miR396a-5p$	Rsa1.0_00056.1_g000044.1	
31 32	miR396b-5p,miR396a-5p	$\frac{1.5a1.0}{0.01844.1} = 00002.1$	
33	miR396b 5p miR396a 5p	$R_{sa1.0}_{07424.1} = 000001.1$	
34	miR396b 5p miR396a 5p	$\frac{1.5a_{1.0}}{2} = 0.041961 = 0.000011$	
35	miR3900-5p,miR390a-5p	1100000000000000000000000000000000000	
36 37	miR397a	$R_{sa1.0}_{00054.1}_{000051}_{0000361}$	
38	miP307a	$R_{sa1.0} = 00003.1 = g00030.1$	
39	miP307a	$\frac{\text{Rsa1.0}_{00034.1}_{00040.1}}{\text{Psa1.0}_{00054.1}_{00012.1}}$	
40	miR397a	$\frac{\text{Rsa1.0}_{00034.1}\text{g}00012.1}{\text{g}00011}$	
41 42	miR397a	$Rsa1.0_0/894.1_{00001.1}$	
42	miR397a	Rsa1.0_08885.1_g00001.1	
44	miR397a	Rsa1.0_00343.1_g00002.1	
45	miR397a	Rsa1.0_01435.1_g00005.1	
46 47	m1R397a	Rsa1.0_03355.1_g00004.1	
47 48		Rsa1.0_00328.1_g00010.1	
49	miR39/a	Rsa1.0_02282.1_g00002.1	
50	m1R39/a	Rsa1.0_00415.1_g00010.1	
51	m1R39/a	Rsa1.0_00099.1_g00001.1	
52 53	m1R39/a	Rsa1.0_20916.1_g00001.1	
54	m1R39/a	Rsa1.0_00048.1_g00023.1	
55	miK398a-3p	Ksa1.0_02319.1_g00005.1	
56	m1R398a-3p	Ksa1.0_09097.1_g00002.1	
57 58	m1R398a-3p	Ksa1.0_03668.1_g00004.1	
59	miR398a-3p,miR398b-3p	Rsa1.0_03067.1_g00006.1	
60	m1R398b-5p	Rsa1.0_04335.1_g00001.1	
	m1R398b-5p	Rsa1.0_01453.1_g00012.1	

1			
2	miR398b-5p	Rsa1.0_00050.1_g00020.1	
3	miR398b-5p	Rsa1.0_41706.1_g00001.1	
4	miR398b-5p	Rsa1.0_06177.1_g00001.1	
6	miR398b-5p	Rsa1.0_00131.1_g00056.1	
7	miR398b-5p	Rsa1.0 00797.1 g00006.1	
8	miR398b-5p	Rsa1.0 08375.1 g00002.1	
9	miR398b-5p	Rsa1.0 00484.1 g00009.1	
10	miR398b-5p	Rsa1.0 00498.1 g00009.1	
11	miR 398b-5p	Rsa1 0 00237 1 g00001 1	
13	miR 398b-5p	Rsa1.0_00053.1_g00007.1	
14	miR398b 5n miR156i	$R_{sa1.0} = 00055.1 = g00007.1$	
15	miR3980-5p,miR130j	$R_{sa1.0}_{0.0253221} = g00001.1$	
16	miR3990	$Rsa1.0_02332.1_g00001.1$	
1/ 18	mik3990	Rsa1.0_03604.1_g00001.1	
10	miR3996	Rsa1.0_58331.1_g00001.1	
20	m1R399b	Rsa1.0_01192.1_g00002.1	
21	miR399b	Rsa1.0_08861.1_g00002.1	
22	miR399b	Rsa1.0_00165.1_g00016.1	
23	miR399b	Rsa1.0_09006.1_g00001.1	
25	miR399f	Rsa1.0_00365.1_g00014.1	
26	miR399f	Rsa1.0_08706.1_g00001.1	
27	miR399f	Rsa1.0_00671.1_g00002.1	
28	miR399f,miR399b	Rsa1.0_00111.1_g00037.1	
29 30	miR399f,miR399b	Rsa1.0_00086.1_g00012.1	
31	miR400	Rsa1.0_00488.1_g00003.1	
32	miR400	Rsa1.0_00589.1_g00023.1	
33	miR400	Rsa1.0_08377.1_g00001.1	
34	miR400	Rsa1.0 01351.1 g00005.1	
36	miR400	Rsa1.0 46818.1 g00001.1	
37	miR400	Rsa1.0 02154.1 g00004.1	
38	miR400	Rsa1.0 02032.1 g00005.1	
39	miR400	Rsa1.0 00596.1 g00017.1	
40	miR400	Rsa1.0 00059.1 g00011.1	
42	miR400	Rsa1.0 39362.1 g00001.1	
43	miR400	Rsa1.0 05188.1 g00001.1	
44	miR400	Rsa1.0 20921.1 g00001.1	
45 46	miR400	Rsa1.0 04165.1 g00005.1	
47	miR400	Rsa1 0 10113 1 g00001 1	
48	miR400	Rsa1.0_18167.1_g00001.1	
49	miR400	$R_{sal} = 0.03142 \pm 0.00005 \pm 0.00005 \pm 0.000005 \pm 0.0000000000$	
50 51	miR400	Rsa1.0_00745.1_g00001.1	
51 52	miR400	$\frac{1}{2} \frac{1}{2} \frac{1}$	
53	miR400	$R_{sa1.0}_{01337.1}g00002.1$	
54	miR400	1000000000000000000000000000000000000	
55	miR400	$1.5a1.0_0+0.052.1_g000000.1$	
56 57	IIIIK400	Ksa1.0_04159.1_g00001.1	
58	miK400	Ksa1.0_00869.1_g00007.1	
59	m1K400	Ksa1.0_00224.1_g00044.1	
60	m1K400	Ksa1.0_02652.1_g00001.1	
	m1R400	Rsa1.0_10155.1_g00002.1	

1			1
2	miR400	Rsa1.0_05188.1_g00003.1	
3	miR400	Rsa1.0_01776.1_g00002.1	
4	miR400	Rsa1.0_09637.1_g00001.1	
6	miR400	Rsa1.0_30585.1_g00001.1	
7	miR400	Rsa1.0_05787.1_g00001.1	
8	miR400	Rsa1.0_00239.1_g00005.1	
9	miR400	Rsa1.0_00239.1_g00011.1	
10 11	miR400	Rsa1.0 20310.1 g00001.1	
12	miR400	Rsa1.0 03786.1 g00003.1	
13	miR400	Rsa1.0 03943.1 g00006.1	
14	miR400	Rsa1.0 00407.1 g00015.1	
15	miR400	Rsa1.0 03686.1 g00004.1	
10	miR400	Rsa1 0 01171 1 g00007 1	
18	miR400	Rsa1 0, 00036 1, g00032 1	
19	miR/00	1000000000000000000000000000000000000	
20	miR400	1100000000000000000000000000000000000	
21	miR400	$R_{sa1.0}_{01794.1}g00002.1$	
22	miR400	$R_{sa1.0}_{005201} = 000061$	
24	miR400	Rsa1.0_00339.1_g00000.1	
25	miR400	Rsa1.0_000/3.1_g00006.1	
26	m1R400	Rsa1.0_00863.1_g00005.1	
2/	m1R400	Rsa1.0_01090.1_g00006.1	
20 29	m1R400	Rsa1.0_01329.1_g00001.1	
30	miR403-3p	Rsa1.0_05146.1_g00001.1	
31	miR403-3p	Rsa1.0_03659.1_g00001.1	
32	miR403-3p	Rsa1.0_10460.1_g00002.1	
33	miR403-3p	Rsa1.0_00459.1_g00001.1	
34 35	miR403-3p	Rsa1.0_06826.1_g00001.1	
36	miR403-5p	Rsa1.0_00616.1_g00002.1	
37	miR403-5p	Rsa1.0_21206.1_g00001.1	
38	miR403-5p	Rsa1.0_00073.1_g00017.1	
39	miR403-5p	Rsa1.0_00064.1_g00010.1	
40	miR403-5p	Rsa1.0 01722.1 g00002.1	4
42	miR403-5p	Rsa1.0 47333.1 g00001.1	
43	miR403-5p	Rsa1.0 01853.1 g00017.1	
44	miR403-5p	Rsa1.0 00015.1 g00088.1	
45 46	miR403-5p	Rsa1.0 08897.1 g00001.1	
47	miR403-5p	Rsa1 0 00184 1 g00018 1	
48	miR403-5n	Rsa1.0_00183.1_g00006.1	
49	miR(105/5p	Rsa1.0_00878.1_g000014.1	
50	miR403.5p	1100000000000000000000000000000000000	
51 52	miR(+03-5p	$R_{sa1.0}_{00157.1}_{000051}$	
53	miR409-5p	$R_{sa1.0}_{01704.1}g00005.1$	
54	miR408-3p	$R_{sa1.0}_{00008.1}_{000021}$	
55	miR400-5p	$Rsa1.0_02252.1_g00005.1$	
56	mik408-3p	Ksa1.0_0/4/8.1_g00002.1	
57 58	m1K408-3p	Ksa1.0_01611.1_g00001.1	
59	m1R408-3p	Ksa1.0_14747.1_g00001.1	
60	m1R408-3p	Ksa1.0_00117.1_g00027.1	
	miR408-5p	Rsa1.0_07094.1_g00002.1	

1			1
2	miR408-5p	Rsa1.0_00359.1_g00009.1	
3	miR408-5p	Rsa1.0_02857.1_g00003.1	
4 5	miR408-5p	Rsa1.0_08288.1_g00001.1	
6	miR408-5p	Rsa1.0_00560.1_g00009.1	
7	miR408-5p	Rsa1.0_09048.1_g00001.1	
8	miR408-5p	Rsa1.0_00243.1_g00026.1	
9	miR408-5p	Rsa1.0 00238.1 g00017.1	
10 11	miR408-5p	Rsa1.0 03434.1 g00004.1	
12	miR408-5p	Rsa1.0 00033.1 g00020.1	
13	miR408-5p	Rsa1.0 01867.1 g00008.1	
14	miR408-5p	Rsa1.0 02255.1 g00003.1	
15 16	miR408-5p	Rsa1.0 00058.1 g00034.1	
17	miR408-5p	Rsa1.0 02559.1 g00004.1	
18	miR408-5p	Rsa1 0 01636 1 g00004 1	
19	miR408-5p	Rsa1 0 02070 1 g00009 1	
20	miR408-5p	Rsa1 0 04336 1 g00001 1	
21	miR 408-5p	Rsa1.0_00341.1_g00034.1	
23	miR 5630a	$R_{sal} = 0.192481 \pm 0.00011$	
24	miR5050a	$R_{sa1.0} 19248.1 g00001.1$	
25	miR5050a	$R_{sa1.0}_{00855.1}g00002.1$	
26 27	miR5050a	Rsa1.0_14001.1_g00001.1	
27 28	miR5030a	Rsa1.0_01199.1_g00015.1	
29	mik5630a	Rsa1.0_00/1/.1_g00002.1	
30	miR5630a	Rsa1.0_012/8.1_g00001.1	
31	miR5630a	Rsa1.0_03200.1_g00003.1	
32	m1R5630a	Rsa1.0_01526.1_g00007.1	
33 34	miR5658	Rsa1.0_00399.1_g00019.1	
35	miR5658	Rsa1.0_06619.1_g00001.1	
36	miR5658	Rsa1.0_15067.1_g00001.1	
37	miR5658	Rsa1.0_01565.1_g00012.1	
38 39	miR5658	Rsa1.0_00476.1_g00007.1	
40	miR5658	Rsa1.0_00113.1_g00019.1	
41	miR5658	Rsa1.0_00090.1_g00014.1	7
42	miR5658	Rsa1.0_02561.1_g00003.1	
43 44	miR5658	Rsa1.0_00008.1_g00064.1	
44	miR5658	Rsa1.0_00654.1_g00015.1	
46	miR5658	Rsa1.0_00037.1_g00035.1	
47	miR5658	Rsa1.0_02810.1_g00004.1	
48	miR5658	Rsa1.0_00554.1_g00010.1	
49 50	miR5658	Rsa1.0_18100.1_g00001.1	
51	miR5658	Rsa1.0 02031.1 g00003.1	
52	miR5658	Rsa1.0 04716.1 g00002.1	
53	miR5658	Rsa1.0 00898.1 g00005.1	
54 55	miR5658	Rsa1.0 00495.1 g00003.1	
55 56	miR5658	Rsa1.0 00909.1 g00008.1	
57	miR5658	Rsa1.0 01257.1 g00005 1	
58	miR5658	Rsa1.0 01355 1 g00002 1	
59	miR5658	Rsa1 0 00749 1 000014 1	
60	miR 5658	Rsa1 0 00708 1 000007 1	
			j –

1			1
2	miR5658	Rsa1.0_01789.1_g00002.1	
3	miR5658	Rsa1.0_04208.1_g00001.1	
4	miR5658	Rsa1.0_00085.1_g00019.1	
5	miR5658	Rsa1.0_01218.1_g00002.1	
7	miR5658	Rsa1.0_01488.1_g00008.1	
8	miR5658	Rsa1.0 01464.1 g00001.1	
9	miR5658	Rsa1.0 00213.1 g00016.1	
10	miR5658	Rsa1.0 02234.1 g00006.1	
12	miR5658	Rsa1.0 00477.1 g00011.1	
13	miR5658	Rsa1.0 01940.1 g00001.1	
14	miR5658	Rsa1.0 00331.1 g00012.1	
15	miR5658	Rsa1 0 35690 1 g00001 1	
10	miR 5658	Rsa1 0 02698 1 g00007 1	
18	miR 5658	Rsa1.0_16835.1_g00001.1	
19	miR 5658	Rsa1.0_00111_1_g00055_1	
20	miR 5658	Rsa1.0_03024.1_g00004.1	
21	miR 5658	1000000000000000000000000000000000000	
23	miR5658	$R_{sa1.0} = 00107.1 \pm 000017.1$	
24	miR 5658	$R_{sal} = 0.00107.1 \pm 0.00028.1$	
25	miR5058	$R_{sa1.0}_{006531} = 00014.1$	
26 27	miD 5659	$R_{sa1.0} = 00055.1 \pm 0000014.1$	
27	miR5058	$R_{sa1.0} = 0000000000000000000000000000000000$	
29	miR5058	Rsa1.0_02329.1_g00003.1	
30	miR5058	Rsa1.0_00706.1_g00013.1	
31	m1R5658	Rsa1.0_00265.1_g00017.1	
32 33	m1R5658	Rsa1.0_00162.1_g00025.1	
34	m1R5658	Rsa1.0_01939.1_g00005.1	
35	m1R5658	Rsa1.0_00367.1_g00006.1	
36	m1R5658	Rsa1.0_00087.1_g00062.1	
3/	m1R5658	Rsa1.0_04528.1_g00002.1	
39	m1R5658	Rsa1.0_20843.1_g00001.1	
40	m1R5658	Rsa1.0_02749.1_g00005.1	
41	miR5658	Rsa1.0_00867.1_g00002.1	
42	miR5658	Rsa1.0_12809.1_g00001.1	
45 44	miR5658	Rsa1.0_00104.1_g00012.1	
45	miR5658	Rsa1.0_04779.1_g00002.1	
46	miR5658	Rsa1.0_00476.1_g00037.1	
47	miR5658	Rsa1.0_03374.1_g00002.1	
48 49	miR5658	Rsa1.0_00894.1_g00001.1	
50	miR5658	Rsa1.0_02020.1_g00005.1	
51	miR5658	Rsa1.0_00318.1_g00007.1	
52	miR5658	Rsa1.0_01311.1_g00002.1	
53 54	miR5658	Rsa1.0_07243.1_g00001.1	
55	miR5658	Rsa1.0_03785.1_g00001.1	
56	miR5658	Rsa1.0_14130.1_g00001.1	
57	miR5658	Rsa1.0_01310.1_g00002.1	
58 50	miR5658	Rsa1.0_02379.1_g00009.1	
60	miR5658	Rsa1.0_00040.1_g00002.1	
	miR5658	Rsa1.0_00208.1_g00009.1	

1		
2	miR5658	Rsa1.0_02791.1_g00003.1
3	miR5658	Rsa1.0_05726.1_g00001.1
4	miR5658	Rsa1.0_00262.1_g00013.1
5	miR5658	Rsa1.0 07021.1 g00004.1
7	miR5658	Rsa1.0 13617.1 g00001.1
8	miR5658	Rsa1.0 00107.1 g00006.1
9	miR5658	Rsa1.0 02160.1 g00004.1
10	miR5658	Rsa1.0 00039.1 g00050.1
11	miR 5658	Rsa1 0 00445 1 g00002 1
13	miR 5658	Rsa1.0_04230.1_g00001.1
14	miR 5658	Rsa1.0_02358.1_g00008.1
15	miR 5658	Rsa1.0_02330.1_g00000.1
16 17	miR 5658	Rsa1.0_00355.1_g00016.1
17	miR 5658	$\frac{R_{sa1.0} - 00335.1 - g00010.1}{R_{sa1.0} - 00116.1 - g00027.1}$
19	miD 5658	$R_{sa1.0} = 00110.1 \pm g00027.1$
20	miD 5659	Rsa1.0_00498.1_g000002.1
21	miD 5 6 5 9	Rsa1.0_13327.1_g00002.1
22 23	miR5058	Rsa1.0_01485.1_g00002.1
24	mik3638	Rsa1.0_1//6/.1_g00001.1
25	mik3638	Rsa1.0_01206.1_g00004.1
26	miR5658	Rsa1.0_02/9/.1_g00005.1
27 20	miR5658	Rsa1.0_01200.1_g00009.1
28 29	miR5658	Rsa1.0_00743.1_g00002.1
30	miR5658	Rsa1.0_02288.1_g00005.1
31	miR5658	Rsa1.0_03056.1_g00003.1
32	miR5658	Rsa1.0_02382.1_g00005.1
33 34	miR5658	Rsa1.0_00540.1_g00012.1
35	miR5658	Rsa1.0_00153.1_g00041.1
36	miR5658	Rsa1.0_00129.1_g00022.1
37	miR5658	Rsa1.0_00821.1_g00017.1
38	miR5658	Rsa1.0_01799.1_g00005.1
39 40	miR5658	Rsa1.0_01798.1_g00003.1
41	miR5658	Rsa1.0_00425.1_g00024.1
42	miR5658	Rsa1.0_01560.1_g00002.1
43	miR5658	Rsa1.0_00856.1_g00008.1
44 45	miR5658	Rsa1.0_02159.1_g00005.1
46	miR5658	Rsa1.0_31408.1_g00001.1
47	miR5658	Rsa1.0_06844.1_g00002.1
48	miR5658	Rsa1.0 01994.1 g00003.1
49 50	miR5658	Rsa1.0 03483.1 g00003.1
50 51	miR5658	Rsa1.0 00434.1 g00020.1
52	miR5658	Rsa1.0 00048.1 g00015.1
53	miR5658	Rsa1.0 00678.1 g00017.1
54 55	miR5658	Rsa1.0 14744.1 g00001.1
55 56	miR5658	Rsa1 0 03563 1 900001 1
57	miR 5658	Rsa1 0 00100 1 000010 1
58	miR 5658	Rsa1 0 00313 1 000009 1
59	miR5658	Rsa1 0 00012 1 000021 1
60	miR 5658	Rsa1.0_00340.1_g00007.1
		<u>1.5m1.0_00010.1_600007.1</u>

1		·	1
2	miR5658	Rsa1.0_05893.1_g00002.1	
3	miR5658	Rsa1.0_00028.1_g00044.1	
4	miR5658	Rsa1.0_00061.1_g00027.1	
5	miR5658	Rsa1.0_04574.1_g00002.1	
7	miR5658	Rsa1.0 03607.1 g00003.1	
8	miR5658	Rsa1.0 00784.1 g00010.1	
9	miR5658	Rsa1.0 00494.1 g00016.1	
10	miR5658	Rsa1.0_00016.1_g00058.1	
12	miR 5658	Rsa1 0 00577 1 g00018 1	
13	miR 5658	Rsa1.0_01209.1_g00007.1	
14	miR 5658	Rsa1.0_06735.1_g00002.1	
15	miR 5658	Rsa1.0_13251.1_g00001.1	
16 17	miR5658	$R_{sa1.0}_{19291.1}_{2000001.1}$	
17	miR5658	$\frac{1}{2} \frac{1}{2} \frac{1}$	
19	miR5058	$R_{sa1.0}_{003281} = g_{000011}$	
20	miD5659	Rsa1.0_00338.1_g00001.1	
21	miR5058	Rsa1.0_02929.1_g00008.1	
22	miR5058	Rsa1.0_00002.1_g00042.1	
24	m1R5658	Rsa1.0_01618.1_g00003.1	
25	m1R5658	Rsa1.0_01244.1_g00001.1	
26	m1R5658	Rsa1.0_00401.1_g00020.1	
27 28	m1R5658	Rsa1.0_04036.1_g00002.1	
20	m1R5658	Rsa1.0_01595.1_g00011.1	
30	miR5658	Rsa1.0_00083.1_g00022.1	
31	miR5658	Rsa1.0_02051.1_g00006.1	
32	miR5658	Rsa1.0_03818.1_g00002.1	
33 34	miR5658	Rsa1.0_00236.1_g00018.1	
35	miR5658	Rsa1.0_00610.1_g00004.1	
36	miR5658	Rsa1.0_00542.1_g00005.1	
37	miR5658	Rsa1.0_00030.1_g00048.1	
38	miR5658	Rsa1.0_00775.1_g00014.1	
40	miR5658	Rsa1.0_00701.1_g00010.1	
41	miR5658	Rsa1.0_01581.1_g00002.1	1
42	miR5658	Rsa1.0_00081.1_g00023.1	
43	miR5658	Rsa1.0_00302.1_g00016.1	
44 45	miR5658	Rsa1.0_06721.1_g00001.1	
46	miR5658	Rsa1.0_00016.1_g00111.1	
47	miR5658	Rsa1.0_05547.1_g00002.1	
48	miR5658	Rsa1.0_01829.1_g00006.1	
49 50	miR5658	Rsa1.0 00602.1 g00015.1	
50	miR5658	Rsa1.0 08814.1 g00001.1	
52	miR5658	Rsa1.0 00626.1 g00002.1	
53	miR5658	Rsa1.0 00620.1 g00004.1	
54 55	miR5658	Rsa1.0 01300.1 g00010.1	
55 56	miR5658	Rsa1.0 02046.1 200009.1	
57	miR5658	Rsa1.0 01233.1 g00009.1	
58	miR5658	Rsa1.0 00550.1 g000111	
59	miR5658	Rsa1.0 00284 1 g00025 1	
U	miR5658	Rsa1.0 00417.1 g00008.1	
			1

1		7	
2	miR5658	Rsa1.0_00005.1_g00021.1	
3	miR5658	Rsa1.0_00131.1_g00012.1	
4	miR5658	Rsa1.0 01965.1 g00005.1	
5	miR5658	Rsa1.0 03926.1 g00004.1	
7	miR5658	Rsa1.0 01936.1 g00002.1	
8	miR 5658	Rsa1 0 02670 1 g00002 1	
9	miR 5658	Rsa1.0_14681.1_g00001.1	
10	miR 5658	$R_{sal} = 0.044561 \pm 0.000041$	
11	miR(5058	$R_{aa1.0} 04450.1 g00004.1$	
12	miR5058	Rsa1.0_00038.1_g00019.1	
14	miR3638	Rsa1.0_04124.1_g00004.1	
15	miR5658	Rsa1.0_01459.1_g00003.1	
16	m1R5658	Rsa1.0_00361.1_g00009.1	
17	miR5658	Rsa1.0_03337.1_g00004.1	
18	miR5658	Rsa1.0_25451.1_g00001.1	
19 20	miR5658	Rsa1.0_00751.1_g00006.1	
21	miR5658	Rsa1.0_00127.1_g00033.1	
22	miR5658	Rsa1.0_06637.1_g00001.1	
23	miR5658	Rsa1.0_00167.1_g00022.1	
24	miR5658	Rsa1.0 08213.1 g00001.1	
25 26	miR5658	Rsa1.0 01344.1 g00009.1	
27	miR5658	Rsa1.0 00612.1 g00017.1	
28	miR5658	Rsa1.0 00002.1 g00077.1	
29	miR 5658	Rsa1 0 00576 1 g00012 1	
30 21	miR 5658	Rsa1 0 00056 1 g00030 1	
32	miR 5658	Rsa1 0 02089 1 g00003 1	
33	miR 5658	Rsa1.0_02178.1_g00005.1	
34	miR 5658	Rsa1 0 01246 1 g00003 1	
35	miR 5658	$R_{sal} = 0.038/8 \pm 0.000021$	
30 37	miR 5658	$R_{sa1.0}_{0.06081}_{0.000161}$	
38	miR5058	$R_{sa1.0} = 00008.1 = g00010.1$	
39	miR5058	$R_{sa1.0}_{0.00081} = 0.0000000000000000000000000000000000$	
40	miR5058	Rsa1.0_00008.1_g00009.1	
41	mik3638	Rsa1.0_01123.1_g00008.1	
42 43	mik3638	Rsa1.0_31593.1_g00001.1	
44	miK5658	Rsa1.0_02207.1_g00005.1	
45	m1R5658	Rsa1.0_00019.1_g00005.1	
46	m1R5658	Rsa1.0_00577.1_g00014.1	
47	miR5658	Rsa1.0_01760.1_g00003.1	
40 49	miR5658	Rsa1.0_00688.1_g00012.1	
50	miR5658	Rsa1.0_03191.1_g00001.1	
51	miR5658	Rsa1.0_14949.1_g00002.1	
52	miR5658	Rsa1.0_02068.1_g00006.1	
53 54	miR5658	Rsa1.0_00497.1_g00002.1	
55	miR5658	Rsa1.0_00945.1_g00012.1	
56	miR5658	Rsa1.0_00200.1_g00010.1	
57	miR5658	Rsa1.0_00200.1_g00011.1	
58	miR5658	Rsa1.0_01529.1_g00001.1	
59 60	miR5658	Rsa1.0 01506.1 g00002.1	
00	miR 5658	Rsa1 0 01179 1 g00005 1	

1		·	
2	miR5658	Rsa1.0_03852.1_g00002.1	l
3	miR5658	Rsa1.0_03479.1_g00003.1	1
4	miR5658	Rsa1.0_00527.1_g00001.1	1
5 6	miR5658	Rsa1.0 00037.1 g00036.1	1
7	miR5658	Rsa1.0 00087.1 g00121.1	1
8	miR5658	Rsa1.0 00815.1 g00008.1	1
9	miR5658	Rsa1.0 00041.1 g00035.1	1
10	miR5658	Rsa1.0 01440.1 g00009.1	1
11	miR 5658	Rsa1 0 00179 1 g00026 1	
13	miR 5658	Rsa1 0 00045 1 000047 1	
14	miR 5658	Rsa1.0_17085.1_g00001.1	
15	miR 5658	$\frac{1.5 \times 1.0}{1.000141} = \frac{1700011}{1.0000171}$	
16 17	miR 5658	$R_{sa1.0}_{00065.1}_{000075.1}$	1
17	miR5058	$R_{sa1.0} = 00005.1 \pm 000075.1$	1
19	miR5058	$R_{sa1.0}_{0000} = 0000000000000000000000000000000$	
20	miD 5 6 5 9	$R_{sa1.0}_{02030.1}_{000008.1}$	
21	miR5058	Rsa1.0_00302.1_g00017.1	
22	mik3638	Rsa1.0_00/62.1_g0000/.1	
24	miR5658	Rsa1.0_04318.1_g00001.1	
25	m1K5658	Rsa1.0_009/1.1_g00012.1	
26	miR5658	Rsa1.0_03181.1_g00003.1	
27 20	miR5658	Rsa1.0_01920.1_g00012.1	
20 29	m1R5658	Rsa1.0_00541.1_g00017.1	
30	miR5658	Rsa1.0_03037.1_g00003.1	
31	miR5658	Rsa1.0_00552.1_g00003.1	l
32	miR5658	Rsa1.0_00854.1_g00003.1	l
33 34	miR5658	Rsa1.0_14784.1_g00001.1	l .
35	miR5658	Rsa1.0_00186.1_g00012.1	
36	miR5658	Rsa1.0_00110.1_g00020.1	
37	miR5658	Rsa1.0_00157.1_g00004.1	
38	miR5658	Rsa1.0_02459.1_g00003.1	
40	miR5658	Rsa1.0_03399.1_g00004.1	
41	miR5658	Rsa1.0_07254.1_g00001.1	1
42	miR5658	Rsa1.0_02960.1_g00002.1	
43	miR5658	Rsa1.0_02809.1_g00001.1	
44 45	miR5658	Rsa1.0_01315.1_g00012.1	1
46	miR5658	Rsa1.0_03673.1_g00003.1	
47	miR5658	Rsa1.0_02951.1_g00001.1	
48	miR5658	Rsa1.0_02135.1_g00003.1	
49 50	miR5658	Rsa1.0_00422.1_g00020.1	
50	miR5658	Rsa1.0 00422.1 g00019.1	
52	miR5658	Rsa1.0 01961.1 g00002.1	
53	miR5658	Rsa1.0 00050.1 g00021.1	
54 55	miR5658	Rsa1.0 01554.1 g00002.1	
55 56	miR5658	Rsa1.0 00275.1 g00030.1	
57	miR5658	Rsa1.0 00030.1 g00023.1	
58	miR5658	Rsa1.0 00469 1 g00010 1	
59	miR5658	Rsa1 0 02265 1 g00008 1	
bU	miR5658	Rsa1.0_06781_1_g00001_1	

1			
2	miR5658	Rsa1.0_03397.1_g00002.1	
3	miR5658	Rsa1.0_03200.1_g00005.1	
4	miR5658	Rsa1.0 02823.1 g00002.1	
5	miR5658	Rsa1.0 02648.1 g00005.1	
7	miR5658	Rsa1.0 02786.1 g00002.1	
8	miR5658	Rsa1 0 02982 1 g00002 1	
9	miR 5658	Rsa1 0 40732 1 g00001 1	
10	miR 5658	$\frac{10752.1}{9000101}$	
11	miD5659	$R_{aa1.0}_{00049.1}_{0000021}$	
12	miR5058	$Rsa1.0_08239.1_{g00002.1}$	
14	mik3038	Rsa1.0_06908.1_g00001.1	
15	m1R5658	Rsa1.0_03943.1_g00005.1	
16	m1R5658	Rsa1.0_02895.1_g00004.1	
17	miR5658	Rsa1.0_01469.1_g00005.1	
18	miR5658	Rsa1.0_00149.1_g00003.1	
20	miR5658	Rsa1.0_03809.1_g00002.1	
21	miR5658	Rsa1.0_03809.1_g00003.1	
22	miR5658	Rsa1.0_00936.1_g00003.1	
23	miR5658	Rsa1.0 00571.1 g00010.1	
24	miR5658	Rsa1.0 01558.1 g00008.1	
25 26	miR5658	Rsa1.0 00333.1 g00011.1	
20	miR 5658	Rsa1 0, 00022 1, g00035 1	
28	miR 5658	Rsa1 0, 00632 1, g00019 1	
29	miR 5658	$R_{sa1.0} = 00052.1 \pm 000017.1$	
30	miR 5658	$R_{sal} = 0.01118 \pm 0.0004 \pm 0.0004 \pm 0.0004 \pm 0.00004 \pm 0.0000000000$	
31	miD 5658	$R_{sa1.0}_{01110.1}g00004.1$	
33	miD 5659	$R_{sa1.0} 14048.1 g00001.1$	
34	miD 5 6 5 9	$R_{aa1.0}_{00505.1}_{00001.1}$	
35	miR5058	Rsa1.0_10391.1_g00001.1	
36	IIIIK3038	Rsa1.0_00240.1_g00000.1	
37 38	mik5658	Rsa1.0_00260.1_g00002.1	
39	m1K5658	Rsa1.0_00939.1_g00015.1	
40	m1K5658	Rsa1.0_01056.1_g00006.1	
41	m1R5658	Rsa1.0_01081.1_g00003.1	
42	miR5658	Rsa1.0_01669.1_g00003.1	
45 44	miR5658	Rsa1.0_07124.1_g00002.1	
45	miR5658	Rsa1.0_04081.1_g00003.1	
46	miR5658	Rsa1.0_01078.1_g00015.1	
47	miR5658	Rsa1.0_00718.1_g00003.1	
48	miR5658	Rsa1.0_08306.1_g00001.1	
49 50	miR5658	Rsa1.0_00384.1_g00007.1	
51	miR5658	Rsa1.0_00538.1_g00004.1	
52	miR5658	Rsa1.0 00434.1 g00004.1	
53	miR5658	Rsa1.0 01389.1 g00004.1	
54 55	miR5658	Rsa1.0 00342.1 g00002.1	
55 56	miR5658	Rsa1.0 00435 1 g00017 1	
57	miR5658	Rsa1 0 00464 1 g00018 1	
58	miR 5658	Rsa1 0 00301 1 000032 1	
59	miR 5658	Rsa1 0 00098 1 000073 1	
60	miR 5658	Rsa1.0_01182.1_000023.1	

1		·	
2	miR5658	Rsa1.0_01599.1_g00003.1	l
3	miR5658	Rsa1.0_16360.1_g00001.1	1
4	miR5658	Rsa1.0_01595.1_g00006.1	1
5 6	miR5658	Rsa1.0 04531.1 g00002.1	1
7	miR5658	Rsa1.0 03505.1 g00001.1	1
8	miR5658	Rsa1.0 00409.1 g00006.1	1
9	miR5658	Rsa1.0 08628.1 g00001.1	1
10	miR5658	Rsa1.0_03781.1_g00006.1	1
11	miR 5658	Rsa1 0 00571 1 g00029 1	l I
13	miR 5658	Rsa1.0_00185.1_g00008.1	l I
14	miR 5658	Rsa1.0_03187.1_g00001.1	l I
15	miR 5658	$\frac{1.5 \times 1.0}{2.5 \times 10^{-10}} = \frac{1.5 \times 10^{-10}}{1.5 \times 10^{-10}}$	1
16 17	miR 5658	$R_{sa1.0}_{00001451}$	1
17	miR5058	$P_{so1} = 0.02149 \pm 0.000021$	1
19	miR5058	$R_{sa1.0}_{02149.1}$ g00002.1	l I
20	miD 5 6 5 9	Rsa1.0_00190.1_g000038.1	l I
21	miR5058	Rsa1.0_03290.1_g00003.1	l I
22	mik3638	Rsa1.0_00341.1_g00003.1	l I
24	mik5658	Rsa1.0_00090.1_g00035.1	1
25	m1K5658	Rsa1.0_00017.1_g00108.1	l I
26	miR5658	Rsa1.0_01/32.1_g00008.1	
27 20	miR5658	Rsa1.0_00/46.1_g0000/.1	
20 29	m1R5658	Rsa1.0_00088.1_g00018.1	
30	miR5658	Rsa1.0_43846.1_g00001.1	
31	miR5658	Rsa1.0_26854.1_g00001.1	l
32	miR5658	Rsa1.0_02285.1_g00005.1	1
33 34	miR5658	Rsa1.0_00451.1_g00004.1	l
35	miR5658	Rsa1.0_01884.1_g00006.1	
36	miR5658	Rsa1.0_01134.1_g00008.1	
37	miR5658	Rsa1.0_23792.1_g00001.1	
38	miR5658	Rsa1.0_17314.1_g00001.1	
40	miR5658	Rsa1.0_04213.1_g00004.1	
41	miR5658	Rsa1.0_02673.1_g00007.1	7
42	miR5658	Rsa1.0_01925.1_g00001.1	
43	miR5658	Rsa1.0_00034.1_g00035.1	
44 45	miR5658	Rsa1.0_00253.1_g00015.1	
46	miR5658	Rsa1.0_00907.1_g00007.1	
47	miR5658	Rsa1.0_01020.1_g00009.1	
48	miR5658	Rsa1.0 00619.1 g00004.1	
49 50	miR5658	Rsa1.0 00707.1 g00013.1	
50	miR5658	Rsa1.0 28203.1 g00001.1	
52	miR5658	Rsa1.0 08717.1 g00002.1	
53	miR5658	Rsa1.0 00026.1 g00036.1	
54 55	miR5658	Rsa1.0 00362.1 g00023.1	
55 56	miR5658	Rsa1.0 02295.1 g00008.1	
57	miR5658	Rsa1.0 02947.1 g00003.1	
58	miR5658	Rsa1.0 00180.1 g00009 1	
59	miR5658	Rsa1.0 00269 1 g00042 1	
UO	miR5658	Rsa1.0 00621.1 g00002.1	

1			
2	miR5658	Rsa1.0_00868.1_g00009.1	
3	miR5658	Rsa1.0_03422.1_g00003.1	
4	miR5658	Rsa1.0 00140.1 g00004.1	
5	miR5658	Rsa1.0 05366.1 g00001.1	
7	miR5658	Rsa1.0 02279.1 g00002.1	
8	miR5658	Rsa1 0 06555 1 g00001 1	
9	miR 5658	Rsa1.0_00088.1_g000015.1	
10	miR 5658	Rsa1.0_00386.1_g00013.1	
11	miD5659	$R_{aa1.0} = 00300.1 \pm 000056.1$	
12	IIIIK3038	$R_{sa1.0}_{00119.1}g00030.1$	
14	mik3038	Rsa1.0_02114.1_g00003.1	
15	m1R5658	Rsa1.0_000/1.1_g00040.1	
16	m1R5658	Rsa1.0_03/13.1_g00003.1	
17	miR5658	Rsa1.0_00129.1_g00014.1	
18	miR5658	Rsa1.0_03499.1_g00004.1	
20	miR5658	Rsa1.0_02328.1_g00002.1	
21	miR5658	Rsa1.0_07650.1_g00001.1	
22	miR5658	Rsa1.0_01463.1_g00006.1	
23	miR5658	Rsa1.0 01606.1 g00008.1	
24	miR5658	Rsa1.0 00421.1 g00013.1	
25 26	miR5658	Rsa1.0 01571.1 g00007.1	
20	miR 5658	Rsa1 0 00142 1 g00017 1	
28	miR 5658	Rsa1.0_00275.1_g00006.1	
29	miR 5658	Rsa1.0_00/96.1_g00001.1	
30	miR 5658	$R_{sa1.0} = 00490.1 \pm 00001111$	
31	miD 5659	$R_{sa1.0}_{00005.1}g00011.1$	
33	miR5058	$R_{sa1.0}_{01205.1}g00005.1$	
34	IIIIK3038	Rsa1.0_00073.1_g00018.1	
35	mik3038	Rsa1.0_00123.1_g00041.1	
36	mik5658	Rsa1.0_02628.1_g00005.1	
37	m1K5658	Rsa1.0_01965.1_g00004.1	
39	m1K5658	Rsa1.0_00249.1_g00005.1	
40	m1R5658	Rsa1.0_00012.1_g00024.1	
41	miR5658	Rsa1.0_00222.1_g00016.1	
42	miR5658	Rsa1.0_08969.1_g00001.1	
43 44	miR5658	Rsa1.0_01372.1_g00002.1	
45	miR5658	Rsa1.0_01628.1_g00008.1	
46	miR5658	Rsa1.0_11183.1_g00001.1	
47	miR5658	Rsa1.0_06167.1_g00001.1	
48	miR5658	Rsa1.0_00914.1_g00013.1	
49 50	miR5658	Rsa1.0_24607.1_g00001.1	
51	miR5658	Rsa1.0_00900.1_g00010.1	
52	miR5658	Rsa1.0 03472.1 g00002.1	
53	miR5658	Rsa1.0 06476.1 g00001.1	
54 55	miR5658	Rsa1.0 00057.1 g00024.1	
55 56	miR5658	Rsa1.0 02412 1 g00003 1	
57	miR5658	Rsa1 0 02772 1 g00007 1	
58	miR 5658	Rsa1 0 00098 1 σ00033 1	
59	miR 5658	Rsa1 0 02257 1 σ00001 1	
60	miR 5658	Rsa1 0 00413 1 σ00007 1	

1		·	
2	miR5658	Rsa1.0_03384.1_g00001.1	l
3	miR5658	Rsa1.0_02206.1_g00003.1	1
4	miR5658	Rsa1.0_00027.1_g00004.1	1
5	miR5658	Rsa1.0_00285.1_g00012.1	1
7	miR5658	Rsa1.0 00465.1 g00003.1	1
8	miR5658	Rsa1.0 01634.1 g00003.1	1
9	miR5658	Rsa1.0 01190.1 g00012.1	1
10	miR5658	Rsa1.0_00179.1_g00054.1	1
12	miR 5658	Rsa1 0 00449 1 g00011 1	1
13	miR 5658	Rsa1.0_06208.1_g00002.1	
14	miR 5658	Rsa1.0_55669.1_g00001.1	1
15	miR 5658	Rsa1.0_01938.1_g00004.1	
16 17	miR 5658	Rsa1.0_02255.1_g00001.1	1
18	miR 5658	Rsa1.0_02255.1_g00007.1	
19	miR5058	$R_{sa1.0}_{01403.1}g00007.1$	
20	miR5058	$\frac{10000240.1}{200014.1}$	
21	miR5058	Rsa1.0_00838.1_g00010.1	
22	miR5058	Rsa1.0_03003.1_g00003.1	
24	m1R5658	Rsa1.0_00048.1_g00020.1	
25	m1R5658	Rsa1.0_00/88.1_g00001.1	
26	m1R5658	Rsa1.0_05110.1_g00003.1	
27 28	m1R5658	Rsa1.0_01164.1_g00005.1	l
20	m1R5658	Rsa1.0_03388.1_g00001.1	
30	miR5658	Rsa1.0_03692.1_g00001.1	l
31	miR5658	Rsa1.0_00218.1_g00019.1	l
32	miR5658	Rsa1.0_05821.1_g00001.1	
33 34	miR5658	Rsa1.0_00013.1_g00047.1	l .
35	miR5658	Rsa1.0_21290.1_g00001.1	
36	miR5658	Rsa1.0_49703.1_g00001.1	
37	miR5658	Rsa1.0_03384.1_g00003.1	
38	miR5658	Rsa1.0_02067.1_g00003.1	
40	miR5658	Rsa1.0_14734.1_g00001.1	
41	miR5658	Rsa1.0_01986.1_g00004.1	
42	miR5658	Rsa1.0_10201.1_g00003.1	
43	miR5658	Rsa1.0_02727.1_g00001.1	
44 45	miR5658	Rsa1.0_01646.1_g00003.1	l .
46	miR5658	Rsa1.0_02039.1_g00007.1	l I
47	miR5658	Rsa1.0_00016.1_g00094.1	l I
48	miR5658	Rsa1.0_00006.1_g00065.1	l I
49 50	miR5658	Rsa1.0 04449.1 g00003.1	l I
50	miR5658	Rsa1.0 02289.1 g00005.1	l I
52	miR5658	Rsa1.0 05653.1 g00004.1	l I
53	miR5658	Rsa1.0 00036.1 g00021.1	
54 55	miR5658	Rsa1.0 00419.1 g00004.1	
55 56	miR5658	Rsa1.0 04919.1 g00003.1	
57	miR5658	Rsa1.0 00015.1 g00059.1	
58	miR5658	Rsa1.0 04884.1 g00002.1	
59	miR5658	Rsa1.0 00816.1 g00036.1	
00	miR5658	Rsa1.0 02438.1 g00005.1	

1		
2	miR5658	Rsa1.0_02605.1_g00004.1
3	miR5658	Rsa1.0_00079.1_g00007.1
4	miR5658	Rsa1.0_00017.1_g00049.1
5	miR5658	Rsa1.0_01102.1_g00004.1
7	miR5658	Rsa1.0 00033.1 g00036.1
8	miR5658	Rsa1.0 02083.1 g00001.1
9	miR5658	Rsa1.0 01418.1 g00008.1
10	miR5658	Rsa1.0 01333.1 g00001.1
11	miR 5658	Rsa1 0, 00064 1, 900013 1
13	miR 5658	Rsa1.0_00221.1_g00020.1
14	miR 5658	Rsa1.0_00273.1_g00006.1
15	miR 5658	$R_{sa1.0} = 00075.1 \pm g00000.1$
16 17	miD 5658	$R_{sa1.0} = 00087.1 \pm g00000.1$
17	miD 5659	Rsa1.0_00312.1_g000012.1
19	miR5058	Rsa1.0_00300.1_g00002.1
20	miR3038	Rsa1.0_01934.1_g00007.1
21	miR5658	Rsa1.0_02241.1_g00002.1
22	miR5658	Rsa1.0_00011.1_g00005.1
23 24	miR5658	Rsa1.0_00313.1_g00015.1
25	miR5658	Rsa1.0_01198.1_g00004.1
26	miR5658	Rsa1.0_01629.1_g00002.1
27	miR5658	Rsa1.0_00101.1_g00003.1
28 20	miR5658	Rsa1.0_00632.1_g00007.1
30	miR5658	Rsa1.0_04980.1_g00001.1
31	miR5658	Rsa1.0_00135.1_g00025.1
32	miR5658	Rsa1.0_03517.1_g00003.1
33	miR5658	Rsa1.0_00206.1_g00011.1
34 35	miR5658	Rsa1.0_02556.1_g00005.1
36	miR5658	Rsa1.0_00107.1_g00034.1
37	miR5658	Rsa1.0_00003.1_g00003.1
38	miR5658	Rsa1.0_00032.1_g00007.1
39 40	miR5658	Rsa1.0_01534.1_g00009.1
40	miR5658	Rsa1.0 00573.1 g00012.1
42	miR5658	Rsa1.0 00293.1 g00009.1
43	miR5658	Rsa1.0 01609.1 g00009.1
44 45	miR5658	Rsa1.0 06417.1 g00002.1
45 46	miR5658	Rsa1.0 00568.1 g00012.1
47	miR5658	Rsa1.0 04632.1 g00002.1
48	miR 5658	Rsa1 0, 02650 1, g00002 1
49	miR 5658	Rsa1 0 01052 1 000001 1
50 51	miR 5658	Rsa1.0_00245.1_g00013.1
52	miR 5658	Rsa1.0_00370.1_g00002.1
53	miR 5658	Rsa1.0_01989.1_000005.1
54	miR 5658	Rsa1.0_00039.1_g00005.1
55	miD 5658	$P_{so1} = 0.00035 \pm 0.00014 \pm 0.000014 \pm 0.0000000000000000000000000000000000$
56 57	min(5056	Rsa1.0_00055.1_g00014.1
58	miD5659	$R_{a1.0} 10400.1 g00002.1$
59	minK3038	Ksa1.0_01588.1_g00002.1
60	mik5658	Ksa1.0_04689.1_g00001.1
	m1K5658	Ksa1.0_00250.1_g00016.1

1		·	
2	miR5658	Rsa1.0_00271.1_g00021.1	l
3	miR5658	Rsa1.0_03044.1_g00004.1	1
4	miR5658	Rsa1.0_01937.1_g00011.1	l
5 6	miR5658	Rsa1.0 00131.1 g00064.1	1
7	miR5658	Rsa1.0 02967.1 g00001.1	1
8	miR5658	Rsa1.0 00451.1 g00044.1	1
9	miR5658	Rsa1.0 00878.1 g00004.1	l
10	miR5658	Rsa1.0 00874.1 g00002.1	l
11	miR 5658	Rsa1 0 00031 1 g00041 1	
13	miR 5658	Rsa1 0 02299 1 000007 1	
14	miR 5658	Rsa1.0_01164.1_g000010.1	
15	miR 5658	$R_{sal} = 0.04668 \pm 0.00002 \pm 0.00002 \pm 0.000002 \pm 0.0000002 \pm 0.0000002 \pm 0.0000002 \pm 0.0000002 \pm 0.0000000000$	l
16 17	miR 5658	$R_{sa1.0}_{0.028781} = 0.00002.1$	l
18	miR 5658	1000000000000000000000000000000000000	
19	miD 5659	$R_{sa1.0} 10378.1 g00002.1$	
20	miR5058	Rsa1.0_37822.1_g00001.1	
21	miR5058	Rsa1.0_00033.1_g00027.1	
22	mik5658	Rsa1.0_00679.1_g00013.1	
24	m1K5658	Rsa1.0_00965.1_g00001.1	l
25	m1K5658	Rsa1.0_13918.1_g00001.1	
26	m1R5658	Rsa1.0_00442.1_g00003.1	
27 20	m1R5658	Rsa1.0_03431.1_g00002.1	
20 29	miR5658	Rsa1.0_09707.1_g00001.1	
30	miR5658	Rsa1.0_68083.1_g00001.1	l
31	miR5658	Rsa1.0_02019.1_g00002.1	l
32	miR5658	Rsa1.0_00335.1_g00007.1	l
33 34	miR5658	Rsa1.0_01737.1_g00001.1	
35	miR5658	Rsa1.0_00101.1_g00049.1	
36	miR5658	Rsa1.0_02948.1_g00004.1	
37	miR5658	Rsa1.0_00350.1_g00005.1	
38	miR5658	Rsa1.0_02011.1_g00001.1	
40	miR5658	Rsa1.0_01138.1_g00006.1	
41	miR5658	Rsa1.0_04371.1_g00005.1	7
42	miR5658	Rsa1.0_01336.1_g00004.1	
43	miR5658	Rsa1.0_00261.1_g00009.1	1
44 45	miR5658	Rsa1.0_00265.1_g00003.1	
46	miR5658	Rsa1.0_01675.1_g00006.1	
47	miR5658	Rsa1.0_02389.1_g00007.1	
48	miR5658	Rsa1.0 06052.1 g00002.1	
49 50	miR5658	Rsa1.0 00616.1 g00012.1	
50	miR5658	Rsa1.0 15780.1 g00001.1	
52	miR5658	Rsa1.0 04458.1 g00003.1	
53	miR5658	Rsa1.0 00093.1 g00014.1	
54 55	miR5658	Rsa1.0 00213.1 g00003.1	
55 56	miR5658	Rsa1.0 01836.1 200004.1	
57	miR5658	Rsa1.0 00144.1 g00004.1	
58	miR5658	Rsa1.0 02314.1 g00006.1	
59	miR5658	Rsa1.0 00180 1 g00006 1	
UO	miR5658	Rsa1.0 00304.1 g00001.1	

1		
2	miR5658	Rsa1.0_07665.1_g00001.1
3	miR5658	Rsa1.0_02192.1_g00010.1
4	miR5658	Rsa1.0_02678.1_g00002.1
5	miR5658	Rsa1.0_01732.1_g00002.1
7	miR5658	Rsa1.0 02388.1 g00006.1
8	miR5658	Rsa1.0 03073.1 g00002.1
9	miR5658	Rsa1.0 06148.1 g00002.1
10	miR5658	Rsa1.0 00662.1 g00015.1
12	miR5658	Rsa1.0_07538.1_g00002.1
13	miR5658	Rsa1 0 03172 1 g00003 1
14	miR 5658	Bsa1.0_05321.1_g00001.1
15	miR 5658	Rsa1.0_00089.1_g00059.1
16 17	miR 5658	Rsa1.0_00303.1_g00007.1
18	miR 5658	Rsa1.0_00085.1_g00007.1
19	miR 5658	Rsa1.0_02005.1_g00002.1
20	miR 5658	Rsa1.0_00925.1_g00004.1
21	miR5058	Rsa1.0_01000.1_g00002.1
22 23	miD5659	Rsa1.0_00235.1_g00019.1
24	IIIIR 3038	Rsa1.0_01010.1_g000009.1
25	miR3038	Rsa1.0_00760.1_g00003.1
26	m1R5658	Rsa1.0_03365.1_g00003.1
27	m1R5658	Rsa1.0_02110.1_g00004.1
28 29	m1R5658	Rsa1.0_04545.1_g00005.1
30	m1R5658	Rsa1.0_02597.1_g00003.1
31	miR5658	Rsa1.0_02309.1_g00001.1
32	miR5658	Rsa1.0_02960.1_g00003.1
33 34	miR5658	Rsa1.0_01147.1_g00012.1
35	miR5658	Rsa1.0_00711.1_g00008.1
36	miR5658	Rsa1.0_00008.1_g00061.1
37	miR5658	Rsa1.0_01567.1_g00002.1
38	miR5658	Rsa1.0_11719.1_g00001.1
39 40	miR5658	Rsa1.0_04287.1_g00002.1
41	miR5658	Rsa1.0_00272.1_g00022.1
42	miR5658	Rsa1.0_00617.1_g00012.1
43	miR5658	Rsa1.0_00362.1_g00029.1
44 45	miR5658	Rsa1.0_00730.1_g00008.1
46	miR5658	Rsa1.0_01129.1_g00005.1
47	miR5658	Rsa1.0 00871.1 g00006.1
48	miR5658	Rsa1.0 02596.1 g00002.1
49 50	miR5658	Rsa1.0 00097.1 g00035.1
50 51	miR5658	Rsa1.0 00161.1 g00005.1
52	miR5658	Rsa1.0 03506.1 g00002.1
53	miR5658	Rsa1.0 10603.1 g00002.1
54	miR5658	Rsa1.0 01513 1 g00004 1
55 56	miR 5658	Rsa1 0 03334 1 000005 1
57	miR 5658	Rsa1.0_00182.1_g000007.1
58	miR 5658	Rsa1.0_00842_1_g00009_1
59	miR 5658	Rsa1.0_0012.1_g00009.1
60	miR 5658	Rsa1.0_05150.1_g00001.1
	mittoooo	[1\sa1.0_01100.1_g00000.1

1			
2	miR5658	Rsa1.0_10493.1_g00001.1	
3	miR5658	Rsa1.0_00034.1_g00015.1	
4	miR5658	Rsa1.0_07444.1_g00003.1	
5	miR5658	Rsa1.0_00260.1_g00010.1	
7	miR5658	Rsa1.0 00330.1 g00010.1	
8	miR5658	Rsa1.0 00596.1 g00006.1	
9	miR5658	Rsa1.0 00019.1 g00007.1	
10	miR5658	Rsa1.0_00007.1_g00001.1	
12	miR 5658	Rsa1 0 01092 1 g00001 1	
13	miR 5658	Rsa1 0 01571 1 000004 1	
14	miR 5658	Rsa1 0 02122 1 g00004 1	
15	miR 5658	Rsa1.0_07722.1_g00001.1	
16 17	miR 5658	$R_{sa1.0} 0.0703 1 0.000111 1$	
18	miR 5658	$R_{sa1.0} 0070301 g000041$	
19	miP 5658	$R_{sa1.0} = 00050.1 = g000004.1$	
20	miD 5659	$R_{sa1.0}_{01717.1}g00009.1$	
21	miR5058	Rsa1.0_00/16.1_g00014.1	
22	miR3038	Rsa1.0_1/69/.1_g00001.1	
24	mik5658	Rsa1.0_00419.1_g00005.1	
25	mik5658	Rsa1.0_60873.1_g00001.1	
26	m1R5658	Rsa1.0_00473.1_g00012.1	
27 28	m1R5658	Rsa1.0_05847.1_g00002.1	
20	m1R5658	Rsa1.0_02096.1_g00005.1	
30	miR5658	Rsa1.0_04901.1_g00002.1	
31	miR5658	Rsa1.0_00677.1_g00015.1	
32	miR5658	Rsa1.0_02505.1_g00004.1	
33 34	miR5658	Rsa1.0_00945.1_g00010.1	
35	miR5658	Rsa1.0_00940.1_g00015.1	
36	miR5658	Rsa1.0_09224.1_g00002.1	
37	miR5658	Rsa1.0_00207.1_g00027.1	
38	miR5658	Rsa1.0_04116.1_g00004.1	
40	miR5658	Rsa1.0_01421.1_g00010.1	
41	miR5658	Rsa1.0_00323.1_g00036.1	
42	miR5658	Rsa1.0_00600.1_g00008.1	
43	miR5658	Rsa1.0_00661.1_g00003.1	
44 45	miR5658	Rsa1.0_01318.1_g00001.1	
46	miR5658	Rsa1.0_01076.1_g00009.1	
47	miR5658	Rsa1.0_02170.1_g00003.1	
48	miR5658	Rsa1.0_00944.1_g00008.1	
49 50	miR5658	Rsa1.0 01344.1 g00013.1	
50	miR5658	Rsa1.0 01829.1 g00007.1	
52	miR5658	Rsa1.0 02239.1 g00006.1	
53	miR5658	Rsa1.0 02201.1 g00004.1	
54 55	miR5658	Rsa1.0 01410.1 g00009.1	
55 56	miR5658	Rsa1.0 00140.1 g00021.1	
57	miR5658	Rsa1.0 00140.1 g00023.1	
58	miR5658	Rsa1.0 03679.1 g00005.1	
59	miR5658	Rsa1.0 00503.1 g00009.1	
00	miR5658	Rsa1.0 05709.1 g00003.1	

1		1	
2	miR5658	Rsa1.0_04867.1_g00001.1	
3	miR5658	Rsa1.0_00190.1_g00038.1	
4	miR5658	Rsa1.0_00821.1_g00005.1	
5	miR5658	Rsa1.0_11903.1_g00002.1	
7	miR5658	Rsa1.0_02662.1_g00005.1	
8	miR5658	Rsa1.0 01814.1 g00006.1	
9	miR5658	Rsa1.0 01210.1 g00004.1	
10	miR5658	Rsa1.0 00251.1 g00016.1	
12	miR5658	Rsa1.0 01731.1 g00002.1	
13	miR5658	Rsa1.0 18033.1 g00001.1	
14	miR5658	Rsa1.0 03464.1 g00002.1	
15	miR 5658	Rsa1 0 00668 1 g00005 1	
10 17	miR 5658	Rsa1.0_00061.1_g000010.1	
18	miR 5658	Rsa1.0_01333.1_g00005.1	
19	miR 5658	$R_{sal} = 0.01995 1 \pm 0.0005 1$	
20	miR 5658	$R_{sal} = 0.001171 \pm 0.000141$	
21	miR5058	$R_{sa1.0}_{000231}$ g00014.1	
22	miD 5 6 5 9	$R_{aa1.0} = 00033.1 = g00011.1$	
24	miR5058	Rsa1.0_05122.1_c00001.1	
25	miR3038	Rsa1.0_05155.1_g00001.1	
26	mik3638	Rsa1.0_06128.1_g00001.1	
2/	m1R5658	Rsa1.0_00010.1_g00019.1	
20 29	miR5658	Rsa1.0_03336.1_g00005.1	
30	miR5658	Rsa1.0_00016.1_g00046.1	
31	miR5658	Rsa1.0_00120.1_g00014.1	
32	miR5658	Rsa1.0_01739.1_g00002.1	
33 34	miR5658	Rsa1.0_01061.1_g00017.1	
35	miR5658	Rsa1.0_00280.1_g00006.1	
36	miR5658	Rsa1.0_57297.1_g00001.1	
37	miR5658	Rsa1.0_33636.1_g00001.1	
38	miR5658	Rsa1.0_31467.1_g00001.1	0
39 40	miR5658	Rsa1.0_00317.1_g00004.1	
41	miR5658	Rsa1.0_00675.1_g00009.1	7
42	miR5658	Rsa1.0_02221.1_g00004.1	
43	miR5658	Rsa1.0_00056.1_g00002.1	
44 45	miR5658	Rsa1.0 03660.1 g00004.1	
46	miR5658	Rsa1.0 00286.1 g00008.1	
47	miR5658	Rsa1.0 10726.1 g00001.1	
48	miR5658	Rsa1.0 01159.1 g00002.1	
49	miR5658	Rsa1.0 00890.1 g00013.1	
50 51	miR 5658	Rsa1 0 03560 1 g00002 1	
52	miR5658	Rsa1.0 00048 1 g00029 1	
53	miR 5658	Rsa1 0 10409 1 g00002 1	
54	miR 5658	Rsa1 0 02826 1 000005 1	
55 56	miR 5658	Rsa1.0_02020.1_500003.1	
57	miR 5658	Rsa1.0_01571.1_g00012.1	
58	miR 5658	$R_{sa1.0} 01371.1 g00003.1$	
59	miR 5658	$\frac{1.501.0}{1.0} = 00202.1 = \frac{000010.1}{0000011}$	
60	miD 5658	$P_{sol} = 0.07426 \pm 0.00001 \pm 0.00002 \pm 0.000002 \pm 0.0000002 \pm 0.000002 \pm 0.0000002 \pm 0.0000000000$	
	mintjuju	11.5a1.0 07420.1 g00002.1	

1	r		
2	miR5658	Rsa1.0_02499.1_g00003.1	
3	miR5658	Rsa1.0_00007.1_g00039.1	
4	miR5658	Rsa1.0_13783.1_g00001.1	
6	miR5658	Rsa1.0_60070.1_g00001.1	
7	miR5658	Rsa1.0_01195.1_g00006.1	
8	miR5658	Rsa1.0_07474.1_g00001.1	
9	miR5658	Rsa1.0_30688.1_g00001.1	
10	miR5658	Rsa1.0_00006.1_g00048.1	
12	miR5658	Rsa1.0 03508.1 g00001.1	
13	miR5658	Rsa1.0 06236.1 g00002.1	
14	miR5658,miR156j	Rsa1.0 04649.1 g00003.1	
15 16	miR5658,miR156j	Rsa1.0 00170.1 g00008.1	
17	miR5658,miR156j	Rsa1.0 07565.1 g00003.1	
18	miR5658.miR156j	Rsa1.0 00079.1 g00039.1	
19	miR5658.miR162a-5p	Rsa1.0 04270.1 g00001.1	
20	miR5658 miR165a-5p	Rsa1 0 02113 1 g00004 1	
21	miR 5658 miR 165a-5p	Rsa1 0 02113 1 g00007 1	
23	miR 5658 miR 172e-3p	Rsa1.0_00350.1_g00002.1	
24	miR 5658 miR 172e-3n miR 172a	Rsa1 0 00629 1 g00004 1	
25	miR 5658 miR 390a-5p	Rsa1 0 00642 1 g00025 1	
20 27	miR 5658 miR 396h-3n	Rsa1.0_01172.1_g00005.1	
28	miR 5658 miR 398h-5n	Rsa1.0_00336.1_g00001.1	
29	miR5658 miR408-5p	$R_{sa1.0} = 0000021 \pm 0000681$	
30	miR5658 miR8171	$R_{sa1.0} = 00002.1 = g00008.1$	
31	miR 8171	$R_{sa1.0} = 00104.1 = g00002.1$	
33	miR0171	$R_{sa1.0} = 00009.1 \pm 000022.1$	
34	miR0171	$R_{sa1.0} = 00023.1 = g00022.1$	
35	miR0171	$R_{sa1.0} 01707.1 g00007.1$	
36 37	miR0171	$\frac{1}{2} \frac{1}{2} \frac{1}$	-
38	miD 8175	$R_{sa1.0}_{01348.1}$ g00004.1	
39	miR8175	$R_{sa1.0}_{000011}$ g00008.1	
40	miR0175	$R_{sa1.0}_{00901.1}_{000003.1}$	1
41	miD 8175	$R_{sa1.0}_{04239.1}g00003.1$	
42	miR8175	Rsa1.0_03123.1_g00002.1	
44	miR8175	$R_{sa1.0}_{00317.1}g00002.1$	
45	miR8175	Rsa1.0_03180.1_g00000.1	
46	IIIIR8173	Rsa1.0_03030.1_g00002.1	
47	miR81/5	Rsa1.0_01342.1_g00008.1	
49	mIR81/5	Rsa1.0_02/31.1_g00002.1	
50	miR81/5	Rsa1.0_00993.1_g00006.1	
51	miR81/5	Rsa1.0_02986.1_g00001.1	
52 53	miR81/5	Rsa1.0_02483.1_g00003.1	
54	m1R81/5	Rsa1.0_04143.1_g00003.1	
55	miK8175	Ksa1.0_067/3.1_g00002.1	
56	miR8175	Ksa1.0_05199.1_g00002.1	
57 58	miR8175	Ksa1.0_01653.1_g00005.1	
59	m1R8175	Rsa1.0_02535.1_g00002.1	
60	miR8175	Rsa1.0_08331.1_g00001.1	
	miR8175	Rsa1.0_04815.1_g00002.1	

1			1
2	miR8175	Rsa1.0_03412.1_g00005.1	
3	miR8175	Rsa1.0_10700.1_g00001.1	
4 5	miR8175	Rsa1.0_01849.1_g00001.1	
6	miR8175	Rsa1.0_04702.1_g00002.1	
7	miR8175	Rsa1.0 06285.1 g00001.1	
8	miR8175	Rsa1.0 01858.1 g00002.1	
9	miR8175	Rsa1.0 08171.1 g00001.1	
10	miR8175	Rsa1.0 12968.1 g00001.1	
11	miR8175	Rsa1 0 09596 1 g00001 1	
13	miR0175	$R_{sal} = 0.01734 \pm 0.0006 \pm 0.00006 \pm 0.00006 \pm 0.000006 \pm 0.0000000000$	
14	miR8175 miR157c-3n	$R_{sal} = 0.05463 \pm 0.00001 \pm 0.00001 \pm 0.000001 \pm 0.0000000000$	
15	miR0175,miR157c-5p	$R_{sa1.0}_{-0.000011} = 0.000011$	
16	miR6175,miR157C-5p	$R_{aa1.0}_{01708.1}g00001.1$	
17 18	miR81/3,miR1/20-3p	Rsa1.0_00337.1_g00003.1	
19	miR824-3p	Rsa1.0_00190.1_g00036.1	
20	miR824-3p	Rsa1.0_192/9.1_g00002.1	
21	miR824-3p	Rsa1.0_16626.1_g00001.1	
22	miR824-3p	Rsa1.0_04849.1_g00002.1	
23 24	miR824-3p	Rsa1.0_00135.1_g00024.1	
25	miR824-3p	Rsa1.0_00217.1_g00001.1	
26	miR824-3p	Rsa1.0_02022.1_g00002.1	
27	miR824-3p	Rsa1.0_01513.1_g00008.1	
28	miR824-3p	Rsa1.0_01146.1_g00011.1	
29 30	miR824-3p,miR398a-3p	Rsa1.0_00716.1_g00008.1	
31	miR824-5p	Rsa1.0_01731.1_g00004.1	
32	miR824-5p	Rsa1.0_01329.1_g00004.1	
33	miR824-5p	Rsa1.0 05752.1 g00001.1	
34 25	miR824-5p	Rsa1.0 02324.1 g00002.1	
35 36	miR824-5p	Rsa1.0 00570.1 g00018.1	
37	miR824-5p	Rsa1.0 11424.1 g00002.1	
38	miR824-5p	Rsa1.0 04330.1 g00001.1	
39	miR824-5p	Rsa1.0 07821.1 g00001.1	
40 41	miR824-5p	Rsa1.0 01061.1 g00007.1	4
42	miR824-5p	Rsa1 0 00266 1 g00010 1	
43	miR824-5p	Rsa1 0 01468 1 g00007 1	
44	miRe21-5p	Rsa1 0 00344 1 g00022 1	
45	miR6215p	Rsa1.0_01135.1_g00005.1	
40 47	miR627	Rsa1.0_01779.1_g00001.1	
48	miR627	$R_{sa1.0}_{01779.1}_{000061}$	
49	miR027	$R_{sa1.0} 02124.1 g00000.1$	
50	miR627	$R_{sol} = 0.000011 \pm 0.0000011$	
51	miR627	$R_{sa1.0}_{00391.1}g00008.1$	
53	miR027	$R_{a1.0} 00136.1 g00001.1$	
54	miR02/	$R_{a1.0} = 0.00264.1 = 0.0010.1$	
55	miK827	Ksa1.0_00364.1_g00010.1	
56	miR827	Ksa1.0_08966.1_g00001.1	
57 58	miR827	Ksa1.0_02038.1_g00003.1	
59	miR827	Rsa1.0_05774.1_g00001.1	
60	miR827	Rsa1.0_08724.1_g00001.1	
	miR827	Rsa1.0_00166.1_g00009.1	

1			
2	miR857	Rsa1.0_01716.1_g00001.1	l
3	miR857	Rsa1.0_00999.1_g00001.1	
4	miR857	Rsa1.0_00973.1_g00009.1	
6	miR857	Rsa1.0_00117.1_g00022.1	l
7	miR857	Rsa1.0_04238.1_g00003.1	
8	miR857	Rsa1.0_01620.1_g00003.1	
9	miR857	Rsa1.0_07981.1_g00001.1	
10	miR857	Rsa1.0_01260.1_g00003.1	1
12	miR857	Rsa1.0 02022.1 g00001.1	
13	miR857	Rsa1.0 28733.1 g00001.1	1
14	miR857	Rsa1.0 03287.1 g00002.1	
15 16	miR857	 Rsa1.0_28713.1_g00001.1	
10	miR857	Rsa1 0 00196 1 g00026 1	
18	miR857	Rsa1.0_01101_1_g00007_1	
19	miR857	Rsa1.0_00261.1_g00007.1	
20	miR057	Rsa1.0_00201.1_g00007.1	
21	miRo57	$\frac{13734.1}{900017.1}$	
22	IIIIK637	Rsa1.0_00013.1_g00017.1	1
24	miR857	Rsa1.0_01253.1_g00004.1	
25	m1R857	Rsa1.0_00451.1_g00023.1	1
26	m1R857	Rsa1.0_00026.1_g00062.1	
27	miR857	Rsa1.0_01055.1_g00006.1	
28 29	miR857	Rsa1.0_25220.1_g00001.1	l
30	miR857	Rsa1.0_01690.1_g00005.1	l
31	miR857	Rsa1.0_00920.1_g00025.1	
32	miR858a	Rsa1.0_00865.1_g00001.1	
33	miR858a	Rsa1.0_53777.1_g00001.1	l
34 35	miR858a	Rsa1.0_51959.1_g00001.1	
36	miR858a	Rsa1.0_00199.1_g00036.1	
37	miR858a	Rsa1.0_01642.1_g00004.1	
38	miR858a,miR858b	Rsa1.0 04490.1 g00001.1	
39 40	miR858a,miR858b	Rsa1.0 14336.1 g00001.1	
40	miR858a,miR858b	Rsa1.0 00640.1 g00007.1	4
42	miR858a.miR858b	Rsa1.0 14223.1 g00001.1	
43	miR858a.miR858b	 Rsa1.0_02496.1_g00006.1	1
44	miR858a miR858b	Rsa1 0 15530 1 g00001 1	
45	miR858b	Rsa1.0_00909.1_g00003.1	
40	miR858b	Rsa1.0_00009.1_g00037.1	1
48	miD858h	$P_{sol} = 0.022811 \pm 0.00021$	1
49	miDeseh	1000000000000000000000000000000000000	
50	miD858b	$Rsa1.0_01370.1_g00007.1$	1
51		Rsa1.0_01880.1_g00001.1	1
52 53	mIR8580	Rsa1.0_02829.1_g00003.1	1
54	m1R858b	Rsa1.0_00015.1_g00085.1	
55	miK858b,miK156g,miK858a	Ksa1.0_00822.1_g00001.1	
56	miR858b,miR159a,miR858a,miR	Ksa1.0_00025.1_g00043.1	
57 58	m1R858b,m1R858a	Rsa1.0_00484.1_g00005.1	
59	miR858b,miR858a	Rsa1.0_00463.1_g00020.1	
60	miR858b,miR858a	Rsa1.0_09985.1_g00001.1	
	miR858b,miR858a	Rsa1.0_00408.1_g00004.1	

1		
2	miR858b,miR858a	Rsa1.0_00088.1_g00009.1
3	miR858b,miR858a	Rsa1.0_00065.1_g00014.1
4	miR858b,miR858a	Rsa1.0_00761.1_g00003.1
5 6	miR858b,miR858a	Rsa1.0_02070.1_g00006.1
7	miR858b,miR858a	Rsa1.0_01629.1_g00005.1
8	miR858b,miR858a	Rsa1.0_03421.1_g00004.1
9	novel_35,miR164a,miR164c-5p	Rsa1.0_07584.1_g00001.1
10	novel_35,miR164a,miR164c-5p	Rsa1.0_00166.1_g00017.1
12	novel_35,miR164a,miR164c-5p	Rsa1.0_00428.1_g00008.1
13	novel_35,miR164a,miR164c-5p	Rsa1.0_02628.1_g00006.1
14	novel_35,miR164a,miR164c-5p	Rsa1.0_00377.1_g00002.1
15		· · · · · · · · · · · · · · · · · · ·

3	l miRNAs
ĺ	Annotation
	POP3 ARATH Probable protein Pop3
	DCMC_HUMAN Malonyl-CoA_decarboxylase_mitochondrial
	COG1_MOUSE Conserved oligometric Golgi complex subunit 1
	V_{3471} ARATH Putative recentor like protein kinase $\Lambda t_{3}^{3} a \pi 7110$
ł	V_{2608} APATH P3 domain containing protein $At_{2g_{2}6080}$
ł	TT12 ADATH Drotoin TDANSDADENT TESTA 12
ł	DCAT2 ADATH Protein TRANSFARENT TESTA 12
ł	DCA1_ARATH Branched-chani-annuo-acid annuotanisterase 5, chioroplastic
ł	BCA1_ARATH Beta carbonic annyulase 1, chloroplastic
ŀ	CSON1 ADATH Sulfactual acidese 1
ł	QSOA1_ARATH Sullhydryl oxidase 1
ļ	PRS8A_ARATH 26S protease regulatory subunit 8 homolog A
ļ	PRP3_ARATH Proline-rich protein 3
ļ	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
ł	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
ŀ	AAP4_ARATH Amino acid permease 4
ļ	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
ļ	LTO1_ARATH Thiol-disulfide oxidoreductase LTO1
ļ	LORF2_MOUSE LINE-1 retrotransposable element ORF2 protein
ļ	F188A_MOUSE Protein FAM188A
ļ	EIF3I_ARATH Eukaryotic translation initiation factor 3 subunit I
	DCL_SOLLC Protein DCL, chloroplastic
ļ	WRK19_ARATH Probable WRKY transcription factor 19
ļ	1A15_ARATH 1-aminocyclopropane-1-carboxylate synthase 5
ļ	TRXB2_ARATH Thioredoxin reductase 2
ļ	TCX7_ARATH Protein tesmin/TSO1-like CXC 7
	SIP_ARATH Signal peptide peptidase
	BIG_ARATH Auxin transport protein BIG
	BGL06_ARATH Putative beta-glucosidase 6
	S6PD_MALDO NADP-dependent D-sorbitol-6-phosphate dehydrogenase
	RL32_ARATH 60S ribosomal protein L3-2
ſ	RL32_ARATH 60S ribosomal protein L3-2
ſ	AB18G_ARATH ABC transporter G family member 18
Ì	AAPT1_ARATH Choline/ethanolaminephosphotransferase 1
Ì	NDUA9 ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial
ľ	LORF2 HUMAN LINE-1 retrotransposable element ORF2 protein
Ì	LIN1 NYCCO LINE-1 reverse transcriptase homolog
İ	LIN1 NYCCO LINE-1 reverse transcriptase homolog
ľ	LIN1 NYCCO LINE-1 reverse transcriptase homolog
Ì	IMK3 ARATH Probable leucine-rich repeat receptor-like protein kinase IMK3
ł	SPL5 ARATH Squamosa promoter-binding-like protein 5
ł	SPL10 ARATH Squamosa promoter-binding-like protein 10
ł	CSLC5 ARATH Probable xyloglucan glycosyltransferase 5
}	V1583 ARATH Uncharacterized protein At1g05835
ł	CIPK8 ARATH CBL-interacting serine/threonine-protein kinase 8
ł	LORF2 HUMAN LINE-1 retrotransposable element ORF2 protein
╞	COG1_MOUSE Conserved oligometric Golgi complex subunit 1
1	cost_neost conserved ongoinene ooigi complex subuint i

1	
2	RB24B_XENLA RNA-binding protein 24-B
3	CSE_ARATH Caffeoylshikimate esterase
4	U7E11_ARATH UDP-glycosyltransferase 76E11
5	LORF2 MOUSE LINE-1 retrotransposable element ORF2 protein
7	NUA ARATH Nuclear-pore anchor
8	NUA ARATH Nuclear-pore anchor
9	NUA ARATH Nuclear-pore anchor
10	HSD5_ARATH 11-beta-hydroxysteroid dehydrogenase-like 5
 12	TPR4 ARATH Topless-related protein 4
12	V8250 ORVSLUncharacterized protein Ocl. 027040
14	WTP6 APATH WAT1 related protein At1g25270
15	DAM2 ADATH Data amulase 2 shlaranlastic
16	BAMIS_ARATH Bela-amylase 5, chloroplastic
1/ 10	NRPD1_ARATH DNA-directed RNA polymerase IV subunit 1
10	KU/0_ARATH ATP-dependent DNA helicase 2 subunit KU/0
20	ARAK_ARATH L-arabinokinase
21	GCST_ARATH Aminomethyltransferase, mitochondrial
22	EXPB1_ARATH Expansin-B1
23	DXS1_ORYSJ 1-deoxy-D-xylulose-5-phosphate synthase 1, chloroplastic
24 25	AEDO_DICDI Probable 2-aminoethanethiol dioxygenase
26	DMS3_ARATH Protein DEFECTIVE IN MERISTEM SILENCING 3
27	COPIA_DROME Copia protein
28	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
29 30	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
31	VRN2_ARATH Polycomb group protein VERNALIZATION 2
32	SPA1_ARATH Protein SUPPRESSOR OF PHYA-105 1
33	SOSSB_DICDI SOSS complex subunit B homolog
34 25	BCCIP_ARATH Protein BCCIP homolog
35	ATPF2 HUMAN ATP synthase mitochondrial F1 complex assembly factor 2
37	RBOHG ARATH Putative respiratory burst oxidase homolog protein G
38	PYRB ARATH Aspartate carbamoyltransferase, chloroplastic
39	NLAL1 ARATH Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1
40 41	MYO17 ARATH Myosin-17
42	MPK16 ARATH Mitogen-activated protein kinase 16
43	KIN17 MOUSE DNA/RNA-binding protein KIN17
44	COPIA DROME Conja protein
45 46	SPL6_ARATH Squamosa promoter-binding-like protein 6
40 47	SPL3_ARATH Squamosa promoter-binding-like protein 3
48	I IN1_NVCCO I INF-1 reverse transcriptase homolog
49	SP13B ARATH Squamosa promoter-binding-like protein 13B
50	GSTT3 ARATH Squanosa promoter-binding-fike protein 15D
51 52	SDL 2 AD ATH Squamosa promoter binding like protein 3
53	A P17C DANDE Alpha/bata hydrologa domain containing protain 17C
54	SD12D ADATU Squemese promotor hinding like protein 12D
55	A A DC CENCI Dutative alvages 6 shoarbats 1 arimeness
56 57	DDL 20 ADATU Drohohla diagage mainten a materia At4-22200
58	SPL 2 AD ATTL S recurses proceed binding in the second sec
59	SPL2_AKATH Squamosa promoter-binding-like protein 2
60	SPL9_AKATH Squamosa promoter-binding-like protein 9
	SPL9_AKATH Squamosa promoter-binding-like protein 9

1	
2	Y1061_ARATH Probably inactive leucine-rich repeat receptor-like protein kinase At1g50610
3	SPL4_ARATH Squamosa promoter-binding-like protein 4
4 5	SP13B_ARATH Squamosa promoter-binding-like protein 13B
6	DHX36_MOUSE ATP-dependent RNA helicase DHX36
7	DF184_ARATH Putative defensin-like protein 184
8	DESI1 HUMAN Desumoylating isopeptidase 1
9	ADCS ARATH Aminodeoxychorismate synthase, chloroplastic
10	CYSK1 BRAJU Cysteine synthase
12	ACT2 ARATH Actin-2
13	CXE6 ARATH Probable carboxylesterase 6
14	CSLC7 ORYSJ Probable xyloglucan glycosyltransferase 7
15	CSCL5 ARATH Protein OSCA1
10	CRS1_ARATH Chloroplastic group IIA intron splicing facilitator CRS1_chloroplastic
18	CRR15 ARATH Cysteine-rich repeat secretory protein 15
19	CRK10 ARATH Cysteine-rich recentor-like protein kinase 10
20	2ABA_ARATH Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
21	COPIA DROME Conia protein
22	COPIA_DROME Copia protein
24	CL 16A_DICDI Protein CL EC16A homolog
25	CK12 SCHPO Casain kinasa Lhamalag 2
26	ACO2M ADATH Aconitate hydratege 2 mitechandrial
27	ACO12 A DATU Dutative perevisemel cert accurring A cuidese 1.2
29	CIDKK ADATH CDL interacting garing (three pine protein binger 20
30	CIPKK_ARATH CBL-interacting serine/threonine-protein kinase 20
31	CIDIT_ARATH Polyadenylate-binding protein-interacting protein 11
32 33	CDPKY_ARATH Calcium-dependent protein kinase 34
34	CDPK Y_ARATH Calcium-dependent protein kinase 34
35	ZRAB3_MOUSE DNA annealing helicase and endonuclease ZRANB3
36	ZDH13_ARATH Probable protein S-acyltransferase 4
3/	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
39	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
40	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
41	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
42	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
43 44	YSL7_ARATH Probable metal-nicotianamine transporter YSL7
45	YBEG_SCHPO Uncharacterized WD repeat-containing protein C17D11.16
46	Y5614_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g56140
47	Y5566_ARATH Uncharacterized protein At5g65660
48 49	Y5436_ARATH MATH domain-containing protein At5g43560
50	Y5344_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g53440
51	Y4844_ARATH Uncharacterized protein At4g28440
52	Y4759_ARATH WEB family protein At4g27595, chloroplastic
53 54	Y4391_ARATH Probable receptor-like protein kinase At4g39110
55	Y3272_ARATH Kelch repeat-containing protein At3g27220
56	Y2559_ARATH Receptor-like serine/threonine-protein kinase At2g45590
57	Y1839_ARATH Probable serine/threonine-protein kinase At1g18390
58 50	XPP1_MOUSE Xaa-Pro aminopeptidase 1
60 60	WRK74_ARATH Probable WRKY transcription factor 74
	VSR3_ARATH Vacuolar-sorting receptor 3
	VEP1_ARATH 3-oxo-Delta(4,5)-steroid 5-beta-reductase
---	---
	CAMK3_ARATH CDPK-related kinase 3
	UPL4_ARATH E3 ubiquitin-protein ligase UPL4
	UFD1_DICDI Ubiquitin fusion degradation protein 1 homolog
	UBC4_SOLLC Ubiquitin-conjugating enzyme E2-17 kDa
	UBA5_ARATH Ubiquitin-like modifier-activating enzyme 5
)	UB12L_ARATH Probable NEDD8-conjugating enzyme Ubc12-like
	TSJT1_TOBAC Stem-specific protein TSJT1
	C78A5_ARATH Cytochrome P450 78A5
	TPR3_ARATH Topless-related protein 3
	TPL_ARATH Protein TOPLESS
	THIK1_ARATH 3-ketoacyl-CoA thiolase 1, peroxisomal
	TF29_SCHPO Transposon Tf2-9 polyprotein
	TBB1_DAUCA Tubulin beta-1 chain (Fragment)
	BRXL4_ARATH Protein Brevis radix-like 4
	SYV_ARATH ValinetRNA ligase
	BRE1A_ARATH E3 ubiquitin-protein ligase BRE1-like 1
	BOB2_ARATH Protein BOBBER 2
	SWET4_ARATH Bidirectional sugar transporter SWEET4
	STS1_ARATH Strictosidine synthase 1
	SRPK_PHYPO Serine/threonine-protein kinase SRPK
	SR45A_ARATH Serine/arginine-rich splicing factor SR45a
	SPY_ARATH Probable UDP-N-acetylglucosaminepeptide N-acetylglucosaminyltransferase SPINDLY
	SPL7_ARATH Squamosa promoter-binding-like protein 7
	SOT5_ARATH Cytosolic sulfotransferase 5
	SFH14_ARATH Phosphatidylinositol/phosphatidylcholine transfer protein SFH14
	SF3B1_XENLA Splicing factor 3B subunit 1
	SERC3_PONAB Serine incorporator 3
	BH129_ARATH Transcription factor bHLH129
	BGL13_ARATH Beta-glucosidase 13
	BCS1B_DICDI Probable mitochondrial chaperone BCS1-B
	RS92_ARATH 40S ribosomal protein S9-2
	BBX21_ARATH B-box zinc finger protein 21
	BBX19_ARATH B-box zinc finger protein 19
	BAHD2_ARATH BAHD acyltransferase At3g29680
	RRP8_ARATH Ribosomal RNA-processing protein 8
	AVP1_ARATH Pyrophosphate-energized vacuolar membrane proton pump 1
	RNS1_ARATH Ribonuclease 1
	RNG1A_ARATH Putative E3 ubiquitin-protein ligase RING1a
	RLA02_ARATH 60S acidic ribosomal protein P0-2
	RL372_ARATH 60S ribosomal protein L37-2
	ATPG3_ARATH ATP synthase subunit gamma, mitochondrial
	ATPG3_ARATH ATP synthase subunit gamma, mitochondrial
	ATPG3_ARATH ATP synthase subunit gamma, mitochondrial
	RL222_ARATH 60S ribosomal protein L22-2
	RING2_ARATH E3 ubiquitin-protein ligase At1g63170
	RHA2B_ARATH Probable E3 ubiquitin-protein ligase RHA2B
	IRGP2 ARATH UDP-arabinopyranose mutase 2

1	
2	RGAP5_ARATH Rho GTPase-activating protein 5
3	RF4_ARATH Putative E3 ubiquitin-protein ligase RF4
4	REF6_ARATH Lysine-specific demethylase REF6
6	RECA3_ARATH DNA repair protein recA homolog 3, mitochondrial
7	RBPS2_MOUSE RNA-binding protein with multiple splicing 2
8	RB47B_ARATH Polyadenylate-binding protein RBP47B
9	RB45A_ARATH Polyadenylate-binding protein RBP45A
10 11	AB2A ARATH ABC transporter A family member 2
12	PYRG DICDI CTP synthase
13	AB19B ARATH ABC transporter B family member 19
14	PXL1 ARATH Leucine-rich repeat receptor-like protein kinase PXL1
15 16	PUB35 ARATH U-box domain-containing protein 35
10	PUB30 ARATH U-box domain-containing protein 30
18	PTBP3 ARATH Polypyrimidine tract-binding protein homolog 3
19	PSI 4 ARATH Glucosidase 2 subunit beta
20	ATML1 ARATH Homeobox-leucine zinner protein MERISTEM L1
21	ATI 49 ARATH Putative RING-H2 finger protein ATI 49
23	1/339 ARATH 1/2-3-2-like protein GE1/ mu
24	PR10A ARATH Pre-mRNA processing factor 10 homolog 1
25	PPD4 ARATH PshP domain containing protein 4 chloroplastic
26 27	POL 5 DROME Potrovirus related Pol polymetain from transposon onus
27	PLV12 ADATU Probable restate lyace 12
29	PLY12_ARATH Plobable pectate lyase 12 DIS1_ADATH CDD disculokuseral_inspital 2 releanhatidultransformers 1
30	ATDUO ADATU Hemereken lenging singer metein ATUD 0
31	A I BH9_AKA I H Homeobox-leucine zipper protein A I HB-9
32 33	
34	PHGIB_DICDI Putative phagocytic receptor 16
35	PDCB3_ARATH PLASMODESMATA CALLOSE-BINDING PROTEIN 3
36	PAILI_ARATH Patellin-I
3/ 38	PABP2_ARATH Polyadenylate-binding protein 2
39	P4H/_ARATH Probable prolyl 4-hydroxylase /
40	P2A10_ARATH Protein PHLOEM PROTEIN 2-LIKE A10
41	ASPL2_ARATH Aspartic proteinase-like protein 2
42	ASPG2_ARATH Protein ASPARTIC PROTEASE IN GUARD CELL 2
45 44	OP162_ARATH Outer envelope pore protein 16-2, chloroplastic
45	OMT1_ARATH Flavone 3'-O-methyltransferase 1
46	OE64M_ARATH Outer envelope protein 64, mitochondrial
47	ASK21_ARATH SKP1-like protein 21
48 40	ARP_ARATH Apurinic endonuclease-redox protein
50	NRP2_ARATH NAP1-related protein 2
51	NOVA1_RAT RNA-binding protein Nova-1 (Fragment)
52	NIP51_ARATH Probable aquaporin NIP5-1
53	NGDN_HUMAN Neuroguidin
54 55	NFYB9_ARATH Nuclear transcription factor Y subunit B-9
56	NAT6_ARATH Nucleobase-ascorbate transporter 6
57	NACA4_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 4
58	NAC78_ARATH NAC domain-containing protein 78
59 60	MYB46_ARATH Transcription factor MYB46
	MYB40_ANTMA Myb-related protein 340

1	
2	MIZ1_ARATH Protein MIZU-KUSSEI 1
3	MHCKB_DICDI Myosin heavy chain kinase B
4 5	MES10_ARATH Methylesterase 10
6	MDAR4_ARATH Probable monodehydroascorbate reductase, cytoplasmic isoform 4
7	MD33A_ARATH Mediator of RNA polymerase II transcription subunit 33A
8	MCU_MOUSE Calcium uniporter protein, mitochondrial
9 10	MAP21_ARATH Methionine aminopeptidase 2A
10	MAOP2_ARATH NADP-dependent malic enzyme 2
12	M3K3_ARATH Mitogen-activated protein kinase kinase kinase 3
13	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
14	M310 ARATH Uncharacterized mitochondrial protein AtMg00310
15 16	ARID4 ARATH AT-rich interactive domain-containing protein 4
17	LPAI ARATH Phospholipase A I
18	LORF2 HUMAN LINE-1 retrotransposable element ORF2 protein
19	LORF2 HUMAN LINE-1 retrotransposable element ORF2 protein
20	LAG11 ARATH LAG1 longevity assurance homolog 1
21 22	KRR1 SCHPO KRR1 small subunit processome component homolog
23	KN12A ARATH Kinesin-like protein KIN12A
24	KIF4A HUMAN Chromosome-associated kinesin KIF4A
25	KII 47 II 47 _
26 27	KITOD_KAT Kincsin-like protein KITTOD
27 28	KDSB_ARATH 5-deoxy-mainto-octutosonate cytrdytytitalisterase, innochondriat
29	KCOT_ARATH Two-pole polassium channel T
30	ICL ADATH Zing finger protein IACCED like
31	JGL_ARATH Zinc Higer protein JAGGED-like
32 33	
34	HUA2_ARATH ENHANCER OF AG-4 protein 2
35	HOX9_ORYSI Homeobox-leucine zipper protein HOX9
36	HENI_ARATH Small RNA 2'-O-methyltransferase
3/ 38	AOX4_ARATH Ubiquinol oxidase 4, chloroplastic/chromoplastic
39	HAK12_ORYSJ Putative potassium transporter 12
40	H2A7_ARATH Probable histone H2A.7
41	H2A4_WHEAT Histone H2A.4
42 42	GUN12_ARATH Endoglucanase 12
43 44	GRXC6_ARATH Glutaredoxin-C6
45	4HPT_ARATH 4-hydroxybenzoate polyprenyltransferase, mitochondrial
46	GET3_ASPOR ATPase get3
47	GDL28_ARATH GDSL esterase/lipase At1g71250
48 40	GCNT7_HUMAN Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7
49 50	GAT25_ARATH GATA transcription factor 25
51	ALFL6_ARATH PHD finger protein ALFIN-LIKE 6
52	ALFL6_ARATH PHD finger protein ALFIN-LIKE 6
53	ALF5_ARATH MATE efflux family protein ALF5
54 55	FBL30_ARATH F-box/LRR-repeat protein At1g48400
55 56	FBK77 ARATH F-box/kelch-repeat protein At3g61590
57	FBK54 ARATH F-box/kelch-repeat protein At3g13680
58	FBD34 ARATH Putative FBD-associated F-box protein At1g05080
59 60	FBD19 ARATH Putative FBD-associated F-box protein At5g50270
00	FAP3 ARATH Fatty-acid-binding protein 3

1	
2	FAAA_HUMAN Fumarylacetoacetase
3 1	F16P2_BRANA Fructose-1,6-bisphosphatase, cytosolic
+ 5	EXOS7_DICDI Putative exosome complex exonuclease RRP42
6	EXOS7_DICDI Putative exosome complex exonuclease RRP42
7	AIR3_ARATH Subtilisin-like protease SBT5.3
8	ERS2_ARATH Ethylene response sensor 2
9 10	ERS1_ARATH Ethylene response sensor 1
11	AHP2_ARATH Histidine-containing phosphotransfer protein 2
12	AHK5_ARATH Histidine kinase 5
13	AGL18_ARATH Agamous-like MADS-box protein AGL18
14 15	EDR1_ARATH Serine/threonine-protein kinase EDR1
16	AGD5_ARATH Probable ADP-ribosylation factor GTPase-activating protein AGD5
17	DRL29_ARATH Probable disease resistance protein At4g33300
18	DRL29_ARATH Probable disease resistance protein At4g33300
19	ADSL3 ARATH Delta-9 desaturase-like 3 protein
20 21	DOF58 ARATH Dof zinc finger protein DOF5.8
22	DNJ21 ARATH DnaJ protein ERDJ2A
23	2A5I ARATH Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota isoform
24	SPL5 ARATH Squamosa promoter-binding-like protein 5
25 26	CDC21 ARATH Cell division cycle 20.1, cofactor of APC complex
27	GALK1 ARATH Galactokinase
28	YTX2 XENLA Transposon TX1 uncharacterized 149 kDa protein
29	SPL9 ARATH Squamosa promoter-binding-like protein 9
30 31	SPL2 ARATH Squamosa promoter-binding-like protein 2
32	SPL11 ARATH Squamosa promoter-binding-like protein 11
33	SPL10 ARATH Squamosa promoter-binding-like protein 10
34	COPIA DROME Copia protein
35 36	LEUNG ARATH Transcriptional corepressor LEUNIG
30 37	SPB1 EMENI AdoMet-dependent rRNA methyltransferase spb1
38	AAPC_CENCI Putative glucose-6-phosphate 1-epimerase
39	CDPK3 ARATH Calcium-dependent protein kinase 3
40 41	C724B_ORVSI Cytochrome P450 724B1
41 42	THCAS CANSA Tetrahydrocannabinolic acid synthase
43	MV122 ARATH Transcription factor MVB122
44	$\frac{MT122}{MCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$
45 46	PERK9 ARATH Proline-rich recentor-like protein kinase PERK9
46 47	SPL 6 ARATH Squamosa promoter-binding-like protein 6
48	ADEH ADATH Auvin response factor 8
49	RH077 ARATH Transcription factor bHI H77
50	ZDH14 ARATH Probable protein S acultransferase 14
51 52	GR\$13 ARATH Monothial glutaredoxin \$13
53	V1524 APATH Probable LPP recentor like serine/threening protein kingse At1g52420
54	VINA SCHPO Uncharacterized AAA domain containing protain C24D10 100
55	UTD11 ADATU Drehekle U2 amell guelesler DNA sessesisted gratein 11
56 57	SND27 MOUSE 14/16 15 small nucleon rikenveleensetein 27 hDe metein
58	SINK2/_WOUSE 04/00.05 Small nuclear ribonucleoprotein 2/ KDa protein
59	DNUV1_ADATU Dutativa riharualaasa U matain Atla (5750
60	KNHA1_AKA1H Putative ribonuclease H protein At1g65/50 NOSID_DROME Nitrie enite enotherer is the state of the state o
	NUSIP_DROME NITRIC oxide synthase-interacting protein homolog

1

e,

2	MES14_ARATH Putative methylesterase 14, chloroplastic
3	GLRX_SOLLC Glutaredoxin
4	YJNA SCHPO Uncharacterized AAA domain-containing protein C24B10.10c
5	SKIP6_ARATH F-box/kelch-repeat protein SKIP6
0 7	PDI22 ARATH Protein disulfide isomerase like 2-2
8	EDV.68 ADATH Dutativa E boy/kalah rapaat protain At2x2/610
9	EDL 5 AD ATLL Detations E har / EDD/LDD remost martain Atla 22000
10	FDL5_ARATH Putative F-box/FBD/LKR-repeat protein At1g22000
11	TPST_ARATH Protein-tyrosine sulfotransferase
12	AX15A_SOYBN Auxin-induced protein 15A
13	RNHX1_ARATH Putative ribonuclease H protein At1g65750
14 15	GIN1_MACFA Gypsy retrotransposon integrase-like protein 1
15	FBL60_ARATH F-box/LRR-repeat protein At3g58940
17	FBK64 ARATH Putative F-box/kelch-repeat protein At3g20710
18	FB168 ARATH F-box protein At3g20690
19	SPL15_ARATH Squamosa promoter-binding-like protein 15
20	SPL15_ARATH Squamosa promoter binding-like protein 15
21	SPI 11 APATH Squamosa promoter hinding like protein 11
22	DNILV1 ADATH Dutative ribervelesse U protein At166750
24	NNRA1_ARATH Putative Hoonuclease H protein At1g05750
25	PP432_ARATH Pentatricopeptide repeat-containing protein At5g55840
26	RL281_ARATH 60S ribosomal protein L28-1
27	ALN_ARATH Allantoinase
28	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
29 30	Y4200_ARATH Uncharacterized protein At4g02000
31	RNHX1_ARATH Putative ribonuclease H protein At1g65750
32	PRP4_SCHPO Serine/threonine-protein kinase prp4
33	PP142 ARATH Pentatricopeptide repeat-containing protein At2g01860
34	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
35	POL3 DROME Retrovirus-related Pol polyprotein from transposon 17.6
37	POL3 DROME Retrovirus-related Pol polyprotein from transposon 17.6
38	MVP_CVI_CV_Putative movement protein
39	MCM8 APATH Probable DNA haliaasa MCM8
40	MCM6_ARATH Flobable DIVA lielicase MCM8
41	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
42 43	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
44	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
45	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
46	HSP72_SOLLC Heat shock cognate 70 kDa protein 2
47	EF2_BETVU Elongation factor 2
48	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
49 50	CYSD1_ARATH Bifunctional L-3-cyanoalanine synthase/cysteine synthase D1
50	CSP4 ARATH Cold shock domain-containing protein 4
52	CCD1 ARATH Carotenoid 9,10(9' 10')-cleavage dioxygenase 1
53	CAAT5 ARATH Cationic amino acid transporter 5
54	THRC1_ARATH Threonine synthase 1_chloroplastic
55 56	TBC25 HUMAN TBC1 domain family member 25
57	SMD2 DROME Probable small nuclear ribonucleoprotain Sm D2
58	DIC5 ADATH Drofoldin A inhibited avening avelocitide aveloge are to in 5
59	DIGS_AKATI Dieleium A-innoneu guanne nucleonde-exchange protein 5
60	K18AL_AKATH 60S ribosomal protein L18a-like protein
	K18A2_AKATH 60S ribosomal protein L18a-2

1	
2	PP323_ARATH Pentatricopeptide repeat-containing protein At4g19191, mitochondrial
3	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
4 5	AAPC_CENCI Putative glucose-6-phosphate 1-epimerase
6	PAD4_ARATH Lipase-like PAD4
7	ASA1_ORYSI Anthranilate synthase alpha subunit 1, chloroplastic
8	MGST3_MOUSE Microsomal glutathione S-transferase 3
9	LORF2 MOUSE LINE-1 retrotransposable element ORF2 protein
10 11	APC1 ARATH Anaphase-promoting complex subunit 1
12	APC1 ARATH Anaphase-promoting complex subunit 1
13	GLTB2 ARATH Ferredoxin-dependent glutamate synthase 2, chloroplastic
14	GLTB2 ARATH Ferredoxin-dependent glutamate synthase 2. chloroplastic
15 16	DNJC2 BOVIN DnaJ homolog subfamily C member 2
17	CLE11 ARATH CLAVATA3/ESR (CLE)-related protein 11
18	RH31 ARATH DEAD-box ATP-dependent RNA helicase 31
19	PRS7A ARATH 26S protease regulatory subunit 7 homolog A
20	PP181 ARATH Pentatricopentide repeat-containing protein At2g33680
21	APGM_PVRAF 2 3-bisphosphoglycerate-independent phosphoglycerate mutase
23	SPL 5 ARATH Squamosa promoter-binding-like protein 5
24	ARG7_VIGRR Indole-3-acetic acid-induced protein ARG7
25	EDI 5 ARATH Putative E-box/EBD/I RR-repeat protein At1g22000
26	EPD40 APATH FPD associated E box protein At/g10400
27	V5929 ADATH Drobably inactive louging rich report recenter like protein kingse At5g49290
29	LIDD12 ADATH Libiquitin corboxyl terminal hydrologo 12
30	UBP15_AKATH Ublquith carboxyl-terminal hydrolase 15
31	TDS1_DRANA Thioming higger that is higger than a structure DTU1, shippen lastic
32 33	STU 1 AD ATU Drateir STICUEL like 1
34	STILL_ARATH Protein STICHEL-like I
35	SKKI_AKATH Serrate KINA effector molecule
36	REV_ARATH Homeobox-leucine zipper protein REVOLUTA
37 38	ATK2_ARATH Kinesin-2
39	PP210_ARATH Pentatricopeptide repeat-containing protein At3g03580
40	PP11/_ARATH Pentatricopeptide repeat-containing protein At1g/3400, mitochondrial
41	PME44_ARATH Probable pectinesterase/pectinesterase inhibitor 44
42	PHF1_ARATH SEC12-like protein 1
43 44	ASPG1_ARATH Protein ASPARTIC PROTEASE IN GUARD CELL 1
45	GSTUD_ARATH Glutathione S-transferase U13
46	DYAD_ARATH Protein DYAD
47	PP223_ARATH Putative pentatricopeptide repeat-containing protein At3g11460
48 49	PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
50	PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
51	MBOA1_ARATH Lysophospholipid acyltransferase 1
52	FUT2_ARATH Fucosyltransferase 2
53 54	FBL41_ARATH F-box/LRR-repeat protein At3g03030
55	DOF25_ARATH Dof zinc finger protein DOF2.5
56	DNJB1_MOUSE DnaJ homolog subfamily B member 1
57	NAC69_ARATH NAC domain-containing protein 69
58 50	CDR1_ARATH Aspartic proteinase CDR1
59 60	RB47C_ARATH Polyadenylate-binding protein RBP47C
	PPK15_SCHPO Serine/threonine-protein kinase ppk15

1	
2	PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
3	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
4	Y2734_MYCBO Uncharacterized protein Mb2734
5	PP247 ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
7	PP103 ARATH Pentatricopeptide repeat-containing protein At1g64100
8	PP103 ARATH Pentatricopeptide repeat-containing protein At1g64100
9	PP103 ARATH Pentatricopeptide repeat-containing protein At1g64100
10	PP103 ARATH Pentatricopentide repeat-containing protein At1g64100
11	AROF TOBAC Phospho-2-dehydro-3-deoxybentonate aldolase 1 chloronlastic
12	EUT2 APATH Europyltransferaçe 2
14	ED228 ADATH Probable E hav protein At5a20400
15	N282 DACUD Understaniand increases DU0282
16	Y 283_BACHD Uncharacterized isomerase BH0283
1/	SYP22_ARATH Syntaxin-22
10	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
20	ASOL_BRANA L-ascorbate oxidase homolog
21	LBD25_ARATH LOB domain-containing protein 25
22	YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
23	YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
24 25	TF26_SCHPO Transposon Tf2-6 polyprotein
26	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
27	ACT12_ARATH Actin-12
28	CHX6A ARATH Cation/H(+) antiporter 6A 🚫
29	YI31B YEAST Transposon Ty3-I Gag-Pol polyprotein
30 31	YI31B YEAST Transposon Tv3-I Gag-Pol polyprotein
32	GAM1 ORYSJ Transcription factor GAMYB
33	LORF2 HUMAN LINE-1 retrotransposable element ORF2 protein
34	COPB1 ARATH Coatomer subunit beta-1
35	CKB11 ARATH Cyclin-dependent kinase B1-1
37	RHP16 SCHPO ATP-dependent helicase rhp16
38	PFK A3 ARATH ATP-dependent 6-phosphofructokinase 3
39	V4117 ARATH Putative disease resistance protein At4g11170
40	TE20 SCHPO Transnoson Tf2 0 polyprotein
41 42	EDI 40. A P A TH Putativa E box/EPD/L PP repeat protein At5a56810
43	POLY TOPAC Patrovirus related Pol polymetain from transposon TNT 1.04
44	POLA_TOBAC Retrovirus related Pol polyprotein from transposon 207
45	CAML ODVELT representation fraction CAMVD
46	GAMI_ORVELT
47 48	GAMI_ORYSJ Transcription factor GAMYB
49	MY104_ARATH Transcription factor MYB104
50	MY104_ARATH Transcription factor MYB104
51	GAM1_ORYSI Transcription factor GAMYB
52 53	GAM1_ORYSJ Transcription factor GAMYB
55 54	PCLO_HUMAN Protein piccolo
55	GAM1_ORYSI Transcription factor GAMYB
56	POL5_DROME Retrovirus-related Pol polyprotein from transposon opus
57	KAT1_ARATH Potassium channel KAT1
58 50	U74F2_ARATH UDP-glycosyltransferase 74F2
60	SUBL_ARATH Subtilisin-like protease
	JMJ25_ARATH Lysine-specific demethylase JMJ25

1	
2	CRS1_MAIZE Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
3	Y4849_ARATH Uncharacterized protein At4g18490
4	ARFP_ARATH Auxin response factor 16
6	ARFP_ARATH Auxin response factor 16
7	ARFJ_ARATH Auxin response factor 10
8	ARFQ ARATH Auxin response factor 17
9	YI31B YEAST Transposon Ty3-I Gag-Pol polyprotein
10	BH079 ARATH Transcription factor bHLH79
12	NOC2L ARATH Nucleolar complex protein 2 homolog
13	ARID6 ARATH AT-rich interactive domain-containing protein 6
14	Y1972 ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g29720
15 16	AB2A ARATH ABC transporter A family member 2
10	HSP7F ARATH Heat shock 70 kDa protein 6. chloroplastic
18	NC2B ARATH Protein Dr1 homolog
19	TRA1_YEAST Transcription-associated protein 1
20	SUBL ARATH Subtilisin-like protease
21	POK1 ARATH Phragmonlast orienting kinesin-1
23	NLTPC ARATH Non-specific lipid-transfer protein 12
24	NC100 ARATH NAC domain-containing protein 100
25	IIXS4_ARATH IDP-glucuronic acid decarboxylase 4
26 27	NC100 ARATH NAC domain-containing protein 100
28	NAC22 ARATH NAC domain-containing protein 21/22
29	NAC22_ARATH NAC domain containing protein 21/22
30	WSD1 APATH O acultransferaçe WSD1
31	WSD1_ARATH O acyltransferase WSD1
33	V/261 ADATH Drabable I DD recentor like sering/threaning protain kingse At/g26180
34	PS212 APATH 40S ribosomal protain S21.2
35	PS211 APATH 405 ribosomal protein S21-2
36 37	EDS11_ADATH Drotain EAD1 DELATED SEQUENCE 11
38	SDL 14 ADATH Squemess promotor binding like protein 14
39	NC100 ADATU NAC domain containing protain 100
40	UDD1D_WILEAT Transcription factor UDD_1b(c22)
41	DARC ARATU Protoin DA1 moloted (
42	DAR6_ARATH Protein DAT-related 6
44	NC100_ARATH NAC domain-containing protein 100
45	NAC22_ARATH NAC domain-containing protein 21/22
46	NAC98_ARATH Protein CUP-SHAPED COTYLEDON 2
47 48	NAC54_ARATH Protein CUP-SHAPED COTYLEDON I
49	PLCD4_ARATH Phosphoinositide phospholipase C 4
50	EIL3_ARATH ETHYLENE INSENSITIVE 3-like 3 protein
51	CASLI_CANSA Cannabidiolic acid synthase-like I
52 53	UGGG_ARATH UDP-glucose:glycoprotein glucosyltransferase
55	C86B1_AKATH Cytochrome P450 86B1
55	TOM91_ARATH Mitochondrial import receptor subunit TOM9-1
56	PER73_ARATH Peroxidase 73
5/ 58	MPK6_ARATH Mitogen-activated protein kinase 6
59	GAUTC_ARATH Probable galacturonosyltransferase 12
60	IG3OX3 ARATH Gibberellin 3-beta-dioxygenase 3
00	

1

	CDE2 ADATH Dechalle DNA 1-12 CDE2
2	SDE3_AKATH Probable KNA nelicase SDE3
3	ATL32_ARATH RING-H2 finger protein ATL32
4 5	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
5	LIN1 NYCCO LINE-1 reverse transcriptase homolog
7	LIN1 NYCCO LINE-1 reverse transcriptase homolog
8	POL 3 DROME Retrovirus-related Pol polyprotein from transposon 17.6
9	VTV2 VENI A Transposon TV1 uncharacterized 140 kDa protein
10	M210 AD ATH Hushers staries durits show dried protein AtMs 00210
11	MS10_ARATH Uncharacterized mitochondrial protein Attivig00310
12	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
13	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
14	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
16	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
17	M310 ARATH Uncharacterized mitochondrial protein AtMg00310
18	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
19	CLU ARATH Clustered mitochondria protein
20	PP289 ARATH Pentatricopentide repeat-containing protein At3g60960 mitochondrial
21	I PD1 APATH LOP domain containing protein 1
22	AMO AD ATH Deine and an
24	AMO_ARATH Primary amine oxidase
25	CCA34_ARATH Cyclin-A3-4
26	ARFH_ARATH Auxin response factor 8
27	FBK95_ARATH F-box/kelch-repeat protein At4g38940
28	TAF6_ARATH Transcription initiation factor TFIID subunit 6
29	NALD2 MOUSE N-acetylated-alpha-linked acidic dipeptidase 2
30 21	LORF2 HUMAN LINE-1 retrotransposable element ORF2 protein
32	ARFE ARATH Auxin response factor 6
33	ADEE ADATH Auvin response factor 6
34	ND5D1_ADATU NADU_autochromo.h5_roductoco.1
35	NDSK1_ARATH NADHcytochionie os feduciase 1
36	AGOI_ARATH Protein argonaute 1
37	AGO1_ARATH Protein argonaute 1
38 30	CAMK1_ARATH CDPK-related kinase 1
40	CAMK1_ARATH CDPK-related kinase 1
41	NFYA9_ARATH Nuclear transcription factor Y subunit A-9
42	NFYA5 ARATH Nuclear transcription factor Y subunit A-5
43	GSHRP SPIOL Glutathione reductase, chloroplastic (Fragment)
44	NFYA5_ARATH Nuclear transcription factor Y subunit A-5
45	FDI 48 ARATH Putative E-box/FBD/I RR-repeat protein At4g13965
40 47	CIDA APATH Polyadenylate binding protein interacting protein A
48	NEXA 0 A D A TH Next containing protein-interacting protein 4
49	NFYA9_ARATH Nuclear transcription factor Y subunit A-9
50	NFYA9_ARATH Nuclear transcription factor Y subunit A-9
51	NFYA2_ARATH Nuclear transcription factor Y subunit A-2
52	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
53	NFYA1_ARATH Nuclear transcription factor Y subunit A-1
54 55	NFYA1 ARATH Nuclear transcription factor Y subunit A-1
56	NFYA5 ARATH Nuclear transcription factor Y subunit A-5
57	NEYA3 ARATH Nuclear transcription factor Y subunit A-3
58	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1.04
59	CNCC6 ADATH Drobable qualic publication and an abarral 6
60	CNOCO_ANATIT Probable cyclic nucleolide-galed ion channel o
	SKPK3 HUMAN SKSF protein kinase 3

1	
2	NFYA3_ARATH Nuclear transcription factor Y subunit A-3
3	NFYA2_ARATH Nuclear transcription factor Y subunit A-2
4	NFYAA ARATH Nuclear transcription factor Y subunit A-10
5	NFYA6 ARATH Nuclear transcription factor Y subunit A-6
7	NFYA3 ARATH Nuclear transcription factor Y subunit A-3
8	NFYA3 ARATH Nuclear transcription factor Y subunit A-3
9	NFYA2 ARATH Nuclear transcription factor Y subunit A-2
10	NFYA1 ARATH Nuclear transcription factor Y subunit A-1
 12	UBC23 ARATH Probable ubiquitin-conjugating enzyme F2 23
13	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
14	NOP56 SCHPO Nucleolar protain 56
15	NOP56 HUMAN Nucleolar protein 56
16 17	NACK1_APATH Kinesin like protein NACK1
17	POLY TOPAC Patrovirus related Pol polymotein from transposon TNT 1.04
19	CK2 ADATH Drobable chaling kings 2
20	CK5_AKATH PIOUADIE CHOIME KINASE 5 DA SL. A DA TH Drotoin DDE A KINC OF A SYMMETRY IN THE STOMATAL LINEACE
21	DVDC2 VENI A CTD symthese 2
22	PYRG2_XENLA CIP synthase 2
24	PGLR_VII VI Probable polygalacturonase
25	ASPG_LUPAN Isoaspartyl peptidase/L-asparaginase
26	FB94_ARATH Putative F-box protein At2g02030
27 20	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
20 29	HAC12_ARATH Histone acetyltransferase HAC12
30	PP369_ARATH Pentatricopeptide repeat-containing protein At5g08305
31	MPK5_ARATH Mitogen-activated protein kinase 5
32	ALKBH_ARATH Alpha-ketoglutarate-dependent dioxygenase alkB
33 34	SCL27_ARATH Scarecrow-like protein 27
35	SCL15_ARATH Scarecrow-like protein 15
36	COPIA_DROME Copia protein
37	SCL15_ARATH Scarecrow-like protein 15
38	SCL6_ARATH Scarecrow-like protein 6
40	SCL27_ARATH Scarecrow-like protein 27
41	SCL22_ARATH Scarecrow-like protein 22
42	WRK70_ARATH Probable WRKY transcription factor 70
43	RQL1_ARATH ATP-dependent DNA helicase Q-like 1
44 45	PPA28_ARATH Probable inactive purple acid phosphatase 28
46	PP158_ARATH Pentatricopeptide repeat-containing protein At2g17140
47	PNCB_DROME Nicotinate phosphoribosyltransferase
48	P2C46 ARATH Probable protein phosphatase 2C 46
49 50	TT1 ARATH Protein TRANSPARENT TESTA 1
50	SYY PARUW TyrosinetRNA ligase
52	RAX3 ARATH Transcription factor RAX3
53	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
54	GLN15 ARATH Glutamine synthetase cytosolic isozyme 1-5
55 56	E135 ARATH Glucan endo-1,3-beta-glucosidase 5
57	Y4117 ARATH Putative disease resistance protein At4g11170
58	AP2 ARATH Floral homeotic protein APETALA 2
59	DGK2 ARATH Diacylglycerol kinase 2
00	TOE2 ARATH AP2-like ethylene-responsive transcription factor TOE2

1	
2	SAC4_ARATH Phosphoinositide phosphatase SAC4
3	CKS1_ORYSJ Cyclin-dependent kinases regulatory subunit 1
4 5	XPO7_CHICK Exportin-7
6	TT12_ARATH Protein TRANSPARENT TESTA 12
7	TONS_ARATH Protein TONSOKU
8	TBA OXYGR Tubulin alpha chain
9	SPE1 BRAJU Arginine decarboxylase
10	SA145 SCHPO Pre-mRNA-splicing factor sap145
12	RNP1_ARATH Heterogeneous nuclear ribonucleoprotein 1
13	PYL11 ARATH Abscisic acid recentor PYL11
14	OFP61 ARATH Outer envelope protein 61
15	MCE1 MOUSE mRNA_conning enzyme
16 17	MCE1_HUMAN mPNA_comping enzyme
17	MATEO ADATU MATE offlux fomily protoin 0
19	MATEZ ADATUMATE COL C. 1
20	MATE/_ARATH MATE efflux family protein /
21	ARID3_ARATH AT-rich interactive domain-containing protein 3
22	LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
23 24	FBK50_ARATH F-box/kelch-repeat protein At3g06240
25	FBK27_ARATH F-box/kelch-repeat protein At1g64840
26	VPS54_ARATH Vacuolar protein sorting-associated protein 54, chloroplastic
27	TF3A_HUMAN Transcription factor IIIA
28	RNHX1_ARATH Putative ribonuclease H protein At1g65750
29 30	AB6G_ARATH ABC transporter G family member 6
31	PEPK2_ARATH Serine/threonine-protein kinase PEPKR2
32	CSTF1_HUMAN Cleavage stimulation factor subunit 1
33	RBG8_ARATH Glycine-rich RNA-binding protein 8
34	TPS8_ARATH Probable alpha, alpha-trehalose-phosphate synthase [UDP-forming] 8
35 36	TOE3 ARATH AP2-like ethylene-responsive transcription factor TOE3
37	ACO1 ARATH Aconitate hydratase 1
38	Y4117 ARATH Putative disease resistance protein At4g11170
39	WRK46 ARATH Probable WRKY transcription factor 46
40 41	VIL1 ARATH VIN3-like protein 1
42	CALM4_ARATH Calmodulin-4
43	TVW1_ARATH S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase
44	C3H19 ARATH Zinc finger CCCH domain-containing protein 19
45	SDN2 ARATH Small RNA degrading nuclease 2
46 47	R\$7 BRAOL 40S ribosomal protein \$7
48	DS72 AD ATU 40S ribosomal protein S7
49	RS/5_ARATH 405 Hoosonial protein S/-5
50	R15A4_ARATH OUS HOOSOMAI protein L15a-4
51 52	PPR4/_ARATH Putative pentatricopeptide repeat-containing protein At1g1/630
52 53	PP303_ARATH Pentatricopeptide repeat-containing protein At4g04370
54	PP305_AKATH Pentatricopeptide repeat-containing protein At4g045/0
55	PGLK_VII VI Probable polygalacturonase
56	MYB39_ARATH Transcription factor MYB39
5/ 58	MFAP1_CHICK Microfibrillar-associated protein 1
50 59	HPR3_ARATH Glyoxylate/hydroxypyruvate reductase HPR3
60	GRF4_ARATH Growth-regulating factor 4
	GPDH1_ORYSJ Probable glycerol-3-phosphate dehydrogenase [NAD(+)] 1, cytosolic

1	
2	FB167_ARATH Putative F-box protein At3g20030
3	ERF93_ARATH Ethylene-responsive transcription factor 15
4	DOF47_ARATH Dof zinc finger protein DOF4.7
6	CSCL9_ARATH CSC1-like protein At1g10090
7	Y3720_ARATH UPF0481 protein At3g47200
8	C3H62_ARATH Zinc finger CCCH domain-containing protein 62
9	RLP12_ARATH Receptor-like protein 12
10	ATL45_ARATH RING-H2 finger protein ATL45
12	LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
13	SMZ ARATH AP2-like ethylene-responsive transcription factor SMZ
14	RAP27 ARATH Ethylene-responsive transcription factor RAP2-7
15 16	RAP27 ARATH Ethylene-responsive transcription factor RAP2-7
17	JAR1 ARATH Jasmonic acid-amido synthetase JAR1
18	AP2 ARATH Floral homeotic protein APETALA 2
19	PP150 ARATH Pentatricopeptide repeat-containing protein At2g13420, mitochondrial
20	FBK70 ARATH F-box/kelch-repeat protein At3g27150
22	FBK70 ARATH F-box/kelch-repeat protein At3g27150
23	YTX2 XENLA Transposon TX1 uncharacterized 149 kDa protein
24	DNMT1 ARATH DNA (cvtosine-5)-methyltransferase 1
25	DSP8 ARATH Putative dual specificity protein phosphatase DSP8
20	BGL13 ARATH Beta-glucosidase 13
28	DNMT1 ARATH DNA (cvtosine-5)-methyltransferase 1
29	YG31B YEAST Transposon Tv3-G Gag-Pol polyprotein
30 21	CHMP5 PONAB Charged multivesicular body protein 5
32	TCP4 ARATH Transcription factor TCP4
33	TCP4_ARATH Transcription factor TCP4
34	TCP4_ARATH Transcription factor TCP4
35	BOR4 ARATH Boron transporter 4
37	BOR1 ARATH Boron transporter 1
38	BOR1 ARATH Boron transporter 1
39	BGL13 ARATH Beta-glucosidase 13
40 41	JMJ19 ARATH Probable inactive lysine-specific demethylase JMJ19
42	AL221 ARATH Aldehyde dehydrogenase 22A1
43	YG31B YEAST Transposon Tv3-G Gag-Pol polyprotein
44	TF29 SCHPO Transposon Tf2-9 polyprotein
45 46	BGL15 ARATH Beta-glucosidase 15
47	YI31B YEAST Transposon Tv3-I Gag-Pol polyprotein
48	VATG2 ARATH V-type proton ATPase subunit G2
49	TF26 SCHPO Transposon Tf2-6 polyprotein
50 51	RNHX1 ARATH Putative ribonuclease H protein At1g65750
52	LORF2 MOUSE LINE-1 retrotransposable element ORF2 protein
53	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
54	AHP6 ARATH Histidine-containing phosphotransfer protein 6
55 56	Y4885 ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g08850
57	CAF2M ARATH CRS2-associated factor 2 mitochondrial
58	BRI1 SOLLC Brassinosteroid LRR receptor kinase
59	RLP12 ARATH Receptor-like protein 12
00	RLCK7 ARATH Probable serine/threonine-protein kinase RLCKVII

1	
2	PHB2_ARATH Prohibitin-2, mitochondrial
3	GRF8_ARATH Growth-regulating factor 8
4 5	FTSH8_ARATH ATP-dependent zinc metalloprotease FTSH 8, chloroplastic
6	COG5_MOUSE Conserved oligomeric Golgi complex subunit 5
7	CHX9_ARATH Cation/H(+) antiporter 9
8	ACA8_ARATH Calcium-transporting ATPase 8, plasma membrane-type
9 10	ACA10_ARATH Calcium-transporting ATPase 10, plasma membrane-type
10	TIR1_ARATH Protein TRANSPORT INHIBITOR RESPONSE 1
12	TIR1_ARATH Protein TRANSPORT INHIBITOR RESPONSE 1
13	TIR1 ARATH Protein TRANSPORT INHIBITOR RESPONSE 1
14	BH077 ARATH Transcription factor bHLH77
15 16	LIN1 NYCCO LINE-1 reverse transcriptase homolog
17	GRH1 ARATH GRR1-like protein 1
18	GRH1 ARATH GRR1-like protein 1
19	GEX1 ARATH Protein GAMETE EXPRESSED 1
20	AFB3 ARATH Protein AUXIN SIGNALING F-BOX 3
21	AFB2 ARATH Protein AUXIN SIGNALING F-BOX 2
23	AFB2 ARATH Protein AUXIN SIGNALING F-BOX 2
24	RF2_THELT Pentide chain release factor 2
25	RF2_SYNY3 Pentide chain release factor 2
20 27	PMTA_ARATH Probable methyltransferase PMT10
28	P4H12 ARATH Probable prolyl 4-hydroxylase 12
29	FGGY XENLA FGGY carbohydrate kinase domain-containing protein
30	FBX6_ARATH F-box only protein 6
31	CLSV3 ARATH SNF2 domain-containing protein CLASSV 3
33	CLSV3_ARATH SNF2 domain-containing protein CLASSV 3
34	V2172 ARATH B3 domain-containing protein At2g31720
35	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
30 37	PHSD_ARATH Probable polyamine transporter At3g19553
38	PER66 ARATH Perovidase 66
39	APS1 ARATH ATP sulfurylase 1 chloroplastic
40	AOC2 ARATH Allene oxide cyclase 2 chloroplastic
41 42	EVIS DROME Ecotropic viral integration site 5 ortholog
43	SECA1 ADATH Protein translocase subunit SECA1 chloroplastic
44	ADS1_ADATH ATD sulfurvlase 1_ablerenlastic
45	V2085 ADATH DTD/DOZ domain containing protein At2g10850
46 47	TUNE 2 AD ATU Thionin like protoin 2
48	DNULVI ADATU Dutativa rikarualaasa U reatair Atla(5750
49	RNHAI_ARATH Putative ribonuclease H protein At1g65750
50	M210 ADATH Lucheresterized mitechendrich metein AtM200210
51 52	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
53	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
54	M310_ARATH Uncharacterized mitochondrial protein AtMg00310
55	M1250_ARATH Uncharacterized mitochondrial protein AtMg01250
56 57	LAC/_AKATH Laccase-/
57 58	SU121_AKA1H Sulfate transporter 2.1
59	APS4_AKATH ATP sulturylase 4, chloroplastic
60	APS1_ARATH ATP sulturylase 1, chloroplastic
	Y 3475_ARATH Probable LRR receptor-like serine/threonine-protein kinase At3g47570

1	
2	ADNT1_ARATH Mitochondrial adenine nucleotide transporter ADNT1
3	UXS6_ARATH UDP-glucuronic acid decarboxylase 6
4	U76E6_ARATH UDP-glycosyltransferase 76E6
6	TTL3_ARATH Inactive TPR repeat-containing thioredoxin TTL3
7	C90C1_ARATH 3-epi-6-deoxocathasterone 23-monooxygenase
8	TF29_SCHPO Transposon Tf2-9 polyprotein
9	TF26_SCHPO Transposon Tf2-6 polyprotein
10	BOP1_DROME Ribosome biogenesis protein BOP1 homolog
12	SYAP_ARATH Probable alaninetRNA ligase, chloroplastic
13	SMR3_ARATH Cyclin-dependent protein kinase inhibitor SMR3
14	RSLE2 ORYSJ Zinc finger BED domain-containing protein RICESLEEPER 2
15 16	REM12 ARATH B3 domain-containing protein REM12
17	PRP39 SCHPO Pre-mRNA-processing factor 39
18	PP172 ARATH Pentatricopeptide repeat-containing protein At2g27610
19	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
20	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
21	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
23	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
24	PME17 ARATH Probable pectinesterase/pectinesterase inhibitor 17
25	PLCD1_ARATH Phosphoinositide phospholipase C 1
20	P2C54 ARATH Probable protein phosphatase 2C 54
28	MTPC4 ARATH Metal tolerance protein C4
29	MCCB_ARATH Methylcrotonovl-CoA carboxylase beta chain_mitochondrial
30	HI S1_ARATH Probable N-acetyltransferase HI S1
31	GNL1 ARATH ARF guanine-nucleotide exchange factor GNL1
33	GAGT1_ARATH Gamma-glutamyltranspentidase 1
34	FBD19 ARATH Putative FBD-associated F-box protein At5950270
35	FB20 ARATH F-box protein At1930790
30 37	FRE70 ARATH Ethylene-responsive transcription factor FRE070
38	FIF3B_TOBAC Eukarvotic translation initiation factor 3 subunit B
39	TAF1 ARATH Transcription initiation factor TFIID subunit 1
40	BGI 11 ARATH Beta-glucosidase 11
41 42	RI P12 ARATH Becenter-like protein 12
43	PP387 ARATH Receptor-like protein 12
44	PP110 ARATH Putative pentatricopentide repeat containing protein At3g13980, intochondrial
45	MKKA DICDI Mitogen activated protein kinase kinase kinase A
46 47	FILL ADATH Protein FLUODESCENT IN PLUE LIGHT abloroplastic
48	ACI 02 ADATH Agemous like MADS hav protein ACI 02
49	ACL95_ARATH Agamous like MADS hav protein ACL95
50	AGL95_AKATH Agamous-like MADS-box protein AGL95
51	DECP1 APATH Protoco De like 1 oblerentectio
52	CMTA5_ADATH Colmodulin binding transcription activator 5
54	VTV2 VENI A Transmoson TV1 uncharacterized 140 kDa mateir
55	I IAZ_AEINLA Hansposon IAT uncharacterized 149 kDa protein VTV2_VENLA Transposon TV1 uncharacterized 140 l-D. and the
56 57	Y IA2_AENLA Iransposon IA1 uncharacterized 149 KDa protein A CCU2_ADATU 1 amin acceleration and 1 accelerations have 1 accelerations
58	TDNULL AD ATU Tranin and reductors be weller. At 1 = 07440
59	TRNH1_ARATH Tropinone reductase nomolog At1g0/440
60	TCD1 ADATH Tropinone reductase nomolog At1g0/440
	ICP1_AKATH Transcription factor ICP1

1	
2	STR/_ARATH Rhodanese-like domain-containing protein /
3 1	BGAL4_ARATH Beta-galactosidase 4
5	RNE_ARATH Ribonuclease E/G-like protein, chloroplastic
6	RH21_ARATH DEAD-box ATP-dependent RNA helicase 21
7	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
8	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
9 10	LIN1_NYCCO LINE-1 reverse transcriptase homolog
11	HS902_ARATH Heat shock protein 90-2
12	HS902_ARATH Heat shock protein 90-2
13	FH10_ARATH Formin-like protein 10
14	FH10 ARATH Formin-like protein 10
15 16	EF1G1 ARATH Probable elongation factor 1-gamma 1
10	LIN1 NYCCO LINE-1 reverse transcriptase homolog
18	LIN1 NYCCO LINE-1 reverse transcriptase homolog
19	Y5162 ARATH Uncharacterized protein At5g41620
20	U73C3 ARATH UDP-glycosyltransferase 73C3
21	U73C1_ARATH UDP-glycosyltransferase 73C1
23	TRI 12 ARATH Thioredoxin-like 1-2 chloroplastic
24	TF26 SCHPO Transposon Tf2-6 polyprotein
25	SCL 33 ARATH Scarecrow like protein 33
26 27	ADALL ADATH Abaging agid 8 tangs: hudroxylage 1
27	ADAHI_ARATH Abscisic acid 8',-ilydioxylase 1
29	POLA_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
30	MAA3_ARATH Probable helicase MAGATAMA 3
31	GPICI_CAEEL G patch domain-containing protein 1 homolog
32	AGL93_ARATH Agamous-like MADS-box protein AGL93
33 34	AGL93_ARATH Agamous-like MADS-box protein AGL93
35	AGL93_ARATH Agamous-like MADS-box protein AGL93
36	DHX29_XENLA ATP-dependent RNA helicase DHX29
37	BGL19_ARATH Beta-glucosidase 19
38 30	PFPA1_ARATH Pyrophosphatefructose 6-phosphate 1-phosphotransferase subunit alpha 1
40	P5CS_SOLLC Delta-1-pyrroline-5-carboxylate synthase
41	P5CS1_ARATH Delta-1-pyrroline-5-carboxylate synthase A
42	P5CS1_ARATH Delta-1-pyrroline-5-carboxylate synthase A
43	P5CS1_ARATH Delta-1-pyrroline-5-carboxylate synthase A
44 45	MAA3_ARATH Probable helicase MAGATAMA 3
46	LAC4_ARATH Laccase-4
47	LAC4_ARATH Laccase-4
48	LAC2 ARATH Laccase-2
49 50	LAC17 ARATH Laccase-17
51	LAC17 ARATH Laccase-17
52	LAC11 ARATH Laccase-11
53	E137 ARATH Glucan endo-1.3-beta-glucosidase 7
54	CX5BL ARATH Putative cvtochrome c oxidase subunit 5b-like
55 56	RI 313 ARATH 60S ribosomal protein I 31-3
57	RL313 ARATH 60S ribosomal protein L31-3
58	VTX2 XFNI Δ Transposon TX1 uncharacterized 149 kDa protein
59	VG31B VFAST Transposon Tv3-G Gag-Pol polyprotein
60	V4177 AD ATH Uncharacterized protein A+4x17700

1	
2	CAP13_ARATH Putative clathrin assembly protein At1g25240
3	TT12_ARATH Protein TRANSPARENT TESTA 12
+ 5	SDA1_NEMVE Protein SDA1 homolog
5	RH57_ARATH DEAD-box ATP-dependent RNA helicase 57
7	LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
3	LIN1_NYCCO LINE-1 reverse transcriptase homolog
) 10	GALM_PIG Aldose 1-epimerase
10	FBL11_ARATH BTB/POZ domain-containing protein FBL11
12	EXEC1_ARATH Protein EXECUTER 1, chloroplastic
3	DRP4C_ARATH Dynamin-related protein 4C
4 5	MYO13_ARATH Myosin-13
5 6	TC120_ARATH Translocase of chloroplast 120, chloroplastic
7	SPA2 ARATH Protein SPA1-RELATED 2
8	SPA2 ARATH Protein SPA1-RELATED 2
9	SFR2 ORYSJ Beta-glucosidase-like SFR2, chloroplastic
0 1	SCP6 ARATH Serine carboxypeptidase-like 6
2	RQL4A ARATH ATP-dependent DNA helicase Q-like 4A
23	GLR36 ARATH Glutamate receptor 3.6
24	DI3L2 ARATH DIS3-like exonuclease 2
25 26	GUF1 ARATH Translation factor GUF1 homolog, mitochondrial
.0 !7	G11A ORYSI Protein kinase G11A
8	UBC24 ARATH Probable ubiquitin-conjugating enzyme E2 24
9	RHM1 ARATH Probable rhamnose biosynthetic enzyme 1
0	CSLD6 ARATH Putative cellulose synthase-like protein D6
2	VAS ARATH Lipid transfer-like protein VAS
3	BAHD1 ARATH BAHD acyltransferase At5g47980
4	PPR97 ARATH Pentatricopeptide repeat-containing protein At1g63070 mitochondrial
5	PPR93 ARATH Pentatricopeptide repeat-containing protein At1g62720
7	PPR93 ARATH Pentatricopentide repeat-containing protein At1g62720
3	PPR92 ARATH Pentatricopeptide repeat-containing protein At1g62680 mitochondrial
)	PPR 56 ARATH Pentatricopeptide repeat-containing protein At1g22000, mitochondrial
)	PPR 56 ARATH Pentatricopentide repeat-containing protein At1g22960 mitochondrial
)	PPP 30 A P A TH Pentatricopentide repeat containing protein At1g12775 mitochondrial
- 3	PPP 37 A P A TH Pentatricopentide repeat containing protein At1g12775, intochondria
ŀ	DDD 27 A D A TH Deptatricopentide repeat-containing protein At1g12620
	DDP 26 A D A TH Deptatricopentide repeat-containing protein At1g12020
	PPRS6_ARATH Pentatricopeptide repeat-containing protein At1g12300, mitochondrial
	PPR36_ARATH Pentatricopeptide repeat-containing protein At1g12300, mitochondrial
	PPR36_ARATH Pentatricopeptide repeat-containing protein At1g12300, mitochondrial
)	PPR36_ARATH Pentatricopeptide repeat-containing protein At1g12300, mitochondrial
	PPR36_ARATH Pentatricopeptide repeat-containing protein At1g12300, mitochondrial
	PPR2/_ARATH Pentatricopeptide repeat-containing protein At1g09820
ļ	PPK20_AKATH Pentatricopeptide repeat-containing protein At1g0//40, mitochondrial
	PP40/_AKATH Pentatricopeptide repeat-containing protein At5g39710
, ,	PP396_ARATH Pentatricopeptide repeat-containing protein At5g24830
	PP389_ARATH Pentatricopeptide repeat-containing protein At5g16640, mitochondrial
)	PP376_ARATH Pentatricopeptide repeat-containing protein At5g12100, mitochondrial
C	PP325_ARATH Pentatricopeptide repeat-containing protein At4g19440, chloroplastic
	PP306_ARATH Pentatricopeptide repeat-containing protein At4g11690

1	
2	PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
3	PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
4 5	PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
6	PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
7	PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
8	PP238 ARATH Putative pentatricopeptide repeat-containing protein At3g16710, mitochondrial
9	PP236 ARATH Pentatricopeptide repeat-containing protein At3g16010
10	PP236 ARATH Pentatricopeptide repeat-containing protein At3g16010
11	PP236 ARATH Pentatricopeptide repeat-containing protein At3g16010
13	PP178 ARATH Pentatricopeptide repeat-containing protein At2g31400, chloroplastic
14	PP177 ARATH Pentatricopeptide repeat-containing protein At2g30780
15	PP149 ARATH Pentatricopeptide repeat-containing protein At2g06000
10	PP133 ARATH Pentatricopentide repeat-containing protein At1g79540
18	PP130 ARATH Pentatricopentide repeat-containing protein At1g77405
19	ORC6 ARATH Origin recognition complex subunit 6
20	MCC08 ARATH MATH domain and coiled-coil domain-containing protein At2g42470
21 22	I RE_ARATH GPL-anchored protein LORELEI
23	KTNB1_ARATH Katanin p80 WD40 repeat-containing subunit B1 homolog
24	IP5P3 ARATH Type I inosital 1.4.5-trisphosphate 5-phosphatase CVP2
25	HPPD ARATH 4-hydroxynhenylnyruyate dioxygenase
26 27	ERE61 ARATH Ethylene-responsive transcription factor ERE061
28	ECA3 ARATH Calcium-transporting ATPase 3 endoplasmic reticulum-type
29	PDK ARATH [Pyruvate dehydrogenase (acetyl-transferring)] kinase mitochondrial
30	I ORE2 HUMAN LINE-1 retrotransposable element ORE2 protein
31 32	AGO2 ARATH Protein argonaute 2
33	AGO2_ARATH Protein argonaute 2
34	AGO2_ARATH Protein argonaute 2
35	COP1 ARATH F3 ubiquitin protein ligase COP1
36 37	V2088 ARATH Lincharacterized protein At2g20880
38	TGA4_ARATH Uncharacterized protein Al2g29880
39	BH070 ARATH Transcription factor bHI H70
40	RNHX1 ARATH Putative ribonuclease H protein At1g65750
41 42	PP205 A P A TH Putative nontatricopantide repeat containing protein At3c01580
43	POLY TOPAC Batravirus related Bal polymotoin from transposon TNT 1.04
44	POLX_TOPAC Retrovirus related Pol polyprotein from transposon TNT 1.04
45	DOLY_TOPAC Retrovinus-related Pol polyprotein from transposon TNT 1.04
46 47	POLX_TOPAC Retrovirus related Pol polyprotein from transposon TNT 1.94
48	A DMAD, HI IMAN, A diposente plasma membrane associated protein
49	E2204 AD ATH LIDE0725 protoin EMD2204
50	DECE1 AD A TH DNA nolymorose engilen estelytic subunit A
51	DNU40 A DA TH Changrong protoin dng L40
53	DADL ADATH Dagig blue protein
54	DADL_ARATH Dask olde plotelli DADC1_ARATH Dask olde plotelli DADC1_ARATH Dask olde plotelli
55 56	DIE1 HUMAN ATP dependent DNA beliege DIE1
50 57	ASO TOBAC L accorbate oxidase
58	IAC12 ARATH Lacesse 12
59	DRIPH ARATH Probable F3 ubiquitin protein liques DRIDU
60	YR35 ARATH Dutative E3 ubiquitin protein ligase VRAT25
	I uauve Lo uoiquiui-piotein iigase ADA155

1	
2	STP4_ARATH Sugar transport protein 4
3	SMBP2_RAT DNA-binding protein SMUBP-2
4	RS261_ARATH 40S ribosomal protein S26-1
6	BAHD2_ARATH BAHD acyltransferase At3g29680
7	RNHX1_ARATH Putative ribonuclease H protein At1g65750
8	RL5_CUCSA 60S ribosomal protein L5
9	RECG SYNY3 ATP-dependent DNA helicase RecG
10 11	RBK2 ARATH Receptor-like cytosolic serine/threonine-protein kinase RBK2
12	PPDK1 ARATH Pyruvate, phosphate dikinase 1, chloroplastic
13	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
14	PHO13 ARATH Phosphate transporter PHO1 homolog 3
15 16	PDCB2 ARATH PLASMODESMATA CALLOSE-BINDING PROTEIN 2
10	PARG2_ARATH Probable poly(ADP-ribose) glycohydrolase 2
18	M310 ARATH Uncharacterized mitochondrial protein AtMg00310
19	ARF2_ORYSI ADP-ribosylation factor 2
20	GOGC1_ARATH Golgin candidate 1
21	GH35_ARATH Indole-3-acetic acid-amido synthetase GH3 5
23	RI 92 ARATH 60S ribosomal protein I 9-2
24	RL92_ARATH 605 ribosomal protein L9-2
25	RL92_ARATH 605 ribosomal protein L9-2
26 27	PL 01 APATH 60S ribosomal protein L 9-1
27	PL 01 APATH 60S ribosomal protein L 9-1
29	RL91_ARATH 00S Holosonnal protein L9-1
30	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
31	FOLA ADATH Esseislin libe and in a slasten metrin 9
32 33	FLA8_ARATH Fasciclin-like arabinogalactan protein 8
34	DNAJ_METTE Chaperone protein Dnaj
35	DNAJ8_ARATH Chaperone protein dnaj 8, chloroplastic
36	DINAJ2_ARATH Chaperone protein dnaj 2
37 38	DJB14_XENLA DnaJ homolog subfamily B member 14
39	DJB13_HUMAN DnaJ homolog subfamily B member 13
40	DJB13_HUMAN DnaJ homolog subfamily B member 13
41	DIV_ANTMA Transcription factor DIVARICATA
42	DIN11_ARATH Probable 2-oxoglutarate-dependent dioxygenase DIN11
45 44	DEGP7_ARATH Protease Do-like 7
45	DAR2_ARATH Protein DA1-related 2
46	DAR1_ARATH Protein DA1-related 1
47	ACY1_PIG Aminoacylase-1
48 49	CYSKP_CAPAN Cysteine synthase, chloroplastic/chromoplastic
50	2NPD_STAAW Probable nitronate monooxygenase
51	CSLCC_ARATH Probable xyloglucan glycosyltransferase 12
52	CSE_ARATH Caffeoylshikimate esterase
53	CSE_ARATH Caffeoylshikimate esterase
55	2ABA_ORYSJ Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
56	CRS1_ARATH Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
57	CRK3_ARATH Cysteine-rich receptor-like protein kinase 3
58	CRK22_ARATH Cysteine-rich receptor-like protein kinase 22
60	CPL4_ARATH RNA polymerase II C-terminal domain phosphatase-like 4
	CPL1_ARATH RNA polymerase II C-terminal domain phosphatase-like 1

2	COQ9_XENTR Ubiquinone biosynthesis protein COQ9, mitochondrial
5	CNG19_ARATH Putative cyclic nucleotide-gated ion channel 19
ŀ	CLSY3_ARATH SNF2 domain-containing protein CLASSY 3
, ,	CLPX_AZOSB ATP-dependent Clp protease ATP-binding subunit ClpX
,	CLL5_ARATH Cullin-like protein 5
3	CLL4_ARATH Putative cullin-like protein 4
)	CLAH2 ARATH Clathrin heavy chain 2
0	CKX1 ARATH Cytokinin dehydrogenase 1
2	CKS2 ARATH Cyclin-dependent kinases regulatory subunit 2
3	ACOC ORYSJ Putative aconitate hydratase, cytoplasmic
4	CIPKH ARATH CBL-interacting serine/threonine-protein kinase 17
5	CIPKD ARATH CBL-interacting serine/threonine-protein kinase 13
7	CIPKD ARATH CBL-interacting serine/threonine-protein kinase 13
3	CIPKD ARATH CBL-interacting serine/threonine-protein kinase 13
)	CIPKD ARATH CBL interacting serine/threenine-protein kinase 13
1	CID6 ARATH Polyadenylate-binding protein-interacting protein 6
	CHX5_ARATH Cation/H(+) antiporter 5
	CHUP1 ARATH Protein CHUP1 chloronlastic
	CHUP1_ARATH Protein CHUP1_chloroplastic
	CHR9 ARATH Switch 2
	CEMA_CVAME Chloroplast anvelopa membrana protein
	CDDVE ADATH Calaium dependent protein kingen 15
	CDFKF_ARATH Calcium-dependent protein kinase 15
	CCD 4D A D A TH Corbon potchalita represent protein 4 homeolog 2
	CCR4B_ARATH Carbon catabolite repressor protein 4 nomolog 2
	ZED2_ADATH Zinc-Inger nomeodomain protein 3
	ZFP3_ARATH Zinc finger protein 3
	ZFP3_ARATH Zine finger protein 3
	ZDS_SOLLC Zeta-carotene desaturase, chloroplastic/chromoplastic
	ZDH19_ARATH Protein S-acyltransferase 8
	ZDH13_ARATH Probable protein S-acyltransferase 4
	YUID_BACSU Uncharacterized membrane protein YuiD
	YTHD2_MOUSE YTH domain-containing family protein 2
	YRP2_SYNPY Uncharacterized protein in rpcF 3'region (Fragment)
	YRDC_RAT YrdC domain-containing protein, mitochondrial
	YPTC5_CHLRE GTP-binding protein YPTC5
	YIPL6_ARATH Protein yippee-like At4g27745
	CCD11_ARATH Cyclin-D1-1
	CCD11_ARATH Cyclin-D1-1
	CCB24_ARATH Cyclin-B2-4
	YF48_SCHPO Uncharacterized WD repeat-containing protein C3H5.08c
	YCF1_CRUWA Putative membrane protein ycf1
	YBEG_SCHPO Uncharacterized WD repeat-containing protein C17D11.16
	CBSX5_ARATH CBS domain-containing protein CBSX5
	CBSX5_ARATH CBS domain-containing protein CBSX5
	Y5986 ARATH Uncharacterized protein At5g39865
	Y5902 ARATH Uncharacterized protein At5g19025
	Y5902 ARATH Uncharacterized protein At5g19025
	Y5843 ARATH Uncharacterized protein At5g08430

1	
2	Y5519_ARATH Uncharacterized protein At5g05190
3	Y5519_ARATH Uncharacterized protein At5g05190
4	Y5436_ARATH MATH domain-containing protein At5g43560
6	Y5161_ARATH Uncharacterized protein At5g01610
7	Y5126_ARATH Probable serine/threonine-protein kinase At5g41260
8	Y4849_ARATH Uncharacterized protein At4g18490
9	Y4523_ARATH Probable serine/threonine-protein kinase At4g35230
10	Y4498_ARATH Uncharacterized protein At4g04980
12	Y4409_ARATH Putative BTB/POZ domain-containing protein At4g04090
13	Y4372 ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g37250
14	Y4312 ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g31250
15 16	Y4291 ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g29180
17	Y4200 ARATH Uncharacterized protein At4g02000
18	Y4117 ARATH Putative disease resistance protein At4g11170
19	Y4117 ARATH Putative disease resistance protein At4g11170
20	Y4117 ARATH Putative disease resistance protein At4g11170
22	Y2559 ARATH Receptor-like serine/threonine-protein kinase At2g45590
23	Y2559 ARATH Receptor-like serine/threonine-protein kinase At2g45590
24	CAX2 ARATH Vacuolar cation/proton exchanger 2
25	Y2241 ARATH Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g24130
20 27	Y2048 ARATH WEB family protein At2g40480
28	V2048 ARATH WEB family protein At2g40480
29	CATB CHICK Cathensin B
30	V1839 ARATH Probable serine/threonine-protein kinase At1g18390
31 32	V1719 ARATH Probable inactive recentor kinase At1g27190
33	V1710 ARATH Probable inactive receptor kinase At1g27190
34	V1686 ARATH Uncharacterized membrane protein Atlg16860
35	V1401 ARATH Uncharacterized protein At1g04010
36 37	V1480 APATH Uncharacterized protein At1g18480
38	V1461 APATH Probable sering/threening protein kingse At1g54610
39	V1448 ADATH Uncharacterized protein At1224485
40	V1164 ADATH DTD/DOZ domain containing materia At1c01640
41	Y 1164_ARATH BTB/POZ domain-containing protein At1g01640
42 43	Y 1112_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase At1g11280
44	Y 1061_ARATH Probably inactive leucine-rich repeat receptor-like protein kinase At1g50610
45	Y 1015_ARATH Uncharacterized protein At1g01500
46	XYLI_ARATH Beta-(1,2)-xylosyltransterase
47 48	XYLI_ARATH Beta-(1,2)-xylosyltransterase
49	XYLT1_RAT Xylosyltransferase 1 (Fragment)
50	XYLL3_ARATH D-xylose-proton symporter-like 3, chloroplastic
51	XRN3_ARATH 5'-3' exoribonuclease 3
52 53	XLG2_ARATH Extra-large guanine nucleotide-binding protein 2
55	XLG2_ARATH Extra-large guanine nucleotide-binding protein 2
55	XB31_ARATH Putative E3 ubiquitin-protein ligase XBAT31
56	WUS_ARATH Protein WUSCHEL
57	WRK70_ARATH Probable WRKY transcription factor 70
58 59	WRK70_ARATH Probable WRKY transcription factor 70
60	WRK57_ARATH Probable WRKY transcription factor 57
	WRK53_ARATH Probable WRKY transcription factor 53

1	
2	WRK53_ARATH Probable WRKY transcription factor 53
3	WRK48_ARATH Probable WRKY transcription factor 48
4	WRK47 ARATH Probable WRKY transcription factor 47
5	WRK25 ARATH Probable WRKY transcription factor 25
7	WRK13 ARATH Probable WRKY transcription factor 13
8	WOX5 ARATH WUSCHEL-related homeobox 5
9	WOX3_ARATH WUSCHEL-related homeobox 3
10	WIT1 ARATH WPP domain-interacting tail-anchored protein 1
11 12	WIP3 ARATH WPP domain interacting protein 3
12	VTI12 ADATH Veriale transport v SNADE 12
14	VIII5_ARATH Vesicle transport v-SNARE 15
15	VIIII_ARATH Vesicle transport V-SNARE II
16	VP3/2_ARATH Vacuolar protein-sorting-associated protein 3/ homolog 2
17	VP281_ARATH Vacuolar protein sorting-associated protein 28 homolog 1
10 19	VP26A_ARATH Vacuolar protein sorting-associated protein 26A
20	VICTR_ARATH Protein VARIATION IN COMPOUND TRIGGERED ROOT growth response
21	VATA_CYACA V-type proton ATPase catalytic subunit A
22	VAR3_ARATH Zinc finger protein VAR3, chloroplastic
23	VAL1_ARATH B3 domain-containing transcription repressor VAL1
24 25	VA727_ARATH Vesicle-associated membrane protein 727
26	VA725_ARATH Vesicle-associated membrane protein 725
27	VA725_ARATH Vesicle-associated membrane protein 725
28	VA0E2_ARATH V-type proton ATPase subunit e2
29	CALS3_ARATH Callose synthase 3
30	UKL1_ARATH Uridine kinase-like protein 1, chloroplastic
32	UGHY_ARATH (S)-ureidoglycine aminohydrolase
33	UBP15 ARATH Ubiquitin carboxyl-terminal hydrolase 15
34	UBC14 ARATH Ubiquitin-conjugating enzyme E2 14
35 36	U80A2 ARATH Sterol 3-beta-glucosyltransferase UGT80A2
37	U80A2 ARATH Sterol 3-beta-glucosyltransferase UGT80A2
38	U71B5 ARATH UDP-glycosyltransferase 71B5
39	U71B2 ARATH UDP-glycosyltransferase 71B2
40 41	CAF1G ARATH Probable CCR4-associated factor 1 homolog 7
42	TYDP2_XENTR_Tyrosyl-DNA_phosphodiesterase 2
43	TT16_ARATH Protein TRANSPARENT TESTA 16
44	TT16_ARATH Protein TRANSPARENT TESTA 16
45	TT12_ARATH Protein TRANSPARENT TESTA 12
40	CAAT4 ARATH Cationic amino acid transporter 4 vacuolar
48	C98A8 ARATH Cytochrome P/50 98A8
49	COOD1 ARATH 3 eni 6 deovocathasterone 23 monoovygenase
50	C9001_ARATH 5-cpi-6-deoxocatilasteroite 25-monooxygenase
51	TD A 1. VEAST Transprintion according to 1
53	TRAT_TEAST Transcription-associated protein 1
54	TPPC8_HOMAN Trafficking protein particle complex subunit 8
55	TPPC4_BOVIN Trafficking protein particle complex subunit 4
56 57	IPPA_AKATH Trenalose-phosphate phosphatase A C2U(2) ODV017: C C2U(2) ODV017: C
57 58	C3H65_OKYSJ Zinc tinger CCCH domain-containing protein 63
59	C3H58_ARATH Zinc tinger CCCH domain-containing protein 58
60	C3H58_ARATH Zinc tinger CCCH domain-containing protein 58
	TPL_ARATH Protein TOPLESS

1	
2	C3H55_ARATH Zinc finger CCCH domain-containing protein 55
3	C3H35_ARATH E3 ubiquitin-protein ligase makorin
4 5	C2D61_ARATH C2 domain-containing protein At1g53590
6	TOM72_ARATH Mitochondrial import receptor subunit TOM7-2
7	TOM71_ARATH Mitochondrial import receptor subunit TOM7-1
8	TOM1_TOBAC Tobamovirus multiplication protein 1
9	TLP9 ARATH Tubby-like F-box protein 9
10 11	TLP2 ARATH Tubby-like F-box protein 2
12	BZP43 ARATH Basic leucine zipper 43
13	BZP43 ARATH Basic leucine zipper 43
14	BZP43 ARATH Basic leucine zipper 43
15 16	TIF5A ARATH Protein TIFY 5A
17	TIF5A ARATH Protein TIFY 5A
18	TIC ARATH Protein TIME FOR COFFEE
19	TIC ARATH Protein TIME FOR COFFEE
20	TIC22 ARATH Protein TIC 22 chloroplastic
21	THI4 ARATH Thiamine thiazole synthase chloroplastic
23	TGT2_ARATH Tribelix transcription factor GT-2
24	TGA5 ARATH Transcription factor TGA5
25	TGA3_ARATH Transcription factor TGA3
26 27	TGA21_TOBAC TGACG-sequence-specific DNA-binding protein TGA-21
28	TCP8 ARATH Transcription factor TCP8
29	TCP5_ARATH Transcription factor TCP5
30	TCP5_ARATH Transcription factor TCP5
31 32	TCP3_ARATH Transcription factor TCP3
33	TCP15_ARATH Transcription factor TCP15
34	TCP15_ARATH Transcription factor TCP15
35	TCP13_ARATH Transcription factor TCP13
36 37	TCP10_APATH Transcription factor TCP10
38	TPLO APATH Protein trichome birefringence like 0
39	TDL 20. A D A TH Protein trichome birefringenee like 20
40	TADA ADATH FIOLEIII IIICiloille olleningence-like 20
41 42	TADA_ARATH (RNA(adenine(34)) deaminase, chloroplastic
42	T184C DAT Terrer endering installer 184C
44	T184C_RAT Transmembrane protein 184C
45	1184C_RAT Transmembrane protein 184C
46	SYWC_SCHPO TryptophantKNA ligase, cytoplasmic
47 48	BRG3_ARATH Probable BOI-related E3 ubiquitin-protein ligase 3
49	BRG2_ARATH Probable BOI-related E3 ubiquitin-protein ligase 2
50	BPS1_ARATH Protein BPS1, chloroplastic
51	BPC6_ARATH Protein BASIC PENTACYSTEINE6
52 53	BPC6_ARATH Protein BASIC PENTACYSTEINE6
54	BPC2_ARATH Protein BASIC PENTACYSTEINE2
55	BON2_ARATH Protein BONZAI 2
56	SYIC_YEAST IsoleucinetRNA ligase, cytoplasmic
57 58	SYIC_MOUSE IsoleucinetRNA ligase, cytoplasmic
59	BOI_ARATH E3 ubiquitin-protein ligase BOI
60	SYFB_ARATH Probable phenylalaninetRNA ligase beta subunit
	BLH4_ARATH BEL1-like homeodomain protein 4

1	
2	BLH3_ARATH BEL1-like homeodomain protein 3
3	BLH3_ARATH BEL1-like homeodomain protein 3
4	BLH2_ARATH BEL1-like homeodomain protein 2
6	BLH2_ARATH BEL1-like homeodomain protein 2
7	SY131_ARATH Putative syntaxin-131
8	SY131_ARATH Putative syntaxin-131
9	SY131 ARATH Putative syntaxin-131
10 11	SY121 ARATH Syntaxin-121
12	SY121 ARATH Syntaxin-121
13	BL1S2 ARATH Biogenesis of lysosome-related organelles complex 1 subunit 2
14	SUVH5 ARATH Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5
15 16	SUVH3 ARATH Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3
10	SUOX ARATH Sulfite oxidase
18	SUCA1 ARATH Succinvl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial
19	STP7 ARATH Sugar transport protein 7
20	STP11 ARATH Sugar transport protein 11
21	STIL4 ARATH Protein STICHEL-like 4
23	SRS3_ARATH Protein SHI RELATED SEQUENCE 3
24	SRPR DICDI Signal recognition particle receptor subunit alpha
25	SRK2E ARATH Serine/threonine-protein kinase SRK2E
20 27	SRK2A_ARATH Serine/threonine-protein kinase SRK2A
28	SRF4_ARATH Protein STRUBBELIG-RECEPTOR FAMILY 4
29	SR45A ARATH Serine/arginine-rich splicing factor SR45a
30	SPZ5_ARATH Probable non-inhibitory serpin-Z5
32	SPT_ARATH Transcription factor SPATILIA
33	SPT16_ARATH FACT complex subunit SPT16
34	SPG1_SCHPO_Sentum-promoting GTP-binding protein 1
35	SODM1_ARATH Superoxide dismutase [Mn] 1_mitochondria]
30 37	SNF4_ARATH Sucrose nonfermenting 4-like protein
38	SMUL ARATH Suppressor of mec-8 and unc-52 protein homolog 1
39	SMG7L ARATH Protein SMG7L
40 41	SMB ARATH Protein SOMBRERO
41	SLU7 ORYST Pre-mRNA-splicing factor SLU7
43	SLAH3 ARATH S-type anion channel SLAH3
44	SLAH3_ARATH S-type anion channel SLAH3
45 46	SKIP5 ARATH F-box protein SKIP5
40 47	SKI17 ARATH F-box protein SKIP17
48	SIGA ARATH RNA polymerase sigma factor sigA
49	SIB1_ARATH Sigma factor binding protein 1_chloroplastic
50 51	SIB1_ARATH Sigma factor binding protein 1, chloroplastic
52	SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
53	SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
54	SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
55 56	SGR2 ARATH Protein STAV-GREEN 2 chloroplastic
57	SFR2_ORYSI Beta-glucosidase-like SFR2_chloroplastic
58	BH130 ARATH Transcription factor bHLH130
59	BH123 ARATH Transcription factor bHLH123
60	BH111 ARATH Transcription factor bHLH111

1	
2	BH093_ARATH Transcription factor bHLH93
3	BH055_ARATH Transcription factor bHLH55
4	BH055_ARATH Transcription factor bHLH55
5	BH047_ARATH Transcription factor bHLH47
7	BH041_ARATH Putative transcription factor bHLH041
8	BH032_ARATH Transcription factor AIG1
9	BH020_ARATH Transcription factor NAI1
10 11	BH013 ARATH Transcription factor bHLH13
12	SDF2 ARATH Stromal cell-derived factor 2-like protein
13	SD31 ARATH G-type lectin S-receptor-like serine/threonine-protein kinase SD3-1
14	SCRK1 ARATH Probable fructokinase-1
15 16	SCP22 ARATH Serine carboxypeptidase-like 22
17	SCP19 ARATH Serine carboxypeptidase-like 19
18	BGL34 ARATH Myrosinase 4
19	SCL31 ARATH Scarecrow-like protein 31
20	SCL31 ARATH Scarecrow-like protein 31
21	SCL31 ARATH Scarecrow-like protein 31
23	SAT2 ARATH Serine acetyltransferase 2
24	SAR1A ARATH GTP-binding protein SAR1A
25	SAP4_ARATH Zinc finger A20 and AN1 domain-containing stress-associated protein 4
20 27	SAC51 ARATH Transcription factor SAC51
28	SAC51_ARATH Transcription factor SAC51
29	S47A2 MOUSE Multidrug and toxin extrusion protein 2
30	S384 A PONAB Putative sodium-coupled neutral amino acid transporter 10
31 32	S384 A MOUSE Putative sodium-coupled neutral amino acid transporter 10
33	RVES ARATH Protein REVEILLES
34	RTEL 1 DROER Regulator of telomere elongation belicase 1 homolog
35	RTELI_DROEK Regulator of clonicle clongation increase it nonloiog
36 37	BELL ARATH Homeobox protein BELL homolog
38	BEE1_ARATH Transcription factor BEE 3
39	RSLE2 ORVSLZing finger BED domain_containing protein RICESLEEPER 2
40	PSI E1_OPVSI Zing finger BED domain containing protein RICESI EEDED 1
41 42	RSEET_OKTSJ Zhie Higer BED domani-containing protein RICESLEETER T
43	BAN ADATH Anthogyanidin reductorse
44	DAM7 ARATH Anthocyanidin reductase
45	DAMI/_ARATH Bela-alliylase /
46 47	DA05_ARATH BAO failing indicular chaperone regulator 5
47 48	RS195_ARATH 405 filosomal protein 519-5
49	B3G1J_ARATH Probable beta-1,3-galactosyltransferase 19
50	B2_DAUCA B2 protein
51 52	RS142_ARATH 40S ribosomal protein S14-2
52 53	RS141_ARATH 40S ribosomal protein S14-1
54	RRP2_SPIOL 30S ribosomal protein 2, chloroplastic
55	RRP2_SPIOL 30S ribosomal protein 2, chloroplastic
56 57	AXX15_SOYBN Auxin-induced protein X15
57 58	AX15A_SOYBN Auxin-induced protein 15A
59	AVT1_YEAST Vacuolar amino acid transporter 1
60	ABR1_ARATH Ethylene-responsive transcription factor ABR1
	RPD1_ARATH Protein ROOT PRIMORDIUM DEFECTIVE 1

1	
2	RNP3_SCHPO Probable ribonuclease P protein subunit 3
3	RNP1_ARATH Heterogeneous nuclear ribonucleoprotein 1
4 5	RNP1_ARATH Heterogeneous nuclear ribonucleoprotein 1
5 6	RNHX1_ARATH Putative ribonuclease H protein At1g65750
7	RNHX1 ARATH Putative ribonuclease H protein At1g65750
8	RNF14 MOUSE E3 ubiquitin-protein ligase RNF14
9	RNF12 MOUSE E3 ubiquitin-protein ligase RLIM
10	RN217 XENLA Probable E3 ubiquitin-protein ligase RNF217
11	RM06 MARPO 60S ribosomal protein I.6. mitochondrial
13	ABKC DICDI Probable serine/threonine-protein kinase abkC
14	ABI3 ARATH B3 domain containing transcription factor ABI3
15	DI E26 ADATH Drotein DALE like 26
16	DL 272 AD ATH FIOLEIN RALF-INE 20
17 18	RL275_ARATH OUS HOUSOINAI protein L27-5
19	RL2/1_ARATH 60S ribosomal protein L2/-1
20	RK6_ARATH 50S ribosomal protein L6, chloroplastic
21	RING1_GOSHI E3 ubiquitin-protein ligase RING1
22	RING1_GOSHI E3 ubiquitin-protein ligase RING1
23 24	RING1_GOSHI E3 ubiquitin-protein ligase RING1
25	RING1_ARATH E3 ubiquitin-protein ligase At1g12760
26	RIC4_ARATH CRIB domain-containing protein RIC4
27	RH37_ARATH DEAD-box ATP-dependent RNA helicase 37
28	RGLG2_ARATH E3 ubiquitin-protein ligase RGLG2
29 30	RGLG1_ARATH E3 ubiquitin-protein ligase RGLG1
31	RF2B_ORYSJ Transcription factor RF2b
32	RF2B_ORYSJ Transcription factor RF2b
33	REN1_ARATH Rho GTPase-activating protein REN1
34 35	REM20_ARATH B3 domain-containing protein REM20
36	REM20_ARATH B3 domain-containing protein REM20
37	REM20_ARATH B3 domain-containing protein REM20
38	REM17 ARATH B3 domain-containing protein REM17
39 40	RDM4 ARATH RNA-directed DNA methylation 4
40 41	RD23B ARATH Ubiquitin receptor RAD23b
42	RBM42 BOVIN RNA-binding protein 42
43	RBM38 HUMAN RNA-binding protein 38
44	RBM24 DANRE RNA-binding protein 24
45 46	RBK1 ARATH Receptor-like cytosolic serine/threonine-protein kinase RBK1
40 47	RAX3 ARATH Transcription factor RAX3
48	RAX2 ARATH Transcription factor RAX2
49	RAX2 ARATH Transcription factor RAX2
50	RANRI TORAC GTP hinding nuclear protein Ran B1
51 52	RANDI_TODAC OTT-onlding nuclear protein Ran-DT
53	PAN1B LOTIA CTP binding nuclear protein Pan1B (Fragment)
54	PAE1 APATH Dybiggo accumulation factor 1, oblerenlactic
55	DAC7 ADATH Doo like CTD kinding protoin ADAC7
56 57	DAC2A ADATH Dag related protein DADC2g
58	KAUZA_AKATH Kas-related protein KABUZa
59	KAUZA_AKATH Kas-related protein KABUZa
60	KABIB_AKATH Kas-related protein KABBID
	KA210_AKATH Ethylene-responsive transcription factor RAP2-10

1		
2	R23A1_ARATH 60S ribosomal protein L23a-1	
3	R13A4_ARATH 60S ribosomal protein L13a-4	
4 5	QWRF8_ARATH QWRF motif-containing protein 8	
6	QWRF2_ARATH QWRF motif-containing protein 2	
7	AB25G_ARATH ABC transporter G family member 25	
8	PYL3_ARATH Abscisic acid receptor PYL3	
9 10	AB17C_DANRE Alpha/beta hydrolase domain-containing protein 17C	
10	AB17C_DANRE Alpha/beta hydrolase domain-containing protein 17C	
12	PUP21_ARATH Probable purine permease 21	
13	PUMP2 ARATH Mitochondrial uncoupling protein 2	
14	PUB50 ARATH Putative U-box domain-containing protein 50	
15 16	PUB18 ARATH U-box domain-containing protein 18	
17	PTR5_ARATH Protein NRT1/ PTR FAMILY 8.2	
18	PTEN DICDI Phosphatidylinositol 3.4.5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase	
19	PSKR2 ARATH Phytosulfokine receptor 2	
20	ATL46 ARATH RING-H2 finger protein ATL46	
21	ATL 3 ARATH RING-H2 finger protein ATL 3	
23	PRN1 ARATH Pirin-1	
24	ATK3 ARATH Kinesin-3	
25	PPR65 ARATH Pentatricopentide repeat-containing protein At1g31430	
26 27	DDD65_ADATH Dentetricopentide repeat containing protein At1221420	
28	PPR 20 ARATH Pentatricopentide repeat containing protein At1g10270	
29	ATCO CPVCA Autophagy related protain 0	
30	DDD1 A DA TH Dentetricementide repeat containing protein At1g01070	
31	DD412 ADATH Pentatricopopulde repeat-containing protein At1g01970	
32 33	PP415_ARATH Pentatricopeptide repeat-containing protein At5g42510, initochondrial	
34	PP389_ARATH Pentatricopeptide repeat-containing protein At5g10040, milochondrial	
35	PP305_ARATH Pentatricopeptide repeat-containing protein At5g04810, chloroplastic	
36	PP235_ARATH Putative pentatricopeptide repeat-containing protein At3g15200	
37 38	PP230_ARATH Pentatricopeptide repeat-containing protein At3g14580, mitochondrial	
39	PP160_ARATH Pentatricopeptide repeat-containing protein At2g17525, mitochondrial	
40	PP110_ARATH Pentatricopeptide repeat-containing protein At1g69290	
41	POT2_ARATH Potassium transporter 2	
42	PORA_ARATH Protochlorophyllide reductase A, chloroplastic	
45 44	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
45	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
46	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
47	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
48 49	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
50	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
51	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
52	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94	
53	POL2_DROME Retrovirus-related Pol polyprotein from transposon 297	
54 55	PNH1_ORYSJ Protein argonaute PNH1	
56	PMTJ_ARATH Probable methyltransferase PMT19	
57	PME8_ARATH Probable pectinesterase 8	
58	PME64_ARATH Probable pectinesterase/pectinesterase inhibitor 64	
59 60	PME56_ARATH Probable pectinesterase 56	
50	PME51 ARATH Probable pectinesterase/pectinesterase inhibitor 51	

1	
2	PME16_ARATH Probable pectinesterase/pectinesterase inhibitor 16
3	PME16_ARATH Probable pectinesterase/pectinesterase inhibitor 16
4	PMA2_ARATH ATPase 2, plasma membrane-type
5	PLY12_ARATH Probable pectate lyase 12
7	PLY12 ARATH Probable pectate lyase 12
8	PLDD1 ARATH Phospholipase D delta
9	PLA15 ARATH Phospholipase A1-Igamma1, chloroplastic
10	PIRL9 ARATH Plant intracellular Ras-group-related LRR protein 9
 12	PIP27 ARATH Aquanorin PIP2-7
12	PHT21 APATH Inorganic phosphate transporter 2.1 chloroplastic
14	DHOT2 ADATH Destationin 2
15	ATCA2 ADATH Alpha astheria anhudraa 2
16	ATCA2_ARATH Alpha carbonic annydrase 2
1/ 19	PHOIS_ARATH Phosphate transporter PHOI nomolog 5
19	A I B20_ARA I H Homeobox-leucine zipper protein A I HB-20
20	PGLR3_ARATH Probable polygalacturonase At3g15720
21	PFKA3_ARATH ATP-dependent 6-phosphofructokinase 3
22	PEX14_ARATH Peroxisomal membrane protein PEX14
23	PERK5_ARATH Proline-rich receptor-like protein kinase PERK5
25	PER21_ARATH Peroxidase 21
26	PEK12_ARATH Proline-rich receptor-like protein kinase PERK12
27	PEK12_ARATH Proline-rich receptor-like protein kinase PERK12
28	PDR2_ARATH Probable manganese-transporting ATPase PDR2
29 30	AAH_ARATH Allantoate deiminase
31	PDAT1_ARATH Phospholipid:diacylglycerol acyltransferase 1
32	PAT1_ARATH Scarecrow-like transcription factor PAT1
33	PAP_CANAL Poly(A) polymerase PAPalpha
34	PAP14_ARATH Probable plastid-lipid-associated protein 14, chloroplastic
36	PAP14 ARATH Probable plastid-lipid-associated protein 14, chloroplastic
37	PAO2 ARATH Probable polyamine oxidase 2
38	P4KA1 ARATH Phosphatidylinositol 4-kinase alpha 1
39	P2C80 ARATH Probable protein phosphatase 2C 80
40 41	P2C66 ARATH Probable protein phosphatase 2C 66
42	P2C43 ARATH Probable protein phosphatase 2C 43
43	OXA1 ARATH Mitochondrial inner membrane protein OXA1
44	OSB3_ARATH Protein OSB3_chloroplastic/mitochondrial
45 46	ASPL1 ARATH Aspartic proteinase-like protein 1
47	ASPG2_ARATH Protein ASPARTIC PROTEASE IN GUARD CELL 2
48	OPA3_SCHPO_OPA3-like protein
49	OFP14 ARATH Transcription repressor OFP14
50 51	OFP14 ARATH Transcription repressor OFP14
52	OCS1_MAIZE Ocs_element_binding factor 1
53	ASHH2 ARATH Histone Jusine N methyltransferase ASHH2
54	NUD12 APATH Nudix bydrologe 12 mitochondrial
55	NTDD_ENTHA Drotoin MrnD
56 57	ADD7 ADATH Two component response resulter ADD7
58	AKK/_AKATH Two-component response regulator AKK/
59	AKK5_AKATH Two-component response regulator AKK5
60	NSA2_DICDI Ribosome biogenesis protein NSA2 homolog
	AKK16_AKATH Two-component response regulator AKR16

1	
2	ARR15_ARATH Two-component response regulator ARR15
3	ARR11_ARATH Two-component response regulator ARR11
4	NPY1_ARATH BTB/POZ domain-containing protein NPY1
6	NPR5_ARATH Regulatory protein NPR5
7	NLTL2_ARATH Non-specific lipid-transfer protein-like protein At2g13820
8	NIPA7 ARATH Probable magnesium transporter NIPA7
9	NGA4 ARATH B3 domain-containing transcription factor NGA4
10 11	NGA4 ARATH B3 domain-containing transcription factor NGA4
12	NGA1 ARATH B3 domain-containing transcription factor NGA1
13	NFYB5 ARATH Nuclear transcription factor Y subunit B-5
14	NEUR DROVI Protein neuralized
15 16	NEK2 ARATH Serine/threonine-protein kinase Nek2
10	NDUS7 ARATH NADH dehvdrogenase [ubiquinone] iron-sulfur protein 7. mitochondrial
18	NACK1_ARATH Kinesin-like protein NACK1
19	NAC8 ARATH NAC domain-containing protein 8
20	NAC8 ARATH NAC domain-containing protein 8
21	NAC8 ARATH NAC domain-containing protein 8
23	NAC86 ARATH NAC domain-containing protein 86
24	NAC7 ARATH NAC domain containing protein 7
25	NAC7_ARATH NAC domain containing protein 7
26 27	NAC7_ARATH NAC domain-containing protein 7
27	NAC/_ARATH NAC domain-containing protein /
29	NAC45_ARATH NAC domain-containing protein 45
30	NAC18_ARATH NAC domain-containing protein 18
31	NAC18_ARATH NAC domain-containing protein 18
32 33	NAATI_HUMAN N-alpha-acetyltransferase 11
34	MYBL_DICDI Myb-like protein L
35	MYB98_ARATH Transcription factor MYB98
36	MYB98_ARATH Transcription factor MYB98
37	MYB98_ARATH Transcription factor MYB98
30 39	MYB86_ARATH Transcription factor MYB86
40	MYB86_ARATH Transcription factor MYB86
41	MYB86_ARATH Transcription factor MYB86
42	MYB86_ARATH Transcription factor MYB86
43 44	MYB86_ARATH Transcription factor MYB86
45	MYB4_ORYSJ Myb-related protein Myb4
46	MYB44_ARATH Transcription factor MYB44
47	MYB44_ARATH Transcription factor MYB44
48	MYB44_ARATH Transcription factor MYB44
49 50	MYB39_ARATH Transcription factor MYB39
51	MYB06_ANTMA Myb-related protein 306
52	MTPB_ARATH Metal tolerance protein B
53	MTP12_ARATH Metal tolerance protein 12
54 55	A4GAT_MOUSE Lactosylceramide 4-alpha-galactosyltransferase
56	A4GAT_GORGO Lactosylceramide 4-alpha-galactosyltransferase (Fragment)
57	MTA70_ARATH N6-adenosine-methyltransferase MT-A70-like
58	MSL6_ARATH Mechanosensitive ion channel protein 6
59 60	MPK7 ARATH Mitogen-activated protein kinase 7
	MPK17_ARATH Mitogen-activated protein kinase 17

1	
2	MO25N_ARATH Putative MO25-like protein At5g47540
3	MNS2_ARATH Mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS2
4	ML328_ARATH MLP-like protein 328
5	ML328_ARATH MLP-like protein 328
7	ML328 ARATH MLP-like protein 328
8	ML328 ARATH MLP-like protein 328
9	MKS1 ARATH Protein MKS1
10	MKKA DICDI Mitogen-activated protein kinase kinase kinase A
11	MIRO DROMF Mitochondrial Rho GTPase
13	MGP_ARATH Zinc finger protein MAGPIF
14	MGP_ARATH Zine finger protein MAGPIE
15	METE2 ARATH 5-methyltetrahydronteroyltriglutamatehomocysteine methyltransferase 2
16 17	METE2_ARATH 5-methyltetrahydropteroyltrightamate_homocysteine methyltransferase 2
18	MEMO1 VENI A Protoin MEMO1
19	MEMOL VENI A Drotoin MEMOL
20	MEMOI_AENLA FIOTEIN MEMOI MED14 ADATH Mediator of DNA polymorogo II transprintion subunit 14
21	MED14_ARATH Mediator of RNA polymerase II transcription subunit 14
22	MD19B_ARATH Probable mediator of RNA polymerase if transcription subunit 190
24	MD15A_ARATH Mediator of RNA polymerase ii transcription subunit 15a
25	MCM6_ARATH DNA replication licensing factor MCM6
26	MCAI_ARATH Metacaspase-1
27 20	MBR2_ARATH E3 ubiquitin-protein ligase MBR2
20 29	MBF1B_ARATH Multiprotein-bridging factor 1b
30	MBD6_ARATH Methyl-CpG-binding domain-containing protein 6
31	MAD16_ORYSJ MADS-box transcription factor 16
32	MA653_ARATH 65-kDa microtubule-associated protein 3
33 34	LUL4_ARATH Probable E3 ubiquitin-protein ligase LUL4
35	LTI65_ARATH Low-temperature-induced 65 kDa protein
36	LSM6_MOUSE U6 snRNA-associated Sm-like protein LSm6
37	LPAAT_ARATH 1-acylglycerol-3-phosphate O-acyltransferase
38	LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
40	LNG2_ARATH Protein LONGIFOLIA 2
41	LK110_ARATH Putative L-type lectin-domain containing receptor kinase I.10
42	LIN1_NYCCO LINE-1 reverse transcriptase homolog
43	LBD36_ARATH LOB domain-containing protein 36
44 45	LBD29_ARATH LOB domain-containing protein 29
46	LBD29_ARATH LOB domain-containing protein 29
47	LBD27_ARATH LOB domain-containing protein 27
48	LACS3 ARATH Long chain acyl-CoA synthetase 3
49 50	KRP4 ARATH Cyclin-dependent kinase inhibitor 4
51	KRP4 ARATH Cyclin-dependent kinase inhibitor 4
52	KPRS4 ARATH Ribose-phosphate pyrophosphokinase 4
53	KPRS3 ARATH Ribose-phosphate pyrophosphokinase 3, chloroplastic
54	KPK2 ARATH Serine/threonine-protein kinase AtPK2/AtPK19
55 56	KNU ARATH Zinc finger protein KNUCKLES
57	KIPK ARATH Serine/threonine-protein kinase KIPK
58	KCS10 ARATH 3-ketoacyl-CoA synthase 10
59	KC1D ARATH Casein kinase Lisoform delta-like
00	KBAY ECOLX D-tagatose-1.6-bisphosphate aldolase subunit KbaY

1		
2	ARFD_ARATH Auxin response factor 4	
3	KAN2_ARATH Probable transcription factor KAN2	
4	KAN1_ARATH Transcription repressor KAN1	
6	KAN1_ARATH Transcription repressor KAN1	
7	KAN1_ARATH Transcription repressor KAN1	
8	JADE1 XENLA Protein Jade-1	
9	IX15L ARATH Protein IRX15-LIKE	
10	ARAE2 ARATH Putative UDP-arabinose 4-epimerase 2	
12	IPO7 HUMAN Importin-7	
13	IP5PD ARATH Type I inositol 1.4.5-trisphosphate 5-phosphatase 13	
14	IDN2 ARATH Protein INVOLVED IN DE NOVO 2	
15	IAR1 ARATH IAA-alanine resistance protein 1	
10	APRR7 ARATH Two-component response regulator-like APRR7	
18	APRR1_ARATH_Two-component response regulator-like APRR1	
19	APL ARATH Myb family transcription factor APL	
20	HMGCL ARATH Hydroxymethylglutaryl-CoA lyase mitochondrial	
21	HMDH1_ARATH 3_hvdrovy_3_methylglutaryl_coenzyme A reductase 1	
22	HMA1 ARATH Probable cadmium/zinc transporting ATPase HMA1 chloroplastic	
24	HEP1 APATH Transcription factor HEP1	
25	ADAE ADATH AD A complex subunit engilen	
26 27	AP4E_ARATH AP 4 complex subunit epsilon	
27	HEADA ODVSL Heat strong transprintion factor ADa	
29	HFA2A_OR Y SJ Heat stress transcription factor A-2a	
30	HERCI_HUMAN Probable E3 ubiquitin-protein ligase HERCI	
31	HERCI_HUMAN Probable E3 ubiquitin-protein ligase HERCI	
32 33	A DAY A DATU A D	
34	AP2M_ARATH AP-2 complex subunit mu	
35	AOPIV_ARATH Probable 2-oxoglutarate-dependent dioxygenase AOPI (Fragment)	
36	HDG8_ARATH Homeobox-leucine zipper protein HDG8	
3/	HDG/_ARATH Homeobox-leucine zipper protein HDG/	
39	HDA11_DICDI Type-1 histone deacetylase 1	
40	HAT7_ARATH Homeobox-leucine zipper protein HAT7	
41	ANP1_ARATH Mitogen-activated protein kinase kinase kinase ANP1	
42	GULDH_MYCTU L-gulono-1,4-lactone dehydrogenase	
43 44	GTL2_ARATH Trihelix transcription factor GTL2	
45	GTL2_ARATH Trihelix transcription factor GTL2	
46	GTL1_ARATH Trihelix transcription factor GTL1	
47	ANM6_ARATH Probable protein arginine N-methyltransferase 6	
48 49	GRS13_ARATH Monothiol glutaredoxin-S13	
50	GRS13_ARATH Monothiol glutaredoxin-S13	
51	GRS13_ARATH Monothiol glutaredoxin-S13	
52	GRP2_SORBI Glycine-rich RNA-binding protein 2	
53	GRF5_ARATH Growth-regulating factor 5	
54 55	GRCR1_HUMAN Glutaredoxin domain-containing cysteine-rich protein 1	
56	GPX6_ARATH Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial	
57	GLYT6_ARATH Probable glycosyltransferase At5g25310	
58	GLYR1_RAT Putative oxidoreductase GLYR1	
60	GLYR1_ARATH Glyoxylate/succinic semialdehyde reductase 1	
	AMS_ARATH Transcription factor ABORTED MICROSPORES	

2	GL13_ARATH Germin-like protein subfamily 1 member 3
i L	4CLL8_ARATH 4-coumarateCoA ligase-like 8
r D	GLD2A_DROME Poly(A) RNA polymerase gld-2 homolog A
5	GL3_ARATH Transcription factor GLABRA 3
,	GID1B_ARATH Gibberellin receptor GID1B
}	GGT1_ARATH Glutamateglyoxylate aminotransferase 1
0	GGR_ARATH Heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic
1	GGPPS_SINAL Geranylgeranyl pyrophosphate synthase, chloroplastic/chromoplastic
2	GEML7_ARATH GEM-like protein 7
}	GDPD2_ARATH Glycerophosphodiester phosphodiesterase GDPD2
	GDL71_ARATH GDSL esterase/lipase At5g03610
	GAUTB_ARATH Probable galacturonosyltransferase 11
	GATL4_ARATH Probable galacturonosyltransferase-like 4
	GATL4_ARATH Probable galacturonosyltransferase-like 4
	GAT2_ARATH Probable GABA transporter 2
	GAT21_ARATH GATA transcription factor 21
	GAT21_ARATH GATA transcription factor 21
	G3PA2_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic
	G3PA2_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic
	FZR2_ARATH Protein FIZZY-RELATED 2
	FY_ARATH Flowering time control protein FY
	FRS10_ARATH Putative protein FAR1-RELATED SEQUENCE 10
	FRO6 ARATH Ferric reduction oxidase 6
	FRO2 ARATH Ferric reduction oxidase 2
	FOLD2 ARATH Bifunctional protein FolD 2
	FLXL4 ARATH Protein FLX-like 4
	FLA21 ARATH Fasciclin-like arabinogalactan protein 21
	FLA21 ARATH Fasciclin-like arabinogalactan protein 21
	FIP2 ARATH FH protein interacting protein FIP2
	FIP1X SCHPO Pre-mRNA polyadenylation factor fip1
	FIMB5 ARATH Fimbrin-5
	FIMB2 ARATH Fimbrin-2
	FH4 ARATH Formin-like protein 4
	FH20 ARATH Formin-like protein 20
	FDL16 ARATH F-box/FBD/LRR-repeat protein At2g26030
	FDH2 ORYSJ Formate dehydrogenase 2, mitochondrial
	FBL4 ARATH F-box/LRR-repeat protein 4
	FBK95 ARATH F-box/kelch-repeat protein At4g38940
	FBK8 ARATH F-box/kelch-repeat protein At1g22040
	FBK42 ARATH Putative F-box/kelch-repeat protein At2g41360
	FBK3 ARATH Putative F-box/kelch-repeat protein At1g13200
	FBK3 ARATH Putative F-box/kelch-repeat protein At1g13200
	FBK28 ARATH F-box/kelch-repeat protein At1g67480
	FBK27 ARATH F-box/kelch-repeat protein At1g64840
	FBK27 ARATH F-box/kelch-repeat protein At1g64840
	FBK27 ARATH F-box/kelch-repeat protein At1g6/8/0
	FBD34 ARATH Putative FBD-associated E-box protein $\Delta t1 g05080$
	FB94 ARATH Putative F-box protein $\Delta t^2 g 02030$
	$\Gamma U = A A A T T T U autive T = 00A protein A (2802030)$

1	
2	FB94_ARATH Putative F-box protein At2g02030
3	FB93_ARATH F-box protein At1g80960
4	FB77_ARATH Putative F-box protein At1g67390
6	FB306_ARATH Putative F-box protein At1g26515
7	FB213_ARATH F-box protein At3g60790
8	FB184_ARATH Putative F-box protein At3g24580
9	FB182_ARATH Putative F-box protein At3g23960
10	FB126_ARATH F-box protein At2g34280
12	FAFL ARATH Protein FAF-like, chloroplastic
13	FAF2A XENLA FAS-associated factor 2-A
14	FAD1 SCHPO Probable FAD synthase
15 16	FAB1A ARATH 1-phosphatidylinositol-3-phosphate 5-kinase FAB1A
17	EZA1 ARATH Histone-lysine N-methyltransferase EZA1
18	EXP17 ARATH Putative expansin-A17
19	EXP11 ARATH Expansin-A11
20	ETR2 ARATH Ethylene receptor 2
21	ERMP1 MOUSE Endoplasmic reticulum metallopentidase 1
23	ERF86 ARATH Ethylene-responsive transcription factor ERF086
24	ERF14 ARATH Ethylene-responsive transcription factor ERF014
25	AIL 5 ARATH AP2-like ethylene-responsive transcription factor AIL 5
20 27	AIFM2 TAEGU Apontosis-inducing factor 2
28	EMEL ARATH Protein EMBRYONIC ELOWER 1
29	EMEL ARATH Protein EMBRYONIC FLOWER 1
30	EMC3 DANRE ER membrane protein complex subunit 3
31	ELES ARATH Protein EARLY ELOWERING 3
33	ELCI_APATH Protein ELC like
34	ELCE_ARATHITIOCHI ELC-like
35	AHV2 ADATH Histiding kingge 2
36	AHK2_ARATH Histidine kinase 2
38	AHK2_AKATH Histidine kinase 2
39	ACL 80 ADATU A compute like MADS have protein ACL 80
40	AOL80_ARATH Agamous-like MADS-box protein AOL80
41	EFGM2_ARATH Elongation factor G-2, mitochondrial
42 43	EFIDI_ARATH Elongation factor 1-delta 1
44	EF10/_ARATH Ethylene-responsive transcription factor ERF10/
45	EF102_ARATH Ethylene-responsive transcription factor 5
46	AGD12_ARATH ADP-ribosylation factor GTPase-activating protein AGD12
47 48	E/0A1_ARATH Exocyst complex component EXO/0A1
49	E1311_ARATH Glucan endo-1,3-beta-glucosidase 11
50	DYL1_YEAST Dynein light chain 1, cytoplasmic
51	DTC_ARATH Mitochondrial dicarboxylate/tricarboxylate transporter DTC
52	DRTS2_ARATH Bifunctional dihydrofolate reductase-thymidylate synthase 2
55 54	DRP1E_ARATH Dynamin-related protein 1E
55	DRL34_ARATH Probable disease resistance protein At5g45440
56	DRE2B_ARATH Dehydration-responsive element-binding protein 2B
57	DRB5_ARATH Double-stranded RNA-binding protein 5
эð 59	DRB3_ARATH Double-stranded RNA-binding protein 3
60	DPNP3_ARATH Probable SAL3 phosphatase
	ADK2_ARATH Adenosine kinase 2

1	
2	DOF56_ARATH Dof zinc finger protein DOF5.6
3	DOF46_ARATH Dof zinc finger protein DOF4.6
4	DOF35 ARATH Dof zinc finger protein DOF3.5
5	DOF35 ARATH Dof zinc finger protein DOF3.5
0 7	DOF25 ARATH Dof zinc finger protein DOF2.5
8	DOF18 ARATH Dof zinc finger protein DOF1 8
9	DOF18 ARATH Dof zing finger protein DOF1.8
10	DOF15_ARATH Dof zinc finger protein DOF1.5
11	DOF15_ARATH Dof zine finger protein DOF1.5
12	DNI40 ADATH Chaparana protain dna 40
14	DID12 HUMAN Dry Lhamala and family Dry and an 12
15	DJB13_HUMAN Dnaj nomolog subramily B member 13
16	ICP15_ARATH Transcription factor ICP15
17	SRO2_ARATH Probable inactive poly [ADP-ribose] polymerase SRO2
18 10	AML5_ARATH Protein MEI2-like 5
20	SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
21	DRTI_DELRE Kunitz-type serine protease inhibitor DrTI
22	DRTI_DELRE Kunitz-type serine protease inhibitor DrTI
23	SYI_TETTH IsoleucinetRNA ligase
24 25	BH087_ARATH Transcription factor bHLH87
26	GRF5_ARATH Growth-regulating factor 5
27	AB33G_ARATH ABC transporter G family member 33
28	HFR1_ARATH Transcription factor HFR1
29	Y1960_ARATH Probable serine/threonine-protein kinase At1g09600
30 31	PIP24 ARATH Probable aquaporin PIP2-4
32	CHX14 ARATH Cation/H(+) antiporter 14
33	SIB2 ARATH Sigma factor binding protein 2, chloroplastic
34 25	MAF5 ARATH Protein MADS AFFECTING FLOWERING 5
35 36	ARAD1 ARATH Probable arabinosyltransferase ARAD1
37	HDG5 ARATH Homeobox-leucine zipper protein HDG5
38	CRK41 ARATH Cysteine-rich receptor-like protein kinase 41
39	COPIA DROME Copia protein
40 41	CNGC7 ARATH Putative cyclic nucleotide-gated ion channel 7
42	YTX2 XENLA Transposon TX1 uncharacterized 149 kDa protein
43	YI31B YEAST Transposon Tv3-I Gag-Pol polyprotein
44	VI31B YEAST Transposon Ty3-I Gag-Pol polyprotein
45	VI31B VFAST Transposon Ty3-I Gag-Pol polyprotein
40 47	VI31B VEAST Transposon Ty3-I Gag-Pol polyprotein
48	VI31B_VEAST_Transposon_Ty3-I Gag_Pol polyprotein
49	VG31B_VEAST Transposon Tv3_G Gag Pol polyprotein
50	VG21P_VEAST Transposon Ty2 G Gag Pol polyprotein
51 52	V2088 ADATH Uncharacterized protein At2g20880
53	TE211 SCHDO Transposon Tf2 11 polymetain
54	DCA12 ADATH Data galacteridase 12
55	BUAI5_ARATH Bela-galaciosidase 15
56 57	KK12B_POPTK SUS filosomal protein S12-B, chloroplastic
57	POL5_DROME Retrovirus-related Pol polyprotein from transposon opus
59	POL4_DROME Retrovirus-related Pol polyprotein from transposon 412
60	POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
	POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6

-	
2	POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
3	POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
4	POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
5 6	POL3 DROME Retrovirus-related Pol polyprotein from transposon 17.6
7	POL3 DROME Retrovirus-related Pol polyprotein from transposon 17.6
8	PEX4 ARATH Protein PEROXIN-4
9	M760 ARATH Uncharacterized mitochondrial protein AtMg00760
10	M750_ARATH Uncharacterized mitochondrial protein AtMg00750
11	M310 ARATH Uncharacterized mitochondrial protein AtMg00310
12	A D1M2 A D A TH A D 1 complex subunit mu 2
14	VTV2_VENLA_Transmagen_TV1_uncharacterized_140 kDa_protain
15	POL EEV Dra Dal nationalization
16	POL_FFV Pro-Pol polyprotein
1/	RNHX1_ARATH Putative ribonuclease H protein At1g65750
10	Y1515_ARATH Uncharacterized TPR repeat-containing protein At1g05150
20	C77A4_ARATH Cytochrome P450 77A4
21	RNHX1_ARATH Putative ribonuclease H protein At1g65750
22	PRS6A_ORYSJ 26S protease regulatory subunit 6A homolog
23	POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
25	POK2_ARATH Phragmoplast orienting kinesin 2
26	MBF1A_ARATH Multiprotein-bridging factor 1a
27	LRK63_ARATH Lectin-domain containing receptor kinase VI.3
28	HASTY_ARATH Protein HASTY 1
29 30	RL313_ARATH 60S ribosomal protein L31-3
31	DNAJ2_ARATH Chaperone protein dnaJ 2
32	COPIA_DROME Copia protein
33	YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
34 35	Y2988_ARATH Uncharacterized protein At2g29880
36	VICTR_ARATH Protein VARIATION IN COMPOUND TRIGGERED ROOT growth response
37	RLK6_ARATH Receptor-like protein kinase At3g21340
37 38	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
37 38 39	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK
37 38 39 40 41	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL ARATH Uncharacterized protein At2g38710
37 38 39 40 41 42	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27 ARATH Putative FBD-associated F-box protein At5g56560
37 38 39 40 41 42 43	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16
37 38 39 40 41 42 43 44	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16
 37 38 39 40 41 42 43 44 45 46 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3
 37 38 39 40 41 42 43 44 45 46 47 	RLK6_ARATH Receptor-like protein kinase At3g21340POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94MHK_ARATH Serine/threonine-protein kinase MHKAMERL_ARATH Uncharacterized protein At2g38710FBD27_ARATH Putative FBD-associated F-box protein At5g56560AGL16_ARATH Agamous-like MADS-box protein AGL16AGL16_ARATH Agamous-like MADS-box protein AGL16CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3COPIA_DROME Copia protein
 37 38 39 40 41 42 43 44 45 46 47 48 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910
 37 38 39 40 41 42 43 44 45 46 47 48 49 52 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13
 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH Transportin-1
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH F3 ubiquitin-protein ligase BAH1
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH F3 ubiquitin-protein ligase BAH1 BAH1_ARATH F3 ubiquitin-protein ligase BAH1
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH F3 ubiquitin-protein ligase BAH1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 PAUX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 55	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH F3 ubiquitin-protein ligase BAH1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH Transportin-1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH F3 ubiquitin-protein ligase BAH1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 PUDB2_ARATH Phospholipase D beta 2
 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH Transportin-1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 PUDB2_ARATH Phospholipase D beta 2 MYB32_ARATH Transcription factor MYB32
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60	RLK6_ARATH Receptor-like protein kinase At3g21340 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 MHK_ARATH Serine/threonine-protein kinase MHK AMERL_ARATH Uncharacterized protein At2g38710 FBD27_ARATH Putative FBD-associated F-box protein At5g56560 AGL16_ARATH Agamous-like MADS-box protein AGL16 AGL16_ARATH Agamous-like MADS-box protein AGL16 CRCK3_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 3 COPIA_DROME Copia protein Y1491_ARATH Uncharacterized protein At1g04910 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 TNPO1_ARATH Transportin-1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 BAH1_ARATH E3 ubiquitin-protein ligase BAH1 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 PLD82_ARATH Phospholipase D beta 2 MYB32_ARATH F-box/LRR-repeat protein At3g60040 FBL69_ARATH F-box/LRR-repeat protein from transposon

1			
2	DF158_ARATH Putative defensin-like protein 158		
3	YODA_ARATH Mitogen-activated protein kinase kinase kinase YODA		
4	Y1561_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g56130		
5	XRCC4_ARATH DNA repair protein XRCC4		
7	TCPB BOVIN T-complex protein 1 subunit beta		
8	SYP42 ARATH Syntaxin-42		
9	RH51 ARATH DEAD-box ATP-dependent RNA helicase 51		
10	PXM16 ARATH Zinc-metallopentidase peroxisomal		
 12	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94		
12	POLY TOBAC Retrovirus related Pol polyprotein from transposon TNT 1.94		
14	POLY_TOPAC Retrovirus related Pol polyprotein from transposon TNT 1.04		
15	POLA_TOBAC Retrovirus related Pol polyprotein from transposon TNT 1-94		
16	POLA_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94		
1/	PGLK_BRANA Polygalacturonase		
10	M1810_ARATH Probable S-adenosylmethionine-dependent methyltransferase At5g38100		
20	M3K1_ARATH Mitogen-activated protein kinase kinase kinase 1		
21	KEA3_ARATH K(+) efflux antiporter 3, chloroplastic		
22	IFRH_ARATH Isoflavone reductase homolog P3		
23	HFA7A_ARATH Heat stress transcription factor A-7a		
24 25	GSTUP_ARATH Glutathione S-transferase U25		
26	GSO1_ARATH LRR receptor-like serine/threonine-protein kinase GSO1		
27	GPDL3_ARATH Glycerophosphodiester phosphodiesterase GDPDL3		
28	FUT9_ARATH Probable fucosyltransferase 9		
29 30	ALDO1_ARATH Indole-3-acetaldehyde oxidase		
31	ENDO2_ARATH Endonuclease 2		
32	DAPF_ARATH Diaminopimelate epimerase, chloroplastic		
33	BGAL9_ARATH Beta-galactosidase 9		
34	BGAL8 ARATH Beta-galactosidase 8		
36	POLX TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94		
37	OCT4 ARATH Organic cation/carnitine transporter 4		
38	MYB48 ARATH Transcription factor MYB48		
39	MYB46 ARATH Transcription factor MYB46		
40 41	MYB46 ARATH Transcription factor MYB46		
42	MYB46 ARATH Transcription factor MYB46		
43	MYB12 ARATH Transcription factor MYB12		
44	GAM1_ORYSLTranscription factor GAMYB		
45	WOX1_ARATH WUSCHEL-related homeobox 1		
47	RAA2B ARATH Res-related protein RABA2b		
48	MYB82 ARATH Transcription factor MYB82		
49	MYB82 ARATH Transcription factor MYB82		
50	MYB52_ARATH Transcription factor MYB59		
51 52	MVB46 ARATH Transcription factor MVB46		
53	MVR46_APATH Transcription factor MVR46		
54	MVD12 ADATH Transcription factor MVD12		
55	GAM1_ODVSLTranscription factor GAMVD		
56 57	WOV1 ADATH WUSCHEL related horseshow 1		
58	WUA1_AKATH WUSUHEL-related nomeobox 1 TT2_ADATH Transportation factor TT2		
59	112_AKATH Transcription factor 112		
60	POLS_DROWE Retrovirus-related Pol polyprotein from transposon opus		
	MYB59_AKATH Transcription factor MYB59		

1

2 3

1	
-	
5	
0	
/	
8	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	
10	
19	
20	
21	
22	
23	
24	
25	
26	
27	
28	
29	
30	
31	
32	
33	
34	
25	
26	
30 27	
3/	
38	
39	
40	
41	
42	
43	
44	
45	
46	
47	
48	
49	
50	
51	
51	

MYB2_PHYPA Myb-related protein Pp2					
MYB1_HORVU Myb-related protein Hv1					
MYB12_ARATH Transcription factor MYB12					
MYB12_ARATH Transcription factor MYB12					
DRL23_ARATH Putative disease resistance protein At4g10780					
DRL23_ARATH Putative disease resistance protein At4g10780					
NC100_ARATH NAC domain-containing protein 100					
NC100_ARATH NAC domain-containing protein 100					
NAC98_ARATH Protein CUP-SHAPED COTYLEDON 2					
NAC54_ARATH Protein CUP-SHAPED COTYLEDON 1					
NAC54_ARATH Protein CUP-SHAPED COTYLEDON 1					
miDNA	miRNA (log ₂ FC)			Targat gana	
------------	-----------------------------	-----------	--------------	----------------------	--
IIIININA	Cd vs. Con	Cd+MT vs.	Cd+MT vs. Cd	Target gene	
miR156c-3p	—	1.5019	—	Rsa1.0_00867.1_g0001	
miR157a-3p	1.6885	1.3531	—	Rsa1.0_01910.1_g0000	
miR158a-3p	1.0073	—	—	Rsa1.0_02387.1_g0000	
miR164a	0.93873	—	—	Rsa1.0_00387.1_g0004	
miR164a	0.93873	—	—	Rsa1.0_00166.1_g0001	
miR164c-5p	0.8825	—	—	Rsa1.0_00568.1_g0000	
miR164c-5p	0.8825	—	—	Rsa1.0_00387.1_g0004	
miR164c-5p	0.8825	—	—	Rsa1.0_00166.1_g0001	
miR172a	_		-1.0199	Rsa1.0_01063.1_g0000	
miR172a	_		-1.0199	Rsa1.0_04013.1_g0000	
miR172b-5p	-2.016	-1.4312		Rsa1.0_00289.1_g0000	
miR172c		_	-1.3389	Rsa1.0_02754.1_g0000	
miR172c	_	_	-1.3389	Rsa1.0_01063.1_g0000	
miR172c			-1.3389	Rsa1.0_04013.1_g0000	
miR172e-3p	_	<u> </u>	-1.4914	Rsa1.0_01063.1_g0000	
miR172e-3p	_	_	-1.4914	Rsa1.0_04013.1_g0000	
miR319c			-0.99209	Rsa1.0_01583.1_g0000	
miR319c		_	-0.99209	Rsa1.0_01271.1_g0000	
miR395b	-2.1303		1.6878	Rsa1.0_00493.1_g0000	
miR395b	-2.1303		1.6878	Rsa1.0_00057.1_g0001	
miR396b-3p	-1.8776	-1.059	~ –	Rsa1.0_00017.1_g0014	
miR396b-5p	0.98777		-	Rsa1.0_08220.1_g0000	
miR396b-5p	0.98777			Rsa1.0_00394.1_g0002	
miR396b-5p	0.98777			Rsa1.0_02616.1_g0000	
miR397a		1.3319	_	Rsa1.0_00328.1_g0001	
miR398b-3p	_	0.99034	1.1971	Rsa1.0_01099.1_g0000	
miR399b	-1.8885		- 7	Rsa1.0_00086.1_g0001	
miR857	1.5394	3.0215	1.4251	Rsa1.0_00015.1_g0001	
miR857	1.5394	3.0215	1.4251	Rsa1.0_01260.1_g0000	
miR858a	2.1258	1.625		Rsa1.0_51959.1_g0000	
miRn4	-2.2535	-0.91179	1.1118	Rsa1.0 00166.1 g0001	

Table S13 Differentially expressed miRNAs and their target genes derived from RNA-Seq.

Note: The positive and negative correlation between miRNA and their corresponding target is highli

2				
3	RNA-seq (log ₂ FC)			
4 5	Cd vs. Con	Cd+MT vs. Con	Cd+MT vs. Cd	
6	2.4121	2.0221	_	
7	-3.1794	-2.634		
8	1.0507	2.914	1.8552	
9	3.5749	3.3839	_	
10	1.8262	_	_	
12		_	1.4656	
13	3.5749	3.3839		
14 15	1.8262			
15 16	-1 7478	-1 9945		
17	-2.8234	-1 4861	1 3298	
18	-1 6479	-1 6359		
19		-2 1528	_2 2917	
20	_1 7/78	-2.1328	-2.2)17	
21 22	-1.7478	-1.9943	1 2 2 0 8	
23	-2.8234	-1.4801	1.5298	
24	-1./4/8	-1.9943	1 2209	
25	-2.8234	-1.4861	1.3298	
26	1.6973	1.8818		
27 29			3.1018	
20 29	5.4636	5.4859		
30	1.1928	1.4988	$- \mathbf{N}$	
31	-2.6732	-7.1352	-4.4716	
32	-1.2513	-1.5025	—	
33	-3.7998	-3.6965		
34 35	-3.834	-3.0539	_	
36	1.5489	1.778	_	
37	2.0394	2.0409	_	
38	-1.9691	-1.8008		
39 40	1.9852	2.2021		
41	1.9374		-1.1275	
42	-2.3329	-1.7899		
43	1.8262			
44				

ighted in blue and red, respectively. "-" means no signi

 Review

3	
4	
-	
5	
6	
7	
0	
0	
9	
10	
11	
11	
12	
13	
14	
1 -	
15	
16	
17	
10	
18	
19	
20	
21	
21	
22	
23	
24	
24	
25	
26	
27	
20	
28	
29	
30	
21	
31	
32	
32 33	
32 33	
32 33 34	
32 33 34 35	
32 33 34 35 36	
32 33 34 35 36 37	
32 33 34 35 36 37	
32 33 34 35 36 37 38	
32 33 34 35 36 37 38 39	
32 33 34 35 36 37 38 39 40	
32 33 34 35 36 37 38 39 40	
32 33 34 35 36 37 38 39 40 41	
 32 33 34 35 36 37 38 39 40 41 42 	
 32 33 34 35 36 37 38 39 40 41 42 43 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 44 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 46 47 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 	
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 	
32 33 35 36 37 38 39 40 41 42 43 44 45 46 47 48 950	
32 33 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50	
32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50	
32 33 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52	
32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 95 51 52 53	
32 33 34 35 37 38 37 38 39 40 41 42 43 44 45 46 47 48 950 51 52 53	
32 33 34 35 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 4	
32 33 34 35 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55	
32 33 34 35 37 38 39 40 41 42 43 44 45 47 48 49 50 52 53 54 55 56	
32 33 34 35 37 38 39 41 42 43 45 467 48 49 512 53 54 55 55 57	
32 33 34 35 36 37 38 39 40 42 44 45 46 47 48 950 52 53 54 55 56 72	

Annotation

7	Protein networked 1A	
8	Glutathione S-transferase tau 13 glutathione S-transferase (GSTU13	3)
9	NAC domain-containing protein 3 (NAC3)	ĺ
10	NAC domain containing protein 100 (NAC100)	
12	NAC domain-containing protein 3 (NAC3)	
13	NAC domain-containing protein 3 (NAC3)	
14	NAC domain containing protein 100 (NAC100)	
15	Target of early activation tagged 1 (RAP2 7)	
10	Target of early activation tagged 3 (TOE3)	
18	TUA: tubulin alpha 2 chain	
19	TOR2, tubulin alpha-2 chain	
20	TFIIIA, transcription factor IIIA	
21	larget of early activation tagged 1 (RAP2./)	
22	Target of early activation tagged 3 (TOE3)	
25 74	Target of early activation tagged 1 (RAP2.7)	
25	Target of early activation tagged 3 (TOE3)	
26	Boron transporter 1 (BOR1)	
27	DNA cytosine-5-methyltransferase 1 (MET1)	
28	Sulfate transporter 2;1 (SULTR2;1)	
29 30	Sulfate Adenylyltransferase (APS4)	
31	Homeobox protein ATH1	
32	Actin-binding FH2 (formin homology 2) family protein	
33 34	Actin-binding FH2 (formin homology 2) family protein	
35	Beta-glucosidase 44 (BGLU44)	
36	IRREGULAR XYLEM 12 (IRX12)	
37	Calcineurin-like phosphoesterase domain-containing protein	
38	NRS/ER; UDP-4-keto-6-deoxy-d-glucose-3,5-epimerase-4-reductas	se 1
40	NmrA-like negative transcriptional regulator-like protein	
41	Zinc-metallopeptidase PXM16	
42	Beta-galactosidase 8 (BGAL8)	
43	NAC100; NAC domain containing protein 100 (NAC100)	
44 45	ificant difference was found in this comparision. log ₂ FC: log ₂ fold c	
.5	· · · · · · · · · · · · · · · · · · ·	

Adenine nucleotide alpha hydrolases-like protein

Journal of Pineal Research

Table S14 Identification of DEGs invovled in ROS scavenging and signaling trans

Gene ID	log ₂ (Cd/Con)	log ₂ (Cd+MT/Con)	log ₂ (Cd+MT/Cd)
Rsa1.0_00052.1_g00025.1	1.8616	1.8557	_
Rsa1.0_05109.1_g00001.1	3.9993	3.7211	
Rsa1.0_10038.1_g00001.1	—	2.1499	
Rsa1.0_36271.1_g00001.1		2.5066	_
Rsa1.0_02737.1_g00002.1	0.80523	1.7287	0.91487
Rsa1.0_03562.1_g00001.1	-1.2158	-4.0875	-2.88
Rsa1.0_01524.1_g00004.1	1.2625	3.1761	1.9054
Rsa1.0_00054.1_g00035.1	-1.658	3.8619	5.5144
Rsa1.0_00002.1_g00012.1	0.59177	1.9641	1.3651
Rsa1.0_01561.1_g00001.1	1.1095	2.0958	0.97899
Rsa1.0_00739.1_g00008.1	1.5854	0.9204	-0.67353
Rsa1.0_00107.1_g00028.1	1.8647	0.8597	-1.0136
Rsa1.0_00151.1_g00017.1	-0.46261	1.2469	1.701
Rsa1.0_01519.1_g00007.1	-1.6352	-0.6919	0.9352
Rsa1.0_00092.1_g00070.1	-1.3803	4.307	5.6822
Rsa1.0_01519.1_g00006.1	-2.8594	-0.078157	2.7739
Rsa1.0_28556.1_g00001.1	1.0767	-3.6256	-4.7118
Rsa1.0_00344.1_g00014.1	-0.2304	1.2213	1.4431
Rsa1.0_02241.1_g00006.1	-4.1247	-2.6137	1.5027
Rsa1.0_00250.1_g00016.1	-2.3307	-0.83969	1.4826
Rsa1.0_01237.1_g00002.1	-3.0049	-1.8237	1.1749
Rsa1.0_00566.1_g00004.1	-2.7072	-3.2184	-0.52216
Rsa1.0_02343.1_g00003.1	2.0539	2.956	0.89339
Rsa1.0_05804.1_g00001.1	2.1628	1.165	-1.0067
Rsa1.0_01917.1_g00006.1	-1.574	0.39976	1.9667
Rsa1.0_00660.1_g00009.1	0.62327	3.6905	3.0588
Rsa1.0_01445.1_g00006.1	2.6108	1.0851	-1.5343
Rsa1.0_02645.1_g00002.1	5.914	4.1862	-1.7345
Rsa1.0_01004.1_g00008.1	-0.31775	1.4642	1.7737
Rsa1.0_10209.1_g00001.1	-6.2475	-2.0379	4.204
Rsa1.0_02009.1_g00004.1	-6.6122	-3.2713	3.3354
Rsa1.0_13777.1_g00001.1	-4.1973	-1.1955	2.9928
Rsa1.0_00120.1_g00037.1	0.59095	-1.7659	-2.3648
Rsa1.0_00613.1_g00008.1	-0.17/3	2.8358	3.0059
Rsa1.0_00101.1_g00034.1	0.55203	1.927	1.367
Rsa1.0_00816.1_g00007.1	-5.6125	-3.0677	2.5369
Ksa1.0_00353.1_g00001.1	2.3401	4.1/98	1.8334
Ksa1.0_1041/.1_g00001.1	1.9123	0.024635	-1.8966
$\kappa_{sa1.0}$ 51814.1 g00001.1	-2.9866	-1.290/	1.0809
Ksa1.0_03364.1_g00001.1	1.4884	4.4165	2.9224
Ksa1.0_00045.1_g00018.1	2.1813	3.498	1.30/9
Ksa1.0_00019.1_g00008.1	-2.182/	-0.0081	1.3001
$Ksa1.0_00026.1_g00056.1$	-/.3124	-11.1/1	-3.0038
$R_{sol} = 0.00122 \pm 0.0007 \pm$	5.8124	<u> </u>	2.0230
$rsa1.0_00152.1_g00007.1$	-0.0/69	-0.9/085	<u> </u>
[KSa1.0_04860.1_g00001.1	2.144/	0.55045	-1.823

1				
2	Rsa1.0_00004.1_g00030.1	-4.4524	-1.9125	2.5323
3	Rsa1.0_00838.1_g00016.1	2.4993	0.98534	-1.5226
4	Rsa1.0_00202.1_g00001.1	-7.2096	-5.6612	1.5427
5	Rsa1.0_16177.1_g00001.1	0.91966	5.7191	4.7938
7	Rsa1.0_00860.1_g00009.1	0.91906	2.6905	1.7636
8	Rsa1.0_00301.1_g00038.1	-1.5076	1.1093	2.6114
9	Rsa1.0_00632.1_g00011.1	-4.7303	-2.4206	2.3038
10	Rsa1.0_00632.1_g00013.1	-1.7827	0.61094	2.3863
12	Rsa1.0_05870.1_g00001.1	-7.8827	-6.8392	1.0342
13	Rsa1.0_00123.1_g00051.1	4.114	6.2727	2.1514
14 15	Rsa1.0_00124.1_g00045.1	1.8003	3.3648	1.5585
15	Rsa1.0_00370.1_g00005.1	2.8988	6.1657	3.26
17	Rsa1.0_02387.1_g00004.1	1.0507	2.914	1.8552
18	Rsa1.0_01072.1_g00006.1	5.7092	6.7561	1.0383
19 20	Rsa1.0_02674.1_g00001.1	2.0435	3.4971	1.4456
20				

Note: The items in blue is listed in the text.

Journal of Pineal Research

sduction.
Annotation
Auxin-responsive protein IAA2
Auxin-responsive protein IAA15
ETHYLENE INSENSITIVE 3-like 3 protein
ETHYLENE INSENSITIVE 3-like 3 protein
CPK9: calmodulin-domain protein kinase 9
CDPK 18: Calcium-dependent protein kinase 18
CMI 11: calmodulin like protein 11
Calmodulin hinding protein
CMI 27: Calaium hinding protein CMI 27
Putative Calcium binding protein CML27
CPV 10: Coloium dependent protein linese 10
CIPK 12: CPL interacting garing/threaning protein kingge 12
CIPK12, CBL-interacting serine/infeonine-protein kinase 12
CIPK1; CBL-interacting serine/threonine-protein kinase 1
CIPK2; CBL-interacting protein kinase 2
CBL-interacting serine/threonine-protein kinase 6
CBL-interacting serine/threonine-protein kinase 10
Calcium-dependent phosphotriesterase sUPerfamily protein
Calcium-dependent lipid-binding domain-containing protein
MAPKK6; mitogen-activated protein kinase kinase 6
MAPK17; mitogen-activated protein kinase 17
MAPK21; mitogen-activated protein kinase 21
MAPK13; mitogen-activated protein kinase 13
MAPKK4; mitogen-activated protein kinase kinase 4
MAPK19; mitogen-activated protein kinase 19
Receptor like protein 24
Putative receptor-like protein kinase
RLP24; receptor like protein 24
RLP54; receptor like protein 54
RFO1; wall-associated receptor kinase-like 22
CRK8; cysteine-rich receptor-like protein kinase 8
CRK8; cysteine-rich receptor-like protein kinase 8
CRK8: cvsteine-rich receptor-like protein kinase 8
CRK8: cysteine-rich receptor-like protein kinase 8
CRK39 [•] putative cysteine-rich receptor-like protein kinase 39
Receptor-like serine/threonine-protein kinase
Probably inactive leucine-rich repeat receptor-like protein kinase
Putative I RR recentor-like serine/threonine_protein kinase
Putative LRR receptor-like serine/threenine-protein kinase
RACK1C AT: recentor for activated C kinase 1C
G type leatin S receptor like sering/threening protein kingse SD1 1
HI ECDV: login recentor kinge
ACT like motoin tracsing kingso family motoin
ACT-like protein tyrosine kinase family protein
ANS, aspartokinase 5
APKZA; protein Kinase ZA
Leucine-rich repeat protein kinase family protein
Leucine-rich repeat protein kinase family protein

1	
2	Leucine-rich repeat transmembrane protein kinase family protein
3	PFK3; 6-phosphofructokinase 3
4	Protein kinase family protein
5	SK13: Shagoy-related protein kinase 13
6 7	Perovidase
7 8	Derovidase 5(
9	Peroxidase 56
10	Peroxidase 69
11	Peroxidase 71
12	Peroxidase 69
13	Peroxidase
14	Peroxidase 45
15	Glutathione S-transferase tau 3
16 17	Chutathione S transforase tau 12
17 18	
10	Glutathione S-transferase IAU 12
20	Glutathione S-transferase TAU 12
21	
22	
23	
24	
25	
26	
27 28	
20 29	
30	
31	
32	
33	
34	
35	
36	
3/	
30	
40	
41	
42	
43	
44	
45	
46 47	
4/ 19	
40 40	
50	
51	
52	
53	
54	
55	
56	
57	
58	
59 60	
00	