Identification and Analysis of miRNAs and siRNAs in *Botrytis cinerea*

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**Abstract**

Small RNAs in *Botrytis cinerea* were analyzed via high-throughput sequencing on BGISEQ-500 platform. A total of 8 novel miRNAs and 110 novel siRNAs were predicted. Sequence information, construction, length distribution, base bias and expression levels of miRNAs and siRNAs were determined as well. Through GO and KEGG enrichment analysis, the miRNA target genes are mostly located in membrane and organelle, possessed binding and catalytic activities, and involved in signal transduction and carbohydrate metabolism. The results will provide a theoretical foundation for understanding the developmental and pathogenic mechanisms of *B. cinerea* at the transcriptional level.

**Keywords**

*Botrytis cinerea*, MicroRNA, Small Interfering RNA, Biological Function

1. Introduction

*Botrytis cinerea* is a necrotrophic plant pathogen with a broad host range, which can cause gray mold disease on crops, fruits and vegetables. This notorious fungus infects nearly all tissues of hosts at both pre-harvest and post-harvest stages, and leads to a huge economic loss worldwide. Owing to the importance in agricultural production, it has been ranked as the second most important plant-pathogenic fungus, and becomes one of the most extensively investigated pathogens [1]. Controlling this pathogen is difficult because of its various attack modes, great reproductive output, high evolutionary potential, and ability to survive for extended periods as conidia and/or small hardened mycelia masses called sclerotia. The application of synthetic fungicide is a conventional but not

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an adequate strategy due to developed resistant strains and adverse effects on the environment and human health [2] [3]. Therefore, exploring the pathogenic mechanisms of *B. cinerea* will provide a fundamental basis for developing new effective and safe control strategies. So far, a gapless genome sequence for *B. cinerea* strain B05.10 has been reported [4], and many advances have been achieved on the developmental and pathogenetic processes of *B. cinerea*, specifically on functional roles of genes in growth, virulence, metabolism, signaling and stress response [5] [6] [7]. These findings indicate the multigenic, variable, and sophisticated nature of necrotrophic pathogenicity of *B. cinerea*. Exploring more specific regulatory networks is necessary.

RNA has received extensive attention and it has been one of the most popular areas of life science research for nearly a decade. Non-coding RNA (ncRNA) does not encode a protein and performs the biological functions at the RNA level, such as ribosomal RNA (rRNA), transfer RNA (tRNA), microRNA (miRNA), small nuclear RNA, small interfering RNA (siRNA) and long non-coding RNA (lncRNA) [8] [9]. Among them, miRNAs are small non-coding RNAs of about 20 - 24 nucleotides, which can inhibit the translation of proteins by binding to 3’-UTR of the target mRNA [10]. Some studies found that miRNAs could interact directly with proteins to regulate gene expression or influence epigenetic mechanisms. Another, siRNAs are double-stranded RNAs of 20 - 25 nt. A guide strand of siRNA is selected and incorporated into the RNA-induced silencing complex (RISC). The siRNA guides RISC to fully complementary sites on target RNA that is then sequence-specifically cleaved by the Argonaute (Ago) protein. This process is named as RNA interference (RNAi) which leads to transcriptional or post-transcriptional gene silencing [11]. Although miRNA and siRNA share many similarities, both are short duplex RNA molecules that exert gene silencing effects by targeting mRNA, yet their mechanisms of action are distinct. The major difference between siRNA and miRNA is that the former is highly specific with only one mRNA target, whereas the latter has multiple targets. Many evidences have indicated that miRNA and siRNA could participate in gene expression, chromosome structure modification, cell differentiation, epigenetic regulation, and human disease. However, the identification and biological function analysis of miRNA and siRNA in fungal pathogens are less reported. In this study, small RNAs in *B. cinerea* were sequenced via high-throughput transcriptomic technology. The detected miRNAs and siRNAs were characterized and target genes of miRNAs were predicted. The results will provide a theoretical foundation for understanding pathogenic genes and regulatory pathways of *B. cinerea* at the transcriptional level.

2. Materials and Methods

2.1. Fungal Physiological Measurement

*Botrytis cinerea* was isolated from a naturally infected tomato fruit with a typical grey mold symptom. The genetic background of fungus has been identified by
morphological observation and rDNA-internal transcribed spacer analysis in the preliminary experiments. The fungus was cultivated on a potato dextrose agar (PDA) plate at 25°C. To evaluate the mycelial growth, a mycelial agar disk (0.5 cm in diameter) was placed in the center of a 9 cm diameter petri dish containing 25 mL PDA. During 10 days of culturing at 25°C, radial growth was measured daily by the decussation method. Meanwhile, the mycelial phenotype was microscopically observed using a Nikon Eclipse Ni-U microscope (Nikon, Japan). Tomato fruit at commercial maturity were bought from local market. After disinfection by 2% sodium hypochlorite, fruit were wounded at the equator utilizing a sterile needle and inoculated with 10 μL spore suspension (1 × 10⁴ spores/mL). The lesion diameter of inoculated fruit was recorded in every two days.

2.2. Small RNA Sequencing

Fresh spore suspensions were prepared by flooding the sporulating cultures of B. cinerea with sterile distilled water containing 0.05% (v/v) Tween-20. A suitable aliquot of the suspension was added to 100 mL potato dextrose broth (PDB) with a final concentration of 1 × 10⁶ spores/mL. After 24 h of shaking culture at 25°C, the harvest spores and mycelia were washed twice with sterile distilled water, and quickly frozen in liquid nitrogen. A biological repeat was carried out, and the two samples were mixed with the same weight. Small RNA sequencing was performed using BGISEQ-500 technology of Beijing Genomics Institute (BGI) Co., Ltd. Briefly, small RNA was separated from total RNA by PAGE gel, and linked with a 5’-adenylated, 3’-blocked single-stranded DNA adapter at 3’ end. After RT primer hybridization, the 5’ adaptor was linked and the first strand cDNA was synthesized. To enrich cDNA of 100 - 120 bp, PCR amplification and PAGE gel separation were carried out. Finally, the library was quantified and pooling cyclization was performed. Each step was under strict quality control.

2.3. Bioinformatic Analysis

After sequencing, the original data were filtered by removing low-quality reads, adaptors and other contaminants to get clean reads. The remaining tags (clean tags or clean reads) were stored in FASTQ format. Bowtie2 was used to map clean reads to the reference genome and to other sRNA [12], and Cmsearch was used for Rfam [13]. sRNA classification followed the priority rule as MiRbase > pirnabank > snoRNA > Rfam > other sRNA. Novel miRNA was predicted by exploring the characteristic hairpin structure of miRNA precursor in miRDeep2 and miRA [14] [15]. siRNA predicting followed the criteria that siRNA was a 22 - 24 nt double-stranded RNA, each strand of which was 2 nt longer than the other [16]. The small RNA expression level was calculated by using TPM (transcripts per million). TPM = C × 10⁴/N. C means miRNA counts number in a sample, and N means total reads number that mapped to the genome [17]. TAPIR and
TargetFinder were used to predict miRNA target genes [18]. The default parameters are as follows, TAPIR: --score 5 --mfe_ratio 0.6; TargetFinder: -c 4. WEGO software was used to perform Gene Ontology (GO) enrichment analysis of miRNA target genes. KEGG database was used to perform pathway enrichment analysis of miRNA target genes. A scatter plot of the KEGG enrichment results and a bar plot of the KEGG terms were generated. A corrected $P$ value $\leq 0.05$ was taken as a threshold.

2.4. Statistical Analysis

Data were pooled across independent repeat experiments. Correlation analysis was carried out to test the significance of the relationship between two or more variables utilizing Statistical Product and Serviced Solutions software (SPSS, USA). Analysis of variance (ANOVA) was used to compare more than two means. Mean separations were analyzed using Duncan’s multiple range test. Differences at $P < 0.05$ were considered to be significant.

3. Results

3.1. Phenotype and Activity of *B. cinerea*

In a previous experiment, the isolate has been identified as *Botrytis cinerea* based on morphological and genetic characteristics. Typically, sclerotia of *B. cinerea* commence growth to produce conidiophores and multinucleate conidia, serving as a primary source of inoculum. Microconidia are also formed as spermatia. The sexual cycle involves the spermatization of sclerotia, leading to the production of apothecia and asci with eight binucleate ascospores. Conidia generation follows a cycle of initiation, production and dissemination that is controlled by changes in light, humidity and temperature. Dry-inoculated conidia produced one or two short germ tubes and no obvious terminal appressoria, whereas conidial within suspension possessed much longer germ tube and extensive secretion of an extracellular matrix. On PDA plate, *B. cinerea* initially formed white colony turning gray or grayish brown (*Figure 1A*). The mycelial extension was fast and the colony could cover the petri dish in 8 days (*Figure 1C*). The hyphae were septate and intertwined (*Figure 1B*). Conidiophores were gray brown, ellipsoidal or ovate.

*B. cinerea* is responsible for a very wide range of symptoms. Soft rots, accompanied by collapse and water-soaking of parenchyma tissues, followed by a rapid appearance of grey masses of conidia are the most typical symptoms on fruit. Soft rotting of mature tomato fruit occurs mainly in postharvest stage. In the present study, at the temperature of 25°C with high relative humidity, the infection of *B. cinerea* on tomato fruit was rapid, resulting in softening of the flesh and a browning skin. On the fruit surface, massive mycelia were visible. Within about a week, the fruit was completely rotten (*Figure 1D*). Therefore, the fungus used in this study presented a typical phenotype of *B. cinerea*, and exhibited a normal growth and pathogenicity.
Figure 1. Phenotype and growth dynamic of Botrytis cinerea. (A) Colonial phenotype; (B) Mycelial phenotype; (C) Mycelial expansion on PDA; (D) Lesion expansion on tomato fruit. Bars represent the standard deviation of the means of three independent experiments. Lower case letters indicate significant differences at P < 0.05 at each time point.

3.2. Small RNA Sequencing Results

The small RNAs were sequenced using BGISEQ-500 technology. A total of 27,872,641 raw tags containing 1,006,245 low quality tags, 875,820 invalid adapter tags, 774 polyA tags, 1,934,729 short valid length tags and 24,055,073 clean tags. The base percentage composition of clean tags was shown in Figure 2(A). The percentage of clean tags, of which quality was more than 20, was 98.80% of all clean tags (Figure 2(B)). The length of small RNAs was in a range of 10 - 44 nt, and the number of small RNAs in a range of 18 - 30 nt was the highest (Figure 2(C)). A total of 20,830,926 clean tags were aligned to the reference genome. Among them, 23,900 snRNAs, 1,187,863 rRNAs, 16,349 snoRNAs, 20,911 tRNAs, 270,355 Rfam other snRnas, and 10,932 precursors were identified. The proportion of all kinds of sRNA was shown in Figure 3(A) and the genome distribution of tags was shown in Figure 3(B).

3.3. Prediction of miRNAs and siRNAs

Only miR-466i-5p as known miRNA was found in B. cinerea. It belonged to mmu-miR-466i-5p family and its hairpin contained 300 bases. Eight novel miRNAs named as Bc-mir1 to Bc-mir8 were predicted. Their expression levels
Figure 2. Sequencing results of small RNA in *B. cinerea*. (A) Base percentage composition of small RNAs; (B) Distribution of base quality on clean tag. Each dot represents the total number of bases with a specific quality value of the corresponding base along a tag, and a darker color indicates a higher base number; (C) Length distribution of small RNAs.

Figure 3. Catalog of small RNA (A) and genome distribution of tags (B). Figure (A) shows the proportion of different types of small RNA. In Figure (B), the X axis shows the relative position in the chromosome, and the Y axis shows the number of tags. The color red indicates tag count, whereas green indicates tag catalogs.

were significantly different. The expression of Bc-mir1 was about 100 times higher than that of Bc-mir8. The sequence information of novel miRNAs was shown in Table 1. The stem loop structure of precursors was shown in Figure 4. A total of 110 novel siRNAs were predicted based on their architectural features. The details of novel siRNAs were shown in Table S1. Their expression levels were represented by the TPM values in a range of 0 to 16.41. Through sequence analysis, the base
Table 1. Information of predicted miRNAs in *Botrytis cinerea*.

| Name   | Chromosome | Strand | Sequence (mature)                          | TPM     |
|--------|------------|--------|-------------------------------------------|---------|
| Bc-mir1| NC_037310.1| +      | CCATAACACAAGCTTCAGATCGGTGGA                | 28,306.92|
| Bc-mir2| NC_037314.1| +      | AGTTCACTGGTAGAATTCTTGCTTTGGG              | 2310.08 |
| Bc-mir3| NC_037317.1| +      | GTGGCTCAGTTGGGTAGACGTTGGTGCTCA           | 2355.44 |
| Bc-mir4| NC_037320.1| +      | TTACTCTGCAGGGCAATCTGTTTTTTGCA            | 680.29  |
| Bc-mir5| NC_037323.1| +      | GTGTCGATTCAAGGGCAATGTTGCA                | 2911.67 |
| Bc-mir6| NC_037323.1| +      | AGACTGAGGAGATTGGGCATCCCGTCCGC          | 13,262.56|
| Bc-mir7| NC_037324.1| +      | CTGCTACATATATATTTGAATTTG                 | 314.38  |
| Bc-mir8| NC_037325.1| +      | GACTGAGAAGATTTGGCATCC                    | 271.62  |

![Figure 4. Stem-loop structure of predicted novel miRNA precursor in *B. cinerea*. (A)-(H) indicate the predicted miRNAs Bc-mir1 to Bc-mir8.](image)

The composition of predicted miRNAs and siRNAs was shown in Figure 5. For novel miRNAs, the first base distribution was G, C, A and U in number from high to low. There were no obvious rules for the base distribution due to the small number. The length of novel siRNAs was mostly less than 21 nt. The first base distribution was U, G, A and C in number from high to low. In the length range of 1 to 22 nt of all novel siRNAs, the third base contained the highest percent of G and lowest percent of U, and the twenty-second base possessed highest percent of U and lowest percent of
Figure 5. The base distribution in predicted miRNA and siRNA sequences in B. cinerea. (A) and (C) respectively indicate the base distribution in predicted miRNA and siRNA sequences; (B) and (D) respectively indicate the first base distribution of predicted miRNA and siRNA sequences.

A. In addition, the twenty-third base of 14 siRNAs did not contain base A.

3.4. Enrichment Analysis of miRNA Target Genes

Software TAPIR and TargetFinder were used to find the target genes of miRNAs in B. cinerea. The intersection results of two softwares contained 300 target genes, and there were 642 target genes in union results (Table S2). The GO enrichment result was shown in Figure 6. Most of the target genes located in membrane and organelle, and possessed binding activity, catalytic activity or transporter activity. The target genes involved in many biological processes including cellular process, biological regulation, metabolic process, single-organism process, etc. The KEGG enrichment result was shown in Figure 7. The items with a larger number of target genes were carbohydrate metabolism, signal transduction, and transport and catabolism. In addition, statistics of pathway enrichment indicated that many target genes were related to the MAPK signaling pathway, amino sugar and nucleotide sugar metabolism, and endocytosis. Meanwhile, target genes involved in the AGE-RAGE signaling pathway, alpha-linolenic acid metabolism, and phosphatidylinositol signaling system possessed higher rich factor value (Figure 8).
4. Discussion

RNAi is a highly conserved biological process in diverse species. It has in common the involvement of miRNAs and siRNAs. miRNAs are essential components of the gene silencing machinery in most eukaryotic organisms, and negatively regulate the expression of a large proportion of cellular mRNAs. Most of the miRNAs are transcribed by RNA polymerase II. The long primary transcript with a hairpin structure is termed as pri-miRNA. In the nucleus, pri-miRNA is converted into pre-miRNA (about 70 nt stem-loop precursor miRNA) under
catalyzing of RNase III type enzyme DROSHA and the double-stranded RNA-binding protein DGCR8. Once exported to the cytoplasm by Exportin-5, the pre-miRNA is processed to form miRNA duplex by another RNase type III enzyme Dicer. miRNA duplex is then incorporated in RISC together with Ago protein, where one strand is selected to become the mature miRNA [19]. The mature miRNA recognizes its complementary sequence in the 3’ untranslated region of their target mRNAs via seed region, typically positions 2 - 7 in the miRNA. Then, miRNA exerts its regulatory functions through mRNA cleavage, deadenylation or translational repression [20] [21]. In addition, many studies have shown that a single miRNA may target multiple mRNAs, and some miRNAs with distinct sequences could repress the same target mRNA. For filamentous fungi, Lee et al. (2010) first found four different pathways for miRNAs
Figure 8. Statistics of pathway enrichment of miRNA target genes in B. cinerea. The rich factor is the ratio of target gene numbers annotated in this pathway term to all gene numbers annotated in this pathway term. The greater rich factor indicates the greater the degree of enrichment. The Q-value is the corrected p-value, and the lower Q-value indicates the greater enrichment level.

and siRNAs production in Neurospora crassa, which used a distinct combination of factors including Dicers, QDE-2, QIP, and MRPL3 [22]. Lin et al. (2015) identified 4 conserved miRNAs and 63 novel predicted miRNAs in Antrodia cinnamomea. Their predicted targets involved in triterpenoid synthesis, mating type recognition, chemical or physical sensory protein and transporters [23]. Wang et al. (2017) reported a novel miRNA (termed Pst-miR1) in Puccinia striiformis f. sp. tritici, which acted as an important pathogenicity factor sup-
pressing host immunity [24]. Jin et al. (2019) identified a novel miRNA VdmilR1 in *Verticillium dahlia* that could target VdHy1 gene at the 3'-UTR for transcriptional repression through increased histone H3K9 methylation of VdHy1 [25]. Hu et al. (2022) found an Ago1-associated miRNA (miR8788) that could target a potato alpha/beta hydrolase-type encoding gene (*StABHI*) and facilitate infection of *Phytophthora infestans* [26].

siRNA is processed from a long double-stranded RNA (dsRNA) which is commonly generated by RNA-dependent RNA polymerase (RdRP). Further, a RNase III-type Dicer ribonuclease cleaves dsRNA into siRNA with two unpaired nucleotides at the 3'-end of each strand. A guide strand is selected and associated with an Ago family protein to form RISC. The siRNA directs RISC to target homologous mRNA, which is then sequence-specifically cleaved by the Ago protein. This process finally leads to target gene silencing by RNA degradation, translational inhibition, or transcriptional silencing initiated by alteration of chromatin state [27] [28] [29]. In fungi, Khatri and Rajam (2007) found that a 23-nucleotide siRNA based on *ODC* (*ornithine decarboxylase*) gene could cause a specific silencing effect, and lead to significant reduction in mycelial growth and cellular polyamine concentration [30]. Hammond et al. (2013) identified and characterized two novel proteins, SAD-4 and SAD-5. Both of them were required for meiotic silencing by unpaired DNA and siRNA generation in *Neurospora crassa* [31]. Deshmukh and Purohit (2014) used synthetic siRNAs to down-regulate secondary metabolite genes *hmgR* and *fpps*, which led to bikaverin overproduction in *Fusarium* sp. HKF15 [32]. Yu et al. (2014) showed that convergent antisense transcription and availability of the Dicer ribonuclease were key determinants for heterochromatin formation and catalyzing siRNA generation in *Schizosaccharomyces pombe* [33]. Yu et al. (2021) found that trimethylguanosine synthase 1 (Tgs1) played critical roles in Swi6/HP1-independent siRNA production and establishment of heterochromatin in fission yeast [34].

Considering the critical roles of miRNAs and siRNAs in gene regulating and biological function in fungi, the specific and sensitive detection is becoming more important. More elaborate regulation mechanisms of miRNAs and siRNAs need to be further explored. Due to the short sequence lengths, large variability in per-cell copy number, and high sequence similarity within families, the relevant studies of miRNAs and siRNAs in *B. cinerea* are limited so far. Our study focuses on finding novel miRNAs and siRNAs, and the targets of miRNAs in *B. cinerea*. The results will provide new knowledge regarding the small RNA transcriptome and new insights into miRNAs function on pathogenicity and growth in *B. cinerea*.

5. Conclusion

In this study, 8 novel miRNAs and 110 novel siRNAs were predicted in *Botrytis cinerea* utilizing high-throughput transcriptomic sequencing. Their sequence information, construction, base bias and expression level were determined as
well. In addition, GO and KEGG enrichment analysis indicated that the miRNA target genes are mostly located in membrane and organelle, possessed binding and catalytic activities, and involved in carbohydrate metabolism and signal transduction. These results will provide new clues to understand the developmental and pathogenic mechanisms of *B. cinerea* at the transcriptional level.

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**Conflicts of Interest**

The authors declare no conflicts of interest regarding the publication of this paper.

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## Supplemental Material

### Table S1. Information of predicted siRNAs in *B. cinerea*.

| Name   | Guide sequence | Passenger sequence | TPM  |
|--------|---------------|--------------------|------|
| Bc-sir1| GGTCGGTCGATCTAAGTCCC | AGCCAGCTAAGATTCAAGGGCC | 0.82 |
| Bc-sir2| CGCTATGATACGATTCCTCCA | TCGCGATACTATGCTAGGGAG | 0.50 |
| Bc-sir3| GCCCTATGCTCAAGTCATTACAG | GTCGCGATACGCTAGGGAG | 0.50 |
| Bc-sir4| AGCGATACCACACTGTTTGATACG | GTTGGTTCAGGGGGGAGCAT | -   |
| Bc-sir5| ATGTGTTCGAAGTCTAGCCAT | CACACAGCTGAGGAGGCTAGA | -   |
| Bc-sir6| TACCAAGGCTCAGATCAGGTA | GTTGGTTCAGGGGGGAGCAT | -   |
| Bc-sir7| AAATGGTTCTACCTGGATGCTCAT | TACCAAGGCGACCTAGGTAAT | 0.91 |
| Bc-sir8| CTGGGTCCTGAAAGCTGATG | GCCAGCAGGACTTGGCAT | 0.82 |
| Bc-sir9| CGCTGGGTCCTGAAAGCTGATG | CGGGCAAGCAGGGACTTGAT | 3.41 |
| Bc-sir10| CGCGGTTCGCTCGAAGCTGATG | GTGGCGGACGGAGACCTGGCAT | 2.45 |
| Bc-sir11| GCCGGGTCTCTGCTGAAAGCTGATG | GCCGGGACGGAGACCTGGCAT | 1.36 |
| Bc-sir12| TACCGTTAATGCTGCTGAAAGCTGATG | GCCGGGACGGAGACCTGGCAT | 0.50 |
| Bc-sir13| TATACCCGATGATACCGAGGCTAGA | GCGGAGACCCGGAGGACTTGAT | 0.50 |
| Bc-sir14| GAACCTTACCAATGCTGCTGAAAGCTGATG | ACCTGAGAGGAGGAGGCTAGA | 0.68 |
| Bc-sir15| TGGGTCCTGAAAGCTGATG | GCCGGGACGGAGACCTGGCAT | 2.45 |
| Bc-sir16| CGCCTGGGTCCTGCTGAAAGCTGATG | GCCGGGACGGAGACCTGGCAT | 1.36 |
| Bc-sir17| GGGTTCTGCTGCTGAAAGCTGATG | GCCGGGACGGAGACCTGGCAT | 0.50 |
| Bc-sir18| GTATCTGATTTATGCTGCTGAGGCT | TACACCTCAGCTGCTGCTGCTG | 2.00 |
| Bc-sir19| GTGTTCGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.73 |
| Bc-sir20| TACATCCTAATTCCTCCCTGAGGCT | CATGTGCTGCTGCTGCTGCTG | 0.64 |
| Bc-sir21| CATCAGCTAATTCCTCCCTGAGGCT | CATGTGCTGCTGCTGCTGCTG | -   |
| Bc-sir22| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 15.04 |
| Bc-sir23| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.45 |
| Bc-sir24| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.86 |
| Bc-sir25| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 1.14 |
| Bc-sir26| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | -   |
| Bc-sir27| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 3.27 |
| Bc-sir28| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.45 |
| Bc-sir29| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.55 |
| Bc-sir30| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 3.27 |
| Bc-sir31| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.45 |
| Bc-sir32| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.55 |
| Bc-sir33| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.77 |
| Bc-sir34| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.64 |
| Bc-sir35| GGGTCCTGCTGCTGCTGCTGCTG | TACACCTCAGCTGCTGCTGCTG | 0.50 |
| Bc-sir  | Sequence 1                          | Sequence 2                          | Score |
|--------|------------------------------------|------------------------------------|-------|
| Bc-sir36 | GCAGCGTTTTGTCTAACCAGGTCTCTTGGCT   | TCGAAAAACAGATTGCGGCGAAT            | 2.68  |
| Bc-sir37 | AAAAAACCAGATTGCCCGAGCTAGT          | GCTTTTGCTCAACGGGCGGCTCT            | -     |
| Bc-sir38 | ATGGAAGAGCCCTGCGAAAAAGT            | CCTTCTCGAGGCTTTTCAGA              | 2.32  |
| Bc-sir39 | AATGGAAGAGCCCTGCGAAAAAGT           | ACTTTCTCGAGGCTTTTCAGA             | 1.32  |
| Bc-sir40 | GAATTCGCGGTAGTGTTAAAAAGT           | TAAGCGCCTACATGTTTTTCAGG            | 0.50  |
| Bc-sir41 | GAGTGCAACCCCTCGCGCAAGT             | TCAAGTTTGAGGGGCGTCGTTCAAT          | -     |
| Bc-sir42 | CAATGTCGCGGTAGTTCAAGGT            | TACCAGCCAGCTAGTTAGTTCAAG           | 0.68  |
| Bc-sir43 | TCCTTGAAACAGACCGTCTGATG           | CAAGGAAACGTTGTCTGCTGAGT           | 0.68  |
| Bc-sir44 | TAATTCGAGGCTAGTGCTGAGT            | AAATTTAGCCTCCCGACTGAGT            | 0.86  |
| Bc-sir45 | CTATATTTCCCTCAACGCAGT             | TATTAGGGAATGCGTAGTCAAG            | 1.50  |
| Bc-sir46 | AAATTTAGTACCTACCGGCTAGT           | TAAATCTAATTGGCGCCGATCGAGA         | -     |
| Bc-sir47 | CTATATAACGGCGTGATGCTGATG          | TATATGCGCCAATGCGCTACAG            | 1.30  |
| Bc-sir48 | TGCAATTTTTTACCTCCTCATGCT          | GTAGCCGTTAAAAATGGGTTAGT           | 0.55  |
| Bc-sir49 | TAACTTCCCTGCTGAAATTTAGT           | TGAAGGAACGTCATTTAATCAAT           | -     |
| Bc-sir50 | TAATGCGAGGCCTCTAAATACGT           | TCAATTACCTCAGGAGTTTACGT           | 0.95  |
| Bc-sir51 | GTGGGTTGAATCTTTTGTCA              | CGCACCCCAACTTAGGAAACGT            | 0.91  |
| Bc-sir52 | GTATATAAAATGTTGTCTTACGT          | TCGCATATATCTATTTCAACACGT          | 0.55  |
| Bc-sir53 | ACTATGCTCACGAGGTTAGCT             | ATACGAGTCTCCATCTGACCA             | 0.82  |
| Bc-sir54 | CTCAGCTACTAAATTTCTGCTCAGT       | CAGAGTTTCTAATTTCTGCTGAGT          | 0.45  |
| Bc-sir55 | CGGATCCTCTTTTGGTTCTGCGCATC     | TGTCCCTAGAAACAACAGACGCT          | 0.64  |
| Bc-sir56 | TAATATAACCCAGTAATAGCAGT          | GTATTATAGGATGTCCTAGCT             | 2.36  |
| Bc-sir57 | TCAGGGGTTGCTCGCTCAGCATC          | AAATCCCTCCACGGGACGATCG            | 2.41  |
| Bc-sir58 | ACTAACTACTCGGAAGAACATT           | TCTGATGTGAGCTGGCTTCTG            | 0.55  |
| Bc-sir59 | GCATTGCCAGCCGTCGCAAGGT           | TAAAGCTGTCAGGCGGCTAGGCA          | 0.64  |
| Bc-sir60 | GCAAGTATAAGATAATAGG               | TCTCTATTATTTCAATCCG              | 2.23  |
| Bc-sir61 | TCGCGATCATCTAGTCCTAGG             | CGCTATGACAGTATGTCCTCAAT           | 0.45  |
| Bc-sir62 | TGACTAAAATCTCGGACGCT             | TGGTTTTAGAGCTCGCTAGT             | 0.45  |
| Bc-sir63 | GGACTGAATAATTTAGCTAGTT           | TGCATTATTTATCTGAGCT             | 3.14  |
| Bc-sir64 | TGCTCTGGGCTCGCGCGGCGG            | AGGACCAGCCCGGCCGCCGCACT           | 0.59  |
| Bc-sir65 | AGTCTCTGGCCTCCGCGCGGC            | AGGACCAGCCCGGCCGCCGCACT          | 16.41 |
| Bc-sir66 | TATCCCTCATCAACCGAACCAT           | GTATAGGGAATGTTGTGCTGCTG           | 0.59  |
| Bc-sir67 | AGATAGTATAAGCTCGCCAGG            | TATCAATTTGGCGCTCCCA             | 0.45  |
| Bc-sir68 | TCCTCTGGCCAGGACTGCGCTG           | ATGACCGGGTTCATGCCCCACTG          | 0.50  |
| Bc-sir69 | TATGATGCAAGTCTGCGGT             | ACTACGTTGCAAGCCACCA             | 0.68  |
| Bc-sir70 | TTATGATGCAAGTCTGCGGT             | TACTAAGTCCAGGACCACG             | 2.82  |
| Bc-sir71 | CGAAAGACTAATCGAACCACAT           | CCGGCTTCTGATTAGCTGTG            | 0.55  |
| Bc-sir72 | GCGAAAGACTAATCGAACCACAT         | CCGGCTTCTGATTAGCTGT             | 0.86  |
Continued

| Accession | Primers | Log2FC | TPM          |
|-----------|---------|--------|--------------|
| Bc-sir73  | CCACTCCGCCTGGCCGGTTGGT TGAGGCGGACCGGCCAACCAGG | 4.86 |            |
| Bc-sir74  | TGATTACTCAGGGCCTAATGTTGA GGAAGTTGAGGCAATAACAGG | 0.73 |            |
| Bc-sir75  | ATGCTCAGGAGGTAACCTGGT TGAGGCGGACCGGCCAACCAGG | 1.82 |            |
| Bc-sir76  | CTATGCTCAGGGCTAATGTTGA GGAAGTTGAGGCAATAACAGG | 1.32 |            |
| Bc-sir77  | ATGCTCAGGAGGTAACCTGGT TGAGGCGGACCGGCCAACCAGG | 0.59 |            |
| Bc-sir78  | GGAAGTTGAGGCAATAACAGG | 0.73 |            |
| Bc-sir79  | TGATCGGGGCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 2.54 |            |
| Bc-sir80  | TGAGTCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 2.77 |            |
| Bc-sir81  | TGAGTCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.45 |            |
| Bc-sir82  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.68 |            |
| Bc-sir83  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.14 |            |
| Bc-sir84  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir85  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir86  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir87  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir88  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.32 |            |
| Bc-sir89  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.64 |            |
| Bc-sir90  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.59 |            |
| Bc-sir91  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.77 |            |
| Bc-sir92  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir93  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir94  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.14 |            |
| Bc-sir95  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir96  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.55 |            |
| Bc-sir97  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.50 |            |
| Bc-sir98  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.41 |            |
| Bc-sir99  | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.68 |            |
| Bc-sir100 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.64 |            |
| Bc-sir101 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 14.31 |           |
| Bc-sir102 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.14 |            |
| Bc-sir103 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.45 |            |
| Bc-sir104 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.68 |            |
| Bc-sir105 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 0.68 |            |
| Bc-sir106 | TGATCTCAGGGCTTATTGA GGAAGTTGAGGCAATAACAGG | 1.23 |            |

TPM: transcripts per kilobase million; the “-” indicates “not applicable.”
| miRNA ID  | Target ID      | TAPIR Score | TAPIR MFE | Target Finder Score | Pathway | NR ID       |
|----------|----------------|-------------|-----------|---------------------|---------|-------------|
| miR-1277-5p_2 | BCIN_01g00260 | 4.5         | -22.8     | 3.5                 | K00102  | XP_001545605.1 |
| miR-1277-5p_2 | BCIN_01g00440 | 3           | -20.7     | 3                   | K00667  | XP_018068696.1  |
| miR-1277-5p_2 | BCIN_01g00550 | 2.5         | -23.7     | 3                   | K07901  | XP_001547449.1  |
| miR-1277-5p_2 | BCIN_01g00560 | 2.5         | -22.1     | -                   | -       | EMR89982.1    |
| miR-1277-5p_2 | BCIN_01g00750 | 5           | -20.3     | 3                   | K05740  | XP_001547248.1  |
| miR-1277-5p_2 | BCIN_01g00830 | 3.5         | -26.6     | -                   | K11294  | XP_001547258.1  |
| miR-1277-5p_2 | BCIN_01g03250 | 2           | -21.1     | 2                   | -       | XP_001550948.1  |
| miR-1277-5p_2 | BCIN_01g03470 | 3           | -24.8     | 2                   | K08869  | XP_001549015.1  |
| miR-1277-5p_2 | BCIN_01g04580 | - NA        | NA        | 3                   | K11244  | CCD55062.1 |
| miR-1277-5p_2 | BCIN_01g08210 | 5           | -21.4     | 2.5                 | K03260  | EMR899818.1    |
| miR-1277-5p_2 | BCIN_01g08890 | 3           | -20.5     | 3                   | -       | CCD45998.1    |
| miR-1277-5p_2 | BCIN_01g09710 | - NA        | NA        | 3.5                 | -       | EMR81406.1    |
| miR-1277-5p_2 | BCIN_02g01810 | 3           | -22.4     | 2.5                 | K05770  | XP_001597624.1  |
| miR-1277-5p_2 | BCIN_02g01870 | 5           | -21.6     | 2.5                 | K05894  | XP_001558929.1  |
| miR-1277-5p_2 | BCIN_02g02400 | 3.5         | -26.2     | 3.5                 | K10958  | CCD48604.1 |
| miR-1277-5p_2 | BCIN_02g02900 | 3.5         | -23.3     | -                   | K14309  | EMR82742.1 |
| miR-1277-5p_2 | BCIN_02g05750 | - NA        | NA        | 3.5                 | K03469  | XP_001552711.1  |
| miR-1277-5p_2 | BCIN_02g07730 | - NA        | NA        | 3.5                 | -       | EMR81378.1 |
| miR-1277-5p_2 | BCIN_03g01840 | 2           | -21.2     | 2                   | K08773  | CCD44002.1 |
| miR-1277-5p_2 | BCIN_03g03300 | - NA        | NA        | 3                   | K06004  | XP_001560517.1  |
| miR-1277-5p_2 | BCIN_03g03920 | NA          | NA        | 3                   | -       | XP_001560602.1  |
| miR-1277-5p_2 | BCIN_03g05330 | 2           | -21.1     | 2                   | K06215  | CCD51582.1 |
| miR-1277-5p_2 | BCIN_03g05820 | 3.5         | -24.2     | 2                   | K01728  | XP_001560884.1  |
| miR-1277-5p_2 | BCIN_03g07100 | 2           | -21.2     | 2                   | K11702  | CCD51306.1 |
| miR-1277-5p_2 | BCIN_03g07560 | 3           | -26.5     | 3                   | K11501  | EMR83782.1 |
| miR-1277-5p_2 | BCIN_03g08670 | - NA        | NA        | 3.5                 | K17808  | XP_001554883.1  |
| miR-1277-5p_2 | BCIN_04g02270 | 1           | -26.3     | 1                   | K18626  | XP_001557298.1  |
| miR-1277-5p_2 | BCIN_04g05390 | 3.5         | -29.6     | -                   | K14963  | XP_001557671.1  |
| miR-1277-5p_2 | BCIN_05g00590 | 1.5         | -23       | 1.5                 | K21820  | XP_001552023.1  |
| miR-1277-5p_2 | BCIN_05g00860 | 5           | -21.4     | 2.5                 | K01674  | XP_001552065.1  |
| miR-1277-5p_2 | BCIN_05g02150 | 3.5         | -26.6     | -                   | -       | CCD34040.1 |
| miR-1277-5p_2 | BCIN_05g02180 | 3           | -26.3     | -                   | -       | EMR89408.1 |
| miR-1277-5p_2 | BCIN_05g05050 | 3.5         | -21.8     | 3.5                 | -       | CCD53614.1 |
| miR-1277-5p_2 | BCIN_05g06080 | 3           | -25.8     | -                   | -       | XP_001559616.1 |
| miR-1277-5p_2 | BCIN_05g06090 | 2.5         | -26.1     | 2.5                 | -       | XP_001559615.1 |
miR-1277-5p_2  BCIN_05g06840  2  -23.8  2  K07300  EMR80478.1
miR-1277-5p_2  BCIN_05g08020  1.5  -26.6  1.5  K00088  CCD34394.1
miR-1277-5p_2  BCIN_05g08280  4.5  -20.7  3  K00088  XP_001548411.1
miR-1277-5p_2  BCIN_06g01060  3.5  -19.4  -  K03380  XP_001560250.1
miR-1277-5p_2  BCIN_06g03920  3.5  -26.6  2  K01183  CCD48175.1
miR-1277-5p_2  BCIN_06g05580  -  -  3  -  CCD56961.1
miR-1277-5p_2  BCIN_06g06140  2  -26.3  2  K11681  XP_001549229.1
miR-1277-5p_2  BCIN_06g06150  5  -20.3  3  K20307  XP_001549231.1
miR-1277-5p_2  BCIN_06g07080  2  -21.2  2  K13341  XP_001596816.1
miR-1277-5p_2  BCIN_06g07120  3.5  -21.7  3.5  K00480  EMR90947.1
miR-1277-5p_2  BCIN_06g07250  1.5  -22.8  1.5  -  XP_001545249.1
miR-1277-5p_2  BCIN_07g02120  5  -24.4  3  K09419  CCD46226.1
miR-1277-5p_2  BCIN_07g03250  4  -23.1  3  -  EMR80900.1
miR-1277-5p_2  BCIN_07g07090  1  -24.3  1  -  XP_001549837.1
miR-1277-5p_2  BCIN_08g01170  -  -  2.5  -  XP_001548743.1
miR-1277-5p_2  BCIN_08g01730  -  -  3  -  K19898  CCD34005.1
miR-1277-5p_2  BCIN_08g02270  -  -  3  -  XP_001551936.1
miR-1277-5p_2  BCIN_08g02590  2  -24.4  2  K19851  XP_001551972.1
miR-1277-5p_2  BCIN_08g02920  -  -  2.5  K07836  APA11004.1
miR-1277-5p_2  BCIN_08g03490  2.5  -22.5  2.5  K20059  XP_001554617.1
miR-1277-5p_2  BCIN_08g03500  2  -21.1  2.5  K15505  XP_001554616.1
miR-1277-5p_2  BCIN_08g03550  2.5  -23.3  NA  K02265  XP_001554609.1
miR-1277-5p_2  BCIN_08g04630  4.5  -22.8  2.5  -  XP_001552328.1
miR-1277-5p_2  BCIN_08g04770  1.5  -22.9  1.5  K02858  XP_001552345.1
miR-1277-5p_2  BCIN_08g04810  3  -20.5  3  K01288  XP_001552353.1
miR-1277-5p_2  BCIN_08g05880  3.5  -23.5  -  -  EMR85246.1
miR-1277-5p_2  BCIN_08g06160  5  -21.5  3.5  K01224  CCD55537.1
miR-1277-5p_2  BCIN_08g06660  3.5  -18.8  -  K11294  EMR85173.1
miR-1277-5p_2  BCIN_09g03880  1  -24.4  1  K16261  XP_001551566.1
miR-1277-5p_2  BCIN_09g05430  -  -  3.5  K02974  EMR83128.1
miR-1277-5p_2  BCIN_09g05440  3.5  -25.5  NA  -  CCD33681.1
miR-1277-5p_2  BCIN_09g06600  -  -  3.5  -  CCD50123.1
miR-1277-5p_2  BCIN_10g00480  -  -  3.5  K01183  ESZ93861.1
miR-1277-5p_2  BCIN_10g00790  3.5  -25.3  NA  K08853  CCD49512.1
miR-1277-5p_2  BCIN_10g01210  2  -21.1  2  -  KIV87681.1
miR-1277-5p_2  BCIN_10g03450  2  -21.1  2  -  CCD49648.1
miR-1277-5p_2  BCIN_10g03890  3  -23.4  3  K00223  XP_001546106.1
| miR-1277-5p_2 BCIN_10g03900 | 3 | −22.6 | 3.5 | - | EMR89744.1 |
| miR-1277-5p_2 BCIN_10g04000 | 3 | −24.1 | 3.5 | K10733 | CCD43707.1 |
| miR-1277-5p_2 BCIN_10g04240 | - | - | 3.5 | - | CCD50947.1 |
| miR-1277-5p_2 BCIN_10g05170 | 2 | −21.2 | 2.5 | K10733 | CCD47615.1 |
| miR-1277-5p_2 BCIN_11g01410 | 5 | −20.6 | 2.5 | K19898 | CCD47637.1 |
| miR-1277-5p_2 BCIN_11g01560 | 3.5 | −19.7 | 3.5 | - | CCD47723.1 |
| miR-1277-5p_2 BCIN_11g02190 | - | - | 3.5 | - | CCD47723.1 |
| miR-1277-5p_2 BCIN_11g02230 | 3 | −22.6 | 2.5 | K11761 | CCD47729.1 |
| miR-1277-5p_2 BCIN_12g03700 | 3 | −26.3 | 3.5 | - | CCD47816.1 |
| miR-1277-5p_2 BCIN_12g04550 | 2 | −21.3 | 2.5 | - | XP_001553933.1 |
| miR-1277-5p_2 BCIN_13g01860 | 4 | −20.1 | 3.5 | K03488 | CCD54998.1 |
| miR-1277-5p_2 BCIN_13g02020 | 2.5 | −26.5 | 2.5 | K11761 | CCD54378.1 |
| miR-1277-5p_2 BCIN_13g02670 | 1 | −28.5 | 1.5 | K03381 | CCD43638.1 |
| miR-1277-5p_2 BCIN_13g03630 | 2 | −21.2 | 2.5 | K08257 | CCD47037.1 |
| miR-1277-5p_2 BCIN_13g04680 | 3 | −24.7 | 3.5 | K08257 | CCD52364.1 |
| miR-1277-5p_2 BCIN_14g03850 | - | - | 2.5 | K04043 | ESZ96837.1 |
| miR-1277-5p_2 BCIN_15g03180 | - | - | 3.5 | - | - |
| miR-1277-5p_2 BCIN_15g04430 | 3.5 | −19.6 | 3.5 | K00898 | EMR89147.1 |
| miR-1277-5p_2 BCIN_15g04990 | 3 | −20.4 | 3.5 | - | XP_001545815.1 |
| miR-1277-5p_2 BCIN_14g05220 | 1.5 | −22.4 | 1.5 | K03380 | CCD47638.1 |
| miR-1277-5p_2 BCIN_15g01340 | 1.5 | −23.5 | 1.5 | K19851 | CCP26832.1 |
| miR-1277-5p_2 BCIN_15g03180 | - | - | 3.5 | - | - |
| miR-1277-5p_2 BCIN_15g04440 | - | - | 2.5 | K12604 | XP_001545805.1 |
| miR-1277-5p_2 BCIN_15g04470 | - | - | 3.5 | K05906 | XP_001545802.1 |
| miR-1277-5p_2 BCIN_15g04990 | 3.5 | −21.2 | 3.5 | - | APA13791.1 |
| miR-1277-5p_2 BCIN_15g05690 | 2 | −21.1 | 2.5 | K00898 | XP_001545801.1 |
| miR-1277-5p_2 BCIN_16g04560 | 3 | −21.2 | 3.5 | K00898 | EMR89147.1 |
| miR-4003c-5p BCIN_04g02950 | 3.5 | −26.7 | 3.5 | - | EMR88909.1 |
| miR-4003c-5p BCIN_05g02800 | 3.5 | −26.7 | 3.5 | K03380 | CCD46646.1 |
| miR-4003c-5p BCIN_05g03030 | 3.5 | −26.7 | 3.5 | K20178 | CCD46610.1 |
| miR-4003c-5p BCIN_06g01320 | 3.5 | −24.7 | 3.5 | K20178 | CCD49174.1 |
| miR-4003c-5p BCIN_10g05790 | 3 | −26.6 | 3.5 | - | EMR89982.1 |
| miR-466b-2-3p | BCIN_01g03160 | 3 | −23.8 | 3 | K00101 | EMR80850.1 |
| miR-466b-2-3p | BCIN_01g06270 | 2 | −30.3 | 2 | K01613 | XP_001561287.1 |
| miR-466b-2-3p | BCIN_02g02180 | 3.5 | −36.4 | 3.5 | - | XP_001558889.1 |
| miR-466b-2-3p | BCIN_02g08160 | 3 | −31.6 | 4 | K16261 | ESZ96655.1 |
| miR-466b-2-3p | BCIN_03g01480 | 3 | −30.3 | 3 | K00432 | EMR87195.1 |
| miR-466b-2-3p | BCIN_03g07700 | 5 | −30.5 | 2 | K14692 | XP_001546498.1 |
| miR-466b-2-3p | BCIN_04g05380 | 4 | −31.3 | 3 | K05747 | CCD45013.1 |
| miR-466b-2-3p | BCIN_05g02470 | 3 | −30.3 | 4 | K10273 | XP_001560064.1 |
| miR-466b-2-3p | BCIN_05g06080 | 4 | −26.6 | 3 | - | XP_001559616.1 |
| miR-466b-2-3p | BCIN_05g07010 | 2 | −36.3 | 2 | K10798 | XP_001548102.1 |
| miR-466b-2-3p | BCIN_06g05240 | 2 | −30.2 | 3.5 | - | CCD56908.1 |
| miR-466b-2-3p | BCIN_07g02120 | 2 | −28.2 | - | K09419 | CCD46226.1 |
| miR-466b-2-3p | BCIN_07g04210 | 2.5 | −36.4 | 2.5 | - | - |
| miR-466b-2-3p | BCIN_07g06160 | 3.5 | −36.4 | 3.5 | K08675 | CCD55346.1 |
| miR-466b-2-3p | BCIN_07g06450 | 3.5 | −36.3 | 2.5 | K12604 | XP_001547376.1 |
| miR-466b-2-3p | BCIN_07g06530 | 4.5 | −31.1 | 3.5 | - | XP_001547772.1 |
| miR-466b-2-3p | BCIN_08g02920 | - | - | 3.5 | K07836 | APA11004.1 |
| miR-466b-2-3p | BCIN_08g05880 | - | - | 3 | - | EMR85246.1 |
| miR-466b-2-3p | BCIN_09g05170 | 4.5 | −35.7 | 3.5 | K01046 | XP_001551716.1 |
| miR-466b-2-3p | BCIN_10g01690 | 3.5 | −36.4 | 3.5 | K01183 | EMR81038.1 |
| miR-466b-2-3p | BCIN_10g02860 | 2.5 | −35.6 | 2.5 | K11294 | XP_001556948.1 |
| miR-466b-2-3p | BCIN_10g03010 | 2.5 | −36.4 | 1.5 | - | XP_001556928.1 |
| miR-466b-2-3p | BCIN_10g03210 | 2.5 | −36.2 | 2.5 | K14213 | XP_001548054.1 |
| miR-466b-2-3p | BCIN_10g04260 | 3.5 | −36.3 | 3.5 | - | EMR82279.1 |
| miR-466b-2-3p | BCIN_10g04530 | 4 | −26.4 | 3 | K11294 | XP_001557411.1 |
| miR-466b-2-3p | BCIN_10g05100 | 3 | −30.4 | 3 | K01183 | EMR81430.1 |
| miR-466b-2-3p | BCIN_12g01280 | 2 | −36.3 | 2 | K20521 | CCD53768.1 |
| miR-466b-2-3p | BCIN_12g03680 | 2 | −28.2 | 2.5 | K01183 | XP_001552242.1 |
| miR-466b-2-3p | BCIN_13g03710 | 3.5 | −30.8 | 3.5 | K01537 | CCD47027.1 |
| miR-466b-2-3p | BCIN_13g04920 | 4.5 | −36 | 3.5 | K11173 | ESZ95094.1 |
| miR-466b-2-3p | BCIN_14g00530 | 3 | −27.4 | 4 | - | XP_001547926.1 |
| miR-466b-2-3p | BCIN_15g04120 | - | - | 3.5 | K20042 | EMR82018.1 |
| miR-466b-2-3p | BCIN_15g04440 | 3.5 | −36.4 | 1.5 | K12604 | XP_001548505.1 |
| miR-466b-2-3p | BCIN_15g04460 | 4 | −26.6 | 3 | K05747 | CCD34183.1 |
| miR-466b-2-3p | BCIN_15g04990 | 3 | −27.4 | 3 | K11314 | APA13791.1 |
| miR-466b-2-3p | BCIN_16g00770 | 3.5 | −36.4 | 3 | K21293 | CCD35042.1 |
| miR-466i-5p | BCIN_01g00430 | 1 | −38.1 | 1 | - | XP_001547466.1 |
| miR-466i-5p | BCIN_01g00550 | 3 | −34.2 | 3 | K07901 | XP_001547449.1 |
| miR-466i-5p | BCIN_01g00920 | 3.5 | −32.9 | 3.5 | - | XP_001555522.1 |
| miR-466i-5p | BCIN_01g00950 | 5 | −32.8 | 0 | K09885 | XP_001555528.1 |
| miR-466i-5p | BCIN_01g01790 | 2.5 | −36.2 | 2.5 | K00102 | EMR89872.1 |
| miR-466i-5p | BCIN_01g02580 | 3 | −37.1 | 3 | K06630 | APA06607.1 |
| miR-466i-5p | BCIN_01g02740 | 0 | −41.9 | 0 | - | EMR81600.1 |
| miR-466i-5p | BCIN_01g03480 | 3 | −33.2 | - | K05857 | CCD54920.1 |
| miR-466i-5p | BCIN_01g03660 | 0 | −41.8 | 0 | K08773 | XP_001551000.1 |
| miR-466i-5p | BCIN_01g04580 | 5 | −27.8 | 0 | K11244 | CCD55062.1 |
| miR-466i-5p | BCIN_01g05040 | 1.5 | −38.1 | 1.5 | - | EMR86089.1 |
| miR-466i-5p | BCIN_01g05350 | 3.5 | −34.1 | 3.5 | - | ESZ92622.1 |
| miR-466i-5p | BCIN_01g06010 | 1 | −41.1 | 1 | K11244 | APA06865.1 |
| miR-466i-5p | BCIN_01g06260 | 0.5 | −41.5 | 0.5 | K19691 | AAL30826.1 |
| miR-466i-5p | BCIN_01g06420 | 3 | −34.8 | 3 | K12488 | ESZ98859.1 |
| miR-466i-5p | BCIN_01g06740 | 3.5 | −34.1 | 1.5 | - | XP_001561229.1 |
| miR-466i-5p | BCIN_01g07410 | - | - | 2.5 | - | XP_001561128.1 |
| miR-466i-5p | BCIN_01g07600 | 3.5 | −32.6 | 3.5 | - | XP_001561105.1 |
| miR-466i-5p | BCIN_01g07870 | 2 | −38.1 | 2 | K22193 | CCD45851.1 |
| miR-466i-5p | BCIN_01g09100 | 5 | −30 | 0 | K16055 | XP_001586238.1 |
| miR-466i-5p | BCIN_01g10630 | 0.5 | −39.8 | 0.5 | - | CCD43118.1 |
| miR-466i-5p | BCIN_02g01080 | 4.5 | −35.4 | 3.5 | K03282 | XP_001597483.1 |
| miR-466i-5p | BCIN_02g01870 | 3.5 | −33.9 | 3.5 | K05894 | XP_001558929.1 |
| miR-466i-5p | BCIN_02g02310 | 3 | −35 | 3 | K17262 | XP_001558870.1 |
| miR-466i-5p | BCIN_02g02410 | 3 | −33.3 | 2.5 | K01183 | PBP23908.1 |
| miR-466i-5p | BCIN_02g03320 | 4.5 | −32.9 | 2 | K08064 | EMR82704.1 |
| miR-466i-5p | BCIN_02g03490 | 2 | −38.3 | 2 | K01758 | KIM97697.1 |
| miR-466i-5p | BCIN_02g04210 | 3 | −35.8 | 3 | - | XP_001553733.1 |
| miR-466i-5p | BCIN_02g04230 | 1.5 | −38.1 | 1.5 | K01183 | EMR87251.1 |
| miR-466i-5p | BCIN_02g05030 | 1.5 | −41.1 | 1.5 | K21631 | XP_001546736.1 |
| miR-466i-5p | BCIN_02g05460 | 5 | −32.8 | 3 | K21632 | EMR82905.1 |
| miR-466i-5p | BCIN_02g05590 | 3 | −33 | - | K14568 | EMR82918.1 |
| miR-466i-5p | BCIN_02g07390 | 1 | −40 | 1 | K01183 | EMR81569.1 |
| miR-466i-5p | BCIN_03g00940 | 1 | −40 | 1 | K11294 | XP_001559444.1 |
| miR-466i-5p | BCIN_03g01710 | 4 | −31.7 | 3 | K19851 | CCD43982.1 |
| miR-466i-5p | BCIN_03g01790 | 3 | −35.3 | 3 | K03260 | XP_001559323.1 |
| miR-466i-5p | BCIN_03g02860 | 2 | −38 | 2 | K09510 | XP_001555002.1 |
| miR-466i-5p | BCIN_03g03450 | 3 | −35 | - | K12274 | CCD51846.1 |
| miR-466i-5p | BCIN_03g03920   | 0   | −42.1 | 0   | - | XP_001560602.1 |
| miR-466i-5p | BCIN_03g05330   | 2   | −37.2 | 1.5 | K06215 | CCD51582.1 |
| miR-466i-5p | BCIN_03g06450   | 2.5 | −36.4 | 2.5 | K20100 | CCD51406.1 |
| miR-466i-5p | BCIN_03g07700   | 3   | −35.9 | 3   | K14692 | XP_001546498.1 |
| miR-466i-5p | BCIN_03g08150   | 3.5 | −34.6 | 3   | - | EMR81292.1 |
| miR-466i-5p | BCIN_03g08390   | 0   | −42.1 | 0   | - | XP_001554920.1 |
| miR-466i-5p | BCIN_03g08670   | 5   | −31.1 | 2   | K17808 | XP_001554883.1 |
| miR-466i-5p | BCIN_04g00220   | 4   | −36.4 | 3.5 | K20301 | CCD34150.1 |
| miR-466i-5p | BCIN_04g01650   | 3.5 | −33.1 | 3.5 | K13289 | XP_001554862.1 |
| miR-466i-5p | BCIN_04g02120   | 1.5 | −40.4 | 1.5 | K18045 | XP_001557315.1 |
| miR-466i-5p | BCIN_04g03510   | 3   | −32.8 | -   | K01183 | XP_001546962.1 |
| miR-466i-5p | BCIN_04g05140   | 1.5 | −38.1 | 1.5 | - | EMR86951.1 |
| miR-466i-5p | BCIN_04g06150   | 3   | −34.9 | 3   | K08257 | XP_001557784.1 |
| miR-466i-5p | BCIN_05g00480   | 2   | −37.7 | 2   | K00759 | XP_001550336.1 |
| miR-466i-5p | BCIN_05g01210   | 3.5 | −36.2 | 2.5 | K08257 | A0A0B5L7R4.1 |
| miR-466i-5p | BCIN_05g01350   | 2   | −38.3 | 2   | K03141 | XP_001549029.1 |
| miR-466i-5p | BCIN_05g01560   | 1   | −38.7 | 1   | K17550 | CCD33804.1 |
| miR-466i-5p | BCIN_05g01760   | 3   | −32.7 | -   | - | XP_001548220.1 |
| miR-466i-5p | BCIN_05g02760   | 4   | −34.8 | 3.5 | K03316 | XP_001560021.1 |
| miR-466i-5p | BCIN_05g03070   | -   | -     | 2.5 | - | XP_001559970.1 |
| miR-466i-5p | BCIN_05g04230   | 2.5 | −37   | 2   | K12198 | XP_001559801.1 |
| miR-466i-5p | BCIN_05g06680   | 3   | −36.5 | 2   | K13120 | XP_001559538.1 |
| miR-466i-5p | BCIN_05g06880   | 4   | −31.1 | 2.5 | K08286 | XP_001548082.1 |
| miR-466i-5p | BCIN_05g07180   | -   | -     | 3   | K01539 | XP_001548124.1 |
| miR-466i-5p | BCIN_05g07560   | 4   | −32.8 | 3   | - | XP_001552695.1 |
| miR-466i-5p | BCIN_05g07590   | 1   | −41.7 | 1   | K00108 | XP_001550662.1 |
| miR-466i-5p | BCIN_05g03070   | 3.5 | −33.5 | -   | K01749 | XP_001560154.1 |
| miR-466i-5p | BCIN_05g02840   | -   | -     | 3.5 | - | XP_001560498.1 |
| miR-466i-5p | BCIN_06g02870   | 3   | −36   | 3   | K14758 | EMR88544.1 |
| miR-466i-5p | BCIN_06g02920   | 2   | −36   | 2   | K10689 | XP_001556264.1 |
| miR-466i-5p | BCIN_06g03910   | 3   | −36.8 | 3.5 | K20523 | XP_001556115.1 |
| miR-466i-5p | BCIN_06g03970   | 1   | −40   | 1   | K07297 | EMR86394.1 |
| miR-466i-5p | BCIN_06g04320   | 2.5 | −36.2 | 2.5 | - | CCD56774.1 |
| miR-466i-5p | BCIN_06g05000   | 1.5 | −38.3 | 1.5 | K11552 | EMR87611.1 |
| miR-466i-5p | BCIN_06g05800   | 1.5 | −39.8 | 2   | K21543 | CCD56999.1 |
| miR-466i-5p | BCIN_06g05940   | 4.5 | −33.5 | 3   | K19475 | CCD57022.1 |
| miR-466i-5p | BCIN_06g06360 | 4 | −31.4 | 0 | K11380 | XP_001549253.1 |
| miR-466i-5p | BCIN_06g06500 | - | - | 2.5 | K09584 | XP_001555206.1 |
| miR-466i-5p | BCIN_06g07290 | 3 | −35.1 | 3 | - | XP_001547338.1 |
| miR-466i-5p | BCIN_07g00760 | 3 | −33.4 | 3.5 | K01183 | XP_001556067.1 |
| miR-466i-5p | BCIN_07g01110 | 2 | −36.5 | 2 | K20872 | XP_001551517.1 |
| miR-466i-5p | BCIN_07g01410 | 3.5 | −29.9 | 3.5 | - | EMR91000.1 |
| miR-466i-5p | BCIN_07g01650 | - | - | 3 | - | EMR88033.1 |
| miR-466i-5p | BCIN_07g03500 | 3 | −35.1 | 3 | - | CCD53038.1 |
| miR-466i-5p | BCIN_07g03890 | 0 | −41.9 | 0 | K11294 | CCD52989.1 |
| miR-466i-5p | BCIN_07g04210 | 4 | −33 | 3 | - | - |
| miR-466i-5p | BCIN_07g04420 | 0 | −41.9 | 0 | K19851 | XP_001589337.1 |
| miR-466i-5p | BCIN_07g04430 | 5 | −27.8 | 3 | K19838 | EMR81973.1 |
| miR-466i-5p | BCIN_07g04660 | 5 | −27.7 | 3 | K11872 | CCD52867.1 |
| miR-466i-5p | BCIN_07g04720 | 4 | −33 | 1 | K10688 | XP_001554092.1 |
| miR-466i-5p | BCIN_07g06500 | 3 | −36.4 | 3 | - | EMR91055.1 |
| miR-466i-5p | BCIN_07g06960 | 2 | −37.8 | 2 | K11262 | XP_001592109.1 |
| miR-466i-5p | BCIN_08g00550 | 3 | −36.2 | 3 | K01120 | XP_001552552.1 |
| miR-466i-5p | BCIN_08g01040 | 1.5 | −38.5 | 1.5 | K12879 | CCD43777.1 |
| miR-466i-5p | BCIN_08g01620 | 3 | −33 | - | K19848 | KGY15063.1 |
| miR-466i-5p | BCIN_08g02810 | 3 | −32.4 | 3 | K16216 | XP_001551998.1 |
| miR-466i-5p | BCIN_08g02920 | 3 | −36.2 | 3 | K07836 | APA11004.1 |
| miR-466i-5p | BCIN_08g03300 | 1 | −40 | 1 | - | CCD54028.1 |
| miR-466i-5p | BCIN_08g03490 | 3 | −33.2 | 0 | K20059 | XP_001554617.1 |
| miR-466i-5p | BCIN_08g03550 | 1 | −41.4 | 1 | K02265 | XP_001554609.1 |
| miR-466i-5p | BCIN_08g04300 | 2 | −40.7 | 2.5 | K03099 | CCD51965.1 |
| miR-466i-5p | BCIN_08g05150 | 4.5 | −27 | 2.5 | K11246 | EMR85582.1 |
| miR-466i-5p | BCIN_08g05880 | 0 | −42.1 | 0 | - | EMR85246.1 |
| miR-466i-5p | BCIN_08g06660 | 3.5 | −33 | - | K11294 | EMR85173.1 |
| miR-466i-5p | BCIN_09g00920 | 5 | −25.7 | 2.5 | K09051 | EMR83531.1 |
| miR-466i-5p | BCIN_09g01230 | 3 | −34.9 | 3 | K01115 | CCD55073.1 |
| miR-466i-5p | BCIN_09g02560 | 3 | −34.8 | 3 | K20520 | CCD44478.1 |
| miR-466i-5p | BCIN_09g03930 | 4.5 | −30.1 | 3.5 | K14171 | XP_001551558.1 |
| miR-466i-5p | BCIN_09g04170 | 2 | −36.7 | 2.5 | K00844 | EMR80470.1 |
| miR-466i-5p | BCIN_09g04550 | 1.5 | −38.6 | 1.5 | K03114 | EMR90311.1 |
| miR-466i-5p | BCIN_09g04580 | 3.5 | −31.1 | 3 | K14692 | XP_001593574.1 |
| miR-466i-5p | BCIN_09g04680 | 4 | −33 | 2.5 | K05747 | EMR90324.1 |
| miR-466i-5p | BCIN_09g06110 | 0 | −42.1 | 0 | K01638 | CZT05650.1 |
| miR-466i-5p | BCIN_09g06400 | - | - | 3.5 | K21421 | CCD50097.1 |
| miR-466i-5p | BCIN_10g00500 | - | - | 2.5 | - | XP_001554208.1 |
| miR-466i-5p | BCIN_10g00940 | 3 | −36.2 | 3.5 | - | CCD49535.1 |
| miR-466i-5p | BCIN_10g01220 | 0 | −41.8 | 4 | K03360 | XP_001555738.1 |
| miR-466i-5p | BCIN_10g01230 | 2.5 | −36 | 2.5 | K03006 | XP_001555736.1 |
| miR-466i-5p | BCIN_10g01600 | 3.5 | −36.2 | 3.5 | K01469 | XP_001555688.1 |
| miR-466i-5p | BCIN_10g02300 | 2.5 | −36.8 | 3.5 | K11397 | XP_001557022.1 |
| miR-466i-5p | BCIN_10g02590 | 3 | −34.2 | 3 | K16186 | EMR82676.1 |
| miR-466i-5p | BCIN_10g03080 | 2.5 | −34.8 | 2 | K00306 | CCD44963.1 |
| miR-466i-5p | BCIN_10g03170 | 3 | −38.3 | - | K10669 | XP_001548061.1 |
| miR-466i-5p | BCIN_10g03190 | 4.5 | −34.1 | 3.5 | K11240 | XP_001548056.1 |
| miR-466i-5p | BCIN_10g03450 | 4 | −31.3 | 1 | - | CCD49648.1 |
| miR-466i-5p | BCIN_10g04090 | 1 | −38.1 | 1 | K01210 | CCD43696.1 |
| miR-466i-5p | BCIN_10g04630 | 2.5 | −36.4 | 3 | K00002 | XP_001557399.1 |
| miR-466i-5p | BCIN_10g04640 | 3.5 | −34.6 | 3 | K01183 | CCD51011.1 |
| miR-466i-5p | BCIN_10g05690 | 4.5 | −30.3 | 1.5 | - | CCD50870.1 |
| miR-466i-5p | BCIN_10g05760 | 3 | −32.9 | - | K01183 | XP_001551433.1 |
| miR-466i-5p | BCIN_10g05970 | 3.5 | −34 | 3 | K03260 | CCD34756.1 |
| miR-466i-5p | BCIN_10g06070 | 1 | −41.3 | 1 | K20523 | XP_001554980.1 |
| miR-466i-5p | BCIN_10g06080 | 3.5 | −35.6 | - | K05857 | CCD34776.1 |
| miR-466i-5p | BCIN_11g00690 | 1.5 | −40.7 | 1.5 | - | CCD34074.1 |
| miR-466i-5p | BCIN_11g00730 | 2 | −38.1 | 2 | - | CCD49456.1 |
| miR-466i-5p | BCIN_11g02230 | 4.5 | −28.8 | 2 | K11761 | CCD47729.1 |
| miR-466i-5p | BCIN_11g02410 | 3.5 | −35 | - | K21989 | EMR89730.1 |
| miR-466i-5p | BCIN_11g03290 | 2.5 | −37.7 | 2.5 | K21543 | XP_001556845.1 |
| miR-466i-5p | BCIN_11g04340 | 1 | −41.4 | 0.5 | K11680 | XP_001558503.1 |
| miR-466i-5p | BCIN_11g05770 | 3.5 | −36.1 | 3.5 | K03321 | EMR90820.1 |
| miR-466i-5p | BCIN_11g05820 | 2.5 | −32.2 | 2.5 | - | CCD50386.1 |
| miR-466i-5p | BCIN_11g06110 | 3 | −34.4 | - | K19800 | EMR84088.1 |
| miR-466i-5p | BCIN_12g00490 | 3.5 | −34.5 | 3.5 | K01183 | CCD45324.1 |
| miR-466i-5p | BCIN_12g00740 | 3.5 | −33 | - | K17652 | XP_001557920.1 |
| miR-466i-5p | BCIN_12g01240 | 4 | −36.8 | 2 | - | XP_001557861.1 |
| miR-466i-5p | BCIN_12g01830 | 3.5 | −32.8 | - | K00953 | XP_001550264.1 |
| miR-466i-5p | BCIN_12g01870 | 3.5 | −30.8 | 3.5 | K00344 | XP_001550258.1 |
| miR-466i-5p | BCIN_12g02110 | 2.5 | −34.9 | 3 | - | XP_001558052.1 |
| miR-466i-5p | BCIN_12g03180 | 0 | −41.9 | 0 | K00327 | CZR63224.1 |
| miR-466i-5p | BCIN_12g03620 | 1 | −37.1 | 2 | K00915 | XP_001552249.1 |
| miR-466i-5p | BCIN_12g03630 | 3 | −37.7 | 3 | - | CCD52608.1 |
| miR-466i-5p | BCIN_12g04510 | 1.5 | −38.7 | 4 | K11231 | CCD52712.1 |
| miR-466i-5p | BCIN_13g00890 | 3.5 | −37.4 | 4 | K11254 | CEF85879.1 |
| miR-466i-5p | BCIN_13g01840 | 2.5 | −36.2 | 2.5 | K12734 | CCD54500.1 |
| miR-466i-5p | BCIN_13g02670 | 3.5 | −32.8 | 3.5 | K03381 | CCD54378.1 |
| miR-466i-5p | BCIN_13g04520 | 2.5 | −40.6 | 2.5 | K08052 | APA15577.1 |
| miR-466i-5p | BCIN_13g05060 | 3.5 | −34.3 | 3.5 | - | XP_001554822.1 |
| miR-466i-5p | BCIN_14g01000 | 3 | −34.2 | 3.5 | - | XP_001550102.1 |
| miR-466i-5p | BCIN_14g02450 | 3.5 | −33 | - | K18338 | XP_001553175.1 |
| miR-466i-5p | BCIN_14g03390 | 3 | −35.3 | 3 | K01915 | XP_001549470.1 |
| miR-466i-5p | BCIN_14g03860 | 3 | −34.6 | 4 | K12765 | CCD50088.1 |
| miR-466i-5p | BCIN_14g04700 | 4 | −28.4 | 1 | K07766 | XP_001546171.1 |
| miR-466i-5p | BCIN_14g05050 | 0 | −41.8 | 0 | K03510 | CCD43659.1 |
| miR-466i-5p | BCIN_15g00300 | 3.5 | −35.4 | 3.5 | - | XP_001548800.1 |
| miR-466i-5p | BCIN_15g00970 | 2.5 | −34.9 | 2.5 | K11273 | EMR89121.1 |
| miR-466i-5p | BCIN_15g01330 | 5 | −35.7 | 3 | K19860 | CCD47474.1 |
| miR-466i-5p | BCIN_15g02150 | 3.5 | −34.9 | 3 | K19691 | AAR30107.1 |
| miR-466i-5p | BCIN_15g02270 | 3 | −29.7 | - | K00693 | OWP03119.1 |
| miR-466i-5p | BCIN_15g02310 | 4.5 | −31.1 | 1 | - | XP_001549572.1 |
| miR-466i-5p | BCIN_15g02590 | 1.5 | −37.8 | 1.5 | K01768 | CCD47303.1 |
| miR-466i-5p | BCIN_15g05360 | 4.5 | −32.6 | 2.5 | K00965 | CCD43388.1 |
| miR-466i-5p | BCIN_16g00370 | 2.5 | −36.3 | 2.5 | K04705 | CCD49400.1 |
| miR-466i-5p | BCIN_16g01160 | 2 | −38.5 | 1.5 | K17781 | XP_001545267.1 |
| miR-466i-5p | BCIN_16g01560 | 1 | −37.4 | 1 | K07238 | EMR81335.1 |
| miR-466i-5p | BCIN_16g02440 | 4 | −31.2 | 2 | K00111 | CCD48688.1 |
| miR-466i-5p | BCIN_16g02880 | 3 | −34.3 | 3 | K11877 | XP_001551858.1 |
| miR-466i-5p | BCIN_16g04000 | 0.5 | −40 | 0.5 | K18748 | APA15448.1 |
| miR-466i-5p | BCIN_16g04330 | 5 | −27.7 | 3.5 | K03083 | CCD55978.1 |
| miR-466i-5p | BCIN_16g04910 | 3 | −34.3 | 0 | K11238 | EMR80965.1 |
| novel_mir5 | BCIN_09g00390 | 2 | −43.1 | 2 | - | XP_001552636.1 |
| novel_mir5 | BCIN_14g00350 | 0 | −49.3 | 0 | K21440 | EMR91141.1 |

The “-” indicates “not applicable”; MFE: minimum free energy; NR: non-redundant database.