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**Characterization of microRNAs and their targets in wild barley (*Hordeum
vulgare subsp. spontaneum*) using deep sequencing**

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Abstract

MicroRNAs (miRNA) are a class of small, endogenous RNAs that play a negative regulatory role in various developmental and metabolic processes of plants. Wild barley (*Hordeum vulgare subsp. spontaneum*) as the progenitor of cultivated barley (*Hordeum vulgare subsp. vulgare*), has served as a valuable germplasm resource for barley genetic improvement. To survey miRNAs in wild barley, we sequenced the small RNA library prepared from wild barley using the Illumina deep sequencing technology. A total of 70 known miRNAs and 18 putative novel miRNAs were identified. Sequence analysis revealed that all of the miRNAs identified in wild barley contained the highly conserved hairpin sequences found in barley cultivars. MiRNA target predictions showed that 12 out of 52 miRNA families were predicted to target transcription factors, including 8 highly conserved miRNA families in plants and 4 wheat-barley conserved miRNA families. In addition to transcription factors, other predicted target genes were involved in diverse physiological and metabolic processes and stress defense. Our study for the first time reported the large-scale investigation of small RNAs in wild barley, which will provide essential information for understanding the regulatory role of miRNAs in wild barley and also shed light on future practical utilization of miRNAs for barley improvement.

Keywords: MiRNA; Wild Barley; Sequencing; RT-PCR

Introduction

Wild barley (*Hordeum vulgare subsp. spontaneum*) as the progenitor of cultivated barley (*Hordeum vulgare subsp. vulgare*), originated about 5.5 million years ago in southwest Asia and then spread to the Eastern Mediterranean, Balkans, North Africa, Central Asia, and Tibet (Dai et al. 2012; Hartmann et al. 2006). Wild barley is found to grow over a remarkably wide range of ecological habitats, including deserts and highlands. The long-term coevolution and local adaption to microclimates resulted in wild barley having a high level of genetic diversity and a large number of alleles for many economically important traits (Ellis et al. 2000; Fetch Jr et al. 2003; Roy et al. 2010; Shakhathreh et al. 2010; Steffenson et al. 2007). Previous studies demonstrated that wild barley could display unique and multiple adaptive divergence complexes and remarkable incipient sympatric ecological speciation across an average distance of only 200m (Shen et al. 2013; Yang et al. 2011). Furthermore, wild barley also showed adaptation to extreme climatic conditions, including high temperature, drought and high soil salinity, thus providing an indispensable genetic resource for the breeding of stress-tolerant varieties of the cultivated crop and held the promise for barley improvement to meet the challenges of increasing food demand and changing global climate in the future (The International Barley Genome Sequencing Consortium, 2012).

MicroRNAs (miRNAs) are a class of endogenous, small (19 - 24nt), non-coding RNAs and are now well known as one of the most important factors for gene expression regulation in eukaryotic cells (Bartel 2004; Voinnet 2009). The biogenesis of miRNA begins with transcription of the miRNA gene by RNA polymerase II (Pol II), generating a primary transcript (pri-miRNA) that is both capped and polyadenylated. The pri-miRNA molecule is further folded into a stem-loop structure via intramolecular base-pairing (Xie et al. 2005) and cleaved into precursor-miRNA (pre-miRNA) by

Dicer-like 1 (DCL1) (Kurihara and Watanabe 2004). Pre-miRNA is cleaved again to release a miRNA/miRNA* duplex which is loaded into cytoplasmic *AGO* proteins and transported out of the nucleus by *HASTY* (Park et al. 2005). The post-transcriptional RNA silencing is mediated through complementary binding of miRNA within RNA-induced silencing complex (*RISC*) to the mRNA, resulting in mRNA cleavage, translational inhibition, or mRNA decay (Axtell et al. 2011). The other strand is known as miRNA star (miRNA*) and in the majority of cases is degraded (Kawamata et al. 2011). Extensive studies have revealed that miRNAs play a vital role in organ development, proliferation, abiotic and non-abiotic stress response in plants (Datta and Paul 2015; Voinnet 2009; Wang et al. 2007; Zhang 2015).

Given the significance of miRNAs, a large number of studies have been performed to identify miRNAs and their targets in various plant species over the past years (Datta and Paul 2015; Kozomara and Griffiths-Jones 2014; Zhang 2015). Barley (*H. vulgare*) is the world's fourth most important cereal and widely used for animal feed, beer, and human food (Haberer and Mayer 2015). Previous studies attempted to identify miRNAs associated with development and stress response in barley by computational strategies (Dryanova et al. 2008) or by sequencing the small RNA population (Curaba et al. 2012; Deng et al. 2015; Hackenberg et al. 2013; Hackenberg et al. 2012; Kantar et al. 2010; Kruszka et al. 2013; Lv et al. 2012b; Ozhuner et al. 2013; Schreiber et al. 2011). However, the miRNAs in wild barley are not well understood at present. There is no wild barley miRNA in miRBase database (version 21.0, June 2014) (Kozomara and Griffiths-Jones 2014) and only one found in plant microRNA database (PMRD: November 17, 2014) (Zhang et al. 2010). Furthermore, recent studies have shown that species-specific miRNAs and the spatio-temporal regulation of conserved miRNAs play important roles in shaping variation of morphological, developmental and resistance to abiotic or non-abiotic

stresses among related species during evolution (Datta and Paul 2015; Sun et al. 2014; Taylor et al. 2014). Therefore, the characterization of miRNAs in wild barley will contribute to future germplasm exploration and utilization of wild barley. In this study, we reported the first global analysis of miRNA expression in the wild barley based on the Illumina sequencing platform. The results from this study might provide insights into composition and abundance of miRNA in wild barley and pave the way to reveal the regulatory role of miRNAs in barley and beyond.

Materials and Methods

Plant materials

The wild barley accession 3-25 collected from Mt Gilboa, Israel during an expedition trip in 2009 and stored in our lab, was grown in a growth chamber at a relative humidity of 75% and 26/20 °C day/night temperature with light intensity of 3000 lx (Lv et al. 2012a). Leaves, stems and roots at four different stages (seedling, jointing, heading and filling), and spikes at heading and filling stages were collected to construct the small RNA sequencing library.

Small RNA library preparation and sequencing

Total RNA was extracted from the roots, stems, leaves and spikes using TRIZOL Reagent (Invitrogen, USA) according to the manufacturer's instructions. The RNA quality was examined using gel electrophoresis (28S:18S > 1.5) and Bioanalyzer (Agilent2100, RIN ≥ 8.0). One RNA sample was generated by blending equal quantities of samples from different tissues. Then, this RNA sample was sent to Bioteke Corporation (Beijing, China) to construct a small RNA library and sequence on Illumina HiSeq™ 2000 platform, according to the manufacturer's protocol.

Bioinformatic analysis

The raw sequencing reads were pre-processed as described by Schreiber et al. (Schreiber et al.

2011). In brief, after removing the poor-quality reads (reads with N, homopolymer runs longer than 6 bases, no more than 4 bases whose quality score was lower than 10 and no more than 6 bases whose quality score is lower than 13) and adaptor sequences, the sequences with length of 16 - 30nt were retained for further analysis. Then, the small RNAs that were not miRNAs were removed as follows: 1) wild barley chloroplast genomes (GenBank accession number: gi|521301089 and gi|521301008), allowing no mismatches and separated into chloroplast reads and non-chloroplast reads (nuclear-derived reads); 2) diverse repeat databases TIGR Hordeum Repeats (Ouyang and Buell 2004), TIGR Oryza Repeats (Ouyang and Buell 2004), TIGR Triticum Repeats (Ouyang and Buell 2004), Triticeae repeat sequence database (TREP) (Wicker et al. 2002), RepBase(Jurka et al. 2005), allowing no mismatches; 3) Plant tRNAs, plant snoRNAs and Rfam database (Version 11.0) (Burge et al. 2013), allowing no mismatches excepting Rfam with two mismatches; 4) Wild barley and barley mRNA sequences, allowing two mismatches. After the reads were mapped to a given library, the mapped reads were removed and the remaining reads were used to map to another library.

The remaining clean sRNAs were subjected to miRNA identification using the miRDeep2 software (Friedlander et al. 2012). As the complete genome sequence of wild barley was unavailable, miRNA precursors were determined through mapping to the reference genomes of the barley cultivars Morex, Barke and Bowman (Mayer et al. 2012) and Tibetan barley (Zeng et al. 2015). All of the miRNAs from barley (miRBase 21.0, June 2014; published studies) and 5 grass species (*Oryza sativa*, *Triticum aestivum*, *Zea mays*, *Brachypodium distachyon* and *Aegilops tauschii*) were collected and used as two query data sets for miRDeep2 software, corresponding to ‘mature_ref_this_species’ and ‘mature_ref_other_species’ respectively, resulting in three types of results (known miRNA, homologous miRNA and novel miRNA). The following key criteria were used for miRNA prediction:

(i) the miRNA and miRNA* should be derived from the opposite stem-arms; (ii) there were four or fewer mismatches between the miRNA and other arm of the hairpin including the miRNA*; (iii) although some by-products of miRNA processing (such as length heterogeneity, sequential Dicer cleavage and RNA editing) certainly exist in plants, there should be little heterogeneity in the sequences matching to the non-miRNA or non-miRNA* region of pre-miRNAs. (iv) the number of miRNA reads should be greater than 4 in the library; (v) the free energy value of precursor should be less than -20 Kcal/mol. Homologous miRNAs and novel miRNAs were used as query data sets to search against miRNAs from barley and miRBase for novel variant miRNA identification. Novel variant miRNAs should meet the following criteria as described by Sun *et al.* (2014): (i) miRNA does not perfectly match barley known miRNA (including miRBase 21.0 and published papers); (ii) miRNA with 1 or 2 mismatches to known miRNA from barley or 5 other grass species.

MiRNA validation by qRT-PCR

To validate the identified miRNAs, the stem-loop real-time RT-PCR was performed to investigate the expression of 6 randomly selected miRNAs using the previously described method (Varkonyi-Gasic *et al.* 2007). Total RNAs were extracted from three individual leaves of wild barley at the third leaf stage using TRIZOL Reagent (Invitrogen, USA). Then 1 uL DNase I-treated RNA and 1 uL stem-loop RT primer for each individual miRNA (1uM) were used in first-strand-strand cDNA synthesis with 0.25uL SuperScript III Reverse Transcriptase (Invitrogen, 200units/uL). Real-time RT-PCR was carried out using SYBR Premix Ex *Taq* (Takara) on the ABI PRISM 7300 Real-time PCR System using the following program: 3min at 95 °C followed by 40 cycles of 5 s at 95 °C and 31 s at 60 °C. At the end of each PCR reaction, a melting curve was added to monitor the amplification specificity and only samples with correct annealing temperature were used for subsequent analysis. The

qRT-PCR was performed in four replications. The primers are listed in Table S1 and the housekeeping gene 18s RNA was used as reference.

Results and Discussion

Deep sequencing results of wild barley

To identify miRNAs in wild barley, a small RNA library was constructed by pooling equal quantities of RNAs from different tissues and at various development stages and sequenced on the Illumina HiSeq™ 2000 platform. A total of 19,193,791 raw reads were obtained. After removal of low-quality, adaptor sequences and sequences with the length out of 16-30 nt, 9,885,815 clean reads, representing 1,967,628 unique reads remained (Table S2). Tags removed from raw data mainly focused on low quality, adaptor, length less than 16 and length more than 30, accounting for 7.35% (1,411,696), 0.00% (420), 26.62% (5,108,431) and 13.66% (2,622,257) respectively. Twenty-two nt was the most abundant sequence length (Figure 1A), whereas among total small RNAs the 24 nt was the most abundant (Figure 1B). In general in plants, size distributions of 24-nt and 21-nt sRNAs have been prevalent, the majority of which were associated with repeats and miRNAs respectively (Curaba et al. 2012; Lv et al. 2012b; Zabala et al. 2012). A previous study demonstrated that the 22-nt size class had a significant number of repetitions and function differently from the 21-nt and 24-nt sRNAs (Zabala et al. 2012). Such enrichment of 22-nt sRNAs in our study indicated a possible relevant role of the 22-nt sRNAs in wild barley. Similar results also were observed in wheat (Sun et al. 2014), maize (Zhang et al. 2009b) and soybean (Zabala et al. 2012).

A recent study found that many previously annotated miRNAs were the fragments of long noncoding RNAs such as tRNAs, rRNAs and mRNAs (Taylor et al. 2014). Therefore, the small RNAs

that were not miRNAs were removed before miRNA analysis by matching to a number of other sources such as chloroplast genome, repeats database and Rfam database. Firstly, all the trimmed reads were searched against the wild barley chloroplast genome sequences without mismatch and then separated into chloroplast-derived sRNAs (csRNAs) and nuclear-derived sRNAs. In total, of 3,712,610 reads were identified as csRNAs, accounting for 37.55% of the total reads, of which 84,495 was unique sequence (Figure 2A). Among them, the csRNAs derived from rRNA (64.64%) were the most abundant, followed by chloroplast tRNA (19.88%), intergenic region (13.99%) and chloroplast gene (1.48%) (Figure 2B). This result was similar to the result reported by the previous work on the origin of csRNAs in Chinese cabbage (Wang et al. 2011). Furthermore, we also matched all csRNAs with the chloroplast genome of cultivated barley. Our results displayed that more than 99% of the csRNAs from wild barley mapped perfectly to the chloroplast genome.

On the other hand, a total of 5,740,120 read (58.06%), representing 1,615,447 unique reads matched (no more than 2 mismatches) to the barley genome sequence (cv. Morex) and be considered as nuclear-derived sRNAs (Table S2 and Figure 2A). Since the reference sequence of wild barley was not available, we mapped all nuclear-derived sRNA sequences to the reference genome of barley cultivar Morex for further genomic origin analysis. In this case, we found that more than 60% of the total nuclear-derived sRNAs could perfectly match to the reference genome, accounting for 40% of unique reads. When a mismatch threshold ≤ 2 was applied, more than 90% of the total nuclear-derived sRNAs could match to the reference genome and represented approximately 80% of unique reads.

Non-miRNA reads were further removed by matching the tags against a collection of various plant repeat databases, other small RNA databases and barley genes as described in Materials and Methods. Finally, a total of 2,842,290 reads (521,381 unique reads) were removed, of which 1,709,799 and

323,356 tags were mapped to repeat elements and non-coding RNAs in Rfam, respectively (Figure 2C).

These non-coding RNAs included rRNAs (40.59%), snoRNAs (6.12%), tRNAs (2.24%), snRNAs (0.31%) and unclassified non-coding RNAs (50.74%) (Figure 2D). After this cleanup, 53.96% of the total nucleotide-derived sRNAs were remained to identify conserved and novel miRNAs.

Identification of known and novel miRNAs in wild barley

Recently, around 271 barley miRNAs, belonging to 155 miRNA families putatively associated with development and stress response have been identified by sequencing the small RNA population (Curaba et al. 2012; Deng et al. 2015; Hackenberg et al. 2014; Hackenberg et al. 2013; Hackenberg et al. 2012; Kantar et al. 2010; Kruszka et al. 2013; Lv et al. 2012b; Ozhuner et al. 2013; Schreiber et al. 2011; Zhou et al. 2015). We confirmed that 55 miRNAs from 35 families in wild barley shared the same sequences of miRNAs in cultivated barley (Table S3). In order to find novel variants of known miRNAs, we searched small RNAs with 1 or 2 mismatches to known miRNAs in our small RNA library by homolog analysis, resulting in 15 novel variants belonging to 14 known miRNA families (Table S4). In total, 60 known miRNAs belonging to 38 miRNA families were identified in wild barley. Among them, miR159 was the most abundantly expressed miRNA, with frequencies of 19,623 and followed by miR166, miR167, miR156 (Table S4). It has been demonstrated that these four miRNAs targeted *MYB* transcription factor (Reyes and Chua 2007), homeobox-leucine zipper (Zhu et al. 2011), auxin response factor (Wang et al. 2015), *SPL* (squamosa promoter-binding-like) transcription factor (Wang et al. 2009), respectively. The high expression of these miRNAs suggested that they play a critical role in wild barley growth and development. A total of 7 miRNAs, including 2 known miRNAs (*hvs-miR2023a* and *hvs-miR5049a*) and 5 novel miRNAs (*hvs-miR-n01*, *hvs-miR-n04*, *hvs-miR-n08*,

hvs-miR-n17 and *hvs-miR-n18*) expressed at a very low level (total abundance less than 12), suggesting they might play roles in specific temporal or spatial expression patterns.

Furthermore, among the 20 highly conserved miRNA families in plants (Jones-Rhoades et al. 2006), 16 out of them were present among our reads (miR156, miR159, miR160, miR164, miR166, miR167, miR168, miR171, miR172, miR319, miR390, miR393, miR395, miR396, miR397 and miR399), while the homologues of miR162, miR169, miR394 and miR398 were not found in wild barley the miR162 family is known to regulate the *DCL1* expression which was required for miRNA biogenesis (Xie et al. 2003). However, miR162 has not been found in barley using deep sequencing technologies or precursors searching against barley ESTs that were deposited with the NCBI database. Barley genome analysis also revealed that no homologue could be found in its genome (Mayer et al. 2012), a feature also reported in wheat (Li et al. 2013). These observations indicate that further research is required to study the existence of miR162 in barley. miR169 (targeting *NF-YA* transcription factor), miR394 (targeting *F-box* protein) and miR398 (targeting *Cu/Zn* superoxide dismutase) were recently reported to be differentially regulated by stress conditions and play important roles in abiotic stress responses such as high salinity, drought stress or nitrogen-starvation (Liu et al. 2008; Sunkar et al. 2006; Zhao et al. 2011), thus their absence was expected.

EST (Expressed Sequence Tags) and GSS (genome survey sequences) provided a powerful alternative resource to identify miRNA when the complete genome sequence is not available. Therefore, all the wild barley EST and GSS sequences have been screened to identify new miRNAs which showed low homology to known miRNA as described in Materials and Methods. However, there was no miRNA meeting our prediction criteria although there were 18 miRNAs gained by the miRNA prediction pipeline. We further identified new miRNAs by searching the cultivated barley

genome and ESTs to extend the information of miRNAs in wild barley. Finally, a total of 18 miRNAs were identified and 55.56% (10/18) of them had the expression of the miRNA* (Table S4). The potential mature miRNA sequences showed no similarity to any current entries in miRBase (21.0), indicating that they were novel miRNAs. The length distribution of novel miRNAs ranged from 20-24 nt and the most abundant length was 21 nt (77.78%, 14/18). Details of all predicted miRNAs are given in supplementary table S4 and part of their pre-miRNA secondary structures are showed in Figure 3. To screen the barley specific miRNAs, we explored the presence of 18 novel barley miRNAs across Arabidopsis, soybean, rice, maize, sorghum, barley and Brachypodium. Among them, 7 miRNAs (*hvs-n05*, *hvs-n09*, *hvs-n10*, *hvs-n11*, *hvs-n12*, *hvs-n15* and *hvs-n18*) were found to be barley-specific, while the remaining 11 barley miRNAs were shared with wheat but not other species. Furthermore, most of the newly identified miRNAs were infrequently recovered by deep sequencing, with median read frequencies of only 180. In contrast, conserved miRNAs had a higher expression counts (slightly over 1265 reads, on average), suggesting that non-conserved miRNAs might express in specific cells or growth conditions with generally low expression level in plants (Rajagopalan et al. 2006). In addition, six miRNAs were selected randomly to validate the results from the bioinformatics-based analysis using stem-loop real-time RT-PCR, with 18S rRNA as reference. Results showed that all the selected miRNAs could be detected by qRT-PCR, supporting their actual presence in wild barley (Figure 4).

To characterize the nucleotide diversity of miRNA genes across wild and cultivated barley accessions, we examined all the precursors of miRNAs (53 known miRNAs, 14 novel variants and 18 novel miRNAs) among the current genome assembly of cultivars (Barke, Bowman, Morex and Tibetan barley). Alignment results suggested that they had highly conserved hairpin sequences, especially within the mature miRNA sequence (Figure 5). Similar results also reported in maize (Zhang et al.

2009a). This might due to the important regulatory function of miRNAs, making them highly conserved across barley accessions. In addition, Lv *et al.* (2012a) conducted a similar analysis of miRNA in cultivated barley (cv. Morex) by pooling equal amounts of RNA from four different tissues. A set of 32 miRNAs (14 novel variants and 18 novel miRNAs) obtained in our study were used as database to search against a small RNA sequencing dataset from cultivated barley (NCBI Accession: SRX122678) (Lv *et al.* 2012a). The results indicated that 21 out of those miRNAs (65.63%, including 7 novel variants and 14 novel miRNAs) could be detected in cultivated barley (Table S4). Furthermore, the majority of those miRNAs (95.24%, 20/21) displayed significantly different expression levels between those two materials, but it was not possible to associate function with tissue types as both of these two small RNA sequencing datasets were from pooling of RNAs from different tissues. Considering that most of the miRNAs could detect their precursors in different barley genomes, the role of miRNA contributing to phenotype variation between wild barley and cultivar barley might, in most cases, come from their different expression patterns rather than genomic constitution.

Target prediction for wild barley miRNAs

The targets of miRNA were predicted by searching against the HVGI database (Release 12) using psRNAtarget tool. A total of 708 unique putative genes were targeted by 73 miRNA belonging to 52 families, with an average of 9.70 (708/73) target genes per miRNA (Table S5). Of those target genes, 61.58% of them had the known function, whereas others were not annotated. We found that 12 out of 52 miRNA families were predicted to target transcription factors, such as *SBP*, *MYB* and *HD-ZIP*, suggesting that these miRNA families play key roles in post-transcriptional regulation and transcription networks. Among them, eight miRNA-target pairs (*hvs-miR156* and *SBP*; *hvs-miR159* and *GAMYB*; *hvs-miR160* and Auxin response factor; *hvs-miR164* and *NAC* transcription factor; *hvs-miR172* and

APETALA2-like protein; *hvs*-miR396 and Growth-regulating factor; *hvs*-miR397 and auxin response factor; *hvs*-miR444 and *MIKC-type MADS-box* transcription factor) were highly conserved among plants. One miRNA-target pair (*hvs*-miR2024 and *MIKC-type MADS-box* transcription factor) was conserved in wheat (Sun et al. 2014) and the remaining three (*hvs*-miR2004 and *WRKY* transcription factor; *hvs*-n07 and *ERF* transcriptional factor; *hvs*-n14 and auxin response factor) have only been reported in wild barley. In addition to transcription factors, the predicted target genes were also involved in diverse physiological, metabolic processes and stress defense. Such targets include pentatricopeptide (*PPR*) repeat-containing protein (*hvs*-miR1436), heat shock protein 80 (*hvs*-miR396a), superoxide dismutase (*hvs*-miR528), *GL2*-type homeobox genes (*hvs*-miR6201), cytochrome b (*hvs*-n06), acetolactate synthase (*hvs*-n10), *CBF10B* (*hvs*-n14) and auxin-responsive protein (*hvs*-n16).

Furthermore, all the putative target genes of wild barley miRNAs were subjected to Gene Ontology (GO) analysis to determine their GO terms, which could provide more information on understanding these miRNAs function (Table S6). About 52.97% (375/708) of the target genes involved in 61 miRNAs (45 conserved miRNA and 16 novel miRNAs), could be annotated and classified into 326 biological processes and 355 molecular functions via Blast2GO tool. In Biological Process, cellular process (GO:0009987) and metabolic process (GO:0008152) were the most common annotations, according for 62.9% and 61.9%, respectively. In addition, there were at least 104 miRNA-target pairs (36 miRNAs and 96 unique genes) associated with stress response (GO:0050896), involving in 28 conserved miRNAs (for example, *hvs*-miR159, *hvs*-miR160d, *hvs*-miR164d and *hvs*-miR172a) and 8 novel miRNAs (for example, *hvs*-n01, *hvs*-n02, *hvs*-n06 and *hvs*-n07). Some of classified biological processes associated with biological regulation (GO:0065007), pigmentation

(GO:0043473), reproductive process (GO:0022414), growth (GO:0040007) and death (GO:0016265) were also identified. In Molecular Function section, binding (GO:0005488) and catalytic activity (GO:0003824) were the most represented and at least 27 miRNA-target pairs were associated with regulator activity, such as transcription regulator activity (GO:0030528), translation regulator activity (GO:0045182) and enzyme regulator activity (GO:0030234). GO function enrichment analysis showed that genes targeted by wild barley miRNAs were significantly enriched for 5 Molecular Function (Figure 6A) and 12 Biological Process (Figure 6B). In addition, a total of 11 miRNAs, including 7 novel miRNAs and 4 novel variants of known miRNAs, were not detected in a cultivated barley (Table S4). GO function enrichment analysis of these miRNAs displayed that they were significantly enriched for organelle part (GO:0044422) and transferase activity (GO:0016740) (Figure 6C). Overall, the results of GO analysis revealed that miRNAs and their target genes were closely linked to wild barley development, growth and stress response.

Conclusion

To our knowledge, this is the first report on the large-scale investigation of small RNAs in wild barley utilizing the next-generation sequencing technique. A total of 90 miRNAs were identified in wild barley, comprising of 72 conserved miRNAs and 18 novel miRNAs. To understand the possible function of these miRNAs, 718 unique putative genes were predicted as the potential targets for 53 miRNA families. Gene Ontology (GO)-based functional classification showed that these miRNAs and their targets could play important roles in wild barley development, growth and stress responses. This work provided the base for further exploration of miRNAs from wild barley, and also shed light on future practical utilization of miRNAs for barley improvement.

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Figure Legend

Figure 1. Length, distribution and abundance of wild barley small RNAs. Note: (A) Unique reads and (B) Total reads.

Figure 2. Distribution of different classes of sRNAs derived from wild barley. Note: (A) Distribution of sRNAs derived from wild barley chloroplast and genome. (B) Distribution of different classes of sRNAs derived from wild barley chloroplast. (C) Distribution of different classes of sRNAs derived from wild barley genome. (D) Distribution of different classes of sRNAs among plant Rfam database.

Figure 3. Pre-miRNA stem-loop structures for novel miRNAs identified in this study. Note: Predicted mature miRNA sequences were shown in red.

Figure 4. Quantitative real-time PCR analysis of parts miRNA identified in wild barley. Note: The amount of expression was normalized to the level of 16s RNA.

Figure 5. Partial of syntenic sites harboring miRNA genes in barley and other plants. Note: (A) and (B) showed the syntenic sites harboring *hvs-miR1878* and *hvs-miR395c* respectively.

Figure 6. Go enrichment analysis of miRNA target genes identified in wild barley. Note: (A) and (B) showed the significantly enriched GO terms of Molecular Function and Biological Process for all miRNAs identified in wild barley; (C) showed the significantly enriched GO terms for gene targeted by novel miRNAs and the new variants of known miRNAs in wild barley; Observed, numbers of genes observed in this study; Expected, numbers of genes in this same category in the GO enrichment analysis program.

Supporting Information

Table S1. Information of primers used for quantitative real-time PCR.

Table S2. Summary of unique reads and read count identified as various classes of small RNAs.

Table S3. Profile of the known microRNAs (miRBase 21.0) identified in this study. Note: LM, length of mature miRNA; LP, length of miRNA precursor; MFE, minimum free energy of candidate precursors; MFEI, the minimum free energy index of candidate precursors; pre-miRNA location, the position of candidate precursors in barley genome sequence.

Table S4. Precursors of novel miRNA and novel variants of known miRNAs in wild barley. Note: LM, length of mature miRNA; LP, length of miRNA precursor; MFE, minimum free energy of candidate precursors; MFEI, the minimum free energy index of candidate precursors; pre-miRNA location, the position of candidate precursors in barley genome sequence.

Table S5. List of predicted targets of miRNAs identified in this study. Note: for each miRNAs, total targets, their function and GO annotation were given.

Draft

Figure 1. Length, distribution and abundance of wild barley small RNAs. Note: (A) Unique reads and (B) Total reads.
148x132mm (300 x 300 DPI)

Figure 2. Distribution of different classes of sRNAs derived from wild barley. Note: (A) Distribution of sRNAs derived from wild barley chloroplast and genome. (B) Distribution of different classes of sRNAs derived from wild barley chloroplast. (C) Distribution of different classes of sRNAs derived from wild barley genome. (D) Distribution of different classes of sRNAs among plant Rfam database.
167x129mm (300 x 300 DPI)

Figure 3. Pre-miRNA stem-loop structures for novel miRNAs identified in this study. Note: Predicted mature miRNA sequences were shown in red.
147x97mm (300 x 300 DPI)

Figure 4. Quantitative real-time PCR analysis of parts miRNA identified in wild barley. Note: The amount of expression was normalized to the level of 16s RNA.
64x37mm (300 x 300 DPI)

Figure 5. Partial of syntenic sites harboring miRNA genes in barley and other plants. Note: (A) and (B) showed the syntenic sites harboring hvs-miR1878 and hvs-miR395c respectively.
74x32mm (300 x 300 DPI)

Figure 6. Go enrichment analysis of miRNA target genes identified in wild barley. Note: (A) and (B) showed the significantly enriched GO terms of Molecular Function and Biological Process for all miRNAs identified in wild barley; (C) showed the significantly enriched GO terms for gene targeted by novel miRNAs and the new variants of known miRNAs in wild barley; Observed, numbers of genes observed in this study; Expected, numbers of genes in this same category in the GO enrichment analysis program.

68x29mm (300 x 300 DPI)

Table S1. Information of primers used for quantitative real-time PCR.

Category	Gene Name		Primer Sequence (5'-3')
Control gene	18s rRNA forward	Forward primer	GTGACGGGTGACGGAGAATT
	18s rRNA reverse	Reverse primer	GACACTAATGCGCCCGGTAT
Primer for miRNA quantification by stem-loop RT-PCR	miR1436-F	Forward primer	cgccTACATTATGGGACGG
	miR1436-ST	Stem loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACctccct
	miR2004-F	Forward primer	gcggcTTGTTTTTATGTTATTTG
	miR2004-ST	Stem loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACccttca
	miR6201-F	Forward primer	cgcTGACCCTGAGGCACTC
	miR6201-ST	Stem loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACcggtat
	hvs-n06-F	Forward primer	gggcgCTTTTTTTGGATTT
	hvs-n06-ST	Stem loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACgaccac
	hvs-n07-F	Forward primer	cgccgCTCCCTCTGTAGACT
	hvs-n07-ST	Stem loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACtatatt
	hvs-n14-F	Forward primer	gggcgTCTTATGTTGTGGGA
	hvs-n14-ST	Stem loop Primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACcctcgc
Universal Reverse Primer			GTGCAGGGTCCGAGGT

Draft

Table S2. Summary of unique reads and read count identified as various classes of small RNAs.

Library	Unique reads	total reads
Raw data		19,193,791
Clean data	1,967,628	9,885,815
Chloroplast-derived sRNAs	84,495	3,712,610
Chloroplast gene	19,876	55,141
Chloroplast rRNA	32,836	2,400,015
Chloroplast tRNA	4,673	738,141
Chloroplast Intergenic region	27,110	519,313
Nuclear-derived sRNAs	1,615,447	5,740,120
Repeats	92,781	1,709,799
TIGR_Hordeum_Repeats	38,692	838,037
TIGR_Triticum_Repeats	28,681	795,043
TIGR_Oryza_Repeats	5,964	36,039
TREP	13,837	20,421
repbase17.11	5,607	20,259
Rfam	89,368	323,356
rRNA	13,084	131,243
tRNA	3,295	7,248
snoRNA	8,519	19,803
snRNA	534	1,003
Other	63,936	164,059
Exon	257,774	566,685
Intron	81,458	242,450
miRNA	3352	144162
Unannotation reads	1,090,714	2,753,668
Unmapped sRNAs	267,686	433,085

Table S3. Profile of the known microRNAs (miRBase 21.0) identified in this study.

miRNA fa	miRNA ID	Name provide	miRNA sequence (5'-3')	LM	Read	c LP	MFE (kcal/mol)	MFEI	Genome location	Consensus prec	Secondary structure	Reference
miR1120	hvs-miR1120	hvu-miR1120	acauucuuauuuauugggacgg	24	55	84	-43.1	1.44	barke_contig_1796748:3174...3257	cuacuccuccuuc	..(((((((.(((((((((((((((	miRBase
miR1318	hvs-miR1318	hvu-miR1318	aucaggagagagacacccgg	20	13	63	-20.6	0.61	barke_contig_2818564:191...253	+ ggugugcucuuc	(((((.(((((((.(((((((.(((	(Curaba et al. 2012)
miR1436	hvs-miR1436	hvu-miR1436	uacauuauugggacggaggag	21	17	91	-35	0.85	barke_contig_2781497:579...669	+ ggcuuccugua	(((((.(((((((.(((((((.))))))	((miRBase
miR1436	hvs-miR1436a	hvu-miR1436a	auauuauugggacggaggag	21	11	68	-34.8	1.20	barke_contig_1780432:1741...1808	uccuccgucceau	(((((.(((((((.(((((((.(((	(Schreiber et al. 2011)
miR156	hvs-miR156a	hvu-miR156a	ugacagaagagagagagc	18	6812	254	-148.5	1.09	barke_contig_269597:3223...3106	gcugacagaagaga	(((((.(((((((.(((((((.(((	(miRBase
miR156	hvs-miR156e	hvu-miR156e	ugacagaagagagcagcac	20	124	55	-74.1	0.88	bowman_contig_872374:1437...15	gcuccuguccuau	..(((((((.(((((((((((((((	(lv et al., 2012)
miR159	hvs-miR159	hvu-miR159	uuuggauugaaggagcucug	21	19623	301	-118.3	0.79	barke_contig_1783742:5988...5811	ggugagcuccuau	(((((.(((((((.(((((((.(((	(miRBase
miR160	hvs-miR160d	hvu-miR160d	ugccuggcuccugauugcca	21	181	84	-47.1	0.91	barke_contig_52987:2470...2387	ugccuggcuccug	(((((.(((((((.(((((((.))))	(lv et al., 2012)
miR160	hvs-miR160e	hvu-miR160e	ugccuggcuccugauugcca	21	326	83	-47	0.89	barke_contig_1798897:392...474	+ ugccuggcuccug	(((((.(((((((.(((((((.(((	(lv et al., 2012)
miR164	hvs-miR164d	hvu-miR164d	uggagaagcagggcacugcu	21	164	70	-39.3	0.96	barke_contig_2911825:1...32	+ bo uggagaagcagggc	(((((.(((((((.(((((((.(((	(Schreiber et al. 2011)
miR166	hvs-miR166b	hvu-miR166b	ucggaccaggcucauuccc	21	14954	102	-62.8	1.03	morex_contig_38715:11507...1139	ggggauguguci	(((((.(((((((.(((((((((((((((	(miRBase
miR166	hvs-miR166m	hvu-miR166m	ucggaccaggcucauuccc	21	2536	85	-29.9	0.65	barke_contig_12287:123...207	+ b ucggaccaggcu	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR167	hvs-miR167d	hvu-miR167d	ugaagcugccagcaugaucga	22	8357	77	-40.7	1.13	barke_contig_278740:6973...7049	ugaagcugccagca	(((((.(((((((.(((((((((((((((	(Schreiber et al. 2011; lv et al
miR168	hvs-miR168-5p	hvu-miR168-5p	ucgcuuggugcagauccggac	21	3191	106	-63	0.79	bowman_contig_885914:1...97	+ i guccugcgcgcgcg	(((((((.(((((((.(((((((	(miRBase
miR168	hvs-miR168-3p	hvu-miR168-3p	gauccgccuugcaccaguga	24	1039	106	-63	0.79	bowman_contig_885914:1...97	+ i guccugcgcgcgcg	(((((((.(((((((.(((((((	(miRBase
miR171	hvs-miR171-3p	hvu-miR171-3p	ugauagcggugccauuac	21	890	173	-91.9	0.92	barke_contig_271341:2303...2155	gcggguugauggc	..(((((((.(((((((.(((((((	(miRBase
miR171	hvs-miR171-5p	hvu-miR171-5p	uguuggcugcacucacuga	21	136	173	-91.9	0.92	barke_contig_271341:2303...2155	gcggguugauggc	..(((((((.(((((((.(((((((	(miRBase
miR171	hvs-miR171a	hvu-miR171a	ugaauagccgcgcacauauc	21	249	82	-33.4	0.88	barke_contig_55541:1179...1260	+ uauuggggagguu	(((((.(((((((.(((((((((((((((	(Schreiber et al. 2011)
miR171	hvs-miR171f	hvu-miR171f	ugagccgaaccauauacuc	21	48	71	-35	0.95	barke_contig_60117:5625...5695	+ ugguauugucgcg	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR172	hvs-miR172a	hvu-miR172a	agaauuugaugaugcugcau	21	204	83	-37.1	0.90	barke_contig_281063:381...299	lgcagaccaccaag	(((((.(((((((.(((((((((((((((	(Schreiber et al. 2011; lv et al
miR2012	hvs-miR2012a	hvu-miR2012a	uuggacgugaggugcagcug	21	260	77	-46.8	0.92	barke_contig_72094:214...138	+ buuggacgugagg	(((((.(((((((.(((((((((((((((	(Schreiber et al. 2011)
miR2023	hvs-miR2023a	hvu-miR2023a	uuuugccgguuagacgacca	22	5	119	-55.9	0.87	barke_contig_272245:4913...4798	gcugguuuuuug	(((((.(((((((.(((((((((((((((	(miRBase
miR2024	hvs-miR2024a	hvu-miR2024a	gcaguugcugcucaagcuu	20	44	121	-55.1	1.02	barke_contig_311660:3925...1427	gguggcaccaagca	((.((.(((((((.(((((((((((((((	(miRBase
miR390	hvs-miR390	hvu-miR390	aagcucaggaggauagccgc	21	33	139	-69	0.90	barke_contig_269893:2969...3102	acaauccuagagc	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR319	hvs-miR319a-3p	hvu-miR319a-3p	uuggacugaaggugcuccu	21	91	88	-27.6	0.59	barke_contig_1857314:744...831	+ ggagcguauugcu	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR393	hvs-miR393b	hvu-miR393b	ucagugcgauccucuggaau	21	293	79	-41.8	1.00	barke_contig_372756:487...565	+ uuccaaagggaucg	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR395	hvs-miR395a	hvu-miR395a	ugaaguguuugggggaacuc	20	283	64	-32.9	1.00	barke_contig_370787:1313...1250	guuccugcaggca	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR395	hvs-miR395n	hvu-miR395n	ugaaguguuugggggaacuc	20	482	64	-31.8	1.14	barke_contig_270422:4756...4819	guucucucaagca	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR396	hvs-miR396a	hvu-miR396a	uuccacagcuuucugaucg	21	482	86	-45.2	1.19	barke_contig_306463:3900...3985	uuccacagcuuuc	(((((.(((((((.(((((((((((((((	(Schreiber et al. 2011)
miR397	hvs-miR397a	hvu-miR397a	uugagugcagcguugaagac	21	49	113	-74.2	0.98	bowman_contig_1986701:3734...3	cgagaggugccgu	(((((.(((((((.(((((((((((((((	(miRBase
miR399	hvs-miR399	hvu-miR399	ugccaaaggagauuugcccg	21	29	131	-35.4	0.61	barke_contig_54363:4414...4544	+ ucagaagaacuagg	(((((((.(((((((.(((((((	(miRBase
miR399	hvs-miR399b	hvu-miR399b	ugccaaaggagauuugcccg	21	118	131	-58.3	0.90	barke_contig_56178:1665...1796	uguucaggugag	..(((((((.(((((((.(((((((	(Schreiber et al. 2011; lv et al
miR399	hvs-miR399j	hvu-miR399j	ugccaaaggagauuugcccg	21	118	77	-46.2	1.03	barke_contig_269537:5497...5421	gggcuccucuua	(((((.(((((((.(((((((((((((((	(lv et al., 2012)
miR444	hvs-miR444a	hvu-miR444a	ugcaguugcugccuacagcu	21	458	114	-32.6	0.62	barke_contig_1787882:1228...3288	aggcacaaguagga	(((((.(((((((.(((((((((((((((	(miRBase
miR444	hvs-miR444	hvu-miR444	uugugcguuucugcaagucg	21	15	114	-32.6	0.62	barke_contig_1787882:1228...3288	aggcacaaguagga	(((((.(((((((.(((((((((((((((	(miRBase
miR444	hvs-miR444b	hvu-miR444b	ugcaguugcugcucaagcu	21	44	121	-55.1	1.02	barke_contig_311660:3925...1427	gguggcaccaagca	((.((.(((((((.(((((((((((((((	(miRBase
miR5048	hvs-miR5048a	hvu-miR5048a	uauuugcagguuuuaggcu	22	1680	701	-197.6	0.91	barke_contig_1789351:1080...1422	ucaacaauauau	(((((.(((((((.(((((((((((((((	(miRBase
miR5049	hvs-miR5049c	hvu-miR5049c	agacaauuuuugggacggag	23	46	108	-38.9	1.02	barke_contig_372739:1917...2023	guuucuauucccc	(((((((.(((((((((((((((	(miRBase
miR5049	hvs-miR5049e	hvu-miR5049e	auuuuuuagguuacagagga	21	43	98	-51.5	1.56	barke_contig_274682:7296...7393	aucuuuuuauucc	(((((.(((((((.(((((((((((((((	(miRBase
miR5049	hvs-miR5049d	hvu-miR5049d	uacaaauuuuaggaacggag	21	41	96	-45.9	1.35	barke_contig_275605:5255...5173	auucuaucuccuc	(((((((.(((((((.(((((((	(miRBase
miR5049	hvs-miR5049a	hvu-miR5049a	uccaaauuucugguuggg	21	4	83	-54.9	1.53	barke_contig_55319:437...356	+ bacuccucugucc	(((((.(((((((.(((((((((((((((	(miRBase
miR5051	hvs-miR5051	hvu-miR5051	uuuggcaccuugaacuggga	21	439	105	-62.7	1.23	barke_contig_1790171:1210...1106	gcagguaucguucc	..(((((((.(((((((((((((((	(miRBase
miR5064	hvs-miR5064	hvu-miR5064	ugaauuuguccauagcaucag	21	13	87	-43.3	1.11	barke_contig_1783676:28...114	+ ugaauuuguccau	(((((.(((((((.(((((((((((((((	(Curaba et al. 2012)

Note: LM, length of mature miRNA; LP, length of miRNA precursor; MFE, minimum free energy of candidate precursors; MFEI, the minimum free energy index of candidate precursors; pre-miRNA location, the

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miRNA ID	consensus	mat	consensus	star	sA read	sA* read	LM	LP	FE (kcal/m)	MFEI	consensus	precurs	secondary	stru	precursor	coordinate	homologous	miRNA	name
hvs-miR-n01	uugcgucuuuuua	ucggaaauuuauugac	6	2	21	75	-38.1	1.31	ucggaaauuuauugacg	(((((((((.(((((((7H:471694067.471691WGCSC_chr:	1								
hvs-miR-n02	ccuguuuugucauu	gaaguuuuauagaga	112	44	21	84	-32.1	1.11	ccuguuuugucauuuuaa	..(((((((.(((((((morex_contig_1564131WGCSC_chr:	1								
hvs-miR-n03	gagaaguauaccggc	caucugcccgauca	41	11	22	83	-44.9	1.04	gagaaguauaccggcag	(((((((((.(((((((morex_contig_1351841WGCSC_chr:	4								
hvs-miR-n04	uccuucagaagaac	ugcccaugcucucuc	5	1	20	82	-52.5	1.50	uccuucagaagaacaucg	(((((((((.(((((((morex_contig_39060:1WGCSC_chr:ot detecte									
hvs-miR-n05	acgagcugcuaaac	uggcgcuuaagcagc	14	0	21	81	-58.9	1.18	ucggcuuaagcagcucg	(((((((((.(((((((barke_contig_423851: none	31								
hvs-miR-n06	cuuuuuuuggauu	ccacaaauccaaaaa	43	0	20	81	-37.9	1.22	cuuuuuuuggauuugr	(((((((((.(((((((barke_contig_479896:1WGCSC_chr:	7								
hvs-miR-n07	cucccucuguaag	uauuaguuuuagga	26	0	21	83	-33.7	1.60	cucccucuguaagacua	(((((((((.(((((((morex_contig_55060:1WGCSC_chr:ot detecte									
hvs-miR-n08	aaugacugagaaa	ucuaaguuucucag	8	0	21	81	-52.9	1.89	ucuaaguuucucaguc	(((((((((.(((((((barke_contig_265514:1WGCSC_chr:ot detecte									
hvs-miR-n09	aaccugacgugug	caguucacccacacg	35	0	24	71	-37.9	0.88	caguucacccacacgc	(((((((((.(((((((bowman_contig_6251: none	ot detecte								
hvs-miR-n10	uuggugaugagga	ucacauucuuuccaa	181	0	21	81	-31	1.00	uuggugaugaggaucg	(((((((((.(((((((morex_contig_271314 none	17								
hvs-miR-n11	uagcacuuuaaau	caacccaaauuuuaa	33	5	24	64	-34.7	1.58	caacccaaauuuuaaag	(((((((((.(((((((barke_contig_2566752 none	ot detecte								
hvs-miR-n12	cuagcacuuugaa	caacccaaauuuuaa	76	5	24	63	-43.4	1.89	caacccaaauuuuaaag	(((((((((.(((((((barke_contig_207468: none	72								
hvs-miR-n13	uugaacaucccag	gcgcgucuguggug	2581	1769	21	78	-48.8	1.02	gcgcgucugugguguu	..(((((((.(((((((morex_contig_12327:1WGCSC_chrt	2421								
hvs-miR-n14	ucuaauguugugg	uccgucccaauauu	31	0	21	73	-39.7	1.32	uccgucccaauauum	(((((((((.(((((((barke_contig_512966:1WGCSC_chr:	34								
hvs-miR-n15	uuaaauugugggu	ccacaaugcacaau	25	1	21	83	-49	1.26	uuaaauugugggucv	(((((((((.(((((((barke_contig_61731:1 none	ot detecte								
hvs-miR-n16	uuuugauuuguaa	ccacaaauucacaa	19	0	21	81	-35.1	1.25	ccacaaauuucacaauc	(((((((((.(((((((barke_contig_1790721WGCSC_chr:	3								
hvs-miR-n17	ggagugucucuga	uguuuuuacagguc	8	5	22	81	-35.9	0.94	ggagugucucugaguc	(((((((((.(((((((barke_contig_374794:1WGCSC_chr:ot detecte									
hvs-miR-n18	gaggcgcgcgaua	aaaugauuacaccgc	5	4	21	61	-35.7	1.15	aaaugauuacaccgcc	(((((((((.(((((((bowman_contig_8548: none	1463								

Note: LM, length of mature miRNA; LP, length of miRNA precursor; MFE, minimum free energy of candidate precursors; MFEI, the minimum free energy index of candidate

Table S4. Precursors of novel miRNA and novel variants of known miRNAs in wild barley.

miRNA fa	miRNA ID	homologous	homologous m	miRNA sequence	miRNA* s	miRNA	miRNA* re	LM	LP	MFE (kcal	MFEI	precursor coord	consensus p	secondary struc	miRNA re
miR1120	hvs-miR1120	hvu-miR1120	cauucuuauauua	---uucuuauauuaugggacggag	ccuucccau	52	0	21	70	-33.8	1.47	gi 21165024 gb B	ccuucccauau	((.((((((((((((((((	342
miR157	hvs-miR157	hvu-miR157	uugacagaagaga	-ugacagaagagagugagcac	gcucacucci	6853	215	20	85	-52	1.08	barke_contig_52	ugacagaagag	((((((((((((((((((	153336
miR167	hvs-miR167b	osa-miR167b	aucaugcaugaca	aucaugACugacagccuauu	ugaagcugc	442	675	21	77	-37.4	1.10	barke_contig_27	ugaagcugcca	((.(((.((((((((((((	8
miR168	hvs-miR168-3	hvu-miR168-	gaucgccgccuugc	gaucgccccuugcaccaagugaA	cgcguggug	1036	0	20	66	-33.8	0.66	morex_contig_15	cgcguggugca	((.(((((((.(((.(	3
miR1878	hvs-miR1878	bdi-miR1878	auuuguaguguuc	auuuguaguguucGgauugagui	acuuagucu	246	0	24	81	-34.10	1.55	barke_contig_26	acuuagucuug	(((((((((.((((((((	4
miR2004	hvs-miR2004	hvu-miR2004	uuuuuuuuuau	-uuuuuuuuuauuuuuuguga		5036									15
miR2007	hvs-miR2007	hvu-miR2007	caagauauugggu	-gcaagauauuggguuuuuugaa	gcugcacau	263	0	22	47	-22.7	1.62	barke_contig_72	caaaacuaccu	(((((.((((((((((((	383
miR2016	hvs-miR2016	tae-miR2016	ugaccugaggca	ugaccGugaggcacuauaccg	guaugagug	37	6	22	88	-56.20	1.2773	barke_contig_37	ugaccugagg	(((((.((((((((((((	not detecte
miR393	hvs-miR393	hvu-miR393	uccaaagggaucg	uccaaagggaucgcauugauC	uuccaaagg	2168	809	21	90	-43.5	0.97	barke_contig_37	uccaaaggga	(((((((((((((((((	37
miR395	hvs-miR395c	tae-miR395c	ugaaguguuuggg	-gaaguguuugggggaacucUU	guucccuuc	7	10	20	66	-30.10	1.0033	2H:509428590..5	guucccucaa	(((((.((((((((((((	not detecte
miR395	hvs-miR395o'	zma-miR395c	guucucuuaagc	guucucuuaagcacuuaGg-	ugaaguguu	15	6	21	64	-30.70	1.0964	barke_contig_51	guucucucaa	(((((.((((((((((((	not detecte
miR5049	hvs-miR5049	hvu-miR504	aguauuuaggua	-guauuuagguaacagaggagU	accugaucu	19	0	72	92	-60.8	1.38	barke_contig_27	cauauuggcua	((.((((((((((((	2
miR9674	hvs-miR9674	ata-miR9674	ugaauuuuuccau	uUaaauuuCuccauagcauca	gugcuau	349	21	21	90	-38.60	1.0722	bowman_contig_	uuuuuuuucuc	(((((.((((((((((((	195
miR5067	hvs-miR5067	bdi-miR5067	ucagcgacaacua	uGagcgacaacuaauaugga-	uauuaguua	110	27	20	79	-33.80	1.2071	barke_contig_68	uauuaguuauc	(((((((((.((((((((	not detecte
miR5200	hvs-miR5200	hvu-miR520	uagauacucucua	uagauacucucuaaggcuuGg	aggccuau	237	194	21	82	-30.8	0.96	barke_contig_39	aggccuauag	(((((((((.((((((((	2

Note: LM, length of mature miRNA; LP, length of miRNA precursor; MFE, minimum free energy of candidate precursors; MFEI, the minimum free energy index of candidate precursors; pre-miRNA location, the position of candidate precursors in barley genome sequence.

Table S5. List of predicted targets of miRNAs identified in this study.

miRNA Acc.	Target Acc.	Expectation	Target start	Target end	Inhibition	Target Desc.	Multiplicity	GO annotation
hvs-miR1120	CK566710	2	98	121	Cleavage	TAK14	1	GO:0006468;GO:0005524;G receptor-like protein kinase
hvs-miR1120	TC239725	2	746	769	Cleavage	unknown function	1	
hvs-miR1120	TC245238	3	1654	1677	Cleavage	unknown function	1	GO:0004176;GO:0046872;G lon peptidase n-terminal domain and ring fingi
hvs-miR1120	TC254574	2.5	763	786	Cleavage	unknown function	1	GO:0005739;GO:0004003;G regulator of telomere elongation helicase 1-lik
hvs-miR1120	TC255970	3	976	998	Cleavage	unknown function	1	GO:0008272;GO:0005886;G sulfate transporter
hvs-miR1120	BE231018	2.5	27	50	Cleavage	unknown function	1	GO:0016787 protein
hvs-miR1120	TC247304	2.5	1538	1561	Cleavage	unknown function	1	GO:0008233 aspartic proteinase nepenthesin-2
hvs-miR1120	TC253511	3	393	412	Cleavage	Expressed protein	1	GO:0008270;GO:0046872 btb poz domain-containing protein at3g50780-
hvs-miR1120	TC279469	3	1927	1946	Cleavage	unknown function	1	GO:0016021;GO:0006812;G k(+) efflux antiporter 4-like
hvs-miR1120	TC239276	3	707	727	Cleavage	unknown function	1	GO:0005730;GO:0003735;G 40s ribosomal protein
hvs-miR1318	EX595164	2.5	59	78	Cleavage	unknown function	1	
hvs-miR1318	BI955549	3	201	220	Cleavage	Guanine nucleotide-binding	1	
hvs-miR1318	DN181915	3	366	385	Cleavage	50S ribosomal protein L16	1	
hvs-miR1318	CA009137	3	510	529	Translation	Catalytic activity	1	GO:0044262;GO:0030060;G malate nad-dependent
hvs-miR1318	TC239111	3	473	492	Translation	P-type ATPase	1	GO:0005388;GO:0005516;G calcium-transporting atpase plasma membrane
hvs-miR1318	TC239229	3	110	129	Cleavage	Calcium-dependent calmod	1	GO:0006468;GO:0005509;G calcium-dependent protein kinase
hvs-miR1318	TC242185	3	1056	1075	Translation	P-type ATPase	1	GO:0005388;GO:0005516;G calcium-transporting atpase plasma membrane
hvs-miR1436	TC252597	0	1117	1137	Cleavage	unknown function	1	GO:0046872;GO:0008270 phd-finger family expressed
hvs-miR1436	TC258133	0	79	99	Cleavage	PP-loop domain protein	1	
hvs-miR1436	DN159362	0	470	490	Cleavage	unknown function	1	
hvs-miR1436	TC255021	0.5	1038	1058	Cleavage	Expressed protein	1	GO:0005829;GO:0005886 uncharacterized protein loc100840458
hvs-miR1436	TC259253	1.5	456	476	Cleavage	Peptidase M48, Ste24p	1	
hvs-miR1436	TC256851	1	465	485	Translation	Pentatricopeptide (PPR) rep	1	
hvs-miR1436	TC245238	2	1650	1670	Cleavage	unknown function	1	GO:0004176;GO:0046872;G lon peptidase n-terminal domain and ring fingi
hvs-miR1436	TC253359	2	652	672	Cleavage	Ribulose bisphosphate carb	1	GO:0005618;GO:0046863;G ribulose bisphosphate carboxylase oxygenase
hvs-miR1436	TC272102	2	886	906	Cleavage	unknown function	1	
hvs-miR1436	TC239725	2	742	762	Cleavage	unknown function	1	
hvs-miR1436	TC273876	2	886	906	Cleavage	unknown function	1	
hvs-miR1436	CK566710	2	94	114	Cleavage	TAK14	1	GO:0006468;GO:0005524;G receptor-like protein kinase
hvs-miR1436	BM444318	2	165	185	Cleavage	Carboxy-terminal processin	1	
hvs-miR1436	EX583948	2	42	62	Cleavage	unknown function	1	
hvs-miR1436	TC240537	2.5	970	990	Cleavage	Eukaryotic translation initia	1	GO:0003743;GO:0003746;G eukaryotic translation initiation factor 5a-4
hvs-miR1436	TC249054	2.5	848	868	Cleavage	Plastidic 2-oxoglutarate/ma	1	GO:0009624;GO:0009941;G dicarboxylate transporter chloroplastic-like
hvs-miR1436	TC249924	2.5	471	491	Cleavage	Myosin heavy chain-like pr	1	
hvs-miR1436	BY861244	2.5	57	77	Cleavage	unknown function	1	
hvs-miR1436	TC265845	3	1038	1058	Cleavage	Fasciclin-like protein FLA4	1	
hvs-miR1436	TC254574	3	759	779	Cleavage	unknown function	1	GO:0005739;GO:0004003;G regulator of telomere elongation helicase 1-lik
hvs-miR1436	TC244199	2.5	723	742	Cleavage	unknown function	1	GO:0008312;GO:0005525;G signal recognition particle
hvs-miR1436	TC240673	3	756	776	Cleavage	unknown function	1	GO:0009941;GO:0010177;G 2-isopropylmalate synthase b
hvs-miR1436	DN178864	2.5	454	474	Cleavage	Vinylacetyl-CoA delta-ison	1	
hvs-miR1436	BQ468979	2.5	280	299	Cleavage	Pollen coat oleosin-glycine	1	
hvs-miR1436	BM368186	3	115	135	Cleavage	unknown function	1	
hvs-miR1436	TC240966	3	727	747	Cleavage	Root hair defective 3 GTP-l	1	GO:0005525;GO:0016817;G protein root hair defective 3 homolog 2-like

hvs-miR1436	TC247932	3	311	331	Cleavage	unknown function	1	
hvs-miR1436	TC253552	3	603	623	Cleavage	unknown function	1	GO:0003676;GO:0006810;G glycine-rich rna-binding protein mitochondrial
hvs-miR1436	AL501466	3	128	148	Cleavage	unknown function	1	
hvs-miR1436	CD662567	2.5	30	49	Cleavage	LOC509744 protein	1	
hvs-miR1436	DN159294	2.5	104	123	Cleavage	unknown function	1	
hvs-miR1436	CD664034	3	573	593	Cleavage	COG0008	1	
hvs-miR1436	CA012079	3	37	57	Cleavage	unknown function	1	GO:0006468;GO:0004674;G seven transmembrane domain-containing tyrosine
hvs-miR1436	AJ472881	3	201	220	Cleavage	Potassium voltage-gated ch	1	
hvs-miR1436a	TC245238	0.5	1649	1669	Cleavage	unknown function	1	GO:0004176;GO:0046872;G lon peptidase n-terminal domain and ring finger
hvs-miR1436a	TC253359	0.5	651	671	Cleavage	Ribulose biphosphate carb	1	GO:0005618;GO:0046863;G ribulose biphosphate carboxylase oxygenase
hvs-miR1436a	TC252597	0.5	1116	1136	Cleavage	unknown function	1	GO:0046872;GO:0008270 phd-finger family expressed
hvs-miR1436a	TC272102	0.5	885	905	Cleavage	unknown function	1	
hvs-miR1436a	TC239725	0.5	741	761	Cleavage	unknown function	1	
hvs-miR1436a	TC273876	0.5	885	905	Cleavage	unknown function	1	
hvs-miR1436a	TC258133	0.5	78	98	Cleavage	PP-loop domain protein	1	
hvs-miR1436a	DN159362	0.5	469	489	Cleavage	unknown function	1	
hvs-miR1436a	TC262648	1	797	817	Cleavage	Integral membrane protein-i	1	GO:0016021 transmembrane protein 19-like
hvs-miR1436a	TC255021	1	1037	1057	Cleavage	Expressed protein	1	GO:0005829;GO:0005886 uncharacterized protein loc100840458
hvs-miR1436a	TC240537	1	969	989	Cleavage	Eukaryotic translation initia	1	GO:0003743;GO:0003746;G eukaryotic translation initiation factor 5a-4
hvs-miR1436a	TC249054	1	847	867	Cleavage	Plastidic 2-oxoglutarate/ma	1	GO:0009624;GO:0009941;G dicarboxylate transporter chloroplastic-like
hvs-miR1436a	BY861244	1	56	76	Cleavage	unknown function	1	
hvs-miR1436a	CK566710	0.5	94	113	Cleavage	TAK14	1	GO:0006468;GO:0005524;G receptor-like protein kinase
hvs-miR1436a	TC265845	1.5	1037	1057	Cleavage	Fasciclin-like protein FLA4	1	
hvs-miR1436a	TC254574	1.5	758	778	Cleavage	unknown function	1	GO:0005739;GO:0004003;G regulator of telomere elongation helicase 1-like
hvs-miR1436a	TC240673	1.5	755	775	Cleavage	unknown function	1	GO:0009941;GO:0010177;G 2-isopropylmalate synthase b
hvs-miR1436a	BM368186	1.5	114	134	Cleavage	unknown function	1	
hvs-miR1436a	TC256560	2	914	934	Cleavage	Chloroplast ornithine carba	1	GO:0006591;GO:0004585;G ornithine carbamoyltransferase
hvs-miR1436a	TC275846	1.5	906	926	Cleavage	unknown function	1	GO:0006260;GO:0003697;G single-stranded dna-binding mitochondrial
hvs-miR1436a	TC259253	2	455	475	Cleavage	Peptidase M48, Ste24p	1	
hvs-miR1436a	TC256851	1.5	464	484	Translation	Pentatricopeptide (PPR) rep	1	
hvs-miR1436a	TC244520	2	459	479	Cleavage	unknown function	1	
hvs-miR1436a	TC253552	2	602	622	Cleavage	unknown function	1	GO:0003676;GO:0006810;G glycine-rich rna-binding protein mitochondrial
hvs-miR1436a	BG344337	1.5	468	488	Translation	MGC86555 protein	1	
hvs-miR1436a	BM377451	2	59	79	Cleavage	unknown function	1	
hvs-miR1436a	TC275228	2	303	323	Cleavage	unknown function	1	GO:0016020;GO:0006633;G 3-ketoacyl- synthase 6-like
hvs-miR1436a	BQ766864	2	374	394	Cleavage	unknown function	1	
hvs-miR1436a	AL501466	1.5	127	147	Cleavage	unknown function	1	
hvs-miR1436a	TC239563	3	1133	1153	Cleavage	At4g16765	1	GO:0005777;GO:0005506;G gibberellin 20-oxidase
hvs-miR1436a	TC276245	3	847	867	Cleavage	Expansin-B18 precursor	1	GO:0005576;GO:0019953 exb14_orys ame: full= expansin-b14 ame: full
hvs-miR1436a	TC266554	2.5	1318	1338	Cleavage	unknown function	1	GO:0006457;GO:0031072;G chaperone -domain-containing protein
hvs-miR1436a	TC240119	2.5	1183	1203	Cleavage	AMP-binding enzyme fami	1	GO:0010193;GO:0008152;G amp-binding protein
hvs-miR1436a	TC243055	2.5	663	683	Cleavage	unknown function	1	GO:0005515 chaperone -domain-containing protein
hvs-miR1436a	TC251083	2	751	771	Cleavage	Ubiquitin-conjugating enzy	1	GO:0009910;GO:0033523;G ubiquitin-conjugating enzyme e2 2-like
hvs-miR1436a	TC258212	2.5	362	382	Cleavage	unknown function	1	GO:0016491;GO:0009706;G short chain dehydrogenase reductase family ex
hvs-miR1436a	TC239954	2.5	1497	1517	Cleavage	unknown function	1	GO:0005634 ribonuclease h2 subunit b-like

hvs-miR1436a	TC251995	2.5	866	886	Cleavage	Glutathione-S-transferase 2	1	GO:0009628;GO:0009791;G probable glutathione s-transferase gstu6-like
hvs-miR1436a	TC272422	2.5	563	583	Cleavage	OJ000223_09.17 protein	1	
hvs-miR1436a	CB865569	2.5	15	35	Cleavage	Pyridoxal-dependent decarb	1	
hvs-miR1436a	TC271886	2.5	611	631	Cleavage	Cysteine proteinase	1	GO:0008234;GO:0006508 cysteine proteinase
hvs-miR1436a	DN160314	2	474	494	Translation	Splicing factor arginine/ser	1	
hvs-miR1436a	EX583948	2.5	41	61	Cleavage	unknown function	1	
hvs-miR1436a	TC271434	2.5	620	640	Cleavage	unknown function	1	GO:0005730;GO:0003735;G 60s ribosomal protein l32-1
hvs-miR1436a	TC240249	3	1363	1383	Cleavage	Cytosine-specific methyltra	1	GO:0010216;GO:0009910;G cytosine-5 dna methyltransferase
hvs-miR1436a	TC239354	3	968	988	Cleavage	unknown function	1	
hvs-miR1436a	TC258307	2.5	753	773	Cleavage	FGF homolog	1	
hvs-miR1436a	TC243686	3	772	792	Cleavage	Leucine Rich Repeat family	1	GO:0006468;GO:0004674;G probable leucine-rich repeat receptor-like prot
hvs-miR1436a	TC239455	3	518	538	Cleavage	CTR1-like kinase kinase kii	1	GO:0006468;GO:0005524;G atp binding protein
hvs-miR1436a	BM097988	3	73	93	Cleavage	unknown function	1	
hvs-miR1436a	GH209030	3	471	491	Cleavage	Transcriptional regulator, C	1	
hvs-miR1436a	BQ756036	3	398	418	Cleavage	Terpene cyclase	1	
hvs-miR1436a	BF628687	3	234	254	Cleavage	unknown function	1	
hvs-miR1436a	CB872762	3	178	198	Cleavage	unknown function	1	
hvs-miR1436a	TC247304	2	1533	1553	Cleavage	unknown function	1	GO:0008233 aspartic proteinase nepenthesin-2
hvs-miR1436a	TC250424	3	198	218	Cleavage	unknown function	1	GO:0004672;GO:0006355;G wrky transcription factor
hvs-miR1436a	TC252903	3	957	977	Cleavage	CFM2	1	GO:0003723 chloroplastic group iia intron splicing facilitat
hvs-miR1436a	TC248415	3	642	662	Cleavage	unknown function	1	
hvs-miR1436a	TC238576	3	908	928	Cleavage	HvCBF10B	1	GO:0006351 c-repeat binding factor 3-like protein
hvs-miR1436a	TC280514	2.5	438	458	Cleavage	Aminotransferase class-III	1	
hvs-miR1436a	TC249924	3	470	490	Cleavage	Myosin heavy chain-like pr	1	
hvs-miR1436a	TC274630	2.5	525	545	Cleavage	Beta3-glucuronyltransferase	1	GO:0016740 probable glucuronosyltransferase os07g06944
hvs-miR1436a	CX626909	2.5	138	158	Cleavage	unknown function	1	
hvs-miR1436a	TC273215	3	16	36	Cleavage	Predicted protein	1	
hvs-miR1436a	TC267617	3	581	601	Cleavage	Vesicle-fusing ATPase	1	GO:0005773;GO:0005524;G n-ethylmaleimide sensitive factor
hvs-miR1436a	TC259615	2.5	107	127	Cleavage	Pathogenesis-related protein	1	
hvs-miR1436a	GH216366	3	261	281	Cleavage	unknown function	1	
hvs-miR1436a	BM444318	2.5	164	184	Cleavage	Carboxy-terminal processin	1	
hvs-miR1436a	TC273832	2.5	380	400	Translation	unknown function	1	GO:0010508;GO:0003677;G uv radiation resistance-associated gene
hvs-miR1436a	BQ767963	3	375	395	Cleavage	Similarity to Serine/arginin	1	
hvs-miR1436a	CB860412	2.5	630	649	Cleavage	unknown function	1	
hvs-miR1436a	AJ465367	3	321	341	Cleavage	unknown function	1	
hvs-miR1436a	TC252433	3	1118	1138	Cleavage	unknown function	1	GO:0005524;GO:0004775;G atp-citrate synthase
hvs-miR1436a	TC277671	2.5	519	539	Cleavage	Nucleotide pyrophosphatase	1	
hvs-miR1436a	TC241325	3	685	705	Translation	Delta-1-pyrroline-5-carboxy	1	GO:0055114;GO:0008270;G delta-1-pyrroline-5-carboxylate dehydrogenase
hvs-miR1436a	TC258367	3	28	48	Cleavage	ER lumen protein retaining	1	GO:0005794;GO:0006621;G er lumen protein retaining receptor
hvs-miR1436a	AV836526	3	238	258	Cleavage	unknown function	1	
hvs-miR156e	TC245963	1	529	548	Cleavage	Squamosa promoter-binding	1	GO:0005634;GO:0003677 teosinte glume architecture 1
hvs-miR156e	TC265421	1	439	458	Cleavage	Squamosa promoter-binding	1	
hvs-miR156e	TC245020	1	376	395	Cleavage	Isoform 2 of Q6H509	1	GO:0005634;GO:0003677 squamosa promoter-binding (sbp domain) tran
hvs-miR156e	CA032492	1	523	542	Cleavage	Squamosa promoter-binding	1	GO:0046872;GO:0003677;G squamosa promoter-binding-like protein 17-lil
hvs-miR156e	BF258419	1	184	203	Cleavage	Promoter binding protein	1	

hvs-miR156e	EX598089	1	241	260	Cleavage	Squamosa promoter-binding	1	
hvs-miR156e	TC252995	2	713	732	Cleavage	Squamosa promoter-binding	1	GO:0005634;GO:0003677;G squamosa promoter-binding-like protein 13-lil
hvs-miR156e	TC246441	2	230	249	Cleavage	Squamosa promoter-binding	1	GO:0006351;GO:0003677;G sbp-box family member protein
hvs-miR156e	BF630636	3	187	206	Cleavage	SBP transcription factor	1	
hvs-miR156e	TC262843	3	1295	1314	Cleavage	F-box domain containing pr	1	
hvs-miR156e	BQ766747	3	508	527	Cleavage	Predicted protein	1	GO:0005840;GO:0003735;G 60s ribosomal protein l39
hvs-miR159	TC259549	2.5	224	244	Cleavage	GAMyb protein	1	GO:0006355;GO:0009908;G transcription partial
hvs-miR159	TC238438	2.5	1236	1256	Cleavage	Transcription factor GAN	1	GO:0006355;GO:0009908;G transcription factor
hvs-miR159	CV062223	2	763	782	Cleavage	60S ribosomal protein L30	1	
hvs-miR159	TC252032	2.5	766	786	Translation	Triosephosphate isomerase,	1	GO:0010038;GO:0071944;G triosephosphate isomerase
hvs-miR159	TC268406	3	333	352	Translation	Zinc finger AN1 and C2H2	1	GO:0008270;GO:0005622;G zinc finger an1 and c2h2 domain-containing st
hvs-miR160d	BU986263	0	189	208	Cleavage	Auxin response factor 22	1	GO:0009734;GO:0006355;G auxin response factor 10
hvs-miR160d	BF622307	1	252	271	Cleavage	Auxin response factor 18	1	GO:0048731;GO:0009734;G auxin response factor 18-like
hvs-miR160d	TC262692	2	432	451	Translation	unknown function	1	
hvs-miR160d	BE196326	2.5	699	718	Cleavage	Protein synthesis inhibitor I	1	GO:0006952;GO:0017148;G ribosome inactivating protein 1
hvs-miR160d	BG369432	3	266	286	Translation	CG13214-PA, isoform A	1	
hvs-miR160d	TC274168	3	797	816	Translation	Protein kinase domain cont	1	GO:0009524;GO:0005886;G serine threonine-protein kinase cbk1-like
hvs-miR160e	BU986263	1	189	208	Cleavage	Auxin response factor 22	1	GO:0009734;GO:0006355;G auxin response factor 10
hvs-miR160e	BG369432	2	266	286	Translation	CG13214-PA, isoform A	1	
hvs-miR160e	BF622307	2	252	271	Cleavage	Auxin response factor 18	1	GO:0048731;GO:0009734;G auxin response factor 18-like
hvs-miR160e	TC262811	3	72	92	Translation	unknown function	1	
hvs-miR160e	TC247125	3	48	67	Translation	Betaine aldehyde dehydrog	1	GO:0016903 betaine-aldehyde partial
hvs-miR160e	TC262692	3	432	451	Translation	unknown function	1	
hvs-miR164d	TC240039	1	806	826	Cleavage	NAC transcription factor	1	
hvs-miR164d	TC248477	1	643	663	Cleavage	NAC domain protein NAC1	1	GO:0003677;GO:0006355 nac domain-containing protein 21 22
hvs-miR164d	TC251797	1	359	379	Cleavage	NAC domain protein NAC1	1	GO:0003677;GO:0006355 nac domain-containing protein 21 22
hvs-miR164d	TC254954	2	720	740	Cleavage	unknown function	1	GO:0003677;GO:0006355 nac domain-containing protein 21 22
hvs-miR164d	TC256476	1.5	119	138	Cleavage	Mitogen-activated protein k	1	GO:0004707;GO:0000165;G mitogen-activated protein kinase 4
hvs-miR164d	DN183772	3	338	358	Translation	Expressed protein	1	GO:0043234;GO:0019375;G dgd1 suppressor 1
hvs-miR164d	DN156119	3	309	329	Translation	Sperm protamine-P1	1	
hvs-miR164d	TC272251	3	359	379	Cleavage	unknown function	1	
hvs-miR164d	TC269623	3	153	172	Cleavage	Phytosulfokine-alpha 1 prec	1	
hvs-miR164d	BI956904	3	42	61	Cleavage	Pherophorin-C1 protein pre	1	
hvs-miR166b	CV063912	3	660	679	Cleavage	unknown function	1	
hvs-miR166m	CV063912	3	660	679	Cleavage	unknown function	1	
hvs-miR167d	DN178141	3	249	269	Translation	Serine/threonine-protein kir	1	GO:0006468;GO:0004674;G serine threonine-protein kinase nek5
hvs-miR167d	TC253839	3	401	421	Cleavage	unknown function	1	GO:0055085;GO:0006468;G probable anion transporter chloroplastic-like
hvs-miR168-5p	NP315934	1.5	713	733	Translation	unknown function	1	
hvs-miR168-5p	TC258904	3	214	233	Translation	unknown function	1	
hvs-miR168-5p	TC276022	3	704	723	Translation	Diadenosine tetraphosphata	1	GO:0048482;GO:0046872;G calcineurin-like metallo-phosphoesterase supe
hvs-miR168-3p	BQ758060	3	284	307	Cleavage	unknown function	1	
hvs-miR171-3p	CD054872	3	141	160	Translation	Protein FAN	1	GO:0009737;GO:0009825;G beach domain-containing protein lvs-like
hvs-miR171f	TC239462	3	176	195	Cleavage	unknown function	1	GO:0006468;GO:0005524;G lrr receptor-like serine threonine-protein kinas
hvs-miR172a	TC278536	0.5	282	301	Cleavage	unknown function	2	GO:0006351 floral homeotic protein apetala 2
hvs-miR172a	TC278536	0.5	418	437	Cleavage	unknown function	2	GO:0006351 floral homeotic protein apetala 2

hvs-miR172a	TC242534	0.5	614	633	Cleavage	unknown function	1	GO:0006355;GO:0003677;G ap2 erebp transcription factor superfamily prot
hvs-miR172a	TC240202	0.5	1465	1484	Cleavage	APETALA2-like protein	1	GO:0003700;GO:0003677;G floral homeotic protein
hvs-miR172a	TC266609	3	252	272	Cleavage	Sporulation related precurs	1	
hvs-miR172a	AL499992	2.5	290	309	Cleavage	Succinyl-CoA ligase [GDP-	1	
hvs-miR172a	AL501298	2.5	254	273	Cleavage	Succinyl-CoA ligase [GDP-	1	GO:0004776;GO:0005507;G succinyl- ligase
hvs-miR172a	TC248970	2.5	1203	1223	Cleavage	Protein kinase domain cont	1	GO:0006468;GO:0005524;G protein kinase
hvs-miR172a	TC272816	3	482	502	Translation	unknown function	1	
hvs-miR172a	TC268550	3	94	113	Cleavage	unknown function	1	
hvs-miR172a	TC242934	3	615	634	Cleavage	AIG1 family protein, expre:	1	GO:0016817;GO:0019031;G translocase of chloroplast chloroplastic-like
hvs-miR2012a	TC257133	2.5	54	74	Cleavage	DnaJ protein family-like	1	GO:0006457;GO:0031072;G chaperone protein dnaj 10
hvs-miR2012a	TC269048	3	443	463	Cleavage	Ribonuclease	1	GO:0005618;GO:0003723;G ribonuclease t2
hvs-miR2012a	TC244274	3	771	790	Cleavage	unknown function	1	GO:0042127;GO:0005886;G arm repeat protein interacting with abf2-like
hvs-miR2012a	TC245278	2.5	542	561	Cleavage	Contig An10c0020, comple	1	
hvs-miR2012a	TC267248	3	25	45	Cleavage	Gastric mucin-like protein	1	
hvs-miR2012a	TC267365	3	345	365	Translation	Expansin EXPA8	1	GO:0009505;GO:0009664;G expansin expa8
hvs-miR2012a	BQ766646	3	393	413	Translation	Expansin EXPA8	1	GO:0009505;GO:0009664;G expansin expa8
hvs-miR2012a	TC243840	3	1678	1697	Translation	unknown function	1	GO:0003676;GO:0032259;G methyltransferase-like protein 1-like
hvs-miR2012a	TC263561	3	534	553	Cleavage	unknown function	1	
hvs-miR2012a	TC264503	3	505	524	Translation	Photosystem I reaction cent	1	GO:0009522;GO:0009535 photosystem i reaction center subunit n
hvs-miR2023a	TC253033	2	304	324	Cleavage	unknown function	1	
hvs-miR2023a	TC266596	3	73	92	Cleavage	unknown function	1	
hvs-miR2023a	TC251896	3	1849	1868	Cleavage	unknown function	1	
hvs-miR2023a	BM373527	3	57	78	Cleavage	Emb CAB72159.1	1	
hvs-miR2023a	TC274041	3	2	23	Cleavage	unknown function	1	
hvs-miR2023a	TC255070	3	606	627	Cleavage	Chlorophyll synthase, chlor	1	
hvs-miR2023a	TC252812	3	1501	1520	Translation	unknown function	1	GO:0005794;GO:0004571;G mannosyl-oligosaccharide -alpha-mannosidase
hvs-miR2024a	TC242029	2.5	150	169	Cleavage	Expressed protein	1	
hvs-miR2024a	GH228935	2.5	246	265	Cleavage	MIKC-type MADS-box tr	1	
hvs-miR2024a	TC243711	3	620	639	Cleavage	F-box domain containing pr	1	
hvs-miR2024a	TC274417	2.5	326	345	Cleavage	MIKC-type MADS-box tr	1	
hvs-miR2024a	TC254804	3	556	575	Cleavage	F-box domain containing pr	1	
hvs-miR2024a	TC240629	2.5	104	123	Cleavage	MIKC-type MADS-box tr	1	
hvs-miR2024a	BI958665	3	143	162	Cleavage	unknown function	1	GO:0016772 f-box protein atlg78280-like
hvs-miR2024a	BF258360	3	688	707	Translation	unknown function	1	
hvs-miR2024a	NP1772588	3	594	613	Translation	unknown function	1	GO:0008270;GO:0005622 vef family protein
hvs-miR319a-3p	TC264933	2.5	440	459	Cleavage	unknown function	1	
hvs-miR319a-3p	BM370389	3	360	380	Cleavage	Predicted protein	1	
hvs-miR319a-3p	CA004040	3	182	202	Cleavage	Polyhedral envelope proteir	1	
hvs-miR319a-3p	TC250057	2.5	80	99	Cleavage	unknown function	1	GO:0080049;GO:0050660;G l-galactono- -lactone dehydrogenase mitochon
hvs-miR319a-3p	TC258104	3	269	288	Cleavage	unknown function	1	GO:0006468;GO:0005524;G transmembrane protein kinase family protein
hvs-miR393b	TC279715	3	279	299	Translation	unknown function	1	GO:0016798;GO:0003723;G rna pseudourine synthase 7-like
hvs-miR395a	TC262830	1	383	402	Cleavage	Plastidic ATP sulfurylase	1	GO:0046686;GO:0004781;G atp sulfurylase
hvs-miR395n	TC262830	1	383	402	Cleavage	Plastidic ATP sulfurylase	1	GO:0046686;GO:0004781;G atp sulfurylase
hvs-miR396a	AV913958	2.5	444	464	Cleavage	Uncharacterized protein At	1	GO:0048564;GO:0009535 uncharacterized protein ycf37-like
hvs-miR396a	TC269943	3	295	315	Cleavage	unknown function	1	GO:0003743;GO:0009860;G transcription initiation factor tfiid subunit 6-lik

hvs-miR396a	TC250287	2.5	197	217	Cleavage	unknown function	1	GO:0048564;GO:0009535	tetratricopeptide expressed
hvs-miR396a	TC244394	2	1613	1632	Cleavage	MutT/nudix protein-like	1	GO:0016787;GO:0005773	nudix hydrolase 3-like
hvs-miR396a	CA026441	2	139	160	Cleavage	Transcription activator	1		
hvs-miR396a	NP611500	3	355	375	Translation	unknown function	1		
hvs-miR396a	CB860915	2	98	119	Cleavage	Growth-regulating factor	1		
hvs-miR396a	TC279628	2	257	278	Cleavage	Growth-regulating factor 3	1	GO:0006355;GO:0005524;G	growth-regulating factor 1
hvs-miR396a	GH213244	2	212	231	Cleavage	Growth-regulating factor 6	1	GO:0006355;GO:0005524;G	growth-regulating factor 1
hvs-miR396a	TC272166	2	521	542	Cleavage	Growth-regulating factor 1	1	GO:0009739;GO:0006355;G	growth-regulating factor 11
hvs-miR396a	TC270705	2	536	557	Cleavage	Growth-regulating factor 3	1	GO:0006355;GO:0005524;G	growth-regulating factor 1
hvs-miR396a	TC253960	2	397	418	Cleavage	Growth-regulating factor 3	1	GO:0006355;GO:0005524;G	growth-regulating factor 1
hvs-miR396a	BG342891	2.5	306	325	Cleavage	Molecular chaperone Hsp90	1	GO:0006952;GO:0005829;G	heat shock protein 90
hvs-miR396a	TC246704	3	121	140	Translation	AT3g14110/MAG2_6	1	GO:0009941;GO:0000304;G	protein fluorescent in blue chloroplastic-like
hvs-miR396a	TC261739	3	740	759	Translation	unknown function	1	GO:0010380;GO:0016020;G	protein fluorescent in blue chloroplastic-like
hvs-miR396a	TC255527	2	107	126	Cleavage	Growth-regulating factor 6	1		
hvs-miR396a	TC260953	2	531	550	Cleavage	Growth-regulating factor 8	1	GO:0006355;GO:0005524;G	growth-regulating factor 2
hvs-miR396a	GH211677	3	127	146	Translation	unknown function	1		
hvs-miR396a	BG414689	3	462	481	Translation	F8A5.21 protein	1	GO:0016491	aldo keto
hvs-miR396a	TC260189	3	284	303	Cleavage	unknown function	1	GO:0009651;GO:0022626	nascent polypeptide associated complex alpha
hvs-miR396a	BJ478709	3	219	238	Cleavage	Heat shock protein 80	1	GO:0006952;GO:0005829;G	heat shock protein 90
hvs-miR396a	BF627785	3	60	79	Cleavage	unknown function	1	GO:0009651;GO:0022626	nascent polypeptide-associated complex subur
hvs-miR396a	TC257291	3	232	251	Cleavage	Alpha chain of nascent poly	1		
hvs-miR396a	TC281337	3	69	88	Cleavage	Heat shock protein 80	1	GO:0006952;GO:0005829;G	heat shock protein 90
hvs-miR396a	TC245999	3	1005	1024	Cleavage	Heat shock protein 80	1	GO:0006952;GO:0005829;G	heat shock protein 90
hvs-miR397a	TC275983	0	38	58	Cleavage	unknown function	1		
hvs-miR397a	TC262144	0.5	732	751	Cleavage	Laccase-23 precursor	1	GO:0046872;GO:0016491;G	laccase 90c
hvs-miR397a	BI960433	2.5	219	239	Cleavage	Laccase-10 precursor	1		
hvs-miR397a	BY839519	2.5	280	300	Translation	Laccase-12/13 precursor	1	GO:0009414;GO:0005507;G	laccase-12 13-like
hvs-miR397a	GH208933	3	532	552	Translation	unknown function	1	GO:0009570	uncharacterized protein loc100829963
hvs-miR397a	BI960140	2.5	191	211	Translation	Laccase-12/13 precursor	1	GO:0009414;GO:0005507;G	laccase precursor
hvs-miR397a	TC274250	2.5	415	435	Cleavage	Laccase-10 precursor	1	GO:0009414;GO:0005507;G	uncharacterized protein loc100193025 precurs
hvs-miR397a	TC252167	3	368	388	Translation	At5g45170	1	GO:0009570	haloacid dehalogenase-like hydrolase superfar
hvs-miR397a	BY835984	2.5	319	338	Translation	Laccase LAC5-6	1	GO:0009414;GO:0005507;G	laccase-4
hvs-miR397a	BI957301	2.5	85	104	Translation	Laccase LAC5-6	1	GO:0009414;GO:0005507;G	laccase-4
hvs-miR397a	TC263463	2.5	82	101	Translation	Laccase LAC5-6	1	GO:0005507;GO:0052716;G	laccase-4
hvs-miR397a	CK568938	2.5	121	140	Cleavage	unknown function	1		
hvs-miR397a	CV057686	3	129	148	Cleavage	Cystatin Hv-CPI8	1	GO:0010466;GO:0004869	cysteine proteinase inhibitor 8-like
hvs-miR397a	CV060414	3	176	195	Cleavage	Cystatin Hv-CPI8	1	GO:0010466;GO:0004869	cysteine proteinase inhibitor 8
hvs-miR397a	CV058406	3	176	195	Cleavage	Cystatin Hv-CPI8	1	GO:0010466;GO:0004869	cysteine proteinase inhibitor 8-like
hvs-miR397a	CV064261	3	143	162	Cleavage	Cystatin Hv-CPI8	1	GO:0030414	cysteine proteinase inhibitor 8-like
hvs-miR397a	TC259700	3	146	165	Cleavage	Auxin response factor 9	1	GO:0005488;GO:0044699;G	auxin response factor 1
hvs-miR399	AV835204	0	331	351	Cleavage	DNA primase	1		
hvs-miR399	NP398309	3	450	469	Cleavage	unknown function	1	GO:0006952;GO:0043531	rp1-like protein
hvs-miR399	TC253213	3	705	724	Cleavage	unknown function	1		
hvs-miR399b	AV835204	1.5	331	351	Cleavage	DNA primase	1		
hvs-miR399b	CV063173	3	734	754	Cleavage	unknown function	1	GO:0022626;GO:0009941;G	dihydrolipoyllysine-residue acetyltransferase c

hvs-miR399b	TC243905	3	1230	1250	Cleavage	l-aminocyclopropane- l-car	1	GO:0008793;GO:0030170;G l-aminocyclopropane- l-carboxylate synthase
hvs-miR399b	EX581729	3	242	261	Cleavage	Expressed protein	1	GO:0016021
hvs-miR399b	TC265464	3	405	424	Cleavage	Expressed protein	1	GO:0016021
hvs-miR399j	AV835204	1.5	331	351	Cleavage	DNA primase	1	
hvs-miR399j	TC244059	3	371	390	Cleavage	unknown function	1	GO:0017111;GO:0005524
hvs-miR6213	TC278759	0	133	153	Cleavage	180-200 kDa membrane prc	1	atp-dependent clp protease atp-binding subuni
hvs-miR6213	TC270792	0	128	148	Cleavage	unknown function	1	
hvs-miR6213	TC268582	0	264	284	Cleavage	unknown function	1	
hvs-miR6213	BE438007	0	270	290	Cleavage	unknown function	1	
hvs-miR6213	TC258701	0	1517	1537	Cleavage	Ribonuclease BN	1	
hvs-miR6213	TC272013	1	122	142	Cleavage	unknown function	1	
hvs-miR6213	BE437389	1.5	300	320	Cleavage	unknown function	1	
hvs-miR444a	GH228935	2	246	266	Translation	MIKC-type MADS-box tr	1	
hvs-miR444a	TC274417	2	326	346	Translation	MIKC-type MADS-box tr	1	
hvs-miR444a	TC240629	2	104	124	Translation	MIKC-type MADS-box tr	1	
hvs-miR444	TC247725	2.5	212	232	Cleavage	Triosephosphate isomerase,	1	GO:0032504;GO:0080022;G triosephosphate isomerase
hvs-miR444	TC245800	2.5	923	943	Cleavage	Triosephosphate isomerase,	1	GO:0032504;GO:0080022;G triosephosphate isomerase
hvs-miR444	TC248027	3	559	578	Cleavage	unknown function	1	GO:0005773;GO:0042823;G ribonuclease p family protein rpp14 family prc
hvs-miR444b	TC242029	3	150	170	Cleavage	Expressed protein	1	
hvs-miR444b	GH228935	2.5	246	266	Translation	MIKC-type MADS-box tr	1	
hvs-miR444b	TC274417	2.5	326	346	Translation	MIKC-type MADS-box tr	1	
hvs-miR444b	TC253530	3	690	710	Translation	unknown function	1	
hvs-miR444b	TC240629	2.5	104	124	Translation	MIKC-type MADS-box tr	1	
hvs-miR444b	BI958665	3	143	163	Translation	unknown function	1	GO:0016772
hvs-miR444b	TC263174	3	138	158	Translation	Eukaryotic translation initia	1	f-box protein at lg78280-like
hvs-miR5048a	TC250387	0	771	792	Cleavage	unknown function	1	GO:0006468;GO:0005524;G cysteine-rich receptor-like protein kinase 26
hvs-miR5048a	TC281282	1.5	645	666	Cleavage	Jacalin-like lectin domain c	1	GO:0004672;GO:0000166
hvs-miR5048a	TC238421	1.5	1585	1605	Cleavage	Resistance protein	1	cysteine-rich receptor-like protein kinase 15
hvs-miR5048a	TC262711	2.5	82	103	Cleavage	Serine/threonine protein kin	1	GO:0046872;GO:0006468;G barley stem rust resistance protein
hvs-miR5048a	TC261703	2.5	660	681	Cleavage	Protein kinase domain cont	1	GO:0004672;GO:0000166
hvs-miR5048a	TC238427	2.5	403	423	Cleavage	Serine/threonine kinase-like	1	wall-associated receptor kinase 3
hvs-miR5048a	TC238429	2.5	790	810	Cleavage	Serine/threonine kinase-like	1	GO:0006468;GO:0005524;G cysteine-rich receptor-like protein kinase 19
hvs-miR5048a	TC243354	2.5	516	535	Cleavage	unknown function	1	GO:0006468;GO:0004674;G protein kinase chloroplastic-like
hvs-miR5048a	TC268462	2.5	109	129	Cleavage	unknown function	1	GO:0046777;GO:0004674;G protein kinase chloroplastic-like
hvs-miR5048a	TC253610	3	802	821	Cleavage	Cyclin-dependent kinase F-	1	GO:0046872;GO:0006468;G probable leucine-rich repeat receptor-like serir
hvs-miR5048a	TC266645	2.5	651	670	Cleavage	Mitogen-activated protein k	1	GO:0007049;GO:0006468;G serine threonine-protein kinase expressed
hvs-miR5049c	BY872542	1	91	113	Cleavage	unknown function	1	GO:0009864;GO:0006468;G mitogen-activated protein kinase kinase 6
hvs-miR5049c	TC266554	1.5	1322	1344	Cleavage	unknown function	1	
hvs-miR5049c	TC243055	1.5	667	689	Cleavage	unknown function	1	GO:0006457;GO:0031072;G chaperone -domain-containing protein
hvs-miR5049c	CB860412	1.5	633	655	Cleavage	unknown function	1	GO:0005515
hvs-miR5049c	TC253269	2	258	280	Cleavage	unknown function	1	chaperone -domain-containing protein
hvs-miR5049c	TC249455	2	426	448	Cleavage	unknown function	1	
hvs-miR5049c	TC239354	2	972	994	Cleavage	unknown function	1	
hvs-miR5049c	TC243686	2	776	798	Cleavage	Leucine Rich Repeat family	1	GO:0006468;GO:0004674;G probable leucine-rich repeat receptor-like prot
hvs-miR5049c	DN156749	1.5	86	108	Cleavage	Probable histone-lysine N-r	1	

hvs-miR5049c	TC265824	1.5	420	442	Cleavage	Beta-defensin 123 precursor	1	
hvs-miR5049c	TC240249	2.5	1367	1389	Cleavage	Cytosine-specific methyltransferase	1	GO:0010216;GO:0009910;G cytosine-5 dna methyltransferase
hvs-miR5049c	FD523641	2.5	361	383	Cleavage	unknown function	1	
hvs-miR5049c	EX591130	1.5	514	535	Cleavage	unknown function	1	
hvs-miR5049c	TC249543	2	491	513	Cleavage	unknown function	1	GO:0005886;GO:0006468;G receptor-like protein kinase hsl1-like
hvs-miR5049c	AL500722	2.5	32	54	Cleavage	Glutathione S-transferase T	1	
hvs-miR5049c	CB872762	2.5	182	204	Cleavage	unknown function	1	
hvs-miR5049c	TC256737	2.5	908	930	Cleavage	Sulfolipid synthase	1	GO:0046510;GO:0009941;G glycosyl group 1 family protein
hvs-miR5049c	BM097988	3	77	99	Cleavage	unknown function	1	
hvs-miR5049c	TC262832	2.5	1104	1126	Cleavage	Glucose-6-phosphate 1-dehydrogenase	1	GO:0050661;GO:0004345;G glucose-6-phosphate 1-dehydrogenase
hvs-miR5049c	TC260184	2.5	294	316	Cleavage	unknown function	1	
hvs-miR5049c	AJ474659	2.5	396	418	Cleavage	unknown function	1	
hvs-miR5049c	TC254299	2.5	430	451	Cleavage	Endonuclease/exonuclease/	1	GO:0008270;GO:0003676 carbon catabolite repressor protein 4 homolog
hvs-miR5049c	TC243595	3	590	612	Cleavage	unknown function	1	
hvs-miR5049c	TC272572	3	41	63	Cleavage	unknown function	1	
hvs-miR5049c	TC257743	3	720	742	Cleavage	Boron transporter	1	GO:0035445;GO:0005768;G probable boron transporter 2-like
hvs-miR5049c	TC244093	2	548	570	Cleavage	UMP synthase	1	GO:0009220;GO:0009116;G uridine 5 -monophosphate synthase-like
hvs-miR5049c	TC256008	3	577	599	Cleavage	Nigrosin-OG1 antimicrobia	1	
hvs-miR5049c	GH217058	3	441	463	Cleavage	unknown function	1	
hvs-miR5049c	TC250371	2.5	555	577	Cleavage	General secretion pathway 1	1	
hvs-miR5049c	TC257880	2.5	1605	1627	Cleavage	unknown function	1	GO:0005634;GO:0005737 proteasomal ubiquitin receptor adrm1
hvs-miR5049c	TC265563	3	742	764	Cleavage	unknown function	1	
hvs-miR5049c	TC241253	2.5	812	834	Cleavage	unknown function	1	GO:0017111;GO:0005524 cell division control protein 48 homolog c-like
hvs-miR5049c	BI950288	3	393	415	Cleavage	40S ribosomal protein S3aE	1	GO:0003746;GO:0005853;G elongation factor 1-gamma
hvs-miR5049c	TC251577	2.5	510	532	Cleavage	Myosin heavy chain-like pr	1	
hvs-miR5049c	DN189237	2	387	409	Cleavage	unknown function	1	
hvs-miR5049c	TC274933	3	784	806	Cleavage	Malate dehydrogenase	1	GO:0030060;GO:0009651;G malate dehydrogenase
hvs-miR5049c	TC258328	3	809	831	Cleavage	Cell envelope-related transc	1	
hvs-miR5049c	BU996683	3	304	326	Cleavage	Transcriptional regulator, C	1	
hvs-miR5049c	TC255389	0	687	707	Cleavage	unknown function	1	GO:0006468;GO:0004674;G protein kinase and pp2c-like domain-contains
hvs-miR5049c	TC256535	0	972	992	Cleavage	Expressed protein	1	
hvs-miR5049c	TC242358	0	982	1002	Cleavage	unknown function	1	GO:0008270;GO:0003676 family transposase isoform 1
hvs-miR5049c	TC266552	0.5	1214	1234	Cleavage	GAMYB-binding protein	1	
hvs-miR5049c	TC267500	1	830	850	Cleavage	Early transcribed membrane	1	
hvs-miR5049c	FD522424	1.5	521	541	Cleavage	Type II and III secretion sy	1	
hvs-miR5049c	TC242241	1	787	807	Translation	Surface antigen protein 2	1	
hvs-miR5049c	TC252029	1.5	886	906	Cleavage	unknown function	1	
hvs-miR5049c	TC263351	1	1361	1381	Cleavage	unknown function	1	
hvs-miR5049c	TC278477	1	492	511	Cleavage	unknown function	1	
hvs-miR5049c	CD057330	1.5	55	75	Cleavage	unknown function	1	
hvs-miR5049c	BJ450193	1.5	323	343	Cleavage	Pathogenesis-related protein	1	
hvs-miR5049c	CX626387	1.5	589	609	Cleavage	TSBP protein	1	
hvs-miR5049c	TC260883	1.5	507	527	Cleavage	unknown function	1	GO:0016630;GO:0009706;G retinol dehydrogenase 14
hvs-miR5049c	TC271384	1.5	632	652	Cleavage	unknown function	1	
hvs-miR5049c	TC254898	1.5	332	352	Cleavage	Predicted protein	1	

hvs-miR5049e	TC261514	1.5	614	634	Translation	Zinc finger protein	1	GO:0046872;GO:0005886	protein brevis radix-like 4-like
hvs-miR5049e	TC271832	1.5	753	773	Cleavage	unknown function	1		
hvs-miR5049e	TC239858	2	975	995	Cleavage	At3g03330/T21P5_25	1	GO:0016491;GO:0055114;G	dehydrogenase reductase sdr family member 7
hvs-miR5049e	AJ473037	2	190	210	Translation	unknown function	1		
hvs-miR5049e	GH228939	2	60	80	Cleavage	Laccase LAC12	1	GO:0009414;GO:0005507;G	laccase 17 isoform 1
hvs-miR5049e	BU974512	2.5	311	331	Cleavage	Meiotically up-regulated ge	1		
hvs-miR5049e	BU995668	2.5	43	63	Translation	Transmembrane amino acid	1	GO:0016021	amino acid permease 3-like
hvs-miR5049e	TC240827	2	807	827	Cleavage	Predicted protein	1		
hvs-miR5049e	TC247285	2.5	1120	1140	Cleavage	unknown function	1	GO:0005509	caleosin 3
hvs-miR5049e	TC260565	2.5	1405	1425	Cleavage	unknown function	1		
hvs-miR5049e	BI779287	2.5	53	73	Cleavage	unknown function	1		
hvs-miR5049e	TC256737	2.5	906	926	Translation	Sulfolipid synthase	1	GO:0046510;GO:0009941;G	glycosyl group 1 family protein
hvs-miR5049e	TC266779	3	614	634	Translation	Ethylene receptor-like prote	1	GO:0000156;GO:0035556;G	ethylene receptor
hvs-miR5049e	TC243055	3	665	685	Translation	unknown function	1	GO:0005515	chaperone -domain-containing protein
hvs-miR5049e	TC253269	3	256	276	Translation	unknown function	1		
hvs-miR5049e	TC266554	3	1320	1340	Translation	unknown function	1	GO:0006457;GO:0031072;G	chaperone -domain-containing protein
hvs-miR5049d	CX626387	2	592	612	Cleavage	TSBP protein	1		
hvs-miR5049d	TC260883	2	510	530	Cleavage	unknown function	1	GO:0016630;GO:0009706;G	retinol dehydrogenase 14
hvs-miR5049d	TC255389	1.5	690	710	Cleavage	unknown function	1	GO:0006468;GO:0004674;G	protein kinase and pp2c-like domain-containin
hvs-miR5049d	TC256535	1.5	975	995	Cleavage	Expressed protein	1		
hvs-miR5049d	BF064522	1.5	447	466	Cleavage	UDP-glucuronosyl and UDI	1	GO:0016758;GO:0008152	cytokinin-o-glucosyltransferase 2
hvs-miR5049d	TC264730	1.5	486	505	Cleavage	UDP-glucuronosyl and UDI	1	GO:0016758;GO:0008152	anthocyanin 5-o-glucosyltransferase
hvs-miR5049d	TC260502	1.5	1108	1127	Cleavage	Cyanate hydratase	2	GO:0043565;GO:0008824;G	cyanate hydratase
hvs-miR5049d	TC260502	1.5	1134	1153	Cleavage	Cyanate hydratase	2	GO:0043565;GO:0008824;G	cyanate hydratase
hvs-miR5049d	TC272572	2.5	42	62	Cleavage	unknown function	1		
hvs-miR5049d	TC253269	2	259	279	Cleavage	unknown function	1		
hvs-miR5049d	TC257882	2	811	831	Cleavage	Protein kinase-like protein	1	GO:0004674;GO:0043167;G	calcium-dependent protein kinase 7-like
hvs-miR5049d	BY872542	2.5	92	112	Cleavage	unknown function	1		
hvs-miR5049d	BQ470677	3	411	431	Cleavage	unknown function	1	GO:0044763;GO:0006811;G	potassium channel kat1-like
hvs-miR5049d	BU974512	3	314	334	Cleavage	Meiotically up-regulated ge	1		
hvs-miR5049d	CK566281	3	46	66	Cleavage	HV1LRR1	1	GO:0006952;GO:0043531	disease resistance protein rpm1
hvs-miR5049d	TC240249	2.5	1368	1388	Cleavage	Cytosine-specific methyltra	1	GO:0010216;GO:0009910;G	cytosine-5 dna methyltransferase
hvs-miR5049d	TC240827	2	810	830	Cleavage	Predicted protein	1		
hvs-miR5049d	TC263351	2.5	1364	1384	Cleavage	unknown function	1		
hvs-miR5049d	TC242241	2.5	790	810	Cleavage	Surface antigen protein 2	1		
hvs-miR5049d	TC265572	3	105	124	Cleavage	Peptidyl-prolyl cis-trans iso	1	GO:0005737;GO:0006457;G	peptidyl-prolyl cis-trans isomerase cyp40-like
hvs-miR5049d	TC252029	2.5	889	909	Cleavage	unknown function	1		
hvs-miR5049d	TC242358	3	985	1005	Cleavage	unknown function	1	GO:0008270;GO:0003676	family transposase isoform 1
hvs-miR5049d	TC266552	3	1217	1237	Cleavage	GAMYB-binding protein	1		
hvs-miR5049d	AJ473037	2.5	193	213	Cleavage	unknown function	1		
hvs-miR5049d	TC271384	2.5	635	655	Cleavage	unknown function	1		
hvs-miR5049d	TC261514	2.5	617	637	Cleavage	Zinc finger protein	1	GO:0046872;GO:0005886	protein brevis radix-like 4-like
hvs-miR5049d	TC271832	3	756	776	Cleavage	unknown function	1		
hvs-miR5049d	TC261197	3	1	21	Cleavage	TATA box-binding protein	1	GO:0006352;GO:0003743;G	transcription initiation factor tfiid subunit 10
hvs-miR5049a	TC254787	1	406	426	Cleavage	Tubby protein-like	1		

hvs-miR5049a	TC246769	1	792	812	Cleavage	Non-specific lipid-transfer p	1	
hvs-miR5049a	TC254069	2.5	996	1016	Cleavage	Resistance-related receptor-	1	GO:0006468;GO:0005524;G receptor-like protein kinase
hvs-miR5049a	BI779287	3	92	113	Cleavage	unknown function	1	
hvs-miR5049a	DN158159	2	49	68	Translation	Predicted protein	1	
hvs-miR5049a	TC251541	2.5	816	835	Translation	Lipase class 3-like	1	GO:0004806;GO:0016042;G gdsI esterase lipase at4g10955-like
hvs-miR5049a	BM101048	3	159	178	Cleavage	HcrVfI protein-like	1	
hvs-miR5049a	TC241518	3	1303	1323	Translation	Farnesyl pyrophosphate syn	1	GO:0004337;GO:0004161;G farnesyl pyrophosphate synthetase
hvs-miR5049a	GH206526	3	153	173	Translation	TAK14	1	GO:0006468;GO:0005524;G receptor-like protein kinase
hvs-miR5064	TC276556	2.5	531	551	Cleavage	Peptidyl-prolyl cis-trans iso	1	GO:0006457;GO:0005794;G cyclophilin-like peptidyl-prolyl cis-trans isom
hvs-miR5064	DN177741	2.5	448	468	Cleavage	unknown function	1	GO:0003824 carbohydrate esterase family 4 protein
hvs-miR5064	TC253465	2.5	367	387	Translation	Nucleolar phosphoprotein p	1	
hvs-miR5064	TC240804	3	15	35	Cleavage	Probable methionyl-tRNA s	1	GO:0046872;GO:0004825;G methionyl-trna synthetase
hvs-miR5064	TC261152	3	661	681	Cleavage	Bifunctional xylanase/deacc	1	GO:0003824 chitin deacetylase
hvs-miR5064	TC241092	3	744	763	Translation	Neutral/alkaline invertase	1	GO:0004575;GO:0048825;G alkaline neutral invertase
hvs-miR5064	TC267214	3	224	243	Cleavage	unknown function	1	GO:0015031 charged multivesicular body protein 5
hvs-miR5064	TC255507	3	926	945	Cleavage	unknown function	1	GO:0015031 charged multivesicular body protein 5-like
hvs-miR528	CB864936	1.5	238	258	Translation	Src homology-3 domain pro	1	
hvs-miR528	TC274798	2	411	430	Cleavage	Zgc	1	GO:0005507;GO:0009055;G protein
hvs-miR528	TC252641	2	506	525	Cleavage	unknown function	1	GO:0005507;GO:0009055;G protein
hvs-miR528	BQ759855	2	235	254	Cleavage	Phytocyanin homolog	1	GO:0005507;GO:0009055;G early nodulin-like protein
hvs-miR528	TC253210	2.5	122	141	Cleavage	Superoxide dismutase [Cu-/Zn-]	1	GO:0046872;GO:0006979;G cu zn superoxide dismutase
hvs-miR528	TC238743	2.5	97	116	Cleavage	Superoxide dismutase [Cu-/Zn-]	1	GO:0046872;GO:0006979;G cu zn superoxide dismutase
hvs-miR528	TC241307	2.5	55	74	Cleavage	Superoxide dismutase [Cu-/Zn-]	1	GO:0046872;GO:0006979;G cu zn superoxide dismutase
hvs-miR528	BM374154	2.5	139	158	Cleavage	Superoxide dismutase [Cu-/Zn-]	1	
hvs-miR528	BI952967	2.5	48	67	Cleavage	unknown function	1	
hvs-miR528	CK568202	3	62	82	Translation	unknown function	1	
hvs-miR528	TC247699	3	541	560	Translation	unknown function	1	GO:0009507 fanconi anemia group d2 protein homolog
hvs-miR528	CV054395	3	226	245	Translation	unknown function	1	
hvs-miR6191	TC269763	0	33	52	Cleavage	unknown function	1	
hvs-miR6191	TC257491	1	533	552	Cleavage	unknown function	1	
hvs-miR6191	TC251008	2	585	604	Cleavage	unknown function	1	GO:0008233;GO:0006508 actin-like atpase superfamily protein
hvs-miR6191	TC259658	3	10	29	Cleavage	Predicted protein	1	
hvs-miR6191	BJ460072	3	16	35	Cleavage	Anthranilate phosphoribosy	1	GO:0009507 multiple c2 and transmembrane domain-contai
hvs-miR6191	CA024142	3	21	40	Cleavage	unknown function	1	
hvs-miR6191	TC262714	2.5	23	42	Cleavage	unknown function	1	GO:0005737;GO:0004830;G predicted protein [Hordeum vulgare subsp. vu]
hvs-miR6191	EX572959	3	284	303	Cleavage	unknown function	1	
hvs-miR6198	BQ662754	0	164	185	Cleavage	unknown function	1	
hvs-miR6198	BQ662913	0	140	161	Cleavage	CDNA FLJ45600 fis clone	1	
hvs-miR6198	TC245291	0	114	135	Cleavage	Predicted protein	1	
hvs-miR6198	TC240252	0	135	156	Cleavage	unknown function	1	
hvs-miR6198	TC278401	2.5	119	141	Cleavage	Sucrose transporter	1	
hvs-miR6198	TC267105	3	590	610	Cleavage	Quinone reductase 2	1	GO:0016655;GO:0055114;G flavoprotein wrba
hvs-miR6201	TC268312	3	893	912	Translation	GL2-type homeobox genes	1	GO:0048364;GO:0006355;G probable dna replication complex gins protein
hvs-miR6213	TC281545	1.5	72	92	Cleavage	unknown function	1	
hvs-miR6213	TC266970	1	717	737	Cleavage	unknown function	1	

hvs-miR6213	BM373879	1.5	162	182 Cleavage	unknown function	1	
hvs-miR6213	CA021035	2	301	321 Cleavage	GA17159-PA	1	
hvs-miR6213	BE437939	1	181	200 Cleavage	Homolog of Homo sapiens	1	
hvs-miR6213	TC280803	1.5	809	828 Cleavage	Ribonuclease BN	1	
hvs-miR6213	BE437428	2.5	198	218 Cleavage	unknown function	1	
hvs-miR6213	TC240341	3	1138	1157 Cleavage	unknown function	1	
hvs-miR6213	TC244889	3	1610	1629 Cleavage	Probable serine/threonine-p	1	GO:0046777;GO:0004674;G protein kinase chloroplastic-like

Draft

miRNA Acc.	Target Acc	Expect	Target	Target	Inhibition	Target Desc.	Multiplicity	GO annotation
hvs-miR1120	CK566710	0.5	98	118	Cleavage	TAK14	1	GO:0006468;GO:0005524;GO:0004 receptor-like protein kinase
hvs-miR1120	TC245238	0.5	1654	1674	Cleavage	unknown function	1	GO:0004176;GO:0046872;GO:0006 lon peptidase n-terminal domain and ring finger
hvs-miR1120	TC239725	1	746	766	Cleavage	unknown function	1	
hvs-miR1120	AL501466	1.5	132	152	Cleavage	unknown function	1	
hvs-miR1120	DN159362	1.5	474	494	Cleavage	unknown function	1	
hvs-miR1120	TC252597	1.5	1121	1141	Cleavage	unknown function	1	GO:0046872;GO:0008270 phd-finger family expressed
hvs-miR1120	TC254574	1	763	783	Translation	unknown function	1	GO:0005739;GO:0004003;GO:0002 regulator of telomere elongation helicase 1-like
hvs-miR1120	BQ468979	2	283	303	Cleavage	Pollen coat oleosin-glycine 1	1	
hvs-miR1120	TC244199	2	726	746	Cleavage	unknown function	1	GO:0008312;GO:0005525;GO:0006 signal recognition particle
hvs-miR1120	BQ766864	1.5	379	399	Cleavage	unknown function	1	
hvs-miR1120	TC273876	2	890	910	Cleavage	unknown function	1	
hvs-miR1120	TC253359	3	656	676	Cleavage	Ribulose biphosphate carb	1	GO:0005618;GO:0046863;GO:0043 ribulose biphosphate carboxylase oxygenase c
hvs-miR1120	TC240673	2	760	780	Translation	unknown function	1	GO:0009941;GO:0010177;GO:0003 2-isopropylmalate synthase b
hvs-miR1120	TC255970	1.5	976	995	Cleavage	unknown function	1	GO:0008272;GO:0005886;GO:0005 sulfate transporter
hvs-miR1120	TC275228	2	308	328	Translation	unknown function	1	GO:0016020;GO:0006633;GO:0016 3-ketoacyl- synthase 6-like
hvs-miR1120	BE231018	2	27	47	Cleavage	unknown function	1	GO:0016787 protein
hvs-miR1120	TC240537	2.5	974	994	Cleavage	Eukaryotic translation initial	1	GO:0003743;GO:0003746;GO:0006 eukaryotic translation initiation factor 5a-4
hvs-miR1120	BM368186	3	119	139	Cleavage	unknown function	1	
hvs-miR1120	BM444318	3	169	189	Cleavage	Carboxy-terminal processing	1	
hvs-miR1120	TC244992	2.5	476	496	Translation	Hydroxypyruvate reductase	1	GO:0051287;GO:0005777;GO:0008 hydroxypyruvate reductase
hvs-miR1120	TC256851	2.5	469	489	Cleavage	Pentatricopeptide (PPR) rep	1	
hvs-miR1120	TC265845	3	1042	1062	Cleavage	Fasciclin-like protein FLA4	1	
hvs-miR1120	TC273832	2	385	405	Translation	unknown function	1	GO:0010508;GO:0003677;GO:0003 uv radiation resistance-associated gene
hvs-miR1120	CV062553	2.5	33	53	Cleavage	unknown function	1	GO:0071944 cobra-like protein 1-like
hvs-miR1120	TC249649	2.5	471	491	Cleavage	unknown function	1	
hvs-miR1120	CV062087	2.5	33	53	Cleavage	unknown function	1	
hvs-miR1120	TC256884	2.5	1105	1125	Cleavage	Expressed protein	1	
hvs-miR1120	TC241917	2.5	1156	1176	Cleavage	Expressed protein	1	
hvs-miR1120	TC271886	3	616	636	Translation	Cysteine proteinase	1	GO:0008234;GO:0006508 cysteine proteinase
hvs-miR1120	TC251378	3	248	268	Cleavage	unknown function	1	GO:0008270;GO:0005634 nuclear-interacting partner of alk
hvs-miR1120	TC252903	3	962	982	Translation	CFM2	1	GO:0003723 chloroplastic group iia intron splicing facilitato
hvs-miR157	TC245963	1	529	548	Cleavage	Squamosa promoter-binding	1	GO:0005634;GO:0003677 teosinte glume architecture 1
hvs-miR157	TC265421	1	439	458	Cleavage	Squamosa promoter-binding	1	
hvs-miR157	TC245020	1	376	395	Cleavage	Isoform 2 of Q6H509	1	GO:0005634;GO:0003677 squamosa promoter-binding (sbp domain) trans
hvs-miR157	CA032492	1	523	542	Cleavage	Squamosa promoter-binding	1	GO:0046872;GO:0003677;GO:0005 squamosa promoter-binding-like protein 17-like
hvs-miR157	BF258419	1	184	203	Cleavage	Promoter binding protein	1	
hvs-miR157	EX598089	1	241	260	Cleavage	Squamosa promoter-binding	1	
hvs-miR157	TC252995	2	713	732	Cleavage	Squamosa promoter-binding	1	GO:0005634;GO:0003677;GO:0010 squamosa promoter-binding-like protein 13-like
hvs-miR157	TC246441	2	230	249	Cleavage	Squamosa promoter-binding	1	GO:0006351;GO:0003677;GO:0005 sbp-box family member protein
hvs-miR157	BF630636	3	187	206	Cleavage	SBP transcription factor	1	
hvs-miR157	TC241815	3	775	794	Cleavage	unknown function	1	
hvs-miR157	TC279246	3	75	94	Translation	Mitogen-activated protein ki	1	GO:0004707;GO:0000165;GO:0006 mitogen-activated protein kinase 10-like
hvs-miR157	BF628940	3	1	21	Cleavage	Sensor protein	1	

hvs-miR167b	TC277075	2.5	43	63	Cleavage	unknown function	1		
hvs-miR167b	TC274770	3	138	157	Cleavage	unknown function	1		
hvs-miR167b	TC243580	3	301	320	Cleavage	unknown function	1		
hvs-miR168-3p	CV057005	3	356	375	Cleavage	Ubiquitin family protein, ex	1		
hvs-miR1878	CA006752	3	488	511	Cleavage	Oxysterol-binding protein, e	1	GO:0005543	oxysterol-binding protein 1d-like
hvs-miR1878	TC261829	3	1540	1563	Cleavage	unknown function	1		
hvs-miR1878	CA011549	3	189	212	Cleavage	unknown function	1		
hvs-miR1878	DN184503	2.5	157	177	Cleavage	unknown function	1	GO:0006468;GO:0005524;GO:0004	calcium binding egf domain containing express
hvs-miR1878	TC245264	3	459	481	Cleavage	unknown function	1	GO:0047220;GO:0048531;GO:0005	beta- -galactosyltransferase 7-like
hvs-miR1878	TC252724	3	2071	2090	Cleavage	unknown function	1	GO:0046872;GO:0005618;GO:0003	probable inactive purple acid phosphatase 27-li
hvs-miR1878	TC255323	2.5	438	457	Cleavage	Expressed protein	1		
hvs-miR2004	TC252839	3	213	236	Translation	unknown function	1	GO:0005829;GO:0010102;GO:000C	exocyst subunit exo70 family protein a1
hvs-miR2004	TC255601	3	1158	1181	Translation	unknown function	1	GO:0005829;GO:0010102;GO:000C	exocyst complex component 7-like
hvs-miR2004	FD522458	2.5	271	292	Translation	unknown function	1		
hvs-miR2004	TC278292	3	610	634	Cleavage	Photosystem I reaction cente	1		
hvs-miR2004	BG415655	2	37	58	Translation	Mitochondrial ATPase subu	1	GO:0005743;GO:0015986;GO:0045	atpase subunit 6
hvs-miR2004	TC272535	2	723	744	Translation	AGR075Wp	1		
hvs-miR2004	TC240071	3	984	1005	Cleavage	Protein synthesis inhibitor I	1	GO:0006952;GO:0017148;GO:003C	protein synthesis inhibitor ii
hvs-miR2004	AV926567	3	25	47	Cleavage	Chloroplast 50S ribosomal p	1	GO:0005840;GO:0003735;GO:0005	ribosomal protein l23
hvs-miR2004	DN181374	3	106	130	Translation	Conserved protein	1		
hvs-miR2004	TC262284	2.5	449	471	Cleavage	Phosphate translocator-like	1		
hvs-miR2004	TC242850	3	108	128	Cleavage	unknown function	1		
hvs-miR2004	TC263928	3	835	855	Cleavage	CRS1	1	GO:0003723	chloroplastic group iia intron splicing facilitato
hvs-miR2004	TC251464	2.5	916	938	Cleavage	unknown function	1	GO:0048046	tetratricopeptide repeat protein 27 homolog
hvs-miR2004	TC266958	3	1165	1185	Cleavage	CRS1	1	GO:0003723	chloroplastic group iia intron splicing facilitato
hvs-miR2004	GH226861	2.5	530	550	Cleavage	unknown function	1		
hvs-miR2004	BG309460	2	660	680	Translation	Ribulose bisphosphate carbo	1	GO:0044710;GO:0003824	ribulose- -bisphosphate carboxylase oxygenase
hvs-miR2004	CX631847	3	56	78	Translation	unknown function	1		
hvs-miR2004	GH226364	3	95	116	Translation	Aconitate hydratase-like pro	1	GO:0005829;GO:0019541;GO:0003	aconitate hydratase
hvs-miR2004	EX582129	2.5	43	63	Translation	unknown function	1	GO:0016192;GO:0006886;GO:003C	ap-1 complex subunit mu-1
hvs-miR2004	TC280148	3	438	458	Translation	unknown function	1		
hvs-miR2004	TC273452	3	518	538	Translation	unknown function	1		
hvs-miR2004	TC252746	3	540	563	Translation	HMG CoA reductase	1	GO:0050661;GO:0008299;GO:001C	3-hydroxy-3-methylglutaryl-coenzyme a reduc
hvs-miR2004	TC254934	3	1768	1788	Translation	unknown function	1	GO:0000304;GO:0042651	protein executor chloroplastic-like
hvs-miR2004	TC279282	3	775	796	Translation	Pyridoxal kinase	1	GO:0042538;GO:0009443;GO:001C	pyridoxal kinase
hvs-miR2004	TC275171	2.5	240	259	Translation	WRKY transcription facto	1	GO:0003700;GO:0043565;GO:000C	wrky transcription factor 40
hvs-miR2004	TC273753	2.5	73	92	Translation	Expressed protein	1		
hvs-miR2004	TC238673	3	2	22	Translation	HvCBF11	1	GO:0006355;GO:0009409;GO:0003	cbf protein 1
hvs-miR2007	TC272654	2.5	523	544	Translation	Polyprotein	1	GO:0043169	uncharacterized protein partial
hvs-miR2007	TC253755	3	383	402	Cleavage	unknown function	1		
hvs-miR2007	TC254958	3	767	788	Cleavage	unknown function	1	GO:0003676;GO:0000398;GO:0005	rna-binding protein 5
hvs-miR2016	TC268937	3	361	382	Cleavage	unknown function	1		
hvs-miR393	TC249771	2	85	104	Cleavage	unknown function	1	GO:0000822;GO:0010011;GO:001C	auxin signaling f-box 1
hvs-miR393	TC257470	2	420	439	Cleavage	Protein AUXIN SIGNALIN	1	GO:0009734;GO:0000822	auxin signaling f-box 3
hvs-miR393	TC254168	2	1200	1219	Cleavage	unknown function	1	GO:0000822;GO:0010011;GO:001C	transport inhibitor response 1

hvs-miR393	CD663029	2	24	43	Cleavage	unknown function	1	
hvs-miR393	TC280604	2.5	633	652	Cleavage	unknown function	1	GO:0044431;GO:0048827;GO:0006 protein clp1 homolog
hvs-miR393	TC250749	2.5	207	226	Cleavage	unknown function	1	GO:0044431;GO:0048827;GO:0006 protein clp1 homolog
hvs-miR393	BI953281	3	210	229	Cleavage	unknown function	1	GO:0000822;GO:0010011;GO:0010 tir1
hvs-miR393	CX626993	3	64	83	Translation	unknown function	1	
hvs-miR395c	BU988654	2.5	81	100	Cleavage	Phosphodiesterase/alkaline p	1	
hvs-miR395c	TC248628	2.5	1054	1073	Cleavage	At1g14020	1	
hvs-miR395c	TC262830	3	381	400	Cleavage	Plastidic ATP sulfurylase	1	GO:0046686;GO:0004781;GO:0005 atp sulfurylase
hvs-miR395c	BQ756651	3	119	138	Cleavage	unknown function	1	
hvs-miR395c	TC281174	3	539	558	Cleavage	unknown function	1	
hvs-miR395c	DN160133	3	379	399	Cleavage	unknown function	1	
hvs-miR395c	DN159988	3	167	186	Translation	unknown function	1	GO:0009965;GO:0008757;GO:0008 ribosomal rna methyltransferase nop2-like
hvs-miR395c	BG366141	3	180	199	Cleavage	unknown function	1	GO:0000325;GO:0015079;GO:0005 potassium transporter 7-like
hvs-miR395c	TC276756	3	171	190	Cleavage	unknown function	1	GO:0000325;GO:0015079;GO:0005 potassium transporter 14
hvs-miR395c	BG368777	3	500	519	Translation	unknown function	1	
hvs-miR395o	TC275846	2.5	196	215	Cleavage	unknown function	1	GO:0006260;GO:0003697;GO:0005 single-stranded dna-binding mitochondrial
hvs-miR395o	CV059408	3	17	36	Cleavage	Similarity to ATPF3	1	
hvs-miR395o	TC249333	3	430	449	Translation	unknown function	1	
hvs-miR395o	TC260215	2.5	125	144	Cleavage	unknown function	1	GO:0006468;GO:0005524;GO:0004 tpa: leucine-rich repeat receptor-like protein kii
hvs-miR395o	TC278479	2.5	708	727	Cleavage	unknown function	1	GO:0016772 tpa: leucine-rich repeat receptor-like protein kii
hvs-miR395o	TC268144	3	368	387	Translation	VacJ family lipoprotein prec	1	
hvs-miR395o	TC269282	3	177	196	Translation	Homocysteine S-methyltran	1	GO:0033528;GO:0005886;GO:0008 homocysteine s-methyltransferase 4
hvs-miR395o	TC253520	3	450	469	Cleavage	unknown function	1	GO:0002161;GO:0004823;GO:0006 leucyl-trna cytoplasmic
hvs-miR5049b	TC256535	1	970	990	Cleavage	Expressed protein	1	
hvs-miR5049b	TC242358	1	980	1000	Cleavage	unknown function	1	GO:0008270;GO:0003676 family transposase isoform 1
hvs-miR5049b	TC255389	1	685	705	Cleavage	unknown function	1	GO:0006468;GO:0004674;GO:0005 protein kinase and pp2c-like domain-containing
hvs-miR5049b	TC239858	1.5	973	993	Cleavage	At3g03330/T21P5_25	1	GO:0016491;GO:0055114;GO:0006 dehydrogenase reductase sdr family member 7-
hvs-miR5049b	TC266552	1.5	1212	1232	Cleavage	GAMYB-binding protein	1	
hvs-miR5049b	TC246709	1	1278	1298	Cleavage	Glucose and ribitol dehydro	1	GO:0016491;GO:0055114;GO:0006 glucose and ribitol dehydrogenase-like protein
hvs-miR5049b	TC252029	2	884	904	Cleavage	unknown function	1	
hvs-miR5049b	BM376524	1.5	116	136	Translation	Phenylalanyl-tRNA synthet	1	
hvs-miR5049b	BU974512	1.5	309	329	Translation	Meiotically up-regulated ger	1	
hvs-miR5049b	BU988612	1.5	595	615	Cleavage	unknown function	1	GO:0055085;GO:0016021 uncharacterized transporter
hvs-miR5049b	CK569067	1.5	623	643	Translation	unknown function	1	
hvs-miR5049b	TC242133	1.5	769	789	Translation	Cyclic nucleotide-gated ion	1	GO:0006816;GO:0055085;GO:0005 cyclic nucleotide-gated ion channel 1
hvs-miR5049b	TC280947	1.5	449	469	Translation	unknown function	1	
hvs-miR5049b	TC268011	1.5	870	890	Cleavage	unknown function	1	
hvs-miR5049b	TC254020	1.5	935	955	Translation	unknown function	1	GO:0005681;GO:0000398 pre-mrna-processing-splicing factor 8
hvs-miR5049b	TC281296	1.5	1098	1118	Translation	unknown function	1	GO:0003700;GO:0043565;GO:0006 wrky transcription factor 44
hvs-miR5049b	TC269747	2	1318	1338	Cleavage	Hydrolase, alpha/beta fold f	1	GO:0008152;GO:0016787 aminoacylate hydrolase -like
hvs-miR5049b	TC262714	2	96	116	Cleavage	unknown function	1	GO:0005737;GO:0004830;GO:0006 predicted protein [Hordeum vulgare subsp. vul]
hvs-miR5049b	FD522424	2.5	519	539	Cleavage	Type II and III secretion sys	1	
hvs-miR5049b	TC267500	2.5	828	848	Cleavage	Early transcribed membrane	1	
hvs-miR5049b	TC263351	2	1359	1379	Cleavage	unknown function	1	
hvs-miR5049b	BI954430	2	352	372	Cleavage	Pathogenesis-related protein	1	GO:0009651;GO:0042742;GO:0005 pathogenesis-related protein 4

hvs-miR5049b	DN160611	2	276	296	Translation	unknown function	1	
hvs-miR5049b	TC242392	2	388	408	Cleavage	WIR1 protein	1	
hvs-miR5049b	TC265005	2	608	628	Cleavage	Pathogenesis-related protein 1	1	GO:0009651;GO:0042742;GO:0005 vacuolar defense protein
hvs-miR5049b	TC239033	2	645	665	Cleavage	Pathogenesis-related protein 1	1	GO:0009651;GO:0042742;GO:0005 pathogenesis-related protein 4
hvs-miR5049b	TC252977	2.5	883	903	Cleavage	unknown function	1	GO:0030001;GO:0046872 metal ion binding protein
hvs-miR5049b	TC247711	2	1183	1203	Translation	unknown function	1	
hvs-miR5049b	BJ450193	2.5	321	341	Cleavage	Pathogenesis-related protein 1	1	
hvs-miR5049b	CX626387	2.5	587	607	Translation	TSBP protein	1	
hvs-miR5049b	TC260883	2.5	505	525	Translation	unknown function	1	GO:0016630;GO:0009706;GO:0055 retinol dehydrogenase 14
hvs-miR5049b	TC254898	2.5	330	350	Cleavage	Predicted protein	1	
hvs-miR5049b	TC261514	2.5	612	632	Cleavage	Zinc finger protein	1	GO:0046872;GO:0005886 protein brevis radix-like 4-like
hvs-miR5049b	TC242241	2.5	785	805	Translation	Surface antigen protein 2	1	
hvs-miR5049b	TC271832	2.5	751	771	Cleavage	unknown function	1	
hvs-miR5049b	TC271580	2	83	103	Translation	Quinone reductase	1	
hvs-miR5049b	TC273020	2	309	329	Translation	Thaumatococcus-like protein PW1	1	
hvs-miR5049b	TC280052	2	373	393	Translation	Pathogenesis-related protein 1	1	
hvs-miR5049b	BQ762328	2	543	563	Translation	Pathogenesis-related protein 1	1	
hvs-miR5049b	TC253150	2.5	49	69	Translation	Calcium sensing protein	1	GO:0010035;GO:0005509;GO:0005 calcineurin b-like protein 4
hvs-miR5049b	TC266790	2.5	484	504	Cleavage	unknown function	1	
hvs-miR5049b	TC255672	2.5	607	627	Translation	Cytochrome P450 family pr	1	GO:0020037;GO:0016705;GO:0004 cytochrome p450 86a2
hvs-miR5049b	CK566281	2	41	61	Translation	HV1LRR1	1	GO:0006952;GO:0043531 disease resistance protein rpm1
hvs-miR5049b	TC248531	2.5	631	651	Translation	unknown function	1	
hvs-miR5049b	TC243412	2	458	478	Translation	Zinc finger, C3HC4 type far	1	
hvs-miR5049b	NP315666	2	629	649	Translation	unknown function	1	
hvs-miR5049b	TC281666	2	770	790	Translation	unknown function	1	GO:0009911;GO:0016926;GO:0016 ubiquitin-like-specific protease esd4-like
hvs-miR5049b	TC240649	2	696	716	Translation	Pathogenesis-related protein 1	1	
hvs-miR5049b	TC239078	2.5	596	616	Cleavage	unknown function	1	
hvs-miR5049b	TC250276	2	1007	1027	Translation	Biotin synthase	1	GO:0004076;GO:0051536;GO:0005 biotin synthase
hvs-miR5049b	TC257019	2	186	206	Translation	Vitellogenin-1 precursor (Vi	1	
hvs-miR5049b	AJ473037	3	188	208	Translation	unknown function	1	
hvs-miR5049b	TC258337	3	266	286	Translation	Protease inhibitor-like	1	GO:0004867;GO:0009611 subtilisin-chymotrypsin inhibitor-2a
hvs-miR5049b	CD057330	3	53	73	Cleavage	unknown function	1	
hvs-miR5049b	TC274711	3	587	607	Cleavage	TA9 protein-like	1	
hvs-miR5049b	CX627988	2.5	130	150	Translation	unknown function	1	
hvs-miR5049b	CX631852	2.5	93	113	Translation	unknown function	1	
hvs-miR5049b	BF266889	2.5	220	240	Translation	Endonuclease Staphylococci	1	
hvs-miR5049b	CB863687	3	59	79	Cleavage	Predicted protein	1	
hvs-miR5049b	BU989524	2.5	122	142	Translation	unknown function	1	
hvs-miR5049b	TC272428	2.5	336	356	Translation	Calcium homeostasis regula	1	
hvs-miR5049b	BY873084	2.5	201	221	Translation	unknown function	1	
hvs-miR5049b	BY869849	2.5	53	73	Translation	Embryonic abundant protein	1	GO:0008168;GO:0032259 uncharacterized protein loc100824390
hvs-miR5049b	TC269247	2.5	217	237	Translation	unknown function	1	
hvs-miR5049b	BY858312	2.5	90	110	Translation	Heat shock protein HslVU	1	
hvs-miR5049b	BG418841	2.5	136	156	Translation	Inositol monophosphatase	1	
hvs-miR5049b	CA005229	2.5	127	147	Translation	DNA-binding response regu	1	

hvs-miR5049b	AL505935	2.5	208	228	Translation	ATPase	1	
hvs-miR5049b	GH224593	2.5	160	180	Translation	Auxin-responsive protein IA	1	GO:0006355;GO:0046983;GO:0005 predicted protein [Hordeum vulgare subsp. vul;
hvs-miR5049b	TC275256	2.5	539	559	Translation	Transcriptional regulator, L3	1	
hvs-miR5049b	CB863387	2.5	506	526	Translation	unknown function	1	GO:0097159;GO:1901363 rna recognition domain containing protein
hvs-miR5049b	TC250646	2.5	567	587	Translation	unknown function	1	
hvs-miR5049b	TC262159	2.5	151	171	Translation	unknown function	1	GO:0047513;GO:0005975 alpha-l-fucosidase 2
hvs-miR5049b	TC258402	2.5	541	561	Translation	Histidine utilization repress	1	
hvs-miR5049b	TC278320	2.5	605	625	Translation	Uncharacterized protein At1	1	GO:0005737;GO:0016788;GO:0003 holliday junction resolvase-like
hvs-miR5049b	TC270774	2.5	596	616	Translation	unknown function	1	GO:0009507 protein
hvs-miR5049b	TC264401	2.5	442	462	Translation	COG0730	1	
hvs-miR5049b	TC242874	2.5	564	584	Translation	Haploid germ cell-specific n	1	GO:0006468;GO:0005524;GO:0004 serine threonine-protein kinase haspin-like
hvs-miR5049b	CA015005	2.5	294	314	Translation	Emb CAB62636.1	1	GO:0008219;GO:0005739;GO:0005 dnaJ domain containing protein
hvs-miR5049b	TC243164	2.5	629	649	Translation	unknown function	1	
hvs-miR5049b	BU970443	2.5	335	355	Translation	Phospholipid-hydroperoxide	1	GO:0006979;GO:0046686;GO:0005 glutathione partial
hvs-miR5049b	FD518121	2.5	90	110	Translation	unknown function	1	
hvs-miR5049b	TC248672	2.5	576	596	Translation	unknown function	1	GO:0003746;GO:0006511;GO:0005 transcription elongation factor b polypeptide 1
hvs-miR5049b	TC257763	2.5	489	509	Translation	Chitinase 2	1	GO:0008843;GO:0006032;GO:0016 protein
hvs-miR5049b	TC242062	2.5	618	638	Translation	unknown function	1	
hvs-miR5049b	TC240250	2.5	495	515	Translation	unknown function	1	GO:0003746;GO:0006511;GO:0005 transcription elongation factor b polypeptide 1
hvs-miR5049b	TC280959	2.5	473	493	Translation	unknown function	1	
hvs-miR5049b	TC246915	2.5	725	745	Translation	Pathogenesis-related protein	1	
hvs-miR5049b	TC265394	2.5	675	695	Translation	Expressed protein	1	
hvs-miR5049b	TC257182	2.5	736	756	Translation	unknown function	1	GO:0005509 uncharacterized protein loc101765460
hvs-miR5049b	TC264578	2.5	743	763	Translation	SOUL heme-binding protei	1	GO:0009535;GO:0010287 heme-binding-like protein chloroplastic-like
hvs-miR5049b	TC247725	2.5	260	280	Translation	Triosephosphate isomerase,	1	GO:0032504;GO:0080022;GO:0005 triosephosphate isomerase
hvs-miR5049b	TC240134	2.5	493	513	Translation	Haploid germ cell-specific n	1	GO:0004672;GO:0006468;GO:0005 serine threonine-protein kinase haspin
hvs-miR5049b	TC244930	2.5	680	700	Translation	Pathogenesis-related protein	1	
hvs-miR5049b	TC261278	3	575	595	Cleavage	NAD dependent epimerase/c	1	GO:0044237;GO:0016491;GO:0050 bifunctional dihydroflavonol 4-reductase flavai
hvs-miR5049b	TC242170	2.5	860	880	Translation	unknown function	1	GO:0043231;GO:0005737 golgin candidate 5-like
hvs-miR5049b	TC258107	2.5	755	775	Translation	unknown function	1	
hvs-miR5049b	TC249253	2.5	868	888	Translation	CREG2-protein-like	1	GO:0005773;GO:0016491;GO:0055 protein creg1
hvs-miR5049b	TC261500	3	655	675	Cleavage	NAD dependent epimerase/c	1	GO:0044710;GO:0044237;GO:0050 bifunctional dihydroflavonol 4-reductase flavai
hvs-miR5049b	TC238627	2.5	878	898	Translation	Ubiquitin carrier protein	1	GO:0009910;GO:0033523;GO:0005 ubiquitin-conjugating enzyme e2 2-like
hvs-miR5049b	TC275881	2.5	866	886	Translation	Glutathione S-transferase G	1	GO:0009628;GO:0009791;GO:0042 glutathione s-transferase gstu6
hvs-miR5049b	TC251923	2.5	965	985	Translation	Glutathione S-transferase T	1	
hvs-miR5049b	TC258503	2.5	941	961	Translation	ABA induced plasma memb	1	
hvs-miR5049b	TC268439	2.5	1041	1061	Translation	Kinase binding protein	1	GO:0009543;GO:0019898;GO:0005 psbp-like protein chloroplastic-like
hvs-miR5049b	TC279988	2.5	1053	1073	Translation	Hydrolase, alpha/beta fold f	1	GO:0033473;GO:0080030;GO:0048 alpha beta fold family expressed
hvs-miR5049b	TC248415	2.5	642	662	Translation	unknown function	1	
hvs-miR5049b	TC271642	2.5	928	948	Translation	Hydrolase, alpha/beta fold f	1	GO:0033473;GO:0080030;GO:0048 methylesterase 17-like
hvs-miR5049b	TC253336	2.5	863	883	Translation	Cinnamyl alcohol dehydrog	1	GO:0009626;GO:0046872;GO:0005 cinnamyl alcohol dehydrogenase 5
hvs-miR5049b	TC239589	2.5	887	907	Translation	Efflux transporter, RND fan	1	
hvs-miR5049b	TC280177	3	517	537	Translation	unknown function	1	GO:0003676;GO:0005634;GO:0008 sgf29 tudor-like domain-containing protein
hvs-miR5049b	TC267934	2.5	1086	1106	Translation	Glutathione S-transferase G	1	GO:0009704;GO:0048527;GO:0046 glutathione s-transferase gst 34
hvs-miR5049b	TC258286	2.5	409	429	Translation	Phospholipid hydroperoxide	1	GO:0006979;GO:0046686;GO:0005 glutathione peroxidase

hvs-miR5049b	TC242275	2.5	1126	1146	Translation	Glucan endo-1,3-beta-D-glu 1	GO:0004553;GO:0005975;GO:0043	endo-beta- -glucanase
hvs-miR5049b	TC241575	2.5	1145	1165	Translation	Delta(7)-sterol-C5(6)-desatu 1	GO:0006633;GO:0005506;GO:0050	delta-7-sterol-c5
hvs-miR5049b	TC238623	2.5	1168	1188	Translation	HvCBF5		
hvs-miR5049b	TC244590	2.5	1249	1269	Translation	unknown function		
hvs-miR5049b	TC245800	2.5	971	991	Translation	Triosephosphate isomerase, 1	GO:0032504;GO:0080022;GO:0005	triosephosphate isomerase
hvs-miR5049b	TC244458	2.5	1304	1324	Translation	unknown function	GO:0008234;GO:0006508	probable ubiquitin-like-specific protease 2b-lik
hvs-miR5049b	TC248888	2.5	684	704	Translation	Histone H3	GO:0000786;GO:0003677;GO:0006	histone h3
hvs-miR5049b	TC238785	2.5	1403	1423	Translation	Acetylxyylan esterase 1 precu 1		
hvs-miR5049b	TC255529	2.5	1388	1408	Translation	Annexin p33	GO:0009414;GO:0009651;GO:0005	annexin p35
hvs-miR5049b	TC270215	2.5	1168	1188	Translation	unknown function		
hvs-miR5049b	TC247268	2.5	1562	1582	Translation	unknown function	GO:0005886;GO:0005783	uncharacterized protein loc100832879
hvs-miR5049b	TC258392	2.5	1537	1557	Translation	unknown function	GO:0016773;GO:0006139;GO:0005	deoxycytidine kinase
hvs-miR5049b	TC242691	3	615	634	Cleavage	unknown function	GO:0005773;GO:0004046;GO:0010	aminoacylase-1
hvs-miR5049b	TC262694	3	244	264	Translation	Glutathione S-transferase G: 1	GO:0009704;GO:0048527;GO:0046	glutathione s-transferase gstu6
hvs-miR5049b	EX593083	3	59	79	Translation	unknown function		
hvs-miR5049b	EX593083	3	375	395	Translation	unknown function		
hvs-miR5049b	TC240827	3	805	825	Cleavage	Predicted protein		
hvs-miR5049b	TC261486	3	1006	1026	Translation	Isoflavone reductase-like pr 1	GO:0009807;GO:0000166	isoflavone reductase homolog
hvs-miR5049b	TC274398	3	121	141	Translation	unknown function		
hvs-miR5049b	DN158282	3	234	253	Cleavage	unknown function		
hvs-miR5049b	CA006980	3	315	335	Translation	Nitric oxide synthase		
hvs-miR5049b	BY875458	2.5	192	212	Translation	unknown function		
hvs-miR5049b	GH218772	3	150	170	Translation	unknown function		
hvs-miR5049b	TC275787	3	431	451	Translation	unknown function		
hvs-miR5049b	CA015193	3	82	102	Translation	unknown function		
hvs-miR5049b	TC264531	3	386	406	Translation	unknown function		
hvs-miR5049b	TC262369	3	127	147	Translation	CDNA6 protein		
hvs-miR5049b	TC273209	3	464	484	Translation	unknown function	GO:0003777;GO:0005875;GO:0005	uncharacterized protein loc100381510
hvs-miR5049b	TC255566	3	298	318	Translation	Leucine Rich Repeat family 1		
hvs-miR5049b	TC264155	3	423	443	Translation	unknown function	GO:0006470;GO:0046872;GO:0004	protein phosphatase 2c family protein
hvs-miR5049b	TC255104	3	424	444	Translation	unknown function		
hvs-miR5049b	TC255081	3	508	528	Translation	Uncharacterized protein EN: 1		
hvs-miR5049b	BG368276	3	459	479	Translation	unknown function	GO:0009941;GO:0046686;GO:0004	transketolase 1
hvs-miR5049b	CA013466	3	384	404	Translation	unknown function		
hvs-miR9674	TC265885	2.5	485	504	Translation	Dehydration responsive elen 1	GO:0006351	dre binding factor
hvs-miR9674	TC244765	3	142	161	Cleavage	Heme oxygenase 2	GO:0006788;GO:0004392;GO:0010	probable inactive heme oxygenase chloroplasti
hvs-miR9674	TC275768	3	511	530	Cleavage	Predicted protein	GO:0003676;GO:0000166	rna and export factor-binding protein 2-like
hvs-miR9674	DN181354	3	501	520	Translation	unknown function	GO:0005886;GO:0006468;GO:0005	serine threonine-protein kinase ctr1
hvs-miR9674	CX631621	3	111	130	Translation	TNP2-like transposase prote 1		
hvs-miR9674	TC264830	3	250	269	Cleavage	Tetratricopeptide repeat prot 1	GO:0005773	protein unc-45-a-like protein
hvs-miR9674	TC248007	3	626	645	Cleavage	Tetratricopeptide repeat prot 1	GO:0005773	protein unc-45-a-like protein
hvs-miR5067	BU970053	2.5	366	385	Translation	unknown function		
hvs-miR5067	TC254245	3	294	313	Translation	unknown function		
hvs-miR5067	TC255937	3	1075	1095	Translation	Expressed protein		

miRNA Acc.	Target Acc.	Expectation	Target s	Target	Inhibition	Target Desc.	Multiplicity	GO annotation
hvs-n01	TC259113	2.5	315	335	Translation	unknown function	1	GO:0008168;EC:2.1.1.0 probable o-methyltransferase 2-like
hvs-n01	TC268253	2.5	556	576	Translation	O-methyltransferase far	1	GO:0008168;EC:2.1.1.0 probable o-methyltransferase 2-like
hvs-n01	AV836714	3	276	296	Cleavage	Histidine kinase	1	GO:0005034;GO:0009414;GO:0005034 histidine kinase 2
hvs-n01	DN159601	2.5	156	175	Translation	Proline-rich protein	1	
hvs-n01	TC277073	3	190	209	Cleavage	unknown function	1	
hvs-n01	GH226061	3	141	160	Translation	unknown function	1	
hvs-n01	TC242887	3	568	587	Cleavage	unknown function	1	
hvs-n01	AV835517	3	298	316	Translation	unknown function	1	
hvs-n02	DN185097	2	90	110	Cleavage	Cleavage and polyaden	1	
hvs-n02	TC253481	3	551	571	Cleavage	Zinc finger, C3HC4 ty	1	GO:0046872;GO:0008270 tpa: ring zinc finger domain superfamily protein
hvs-n02	TC259390	3	457	477	Translation	unknown function	1	GO:0006457;GO:0051082;GO:0006457 heat shock protein binding protein
hvs-n02	TC280887	3	308	328	Translation	unknown function	1	GO:0006457;GO:0051082;GO:0006457 heat shock protein binding protein
hvs-n02	TC241013	3	199	219	Translation	unknown function	1	GO:0006457;GO:0051082;GO:0006457 heat shock protein binding protein
hvs-n02	AJ474518	3	376	396	Cleavage	unknown function	1	
hvs-n02	TC268287	3	1247	1267	Cleavage	unknown function	1	GO:0043169;GO:0044238;GO:0043169 zinc finger ccch domain-containing protein 19-like
hvs-n03	TC277925	2.5	386	407	Cleavage	Peroxidase 8	1	GO:0006468;GO:0005524;GO:0006468 uncharacterized protein loc100838142 isoform 1
hvs-n03	TC246508	2.5	1381	1402	Cleavage	Sperm protamine P1 (F	1	GO:0004672 uncharacterized protein loc100838142 isoform 1
hvs-n03	TC263785	3	569	588	Cleavage	unknown function	1	
hvs-n03	TC265999	3	567	586	Cleavage	unknown function	1	
hvs-n04	TC249085	2	585	604	Cleavage	Amidase family protei	1	GO:0016884;GO:0016740;EC:6.3.5.1 amidase family expressed
hvs-n04	TC275024	2	1303	1322	Cleavage	Amidase family protei	1	GO:0016884;EC:6.3.5.0 amidase family expressed
hvs-n04	TC280569	3	274	293	Cleavage	SJCHGC01974 protein	1	
hvs-n04	BI952019	3	443	462	Cleavage	TonB-dependent recep	1	
hvs-n04	TC247508	2	11	30	Translation	unknown function	1	
hvs-n04	TC242564	2	899	918	Translation	unknown function	1	
hvs-n04	TC252077	3	48	67	Translation	Telomere binding prote	1	GO:0003677;GO:0003682;GO:0003677 telomere-binding protein 1
hvs-n04	TC248946	3	211	230	Cleavage	DNA-directed RNA po	1	GO:0003899;GO:0005665;GO:0003899 dna-directed rna polymerase ii subunit rpb1-like
hvs-n04	TC280441	3	163	182	Translation	Contig An02c0450, co	1	
hvs-n05	TC265376	2.5	374	393	Cleavage	Deoxyhypusine hydrox	1	GO:0016829 deoxyhypusine hydroxylase-b
hvs-n06	BF621630	3	562	581	Cleavage	unknown function	1	GO:0004143;GO:0007205;GO:0004143 sphingoid long-chain bases kinase 1
hvs-n06	BI952145	3	481	500	Cleavage	T8F5.13 protein	1	GO:0051436;GO:0043123;GO:0051436 ubiquitin-like protein
hvs-n06	BG366135	3	730	749	Cleavage	unknown function	1	
hvs-n06	TC269438	3	207	226	Cleavage	unknown function	1	
hvs-n06	TC259782	3	174	193	Cleavage	Arylsulfatase	1	
hvs-n06	CD056116	3	73	92	Cleavage	unknown function	1	
hvs-n06	TC278709	3	127	146	Cleavage	Ribose import ATP-bir	1	
hvs-n06	TC261877	3	563	582	Translation	unknown function	1	GO:0003700;GO:0008270;GO:0003700 nf-x1-type zinc finger protein nfx12-like
hvs-n06	TC250166	3	678	697	Cleavage	Transcriptional regulat	1	
hvs-n06	TC279091	3	805	824	Translation	Coproporphyrinogen II	1	GO:0006779;GO:0004109;GO:0006779 coproporphyrinogen iii oxidase
hvs-n06	TC263153	3	1259	1278	Translation	Coproporphyrinogen II	1	GO:0006779;GO:0004109;GO:0006779 coproporphyrinogen iii oxidase
hvs-n06	BE195813	3	243	263	Cleavage	Polyubiquitin	1	
hvs-n06	BF267126	3	277	297	Cleavage	Polyubiquitin	1	
hvs-n06	EX577298	3	662	681	Translation	Rac GTPase activating	1	GO:0007165;GO:0005622 rac gtpase activating protein

hvs-n06	TC249195	3	592	611	Cleavage	Glucose-6-phosphate 1	1	GO:0005525	atp binding protein
hvs-n06	TC245409	3	457	476	Translation	unknown function	1	GO:0007165;GO:0005622	rac gtpase activating protein
hvs-n06	TC274718	3	11	30	Translation	Cytochrome b	1		
hvs-n06	TC274695	3	864	883	Translation	unknown function	1	GO:0006950	u-box domain-containing protein 35-like
hvs-n06	TC247650	3	499	518	Cleavage	unknown function	1	GO:0005525	atp binding protein
hvs-n07	TC267321	0.5	624	644	Cleavage	Monosaccharide transp	1	GO:0009624;GO:0005773;GO:0005525	sugar transport protein 1
hvs-n07	TC256317	1	394	414	Cleavage	Predicted protein	1	GO:0006468;GO:0005524;GO:0005525	lrr receptor-like serine threonine-protein kinase
hvs-n07	TC242491	1	508	528	Cleavage	Leucine Rich Repeat f	1	GO:0006468;GO:0005524;GO:0005525	lrr receptor-like serine threonine-protein kinase
hvs-n07	TC239646	1	653	673	Cleavage	Glutathione S-transfer	1	GO:0016740	glutathione transferase
hvs-n07	CA024142	1	66	85	Cleavage	unknown function	1		
hvs-n07	CD055494	1.5	505	525	Cleavage	Afl10-protein	1	GO:0044424	clathrin interactor epsin 1-like
hvs-n07	TC249688	2	16	36	Cleavage	unknown function	1		
hvs-n07	TC276508	2	60	80	Cleavage	Metallo-beta-lactamase	1	GO:0016787	predicted protein [Hordeum vulgare subsp. vulgare]
hvs-n07	TC251948	1.5	1266	1286	Cleavage	unknown function	1	GO:0043987;GO:0000775;GO:0005525	serine threonine-protein kinase aurora-3
hvs-n07	TC256104	2	678	698	Cleavage	unknown function	1	GO:0005743;GO:0005085;GO:0005525	graves disease carrier protein
hvs-n07	TC268732	2	9	29	Cleavage	BTH-induced ERF tr	1	GO:0006355;GO:0003677;GO:0005525	ap2-related transcription factor
hvs-n07	TC280528	2	737	757	Cleavage	NADH dehydrogenase	1		
hvs-n07	TC261210	3	1136	1156	Cleavage	unknown function	1	GO:0050660;GO:0005507;GO:0005525	electron transfer flavoprotein subunit mitochondrial
hvs-n07	TC267818	3	253	273	Cleavage	unknown function	1		
hvs-n07	AJ469724	2.5	150	170	Cleavage	unknown function	1		
hvs-n07	BJ446874	3	380	400	Cleavage	unknown function	1		
hvs-n07	AV833224	2.5	399	419	Translation	unknown function	1		
hvs-n07	TC244960	3	951	971	Cleavage	unknown function	1	GO:0006468;GO:0004674;GO:0005525	cbl-interacting serine threonine-protein kinase 8-like
hvs-n07	TC279618	2.5	297	317	Cleavage	AGAP011395-PA	1	GO:0006633;GO:0016491;GO:0005525	inositolphosphorylceramide-b c-26 hydroxylase
hvs-n07	CX632020	3	167	187	Cleavage	C6 zinc finger domain	1		
hvs-n07	TC247217	3	549	569	Cleavage	Kinesin motor domain	1	GO:0007018;GO:0005875;GO:0005525	kinesin-like protein kif19
hvs-n07	TC250975	3	514	533	Cleavage	Hexokinase-1	1		
hvs-n07	BQ472582	3	511	531	Translation	J2L	1		
hvs-n08	TC259934	3	633	652	Translation	50S ribosomal protein	1	GO:0022626;GO:0042254;GO:0005525	50s ribosomal protein chloroplastic-like
hvs-n08	TC261371	3	1379	1398	Cleavage	Uroporphyrinogen dec	1	GO:0004853;GO:0046686;GO:0005525	uroporphyrinogen decarboxylase
hvs-n10	TC243289	1.5	252	272	Cleavage	Acetolactate synthase	1	GO:0050660;GO:0030976;GO:0005525	acetolactate partial
hvs-n10	TC277905	2	87	107	Cleavage	Phospholipase-like pro	1		
hvs-n10	CV057710	2	62	82	Cleavage	Phospholipase-like pro	1		
hvs-n10	CV062260	2	62	82	Cleavage	Phospholipase-like pro	1		
hvs-n10	TC254118	2	499	519	Cleavage	Acetolactate synthase	1	GO:0050660;GO:0030976;GO:0005525	acetolactate synthase
hvs-n10	FD520403	2.5	360	380	Translation	unknown function	1	GO:0008234;GO:0006508	ubiquitin-like-specific protease 2
hvs-n10	TC239440	2.5	778	797	Cleavage	unknown function	1		
hvs-n10	BI777802	3	205	224	Translation	Non-histone chromoso	1		
hvs-n10	TC243855	3	565	584	Translation	Enolase	1	GO:0016020	uncharacterized protein loc100825844
hvs-n10	TC244917	3	382	401	Translation	unknown function	1		
hvs-n10	TC241445	3	490	509	Translation	unknown function	1	GO:0016020	caax amino terminal protease family protein
hvs-n10	BJ459322	3	214	233	Translation	Predicted protein	1		
hvs-n12	DN157929	3	600	619	Cleavage	Oxidoreductase, aldo/k	1		
hvs-n12	TC246470	3	365	385	Cleavage	unknown function	1	GO:0004822;GO:0002161;GO:0005525	isoleucyl-trna cytoplasmic
hvs-n12	CD056125	3	185	204	Cleavage	Histidinol dehydrogen	1	GO:0009411;GO:0051287;GO:0005525	histidinol chloroplastic-like

hvs-n12	TC267978	3	284	303	Cleavage	Histidinol dehydrogenase	1	GO:0009411;GO:0051287;GO:0005128;GO:0005128;GO:0005128
hvs-n12	TC239435	3	241	260	Cleavage	Histidinol dehydrogenase	1	GO:0009411;GO:0051287;GO:0005128;GO:0005128;GO:0005128
hvs-n13	TC277400	3	147	167	Translation	unknown function	1	
hvs-n13	TC257459	3	662	682	Cleavage	Indole-3-glycerol phosphate	1	GO:0005507;GO:0009570;GO:0005507;GO:0005507;GO:0005507
hvs-n13	TC264206	3	838	857	Translation	Ribosomal protein L19	1	GO:0005730;GO:0003735;GO:0005730;GO:0005730;GO:0005730
hvs-n14	TC252903	0	961	981	Cleavage	CFM2	1	GO:0003723
hvs-n14	TC254574	0.5	762	782	Cleavage	unknown function	1	GO:0005739;GO:0004003;GO:0005739;GO:0005739;GO:0005739
hvs-n14	TC244992	1	475	495	Cleavage	Hydroxypyruvate reductase	1	GO:0051287;GO:0005777;GO:0005777;GO:0005777;GO:0005777
hvs-n14	TC245238	1.5	1653	1673	Cleavage	unknown function	1	GO:0004176;GO:0046872;GO:0004176;GO:0004176;GO:0004176
hvs-n14	TC252597	1.5	1120	1140	Cleavage	unknown function	1	GO:0046872;GO:0008270
hvs-n14	CK566710	1.5	97	117	Cleavage	TAK14	1	GO:0006468;GO:0005524;GO:0005524;GO:0005524;GO:0005524
hvs-n14	DN159362	1.5	473	493	Cleavage	unknown function	1	
hvs-n14	TC239725	2	745	765	Cleavage	unknown function	1	
hvs-n14	TC244199	2	725	745	Cleavage	unknown function	1	GO:0008312;GO:0005525;GO:0005525;GO:0005525;GO:0005525
hvs-n14	TC240673	1.5	759	779	Translation	unknown function	1	GO:0009941;GO:0010177;GO:0009941;GO:0009941;GO:0009941
hvs-n14	TC273832	1.5	384	404	Cleavage	unknown function	1	GO:0010508;GO:0003677;GO:0003677;GO:0003677;GO:0003677
hvs-n14	BQ468979	2	282	302	Cleavage	Pollen coat oleosin-gly	1	
hvs-n14	TC253359	2.5	655	675	Cleavage	Ribulose biphosphate	1	GO:0005618;GO:0046863;GO:0005618;GO:0005618;GO:0005618
hvs-n14	AL501466	1.5	132	151	Cleavage	unknown function	1	
hvs-n14	BQ766864	2.5	378	398	Cleavage	unknown function	1	
hvs-n14	TC249054	3	851	871	Cleavage	Plastidic 2-oxoglutarate	1	GO:0009624;GO:0009941;GO:0009941;GO:0009941;GO:0009941
hvs-n14	TC265845	3	1041	1061	Cleavage	Fasciclin-like protein F	1	
hvs-n14	TC273876	3	889	909	Cleavage	unknown function	1	
hvs-n14	TC256851	2.5	468	488	Cleavage	Pentatricopeptide (PPR)	1	
hvs-n14	TC271886	2.5	615	635	Translation	Cysteine proteinase	1	GO:0008234;GO:0006508
hvs-n14	BE231018	2.5	26	46	Cleavage	unknown function	1	GO:0016787
hvs-n14	TC275228	2.5	307	327	Translation	unknown function	1	GO:0016020;GO:0006633;GO:0006633;GO:0006633;GO:0006633
hvs-n14	BM444318	3	168	188	Cleavage	Carboxy-terminal proc	1	
hvs-n14	BM368186	3	118	138	Cleavage	unknown function	1	
hvs-n14	TC275014	2	863	882	Translation	ER lumen protein retain	1	GO:0046923;GO:0006621;GO:0006621;GO:0006621;GO:0006621
hvs-n14	TC251378	3	247	267	Translation	unknown function	1	GO:0008270;GO:0005634
hvs-n14	TC238576	3	912	932	Translation	HvCBF10B	1	GO:0006351
hvs-n14	TC249924	3	474	494	Translation	Myosin heavy chain-lil	1	
hvs-n14	TC247157	3	8	28	Translation	unknown function	1	
hvs-n14	EX583948	3	45	65	Translation	unknown function	1	
hvs-n14	TC258960	3	698	718	Cleavage	unknown function	1	
hvs-n14	TC244458	3	1308	1328	Translation	unknown function	1	GO:0008234;GO:0006508
hvs-n14	TC242275	3	1130	1150	Translation	Glucan endo-1,3-beta-l	1	GO:0004553;GO:0005975;GO:0005975;GO:0005975;GO:0005975
hvs-n14	TC238627	3	882	902	Translation	Ubiquitin carrier protei	1	GO:0009910;GO:0035523;GO:0009910;GO:0009910;GO:0009910
hvs-n14	TC245270	3	831	851	Translation	unknown function	1	GO:0008233;GO:0005886;GO:0005886;GO:0005886;GO:0005886
hvs-n14	TC240134	3	497	517	Translation	Haploid germ cell-spec	1	GO:0004672;GO:0006468;GO:0006468;GO:0006468;GO:0006468
hvs-n14	TC265394	3	679	699	Translation	Expressed protein	1	
hvs-n14	TC262938	3	274	294	Translation	Predicted protein	1	
hvs-n14	TC256452	3	650	670	Translation	unknown function	1	GO:0016491;GO:0010181;GO:0010181;GO:0010181;GO:0010181
hvs-n14	TC242874	3	568	588	Translation	Haploid germ cell-spec	1	GO:0006468;GO:0005524;GO:0005524;GO:0005524;GO:0005524

hvs-n14	TC255081	3	512	532	Translation	Uncharacterized protei	1	
hvs-n14	CA005944	3	241	261	Translation	Partial_Kinase	1	GO:0006468;GO:0004674;GO:0005102
hvs-n14	BJ480160	3	18	38	Translation	Beta adaptin-like prote	1	GO:0008565;GO:0016192;GO:0005201
hvs-n14	TC259679	3	446	466	Translation	unknown function	1	GO:0090304
hvs-n14	BM101190	3	317	337	Translation	unknown function	1	
hvs-n14	BG367691	3	198	217	Cleavage	Dead/deah box helicase	1	
hvs-n14	TC250766	3	1171	1191	Translation	Auxin response factor	1	GO:0006355;GO:0003677;GO:0005082
hvs-n14	TC257663	3	1152	1172	Translation	Methyltransferase-like	1	GO:0032259;GO:0009507;GO:0005201
hvs-n15	TC242936	2.5	69	89	Cleavage	unknown function	1	GO:0006047;GO:0005886;GO:0005201
hvs-n15	TC248022	3	260	280	Translation	Expressed protein	1	GO:0008017;GO:0010005;GO:0005201
hvs-n15	TC270215	3	512	531	Cleavage	unknown function	1	
hvs-n15	TC273040	3	457	477	Cleavage	Expressed protein, 3'-p	1	
hvs-n16	TC280323	3	319	339	Cleavage	Cytochrome c oxidase	1	
hvs-n16	TC261932	3	184	204	Translation	unknown function	1	
hvs-n16	DN177768	2.5	271	291	Cleavage	L3mbtl3 protein	1	
hvs-n16	FD521136	3	129	148	Cleavage	unknown function	1	GO:0051287;GO:0009561;GO:0005201
hvs-n16	FD521186	3	478	497	Cleavage	unknown function	1	
hvs-n16	TC246526	3	269	289	Translation	SOS2-like protein kina	1	
hvs-n16	BM369309	3	286	305	Translation	Auxin-responsive prote	1	GO:0006355;GO:0046983;GO:0005201
hvs-n16	TC256642	3	365	384	Translation	unknown function	1	
hvs-n16	TC270473	3	327	346	Cleavage	unknown function	1	
hvs-n16	DN181180	3	40	59	Translation	unknown function	1	
hvs-n16	DN187796	3	339	358	Translation	ABC transporter perme	1	
hvs-n16	BG309912	3	291	310	Translation	Predicted protein	1	
hvs-n17	BF259863	3	613	634	Cleavage	unknown function	1	GO:0016020
hvs-n17	FD519759	3	560	581	Translation	unknown function	1	GO:0016301;GO:0016310;GO:0005201
hvs-n17	TC252223	3	960	979	Cleavage	unknown function	1	GO:0008233;GO:0030163;GO:0005201
hvs-n17	BJ460348	3	298	317	Translation	Exostosin-1	1	GO:0050508;GO:0031227;EC:2.4.1.1
hvs-n18	TC251089	3	573	593	Cleavage	E3 ubiquitin-protein lig	1	GO:0016568;GO:0048731;GO:0005201
hvs-n18	TC247855	3	333	353	Cleavage	unknown function	1	GO:0005507;GO:0009055;GO:0005201
hvs-n18	TC280830	3	1003	1023	Cleavage	unknown function	1	GO:0007018;GO:0005875;GO:0005201