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

Running title: Melatonin enhances Cd tolerance in radish

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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 post-transcriptional 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 Cd^{2+} 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 Cd^{2+} 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 P_1B-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 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℃ light and 10h/18℃ 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 μM $CdCl_2$ for 24 h. Thereafter, the foliar portions of radish plants were sprayed with 10, 25, 50, 100 and 200 μM 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 ℃, 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 HNO_3 and $HClO_4$ 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 analysis[36], 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 (50μM), or Cd (50μM)+MT (0, 10, 25, 50, 100 and 200 μM). 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 50μM 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 50μM 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 50μM 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+50μM 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 R^2 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 (miR156a-3p and miR156c-3p) of miR156 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 gene (Rsa1.0_01882.1_g00002.1) and three ABC 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 $CdCl_2$ 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 $CdCl_2$ 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 Cd^{2+} 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 Ca^{2+} 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 Cd^{2+} 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.

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CONFLICT OF INTEREST

The authors have no competing financial interests to declare.

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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 ± 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 $\log_2$ (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 ± 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 ± 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 $CdCl_2$. 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.

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.

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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.

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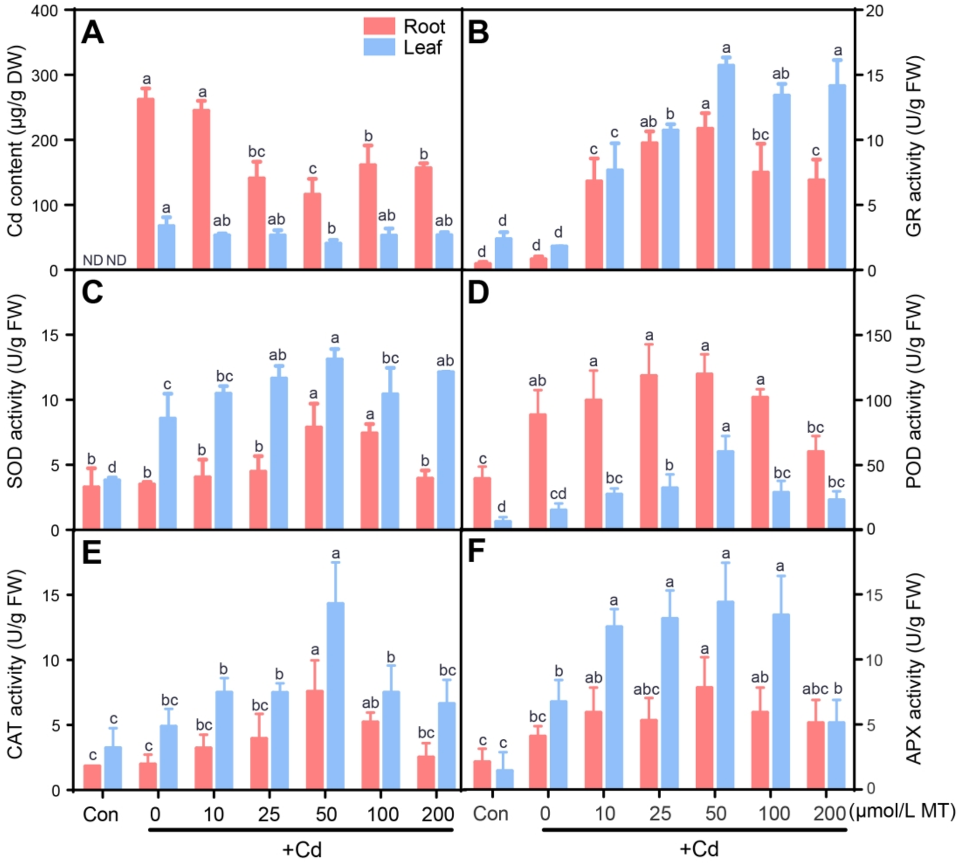
Table S12 Identification of target genes for the known and novel miRNAs.

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.



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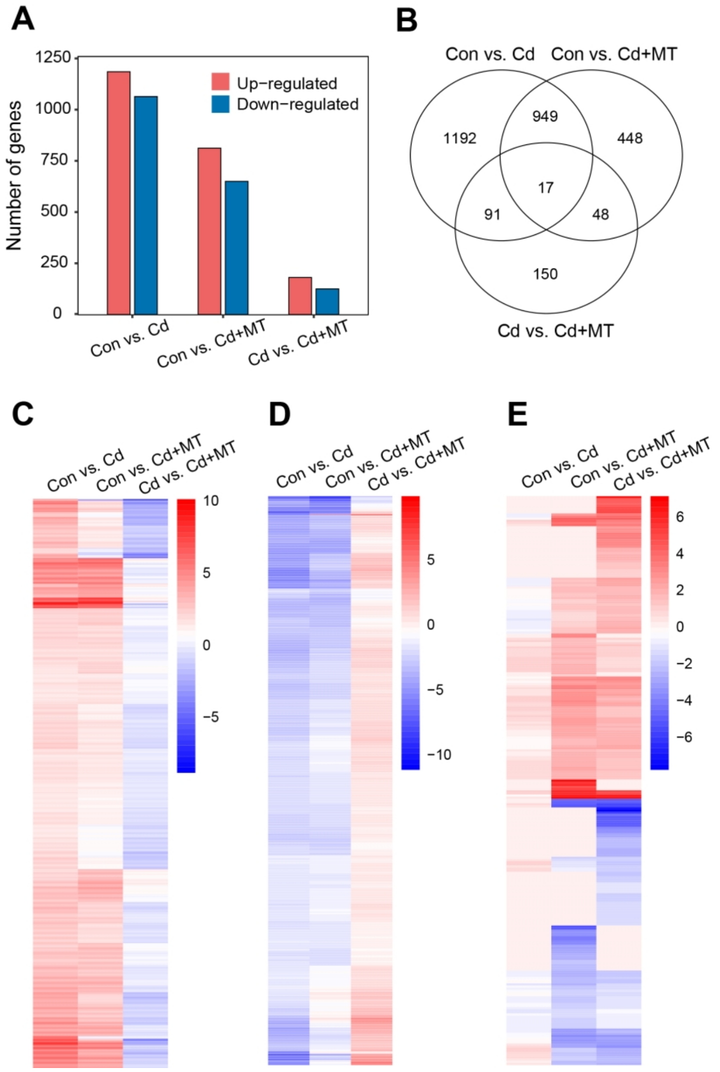

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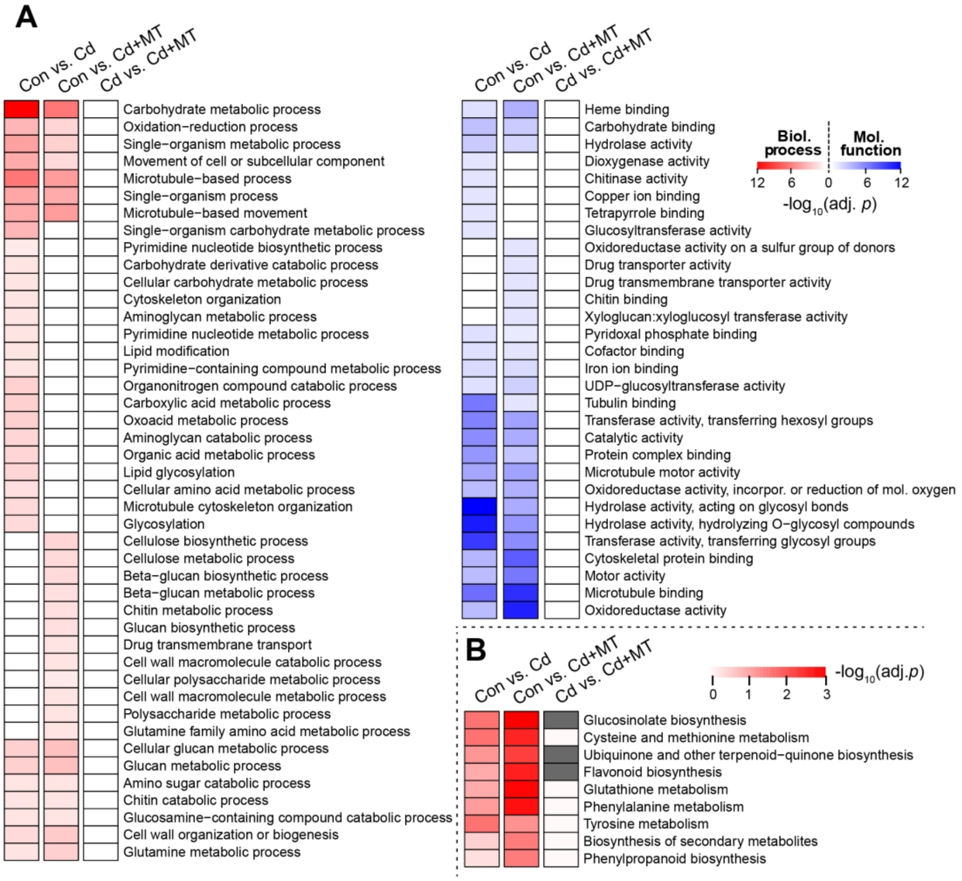

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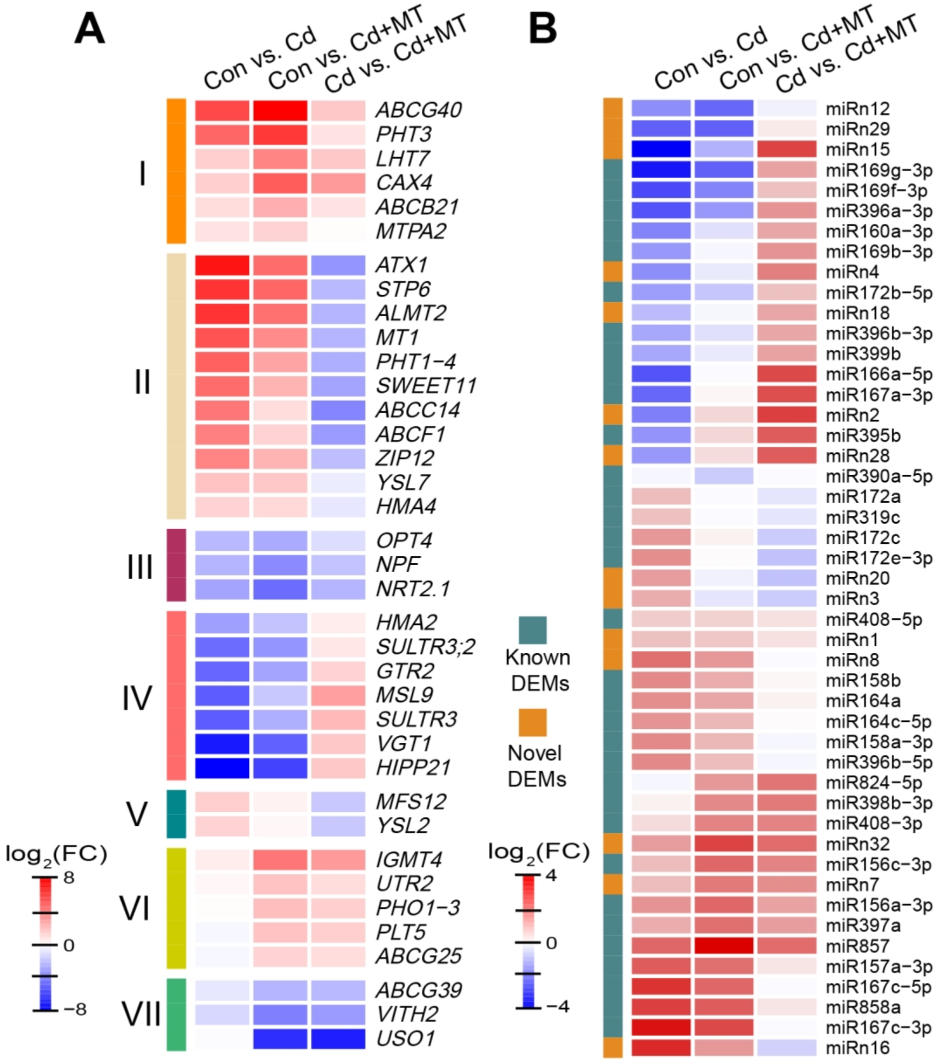

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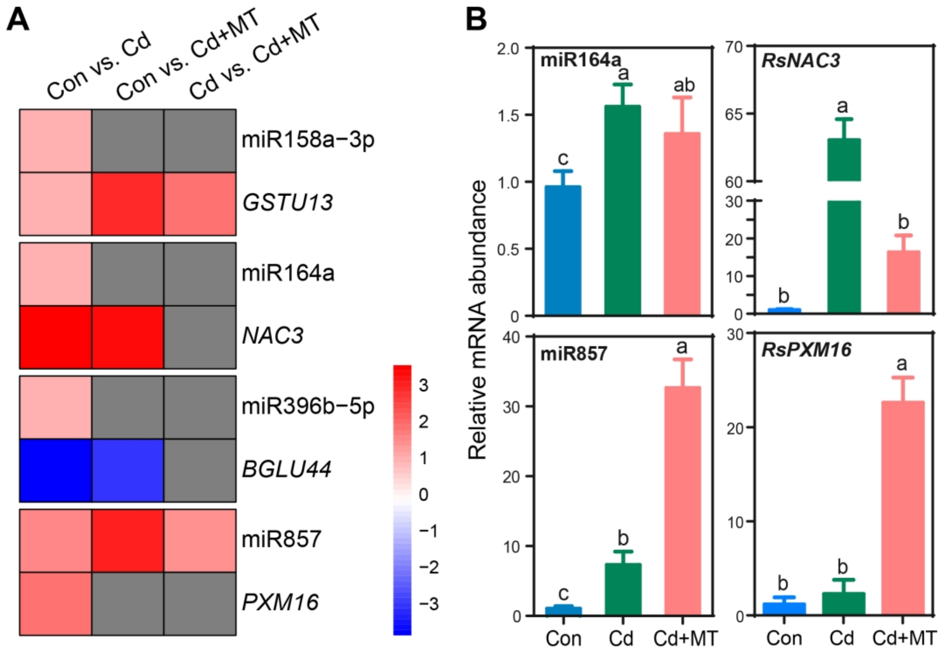

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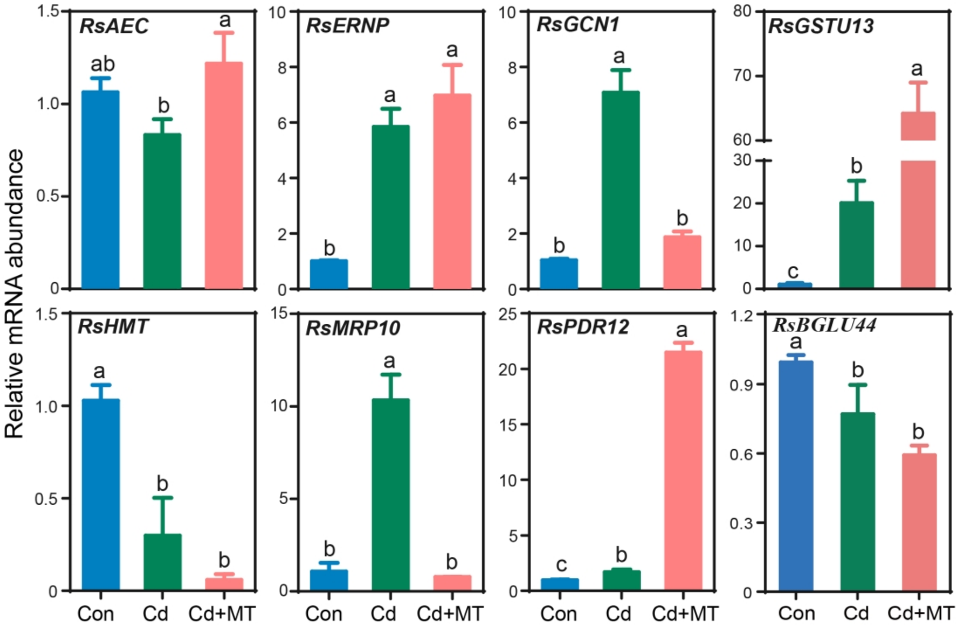

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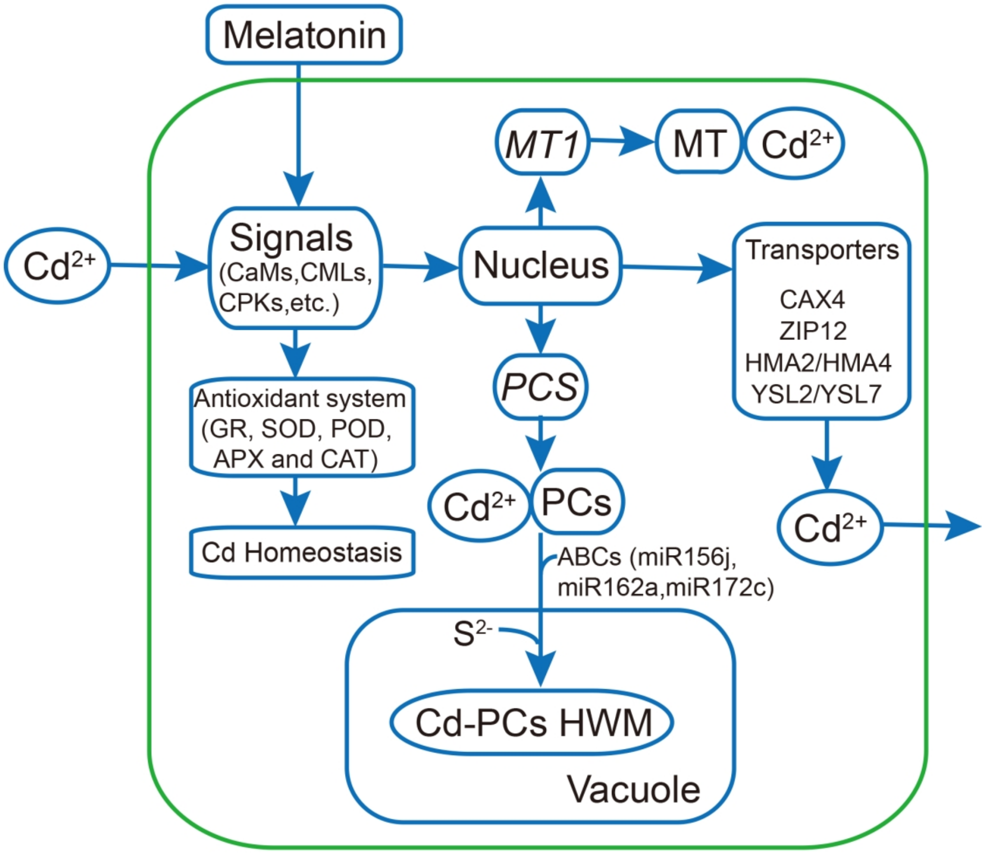

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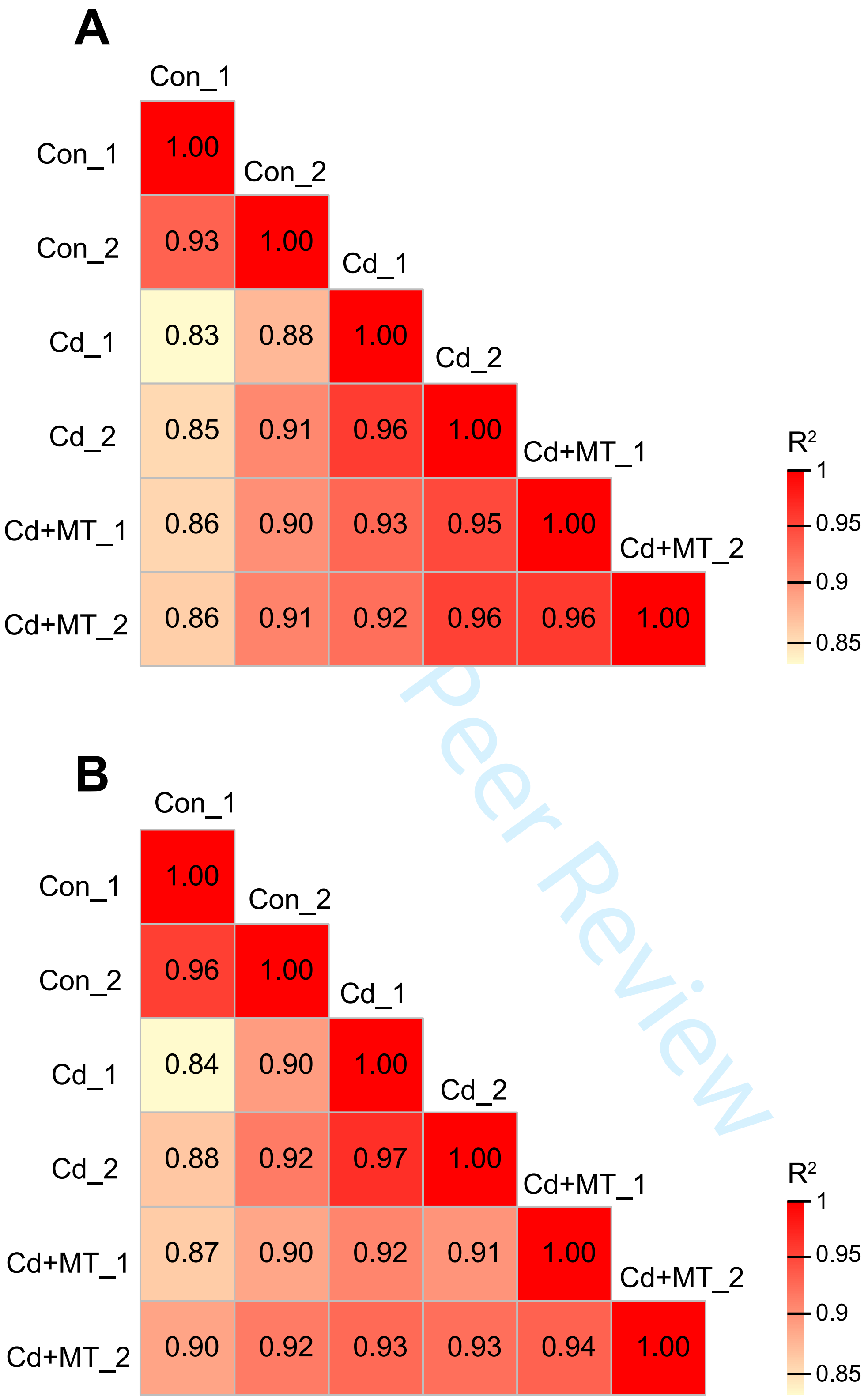

	Con_1	Con_2	Cd_1	Cd_2	Cd+MT_1	Cd+MT_2
Con_1	1.00					
Con_2	0.93	1.00				
Cd_1	0.83	0.88	1.00			
Cd_2	0.85	0.91	0.96	1.00		
Cd+MT_1	0.86	0.90	0.93	0.95	1.00	
Cd+MT_2	0.86	0.91	0.92	0.96	0.96	1.00

	Con_1	Con_2	Cd_1	Cd_2	Cd+MT_1	Cd+MT_2
Con_1	1.00					
Con_2	0.96	1.00				
Cd_1	0.84	0.90	1.00			
Cd_2	0.88	0.92	0.97	1.00		
Cd+MT_1	0.87	0.90	0.92	0.91	1.00	
Cd+MT_2	0.90	0.92	0.93	0.93	0.94	1.00

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.

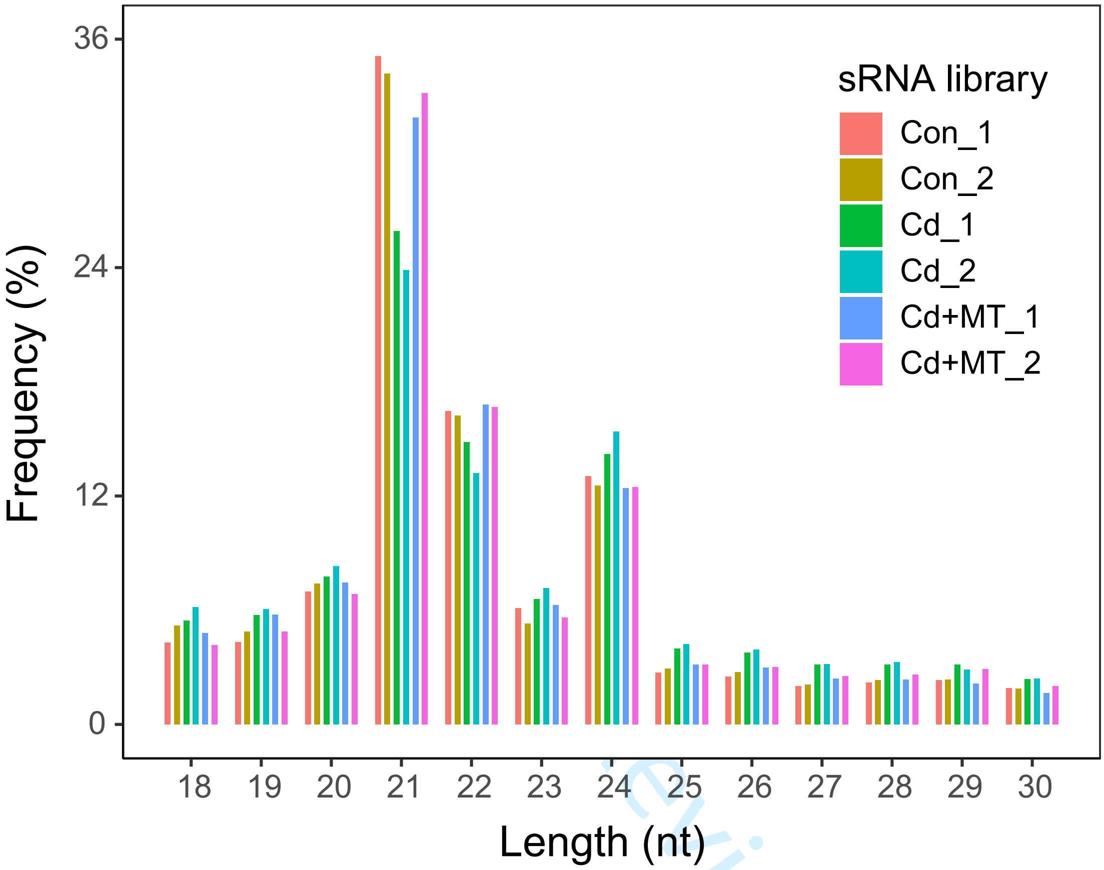

Figure S2 Length distribution of sRNA among six libraries.

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

Gene	Primer	Sequence
RsNAC3	F	GGATTACGAGGTATCAAGAA
	R	CAGGTAGTGGCTTATGAG
RsPXM16	F	TGTCCAGTCTTCAGTTAAG
	R	TCAGTTCTTCCTTCTTCAG
RsAEC	F	GTACAATGTTGGACAAGAC
	R	ACAGTGAGAGCAAGAATG
RsERNP	F	AGAGGTAGTTGAAGAAGAAG
	R	AATGAGACACGAAGGTAG
RsGCN1	F	CGTATCCTTGTTGTGGTA
	R	CTTCATCTGGTTCTCTTCA
RsGSTU13	F	TCACTCAACATCGTTCAG
	R	AGAAGGAAGGATAGAAGGA
RsHMT	F	CCATCTTCTTCCTCTATCG
	R	CTGTTGTTGTTGCTCTTC
RsMRP10	F	GTCCACTCATCAGTTCAA
	R	AAGCATCATATCGGAGAG
RsPDR12	F	AGTAACGAGACAGAAGAAC
	R	CAAGGACATCCATCAGAG
RsBGLU44	F	CTCATAACTCCACCATACC
	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
Clean_Q30 (%)	88.49	88.43	90.06
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.

Sample name	CK_1	CK_2	Cd100_1
Total reads	26333838	26469892	26424742
Total mapped	17002374 (64.56%)	16921713 (63.93%)	17247699 (65.27%)
Multiple mapped	131993 (0.5%)	121414 (0.46%)	128474 (0.49%)
Uniquely mapped	16870381 (64.06%)	16800299 (63.47%)	17119225 (64.78%)
Reads map to '+'	8424346 (31.99%)	8380453 (31.66%)	8548193 (32.35%)
Reads map to '-'	8446035 (32.07%)	8419846 (31.81%)	8571032 (32.44%)

Cd100_2	Cd_50MT1	Cd_50MT2
26245376	26758322	28839030
17308479 (65.95%)	17346360 (64.83%	18889152 (65.5%)
129651 (0.49%)	132339 (0.49%)	143302 (0.5%)
17178828 (65.45%)	17214021 (64.33%	18745850 (65%)
8577378 (32.68%)	8596914 (32.13%)	9360241 (32.46%)
8601450 (32.77%)	8617107 (32.2%)	9385609 (32.54%)

Table S4 The enriched GO categories for the DEGs.

Cd vs. Con

GO_accession	Term_type	Description	DEG_item	Bg_item
GO:0005975	Biological process	carbohydrate metabolic process	179	2346
GO:0007017	Biological process	microtubule-based process	42	360
GO:0044710	Biological process	single-organism metabolic process	419	8562
GO:0044699	Biological process	single-organism process	691	15307
GO:0006928	Biological process	movement of cell or subcellular component	35	346
GO:0007018	Biological process	microtubule-based movement	23	168
GO:0044723	Biological process	single-organism carbohydrate metabolic process	88	1293
GO:0055114	Biological process	oxidation-reduction process	185	3379
GO:0006073	Biological process	cellular glucan metabolic process	21	189
GO:0044042	Biological process	glucan metabolic process	21	189
GO:1901565	Biological process	organonitrogen compound catabolic process	21	195
GO:0019752	Biological process	carboxylic acid metabolic process	92	1530
GO:0043436	Biological process	oxoacid metabolic process	92	1531
GO:0030259	Biological process	lipid glycosylation	13	80
GO:0006082	Biological process	organic acid metabolic process	92	1536
GO:0006026	Biological process	aminoglycan catabolic process	9	44
GO:0070085	Biological process	glycosylation	23	229
GO:0000226	Biological process	microtubule cytoskeleton organization	19	180
GO:0071554	Biological process	cell wall organization or biogenesis	27	302
GO:0006520	Biological process	cellular amino acid metabolic process	65	1046
GO:0006022	Biological process	aminoglycan metabolic process	10	67
GO:0006220	Biological process	pyrimidine nucleotide metabolic process	10	69
GO:0030258	Biological process	lipid modification	14	121
GO:0006541	Biological process	glutamine metabolic process	9	56
GO:1901564	Biological process	organonitrogen compound metabolic process	188	3915
GO:0072527	Biological process	pyrimidine-containing compound metabolic proces	14	127
GO:0006032	Biological process	chitin catabolic process	7	37
GO:0046348	Biological process	amino sugar catabolic process	7	37
GO:1901072	Biological process	glucosamine-containing compound catabolic proce	7	37
GO:1901136	Biological process	carbohydrate derivative catabolic process	12	104
GO:0044262	Biological process	cellular carbohydrate metabolic process	53	821
GO:0007010	Biological process	cytoskeleton organization	32	448
GO:0006221	Biological process	pyrimidine nucleotide biosynthetic process	9	64
GO:0016798	Molecular function	hydrolase activity, acting on glycosyl bonds	104	1093
GO:0004553	Molecular function	hydrolase activity, hydrolyzing O-glycosyl compou	97	1038
GO:0016757	Molecular function	transferase activity, transferring glycosyl groups	90	957
GO:0008017	Molecular function	microtubule binding	35	248
GO:0015631	Molecular function	tubulin binding	35	264
GO:0016758	Molecular function	transferase activity, transferring hexosyl groups	64	691
GO:0003824	Molecular function	catalytic activity	987	22363
GO:0032403	Molecular function	protein complex binding	40	377
GO:0003777	Molecular function	microtubule motor activity	23	159
GO:0008092	Molecular function	cytoskeletal protein binding	50	625
GO:0003774	Molecular function	motor activity	30	288
GO:0016705	Molecular function	oxidoreductase activity, acting on paired donors, w	63	837

GO:0016491	Molecular function	oxidoreductase activity	193	3622
GO:0030246	Molecular function	carbohydrate binding	35	365
GO:0016787	Molecular function	hydrolase activity	404	8556
GO:0005506	Molecular function	iron ion binding	46	625
GO:0020037	Molecular function	heme binding	47	690
GO:0030170	Molecular function	pyridoxal phosphate binding	20	211
GO:0035251	Molecular function	UDP-glucosyltransferase activity	12	91
GO:0048037	Molecular function	cofactor binding	71	1169
GO:0046906	Molecular function	tetrapyrrole binding	48	723
GO:0046527	Molecular function	glucosyltransferase activity	12	94
GO:0004568	Molecular function	chitinase activity	7	37
GO:0005507	Molecular function	copper ion binding	21	242
GO:0051213	Molecular function	dioxygenase activity	25	310

Cd+MT vs. Con

GO_accession	Term_type	Description	DEG_item	Bg_item
GO:0005975	Biological process	carbohydrate metabolic process	115	2346
GO:0007018	Biological process	microtubule-based movement	20	168
GO:0007017	Biological process	microtubule-based process	30	360
GO:0044699	Biological process	single-organism process	474	15307
GO:0006073	Biological process	cellular glucan metabolic process	18	189
GO:0044042	Biological process	glucan metabolic process	18	189
GO:0071554	Biological process	cell wall organization or biogenesis	23	302
GO:0006541	Biological process	glutamine metabolic process	9	56
GO:0044710	Biological process	single-organism metabolic process	278	8562
GO:0055114	Biological process	oxidation-reduction process	125	3379
GO:0030244	Biological process	cellulose biosynthetic process	10	87
GO:0006928	Biological process	movement of cell or subcellular component	22	346
GO:0030243	Biological process	cellulose metabolic process	10	92
GO:0051274	Biological process	beta-glucan biosynthetic process	11	109
GO:0051273	Biological process	beta-glucan metabolic process	11	114
GO:0006030	Biological process	chitin metabolic process	7	46
GO:1901071	Biological process	glucosamine-containing compound metabolic proc	7	46
GO:0009250	Biological process	glucan biosynthetic process	11	119
GO:0016998	Biological process	cell wall macromolecule catabolic process	8	64
GO:0006032	Biological process	chitin catabolic process	6	37
GO:0046348	Biological process	amino sugar catabolic process	6	37
GO:1901072	Biological process	glucosamine-containing compound catabolic proce	6	37
GO:0006855	Biological process	drug transmembrane transport	12	138
GO:0015893	Biological process	drug transport	12	138
GO:0042493	Biological process	response to drug	12	140
GO:0044036	Biological process	cell wall macromolecule metabolic process	8	69
GO:0009064	Biological process	glutamine family amino acid metabolic process	10	109
GO:0005976	Biological process	polysaccharide metabolic process	35	701
GO:0044264	Biological process	cellular polysaccharide metabolic process	33	649
GO:0016798	Molecular function	hydrolase activity, acting on glycosyl bonds	78	1093
GO:0004553	Molecular function	hydrolase activity, hydrolyzing O-glycosyl compou	73	1038
GO:0016757	Molecular function	transferase activity, transferring glycosyl groups	66	957

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

Cd+MT vs. Cd

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

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
2.90E-17	6.43E-14
1.16E-15	1.72E-12
7.16E-14	7.94E-11
3.63E-11	3.22E-08
1.80E-10	1.14E-07
4.71E-10	2.61E-07
1.76E-09	8.66E-07
1.05E-08	4.67E-06
6.18E-08	2.11E-05
6.93E-07	0.00017077
1.04E-06	0.00023699
1.07E-06	0.00023699

1.73E-06	0.00036462
3.10E-06	0.00062447
7.17E-06	0.0013828
6.51E-05	0.0084988
0.00021036	0.024145
0.00021223	0.024145
0.00022541	0.025004
0.00023456	0.025383
0.00030425	0.029999
0.00032073	0.030735
0.00041027	0.033776
0.00041106	0.033776
0.00053182	0.042137

p-value	Corrected_p-value
6.9949E-11	7.7591E-08
1.4373E-08	7.3189E-06
1.4846E-08	7.3189E-06
1.0634E-07	0.000037767
1.8583E-06	0.00045806
1.8583E-06	0.00045806
7.1049E-06	0.0015762
0.00001505	0.0030353
0.000017875	0.0034484
0.000028518	0.0048667
0.000041492	0.006575
0.000059461	0.0087943
0.000073024	0.010452
0.00007978	0.011062
0.00012654	0.016514
0.00016578	0.019819
0.00016578	0.019819
0.00016973	0.019819
0.00027112	0.029089
0.00028846	0.029089
0.00028846	0.029089
0.00028846	0.029089
0.00033663	0.03247
0.00033663	0.03247
0.00037765	0.033513
0.00045925	0.038447
0.00050639	0.041609
0.00051932	0.041895
0.00060002	0.047541
6.1753E-16	2.74E-12
1.2171E-14	2.7001E-11
3.8108E-12	5.6362E-09

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

p-value	Corrected_p-value

Table S5 The enriched KEGG terms for the DEGs.

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

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

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.jp/kegg-bin/show_pathway?ko00940

Corrected p-value	Hyperlink

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)**
Cluster I	ABCG40	5.54	7.54	1.99
	PHT3	4.62	5.87	1.23
	LHT7	1.85	3.80	1.95
	CAX4	1.82	4.96	3.15
	ABCB21	1.31	2.57	1.25
	MTPA2	1.15	1.60	0.44
Cluster II	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
	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
Cluster III	OPT4	-1.44	-1.90	-0.45
	NPF	-1.58	-2.82	-1.26
	NRT2.1	-2.06	-3.66	-1.61
Cluster IV	HMA2	-2.19	-1.25	0.88
	SULTR3;2	-3.60	-2.51	1.08
	GTR2	-3.70	-2.01	1.68
	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
	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
Cluster VII	ABCG39	-0.19	-1.60	-1.41
	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
ABC transporter C family member 14
ABC transporter F family member 1
Zinc transporter 12
Metal-nicotianamine transporter YSL7
Putative cadmium/zinc-transporting ATPase HMA4
OPT4_ARATH Oligopeptide transporter 4
Nitrate/peptide transporter family (NPF) genes
Nitrate transporter 2.1
Cadmium/zinc-transporting ATPase HMA2
Sulfate transporter 3.2
Glucosinolate transporter-2
Mechanosensitive channel of small conductance-like 9
Sulfate transporter 3
Vacuolar glucose transporter 1
Heavy metal transport/detoxification domain-containing protein
MFS12_Major facilitator superfamily domain-containing protein 12
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
VITH2_ARATH Vacuolar iron transporter homolog 2
Intracellular protein transport protein USO1-like protein

Table S7 Summary of data statistics of six sRNA libraries.

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

with ployA/T/G/C	clean reads
45794	14152136 (96.14%)
40456	14447055 (96.75%)
40244	12685671 (96.55%)
38848	13810478 (96.09%)
31123	12560625 (96.22%)
36814	12127487 (96.54%)

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

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

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

Name	Sequence	Length	Con_1	Con_2
miR156a-3p	GCUCACUGCUCUUUCUGUCAGA	22	4.0	10.0
miR156a-5p	UGACAGAAGAGAGUGAGCAC	20	168.0	161.0
miR156c-3p	GCUCACUGCUCUAUCUGUCAGA	22	27.0	29.0
miR156f-3p	GCUCACUCUCUAUCCGUCACC	21	1.0	0.0
miR156g	CGACAGAAGAGAGUGAGCAC	20	1.0	0.0
miR156j	UGACAGAAGAGAGAGAGCAC	20	0.0	0.0
miR157a-3p	GCUCUCUAGCCUUCUGUCAUC	21	18.0	19.0
miR157a-5p	UUGACAGAAGAUAGAGAGCAC	21	18.0	25.0
miR157c-3p	GCUCUCUAUACUUCUGUCACC	21	0.0	0.0
miR157d	UGACAGAAGAUAGAGAGCAC	20	1.0	0.0
miR158a-3p	UCCCAAAUGUAGACAAAGCA	20	17124.0	30442.0
miR158b	CCCCAAAUGUAGACAAAGCA	20	97.0	158.0
miR159a	UUUGGAUUGAAGGGAGCUCUA	21	53959.0	65800.0
miR159b-3p	UUUGGAUUGAAGGGAGCUCUU	21	11025.0	12718.0
miR159c	UUUGGAUUGAAGGGAGCUCCU	21	2713.0	3463.0
miR160a-3p	GCGUAUGAGGAGCCAUGCAUA	21	13.0	10.0
miR160a-5p	UGCCUGGCUCCCUGUAUGCCA	21	315.0	292.0
miR160c-3p	CGUACAAGGAGUCAAGCAUGA	21	3.0	0.0
miR162a-3p	UCGAUAAACCUCUGCAUCCAG	21	7281.0	9183.0
miR162a-5p	UGGAGGCAGCGGUUCAUCGAUC	22	50.0	21.0
miR164a	UGGAGAAGCAGGGCACGUGCA	21	4213.0	5382.0
miR164c-3p	CACGUGUUCUACUACUCCAAC	21	270.0	386.0
miR164c-5p	UGGAGAAGCAGGGCACGUGCG	21	1471.0	1914.0
miR165a-3p	UCGGACCAGGCUUCAUCCCCC	21	875.0	922.0
miR165a-5p	GGAAUGUUGUCUGGAUCGAGG	21	63.0	17.0
miR166a-3p	UCGGACCAGGCUUCAUUCCCC	21	9404.0	10922.0
miR166a-5p	GGACUGUUGUCUGGCUCGAGG	21	122.0	53.0
miR166e-5p	GGAAUGUUGUCUGGCACGAGG	21	0.0	0.0
miR167a-3p	GAUCAUGUUCGCAGUUUCACC	21	134.0	52.0
miR167a-5p	UGAAGCUGCCAGCAUGAUCUA	21	485.0	243.0
miR167c-3p	UAGGUCAUGCUGGUAGUUUCACC	23	23.0	33.0
miR167c-5p	UAAGCUGCCAGCAUGAUCUUG	21	69.0	56.0
miR167d	UGAAGCUGCCAGCAUGAUCUGG	22	235.0	147.0
miR168a-3p	CCCGCCUUGCAUCAACUGAAU	21	668.0	359.0
miR168a-5p	UCGCUUGGUGCAGGUCGGGAA	21	1060.0	924.0
miR169a-5p	CAGCCAAGGAUGACUUGCCGA	21	1.0	4.0
miR169b-3p	GGCAAGUUGUCCUUCGGCUACA	22	27.0	13.0
miR169b-5p	CAGCCAAGGAUGACUUGCCGG	21	8.0	6.0
miR169d	UGAGCCAAGGAUGACUUGCCG	21	1.0	1.0
miR169f-3p	GCAAGUUGACCUUGGCUCUGC	21	41.0	18.0
miR169g-3p	UCCGGCAAGUUGACCUUGGCU	21	121.0	79.0
miR170-3p	UGAUUGAGCCGUGUCAAUAUC	21	0.0	0.0
miR170-5p	UAUUGGCCUGGUUCACUCAGA	21	1.0	1.0
miR171a-3p	UGAUUGAGCCGCGCCAAUAUC	21	18.0	13.0
miR171b-3p	UUGAGCCGUGCCAAUAUCACG	21	1.0	1.0
miR171b-5p	AGAUAUUAGUGCGGUUCAAUC	21	1.0	0.0

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	CUGAAGUGUUUGGGGGGACUC	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
miR398a-3p	UGUGUUCUCAGGUCACCCCUU	21	483.0	446.0
miR398b-3p	UGUGUUCUCAGGUCACCCCUG	21	7021.0	7132.0
miR398b-5p	AGGGUUGAUAUGAGAACACAC	21	0.0	1.0
miR399b	UGCCAAAGGAGAGUUGCCCUG	21	33.0	39.0
miR399f	UGCCAAAGGAGAUUUGCCCGG	21	0.0	0.0
miR400	UAUGAGAGUAUUAUAAGUCAC	21	8.0	8.0
miR403-3p	UUAGAUUCACGCACAAACUCG	21	1514.0	1626.0
miR403-5p	UGUUUUGUGCUUGAAUCUAAUU	22	0.0	0.0
miR408-3p	AUGCACUGCCUCUUCCCUGGC	21	4940.0	6355.0
miR408-5p	ACAGGGAACAAGCAGAGCAUG	21	2891.0	3100.0
miR5630a	GCUAAGAGCGGUUCUGAUGGA	21	0.0	1.0
miR5658	AUGAUGAUGAUGAUGAUGAAA	21	0.0	0.0
miR8171	AUAGGUGGGCCAGUGGUAGGA	21	1.0	0.0
miR8175	GAUCCCCGGCAACGGCGCCA	20	141.0	141.0
miR824-3p	CCUUCUCAUCGAUGGUCUAGA	21	457.0	375.0
miR824-5p	UAGACCAUUUGUGAGAAGGGA	21	128.0	79.0
miR827	UUAGAUGACCAUCAACAAACU	21	1.0	1.0
miR857	UUUUGUAUGUUGAAGGUGUAU	21	8.0	10.0
miR858a	UUUCGUUGUCUGUUCGACCUU	21	15.0	50.0
miR858b	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
0.0	0.0	0.0	0.0

240.0	251.0	86.0	120.0
3.0	11.0	9.0	7.0
967.0	1122.0	318.0	378.0
0.0	0.0	1.0	0.0
1259.0	953.0	248.0	386.0
0.0	0.0	0.0	1.0
1.0	2.0	0.0	5.0
80384.0	135518.0	67006.0	72840.0
14235.0	24959.0	8945.0	7652.0
1.0	1.0	0.0	0.0
256.0	406.0	135.0	208.0
0.0	0.0	1.0	0.0
84.0	120.0	84.0	93.0
2.0	1.0	2.0	0.0
3246.0	2982.0	3001.0	3991.0
78.0	69.0	125.0	176.0
9.0	16.0	36.0	66.0
190.0	318.0	396.0	485.0
9903.0	15220.0	8442.0	9771.0
33.0	38.0	49.0	58.0
14490.0	12275.0	5071.0	8962.0
111.0	66.0	194.0	114.0
295.0	232.0	505.0	551.0
6451.0	3679.0	10577.0	16509.0
0.0	0.0	0.0	1.0
8.0	9.0	8.0	21.0
1.0	0.0	0.0	0.0
1.0	6.0	5.0	3.0
2976.0	1865.0	1526.0	2205.0
1.0	0.0	0.0	0.0
4932.0	5606.0	15317.0	7822.0
2127.0	4895.0	3298.0	1938.0
1.0	0.0	0.0	0.0
1.0	1.0	0.0	2.0
0.0	0.0	0.0	0.0
55.0	161.0	58.0	95.0
333.0	631.0	496.0	342.0
71.0	50.0	203.0	130.0
3.0	4.0	2.0	2.0
36.0	28.0	111.0	87.0
173.0	168.0	61.0	180.0
1.0	3.0	3.0	4.0

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

Name	**Sequence**	**Length**	**Con_1**	**Con_2**	**Cd_1**	**Cd_2**
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	5.0	10.0	8.0	29.0
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
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	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
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
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
miRn4	GGGUCGAUAUGAGAACACAUG	21	6438.0	5878.0	1349.0	1068.0
miRn5	UUCCACAGCUUUCUUGAACUG	21	1.0	0.0	0.0	0.0
miRn6	UUAAGUGUCUGUAUGUAUGGGC	22	1677.0	2144.0	3163.0	3152.0
miRn7	UUUUUCAUGAGAAGUAGAUUUG	22	260.0	752.0	617.0	622.0
miRn8	UGGAGAAGCAGGGCACGUGC	20	55.0	67.0	171.0	188.0
miRn9	AAGCUCAGGAGGGAUAGCGCC	21	3.0	2.0	0.0	1.0

Cd+MT_1	Cd+MT_2	Hairpin.pos
309.0	166.0	Rsa1.0_02734.1:12532..12848:+
196.0	292.0	Rsa1.0_00091.1:100173..100491:-
5.0	10.0	Rsa1.0_01260.1:10666..10983:+
5.0	27.0	Rsa1.0_02040.1:435..750:+
129.0	99.0	Rsa1.0_04538.1:15789..16106:-
184.0	172.0	Rsa1.0_00123.1:201603..201920:-
30.0	21.0	Rsa1.0_00108.1:468042..468359:-
4.0	7.0	Rsa1.0_04552.1:8696..9013:-
8.0	3.0	Rsa1.0_00693.1:160537..160857:-
14.0	21.0	Rsa1.0_00847.1:37258..37575:+
2.0	1.0	Rsa1.0_03744.1:7430..7748:-
9553.0	8385.0	Rsa1.0_21880.1:473..790:+
0.0	4.0	Rsa1.0_11906.1:4267..4585:+
5.0	5.0	Rsa1.0_01069.1:5953..6274:-
1.0	5.0	Rsa1.0_05713.1:12055..12373:-
0.0	5.0	Rsa1.0_01695.1:16219..16540:+
2.0	4.0	Rsa1.0_34995.1:77..394:-
110.0	89.0	Rsa1.0_00110.1:34863..35182:+
3.0	1.0	Rsa1.0_00715.1:12183..12500:-
1.0	1.0	Rsa1.0_11206.1:198..515:-
10881.0	9303.0	Rsa1.0_21880.1:474..789:-
14.0	80.0	Rsa1.0_00022.1:182718..183035:+
1289.0	3975.0	Rsa1.0_00994.1:152493..152810:-
1.0	3.0	Rsa1.0_06717.1:2201..2519:-
33.0	70.0	Rsa1.0_01029.1:122559..122877:+
11.0	6.0	Rsa1.0_02345.1:12625..12943:+
0.0	1.0	Rsa1.0_01801.1:33178..33495:+
2837.0	2752.0	Rsa1.0_00088.1:84940..85258:+
0.0	0.0	Rsa1.0_01001.1:4372..4689:-
2131.0	2682.0	Rsa1.0_36295.1:164..482:+
1542.0	940.0	Rsa1.0_01312.1:34225..34544:-
107.0	93.0	Rsa1.0_00164.1:35281..35597:+
0.0	0.0	Rsa1.0_01154.1:17250..17566:-

Hairpin sequence
gagcuuucuucgguccacucauagaauaauaugugagauuuaauugacucucgacucauucauccaaauaccaaaugaaagauuaugcagacaua
ucgcuuggugcaggucgggaacugauuggcugacaccgccacgugaauuuucacgguuggcuugugagcagggaucggauccugccuuccauca
ugggacauuggaacugugaguuucagaacgauauaaaagaucauggauacaguaaagagauuuaacucaaaugaggcuaguauaucuauggccuu
gcaucaucaucaagauucagaaaucauauucucugaugguucuucguucgagccugucuuuuucugguuugagaaucuugaugaugcugcag
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uccaaagggaucgcauugauccaaauuaagcugaauuauuccccaauaguuauucuuuuccucaaucguaagauguaaagaagacgacuugcuuc
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gugguggugguucaagcugauguaggcucaaaacgauauagaagguguucacuugauguauguuuuggucguacaccaacuuguucccccacca
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uauuuauagucgaccuuuccuccgguuacugggggugcaaagaggucgauugaaugcu
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aagcucaggagggauagcgccaucaugaucacucacaucgauauuuuuggcgcuguccauccugaguuuc

ugugaacccccauuaguuucacuaauggggaugcucua

ugggccccacugacacgug

gcucu

g

Table S11 Identification of differential expressed miRNAs among three comparisions.

miRNA	Cd vs. Con			Cd+MT vs. Con			Cd+MT vs. C	
	$\log_2$(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	—	—	—	—	—	—	-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	—	—
miR396b-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
miRn15	-4.3335	7.79E-14	3.31E-12	-1.694	0.000189	0.002146	2.0334	6.89E-05

Note: "—" means no significant difference was found in this comparision. $\log_2(FC)$: $\log_2$(fold change).

Cd
padj
—
—
—
—
—
—
—
—
0.001166
0.000875
—
—
—
—
—
0.043763
0.001386
0.002692
0.029755
—
0.003335
—
—
—
—
0.037944
—
0.043763
0.024563
0.006061
—
—
—
0.044734
4.27E-05
—
0.027001
—
0.024563
—
—
—
3.12E-08
0.001386

Table S12 Identification of target genes for the known and nove

miRNA	Target gene ID
miR156a-3p	Rsa1.0_00667.1_g00013.1
miR156a-5p	Rsa1.0_00316.1_g00008.1
miR156a-5p	Rsa1.0_04852.1_g00005.1
miR156a-5p	Rsa1.0_00894.1_g00014.1
miR156a-5p	Rsa1.0_00672.1_g00002.1
miR156a-5p	Rsa1.0_00943.1_g00007.1
miR156a-5p	Rsa1.0_01020.1_g00007.1
miR156a-5p	Rsa1.0_01068.1_g00001.1
miR156a-5p	Rsa1.0_01022.1_g00011.1
miR156a-5p	Rsa1.0_02675.1_g00008.1
miR156a-5p	Rsa1.0_08717.1_g00001.1
miR156a-5p	Rsa1.0_07943.1_g00001.1
miR156a-5p	Rsa1.0_01256.1_g00004.1
miR156a-5p	Rsa1.0_01104.1_g00029.1
miR156a-5p	Rsa1.0_02413.1_g00008.1
miR156a-5p	Rsa1.0_10928.1_g00001.1
miR156a-5p	Rsa1.0_02931.1_g00002.1
miR156a-5p	Rsa1.0_00003.1_g00030.1
miR156a-5p	Rsa1.0_02460.1_g00002.1
miR156a-5p	Rsa1.0_02713.1_g00001.1
miR156a-5p,miR156g	Rsa1.0_03451.1_g00003.1
miR156a-5p,miR156g	Rsa1.0_02846.1_g00003.1
miR156a-5p,miR156g	Rsa1.0_00071.1_g00047.1
miR156a-5p,miR156g	Rsa1.0_08401.1_g00001.1
miR156a-5p,miR156g	Rsa1.0_00870.1_g00006.1
miR156a-5p,miR156g	Rsa1.0_04892.1_g00002.1
miR156a-5p,miR156g	Rsa1.0_00078.1_g00028.1
miR156a-5p,miR156g	Rsa1.0_04399.1_g00001.1
miR156a-5p,miR156g	Rsa1.0_11699.1_g00001.1
miR156a-5p,miR156g	Rsa1.0_03385.1_g00003.1
miR156a-5p,miR156g	Rsa1.0_09711.1_g00001.1
miR156a-5p,miR156g	Rsa1.0_06163.1_g00001.1
miR156a-5p,miR156g	Rsa1.0_00018.1_g00013.1
miR156a-5p,miR156g	Rsa1.0_01145.1_g00010.1
miR156a-5p,miR156g	Rsa1.0_00294.1_g00023.1
miR156a-5p,miR156g	Rsa1.0_00106.1_g00018.1
miR156a-5p,miR156g	Rsa1.0_00984.1_g00002.1
miR156a-5p,miR156g	Rsa1.0_09064.1_g00002.1
miR156a-5p,miR156g	Rsa1.0_03959.1_g00003.1
miR156a-5p,miR156j,miR156g	Rsa1.0_01148.1_g00009.1
miR156a-5p,miR157a-5p,miR157	Rsa1.0_04786.1_g00004.1
miR156a-5p,miR157d,miR156j	Rsa1.0_00092.1_g00050.1
miR156a-5p,miR157d,miR156j	Rsa1.0_00043.1_g00002.1
miR156a-5p,miR157d,miR156j,n	Rsa1.0_00001.1_g00030.1
miR156a-5p,miR157d,miR156j,n	Rsa1.0_00011.1_g00004.1
miR156a-5p,miR158b,miR158a-	Rsa1.0_00620.1_g00003.1

miR156a-5p,miR5658	Rsa1.0_00656.1_g00015.1
miR156c-3p	Rsa1.0_00868.1_g00005.1
miR156c-3p	Rsa1.0_30652.1_g00001.1
miR156c-3p	Rsa1.0_03030.1_g00003.1
miR156f-3p	Rsa1.0_17495.1_g00001.1
miR156f-3p	Rsa1.0_00719.1_g00005.1
miR156f-3p	Rsa1.0_20060.1_g00001.1
miR156f-3p	Rsa1.0_00851.1_g00010.1
miR156f-3p,miR5658	Rsa1.0_00657.1_g00017.1
miR156g	Rsa1.0_04511.1_g00002.1
miR156g	Rsa1.0_00249.1_g00017.1
miR156g	Rsa1.0_00246.1_g00007.1
miR156g	Rsa1.0_17474.1_g00001.1
miR156g	Rsa1.0_00236.1_g00006.1
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_00372.1_g00015.1
miR156g,miR156a-5p	Rsa1.0_00130.1_g00021.1
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_g00003.1
miR156g,miR156a-5p	Rsa1.0_04369.1_g00002.1
miR156g,miR156a-5p	Rsa1.0_00201.1_g00024.1
miR156g,miR156a-5p	Rsa1.0_01983.1_g00004.1
miR156g,miR156a-5p	Rsa1.0_01305.1_g00004.1
miR156g,miR156a-5p	Rsa1.0_01502.1_g00006.1
miR156g,miR156a-5p	Rsa1.0_02106.1_g00003.1
miR156g,miR156a-5p	Rsa1.0_00990.1_g00012.1
miR156g,miR156a-5p	Rsa1.0_07110.1_g00001.1
miR156g,miR156a-5p	Rsa1.0_00664.1_g00008.1
miR156g,miR156a-5p	Rsa1.0_00075.1_g00005.1
miR156g,miR156a-5p	Rsa1.0_01997.1_g00007.1
miR156g,miR156a-5p,miR156j	Rsa1.0_00454.1_g00003.1
miR156g,miR156a-5p,miR156j	Rsa1.0_00012.1_g00032.1
miR156g,miR156a-5p,miR156j	Rsa1.0_03890.1_g00004.1
miR156g,miR156a-5p,miR156j	Rsa1.0_00071.1_g00026.1
miR156g,miR156a-5p,miR157a-	Rsa1.0_00158.1_g00006.1
miR156g,miR156j	Rsa1.0_00435.1_g00007.1
miR156g,miR156j,miR156a-5p	Rsa1.0_00948.1_g00009.1
miR156g,miR156j,miR156a-5p	Rsa1.0_00001.1_g00062.1
miR156g,miR156j,miR156a-5p,	Rsa1.0_02545.1_g00001.1
miR156g,miR156j,miR156a-5p,	Rsa1.0_00340.1_g00014.1
miR156g,miR156j,miR157d,miR	Rsa1.0_00374.1_g00009.1
miR156g,miR157a-5p,miR157d,	Rsa1.0_00351.1_g00013.1
miR156g,miR157a-5p,miR157d,	Rsa1.0_23904.1_g00001.1
miR156g,miR157a-5p,miR157d,	Rsa1.0_41914.1_g00001.1

miR156g,miR157d,miR156a-5p,	Rsa1.0_05583.1_g00003.1
miR156g,miR157d,miR157a-5p,	Rsa1.0_06065.1_g00002.1
miR156g,miR157d,miR157a-5p,	Rsa1.0_00158.1_g00005.1
miR156j	Rsa1.0_02527.1_g00005.1
miR156j	Rsa1.0_11225.1_g00001.1
miR156j	Rsa1.0_00376.1_g00011.1
miR156j	Rsa1.0_02415.1_g00003.1
miR156j	Rsa1.0_00033.1_g00032.1
miR156j	Rsa1.0_02848.1_g00006.1
miR156j	Rsa1.0_01123.1_g00003.1
miR156j	Rsa1.0_00017.1_g00030.1
miR156j	Rsa1.0_00316.1_g00006.1
miR156j	Rsa1.0_00117.1_g00019.1
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miR156j	Rsa1.0_03015.1_g00005.1
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miR156j	Rsa1.0_01869.1_g00002.1
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miR156j	Rsa1.0_04298.1_g00002.1
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miR156j	Rsa1.0_00531.1_g00009.1
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miR156j	Rsa1.0_00094.1_g00029.1
miR156j	Rsa1.0_00278.1_g00011.1
miR156j	Rsa1.0_02158.1_g00001.1
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miR156j	Rsa1.0_00037.1_g00025.1
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miR156j	Rsa1.0_00323.1_g00007.1
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miR156j	Rsa1.0_00302.1_g00010.1
miR156j	Rsa1.0_00915.1_g00001.1
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miR156j	Rsa1.0_00706.1_g00011.1
miR156j	Rsa1.0_00049.1_g00020.1
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miR156j	Rsa1.0_01073.1_g00004.1
miR156j	Rsa1.0_03235.1_g00006.1
miR156j,miR156a-5p	Rsa1.0_00293.1_g00040.1
miR156j,miR156a-5p,miR156g	Rsa1.0_02584.1_g00008.1
miR156j,miR156a-5p,miR157a-5	Rsa1.0_00237.1_g00024.1
miR156j,miR156a-5p,miR157a-5	Rsa1.0_00793.1_g00003.1
miR156j,miR156a-5p,miR157d,n	Rsa1.0_03583.1_g00002.1
miR156j,miR156a-5p,miR157d,n	Rsa1.0_00469.1_g00014.1
miR156j,miR156a-5p,miR157d,n	Rsa1.0_00986.1_g00007.1
miR156j,miR156a-5p,miR157d,n	Rsa1.0_04786.1_g00005.1
miR156j,miR156a-5p,miR157d,n	Rsa1.0_04683.1_g00002.1
miR156j,miR156g	Rsa1.0_00565.1_g00011.1
miR156j,miR156g	Rsa1.0_00237.1_g00041.1
miR156j,miR157a-5p,miR157d	Rsa1.0_05244.1_g00002.1
miR156j,miR157a-5p,miR157d,n	Rsa1.0_00138.1_g00022.1
miR156j,miR157d	Rsa1.0_02356.1_g00006.1
miR156j,miR157d	Rsa1.0_04695.1_g00003.1
miR156j,miR157d	Rsa1.0_01150.1_g00004.1
miR156j,miR157d	Rsa1.0_02553.1_g00001.1
miR156j,miR157d	Rsa1.0_00567.1_g00010.1
miR156j,miR157d,miR156a-5p,n	Rsa1.0_05648.1_g00002.1
miR156j,miR157d,miR157a-5p,n	Rsa1.0_00829.1_g00019.1
miR156j,miR167c-5p,miR167a-5	Rsa1.0_00548.1_g00007.1
miR156j,miR393a-5p	Rsa1.0_03774.1_g00002.1
miR156j,miR5658	Rsa1.0_00638.1_g00003.1
miR156j,miR5658	Rsa1.0_00556.1_g00022.1
miR156j,miR5658,miR157d	Rsa1.0_02071.1_g00002.1
miR157a-3p	Rsa1.0_00173.1_g00033.1
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miR157a-3p	Rsa1.0_03247.1_g00003.1

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miR157a-3p	Rsa1.0_01083.1_g00002.1
miR157a-3p,miR857	Rsa1.0_05206.1_g00004.1
miR157a-5p	Rsa1.0_04128.1_g00002.1
miR157a-5p	Rsa1.0_00190.1_g00049.1
miR157a-5p	Rsa1.0_02923.1_g00003.1
miR157a-5p,miR156j	Rsa1.0_16217.1_g00001.1
miR157a-5p,miR157d	Rsa1.0_00832.1_g00003.1
miR157a-5p,miR157d	Rsa1.0_04527.1_g00007.1
miR157a-5p,miR157d	Rsa1.0_00326.1_g00027.1
miR157a-5p,miR157d	Rsa1.0_05468.1_g00003.1
miR157a-5p,miR157d	Rsa1.0_01930.1_g00003.1
miR157a-5p,miR157d	Rsa1.0_00790.1_g00004.1
miR157a-5p,miR157d	Rsa1.0_06033.1_g00004.1
miR157a-5p,miR157d,miR156a-	Rsa1.0_04235.1_g00002.1
miR157a-5p,miR157d,miR156a-	Rsa1.0_01094.1_g00010.1
miR157a-5p,miR157d,miR156a-	Rsa1.0_04683.1_g00003.1
miR157a-5p,miR157d,miR156a-	Rsa1.0_00722.1_g00009.1
miR157a-5p,miR157d,miR156a-	Rsa1.0_00026.1_g00007.1
miR157a-5p,miR157d,miR156j	Rsa1.0_00660.1_g00005.1
miR157a-5p,miR157d,miR156j	Rsa1.0_05719.1_g00002.1
miR157c-3p	Rsa1.0_13653.1_g00001.1
miR157c-3p	Rsa1.0_02281.1_g00005.1
miR157c-3p	Rsa1.0_01443.1_g00003.1
miR157c-3p	Rsa1.0_00038.1_g00033.1
miR157c-3p	Rsa1.0_03415.1_g00005.1
miR157c-3p	Rsa1.0_04916.1_g00001.1
miR157c-3p	Rsa1.0_07517.1_g00001.1
miR157c-3p	Rsa1.0_01804.1_g00001.1
miR157c-3p	Rsa1.0_02318.1_g00001.1
miR157c-3p	Rsa1.0_00339.1_g00006.1
miR157c-3p	Rsa1.0_02667.1_g00005.1
miR157c-3p	Rsa1.0_08242.1_g00002.1
miR157c-3p	Rsa1.0_05224.1_g00001.1
miR157c-3p	Rsa1.0_00234.1_g00012.1
miR157c-3p	Rsa1.0_03018.1_g00002.1
miR157c-3p	Rsa1.0_03189.1_g00003.1
miR157c-3p,miR8175	Rsa1.0_00984.1_g00004.1
miR157d	Rsa1.0_00087.1_g00056.1
miR157d	Rsa1.0_03992.1_g00004.1
miR157d	Rsa1.0_04073.1_g00003.1
miR157d	Rsa1.0_00752.1_g00002.1
miR157d	Rsa1.0_01352.1_g00004.1
miR157d	Rsa1.0_00284.1_g00002.1
miR157d	Rsa1.0_02346.1_g00002.1
miR157d	Rsa1.0_00651.1_g00018.1
miR157d	Rsa1.0_02405.1_g00005.1
miR157d	Rsa1.0_01232.1_g00003.1

miR157d	Rsa1.0_01674.1_g00006.1
miR157d	Rsa1.0_00394.1_g00002.1
miR157d	Rsa1.0_02541.1_g00004.1
miR157d	Rsa1.0_00811.1_g00007.1
miR157d	Rsa1.0_04279.1_g00002.1
miR157d	Rsa1.0_00179.1_g00010.1
miR157d	Rsa1.0_01645.1_g00005.1
miR157d	Rsa1.0_17001.1_g00001.1
miR157d	Rsa1.0_12678.1_g00001.1
miR157d	Rsa1.0_07376.1_g00001.1
miR157d	Rsa1.0_11656.1_g00001.1
miR157d	Rsa1.0_00940.1_g00002.1
miR157d,miR156a-5p,miR156j,	Rsa1.0_00349.1_g00013.1
miR157d,miR157a-5p	Rsa1.0_00722.1_g00017.1
miR157d,miR157a-5p	Rsa1.0_06750.1_g00001.1
miR157d,miR157a-5p	Rsa1.0_04028.1_g00003.1
miR157d,miR157a-5p,miR156a-	Rsa1.0_00294.1_g00025.1
miR157d,miR157a-5p,miR156a-	Rsa1.0_04403.1_g00002.1
miR157d,miR157a-5p,miR156j	Rsa1.0_00876.1_g00001.1
miR157d,miR157a-5p,miR156j	Rsa1.0_02198.1_g00008.1
miR157d,miR157a-5p,miR156j	Rsa1.0_02725.1_g00006.1
miR158a-3p	Rsa1.0_02858.1_g00003.1
miR158a-3p	Rsa1.0_03019.1_g00002.1
miR158a-3p	Rsa1.0_00784.1_g00005.1
miR158a-3p	Rsa1.0_00059.1_g00013.1
miR158a-3p	Rsa1.0_05353.1_g00001.1
miR158a-3p	Rsa1.0_22303.1_g00001.1
miR158a-3p	Rsa1.0_01086.1_g00002.1
miR158a-3p	Rsa1.0_02069.1_g00002.1
miR158a-3p	Rsa1.0_01285.1_g00007.1
miR158a-3p	Rsa1.0_02683.1_g00001.1
miR158a-3p	Rsa1.0_00668.1_g00006.1
miR158a-3p	Rsa1.0_01389.1_g00008.1
miR158a-3p	Rsa1.0_03554.1_g00002.1
miR158a-3p	Rsa1.0_02387.1_g00004.1
miR158a-3p	Rsa1.0_03157.1_g00002.1
miR158a-3p,miR158b	Rsa1.0_01308.1_g00009.1
miR158a-3p,miR158b	Rsa1.0_09853.1_g00001.1
miR158a-3p,miR158b	Rsa1.0_18616.1_g00001.1
miR158a-3p,miR158b	Rsa1.0_00018.1_g00064.1
miR158a-3p,miR158b	Rsa1.0_03991.1_g00002.1
miR158a-3p,miR158b	Rsa1.0_00008.1_g00043.1
miR158a-3p,miR158b	Rsa1.0_00853.1_g00007.1
miR158a-3p,miR158b	Rsa1.0_00273.1_g00039.1
miR158a-3p,miR170-5p	Rsa1.0_04448.1_g00004.1
miR158b	Rsa1.0_01405.1_g00014.1
miR158b	Rsa1.0_05086.1_g00002.1
miR158b	Rsa1.0_04092.1_g00002.1

miR158b	Rsa1.0_00204.1_g00023.1
miR158b	Rsa1.0_24716.1_g00001.1
miR158b,miR158a-3p	Rsa1.0_01077.1_g00014.1
miR158b,miR158a-3p	Rsa1.0_16565.1_g00001.1
miR158b,miR158a-3p	Rsa1.0_07407.1_g00002.1
miR158b,miR158a-3p	Rsa1.0_01467.1_g00008.1
miR158b,miR158a-3p	Rsa1.0_07590.1_g00001.1
miR158b,miR158a-3p	Rsa1.0_34975.1_g00001.1
miR158b,miR158a-3p	Rsa1.0_00433.1_g00014.1
miR158b,miR158a-3p	Rsa1.0_02124.1_g00002.1
miR158b,miR158a-3p	Rsa1.0_01209.1_g00003.1
miR159a	Rsa1.0_11027.1_g00002.1
miR159a	Rsa1.0_04428.1_g00004.1
miR159a	Rsa1.0_00133.1_g00019.1
miR159a	Rsa1.0_01556.1_g00005.1
miR159a	Rsa1.0_04138.1_g00005.1
miR159a,miR159b-3p,miR159c	Rsa1.0_00982.1_g00005.1
miR159a,miR159b-3p,miR159c	Rsa1.0_09089.1_g00001.1
miR159a,miR159b-3p,miR159c	Rsa1.0_03293.1_g00003.1
miR159a,miR159b-3p,miR159c	Rsa1.0_04154.1_g00002.1
miR159a,miR159c,miR159b-3p	Rsa1.0_03477.1_g00001.1
miR159a,miR159c,miR159b-3p	Rsa1.0_00404.1_g00009.1
miR159a,miR159c,miR159b-3p	Rsa1.0_00840.1_g00012.1
miR159a,miR159c,miR159b-3p	Rsa1.0_25994.1_g00001.1
miR159a,miR159c,miR159b-3p	Rsa1.0_00207.1_g00028.1
miR159a,miR159c,miR319c,miR	Rsa1.0_06447.1_g00002.1
miR159b-3p	Rsa1.0_00092.1_g00058.1
miR159b-3p	Rsa1.0_22548.1_g00001.1
miR159b-3p	Rsa1.0_00190.1_g00053.1
miR159b-3p	Rsa1.0_07916.1_g00002.1
miR159b-3p,miR159a	Rsa1.0_00002.1_g00074.1
miR159b-3p,miR159c	Rsa1.0_09080.1_g00001.1
miR159b-3p,miR159c	Rsa1.0_04267.1_g00001.1
miR159b-3p,miR159c,miR159a	Rsa1.0_02516.1_g00003.1
miR159b-3p,miR159c,miR159a	Rsa1.0_02581.1_g00006.1
miR159b-3p,miR159c,miR159a	Rsa1.0_01027.1_g00010.1
miR159b-3p,miR159c,miR159a	Rsa1.0_01249.1_g00010.1
miR159b-3p,miR319c,miR159c,r	Rsa1.0_01813.1_g00006.1
miR159b-3p,miR319c,miR159c,r	Rsa1.0_01000.1_g00006.1
miR159b-3p,miR319c,miR159c,r	Rsa1.0_01308.1_g00007.1
miR159b-3p,miR5658,miR159c,r	Rsa1.0_04131.1_g00003.1
miR159c	Rsa1.0_00955.1_g00004.1
miR159c,miR159a	Rsa1.0_08538.1_g00001.1
miR159c,miR159b-3p,miR159a	Rsa1.0_06290.1_g00002.1
miR159c,miR159b-3p,miR159a	Rsa1.0_00154.1_g00027.1
miR160a-3p	Rsa1.0_00646.1_g00014.1
miR160a-3p	Rsa1.0_00897.1_g00008.1
miR160a-3p	Rsa1.0_00187.1_g00026.1

miR160a-5p	Rsa1.0_00381.1_g00005.1
miR160a-5p	Rsa1.0_00119.1_g00039.1
miR160a-5p	Rsa1.0_00897.1_g00011.1
miR160a-5p	Rsa1.0_00124.1_g00036.1
miR160a-5p	Rsa1.0_02992.1_g00004.1
miR160a-5p,miR156j	Rsa1.0_03073.1_g00005.1
miR160c-3p	Rsa1.0_09283.1_g00002.1
miR160c-3p	Rsa1.0_05041.1_g00001.1
miR160c-3p	Rsa1.0_01283.1_g00006.1
miR160c-3p	Rsa1.0_05093.1_g00003.1
miR162a-3p	Rsa1.0_00079.1_g00053.1
miR162a-3p	Rsa1.0_09923.1_g00001.1
miR162a-3p	Rsa1.0_08779.1_g00004.1
miR162a-5p,miR162a-3p	Rsa1.0_00058.1_g00021.1
miR164a	Rsa1.0_00611.1_g00008.1
miR164a	Rsa1.0_00305.1_g00014.1
miR164a	Rsa1.0_08720.1_g00002.1
miR164a	Rsa1.0_00381.1_g00015.1
miR164a,miR164c-5p,miR172d-	Rsa1.0_00568.1_g00009.1
miR164a,novel_35,miR164c-5p	Rsa1.0_07738.1_g00002.1
miR164a,novel_35,miR164c-5p	Rsa1.0_01302.1_g00005.1
miR164a,novel_35,miR164c-5p	Rsa1.0_00541.1_g00022.1
miR164a,novel_35,miR164c-5p	Rsa1.0_00278.1_g00019.1
miR164c-3p	Rsa1.0_04657.1_g00001.1
miR164c-3p	Rsa1.0_00379.1_g00011.1
miR164c-5p	Rsa1.0_00014.1_g00019.1
miR164c-5p	Rsa1.0_00842.1_g00011.1
miR164c-5p	Rsa1.0_00251.1_g00024.1
miR164c-5p	Rsa1.0_00605.1_g00016.1
miR164c-5p,miR164a	Rsa1.0_00253.1_g00028.1
miR164c-5p,miR164a	Rsa1.0_00387.1_g00044.1
miR164c-5p,miR164a	Rsa1.0_05504.1_g00002.1
miR164c-5p,miR164a,novel_35	Rsa1.0_00176.1_g00021.1
miR164c-5p,miR164a,novel_35	Rsa1.0_00492.1_g00005.1
miR164c-5p,miR164a,novel_35	Rsa1.0_00314.1_g00012.1
miR164c-5p,novel_35,miR164a	Rsa1.0_06642.1_g00002.1
miR164c-5p,novel_35,miR164a	Rsa1.0_00466.1_g00002.1
miR165a-3p	Rsa1.0_05218.1_g00004.1
miR165a-3p	Rsa1.0_01115.1_g00008.1
miR165a-5p	Rsa1.0_00662.1_g00018.1
miR165a-5p	Rsa1.0_02004.1_g00001.1
miR165a-5p	Rsa1.0_01828.1_g00006.1
miR165a-5p	Rsa1.0_00556.1_g00038.1
miR165a-5p	Rsa1.0_03962.1_g00004.1
miR165a-5p	Rsa1.0_26999.1_g00001.1
miR165a-5p	Rsa1.0_00207.1_g00021.1
miR165a-5p	Rsa1.0_00234.1_g00019.1
miR166a-3p	Rsa1.0_00733.1_g00006.1

miR166a-3p	Rsa1.0_00085.1_g00017.1
miR166a-3p	Rsa1.0_02161.1_g00003.1
miR166a-3p	Rsa1.0_07052.1_g00001.1
miR166a-3p	Rsa1.0_01043.1_g00006.1
miR166a-3p	Rsa1.0_11222.1_g00001.1
miR166a-5p	Rsa1.0_06046.1_g00002.1
miR166e-5p	Rsa1.0_00622.1_g00011.1
miR166e-5p	Rsa1.0_06029.1_g00001.1
miR166e-5p	Rsa1.0_04440.1_g00001.1
miR166e-5p	Rsa1.0_01946.1_g00002.1
miR166e-5p	Rsa1.0_00698.1_g00003.1
miR166e-5p	Rsa1.0_00230.1_g00011.1
miR166e-5p	Rsa1.0_03322.1_g00004.1
miR166e-5p,miR165a-5p	Rsa1.0_00977.1_g00003.1
miR167a-3p	Rsa1.0_00380.1_g00018.1
miR167a-3p	Rsa1.0_00064.1_g00028.1
miR167a-3p	Rsa1.0_00566.1_g00002.1
miR167a-3p	Rsa1.0_01407.1_g00002.1
miR167a-5p	Rsa1.0_03078.1_g00004.1
miR167a-5p,miR167c-5p	Rsa1.0_01882.1_g00004.1
miR167a-5p,miR167c-5p	Rsa1.0_01113.1_g00009.1
miR167c-5p	Rsa1.0_00329.1_g00008.1
miR167c-5p	Rsa1.0_05490.1_g00001.1
miR167c-5p	Rsa1.0_01823.1_g00002.1
miR167c-5p	Rsa1.0_00519.1_g00011.1
miR167c-5p,miR5658	Rsa1.0_03113.1_g00003.1
miR168a-3p	Rsa1.0_02173.1_g00002.1
miR168a-5p	Rsa1.0_02946.1_g00003.1
miR168a-5p	Rsa1.0_02490.1_g00004.1
miR169a-5p	Rsa1.0_00029.1_g00024.1
miR169a-5p	Rsa1.0_02937.1_g00005.1
miR169a-5p	Rsa1.0_02655.1_g00005.1
miR169a-5p	Rsa1.0_01797.1_g00006.1
miR169a-5p	Rsa1.0_00506.1_g00002.1
miR169a-5p,miR169b-5p,miR16	Rsa1.0_02406.1_g00004.1
miR169a-5p,miR169b-5p,miR16	Rsa1.0_00694.1_g00010.1
miR169b-5p	Rsa1.0_00032.1_g00024.1
miR169b-5p	Rsa1.0_00977.1_g00014.1
miR169b-5p	Rsa1.0_14221.1_g00002.1
miR169b-5p	Rsa1.0_01811.1_g00005.1
miR169b-5p,miR169a-5p	Rsa1.0_00429.1_g00001.1
miR169b-5p,miR169a-5p	Rsa1.0_00083.1_g00034.1
miR169b-5p,miR169a-5p	Rsa1.0_00509.1_g00014.1
miR169b-5p,miR169a-5p,miR16	Rsa1.0_01436.1_g00005.1
miR169b-5p,miR169a-5p,miR16	Rsa1.0_00046.1_g00029.1
miR169b-5p,miR169d,miR396b-	Rsa1.0_00518.1_g00006.1
miR169d	Rsa1.0_03544.1_g00001.1
miR169d	Rsa1.0_00306.1_g00012.1

miR169d,miR169a-5p,miR169b-	Rsa1.0_01855.1_g00009.1
miR169d,miR169b-5p	Rsa1.0_09683.1_g00001.1
miR169d,miR169b-5p,miR169a-	Rsa1.0_00553.1_g00014.1
miR169d,miR169b-5p,miR169a-	Rsa1.0_00307.1_g00009.1
miR169d,miR169b-5p,miR169a-	Rsa1.0_00060.1_g00008.1
miR169d,miR169b-5p,miR169a-	Rsa1.0_00046.1_g00028.1
miR169d,miR169b-5p,miR169a-	Rsa1.0_00055.1_g00053.1
miR169d,miR169b-5p,miR169a-	Rsa1.0_00016.1_g00003.1
miR169f-3p	Rsa1.0_03010.1_g00003.1
miR169f-3p	Rsa1.0_00337.1_g00007.1
miR169f-3p	Rsa1.0_03111.1_g00002.1
miR169f-3p	Rsa1.0_00278.1_g00013.1
miR169f-3p	Rsa1.0_05059.1_g00001.1
miR169f-3p,miR169b-5p,miR16	Rsa1.0_03674.1_g00004.1
miR169g-3p	Rsa1.0_01499.1_g00003.1
miR169g-3p	Rsa1.0_00576.1_g00024.1
miR170-3p	Rsa1.0_01434.1_g00006.1
miR170-3p	Rsa1.0_06840.1_g00002.1
miR170-3p	Rsa1.0_00058.1_g00028.1
miR170-3p,miR171b-3p	Rsa1.0_00152.1_g00017.1
miR170-5p	Rsa1.0_62908.1_g00001.1
miR170-5p	Rsa1.0_00734.1_g00004.1
miR171a-3p	Rsa1.0_03527.1_g00004.1
miR171a-3p	Rsa1.0_00474.1_g00005.1
miR171a-3p	Rsa1.0_00081.1_g00022.1
miR171a-3p,miR170-3p,miR171	Rsa1.0_01373.1_g00003.1
miR171a-3p,miR170-3p,miR171	Rsa1.0_02830.1_g00004.1
miR171b-3p	Rsa1.0_15744.1_g00001.1
miR171b-3p	Rsa1.0_00037.1_g00020.1
miR171b-3p,miR170-3p,miR171	Rsa1.0_03244.1_g00001.1
miR171b-3p,miR171a-3p,miR17	Rsa1.0_01094.1_g00004.1
miR171b-3p,miR171a-3p,miR17	Rsa1.0_00693.1_g00004.1
miR171b-5p	Rsa1.0_06227.1_g00001.1
miR171b-5p	Rsa1.0_01811.1_g00010.1
miR171b-5p	Rsa1.0_00024.1_g00015.1
miR171b-5p	Rsa1.0_00352.1_g00007.1
miR171b-5p	Rsa1.0_00621.1_g00005.1
miR171b-5p	Rsa1.0_02860.1_g00004.1
miR172a	Rsa1.0_00767.1_g00007.1
miR172a	Rsa1.0_00008.1_g00021.1
miR172a	Rsa1.0_00071.1_g00046.1
miR172a	Rsa1.0_04207.1_g00003.1
miR172a	Rsa1.0_00887.1_g00003.1
miR172a	Rsa1.0_02358.1_g00002.1
miR172a,miR172c,miR172e-3p	Rsa1.0_01717.1_g00004.1
miR172a,miR172c,miR172e-3p	Rsa1.0_01237.1_g00007.1
miR172a,miR172e-3p	Rsa1.0_10548.1_g00001.1
miR172a,miR172e-3p,miR172c	Rsa1.0_00099.1_g00005.1

miR172a,miR5658,miR172e-3p	Rsa1.0_00483.1_g00005.1
miR172b-5p	Rsa1.0_02092.1_g00009.1
miR172b-5p	Rsa1.0_04890.1_g00001.1
miR172b-5p	Rsa1.0_27165.1_g00001.1
miR172b-5p	Rsa1.0_00546.1_g00002.1
miR172b-5p	Rsa1.0_00289.1_g00002.1
miR172b-5p	Rsa1.0_00599.1_g00016.1
miR172b-5p	Rsa1.0_09807.1_g00001.1
miR172b-5p	Rsa1.0_00111.1_g00015.1
miR172b-5p	Rsa1.0_05636.1_g00002.1
miR172b-5p	Rsa1.0_00728.1_g00011.1
miR172b-5p	Rsa1.0_03448.1_g00004.1
miR172b-5p	Rsa1.0_17189.1_g00001.1
miR172b-5p	Rsa1.0_05518.1_g00001.1
miR172b-5p	Rsa1.0_00038.1_g00052.1
miR172b-5p	Rsa1.0_00763.1_g00004.1
miR172b-5p	Rsa1.0_01685.1_g00010.1
miR172b-5p	Rsa1.0_04225.1_g00001.1
miR172b-5p	Rsa1.0_00754.1_g00001.1
miR172b-5p,miR164a,miR164c-	Rsa1.0_00003.1_g00029.1
miR172c	Rsa1.0_02754.1_g00005.1
miR172c	Rsa1.0_25366.1_g00001.1
miR172c	Rsa1.0_00218.1_g00024.1
miR172c	Rsa1.0_00018.1_g00066.1
miR172c,miR172a	Rsa1.0_00576.1_g00016.1
miR172c,miR172b-5p,miR172e-	Rsa1.0_00285.1_g00011.1
miR172c,miR172e-3p,miR172a	Rsa1.0_04622.1_g00002.1
miR172c,miR172e-3p,miR172a,	Rsa1.0_04013.1_g00001.1
miR172d-5p	Rsa1.0_01634.1_g00010.1
miR172d-5p	Rsa1.0_00340.1_g00015.1
miR172d-5p	Rsa1.0_01742.1_g00005.1
miR172d-5p	Rsa1.0_01868.1_g00004.1
miR172d-5p	Rsa1.0_01785.1_g00002.1
miR172d-5p	Rsa1.0_01419.1_g00007.1
miR172d-5p	Rsa1.0_34341.1_g00001.1
miR172d-5p	Rsa1.0_02149.1_g00004.1
miR172d-5p	Rsa1.0_21756.1_g00001.1
miR172d-5p	Rsa1.0_06648.1_g00003.1
miR172d-5p	Rsa1.0_02435.1_g00004.1
miR172d-5p	Rsa1.0_04744.1_g00003.1
miR172d-5p	Rsa1.0_15547.1_g00001.1
miR172d-5p	Rsa1.0_23672.1_g00001.1
miR172d-5p	Rsa1.0_01789.1_g00004.1
miR172d-5p	Rsa1.0_01774.1_g00003.1
miR172d-5p	Rsa1.0_02827.1_g00003.1
miR172d-5p	Rsa1.0_02733.1_g00001.1
miR172d-5p	Rsa1.0_00368.1_g00001.1
miR172d-5p	Rsa1.0_00105.1_g00019.1

miR172d-5p	Rsa1.0_00359.1_g00004.1
miR172d-5p	Rsa1.0_00496.1_g00003.1
miR172d-5p	Rsa1.0_00426.1_g00011.1
miR172e-3p	Rsa1.0_01092.1_g00002.1
miR172e-3p	Rsa1.0_00319.1_g00019.1
miR172e-3p	Rsa1.0_01109.1_g00008.1
miR172e-3p	Rsa1.0_02149.1_g00003.1
miR172e-3p	Rsa1.0_00159.1_g00043.1
miR172e-3p,miR172a	Rsa1.0_04939.1_g00001.1
miR172e-3p,miR172c,miR172a	Rsa1.0_00324.1_g00001.1
miR172e-3p,miR172c,miR172a	Rsa1.0_02242.1_g00002.1
miR172e-3p,miR172c,miR172a	Rsa1.0_01063.1_g00001.1
miR172e-3p,miR172c,miR172a	Rsa1.0_00201.1_g00027.1
miR172e-3p,miR172c,miR172a	Rsa1.0_00621.1_g00004.1
miR2111a-3p	Rsa1.0_00156.1_g00014.1
miR2111a-5p	Rsa1.0_00300.1_g00021.1
miR2111a-5p	Rsa1.0_00252.1_g00018.1
miR319a	Rsa1.0_12335.1_g00001.1
miR319a	Rsa1.0_02059.1_g00003.1
miR319a,miR159c,miR159b-3p,	Rsa1.0_01523.1_g00007.1
miR319a,miR159c,miR319c	Rsa1.0_01779.1_g00003.1
miR319a,miR319c	Rsa1.0_01271.1_g00009.1
miR319a,miR396b-5p,miR396a-	Rsa1.0_24799.1_g00001.1
miR319c	Rsa1.0_25214.1_g00001.1
miR319c	Rsa1.0_00466.1_g00013.1
miR319c	Rsa1.0_20996.1_g00001.1
miR319c	Rsa1.0_00377.1_g00011.1
miR319c	Rsa1.0_00703.1_g00002.1
miR319c	Rsa1.0_01583.1_g00006.1
miR319c	Rsa1.0_02070.1_g00011.1
miR319c	Rsa1.0_03198.1_g00001.1
miR319c	Rsa1.0_06859.1_g00002.1
miR319c	Rsa1.0_00793.1_g00010.1
miR319c,miR159c,miR319a	Rsa1.0_06149.1_g00004.1
miR319c,miR159c,miR319a	Rsa1.0_12766.1_g00001.1
miR319c,miR159c,miR319a	Rsa1.0_04329.1_g00001.1
miR319c,miR319a	Rsa1.0_13515.1_g00001.1
miR319c,miR319a	Rsa1.0_00340.1_g00017.1
miR319c,miR319a	Rsa1.0_10084.1_g00001.1
miR319c,miR319a	Rsa1.0_03106.1_g00001.1
miR319c,miR319a	Rsa1.0_00786.1_g00008.1
miR390a-3p	Rsa1.0_00352.1_g00013.1
miR390a-3p,miR390b-3p	Rsa1.0_15672.1_g00001.1
miR390a-5p	Rsa1.0_01281.1_g00013.1
miR390a-5p	Rsa1.0_03430.1_g00005.1
miR390a-5p	Rsa1.0_00002.1_g00063.1
miR390a-5p	Rsa1.0_07699.1_g00003.1
miR390a-5p	Rsa1.0_00157.1_g00044.1

miR390a-5p	Rsa1.0_00556.1_g00023.1
miR390a-5p	Rsa1.0_00001.1_g00002.1
miR390a-5p	Rsa1.0_00009.1_g00011.1
miR390b-3p,miR390a-3p	Rsa1.0_00398.1_g00019.1
miR391-5p	Rsa1.0_00412.1_g00008.1
miR391-5p	Rsa1.0_06930.1_g00001.1
miR391-5p	Rsa1.0_00124.1_g00026.1
miR393a-5p	Rsa1.0_00031.1_g00028.1
miR393a-5p	Rsa1.0_00332.1_g00003.1
miR393a-5p	Rsa1.0_00330.1_g00013.1
miR393a-5p	Rsa1.0_02710.1_g00004.1
miR393a-5p	Rsa1.0_00002.1_g00071.1
miR393a-5p	Rsa1.0_00417.1_g00019.1
miR393a-5p	Rsa1.0_04434.1_g00002.1
miR393a-5p	Rsa1.0_09417.1_g00001.1
miR393a-5p	Rsa1.0_02127.1_g00001.1
miR393a-5p	Rsa1.0_00202.1_g00005.1
miR393a-5p	Rsa1.0_00020.1_g00021.1
miR394a	Rsa1.0_04167.1_g00002.1
miR394a	Rsa1.0_01455.1_g00006.1
miR394a	Rsa1.0_00299.1_g00005.1
miR394a	Rsa1.0_02830.1_g00002.1
miR394a	Rsa1.0_00460.1_g00009.1
miR394a	Rsa1.0_05076.1_g00007.1
miR395a	Rsa1.0_70604.1_g00001.1
miR395a	Rsa1.0_08869.1_g00002.1
miR395a	Rsa1.0_05783.1_g00001.1
miR395a	Rsa1.0_07396.1_g00002.1
miR395a	Rsa1.0_01569.1_g00004.1
miR395a	Rsa1.0_03819.1_g00003.1
miR395a	Rsa1.0_00033.1_g00053.1
miR395a	Rsa1.0_00886.1_g00015.1
miR395a	Rsa1.0_13934.1_g00001.1
miR395a,miR395b	Rsa1.0_04988.1_g00002.1
miR395a,miR395b	Rsa1.0_00468.1_g00009.1
miR395b	Rsa1.0_01740.1_g00002.1
miR395b	Rsa1.0_01776.1_g00006.1
miR395b	Rsa1.0_02280.1_g00005.1
miR395b	Rsa1.0_00184.1_g00005.1
miR395b	Rsa1.0_00789.1_g00002.1
miR395b	Rsa1.0_14196.1_g00001.1
miR395b	Rsa1.0_02838.1_g00001.1
miR395b	Rsa1.0_08670.1_g00002.1
miR395b	Rsa1.0_01131.1_g00002.1
miR395b,miR395a	Rsa1.0_00493.1_g00009.1
miR395b,miR395a	Rsa1.0_00057.1_g00018.1
miR395b,miR395a	Rsa1.0_01524.1_g00007.1
miR396a-3p	Rsa1.0_05599.1_g00005.1

miR396a-3p	Rsa1.0_00187.1_g00013.1
miR396a-5p	Rsa1.0_00559.1_g00015.1
miR396a-5p	Rsa1.0_01430.1_g00005.1
miR396a-5p	Rsa1.0_05819.1_g00002.1
miR396a-5p	Rsa1.0_00037.1_g00016.1
miR396a-5p	Rsa1.0_07051.1_g00001.1
miR396a-5p	Rsa1.0_05986.1_g00002.1
miR396a-5p	Rsa1.0_71688.1_g00001.1
miR396a-5p	Rsa1.0_01351.1_g00002.1
miR396a-5p	Rsa1.0_01986.1_g00002.1
miR396a-5p	Rsa1.0_00949.1_g00001.1
miR396a-5p	Rsa1.0_03679.1_g00003.1
miR396a-5p	Rsa1.0_00556.1_g00039.1
miR396a-5p	Rsa1.0_03832.1_g00002.1
miR396a-5p	Rsa1.0_19817.1_g00001.1
miR396a-5p	Rsa1.0_03174.1_g00004.1
miR396a-5p	Rsa1.0_12795.1_g00002.1
miR396a-5p	Rsa1.0_01084.1_g00006.1
miR396a-5p	Rsa1.0_00675.1_g00001.1
miR396a-5p	Rsa1.0_08879.1_g00001.1
miR396a-5p	Rsa1.0_02988.1_g00003.1
miR396a-5p	Rsa1.0_07592.1_g00002.1
miR396a-5p	Rsa1.0_00019.1_g00045.1
miR396a-5p	Rsa1.0_05235.1_g00001.1
miR396a-5p	Rsa1.0_07559.1_g00001.1
miR396a-5p	Rsa1.0_00531.1_g00013.1
miR396a-5p	Rsa1.0_01368.1_g00005.1
miR396a-5p	Rsa1.0_03268.1_g00002.1
miR396a-5p	Rsa1.0_04164.1_g00003.1
miR396a-5p	Rsa1.0_10285.1_g00001.1
miR396a-5p,miR396b-5p	Rsa1.0_00320.1_g00017.1
miR396a-5p,miR396b-5p	Rsa1.0_02616.1_g00004.1
miR396a-5p,miR396b-5p	Rsa1.0_08623.1_g00002.1
miR396a-5p,miR396b-5p	Rsa1.0_00040.1_g00051.1
miR396a-5p,miR396b-5p	Rsa1.0_00573.1_g00008.1
miR396a-5p,miR396b-5p	Rsa1.0_14703.1_g00001.1
miR396a-5p,miR396b-5p	Rsa1.0_00032.1_g00031.1
miR396a-5p,miR396b-5p	Rsa1.0_09034.1_g00001.1
miR396a-5p,miR5658,miR396b-	Rsa1.0_03276.1_g00003.1
miR396b-3p	Rsa1.0_00017.1_g00146.1
miR396b-5p	Rsa1.0_01509.1_g00001.1
miR396b-5p	Rsa1.0_01415.1_g00004.1
miR396b-5p	Rsa1.0_05908.1_g00002.1
miR396b-5p	Rsa1.0_19380.1_g00001.1
miR396b-5p	Rsa1.0_00407.1_g00011.1
miR396b-5p	Rsa1.0_00002.1_g00030.1
miR396b-5p	Rsa1.0_02919.1_g00002.1
miR396b-5p	Rsa1.0_01228.1_g00007.1

miR396b-5p	Rsa1.0_03034.1_g00003.1
miR396b-5p	Rsa1.0_00090.1_g00011.1
miR396b-5p	Rsa1.0_06561.1_g00002.1
miR396b-5p	Rsa1.0_00024.1_g00022.1
miR396b-5p	Rsa1.0_07720.1_g00002.1
miR396b-5p	Rsa1.0_30464.1_g00001.1
miR396b-5p	Rsa1.0_03358.1_g00003.1
miR396b-5p	Rsa1.0_01896.1_g00003.1
miR396b-5p	Rsa1.0_02870.1_g00004.1
miR396b-5p	Rsa1.0_08220.1_g00002.1
miR396b-5p	Rsa1.0_00394.1_g00027.1
miR396b-5p	Rsa1.0_04355.1_g00001.1
miR396b-5p,miR156f-3p	Rsa1.0_37312.1_g00001.1
miR396b-5p,miR156f-3p	Rsa1.0_01523.1_g00008.1
miR396b-5p,miR396a-5p	Rsa1.0_02734.1_g00002.1
miR396b-5p,miR396a-5p	Rsa1.0_01481.1_g00010.1
miR396b-5p,miR396a-5p	Rsa1.0_00707.1_g00001.1
miR396b-5p,miR396a-5p	Rsa1.0_01359.1_g00007.1
miR396b-5p,miR396a-5p	Rsa1.0_06427.1_g00002.1
miR396b-5p,miR396a-5p	Rsa1.0_00159.1_g00036.1
miR396b-5p,miR396a-5p	Rsa1.0_00107.1_g00067.1
miR396b-5p,miR396a-5p	Rsa1.0_00982.1_g00001.1
miR396b-5p,miR396a-5p	Rsa1.0_01882.1_g00001.1
miR396b-5p,miR396a-5p	Rsa1.0_00056.1_g00044.1
miR396b-5p,miR396a-5p	Rsa1.0_01844.1_g00002.1
miR396b-5p,miR396a-5p	Rsa1.0_07424.1_g00001.1
miR396b-5p,miR396a-5p	Rsa1.0_04196.1_g00001.1
miR397a	Rsa1.0_00834.1_g00007.1
miR397a	Rsa1.0_00005.1_g00036.1
miR397a	Rsa1.0_00034.1_g00040.1
miR397a	Rsa1.0_00654.1_g00012.1
miR397a	Rsa1.0_07894.1_g00001.1
miR397a	Rsa1.0_08883.1_g00001.1
miR397a	Rsa1.0_06343.1_g00002.1
miR397a	Rsa1.0_01433.1_g00003.1
miR397a	Rsa1.0_03355.1_g00004.1
miR397a	Rsa1.0_00328.1_g00010.1
miR397a	Rsa1.0_02282.1_g00002.1
miR397a	Rsa1.0_00415.1_g00010.1
miR397a	Rsa1.0_00099.1_g00001.1
miR397a	Rsa1.0_20916.1_g00001.1
miR397a	Rsa1.0_00048.1_g00023.1
miR398a-3p	Rsa1.0_02319.1_g00005.1
miR398a-3p	Rsa1.0_09097.1_g00002.1
miR398a-3p	Rsa1.0_03668.1_g00004.1
miR398a-3p,miR398b-3p	Rsa1.0_03067.1_g00006.1
miR398b-5p	Rsa1.0_04335.1_g00001.1
miR398b-5p	Rsa1.0_01453.1_g00012.1

miR398b-5p	Rsa1.0_00050.1_g00020.1
miR398b-5p	Rsa1.0_41706.1_g00001.1
miR398b-5p	Rsa1.0_06177.1_g00001.1
miR398b-5p	Rsa1.0_00131.1_g00056.1
miR398b-5p	Rsa1.0_00797.1_g00006.1
miR398b-5p	Rsa1.0_08375.1_g00002.1
miR398b-5p	Rsa1.0_00484.1_g00009.1
miR398b-5p	Rsa1.0_00498.1_g00009.1
miR398b-5p	Rsa1.0_00237.1_g00001.1
miR398b-5p	Rsa1.0_00053.1_g00007.1
miR398b-5p,miR156j	Rsa1.0_03312.1_g00001.1
miR399b	Rsa1.0_02532.1_g00001.1
miR399b	Rsa1.0_03604.1_g00001.1
miR399b	Rsa1.0_58331.1_g00001.1
miR399b	Rsa1.0_01192.1_g00002.1
miR399b	Rsa1.0_08861.1_g00002.1
miR399b	Rsa1.0_00165.1_g00016.1
miR399b	Rsa1.0_09006.1_g00001.1
miR399f	Rsa1.0_00365.1_g00014.1
miR399f	Rsa1.0_08706.1_g00001.1
miR399f	Rsa1.0_00671.1_g00002.1
miR399f,miR399b	Rsa1.0_00111.1_g00037.1
miR399f,miR399b	Rsa1.0_00086.1_g00012.1
miR400	Rsa1.0_00488.1_g00003.1
miR400	Rsa1.0_00589.1_g00023.1
miR400	Rsa1.0_08377.1_g00001.1
miR400	Rsa1.0_01351.1_g00005.1
miR400	Rsa1.0_46818.1_g00001.1
miR400	Rsa1.0_02154.1_g00004.1
miR400	Rsa1.0_02032.1_g00005.1
miR400	Rsa1.0_00596.1_g00017.1
miR400	Rsa1.0_00059.1_g00011.1
miR400	Rsa1.0_39362.1_g00001.1
miR400	Rsa1.0_05188.1_g00001.1
miR400	Rsa1.0_20921.1_g00001.1
miR400	Rsa1.0_04165.1_g00005.1
miR400	Rsa1.0_10113.1_g00001.1
miR400	Rsa1.0_18167.1_g00001.1
miR400	Rsa1.0_03142.1_g00005.1
miR400	Rsa1.0_00745.1_g00001.1
miR400	Rsa1.0_01537.1_g00002.1
miR400	Rsa1.0_04898.1_g00001.1
miR400	Rsa1.0_04632.1_g00003.1
miR400	Rsa1.0_04159.1_g00001.1
miR400	Rsa1.0_00869.1_g00007.1
miR400	Rsa1.0_00224.1_g00044.1
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miR400	Rsa1.0_10155.1_g00002.1

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miR400	Rsa1.0_30585.1_g00001.1
miR400	Rsa1.0_05787.1_g00001.1
miR400	Rsa1.0_00239.1_g00005.1
miR400	Rsa1.0_00239.1_g00011.1
miR400	Rsa1.0_20310.1_g00001.1
miR400	Rsa1.0_03786.1_g00003.1
miR400	Rsa1.0_03943.1_g00006.1
miR400	Rsa1.0_00407.1_g00015.1
miR400	Rsa1.0_03686.1_g00004.1
miR400	Rsa1.0_01171.1_g00007.1
miR400	Rsa1.0_00036.1_g00032.1
miR400	Rsa1.0_03921.1_g00002.1
miR400	Rsa1.0_01794.1_g00002.1
miR400	Rsa1.0_00113.1_g00008.1
miR400	Rsa1.0_00539.1_g00006.1
miR400	Rsa1.0_00073.1_g00006.1
miR400	Rsa1.0_00863.1_g00005.1
miR400	Rsa1.0_01090.1_g00006.1
miR400	Rsa1.0_01329.1_g00001.1
miR403-3p	Rsa1.0_05146.1_g00001.1
miR403-3p	Rsa1.0_03659.1_g00001.1
miR403-3p	Rsa1.0_10460.1_g00002.1
miR403-3p	Rsa1.0_00459.1_g00001.1
miR403-3p	Rsa1.0_06826.1_g00001.1
miR403-5p	Rsa1.0_00616.1_g00002.1
miR403-5p	Rsa1.0_21206.1_g00001.1
miR403-5p	Rsa1.0_00073.1_g00017.1
miR403-5p	Rsa1.0_00064.1_g00010.1
miR403-5p	Rsa1.0_01722.1_g00002.1
miR403-5p	Rsa1.0_47333.1_g00001.1
miR403-5p	Rsa1.0_01853.1_g00017.1
miR403-5p	Rsa1.0_00015.1_g00088.1
miR403-5p	Rsa1.0_08897.1_g00001.1
miR403-5p	Rsa1.0_00184.1_g00018.1
miR403-5p	Rsa1.0_00183.1_g00006.1
miR403-5p	Rsa1.0_00878.1_g00014.1
miR403-5p	Rsa1.0_00157.1_g00028.1
miR403-5p	Rsa1.0_01704.1_g00005.1
miR408-3p	Rsa1.0_00068.1_g00014.1
miR408-3p	Rsa1.0_02232.1_g00003.1
miR408-3p	Rsa1.0_07478.1_g00002.1
miR408-3p	Rsa1.0_01611.1_g00001.1
miR408-3p	Rsa1.0_14747.1_g00001.1
miR408-3p	Rsa1.0_00117.1_g00027.1
miR408-5p	Rsa1.0_07094.1_g00002.1

miR408-5p	Rsa1.0_00359.1_g00009.1
miR408-5p	Rsa1.0_02857.1_g00003.1
miR408-5p	Rsa1.0_08288.1_g00001.1
miR408-5p	Rsa1.0_00560.1_g00009.1
miR408-5p	Rsa1.0_09048.1_g00001.1
miR408-5p	Rsa1.0_00243.1_g00026.1
miR408-5p	Rsa1.0_00238.1_g00017.1
miR408-5p	Rsa1.0_03434.1_g00004.1
miR408-5p	Rsa1.0_00033.1_g00020.1
miR408-5p	Rsa1.0_01867.1_g00008.1
miR408-5p	Rsa1.0_02255.1_g00003.1
miR408-5p	Rsa1.0_00058.1_g00034.1
miR408-5p	Rsa1.0_02559.1_g00004.1
miR408-5p	Rsa1.0_01636.1_g00004.1
miR408-5p	Rsa1.0_02070.1_g00009.1
miR408-5p	Rsa1.0_04336.1_g00001.1
miR408-5p	Rsa1.0_00341.1_g00034.1
miR5630a	Rsa1.0_19248.1_g00001.1
miR5630a	Rsa1.0_00855.1_g00002.1
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miR5630a	Rsa1.0_01199.1_g00015.1
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miR8175	Rsa1.0_02483.1_g00003.1
miR8175	Rsa1.0_04143.1_g00003.1
miR8175	Rsa1.0_06773.1_g00002.1
miR8175	Rsa1.0_05199.1_g00002.1
miR8175	Rsa1.0_01653.1_g00005.1
miR8175	Rsa1.0_02535.1_g00002.1
miR8175	Rsa1.0_08331.1_g00001.1
miR8175	Rsa1.0_04815.1_g00002.1

miR8175	Rsa1.0_03412.1_g00005.1
miR8175	Rsa1.0_10700.1_g00001.1
miR8175	Rsa1.0_01849.1_g00001.1
miR8175	Rsa1.0_04702.1_g00002.1
miR8175	Rsa1.0_06285.1_g00001.1
miR8175	Rsa1.0_01858.1_g00002.1
miR8175	Rsa1.0_08171.1_g00001.1
miR8175	Rsa1.0_12968.1_g00001.1
miR8175	Rsa1.0_09596.1_g00001.1
miR8175	Rsa1.0_01734.1_g00006.1
miR8175,miR157c-3p	Rsa1.0_05463.1_g00001.1
miR8175,miR157c-3p	Rsa1.0_01708.1_g00001.1
miR8175,miR172b-5p	Rsa1.0_00337.1_g00005.1
miR824-3p	Rsa1.0_00190.1_g00056.1
miR824-3p	Rsa1.0_19279.1_g00002.1
miR824-3p	Rsa1.0_16626.1_g00001.1
miR824-3p	Rsa1.0_04849.1_g00002.1
miR824-3p	Rsa1.0_00135.1_g00024.1
miR824-3p	Rsa1.0_00217.1_g00001.1
miR824-3p	Rsa1.0_02022.1_g00002.1
miR824-3p	Rsa1.0_01513.1_g00008.1
miR824-3p	Rsa1.0_01146.1_g00011.1
miR824-3p,miR398a-3p	Rsa1.0_00716.1_g00008.1
miR824-5p	Rsa1.0_01731.1_g00004.1
miR824-5p	Rsa1.0_01329.1_g00004.1
miR824-5p	Rsa1.0_05752.1_g00001.1
miR824-5p	Rsa1.0_02324.1_g00002.1
miR824-5p	Rsa1.0_00570.1_g00018.1
miR824-5p	Rsa1.0_11424.1_g00002.1
miR824-5p	Rsa1.0_04330.1_g00001.1
miR824-5p	Rsa1.0_07821.1_g00001.1
miR824-5p	Rsa1.0_01061.1_g00007.1
miR824-5p	Rsa1.0_00266.1_g00010.1
miR824-5p	Rsa1.0_01468.1_g00007.1
miR824-5p	Rsa1.0_00344.1_g00022.1
miR827	Rsa1.0_01135.1_g00005.1
miR827	Rsa1.0_01779.1_g00001.1
miR827	Rsa1.0_02124.1_g00006.1
miR827	Rsa1.0_00080.1_g00003.1
miR827	Rsa1.0_00391.1_g00008.1
miR827	Rsa1.0_06138.1_g00001.1
miR827	Rsa1.0_00336.1_g00019.1
miR827	Rsa1.0_00364.1_g00010.1
miR827	Rsa1.0_08966.1_g00001.1
miR827	Rsa1.0_02038.1_g00003.1
miR827	Rsa1.0_05774.1_g00001.1
miR827	Rsa1.0_08724.1_g00001.1
miR827	Rsa1.0_00166.1_g00009.1

miR857	Rsa1.0_01716.1_g00001.1
miR857	Rsa1.0_00999.1_g00001.1
miR857	Rsa1.0_00973.1_g00009.1
miR857	Rsa1.0_00117.1_g00022.1
miR857	Rsa1.0_04238.1_g00003.1
miR857	Rsa1.0_01620.1_g00003.1
miR857	Rsa1.0_07981.1_g00001.1
miR857	Rsa1.0_01260.1_g00003.1
miR857	Rsa1.0_02022.1_g00001.1
miR857	Rsa1.0_28733.1_g00001.1
miR857	Rsa1.0_03287.1_g00002.1
miR857	Rsa1.0_28713.1_g00001.1
miR857	Rsa1.0_00196.1_g00026.1
miR857	Rsa1.0_01101.1_g00007.1
miR857	Rsa1.0_00261.1_g00007.1
miR857	Rsa1.0_13754.1_g00001.1
miR857	Rsa1.0_00015.1_g00017.1
miR857	Rsa1.0_01253.1_g00004.1
miR857	Rsa1.0_00451.1_g00023.1
miR857	Rsa1.0_00026.1_g00062.1
miR857	Rsa1.0_01055.1_g00006.1
miR857	Rsa1.0_25220.1_g00001.1
miR857	Rsa1.0_01690.1_g00005.1
miR857	Rsa1.0_00920.1_g00025.1
miR858a	Rsa1.0_00865.1_g00001.1
miR858a	Rsa1.0_53777.1_g00001.1
miR858a	Rsa1.0_51959.1_g00001.1
miR858a	Rsa1.0_00199.1_g00036.1
miR858a	Rsa1.0_01642.1_g00004.1
miR858a,miR858b	Rsa1.0_04490.1_g00001.1
miR858a,miR858b	Rsa1.0_14336.1_g00001.1
miR858a,miR858b	Rsa1.0_00640.1_g00007.1
miR858a,miR858b	Rsa1.0_14223.1_g00001.1
miR858a,miR858b	Rsa1.0_02496.1_g00006.1
miR858a,miR858b	Rsa1.0_15530.1_g00001.1
miR858b	Rsa1.0_00909.1_g00003.1
miR858b	Rsa1.0_00009.1_g00037.1
miR858b	Rsa1.0_03281.1_g00002.1
miR858b	Rsa1.0_01570.1_g00007.1
miR858b	Rsa1.0_01880.1_g00001.1
miR858b	Rsa1.0_02829.1_g00003.1
miR858b	Rsa1.0_00015.1_g00085.1
miR858b,miR156g,miR858a	Rsa1.0_00822.1_g00001.1
miR858b,miR159a,miR858a,miR	Rsa1.0_00025.1_g00043.1
miR858b,miR858a	Rsa1.0_00484.1_g00005.1
miR858b,miR858a	Rsa1.0_00463.1_g00020.1
miR858b,miR858a	Rsa1.0_09985.1_g00001.1
miR858b,miR858a	Rsa1.0_00408.1_g00004.1

miR858b,miR858a	Rsa1.0_00088.1_g00009.1
miR858b,miR858a	Rsa1.0_00065.1_g00014.1
miR858b,miR858a	Rsa1.0_00761.1_g00003.1
miR858b,miR858a	Rsa1.0_02070.1_g00006.1
miR858b,miR858a	Rsa1.0_01629.1_g00005.1
miR858b,miR858a	Rsa1.0_03421.1_g00004.1
novel_35,miR164a,miR164c-5p	Rsa1.0_07584.1_g00001.1
novel_35,miR164a,miR164c-5p	Rsa1.0_00166.1_g00017.1
novel_35,miR164a,miR164c-5p	Rsa1.0_00428.1_g00008.1
novel_35,miR164a,miR164c-5p	Rsa1.0_02628.1_g00006.1
novel_35,miR164a,miR164c-5p	Rsa1.0_00377.1_g00002.1

l miRNAs.

Annotation
POP3_ARATH Probable protein Pop3
DCMC_HUMAN Malonyl-CoA decarboxylase, mitochondrial
COG1_MOUSE Conserved oligomeric Golgi complex subunit 1
Y3471_ARATH Putative receptor-like protein kinase At3g47110
Y2608_ARATH B3 domain-containing protein At2g36080
TT12_ARATH Protein TRANSPARENT TESTA 12
BCAT3_ARATH Branched-chain-amino-acid aminotransferase 3, chloroplastic
BCA1_ARATH Beta carbonic anhydrase 1, chloroplastic
RNHX1_ARATH Putative ribonuclease H protein At1g65750
QSOX1_ARATH Sulfhydryl oxidase 1
PRS8A_ARATH 26S protease regulatory subunit 8 homolog A
PRP3_ARATH Proline-rich protein 3
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
AAP4_ARATH Amino acid permease 4
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
LTO1_ARATH Thiol-disulfide oxidoreductase LTO1
LORF2_MOUSE LINE-1 retrotransposable element ORF2 protein
F188A_MOUSE Protein FAM188A
EIF3I_ARATH Eukaryotic translation initiation factor 3 subunit I
DCL_SOLLC Protein DCL, chloroplastic
WRK19_ARATH Probable WRKY transcription factor 19
1A15_ARATH 1-aminocyclopropane-1-carboxylate synthase 5
TRXB2_ARATH Thioredoxin reductase 2
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
RL32_ARATH 60S ribosomal protein L3-2
AB18G_ARATH ABC transporter G family member 18
AAPT1_ARATH Choline/ethanolaminephosphotransferase 1
NDUA9_ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
LIN1_NYCCO LINE-1 reverse transcriptase homolog
LIN1_NYCCO LINE-1 reverse transcriptase homolog
LIN1_NYCCO LINE-1 reverse transcriptase homolog
IMK3_ARATH Probable leucine-rich repeat receptor-like protein kinase IMK3
SPL5_ARATH Squamosa promoter-binding-like protein 5
SPL10_ARATH Squamosa promoter-binding-like protein 10
CSLC5_ARATH Probable xyloglucan glycosyltransferase 5
Y1583_ARATH Uncharacterized protein At1g05835
CIPK8_ARATH CBL-interacting serine/threonine-protein kinase 8
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
COG1_MOUSE Conserved oligomeric Golgi complex subunit 1

RB24B_XENLA RNA-binding protein 24-B
CSE_ARATH Caffeoylshikimate esterase
U7E11_ARATH UDP-glycosyltransferase 76E11
LORF2_MOUSE LINE-1 retrotransposable element ORF2 protein
NUA_ARATH Nuclear-pore anchor
NUA_ARATH Nuclear-pore anchor
NUA_ARATH Nuclear-pore anchor
HSD5_ARATH 11-beta-hydroxysteroid dehydrogenase-like 5
TPR4_ARATH Topless-related protein 4
Y8359_ORYSI Uncharacterized protein OsI_027940
WTR6_ARATH WAT1-related protein At1g25270
BAM3_ARATH Beta-amylase 3, chloroplastic
NRPD1_ARATH DNA-directed RNA polymerase IV subunit 1
KU70_ARATH ATP-dependent DNA helicase 2 subunit KU70
ARAK_ARATH L-arabinokinase
GCST_ARATH Aminomethyltransferase, mitochondrial
EXPB1_ARATH Expansin-B1
DXS1_ORYSJ 1-deoxy-D-xylulose-5-phosphate synthase 1, chloroplastic
AEDO_DICDI Probable 2-aminoethanethiol dioxygenase
DMS3_ARATH Protein DEFECTIVE IN MERISTEM SILENCING 3
COPIA_DROME Copia protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
VRN2_ARATH Polycomb group protein VERNALIZATION 2
SPA1_ARATH Protein SUPPRESSOR OF PHYA-105 1
SOSSB_DICDI SOSS complex subunit B homolog
BCCIP_ARATH Protein BCCIP homolog
ATPF2_HUMAN ATP synthase mitochondrial F1 complex assembly factor 2
RBOHG_ARATH Putative respiratory burst oxidase homolog protein G
PYRB_ARATH Aspartate carbamoyltransferase, chloroplastic
NLAL1_ARATH Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1
MYO17_ARATH Myosin-17
MPK16_ARATH Mitogen-activated protein kinase 16
KIN17_MOUSE DNA/RNA-binding protein KIN17
COPIA_DROME Copia protein
SPL6_ARATH Squamosa promoter-binding-like protein 6
SPL3_ARATH Squamosa promoter-binding-like protein 3
LIN1_NYCCO LINE-1 reverse transcriptase homolog
SP13B_ARATH Squamosa promoter-binding-like protein 13B
GSTT3_ARATH Glutathione S-transferase T3
SPL3_ARATH Squamosa promoter-binding-like protein 3
AB17C_DANRE Alpha/beta hydrolase domain-containing protein 17C
SP13B_ARATH Squamosa promoter-binding-like protein 13B
AAPC_CENCI Putative glucose-6-phosphate 1-epimerase
DRL29_ARATH Probable disease resistance protein At4g33300
SPL2_ARATH Squamosa promoter-binding-like protein 2
SPL9_ARATH Squamosa promoter-binding-like protein 9
SPL9_ARATH Squamosa promoter-binding-like protein 9

Y1061_ARATH Probably inactive leucine-rich repeat receptor-like protein kinase At1g50610
SPL4_ARATH Squamosa promoter-binding-like protein 4
SP13B_ARATH Squamosa promoter-binding-like protein 13B
DHX36_MOUSE ATP-dependent RNA helicase DHX36
DF184_ARATH Putative defensin-like protein 184
DESI1_HUMAN Desumoylating isopeptidase 1
ADCS_ARATH Aminodeoxychorismate synthase, chloroplastic
CYSK1_BRAJU Cysteine synthase
ACT2_ARATH Actin-2
CXE6_ARATH Probable carboxylesterase 6
CSLC7_ORYSJ Probable xyloglucan glycosyltransferase 7
CSCL5_ARATH Protein OSCA1
CRS1_ARATH Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
CRR15_ARATH Cysteine-rich repeat secretory protein 15
CRK10_ARATH Cysteine-rich receptor-like protein kinase 10
2ABA_ARATH Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
COPIA_DROME Copia protein
COPIA_DROME Copia protein
CL16A_DICDI Protein CLEC16A homolog
CKI2_SCHPO Casein kinase I homolog 2
ACO3M_ARATH Aconitate hydratase 3, mitochondrial
ACO12_ARATH Putative peroxisomal acyl-coenzyme A oxidase 1.2
CIPKK_ARATH CBL-interacting serine/threonine-protein kinase 20
CID11_ARATH Polyadenylate-binding protein-interacting protein 11
CDPKY_ARATH Calcium-dependent protein kinase 34
CDPKY_ARATH Calcium-dependent protein kinase 34
ZRAB3_MOUSE DNA annealing helicase and endonuclease ZRANB3
ZDH13_ARATH Probable protein S-acyltransferase 4
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YSL7_ARATH Probable metal-nicotianamine transporter YSL7
YBEG_SCHPO Uncharacterized WD repeat-containing protein C17D11.16
Y5614_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g56140
Y5566_ARATH Uncharacterized protein At5g65660
Y5436_ARATH MATH domain-containing protein At5g43560
Y5344_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g53440
Y4844_ARATH Uncharacterized protein At4g28440
Y4759_ARATH WEB family protein At4g27595, chloroplastic
Y4391_ARATH Probable receptor-like protein kinase At4g39110
Y3272_ARATH Kelch repeat-containing protein At3g27220
Y2559_ARATH Receptor-like serine/threonine-protein kinase At2g45590
Y1839_ARATH Probable serine/threonine-protein kinase At1g18390
XPP1_MOUSE Xaa-Pro aminopeptidase 1
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 Valine--tRNA 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-acetylglucosamine--peptide 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
RGP2_ARATH UDP-arabinopyranose mutase 2

RGAP5_ARATH Rho GTPase-activating protein 5
RF4_ARATH Putative E3 ubiquitin-protein ligase RF4
REF6_ARATH Lysine-specific demethylase REF6
RECA3_ARATH DNA repair protein recA homolog 3, mitochondrial
RBPS2_MOUSE RNA-binding protein with multiple splicing 2
RB47B_ARATH Polyadenylate-binding protein RBP47B
RB45A_ARATH Polyadenylate-binding protein RBP45A
AB2A_ARATH ABC transporter A family member 2
PYRG_DICDI CTP synthase
AB19B_ARATH ABC transporter B family member 19
PXL1_ARATH Leucine-rich repeat receptor-like protein kinase PXL1
PUB35_ARATH U-box domain-containing protein 35
PUB30_ARATH U-box domain-containing protein 30
PTBP3_ARATH Polypyrimidine tract-binding protein homolog 3
PSL4_ARATH Glucosidase 2 subunit beta
ATML1_ARATH Homeobox-leucine zipper protein MERISTEM L1
ATL49_ARATH Putative RING-H2 finger protein ATL49
14339_ARATH 14-3-3-like protein GF14 mu
PR19A_ARATH Pre-mRNA-processing factor 19 homolog 1
PPD4_ARATH PsbP domain-containing protein 4, chloroplastic
POL5_DROME Retrovirus-related Pol polyprotein from transposon opus
PLY12_ARATH Probable pectate lyase 12
PIS1_ARATH CDP-diacylglycerol--inositol 3-phosphatidyltransferase 1
ATBH9_ARATH Homeobox-leucine zipper protein ATHB-9
PHL1_ARATH Protein PHR1-LIKE 1
PHG1B_DICDI Putative phagocytic receptor 1b
PDCB3_ARATH PLASMODESMATA CALLOSE-BINDING PROTEIN 3
PATL1_ARATH Patellin-1
PABP2_ARATH Polyadenylate-binding protein 2
P4H7_ARATH Probable prolyl 4-hydroxylase 7
P2A10_ARATH Protein PHLOEM PROTEIN 2-LIKE A10
ASPL2_ARATH Aspartic proteinase-like protein 2
ASPG2_ARATH Protein ASPARTIC PROTEASE IN GUARD CELL 2
OP162_ARATH Outer envelope pore protein 16-2, chloroplastic
OMT1_ARATH Flavone 3'-O-methyltransferase 1
OE64M_ARATH Outer envelope protein 64, mitochondrial
ASK21_ARATH SKP1-like protein 21
ARP_ARATH Apurinic endonuclease-redox protein
NRP2_ARATH NAP1-related protein 2
NOVA1_RAT RNA-binding protein Nova-1 (Fragment)
NIP51_ARATH Probable aquaporin NIP5-1
NGDN_HUMAN Neuroguidin
NFYB9_ARATH Nuclear transcription factor Y subunit B-9
NAT6_ARATH Nucleobase-ascorbate transporter 6
NACA4_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 4
NAC78_ARATH NAC domain-containing protein 78
MYB46_ARATH Transcription factor MYB46
MYB40_ANTMA Myb-related protein 340

MIZ1_ARATH Protein MIZU-KUSSEI 1
MHCKB_DICDI Myosin heavy chain kinase B
MES10_ARATH Methylesterase 10
MDAR4_ARATH Probable monodehydroascorbate reductase, cytoplasmic isoform 4
MD33A_ARATH Mediator of RNA polymerase II transcription subunit 33A
MCU_MOUSE Calcium uniporter protein, mitochondrial
MAP21_ARATH Methionine aminopeptidase 2A
MAOP2_ARATH NADP-dependent malic enzyme 2
M3K3_ARATH Mitogen-activated protein kinase kinase kinase 3
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
ARID4_ARATH AT-rich interactive domain-containing protein 4
LPAI_ARATH Phospholipase A I
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
LAG11_ARATH LAG1 longevity assurance homolog 1
KRR1_SCHPO KRR1 small subunit processome component homolog
KN12A_ARATH Kinesin-like protein KIN12A
KIF4A_HUMAN Chromosome-associated kinesin KIF4A
KI18B_RAT Kinesin-like protein KIF18B
KDSB_ARATH 3-deoxy-manno-octulosonate cytidylyltransferase, mitochondrial
KCO1_ARATH Two-pore potassium channel 1
KASC2_ARATH 3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic
JGL_ARATH Zinc finger protein JAGGED-like
IST1L_DICDI IST1-like protein
HUA2_ARATH ENHANCER OF AG-4 protein 2
HOX9_ORYSI Homeobox-leucine zipper protein HOX9
HEN1_ARATH Small RNA 2'-O-methyltransferase
AOX4_ARATH Ubiquinol oxidase 4, chloroplastic/chromoplastic
HAK12_ORYSJ Putative potassium transporter 12
H2A7_ARATH Probable histone H2A.7
H2A4_WHEAT Histone H2A.4
GUN12_ARATH Endoglucanase 12
GRXC6_ARATH Glutaredoxin-C6
4HPT_ARATH 4-hydroxybenzoate polyprenyltransferase, mitochondrial
GET3_ASPOR ATPase get3
GDL28_ARATH GDSL esterase/lipase At1g71250
GCNT7_HUMAN Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7
GAT25_ARATH GATA transcription factor 25
ALFL6_ARATH PHD finger protein ALFIN-LIKE 6
ALFL6_ARATH PHD finger protein ALFIN-LIKE 6
ALF5_ARATH MATE efflux family protein ALF5
FBL30_ARATH F-box/LRR-repeat protein At1g48400
FBK77_ARATH F-box/kelch-repeat protein At3g61590
FBK54_ARATH F-box/kelch-repeat protein At3g13680
FBD34_ARATH Putative FBD-associated F-box protein At1g05080
FBD19_ARATH Putative FBD-associated F-box protein At5g50270
FAP3_ARATH Fatty-acid-binding protein 3

FAAA_HUMAN Fumarylacetoacetase
F16P2_BRANA Fructose-1,6-bisphosphatase, cytosolic
EXOS7_DICDI Putative exosome complex exonuclease RRP42
EXOS7_DICDI Putative exosome complex exonuclease RRP42
AIR3_ARATH Subtilisin-like protease SBT5.3
ERS2_ARATH Ethylene response sensor 2
ERS1_ARATH Ethylene response sensor 1
AHP2_ARATH Histidine-containing phosphotransfer protein 2
AHK5_ARATH Histidine kinase 5
AGL18_ARATH Agamous-like MADS-box protein AGL18
EDR1_ARATH Serine/threonine-protein kinase EDR1
AGD5_ARATH Probable ADP-ribosylation factor GTPase-activating protein AGD5
DRL29_ARATH Probable disease resistance protein At4g33300
DRL29_ARATH Probable disease resistance protein At4g33300
ADSL3_ARATH Delta-9 desaturase-like 3 protein
DOF58_ARATH Dof zinc finger protein DOF5.8
DNJ21_ARATH DnaJ protein ERDJ2A
2A5I_ARATH Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota isoform
SPL5_ARATH Squamosa promoter-binding-like protein 5
CDC21_ARATH Cell division cycle 20.1, cofactor of APC complex
GALK1_ARATH Galactokinase
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
SPL9_ARATH Squamosa promoter-binding-like protein 9
SPL2_ARATH Squamosa promoter-binding-like protein 2
SPL11_ARATH Squamosa promoter-binding-like protein 11
SPL10_ARATH Squamosa promoter-binding-like protein 10
COPIA_DROME Copia protein
LEUNG_ARATH Transcriptional corepressor LEUNIG
SPB1_EMENI AdoMet-dependent rRNA methyltransferase spb1
AAPC_CENCI Putative glucose-6-phosphate 1-epimerase
CDPK3_ARATH Calcium-dependent protein kinase 3
C724B_ORYSJ Cytochrome P450 724B1
THCAS_CANSA Tetrahydrocannabinolic acid synthase
MY122_ARATH Transcription factor MYB122
FBK98_ARATH F-box/kelch-repeat protein At4g39550
PERK9_ARATH Proline-rich receptor-like protein kinase PERK9
SPL6_ARATH Squamosa promoter-binding-like protein 6
ARFH_ARATH Auxin response factor 8
BH077_ARATH Transcription factor bHLH77
ZDH14_ARATH Probable protein S-acyltransferase 14
GRS13_ARATH Monothiol glutaredoxin-S13
Y1534_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g53420
YJNA_SCHPO Uncharacterized AAA domain-containing protein C24B10.10c
UTP11_ARATH Probable U3 small nucleolar RNA-associated protein 11
SNR27_MOUSE U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein
SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
RNHX1_ARATH Putative ribonuclease H protein At1g65750
NOSIP_DROME Nitric oxide synthase-interacting protein homolog

MES14_ARATH Putative methylesterase 14, chloroplastic
GLRX_SOLLC Glutaredoxin
YJNA_SCHPO Uncharacterized AAA domain-containing protein C24B10.10c
SKIP6_ARATH F-box/kelch-repeat protein SKIP6
PDI22_ARATH Protein disulfide-isomerase like 2-2
FBK68_ARATH Putative F-box/kelch-repeat protein At3g24610
FDL5_ARATH Putative F-box/FBD/LRR-repeat protein At1g22000
TPST_ARATH Protein-tyrosine sulfotransferase
AX15A_SOYBN Auxin-induced protein 15A
RNHX1_ARATH Putative ribonuclease H protein At1g65750
GIN1_MACFA Gypsy retrotransposon integrase-like protein 1
FBL60_ARATH F-box/LRR-repeat protein At3g58940
FBK64_ARATH Putative F-box/kelch-repeat protein At3g20710
FB168_ARATH F-box protein At3g20690
SPL15_ARATH Squamosa promoter-binding-like protein 15
SPL15_ARATH Squamosa promoter-binding-like protein 15
SPL11_ARATH Squamosa promoter-binding-like protein 11
RNHX1_ARATH Putative ribonuclease H protein At1g65750
PP432_ARATH Pentatricopeptide repeat-containing protein At5g55840
RL281_ARATH 60S ribosomal protein L28-1
ALN_ARATH Allantoinase
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
Y4200_ARATH Uncharacterized protein At4g02000
RNHX1_ARATH Putative ribonuclease H protein At1g65750
PRP4_SCHPO Serine/threonine-protein kinase prp4
PP142_ARATH Pentatricopeptide repeat-containing protein At2g01860
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
MVP_CYLCV Putative movement protein
MCM8_ARATH Probable DNA helicase MCM8
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
HSP72_SOLLC Heat shock cognate 70 kDa protein 2
EF2_BETVU Elongation factor 2
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
CYSD1_ARATH Bifunctional L-3-cyanoalanine synthase/cysteine synthase D1
CSP4_ARATH Cold shock domain-containing protein 4
CCD1_ARATH Carotenoid 9,10(9',10')-cleavage dioxygenase 1
CAAT5_ARATH Cationic amino acid transporter 5
THRC1_ARATH Threonine synthase 1, chloroplastic
TBC25_HUMAN TBC1 domain family member 25
SMD2_DROME Probable small nuclear ribonucleoprotein Sm D2
BIG5_ARATH Brefeldin A-inhibited guanine nucleotide-exchange protein 5
R18AL_ARATH 60S ribosomal protein L18a-like protein
R18A2_ARATH 60S ribosomal protein L18a-2

PP323_ARATH Pentatricopeptide repeat-containing protein At4g19191, mitochondrial
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
AAPC_CENCI Putative glucose-6-phosphate 1-epimerase
PAD4_ARATH Lipase-like PAD4
ASA1_ORYSI Anthranilate synthase alpha subunit 1, chloroplastic
MGST3_MOUSE Microsomal glutathione S-transferase 3
LORF2_MOUSE LINE-1 retrotransposable element ORF2 protein
APC1_ARATH Anaphase-promoting complex subunit 1
APC1_ARATH Anaphase-promoting complex subunit 1
GLTB2_ARATH Ferredoxin-dependent glutamate synthase 2, chloroplastic
GLTB2_ARATH Ferredoxin-dependent glutamate synthase 2, chloroplastic
DNJC2_BOVIN DnaJ homolog subfamily C member 2
CLE11_ARATH CLAVATA3/ESR (CLE)-related protein 11
RH31_ARATH DEAD-box ATP-dependent RNA helicase 31
PRS7A_ARATH 26S protease regulatory subunit 7 homolog A
PP181_ARATH Pentatricopeptide repeat-containing protein At2g33680
APGM_PYRAE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
SPL5_ARATH Squamosa promoter-binding-like protein 5
ARG7_VIGRR Indole-3-acetic acid-induced protein ARG7
FDL5_ARATH Putative F-box/FBD/LRR-repeat protein At1g22000
FBD40_ARATH FBD-associated F-box protein At4g10400
Y5838_ARATH Probably inactive leucine-rich repeat receptor-like protein kinase At5g48380
UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13
U76C1_ARATH UDP-glycosyltransferase 76C1
TPS1_BRANA Thiamine biosynthetic bifunctional enzyme BTH1, chloroplastic
STIL1_ARATH Protein STICHEL-like 1
SRRT_ARATH Serrate RNA effector molecule
REV_ARATH Homeobox-leucine zipper protein REVOLUTA
ATK2_ARATH Kinesin-2
PP210_ARATH Pentatricopeptide repeat-containing protein At3g03580
PP117_ARATH Pentatricopeptide repeat-containing protein At1g73400, mitochondrial
PME44_ARATH Probable pectinesterase/pectinesterase inhibitor 44
PHF1_ARATH SEC12-like protein 1
ASPG1_ARATH Protein ASPARTIC PROTEASE IN GUARD CELL 1
GSTUD_ARATH Glutathione S-transferase U13
DYAD_ARATH Protein DYAD
PP223_ARATH Putative pentatricopeptide repeat-containing protein At3g11460
PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
MBOA1_ARATH Lysophospholipid acyltransferase 1
FUT2_ARATH Fucosyltransferase 2
FBL41_ARATH F-box/LRR-repeat protein At3g03030
DOF25_ARATH Dof zinc finger protein DOF2.5
DNJB1_MOUSE DnaJ homolog subfamily B member 1
NAC69_ARATH NAC domain-containing protein 69
CDR1_ARATH Aspartic proteinase CDR1
RB47C_ARATH Polyadenylate-binding protein RBP47C
PPK15_SCHPO Serine/threonine-protein kinase ppk15

PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
Y2734_MYCBO Uncharacterized protein Mb2734
PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
PP103_ARATH Pentatricopeptide repeat-containing protein At1g64100
AROF_TOBAC Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic
FUT2_ARATH Fucosyltransferase 2
FB338_ARATH Probable F-box protein At5g39490
Y283_BACHD Uncharacterized isomerase BH0283
SYP22_ARATH Syntaxin-22
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
ASOL_BRANA L-ascorbate oxidase homolog
LBD25_ARATH LOB domain-containing protein 25
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
TF26_SCHPO Transposon Tf2-6 polyprotein
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
ACT12_ARATH Actin-12
CHX6A_ARATH Cation/H(+) antiporter 6A
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
GAM1_ORYSJ Transcription factor GAMYB
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
COPB1_ARATH Coatomer subunit beta-1
CKB11_ARATH Cyclin-dependent kinase B1-1
RHP16_SCHPO ATP-dependent helicase rhp16
PFKA3_ARATH ATP-dependent 6-phosphofructokinase 3
Y4117_ARATH Putative disease resistance protein At4g11170
TF29_SCHPO Transposon Tf2-9 polyprotein
FDL40_ARATH Putative F-box/FBD/LRR-repeat protein At5g56810
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POL2_DROME Retrovirus-related Pol polyprotein from transposon 297
GAM1_ORYSJ Transcription factor GAMYB
GAM1_ORYSJ Transcription factor GAMYB
MY104_ARATH Transcription factor MYB104
MY104_ARATH Transcription factor MYB104
GAM1_ORYSI Transcription factor GAMYB
GAM1_ORYSJ Transcription factor GAMYB
PCLO_HUMAN Protein piccolo
GAM1_ORYSI Transcription factor GAMYB
POL5_DROME Retrovirus-related Pol polyprotein from transposon opus
KAT1_ARATH Potassium channel KAT1
U74F2_ARATH UDP-glycosyltransferase 74F2
SUBL_ARATH Subtilisin-like protease
JMJ25_ARATH Lysine-specific demethylase JMJ25

CRS1_MAIZE Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
Y4849_ARATH Uncharacterized protein At4g18490
ARFP_ARATH Auxin response factor 16
ARFP_ARATH Auxin response factor 16
ARFJ_ARATH Auxin response factor 10
ARFQ_ARATH Auxin response factor 17
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
BH079_ARATH Transcription factor bHLH79
NOC2L_ARATH Nucleolar complex protein 2 homolog
ARID6_ARATH AT-rich interactive domain-containing protein 6
Y1972_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g29720
AB2A_ARATH ABC transporter A family member 2
HSP7F_ARATH Heat shock 70 kDa protein 6, chloroplastic
NC2B_ARATH Protein Dr1 homolog
TRA1_YEAST Transcription-associated protein 1
SUBL_ARATH Subtilisin-like protease
POK1_ARATH Phragmoplast orienting kinesin-1
NLTPC_ARATH Non-specific lipid-transfer protein 12
NC100_ARATH NAC domain-containing protein 100
UXS4_ARATH UDP-glucuronic acid decarboxylase 4
NC100_ARATH NAC domain-containing protein 100
NAC22_ARATH NAC domain-containing protein 21/22
NAC22_ARATH NAC domain-containing protein 21/22
WSD1_ARATH O-acyltransferase WSD1
WSD1_ARATH O-acyltransferase WSD1
Y4361_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g36180
RS212_ARATH 40S ribosomal protein S21-2
RS211_ARATH 40S ribosomal protein S21-1
FRS11_ARATH Protein FAR1-RELATED SEQUENCE 11
SPL14_ARATH Squamosa promoter-binding-like protein 14
NC100_ARATH NAC domain-containing protein 100
HBP1B_WHEAT Transcription factor HBP-1b(c38)
DAR6_ARATH Protein DA1-related 6
NC100_ARATH NAC domain-containing protein 100
NAC22_ARATH NAC domain-containing protein 21/22
NAC98_ARATH Protein CUP-SHAPED COTYLEDON 2
NAC54_ARATH Protein CUP-SHAPED COTYLEDON 1
PLCD4_ARATH Phosphoinositide phospholipase C 4
EIL3_ARATH ETHYLENE INSENSITIVE 3-like 3 protein
CASL1_CANSA Cannabidiolic acid synthase-like 1
UGGG_ARATH UDP-glucose:glycoprotein glucosyltransferase
C86B1_ARATH Cytochrome P450 86B1
TOM91_ARATH Mitochondrial import receptor subunit TOM9-1
PER73_ARATH Peroxidase 73
MPK6_ARATH Mitogen-activated protein kinase 6
GAUTC_ARATH Probable galacturonosyltransferase 12
G3OX3_ARATH Gibberellin 3-beta-dioxygenase 3
SEC22_ARATH 25.3 kDa vesicle transport protein

SDE3_ARATH Probable RNA helicase SDE3
ATL32_ARATH RING-H2 finger protein ATL32
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
LIN1_NYCCO LINE-1 reverse transcriptase homolog
LIN1_NYCCO LINE-1 reverse transcriptase homolog
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
CLU_ARATH Clustered mitochondria protein
PP289_ARATH Pentatricopeptide repeat-containing protein At3g60960, mitochondrial
LBD1_ARATH LOB domain-containing protein 1
AMO_ARATH Primary amine oxidase
CCA34_ARATH Cyclin-A3-4
ARFH_ARATH Auxin response factor 8
FBK95_ARATH F-box/kelch-repeat protein At4g38940
TAF6_ARATH Transcription initiation factor TFIID subunit 6
NALD2_MOUSE N-acetylated-alpha-linked acidic dipeptidase 2
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
ARFF_ARATH Auxin response factor 6
ARFF_ARATH Auxin response factor 6
NB5R1_ARATH NADH--cytochrome b5 reductase 1
AGO1_ARATH Protein argonaute 1
AGO1_ARATH Protein argonaute 1
CAMK1_ARATH CDPK-related kinase 1
CAMK1_ARATH CDPK-related kinase 1
NFYA9_ARATH Nuclear transcription factor Y subunit A-9
NFYA5_ARATH Nuclear transcription factor Y subunit A-5
GSHRP_SPIOL Glutathione reductase, chloroplastic (Fragment)
NFYA5_ARATH Nuclear transcription factor Y subunit A-5
FDL48_ARATH Putative F-box/FBD/LRR-repeat protein At4g13965
CID4_ARATH Polyadenylate-binding protein-interacting protein 4
NFYA9_ARATH Nuclear transcription factor Y subunit A-9
NFYA9_ARATH Nuclear transcription factor Y subunit A-9
NFYA2_ARATH Nuclear transcription factor Y subunit A-2
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
NFYA1_ARATH Nuclear transcription factor Y subunit A-1
NFYA1_ARATH Nuclear transcription factor Y subunit A-1
NFYA5_ARATH Nuclear transcription factor Y subunit A-5
NFYA3_ARATH Nuclear transcription factor Y subunit A-3
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
CNGC6_ARATH Probable cyclic nucleotide-gated ion channel 6
SRPK3_HUMAN SRSF protein kinase 3

NFYA3_ARATH Nuclear transcription factor Y subunit A-3
NFYA2_ARATH Nuclear transcription factor Y subunit A-2
NFYAA_ARATH Nuclear transcription factor Y subunit A-10
NFYA6_ARATH Nuclear transcription factor Y subunit A-6
NFYA3_ARATH Nuclear transcription factor Y subunit A-3
NFYA3_ARATH Nuclear transcription factor Y subunit A-3
NFYA2_ARATH Nuclear transcription factor Y subunit A-2
NFYA1_ARATH Nuclear transcription factor Y subunit A-1
UBC23_ARATH Probable ubiquitin-conjugating enzyme E2 23
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
NOP56_SCHPO Nucleolar protein 56
NOP56_HUMAN Nucleolar protein 56
NACK1_ARATH Kinesin-like protein NACK1
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
CK3_ARATH Probable choline kinase 3
BASL_ARATH Protein BREAKING OF ASYMMETRY IN THE STOMATAL LINEAGE
PYRG2_XENLA CTP synthase 2
PGLR_VITVI Probable polygalacturonase
ASPG_LUPAN Isoaspartyl peptidase/L-asparaginase
FB94_ARATH Putative F-box protein At2g02030
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
HAC12_ARATH Histone acetyltransferase HAC12
PP369_ARATH Pentatricopeptide repeat-containing protein At5g08305
MPK5_ARATH Mitogen-activated protein kinase 5
ALKBH_ARATH Alpha-ketoglutarate-dependent dioxygenase alkB
SCL27_ARATH Scarecrow-like protein 27
SCL15_ARATH Scarecrow-like protein 15
COPIA_DROME Copia protein
SCL15_ARATH Scarecrow-like protein 15
SCL6_ARATH Scarecrow-like protein 6
SCL27_ARATH Scarecrow-like protein 27
SCL22_ARATH Scarecrow-like protein 22
WRK70_ARATH Probable WRKY transcription factor 70
RQL1_ARATH ATP-dependent DNA helicase Q-like 1
PPA28_ARATH Probable inactive purple acid phosphatase 28
PP158_ARATH Pentatricopeptide repeat-containing protein At2g17140
PNCB_DROME Nicotinate phosphoribosyltransferase
P2C46_ARATH Probable protein phosphatase 2C 46
TT1_ARATH Protein TRANSPARENT TESTA 1
SYY_PARUW Tyrosine--tRNA ligase
RAX3_ARATH Transcription factor RAX3
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
GLN15_ARATH Glutamine synthetase cytosolic isozyme 1-5
E135_ARATH Glucan endo-1,3-beta-glucosidase 5
Y4117_ARATH Putative disease resistance protein At4g11170
AP2_ARATH Floral homeotic protein APETALA 2
DGK2_ARATH Diacylglycerol kinase 2
TOE2_ARATH AP2-like ethylene-responsive transcription factor TOE2

SAC4_ARATH Phosphoinositide phosphatase SAC4
CKS1_ORYSJ Cyclin-dependent kinases regulatory subunit 1
XPO7_CHICK Exportin-7
TT12_ARATH Protein TRANSPARENT TESTA 12
TONS_ARATH Protein TONSOKU
TBA_OXYGR Tubulin alpha chain
SPE1_BRAJU Arginine decarboxylase
SA145_SCHPO Pre-mRNA-splicing factor sap145
RNP1_ARATH Heterogeneous nuclear ribonucleoprotein 1
PYL11_ARATH Abscisic acid receptor PYL11
OEP61_ARATH Outer envelope protein 61
MCE1_MOUSE mRNA-capping enzyme
MCE1_HUMAN mRNA-capping enzyme
MATE9_ARATH MATE efflux family protein 9
MATE7_ARATH MATE efflux family protein 7
ARID3_ARATH AT-rich interactive domain-containing protein 3
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
FBK50_ARATH F-box/kelch-repeat protein At3g06240
FBK27_ARATH F-box/kelch-repeat protein At1g64840
VPS54_ARATH Vacuolar protein sorting-associated protein 54, chloroplastic
TF3A_HUMAN Transcription factor IIIA
RNHX1_ARATH Putative ribonuclease H protein At1g65750
AB6G_ARATH ABC transporter G family member 6
PEPK2_ARATH Serine/threonine-protein kinase PEPKR2
CSTF1_HUMAN Cleavage stimulation factor subunit 1
RBG8_ARATH Glycine-rich RNA-binding protein 8
TPS8_ARATH Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 8
TOE3_ARATH AP2-like ethylene-responsive transcription factor TOE3
ACO1_ARATH Aconitate hydratase 1
Y4117_ARATH Putative disease resistance protein At4g11170
WRK46_ARATH Probable WRKY transcription factor 46
VIL1_ARATH VIN3-like protein 1
CALM4_ARATH Calmodulin-4
TYW1_ARATH S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase
C3H19_ARATH Zinc finger CCCH domain-containing protein 19
SDN2_ARATH Small RNA degrading nuclease 2
RS7_BRAOL 40S ribosomal protein S7
RS73_ARATH 40S ribosomal protein S7-3
R13A4_ARATH 60S ribosomal protein L13a-4
PPR47_ARATH Putative pentatricopeptide repeat-containing protein At1g17630
PP303_ARATH Pentatricopeptide repeat-containing protein At4g04370
PP303_ARATH Pentatricopeptide repeat-containing protein At4g04370
PGLR_VITVI Probable polygalacturonase
MYB39_ARATH Transcription factor MYB39
MFAP1_CHICK Microfibrillar-associated protein 1
HPR3_ARATH Glyoxylate/hydroxypyruvate reductase HPR3
GRF4_ARATH Growth-regulating factor 4
GPDH1_ORYSJ Probable glycerol-3-phosphate dehydrogenase [NAD(+)] 1, cytosolic

FB167_ARATH Putative F-box protein At3g20030
ERF93_ARATH Ethylene-responsive transcription factor 15
DOF47_ARATH Dof zinc finger protein DOF4.7
CSCL9_ARATH CSC1-like protein At1g10090
Y3720_ARATH UPF0481 protein At3g47200
C3H62_ARATH Zinc finger CCCH domain-containing protein 62
RLP12_ARATH Receptor-like protein 12
ATL45_ARATH RING-H2 finger protein ATL45
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
SMZ_ARATH AP2-like ethylene-responsive transcription factor SMZ
RAP27_ARATH Ethylene-responsive transcription factor RAP2-7
RAP27_ARATH Ethylene-responsive transcription factor RAP2-7
JAR1_ARATH Jasmonic acid-amido synthetase JAR1
AP2_ARATH Floral homeotic protein APETALA 2
PP150_ARATH Pentatricopeptide repeat-containing protein At2g13420, mitochondrial
FBK70_ARATH F-box/kelch-repeat protein At3g27150
FBK70_ARATH F-box/kelch-repeat protein At3g27150
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
DNMT1_ARATH DNA (cytosine-5)-methyltransferase 1
DSP8_ARATH Putative dual specificity protein phosphatase DSP8
BGL13_ARATH Beta-glucosidase 13
DNMT1_ARATH DNA (cytosine-5)-methyltransferase 1
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
CHMP5_PONAB Charged multivesicular body protein 5
TCP4_ARATH Transcription factor TCP4
TCP4_ARATH Transcription factor TCP4
TCP4_ARATH Transcription factor TCP4
BOR4_ARATH Boron transporter 4
BOR1_ARATH Boron transporter 1
BOR1_ARATH Boron transporter 1
BGL13_ARATH Beta-glucosidase 13
JMJ19_ARATH Probable inactive lysine-specific demethylase JMJ19
AL221_ARATH Aldehyde dehydrogenase 22A1
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
TF29_SCHPO Transposon Tf2-9 polyprotein
BGL15_ARATH Beta-glucosidase 15
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
VATG2_ARATH V-type proton ATPase subunit G2
TF26_SCHPO Transposon Tf2-6 polyprotein
RNHX1_ARATH Putative ribonuclease H protein At1g65750
LORF2_MOUSE LINE-1 retrotransposable element ORF2 protein
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
AHP6_ARATH Histidine-containing phosphotransfer protein 6
Y4885_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g08850
CAF2M_ARATH CRS2-associated factor 2, mitochondrial
BRI1_SOLLC Brassinosteroid LRR receptor kinase
RLP12_ARATH Receptor-like protein 12
RLCK7_ARATH Probable serine/threonine-protein kinase RLCKVII

PHB2_ARATH Prohibitin-2, mitochondrial
GRF8_ARATH Growth-regulating factor 8
FTSH8_ARATH ATP-dependent zinc metalloprotease FTSH 8, chloroplastic
COG5_MOUSE Conserved oligomeric Golgi complex subunit 5
CHX9_ARATH Cation/H(+) antiporter 9
ACA8_ARATH Calcium-transporting ATPase 8, plasma membrane-type
ACA10_ARATH Calcium-transporting ATPase 10, plasma membrane-type
TIR1_ARATH Protein TRANSPORT INHIBITOR RESPONSE 1
TIR1_ARATH Protein TRANSPORT INHIBITOR RESPONSE 1
TIR1_ARATH Protein TRANSPORT INHIBITOR RESPONSE 1
BH077_ARATH Transcription factor bHLH77
LIN1_NYCCO LINE-1 reverse transcriptase homolog
GRH1_ARATH GRR1-like protein 1
GRH1_ARATH GRR1-like protein 1
GEX1_ARATH Protein GAMETE EXPRESSED 1
AFB3_ARATH Protein AUXIN SIGNALING F-BOX 3
AFB2_ARATH Protein AUXIN SIGNALING F-BOX 2
AFB2_ARATH Protein AUXIN SIGNALING F-BOX 2
RF2_THELT Peptide chain release factor 2
RF2_SYNY3 Peptide chain release factor 2
PMTA_ARATH Probable methyltransferase PMT10
P4H12_ARATH Probable prolyl 4-hydroxylase 12
FGGY_XENLA FGGY carbohydrate kinase domain-containing protein
FBX6_ARATH F-box only protein 6
CLSY3_ARATH SNF2 domain-containing protein CLASSY 3
CLSY3_ARATH SNF2 domain-containing protein CLASSY 3
Y2172_ARATH B3 domain-containing protein At2g31720
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
PHSD_ARATH Probable polyamine transporter At3g19553
PER66_ARATH Peroxidase 66
APS1_ARATH ATP sulfurylase 1, chloroplastic
AOC2_ARATH Allene oxide cyclase 2, chloroplastic
EVI5_DROME Ecotropic viral integration site 5 ortholog
SECA1_ARATH Protein translocase subunit SECA1, chloroplastic
APS1_ARATH ATP sulfurylase 1, chloroplastic
Y3985_ARATH BTB/POZ domain-containing protein At3g19850
THNL2_ARATH Thionin-like protein 2
RNHX1_ARATH Putative ribonuclease H protein At1g65750
RNHX1_ARATH Putative ribonuclease H protein At1g65750
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
M1250_ARATH Uncharacterized mitochondrial protein AtMg01250
LAC7_ARATH Laccase-7
SUT21_ARATH Sulfate transporter 2.1
APS4_ARATH ATP sulfurylase 4, chloroplastic
APS1_ARATH ATP sulfurylase 1, chloroplastic
Y3475_ARATH Probable LRR receptor-like serine/threonine-protein kinase At3g47570

ADNT1_ARATH Mitochondrial adenine nucleotide transporter ADNT1
UXS6_ARATH UDP-glucuronic acid decarboxylase 6
U76E6_ARATH UDP-glycosyltransferase 76E6
TTL3_ARATH Inactive TPR repeat-containing thioredoxin TTL3
C90C1_ARATH 3-epi-6-deoxocathasterone 23-monooxygenase
TF29_SCHPO Transposon Tf2-9 polyprotein
TF26_SCHPO Transposon Tf2-6 polyprotein
BOP1_DROME Ribosome biogenesis protein BOP1 homolog
SYAP_ARATH Probable alanine--tRNA ligase, chloroplastic
SMR3_ARATH Cyclin-dependent protein kinase inhibitor SMR3
RSLE2_ORYSJ Zinc finger BED domain-containing protein RICESLEEPER 2
REM12_ARATH B3 domain-containing protein REM12
PRP39_SCHPO Pre-mRNA-processing factor 39
PP172_ARATH Pentatricopeptide repeat-containing protein At2g27610
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
PME17_ARATH Probable pectinesterase/pectinesterase inhibitor 17
PLCD1_ARATH Phosphoinositide phospholipase C 1
P2C54_ARATH Probable protein phosphatase 2C 54
MTPC4_ARATH Metal tolerance protein C4
MCCB_ARATH Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
HLS1_ARATH Probable N-acetyltransferase HLS1
GNL1_ARATH ARF guanine-nucleotide exchange factor GNL1
GAGT1_ARATH Gamma-glutamyltranspeptidase 1
FBD19_ARATH Putative FBD-associated F-box protein At5g50270
FB20_ARATH F-box protein At1g30790
ERF70_ARATH Ethylene-responsive transcription factor ERF070
EIF3B_TOBAC Eukaryotic translation initiation factor 3 subunit B
TAF1_ARATH Transcription initiation factor TFIID subunit 1
BGL44_ARATH Beta-glucosidase 44
RLP12_ARATH Receptor-like protein 12
PP387_ARATH Pentatricopeptide repeat-containing protein At5g15980, mitochondrial
PP119_ARATH Putative pentatricopeptide repeat-containing protein At1g74400
MKKA_DICDI Mitogen-activated protein kinase kinase kinase A
FLU_ARATH Protein FLUORESCENT IN BLUE LIGHT, chloroplastic
AGL93_ARATH Agamous-like MADS-box protein AGL93
AGL93_ARATH Agamous-like MADS-box protein AGL93
ATH1_ARATH Homeobox protein ATH1
DEGP1_ARATH Protease Do-like 1, chloroplastic
CMTA5_ARATH Calmodulin-binding transcription activator 5
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
ACCH3_ARATH 1-aminocyclopropane-1-carboxylate oxidase homolog 3
TRNH1_ARATH Tropinone reductase homolog At1g07440
TRNH1_ARATH Tropinone reductase homolog At1g07440
TCP1_ARATH Transcription factor TCP1

STR7_ARATH Rhodanese-like domain-containing protein 7
BGAL4_ARATH Beta-galactosidase 4
RNE_ARATH Ribonuclease E/G-like protein, chloroplastic
RH21_ARATH DEAD-box ATP-dependent RNA helicase 21
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
LIN1_NYCCO LINE-1 reverse transcriptase homolog
HS902_ARATH Heat shock protein 90-2
HS902_ARATH Heat shock protein 90-2
FH10_ARATH Formin-like protein 10
FH10_ARATH Formin-like protein 10
EF1G1_ARATH Probable elongation factor 1-gamma 1
LIN1_NYCCO LINE-1 reverse transcriptase homolog
LIN1_NYCCO LINE-1 reverse transcriptase homolog
Y5162_ARATH Uncharacterized protein At5g41620
U73C3_ARATH UDP-glycosyltransferase 73C3
U73C1_ARATH UDP-glycosyltransferase 73C1
TRL12_ARATH Thioredoxin-like 1-2, chloroplastic
TF26_SCHPO Transposon Tf2-6 polyprotein
SCL33_ARATH Scarecrow-like protein 33
ABAH1_ARATH Abscisic acid 8'-hydroxylase 1
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
MAA3_ARATH Probable helicase MAGATAMA 3
GPTC1_CAEEL G patch domain-containing protein 1 homolog
AGL93_ARATH Agamous-like MADS-box protein AGL93
AGL93_ARATH Agamous-like MADS-box protein AGL93
AGL93_ARATH Agamous-like MADS-box protein AGL93
DHX29_XENLA ATP-dependent RNA helicase DHX29
BGL19_ARATH Beta-glucosidase 19
PFPA1_ARATH Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 1
P5CS_SOLLC Delta-1-pyrroline-5-carboxylate synthase
P5CS1_ARATH Delta-1-pyrroline-5-carboxylate synthase A
P5CS1_ARATH Delta-1-pyrroline-5-carboxylate synthase A
P5CS1_ARATH Delta-1-pyrroline-5-carboxylate synthase A
MAA3_ARATH Probable helicase MAGATAMA 3
LAC4_ARATH Laccase-4
LAC4_ARATH Laccase-4
LAC2_ARATH Laccase-2
LAC17_ARATH Laccase-17
LAC17_ARATH Laccase-17
LAC11_ARATH Laccase-11
E137_ARATH Glucan endo-1,3-beta-glucosidase 7
CX5BL_ARATH Putative cytochrome c oxidase subunit 5b-like
RL313_ARATH 60S ribosomal protein L31-3
RL313_ARATH 60S ribosomal protein L31-3
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
Y4177_ARATH Uncharacterized protein At4g17700

CAP13_ARATH Putative clathrin assembly protein At1g25240
TT12_ARATH Protein TRANSPARENT TESTA 12
SDA1_NEMVE Protein SDA1 homolog
RH57_ARATH DEAD-box ATP-dependent RNA helicase 57
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
LIN1_NYCCO LINE-1 reverse transcriptase homolog
GALM_PIG Aldose 1-epimerase
FBL11_ARATH BTB/POZ domain-containing protein FBL11
EXEC1_ARATH Protein EXECUTER 1, chloroplastic
DRP4C_ARATH Dynamin-related protein 4C
MYO13_ARATH Myosin-13
TC120_ARATH Translocase of chloroplast 120, chloroplastic
SPA2_ARATH Protein SPA1-RELATED 2
SPA2_ARATH Protein SPA1-RELATED 2
SFR2_ORYSJ Beta-glucosidase-like SFR2, chloroplastic
SCP6_ARATH Serine carboxypeptidase-like 6
RQL4A_ARATH ATP-dependent DNA helicase Q-like 4A
GLR36_ARATH Glutamate receptor 3.6
DI3L2_ARATH DIS3-like exonuclease 2
GUF1_ARATH Translation factor GUF1 homolog, mitochondrial
G11A_ORYSI Protein kinase G11A
UBC24_ARATH Probable ubiquitin-conjugating enzyme E2 24
RHM1_ARATH Probable rhamnose biosynthetic enzyme 1
CSLD6_ARATH Putative cellulose synthase-like protein D6
VAS_ARATH Lipid transfer-like protein VAS
BAHD1_ARATH BAHD acyltransferase At5g47980
PPR97_ARATH Pentatricopeptide repeat-containing protein At1g63070, mitochondrial
PPR93_ARATH Pentatricopeptide repeat-containing protein At1g62720
PPR93_ARATH Pentatricopeptide repeat-containing protein At1g62720
PPR92_ARATH Pentatricopeptide repeat-containing protein At1g62680, mitochondrial
PPR56_ARATH Pentatricopeptide repeat-containing protein At1g22960, mitochondrial
PPR56_ARATH Pentatricopeptide repeat-containing protein At1g22960, mitochondrial
PPR39_ARATH Pentatricopeptide repeat-containing protein At1g12775, mitochondrial
PPR37_ARATH Pentatricopeptide repeat-containing protein At1g12620
PPR37_ARATH Pentatricopeptide repeat-containing protein At1g12620
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
PPR36_ARATH Pentatricopeptide repeat-containing protein At1g12300, mitochondrial
PPR27_ARATH Pentatricopeptide repeat-containing protein At1g09820
PPR20_ARATH Pentatricopeptide repeat-containing protein At1g07740, mitochondrial
PP407_ARATH 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
PP325_ARATH Pentatricopeptide repeat-containing protein At4g19440, chloroplastic
PP306_ARATH Pentatricopeptide repeat-containing protein At4g11690

PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
PP247_ARATH Pentatricopeptide repeat-containing protein At3g22470, mitochondrial
PP238_ARATH Putative pentatricopeptide repeat-containing protein At3g16710, mitochondrial
PP236_ARATH Pentatricopeptide repeat-containing protein At3g16010
PP236_ARATH Pentatricopeptide repeat-containing protein At3g16010
PP236_ARATH Pentatricopeptide repeat-containing protein At3g16010
PP178_ARATH Pentatricopeptide repeat-containing protein At2g31400, chloroplastic
PP177_ARATH Pentatricopeptide repeat-containing protein At2g30780
PP149_ARATH Pentatricopeptide repeat-containing protein At2g06000
PP133_ARATH Pentatricopeptide repeat-containing protein At1g79540
PP130_ARATH Pentatricopeptide repeat-containing protein At1g77405
ORC6_ARATH Origin recognition complex subunit 6
MCC08_ARATH MATH domain and coiled-coil domain-containing protein At2g42470
LRE_ARATH GPI-anchored protein LORELEI
KTNB1_ARATH Katanin p80 WD40 repeat-containing subunit B1 homolog
IP5P3_ARATH Type I inositol 1,4,5-trisphosphate 5-phosphatase CVP2
HPPD_ARATH 4-hydroxyphenylpyruvate dioxygenase
ERF61_ARATH Ethylene-responsive transcription factor ERF061
ECA3_ARATH Calcium-transporting ATPase 3, endoplasmic reticulum-type
PDK_ARATH [Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
AGO2_ARATH Protein argonaute 2
AGO2_ARATH Protein argonaute 2
AGO2_ARATH Protein argonaute 2
COP1_ARATH E3 ubiquitin-protein ligase COP1
Y2988_ARATH Uncharacterized protein At2g29880
TGA4_ARATH Transcription factor TGA4
BH070_ARATH Transcription factor bHLH70
RNHX1_ARATH Putative ribonuclease H protein At1g65750
PP205_ARATH Putative pentatricopeptide repeat-containing protein At3g01580
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
APMAP_HUMAN Adipocyte plasma membrane-associated protein
E2204_ARATH UPF0725 protein EMB2204
DPOE1_ARATH DNA polymerase epsilon catalytic subunit A
DNJ49_ARATH Chaperone protein dnaJ 49
BABL_ARATH Basic blue protein
RABC1_ARATH Ras-related protein RABC1
PIF1_HUMAN ATP-dependent DNA helicase PIF1
ASO_TOBAC L-ascorbate oxidase
LAC12_ARATH Laccase-12
DRIPH_ARATH Probable E3 ubiquitin protein ligase DRIPH
XB35_ARATH Putative E3 ubiquitin-protein ligase XBAT35

STP4_ARATH Sugar transport protein 4
SMBP2_RAT DNA-binding protein SMUBP-2
RS261_ARATH 40S ribosomal protein S26-1
BAHD2_ARATH BAHD acyltransferase At3g29680
RNHX1_ARATH Putative ribonuclease H protein At1g65750
RL5_CUCSA 60S ribosomal protein L5
RECG_SYNY3 ATP-dependent DNA helicase RecG
RBK2_ARATH Receptor-like cytosolic serine/threonine-protein kinase RBK2
PPDK1_ARATH Pyruvate, phosphate dikinase 1, chloroplastic
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
PHO13_ARATH Phosphate transporter PHO1 homolog 3
PDCB2_ARATH PLASMODESMATA CALLOSE-BINDING PROTEIN 2
PARG2_ARATH Probable poly(ADP-ribose) glycohydrolase 2
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
ARF2_ORYSJ ADP-ribosylation factor 2
GOGC1_ARATH Golgin candidate 1
GH35_ARATH Indole-3-acetic acid-amido synthetase GH3.5
RL92_ARATH 60S ribosomal protein L9-2
RL92_ARATH 60S ribosomal protein L9-2
RL91_ARATH 60S ribosomal protein L9-1
RL91_ARATH 60S ribosomal protein L9-1
RL91_ARATH 60S ribosomal protein L9-1
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
FLA8_ARATH Fasciclin-like arabinogalactan protein 8
DNAJ_METTE Chaperone protein DnaJ
DNAJ8_ARATH Chaperone protein dnaJ 8, chloroplastic
DNAJ2_ARATH Chaperone protein dnaJ 2
DJB14_XENLA DnaJ homolog subfamily B member 14
DJB13_HUMAN DnaJ homolog subfamily B member 13
DJB13_HUMAN DnaJ homolog subfamily B member 13
DIV_ANTMA Transcription factor DIVARICATA
DIN11_ARATH Probable 2-oxoglutarate-dependent dioxygenase DIN11
DEGP7_ARATH Protease Do-like 7
DAR2_ARATH Protein DA1-related 2
DAR1_ARATH Protein DA1-related 1
ACY1_PIG Aminoacylase-1
CYSKP_CAPAN Cysteine synthase, chloroplastic/chromoplastic
2NPD_STAAW Probable nitronate monooxygenase
CSLCC_ARATH Probable xyloglucan glycosyltransferase 12
CSE_ARATH Caffeoylshikimate esterase
CSE_ARATH Caffeoylshikimate esterase
2ABA_ORYSJ Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
CRS1_ARATH Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
CRK3_ARATH Cysteine-rich receptor-like protein kinase 3
CRK22_ARATH Cysteine-rich receptor-like protein kinase 22
CPL4_ARATH RNA polymerase II C-terminal domain phosphatase-like 4
CPL1_ARATH RNA polymerase II C-terminal domain phosphatase-like 1

COQ9_XENTR Ubiquinone biosynthesis protein COQ9, mitochondrial
CNG19_ARATH Putative cyclic nucleotide-gated ion channel 19
CLSY3_ARATH SNF2 domain-containing protein CLASSY 3
CLPX_AZOSB ATP-dependent Clp protease ATP-binding subunit ClpX
CLL5_ARATH Cullin-like protein 5
CLL4_ARATH Putative cullin-like protein 4
CLAH2_ARATH Clathrin heavy chain 2
CKX1_ARATH Cytokinin dehydrogenase 1
CKS2_ARATH Cyclin-dependent kinases regulatory subunit 2
ACOC_ORYSJ Putative aconitate hydratase, cytoplasmic
CIPKH_ARATH CBL-interacting serine/threonine-protein kinase 17
CIPKD_ARATH CBL-interacting serine/threonine-protein kinase 13
CIPKD_ARATH CBL-interacting serine/threonine-protein kinase 13
CIPKD_ARATH CBL-interacting serine/threonine-protein kinase 13
CIPKD_ARATH CBL-interacting serine/threonine-protein kinase 13
CID6_ARATH Polyadenylate-binding protein-interacting protein 6
CHX5_ARATH Cation/H(+) antiporter 5
CHUP1_ARATH Protein CHUP1, chloroplastic
CHUP1_ARATH Protein CHUP1, chloroplastic
CHR9_ARATH Switch 2
CEMA_CYAME Chloroplast envelope membrane protein
CDPKF_ARATH Calcium-dependent protein kinase 15
ACER3_MOUSE Alkaline ceramidase 3
CCR4B_ARATH Carbon catabolite repressor protein 4 homolog 2
ZHD3_ARATH Zinc-finger homeodomain protein 3
ZFP3_ARATH Zinc finger protein 3
ZFP3_ARATH Zinc 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

Y5519_ARATH Uncharacterized protein At5g05190
Y5519_ARATH Uncharacterized protein At5g05190
Y5436_ARATH MATH domain-containing protein At5g43560
Y5161_ARATH Uncharacterized protein At5g01610
Y5126_ARATH Probable serine/threonine-protein kinase At5g41260
Y4849_ARATH Uncharacterized protein At4g18490
Y4523_ARATH Probable serine/threonine-protein kinase At4g35230
Y4498_ARATH Uncharacterized protein At4g04980
Y4409_ARATH Putative BTB/POZ domain-containing protein At4g04090
Y4372_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g37250
Y4312_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g31250
Y4291_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g29180
Y4200_ARATH Uncharacterized protein At4g02000
Y4117_ARATH Putative disease resistance protein At4g11170
Y4117_ARATH Putative disease resistance protein At4g11170
Y4117_ARATH Putative disease resistance protein At4g11170
Y2559_ARATH Receptor-like serine/threonine-protein kinase At2g45590
Y2559_ARATH Receptor-like serine/threonine-protein kinase At2g45590
CAX2_ARATH Vacuolar cation/proton exchanger 2
Y2241_ARATH Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g24130
Y2048_ARATH WEB family protein At2g40480
Y2048_ARATH WEB family protein At2g40480
CATB_CHICK Cathepsin B
Y1839_ARATH Probable serine/threonine-protein kinase At1g18390
Y1719_ARATH Probable inactive receptor kinase At1g27190
Y1719_ARATH Probable inactive receptor kinase At1g27190
Y1686_ARATH Uncharacterized membrane protein At1g16860
Y1491_ARATH Uncharacterized protein At1g04910
Y1480_ARATH Uncharacterized protein At1g18480
Y1461_ARATH Probable serine/threonine-protein kinase At1g54610
Y1448_ARATH Uncharacterized protein At1g24485
Y1164_ARATH BTB/POZ domain-containing protein At1g01640
Y1112_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase At1g11280
Y1061_ARATH Probably inactive leucine-rich repeat receptor-like protein kinase At1g50610
Y1015_ARATH Uncharacterized protein At1g01500
XYLT_ARATH Beta-(1,2)-xylosyltransferase
XYLT_ARATH Beta-(1,2)-xylosyltransferase
XYLT1_RAT Xylosyltransferase 1 (Fragment)
XYLL3_ARATH D-xylose-proton symporter-like 3, chloroplastic
XRN3_ARATH 5'-3' exoribonuclease 3
XLG2_ARATH Extra-large guanine nucleotide-binding protein 2
XLG2_ARATH Extra-large guanine nucleotide-binding protein 2
XB31_ARATH Putative E3 ubiquitin-protein ligase XBAT31
WUS_ARATH Protein WUSCHEL
WRK70_ARATH Probable WRKY transcription factor 70
WRK70_ARATH Probable WRKY transcription factor 70
WRK57_ARATH Probable WRKY transcription factor 57
WRK53_ARATH Probable WRKY transcription factor 53

WRK53_ARATH Probable WRKY transcription factor 53
WRK48_ARATH Probable WRKY transcription factor 48
WRK47_ARATH Probable WRKY transcription factor 47
WRK25_ARATH Probable WRKY transcription factor 25
WRK13_ARATH Probable WRKY transcription factor 13
WOX5_ARATH WUSCHEL-related homeobox 5
WOX3_ARATH WUSCHEL-related homeobox 3
WIT1_ARATH WPP domain-interacting tail-anchored protein 1
WIP3_ARATH WPP domain-interacting protein 3
VTI13_ARATH Vesicle transport v-SNARE 13
VTI11_ARATH Vesicle transport v-SNARE 11
VP372_ARATH Vacuolar protein-sorting-associated protein 37 homolog 2
VP281_ARATH Vacuolar protein sorting-associated protein 28 homolog 1
VP26A_ARATH Vacuolar protein sorting-associated protein 26A
VICTR_ARATH Protein VARIATION IN COMPOUND TRIGGERED ROOT growth response
VATA_CYACA V-type proton ATPase catalytic subunit A
VAR3_ARATH Zinc finger protein VAR3, chloroplastic
VAL1_ARATH B3 domain-containing transcription repressor VAL1
VA727_ARATH Vesicle-associated membrane protein 727
VA725_ARATH Vesicle-associated membrane protein 725
VA725_ARATH Vesicle-associated membrane protein 725
VA0E2_ARATH V-type proton ATPase subunit e2
CALS3_ARATH Callose synthase 3
UKL1_ARATH Uridine kinase-like protein 1, chloroplastic
UGHY_ARATH (S)-ureidoglycine aminohydrolase
UBP15_ARATH Ubiquitin carboxyl-terminal hydrolase 15
UBC14_ARATH Ubiquitin-conjugating enzyme E2 14
U80A2_ARATH Sterol 3-beta-glucosyltransferase UGT80A2
U80A2_ARATH Sterol 3-beta-glucosyltransferase UGT80A2
U71B5_ARATH UDP-glycosyltransferase 71B5
U71B2_ARATH UDP-glycosyltransferase 71B2
CAF1G_ARATH Probable CCR4-associated factor 1 homolog 7
TYDP2_XENTR Tyrosyl-DNA phosphodiesterase 2
TT16_ARATH Protein TRANSPARENT TESTA 16
TT16_ARATH Protein TRANSPARENT TESTA 16
TT12_ARATH Protein TRANSPARENT TESTA 12
CAAT4_ARATH Cationic amino acid transporter 4, vacuolar
C98A8_ARATH Cytochrome P450 98A8
C90D1_ARATH 3-epi-6-deoxocathasterone 23-monooxygenase
C90A1_ARATH Cytochrome P450 90A1
TRA1_YEAST Transcription-associated protein 1
TPPC8_HUMAN Trafficking protein particle complex subunit 8
TPPC4_BOVIN Trafficking protein particle complex subunit 4
TPPA_ARATH Trehalose-phosphate phosphatase A
C3H63_ORYSJ Zinc finger CCCH domain-containing protein 63
C3H58_ARATH Zinc finger CCCH domain-containing protein 58
C3H58_ARATH Zinc finger CCCH domain-containing protein 58
TPL_ARATH Protein TOPLESS

C3H55_ARATH Zinc finger CCCH domain-containing protein 55
C3H35_ARATH E3 ubiquitin-protein ligase makorin
C2D61_ARATH C2 domain-containing protein At1g53590
TOM72_ARATH Mitochondrial import receptor subunit TOM7-2
TOM71_ARATH Mitochondrial import receptor subunit TOM7-1
TOM1_TOBAC Tobamovirus multiplication protein 1
TLP9_ARATH Tubby-like F-box protein 9
TLP2_ARATH Tubby-like F-box protein 2
BZP43_ARATH Basic leucine zipper 43
BZP43_ARATH Basic leucine zipper 43
BZP43_ARATH Basic leucine zipper 43
TIF5A_ARATH Protein TIFY 5A
TIF5A_ARATH Protein TIFY 5A
TIC_ARATH Protein TIME FOR COFFEE
TIC_ARATH Protein TIME FOR COFFEE
TIC22_ARATH Protein TIC 22, chloroplastic
THI4_ARATH Thiamine thiazole synthase, chloroplastic
TGT2_ARATH Trihelix transcription factor GT-2
TGA5_ARATH Transcription factor TGA5
TGA3_ARATH Transcription factor TGA3
TGA21_TOBAC TGACG-sequence-specific DNA-binding protein TGA-2.1
TCP8_ARATH Transcription factor TCP8
TCP5_ARATH Transcription factor TCP5
TCP5_ARATH Transcription factor TCP5
TCP3_ARATH Transcription factor TCP3
TCP15_ARATH Transcription factor TCP15
TCP15_ARATH Transcription factor TCP15
TCP13_ARATH Transcription factor TCP13
TCP10_ARATH Transcription factor TCP10
TBL9_ARATH Protein trichome birefringence-like 9
TBL20_ARATH Protein trichome birefringence-like 20
TADA_ARATH tRNA(adenine(34)) deaminase, chloroplastic
T2FA_ARATH Transcription initiation factor IIF subunit alpha
T184C_RAT Transmembrane protein 184C
T184C_RAT Transmembrane protein 184C
SYWC_SCHPO Tryptophan--tRNA ligase, cytoplasmic
BRG3_ARATH Probable BOI-related E3 ubiquitin-protein ligase 3
BRG2_ARATH Probable BOI-related E3 ubiquitin-protein ligase 2
BPS1_ARATH Protein BPS1, chloroplastic
BPC6_ARATH Protein BASIC PENTACYSTEINE6
BPC6_ARATH Protein BASIC PENTACYSTEINE6
BPC2_ARATH Protein BASIC PENTACYSTEINE2
BON2_ARATH Protein BONZAI 2
SYIC_YEAST Isoleucine--tRNA ligase, cytoplasmic
SYIC_MOUSE Isoleucine--tRNA ligase, cytoplasmic
BOI_ARATH E3 ubiquitin-protein ligase BOI
SYFB_ARATH Probable phenylalanine--tRNA ligase beta subunit
BLH4_ARATH BEL1-like homeodomain protein 4

BLH3_ARATH BEL1-like homeodomain protein 3
BLH3_ARATH BEL1-like homeodomain protein 3
BLH2_ARATH BEL1-like homeodomain protein 2
BLH2_ARATH BEL1-like homeodomain protein 2
SY131_ARATH Putative syntaxin-131
SY131_ARATH Putative syntaxin-131
SY131_ARATH Putative syntaxin-131
SY121_ARATH Syntaxin-121
SY121_ARATH Syntaxin-121
BL1S2_ARATH Biogenesis of lysosome-related organelles complex 1 subunit 2
SUVH5_ARATH Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5
SUVH3_ARATH Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3
SUOX_ARATH Sulfite oxidase
SUCA1_ARATH Succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial
STP7_ARATH Sugar transport protein 7
STP11_ARATH Sugar transport protein 11
STIL4_ARATH Protein STICHEL-like 4
SRS3_ARATH Protein SHI RELATED SEQUENCE 3
SRPR_DICDI Signal recognition particle receptor subunit alpha
SRK2E_ARATH Serine/threonine-protein kinase SRK2E
SRK2A_ARATH Serine/threonine-protein kinase SRK2A
SRF4_ARATH Protein STRUBBELIG-RECEPTOR FAMILY 4
SR45A_ARATH Serine/arginine-rich splicing factor SR45a
SPZ5_ARATH Probable non-inhibitory serpin-Z5
SPT_ARATH Transcription factor SPATULA
SPT16_ARATH FACT complex subunit SPT16
SPG1_SCHPO Septum-promoting GTP-binding protein 1
SODM1_ARATH Superoxide dismutase [Mn] 1, mitochondrial
SNF4_ARATH Sucrose nonfermenting 4-like protein
SMU1_ARATH Suppressor of mec-8 and unc-52 protein homolog 1
SMG7L_ARATH Protein SMG7L
SMB_ARATH Protein SOMBRERO
SLU7_ORYSJ Pre-mRNA-splicing factor SLU7
SLAH3_ARATH S-type anion channel SLAH3
SLAH3_ARATH S-type anion channel SLAH3
SKIP5_ARATH F-box protein SKIP5
SKI17_ARATH F-box protein SKIP17
SIGA_ARATH RNA polymerase sigma factor sigA
SIB1_ARATH Sigma factor binding protein 1, chloroplastic
SIB1_ARATH Sigma factor binding protein 1, chloroplastic
SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
SGR2_ARATH Protein STAY-GREEN 2, chloroplastic
SFR2_ORYSJ Beta-glucosidase-like SFR2, chloroplastic
BH130_ARATH Transcription factor bHLH130
BH123_ARATH Transcription factor bHLH123
BH111_ARATH Transcription factor bHLH111

BH093_ARATH Transcription factor bHLH93
BH055_ARATH Transcription factor bHLH55
BH055_ARATH Transcription factor bHLH55
BH047_ARATH Transcription factor bHLH47
BH041_ARATH Putative transcription factor bHLH041
BH032_ARATH Transcription factor AIG1
BH020_ARATH Transcription factor NAI1
BH013_ARATH Transcription factor bHLH13
SDF2_ARATH Stromal cell-derived factor 2-like protein
SD31_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase SD3-1
SCRK1_ARATH Probable fructokinase-1
SCP22_ARATH Serine carboxypeptidase-like 22
SCP19_ARATH Serine carboxypeptidase-like 19
BGL34_ARATH Myrosinase 4
SCL31_ARATH Scarecrow-like protein 31
SCL31_ARATH Scarecrow-like protein 31
SCL31_ARATH Scarecrow-like protein 31
SAT2_ARATH Serine acetyltransferase 2
SAR1A_ARATH GTP-binding protein SAR1A
SAP4_ARATH Zinc finger A20 and AN1 domain-containing stress-associated protein 4
SAC51_ARATH Transcription factor SAC51
SAC51_ARATH Transcription factor SAC51
S47A2_MOUSE Multidrug and toxin extrusion protein 2
S38AA_PONAB Putative sodium-coupled neutral amino acid transporter 10
S38AA_MOUSE Putative sodium-coupled neutral amino acid transporter 10
RVE8_ARATH Protein REVEILLE 8
RTEL1_DROER Regulator of telomere elongation helicase 1 homolog
RSPH1_MOUSE Radial spoke head 1 homolog
BEL1_ARATH Homeobox protein BEL1 homolog
BEE3_ARATH Transcription factor BEE 3
RSLE2_ORYSJ Zinc finger BED domain-containing protein RICESLEEPER 2
RSLE1_ORYSJ Zinc finger BED domain-containing protein RICESLEEPER 1
BBX22_ARATH B-box zinc finger protein 22
BAN_ARATH Anthocyanidin reductase
BAM7_ARATH Beta-amylase 7
BAG3_ARATH BAG family molecular chaperone regulator 3
RS193_ARATH 40S ribosomal protein S19-3
B3GTJ_ARATH Probable beta-1,3-galactosyltransferase 19
B2_DAUCA B2 protein
RS142_ARATH 40S ribosomal protein S14-2
RS141_ARATH 40S ribosomal protein S14-1
RRP2_SPIOL 30S ribosomal protein 2, chloroplastic
RRP2_SPIOL 30S ribosomal protein 2, chloroplastic
AXX15_SOYBN Auxin-induced protein X15
AX15A_SOYBN Auxin-induced protein 15A
AVT1_YEAST Vacuolar amino acid transporter 1
ABR1_ARATH Ethylene-responsive transcription factor ABR1
RPD1_ARATH Protein ROOT PRIMORDIUM DEFECTIVE 1

RNP3_SCHPO Probable ribonuclease P protein subunit 3
RNP1_ARATH Heterogeneous nuclear ribonucleoprotein 1
RNP1_ARATH Heterogeneous nuclear ribonucleoprotein 1
RNHX1_ARATH Putative ribonuclease H protein At1g65750
RNHX1_ARATH Putative ribonuclease H protein At1g65750
RNF14_MOUSE E3 ubiquitin-protein ligase RNF14
RNF12_MOUSE E3 ubiquitin-protein ligase RLIM
RN217_XENLA Probable E3 ubiquitin-protein ligase RNF217
RM06_MARPO 60S ribosomal protein L6, mitochondrial
ABKC_DICDI Probable serine/threonine-protein kinase abkC
ABI3_ARATH B3 domain-containing transcription factor ABI3
RLF26_ARATH Protein RALF-like 26
RL273_ARATH 60S ribosomal protein L27-3
RL271_ARATH 60S ribosomal protein L27-1
RK6_ARATH 50S ribosomal protein L6, chloroplastic
RING1_GOSHI E3 ubiquitin-protein ligase RING1
RING1_GOSHI E3 ubiquitin-protein ligase RING1
RING1_GOSHI E3 ubiquitin-protein ligase RING1
RING1_ARATH E3 ubiquitin-protein ligase At1g12760
RIC4_ARATH CRIB domain-containing protein RIC4
RH37_ARATH DEAD-box ATP-dependent RNA helicase 37
RGLG2_ARATH E3 ubiquitin-protein ligase RGLG2
RGLG1_ARATH E3 ubiquitin-protein ligase RGLG1
RF2B_ORYSJ Transcription factor RF2b
RF2B_ORYSJ Transcription factor RF2b
REN1_ARATH Rho GTPase-activating protein REN1
REM20_ARATH B3 domain-containing protein REM20
REM20_ARATH B3 domain-containing protein REM20
REM20_ARATH B3 domain-containing protein REM20
REM17_ARATH B3 domain-containing protein REM17
RDM4_ARATH RNA-directed DNA methylation 4
RD23B_ARATH Ubiquitin receptor RAD23b
RBM42_BOVIN RNA-binding protein 42
RBM38_HUMAN RNA-binding protein 38
RBM24_DANRE RNA-binding protein 24
RBK1_ARATH Receptor-like cytosolic serine/threonine-protein kinase RBK1
RAX3_ARATH Transcription factor RAX3
RAX2_ARATH Transcription factor RAX2
RAX2_ARATH Transcription factor RAX2
RANB1_TOBAC GTP-binding nuclear protein Ran-B1
RAN1_ARATH GTP-binding nuclear protein Ran-1
RAN1B_LOTJA GTP-binding nuclear protein Ran1B (Fragment)
RAF1_ARATH Rubisco accumulation factor 1, chloroplastic
RAC7_ARATH Rac-like GTP-binding protein ARAC7
RAC2A_ARATH Ras-related protein RABC2a
RAC2A_ARATH Ras-related protein RABC2a
RAB1B_ARATH Ras-related protein RABB1b
RA210_ARATH Ethylene-responsive transcription factor RAP2-10

R23A1_ARATH 60S ribosomal protein L23a-1
R13A4_ARATH 60S ribosomal protein L13a-4
QWRF8_ARATH QWRF motif-containing protein 8
QWRF2_ARATH QWRF motif-containing protein 2
AB25G_ARATH ABC transporter G family member 25
PYL3_ARATH Abscisic acid receptor PYL3
AB17C_DANRE Alpha/beta hydrolase domain-containing protein 17C
AB17C_DANRE Alpha/beta hydrolase domain-containing protein 17C
PUP21_ARATH Probable purine permease 21
PUMP2_ARATH Mitochondrial uncoupling protein 2
PUB50_ARATH Putative U-box domain-containing protein 50
PUB18_ARATH U-box domain-containing protein 18
PTR5_ARATH Protein NRT1/ PTR FAMILY 8.2
PTEN_DICDI Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase
PSKR2_ARATH Phytosulfokine receptor 2
ATL46_ARATH RING-H2 finger protein ATL46
ATL3_ARATH RING-H2 finger protein ATL3
PRN1_ARATH Pirin-1
ATK3_ARATH Kinesin-3
PPR65_ARATH Pentatricopeptide repeat-containing protein At1g31430
PPR65_ARATH Pentatricopeptide repeat-containing protein At1g31430
PPR29_ARATH Pentatricopeptide repeat-containing protein At1g10270
ATG9_CRYGA Autophagy-related protein 9
PPR1_ARATH Pentatricopeptide repeat-containing protein At1g01970
PP413_ARATH Pentatricopeptide repeat-containing protein At5g42310, mitochondrial
PP389_ARATH Pentatricopeptide repeat-containing protein At5g16640, mitochondrial
PP365_ARATH Pentatricopeptide repeat-containing protein At5g04810, chloroplastic
PP233_ARATH Putative pentatricopeptide repeat-containing protein At3g15200
PP230_ARATH Pentatricopeptide repeat-containing protein At3g14580, mitochondrial
PP160_ARATH Pentatricopeptide repeat-containing protein At2g17525, mitochondrial
PP110_ARATH Pentatricopeptide repeat-containing protein At1g69290
POT2_ARATH Potassium transporter 2
PORA_ARATH Protochlorophyllide reductase A, chloroplastic
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POL2_DROME Retrovirus-related Pol polyprotein from transposon 297
PNH1_ORYSJ Protein argonaute PNH1
PMTJ_ARATH Probable methyltransferase PMT19
PME8_ARATH Probable pectinesterase 8
PME64_ARATH Probable pectinesterase/pectinesterase inhibitor 64
PME56_ARATH Probable pectinesterase 56
PME51_ARATH Probable pectinesterase/pectinesterase inhibitor 51

PME16_ARATH Probable pectinesterase/pectinesterase inhibitor 16
PME16_ARATH Probable pectinesterase/pectinesterase inhibitor 16
PMA2_ARATH ATPase 2, plasma membrane-type
PLY12_ARATH Probable pectate lyase 12
PLY12_ARATH Probable pectate lyase 12
PLDD1_ARATH Phospholipase D delta
PLA15_ARATH Phospholipase A1-Igamma1, chloroplastic
PIRL9_ARATH Plant intracellular Ras-group-related LRR protein 9
PIP27_ARATH Aquaporin PIP2-7
PHT21_ARATH Inorganic phosphate transporter 2-1, chloroplastic
PHOT2_ARATH Phototropin-2
ATCA2_ARATH Alpha carbonic anhydrase 2
PHO15_ARATH Phosphate transporter PHO1 homolog 5
ATB20_ARATH Homeobox-leucine zipper protein ATHB-20
PGLR3_ARATH Probable polygalacturonase At3g15720
PFKA3_ARATH ATP-dependent 6-phosphofructokinase 3
PEX14_ARATH Peroxisomal membrane protein PEX14
PERK5_ARATH Proline-rich receptor-like protein kinase PERK5
PER21_ARATH Peroxidase 21
PEK12_ARATH Proline-rich receptor-like protein kinase PERK12
PEK12_ARATH Proline-rich receptor-like protein kinase PERK12
PDR2_ARATH Probable manganese-transporting ATPase PDR2
AAH_ARATH Allantoate deiminase
PDAT1_ARATH Phospholipid:diacylglycerol acyltransferase 1
PAT1_ARATH Scarecrow-like transcription factor PAT1
PAP_CANAL Poly(A) polymerase PAPalpha
PAP14_ARATH Probable plastid-lipid-associated protein 14, chloroplastic
PAP14_ARATH Probable plastid-lipid-associated protein 14, chloroplastic
PAO2_ARATH Probable polyamine oxidase 2
P4KA1_ARATH Phosphatidylinositol 4-kinase alpha 1
P2C80_ARATH Probable protein phosphatase 2C 80
P2C66_ARATH Probable protein phosphatase 2C 66
P2C43_ARATH Probable protein phosphatase 2C 43
OXA1_ARATH Mitochondrial inner membrane protein OXA1
OSB3_ARATH Protein OSB3, chloroplastic/mitochondrial
ASPL1_ARATH Aspartic proteinase-like protein 1
ASPG2_ARATH Protein ASPARTIC PROTEASE IN GUARD CELL 2
OPA3_SCHPO OPA3-like protein
OFP14_ARATH Transcription repressor OFP14
OFP14_ARATH Transcription repressor OFP14
OCS1_MAIZE Ocs element-binding factor 1
ASHH2_ARATH Histone-lysine N-methyltransferase ASHH2
NUD12_ARATH Nudix hydrolase 12, mitochondrial
NTPR_ENTHA Protein NtpR
ARR7_ARATH Two-component response regulator ARR7
ARR5_ARATH Two-component response regulator ARR5
NSA2_DICDI Ribosome biogenesis protein NSA2 homolog
ARR16_ARATH Two-component response regulator ARR16

ARR15_ARATH Two-component response regulator ARR15
ARR11_ARATH Two-component response regulator ARR11
NPY1_ARATH BTB/POZ domain-containing protein NPY1
NPR5_ARATH Regulatory protein NPR5
NLTL2_ARATH Non-specific lipid-transfer protein-like protein At2g13820
NIPA7_ARATH Probable magnesium transporter NIPA7
NGA4_ARATH B3 domain-containing transcription factor NGA4
NGA4_ARATH B3 domain-containing transcription factor NGA4
NGA1_ARATH B3 domain-containing transcription factor NGA1
NFYB5_ARATH Nuclear transcription factor Y subunit B-5
NEUR_DROVI Protein neuralized
NEK2_ARATH Serine/threonine-protein kinase Nek2
NDUS7_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial
NACK1_ARATH Kinesin-like protein NACK1
NAC8_ARATH NAC domain-containing protein 8
NAC8_ARATH NAC domain-containing protein 8
NAC8_ARATH NAC domain-containing protein 8
NAC86_ARATH NAC domain-containing protein 86
NAC7_ARATH NAC domain-containing protein 7
NAC7_ARATH NAC domain-containing protein 7
NAC7_ARATH NAC domain-containing protein 7
NAC45_ARATH NAC domain-containing protein 45
NAC18_ARATH NAC domain-containing protein 18
NAC18_ARATH NAC domain-containing protein 18
NAA11_HUMAN N-alpha-acetyltransferase 11
MYBL_DICDI Myb-like protein L
MYB98_ARATH Transcription factor MYB98
MYB98_ARATH Transcription factor MYB98
MYB98_ARATH Transcription factor MYB98
MYB86_ARATH Transcription factor MYB86
MYB86_ARATH Transcription factor MYB86
MYB86_ARATH Transcription factor MYB86
MYB86_ARATH Transcription factor MYB86
MYB86_ARATH Transcription factor MYB86
MYB4_ORYSJ Myb-related protein Myb4
MYB44_ARATH Transcription factor MYB44
MYB44_ARATH Transcription factor MYB44
MYB44_ARATH Transcription factor MYB44
MYB39_ARATH Transcription factor MYB39
MYB06_ANTMA Myb-related protein 306
MTPB_ARATH Metal tolerance protein B
MTP12_ARATH Metal tolerance protein 12
A4GAT_MOUSE Lactosylceramide 4-alpha-galactosyltransferase
A4GAT_GORGO Lactosylceramide 4-alpha-galactosyltransferase (Fragment)
MTA70_ARATH N6-adenosine-methyltransferase MT-A70-like
MSL6_ARATH Mechanosensitive ion channel protein 6
MPK7_ARATH Mitogen-activated protein kinase 7
MPK17_ARATH Mitogen-activated protein kinase 17

MO25N_ARATH Putative MO25-like protein At5g47540
MNS2_ARATH Mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS2
ML328_ARATH MLP-like protein 328
ML328_ARATH MLP-like protein 328
ML328_ARATH MLP-like protein 328
ML328_ARATH MLP-like protein 328
MKS1_ARATH Protein MKS1
MKKA_DICDI Mitogen-activated protein kinase kinase kinase A
MIRO_DROME Mitochondrial Rho GTPase
MGP_ARATH Zinc finger protein MAGPIE
MGP_ARATH Zinc finger protein MAGPIE
METE2_ARATH 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2
METE2_ARATH 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2
MEMO1_XENLA Protein MEMO1
MEMO1_XENLA Protein MEMO1
MED14_ARATH Mediator of RNA polymerase II transcription subunit 14
MD19B_ARATH Probable mediator of RNA polymerase II transcription subunit 19b
MD15A_ARATH Mediator of RNA polymerase II transcription subunit 15a
MCM6_ARATH DNA replication licensing factor MCM6
MCA1_ARATH Metacaspase-1
MBR2_ARATH E3 ubiquitin-protein ligase MBR2
MBF1B_ARATH Multiprotein-bridging factor 1b
MBD6_ARATH Methyl-CpG-binding domain-containing protein 6
MAD16_ORYSJ MADS-box transcription factor 16
MA653_ARATH 65-kDa microtubule-associated protein 3
LUL4_ARATH Probable E3 ubiquitin-protein ligase LUL4
LTI65_ARATH Low-temperature-induced 65 kDa protein
LSM6_MOUSE U6 snRNA-associated Sm-like protein LSm6
LPAAT_ARATH 1-acylglycerol-3-phosphate O-acyltransferase
LORF2_HUMAN LINE-1 retrotransposable element ORF2 protein
LNG2_ARATH Protein LONGIFOLIA 2
LK110_ARATH Putative L-type lectin-domain containing receptor kinase I.10
LIN1_NYCCO LINE-1 reverse transcriptase homolog
LBD36_ARATH LOB domain-containing protein 36
LBD29_ARATH LOB domain-containing protein 29
LBD29_ARATH LOB domain-containing protein 29
LBD27_ARATH LOB domain-containing protein 27
LACS3_ARATH Long chain acyl-CoA synthetase 3
KRP4_ARATH Cyclin-dependent kinase inhibitor 4
KRP4_ARATH Cyclin-dependent kinase inhibitor 4
KPRS4_ARATH Ribose-phosphate pyrophosphokinase 4
KPRS3_ARATH Ribose-phosphate pyrophosphokinase 3, chloroplastic
KPK2_ARATH Serine/threonine-protein kinase AtPK2/AtPK19
KNU_ARATH Zinc finger protein KNUCKLES
KIPK_ARATH Serine/threonine-protein kinase KIPK
KCS10_ARATH 3-ketoacyl-CoA synthase 10
KC1D_ARATH Casein kinase I isoform delta-like
KBAY_ECOLX D-tagatose-1,6-bisphosphate aldolase subunit KbaY

ARFD_ARATH Auxin response factor 4
KAN2_ARATH Probable transcription factor KAN2
KAN1_ARATH Transcription repressor KAN1
KAN1_ARATH Transcription repressor KAN1
KAN1_ARATH Transcription repressor KAN1
JADE1_XENLA Protein Jade-1
IX15L_ARATH Protein IRX15-LIKE
ARAE2_ARATH Putative UDP-arabinose 4-epimerase 2
IPO7_HUMAN Importin-7
IP5PD_ARATH Type I inositol 1,4,5-trisphosphate 5-phosphatase 13
IDN2_ARATH Protein INVOLVED IN DE NOVO 2
IAR1_ARATH IAA-alanine resistance protein 1
APRR7_ARATH Two-component response regulator-like APRR7
APRR1_ARATH Two-component response regulator-like APRR1
APL_ARATH Myb family transcription factor APL
HMGCL_ARATH Hydroxymethylglutaryl-CoA lyase, mitochondrial
HMDH1_ARATH 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1
HMA1_ARATH Probable cadmium/zinc-transporting ATPase HMA1, chloroplastic
HFR1_ARATH Transcription factor HFR1
AP4E_ARATH AP-4 complex subunit epsilon
AP4E_ARATH AP-4 complex subunit epsilon
HFA2A_ORYSJ Heat stress transcription factor A-2a
HERC1_HUMAN Probable E3 ubiquitin-protein ligase HERC1
HERC1_HUMAN Probable E3 ubiquitin-protein ligase HERC1
HERC1_HUMAN Probable E3 ubiquitin-protein ligase HERC1
AP2M_ARATH AP-2 complex subunit mu
AOP1V_ARATH Probable 2-oxoglutarate-dependent dioxygenase AOP1 (Fragment)
HDG8_ARATH Homeobox-leucine zipper protein HDG8
HDG7_ARATH Homeobox-leucine zipper protein HDG7
HDA11_DICDI Type-1 histone deacetylase 1
HAT7_ARATH Homeobox-leucine zipper protein HAT7
ANP1_ARATH Mitogen-activated protein kinase kinase kinase ANP1
GULDH_MYCTU L-gulono-1,4-lactone dehydrogenase
GTL2_ARATH Trihelix transcription factor GTL2
GTL2_ARATH Trihelix transcription factor GTL2
GTL1_ARATH Trihelix transcription factor GTL1
ANM6_ARATH Probable protein arginine N-methyltransferase 6
GRS13_ARATH Monothiol glutaredoxin-S13
GRS13_ARATH Monothiol glutaredoxin-S13
GRS13_ARATH Monothiol glutaredoxin-S13
GRP2_SORBI Glycine-rich RNA-binding protein 2
GRF5_ARATH Growth-regulating factor 5
GRCR1_HUMAN Glutaredoxin domain-containing cysteine-rich protein 1
GPX6_ARATH Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial
GLYT6_ARATH Probable glycosyltransferase At5g25310
GLYR1_RAT Putative oxidoreductase GLYR1
GLYR1_ARATH Glyoxylate/succinic semialdehyde reductase 1
AMS_ARATH Transcription factor ABORTED MICROSPORES

GLT3_ARATH Germin-like protein subfamily T member 3
4CLL8_ARATH 4-coumarate--CoA ligase-like 8
GLD2A_DROME Poly(A) RNA polymerase gld-2 homolog A
GL3_ARATH Transcription factor GLABRA 3
GID1B_ARATH Gibberellin receptor GID1B
GGT1_ARATH Glutamate--glyoxylate aminotransferase 1
GGR_ARATH Heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic
GGPPS_SINAL Geranylgeranyl pyrophosphate synthase, chloroplastic/chromoplastic
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 At1g64840
FBD34_ARATH Putative FBD-associated F-box protein At1g05080
FB94_ARATH Putative F-box protein At2g02030

FB94_ARATH Putative F-box protein At2g02030
FB93_ARATH F-box protein At1g80960
FB77_ARATH Putative F-box protein At1g67390
FB306_ARATH Putative F-box protein At1g26515
FB213_ARATH F-box protein At3g60790
FB184_ARATH Putative F-box protein At3g24580
FB182_ARATH Putative F-box protein At3g23960
FB126_ARATH F-box protein At2g34280
FAFL_ARATH Protein FAF-like, chloroplastic
FAF2A_XENLA FAS-associated factor 2-A
FAD1_SCHPO Probable FAD synthase
FAB1A_ARATH 1-phosphatidylinositol-3-phosphate 5-kinase FAB1A
EZA1_ARATH Histone-lysine N-methyltransferase EZA1
EXP17_ARATH Putative expansin-A17
EXP11_ARATH Expansin-A11
ETR2_ARATH Ethylene receptor 2
ERMP1_MOUSE Endoplasmic reticulum metallopeptidase 1
ERF86_ARATH Ethylene-responsive transcription factor ERF086
ERF14_ARATH Ethylene-responsive transcription factor ERF014
AIL5_ARATH AP2-like ethylene-responsive transcription factor AIL5
AIFM2_TAEGU Apoptosis-inducing factor 2
EMF1_ARATH Protein EMBRYONIC FLOWER 1
EMF1_ARATH Protein EMBRYONIC FLOWER 1
EMC3_DANRE ER membrane protein complex subunit 3
ELF3_ARATH Protein EARLY FLOWERING 3
ELCL_ARATH Protein ELC-like
EIN2_ARATH Ethylene-insensitive protein 2
AHK2_ARATH Histidine kinase 2
AHK2_ARATH Histidine kinase 2
AHK2_ARATH Histidine kinase 2
AGL80_ARATH Agamous-like MADS-box protein AGL80
EFGM2_ARATH Elongation factor G-2, mitochondrial
EF1D1_ARATH Elongation factor 1-delta 1
EF107_ARATH Ethylene-responsive transcription factor ERF107
EF102_ARATH Ethylene-responsive transcription factor 5
AGD12_ARATH ADP-ribosylation factor GTPase-activating protein AGD12
E70A1_ARATH Exocyst complex component EXO70A1
E1311_ARATH Glucan endo-1,3-beta-glucosidase 11
DYL1_YEAST Dynein light chain 1, cytoplasmic
DTC_ARATH Mitochondrial dicarboxylate/tricarboxylate transporter DTC
DRTS2_ARATH Bifunctional dihydrofolate reductase-thymidylate synthase 2
DRP1E_ARATH Dynamin-related protein 1E
DRL34_ARATH Probable disease resistance protein At5g45440
DRE2B_ARATH Dehydration-responsive element-binding protein 2B
DRB5_ARATH Double-stranded RNA-binding protein 5
DRB3_ARATH Double-stranded RNA-binding protein 3
DPNP3_ARATH Probable SAL3 phosphatase
ADK2_ARATH Adenosine kinase 2

DOF56_ARATH Dof zinc finger protein DOF5.6
DOF46_ARATH Dof zinc finger protein DOF4.6
DOF35_ARATH Dof zinc finger protein DOF3.5
DOF35_ARATH Dof zinc finger protein DOF3.5
DOF25_ARATH Dof zinc finger protein DOF2.5
DOF18_ARATH Dof zinc finger protein DOF1.8
DOF18_ARATH Dof zinc finger protein DOF1.8
DOF15_ARATH Dof zinc finger protein DOF1.5
DOF15_ARATH Dof zinc finger protein DOF1.5
DNJ49_ARATH Chaperone protein dnaJ 49
DJB13_HUMAN DnaJ homolog subfamily B member 13
TCP15_ARATH Transcription factor TCP15
SRO2_ARATH Probable inactive poly [ADP-ribose] polymerase SRO2
AML5_ARATH Protein MEI2-like 5
SHGR5_ARATH Protein SHOOT GRAVITROPISM 5
DRTI_DELRE Kunitz-type serine protease inhibitor DrTI
DRTI_DELRE Kunitz-type serine protease inhibitor DrTI
SYI_TETTH Isoleucine--tRNA ligase
BH087_ARATH Transcription factor bHLH87
GRF5_ARATH Growth-regulating factor 5
AB33G_ARATH ABC transporter G family member 33
HFR1_ARATH Transcription factor HFR1
Y1960_ARATH Probable serine/threonine-protein kinase At1g09600
PIP24_ARATH Probable aquaporin PIP2-4
CHX14_ARATH Cation/H(+) antiporter 14
SIB2_ARATH Sigma factor binding protein 2, chloroplastic
MAF5_ARATH Protein MADS AFFECTING FLOWERING 5
ARAD1_ARATH Probable arabinosyltransferase ARAD1
HDG5_ARATH Homeobox-leucine zipper protein HDG5
CRK41_ARATH Cysteine-rich receptor-like protein kinase 41
COPIA_DROME Copia protein
CNGC7_ARATH Putative cyclic nucleotide-gated ion channel 7
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
YI31B_YEAST Transposon Ty3-I Gag-Pol polyprotein
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
Y2988_ARATH Uncharacterized protein At2g29880
TF211_SCHPO Transposon Tf2-11 polyprotein
BGA13_ARATH Beta-galactosidase 13
RR12B_POPTR 30S ribosomal protein S12-B, chloroplastic
POL5_DROME Retrovirus-related Pol polyprotein from transposon opus
POL4_DROME Retrovirus-related Pol polyprotein from transposon 412
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6

POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
POL3_DROME Retrovirus-related Pol polyprotein from transposon 17.6
PEX4_ARATH Protein PEROXIN-4
M760_ARATH Uncharacterized mitochondrial protein AtMg00760
M750_ARATH Uncharacterized mitochondrial protein AtMg00750
M310_ARATH Uncharacterized mitochondrial protein AtMg00310
AP1M2_ARATH AP-1 complex subunit mu-2
YTX2_XENLA Transposon TX1 uncharacterized 149 kDa protein
POL_FFV Pro-Pol polyprotein
RNHX1_ARATH Putative ribonuclease H protein At1g65750
Y1515_ARATH Uncharacterized TPR repeat-containing protein At1g05150
C77A4_ARATH Cytochrome P450 77A4
RNHX1_ARATH Putative ribonuclease H protein At1g65750
PRS6A_ORYSJ 26S protease regulatory subunit 6A homolog
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POK2_ARATH Phragmoplast orienting kinesin 2
MBF1A_ARATH Multiprotein-bridging factor 1a
LRK63_ARATH Lectin-domain containing receptor kinase VI.3
HASTY_ARATH Protein HASTY 1
RL313_ARATH 60S ribosomal protein L31-3
DNAJ2_ARATH Chaperone protein dnaJ 2
COPIA_DROME Copia protein
YG31B_YEAST Transposon Ty3-G Gag-Pol polyprotein
Y2988_ARATH Uncharacterized protein At2g29880
VICTR_ARATH Protein VARIATION IN COMPOUND TRIGGERED ROOT growth response
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
PLDB2_ARATH Phospholipase D beta 2
MYB32_ARATH Transcription factor MYB32
FBL69_ARATH F-box/LRR-repeat protein At3g60040
EF104_ARATH Ethylene-responsive transcription factor ERF104

DF158_ARATH Putative defensin-like protein 158
YODA_ARATH Mitogen-activated protein kinase kinase kinase YODA
Y1561_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g56130
XRCC4_ARATH DNA repair protein XRCC4
TCPB_BOVIN T-complex protein 1 subunit beta
SYP42_ARATH Syntaxin-42
RH51_ARATH DEAD-box ATP-dependent RNA helicase 51
PXM16_ARATH Zinc-metallopeptidase, peroxisomal
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
PGLR_BRANA Polygalacturonase
MT810_ARATH Probable S-adenosylmethionine-dependent methyltransferase At5g38100
M3K1_ARATH Mitogen-activated protein kinase kinase kinase 1
KEA3_ARATH K(+) efflux antiporter 3, chloroplastic
IFRH_ARATH Isoflavone reductase homolog P3
HFA7A_ARATH Heat stress transcription factor A-7a
GSTUP_ARATH Glutathione S-transferase U25
GSO1_ARATH LRR receptor-like serine/threonine-protein kinase GSO1
GPDL3_ARATH Glycerophosphodiester phosphodiesterase GDPDL3
FUT9_ARATH Probable fucosyltransferase 9
ALDO1_ARATH Indole-3-acetaldehyde oxidase
ENDO2_ARATH Endonuclease 2
DAPF_ARATH Diaminopimelate epimerase, chloroplastic
BGAL9_ARATH Beta-galactosidase 9
BGAL8_ARATH Beta-galactosidase 8
POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94
OCT4_ARATH Organic cation/carnitine transporter 4
MYB48_ARATH Transcription factor MYB48
MYB46_ARATH Transcription factor MYB46
MYB46_ARATH Transcription factor MYB46
MYB46_ARATH Transcription factor MYB46
MYB12_ARATH Transcription factor MYB12
GAM1_ORYSI Transcription factor GAMYB
WOX1_ARATH WUSCHEL-related homeobox 1
RAA2B_ARATH Ras-related protein RABA2b
MYB82_ARATH Transcription factor MYB82
MYB82_ARATH Transcription factor MYB82
MYB59_ARATH Transcription factor MYB59
MYB46_ARATH Transcription factor MYB46
MYB46_ARATH Transcription factor MYB46
MYB12_ARATH Transcription factor MYB12
GAM1_ORYSJ Transcription factor GAMYB
WOX1_ARATH WUSCHEL-related homeobox 1
TT2_ARATH Transcription factor TT2
POL5_DROME Retrovirus-related Pol polyprotein from transposon opus
MYB59_ARATH Transcription factor MYB59

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

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

miRNA	**miRNA ($\log_2FC$)**			**Target gene**
	Cd vs. Con	**Cd+MT vs.**	**Cd+MT vs. Cd**	
miR156c-3p	—	**1.5019**	—	Rsa1.0_00867.1_g00010.1
miR157a-3p	**1.6885**	**1.3531**	—	Rsa1.0_01910.1_g00004.1
miR158a-3p	**1.0073**	—	—	Rsa1.0_02387.1_g00004.1
miR164a	**0.93873**	—	—	Rsa1.0_00387.1_g00044.1
miR164a	**0.93873**	—	—	Rsa1.0_00166.1_g00017.1
miR164c-5p	0.8825	—	—	Rsa1.0_00568.1_g00009.1
miR164c-5p	**0.8825**	—	—	Rsa1.0_00387.1_g00044.1
miR164c-5p	**0.8825**	—	—	Rsa1.0_00166.1_g00017.1
miR172a	—	—	-1.0199	Rsa1.0_01063.1_g00001.1
miR172a	—	—	-1.0199	Rsa1.0_04013.1_g00001.1
miR172b-5p	**-2.016**	**-1.4312**	—	Rsa1.0_00289.1_g00002.1
miR172c	—	—	-1.3389	Rsa1.0_02754.1_g00005.1
miR172c	—	—	-1.3389	Rsa1.0_01063.1_g00001.1
miR172c	—	—	-1.3389	Rsa1.0_04013.1_g00001.1
miR172e-3p	—	—	-1.4914	Rsa1.0_01063.1_g00001.1
miR172e-3p	—	—	-1.4914	Rsa1.0_04013.1_g00001.1
miR319c	—	—	-0.99209	Rsa1.0_01583.1_g00006.1
miR319c	—	—	-0.99209	Rsa1.0_01271.1_g00009.1
miR395b	**-2.1303**	—	1.6878	Rsa1.0_00493.1_g00009.1
miR395b	**-2.1303**	—	1.6878	Rsa1.0_00057.1_g00018.1
miR396b-3p	**-1.8776**	**-1.059**	—	Rsa1.0_00017.1_g00146.1
miR396b-5p	**0.98777**	—	—	Rsa1.0_08220.1_g00002.1
miR396b-5p	**0.98777**	—	—	Rsa1.0_00394.1_g00027.1
miR396b-5p	**0.98777**	—	—	Rsa1.0_02616.1_g00004.1
miR397a	—	**1.3319**	—	Rsa1.0_00328.1_g00010.1
miR398b-3p	—	**0.99034**	1.1971	Rsa1.0_01099.1_g00002.1
miR399b	**-1.8885**	—	—	Rsa1.0_00086.1_g00012.1
miR857	**1.5394**	**3.0215**	1.4251	Rsa1.0_00015.1_g00017.1
miR857	**1.5394**	3.0215	1.4251	Rsa1.0_01260.1_g00003.1
miR858a	**2.1258**	**1.625**	—	Rsa1.0_51959.1_g00001.1
miRn4	**-2.2535**	-0.91179	1.1118	Rsa1.0_00166.1_g00017.1

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

RNA-seq ($\log_2$FC)		
Cd vs. Con	**Cd+MT vs. Con**	**Cd+MT vs. Cd**
2.4121	**2.0221**	—
-3.1794	**-2.634**	—
1.0507	2.914	1.8552
3.5749	3.3839	—
1.8262	—	—
—	—	1.4656
3.5749	3.3839	—
1.8262	—	—
-1.7478	-1.9945	—
-2.8234	-1.4861	1.3298
-1.6479	**-1.6359**	—
—	-2.1528	-2.2917
-1.7478	-1.9945	—
-2.8234	-1.4861	1.3298
-1.7478	-1.9945	—
-2.8234	-1.4861	1.3298
1.6973	1.8818	—
—	—	3.1018
5.4636	5.4859	—
1.1928	1.4988	—
-2.6732	**-7.1352**	-4.4716
-1.2513	-1.5025	—
-3.7998	-3.6965	—
-3.834	-3.0539	—
1.5489	**1.778**	—
2.0394	**2.0409**	—
-1.9691	-1.8008	—
1.9852	**2.2021**	—
1.9374	—	-1.1275
-2.3329	**-1.7899**	—
1.8262	—	—

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

Annotation
Adenine nucleotide alpha hydrolases-like protein
Protein networked 1A
Glutathione S-transferase tau 13 glutathione S-transferase (GSTU13)
NAC domain-containing protein 3 (NAC3)
NAC domain containing protein 100 (NAC100)
NAC domain-containing protein 3 (NAC3)
NAC domain-containing protein 3 (NAC3)
NAC domain containing protein 100 (NAC100)
Target of early activation tagged 1 (RAP2.7)
Target of early activation tagged 3 (TOE3)
TUA2; tubulin alpha-2 chain
TFIIIA; transcription factor IIIA
Target of early activation tagged 1 (RAP2.7)
Target of early activation tagged 3 (TOE3)
Target of early activation tagged 1 (RAP2.7)
Target of early activation tagged 3 (TOE3)
Boron transporter 1 (BOR1)
DNA cytosine-5-methyltransferase 1 (MET1)
Sulfate transporter 2;1 (SULTR2;1)
Sulfate Adenylyltransferase (APS4)
Homeobox protein ATH1
Actin-binding FH2 (formin homology 2) family protein
Actin-binding FH2 (formin homology 2) family protein
Beta-glucosidase 44 (BGLU44)
IRREGULAR XYLEM 12 (IRX12)
Calcineurin-like phosphoesterase domain-containing protein
NRS/ER; UDP-4-keto-6-deoxy-d-glucose-3,5-epimerase-4-reductase 1
NmrA-like negative transcriptional regulator-like protein
Zinc-metallopeptidase PXM16
Beta-galactosidase 8 (BGAL8)
NAC100; NAC domain containing protein 100 (NAC100)

ificant difference was found in this comparision. $\log_2$FC: $\log_2$fold c

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	-0.1773	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
Rsa1.0_00353.1_g00001.1	2.3401	4.1798	1.8334
Rsa1.0_10417.1_g00001.1	1.9123	0.024635	-1.8966
Rsa1.0_51814.1_g00001.1	-2.9866	-1.2907	1.6869
Rsa1.0_03364.1_g00001.1	1.4884	4.4165	2.9224
Rsa1.0_00645.1_g00018.1	2.1813	3.498	1.3079
Rsa1.0_00019.1_g00008.1	-2.1827	-0.6081	1.5661
Rsa1.0_00026.1_g00056.1	-7.5124	-11.171	-3.6638
Rsa1.0_00453.1_g00009.1	3.8124	5.8423	2.0236
Rsa1.0_00132.1_g00007.1	-6.0769	-0.97685	5.0945
Rsa1.0_04860.1_g00001.1	2.1447	0.33043	-1.823

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

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

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
CDPK18; Calcium-dependent protein kinase 18
CML11; calmodulin-like protein 11
Calmodulin-binding protein
CML37; Calcium-binding protein CML37
Putative Calcium-binding protein CML27
CPK19; Calcium-dependent protein kinase 19
CIPK12; CBL-interacting serine/threonine-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; cysteine-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 LRR receptor-like serine/threonine-protein kinase
Putative LRR receptor-like serine/threonine protein kinase
RACK1C_AT; receptor for activated C kinase 1C
G-type lectin S-receptor-like serine/threonine-protein kinase SD1-1
HLECRK; lectin-receptor kinase
ACT-like protein tyrosine kinase family protein
AK3; aspartokinase 3
APK2A; protein kinase 2A
Leucine-rich repeat protein kinase family protein
Leucine-rich repeat protein kinase family protein

Leucine-rich repeat transmembrane protein kinase family protein
PFK3; 6-phosphofructokinase 3
Protein kinase family protein
SK13; Shaggy-related protein kinase 13
Peroxidase
Peroxidase 56
Peroxidase 69
Peroxidase 71
Peroxidase 69
Peroxidase
Peroxidase 45
Glutathione S-transferase tau 3
Glutathione S-transferase tau 13
Glutathione S-transferase TAU 12
Glutathione S-transferase TAU 12