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Jian Wang, Emory University
Zongcheng Li, Beijing Institute of Basic Medical Sciences
Bailong Liu, Emory University
Guangnan Chen, Emory University
Ningsheng Shao, Beijing Institute of Basic Medical Sciences
Xiaomin Ying, Beijing Institute of Basic Medical Sciences
Ya Wang, Emory University

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Systematic study of cis-antisense miRNAs in animal species reveals miR-3661 to target PPP2CA in human cells

JIAN WANG,1,4 ZONGCHENG LI,2,4 BAILONG LIU,1,3 GUANGNAN CHEN,1 NINGSHENG SHAO,2 XIAOMIN YING,2 and YA WANG1
1Department of Radiation Oncology, Emory University School of Medicine, Winship Cancer Institute of Emory University, Atlanta, Georgia 30322, USA
2Beijing Institute of Basic Medical Sciences, Beijing 100850, China
3The First Norman Bethune Hospital of Jilin University, Changchun 130012, China

ABSTRACT
MicroRNAs (miRNAs) suppress targeting gene expression through blocking translation or triggering mRNA degradation and, in general, act in trans, through a partially complementary interaction with the 3′ untranslated region (3′ UTR) or coding regions of a target gene. Although it has been reported previously that some miRNAs suppress their target genes on the opposite strand with a fully complementary sequence (i.e., natural antisense miRNAs that act in cis), there is no report to systematically study such cis-antisense miRNAs in different animal species. Here we report that cis-antisense miRNAs do exist in different animal species: 48 in Caenorhabditis elegans, 17 in Drosophila, 36 in Mus musculus, and 52 in Homo sapiens using a systematical bioinformatics approach. We show that most of these cis-antisense miRNAs can efficiently reduce the expression levels of their target genes in human cells. We further investigate hsa-miR-3661, one of the predicted cis-antisense miRNAs, in detail and demonstrate that this miRNA directly targets the coding sequence of PPP2CA located on the opposite DNA strand and inhibits the PPP2CA expression. Taken together, these results indicate that cis-antisense miRNAs are conservative and functional in animal species including humans.

Keywords: miRNA; cis-antisense; gene expression; miR-3661; PPP2CA; human cells

INTRODUCTION
MicroRNAs (miRNAs) are a class of small RNA genes with 21–25 nt, which regulate their target genes in various species. Most animal miRNAs regulate the expression of other genes predominantly in trans through partially complementary interactions with 3′ untranslated regions (3′ UTRs) or transcript coding regions of the target genes. However, some animal miRNAs are discovered as transcribed antisense to exons of noncoding or protein-coding genes (Bartel 2004). Such antisense exonic miRNAs, together with the intronic miRNAs and the miRNAs in the sense strand of genes, are termed as intragenic miRNAs (Rodriguez et al. 2004; Hinske et al. 2010, 2014). The function of such antisense exonic miRNAs were investigated in mouse miR-126 and miR-136 that are transcribed antisense of a retrotransposon-like gene (RTL1) and a down-regulated RTL1 mRNA level through a fully complementary sequence match with the target gene (Seitz et al. 2003). These cis-antisense exonic miRNAs are similar to the natural antisense miRNAs (nat-miRNAs) reported later in the plant (Lu et al. 2008), but with one main difference: cis-antisense miRNAs are derived from precursors with a compact hairpin, whereas nat-miRNAs are derived from the precursors with large introns. To date, cis-antisense miRNAs were only reported in mouse; whether these cis-antisense miRNAs functionally exist in various animal species including humans has not been systematically studied.

To address this question, we performed a genome-wide analysis to identify miRNAs that are transcribed antisense to exons of known genes. As a result, we found that such cis-antisense miRNAs with a fully complementary antisense sequence against their target (protein-coding or noncoding) genes exist in different animal species: 48 in C. elegans, 17 in Drosophila, 36 in mouse, and 52 in the human genome (including miR-127/136 as reported [Seitz et al. 2003]). We then demonstrated that almost all of the cis-antisense miRNAs efficiently suppressed the expression levels of their target genes in human cells. We further studied in detail the effects of one cis-antisense miRNA, miR-3661, on its target gene, PPP2CA.

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PP2Acα is the catalytic subunit of PP2A and encoded by the \textit{PPP2CA} gene. PP2A is one of the major cellular serine–threonine phosphatases (Wera and Hemmings 1995). PP2A is a bona fide tumor suppressor consisting of multiple different subunits and targets a multitude of substrates (Janssens and Goris 2001; Sablina and Hahn 2008). PP2Acα is highly conserved from yeast to human. Loss-of-function mutations in PP2A subunits or up-regulation of PP2A-specific inhibitors that contribute to transformation were found in a variety of cancers (Eichhorn et al. 2009). One of the most important dephosphorylating substrates for PP2A is AKT (Andjelković et al. 1996; Meier et al. 1998; Chen et al. 1999; Sato et al. 2000; Ivaska et al. 2002; Resjö et al. 2002). PP2A negatively regulates the AKT pathway by dephosphorylating AKT itself (Ivaska et al. 2002; Resjö et al. 2002). PP2A negatively regulates the AKT pathway by dephosphorylating AKT itself and GSK-3β, an AKT-phosphorylated target (Shaw et al. 1997), which plays a critical role in cell proliferation, unlike the regulation of PP2A at the transcriptional level that has been reported in detail (Altiok et al. 1997; Chen et al. 2009; Liu et al. 2012). There are few reports on the regulation of \textit{PPP2CA} at the post-transcriptional level, particularly via a miRNA-related regulation. Only recently, it was reported that miR-155 can negatively regulate PP2A (Lashine et al. 2015). Our results indicate that miR-3661 can regulate \textit{PPP2CA} expression in human cells in a \textit{cis}-antisense manner. These results demonstrate that the \textit{cis}-antisense miRNAs conservatively and functionally exist in humans.

\section*{RESULTS}

\textbf{Fifty-two potential \textit{cis}-antisense miRNAs and their antisense transcribed genes are identified in the human genome}

We performed a genome-wide analysis to identify miRNAs that are transcribed antisense to known genes (Fig. 1A). In the human (\textit{Homo sapiens}) genome, 432 miRNAs were found in the antisense orientation of 313 protein-coding/noncoding genes. Among the 432 miRNAs, 380 miRNAs that are in the opposite DNA strands at the genomic locus of introns of 280 genes were excluded from this study. Finally 52 miRNAs (including miR-127/136 as reported [Seitz et al. 2003]) were identified as the candidates for suppressing the expression of their 33 antisense target genes in a \textit{cis}-antisense manner with fully complementary sequences (Table 1). Among the 52 miRNAs, 25 miRNAs target coding sequence (CDS) (including miR-127/136 as reported [Seitz et al. 2003]) and 27 miRNAs target noncoding sequence including exons, noncoding genes 3'/5' UTR of protein-coding genes (Table 1). To identify the \textit{cis}-antisense miRNAs in other animal species, we applied the same analysis procedure to \textit{Mus musculus} (\textit{M. musculus}), \textit{Drosophila melanogaster} (\textit{D. melanogaster}), and \textit{Caenorhabditis elegans} (\textit{C. elegans}). As a result, we identified 235 miRNAs in \textit{M. musculus}, 66 miRNAs in \textit{D. melanogaster}, and 177 miRNAs in \textit{C. elegans} genome, in the \textit{cis}-antisense orientation of protein-coding/noncoding genes, respectively. After excluding the miRNA transcribed antisense to the introns of genes, finally 36 (\textit{M. musculus}), 17 (\textit{D. melanogaster}), and, 48 (\textit{C. elegans}) \textit{cis}-antisense miRNAs were obtained (Supplemental Tables 1–3).

\textbf{Most of the identified \textit{cis}-antisense miRNAs functionally suppress their targets in humans}

Next, we were interested in determining whether these human miRNAs can biologically suppress their antisense target genes. Among the 52 miRNAs, 30 miRNAs are from 15 precursors (5p and 3p strands of a pre-miRNA) targeting the same gene (Table 1), and 22 miRNA target genes individually. Therefore, we tested the 37 miRNAs for functional measurement. We obtained 29 commercially available miRNA mimics and the TaqMan assays of their target genes. We transfected these miRNA mimics to 293FT cells and measured their target expressions using a real-time PCR approach. The results showed that most miRNA mimics can efficiently suppress the expression of their targets (Fig. 1B); only three miRNA mimics could not suppress their antisense targets: miR-4665-5p targeting the 5' UTR of KIAA2026, miR-136-5p targeting the CDS of \textit{RL1}, and miR-3665 targeting the CDS of \textit{SLAN1} (Table 1; Fig. 1B). These results indicate that most of the \textit{cis}-antisense miRNAs are functional.

\textbf{MiR-3661 specifically targets \textit{PPP2CA} in human cells}

To further elucidate the functions of miRNAs acting in human cells, we chose miR-3661 because it targets \textit{PPP2CA}, an important catalytic subunit of PP2A. MiR-3661 was first identified in 2010 (Hansen et al. 2010) and then further confirmed by another group (Persson et al. 2011); however, its function remains unclear. We found that miR-3661 is located on the opposite strand of \textit{PPP2CA}, the PP2Acα protein-coding region (Fig. 2A). A perfect complementary sequence exists between miR-3661 and the \textit{PPP2CA} gene (Fig. 2B). The Northern blot data confirmed that miR-3661 is an expressed miRNA (Fig. 2C). To examine the relative expression pattern between miR-3661 and the \textit{PPP2CA} gene, we compared the RNA levels of miR-3661 and \textit{PPP2CA} in different human cell lines. The results showed a moderate positive correlation with high confidence between the expression of miR-3661 and the \textit{PPP2CA} gene (Fig. 2D,E), suggesting that the miR-3661 and \textit{PPP2CA} genes have a correlating expression profile.

Because \textit{PPP2CA} has another isoform, \textit{PPP2CA}-iso (Migueleti et al. 2012), and the two forms share the same miR-3661 target sequence, we then investigated whether \textit{PPP2CA}-iso can also be efficiently targeted by miR-3661. For this purpose, we examined the effects of miR-3661 targeting \textit{PPP2CA} and \textit{PPP2CA}-iso in different cell lines: MRC5SV (transformed fibroblast), Beas2B (transformed lung epithelial cells), H1299 (lung tumor cells), and A549 (lung tumor cells). The results showed that similar to \textit{PPP2CA}, \textit{PPP2CA}-iso is also
efficiently suppressed by miR-3661 (Fig. 3A), indicating that both *PPP2CA* and its isoform are good targets of miR-3661. In addition, the protein levels of PP2Acα were efficiently suppressed by miR-3661 in different cell lines as well (Fig. 3B). To further study the specific effect of miR-3661 on the suppression of *PPP2CA*, we compared the effects of miR-3661 and different miRNAs (including miR-3133, miR-4282, miR-3607, miR-4703, and miR-4277) that are predicted (using miRanda [Betel et al. 2008] and TargetScan software [Lewis et al. 2005]) to have a potential for targeting 3′ UTR of *PPP2CA* in 293FT cells. The results showed that only the miR-3661 mimic efficiently suppressed the PP2Acα protein level, and all other miRNA mimics, similar to the control RNA, had no effect (Fig. 3C). Combining the transfection of the miR-3661 mimic and the miR-3661 inhibitor blocked the suppression effect of the miR-3661 mimic alone on the PP2Acα protein level (Fig. 3D). Next, we designed and constructed a vector encoding a Flag-tagged PPP2CA mutated at the targeting sequence by miR-3661 (Fig. 3E, left panel). The data showed that the mutant Flag-PP2Acα protein level cannot be affected by the miR-3661 mimic although the wild-type Flag-PP2Acα can be suppressed successfully (Fig. 3E, right panel). These results clearly demonstrate that the effect of the miR-3661 on suppressing the PP2Acα protein level is specific.

**Suppression of PP2Acα by miR-3661 increased its target phosphorylation in human cells**

Next, we wanted to know whether pri-miR-3661 can be processed to a mature miRNA in cells and whether the
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*aType of antisense gene includes protein-coding gene and noncoding gene. Some genes encode both protein-coding genes and noncoding genes in alternative isoforms. If a miRNA is in the opposing DNA strand of both protein-coding and noncoding isoforms, both two types will be listed.

bComplementary sites in the gene denotes the sites in the gene that a miRNA might bind it with perfect matches. For protein-coding genes, five types of complementary sites—that is, 5’ UTR, 3’ UTR, CDS, Intron-3’ UTR, and IGR-5’ UTR—are involved. IGR stands for intergenic region. For noncoding genes, exon and intron-exon are involved. If a miRNA is in the opposing DNA strand of both protein-coding and noncoding isoforms, the complementary sites in the two isoforms will be listed correspondingly.
Cis-antisense miRNAs functionally exist in human cells

Most miRNAs are found to suppress the expression of genes prevalently in trans. Some miRNAs are located within genomic regions of protein-coding genes or noncoding genes (Rodriguez et al. 2004; Hinske et al. 2010, 2014). These intragenic miRNAs were studied with their host genes and the results suggest that a complex transcription and regulation relationship exists between them (Monteys et al. 2010; Yan et al. 2011; Son et al. 2014). The subset of intragenic miRNAs, cis-antisense miRNAs that are transcribed antisense to exons of protein-coding or noncoding genes, is rarely studied. Although it has been reported that miR-127/136 in mouse cells is located on the opposite strand of RTL1 (Seitz et al. 2003), there is no report until now to systematically study whether the cis-antisense miRNAs functionally exist in different animal species. In this study, by systematically analyzing genomes from different animal species, we identified 52 cis-antisense miRNAs in the human (Homo sapiens), 48 in the C. elegans, 17 in the Drosophila, and 36 in the mouse (Mus musculus) genome.

Then, we performed biological studies and showed that most cis-antisense miRNAs can suppress their targets well in human cells. We further investigated in detail the relationship between one of our predicted cis-antisense miRNAs, miR-3661, and its target PPP2CA in human cells. Our results showed that miR-3661 can efficiently suppress PPP2CA.

Among the 29 tested cis-antisense miRNAs, three (miR-4665-5p, miR-136-5p, and miR-3665) did not suppress their targets (Fig. 1B), which might be due to the following two reasons. One is that the three miRNAs may only inhibit the translation of the target genes, instead of triggering target degradation. The other is that the three miRNAs are all located near the 5’ end of the target genes and this region may form a complex structure that hinders the interaction of these miRNAs and their target RNAs. Target site accessibility has been found to be very important for miRNA recognition and targeting effectiveness (Kertesz et al. 2007). Of course, these possibilities need to be verified in future studies. Our results, the positive data from 26 among 29 tested miRNAs, indicate that most of the cis-antisense miRNAs are functional. We also investigated whether there were other miRNAs that had the potential to target 3’ UTR of PPP2CA. Using

mature miR-3661 can functionally target PP2Aca. For this purpose, we first constructed the vectors encoding pri-miR-3661 (miR-3661-1 and miR-3661-2) with different lengths at the 5’ and 3’ flanking sequences (Fig. 4A). After transfecting the plasmid into 293FT cells, both pri-miR-3661 plasmids (miR-3661-1 and miR-3661-2) resulted in a significant increase in the mature miR-3661 levels (Fig. 4B), supporting that pri-miR-3661 can be processed well to mature miR-3661 in the cells. At the same time, both pri-miR-3661 plasmid transfections efficiently decreased the levels of PPP2CA mRNA and protein, and increased the phosphorylation levels of AKT or GSK-3β (dephosphorylating substrates of PP2A) (Fig. 4C,D), supporting that pri-miR-3661 functionally targets PP2Aca. These results clearly indicate that the PP2A function is suppressed by miR-3661 to directly target PPP2CA.

DISCUSSION

FIGURE 2. MiR-3661 is located on the opposite strand of the PPP2CA coding region in the human genome. (A) The genomic view of the PPP2CA and miR-3661 genes: coding sequence (CDS), untranslated region (UTR), and miRNA regions are represented as orange, yellow, and green bars, respectively. (AS) antisense strand, (SS) sense strand. The model for cis-antisense miRNA biosynthesis and function: the miRNA processing initiated with the splicing of pri-miRNA transcripts to yield pre-miRNA hairpins that are transported to cytoplasm. After Dicer cleavage, the mature miRNAs bind to target RNAs and direct the translation inhibition or cleavage of the sense transcripts of their targets. (B) The perfect complementary between PPP2CA and miR-3661. The binding positions are shown above (PPP2CA) and below (miR-3661) the sequences. (C) The mature miR-3661 was identified in 293FT cells using a Northern blot. The left lane was the synthetic DNA sequence of the miR-3661, which was as the positive control, and the right lane was the total RNA of 293FT cells. (D) RNA levels of PPP2CA and miR-3661 were measured from various human cell lines as indicated. (E) Scatterplots illustrating the correlation of gene expressions between PPP2CA and Hsa-miR-3661 from various human cell lines as indicated.
miRanda (Betel et al. 2008) and TargetScan software (Lewis et al. 2005), we predicted several miRNAs that target 3’ UTR of PPP2CA; however, none of them could efficiently suppress the PPP2CA expression as miR-3661 does (Fig. 3C). These results indicate that miR-3661 is the most efficient miRNA to target PPP2CA because of its perfect complementarity to the target as compared with other 3’ UTR-targeting miRNAs.

Our results indicate that cis-antisense miRNAs function as a natural post-transcriptional regulator for the antisense transcribed genes. Because cis-antisense miRNAs and their antisense transcribed genes are on opposite strands, it is possible that they have their own transcripational regulation. However, a correlational expression between miRNAs and their targets has been reported previously (Wang and Li 2009), although the underlying mechanism remains unclear. We also found a positive correlation between PPP2CA and miR-3661 ($R^2 = 0.6451$; Fig. 2E). We thought that miR-3661 and PPP2CA might share the same enhancers or silencers or be under the same locus control region (LCR) because of the opposite strand location. Again, the prediction needs to be verified in future studies. In addition, our data do not exclude the other regulations of PPP2CA because of the importance of PP2A for normal physiologic cellular function. When PPP2CA was dramatically decreased by miR-3661, cells may have compensatively up-regulated PPP2CA via other pathways to maintain its normal function. A moderate positive correlation ($R^2 = 0.6451$) between PPP2CA and miR-3661 also suggests the involvement of other regulation pathways. Thus, what we show in this study added miR-3661 as a new regulation factor to maintain the balance of PPP2CA, which contributes to the homeostasis of PP2A function.

In this study, we systematically investigated whether the antisense exonic miRNAs could regulate the target genes in the opposite strand in cis. The results showed that the cis-

FIGURE 3. MiR-3661 specifically targets PPP2CA expression in human cells. (A) RNA levels of PPP2CA and PPP2CA-iso were measured from different human cell lines, MRC5SV, Beas2B, A549, and H1299, that were transfected with the control RNA (mock) or miR-3661 mimic at 30 nM final concentration. (B) The protein levels of PP2Aα were measured from MRC5SV, Beas2B, A549, and H1299 cells transfected with the control RNA (mock) or miR-3661 mimic at 30 nM final concentrations. β-actin was used as the internal loading control. (C) The protein levels of PP2Aα were measured from 293FT cells transfected with 30 nM of a control RNA or the predicted miRNAs as indicated. (D) The protein levels of PP2Aα were measured from 293FT cells transfected with the control RNA (mock), miR-3661 mimic alone or together with a miR-3661 inhibitor at 30 nM final concentration. (E) (Left panel) the top sequence is the mutant plasmid construction of PPP2CA, light gray: the mutated sites of the PPP2CA sequence targeted by Hsa-miR-3661 (bottom sequences). (Right panel) The protein levels of Flag-PP2Aα were measured from 293FT cells transfected with 30 nM of wild-type (WT) or mutant (MT) Flag-PP2Aα together with the mock or miR-3661.

FIGURE 4. Suppression of PP2A by miR-3661 increases its target phosphorylation in human cells. (A) Schematic overview of pri-miR-3661 expression plasmids. (B) The RNA levels of Hsa-miR-3661 were measured from 293FT cells transfected with the control vector and two constructs of pri-miR-3661 expression plasmids. (C) The mRNA levels of PPP2CA and PPP2CA-iso were measured from 293FT cells transfected with the control vector and two constructs of pri-miR-3661 expression plasmids. (D) The protein levels of PP2Aα, phosphorylated AKT (p-AKT), AKT, phosphorylated GSK-3β (p-GSK-3β), and GSK-3β were measured from 293FT cells transfected with the control vector and two constructs of pri-miR-3661 expression plasmids.
antisense miRNAs effectively suppressed the target genes transcribed in the opposite strand. However, cis-antisense miRNAs may also have other targets regulated in trans. For example, hsa-miR-135a-5p is validated to suppress the expression level of antisense transcribed gene GLYCTK in our study (Fig. 1B). It was also reported to regulate the expression of JAK2, NR3C2, APC, HOX10, and MYC in trans from miRTarBase, which contains the largest amount of validated miRNA–target interactions (Supplemental Fig. 1; Kozomara and Griffiths-Jones 2014). Whether cis-antisense miRNAs regulate cis- and trans-targets simultaneously or separately needs further verification.

Taken together, we report for the first time that cis-antisense miRNAs are functional in different animal species, particularly in humans. Such conserved cis-antisense regulation for some miRNAs may play an important role in adjusting their targeting gene expressions.

MATERIALS AND METHODS

Genome-wide identification of potential cis-antisense miRNAs and their antisense transcribed genes

The sequence and genomic annotations of human miRNAs were obtained from a miRBase database release 21 (Kozomara and Griffiths-Jones 2014). The sequences of protein-coding and non-coding genes were downloaded from the RefSeq database (Pruitt et al. 2014) and the genomic annotations from the UCSC genome browser (Karolchik et al. 2014). The genomic annotations of miRNAs and RefSeq genes were both based on the human genome assembly GRCh38. By comparing the genomic loci of miRNAs and exons of RefSeq genes, all the miRNAs that overlapped with the antisense exons were obtained for sequence analysis. The identified miRNAs were further validated by aligning each miRNA to the antisense gene sequences with the parameters “-word_size 11 -perc_identity 100 -strand minus -ungapped” (Altschul et al. 1990). The miRNAs that had a perfect complementary to the antisense miRNAs were validated as potential cis-antisense miRNAs. The same analysis procedure was performed to identify potential cis-antisense miRNAs in the other three species: D. musculus, D. melanogaster, and C. elegans. All the analyses were performed in the R programming language (version 3.0.2).

Cell lines and culture

Human cell lines—293FT (transformed embryo kidney cells, purchased from Invitrogen), MRC5SV (transformed human fibroblasts, as described previously [Liu et al. 2015]), U87MG (brain tumor cells, purchased from ATCC), MIA PaCa-2 (pancreatic carcinoma cells, purchased from ATCC), and T686E (oral squamous cells, obtained from Dr. Georgia Chen’s laboratory [Shin et al. 2013])—were grown in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum (FBS). CEM cells (leukemic cells, purchased from ATCC) were grown in MEM supplemented with 10% FBS. 3KT cells (hTERT-immortalized bronchial epithelial cells, obtained from Dr. Shay’s laboratory [Ramirez et al. 2004]) were grown in keratinocyte-SFM medium (purchased from Invitrogen). Beas2B cells (transformed human bronchial epithelial cells, purchased from ATCC) were grown in Dulbecco’s Modified Eagle’s Medium/Nutrient Mixture F-12 Ham supplemented with 10% FBS. Small cell lung cancer cell lines, DMS114 and DMS153, were purchased from ATCC and grown in Waymouth’s MB 752/1 medium supplemented with 10% FBS. Non-small cell lung cancer (NSCLC) cell lines, A549, H1299, and H460, were purchased from ATCC and grown in RPMI 1640 medium supplemented with 10% FBS. hESC-H9 cells (human embryonic stem cells) were purchased from WISC Stem Cell Bank and grown on BD Matrigel.

RNA isolation, RT-PCR, and real-time PCR

Total RNA was extracted from human cells using miRNasy mini kits (QIAGEN). cDNA was synthesized using 500 ng of total RNA from each sample using the SuperScript VIVO cDNA Synthesis Kit (Life Technologies), followed by triplicate qPCR reactions using TaqMan assays with the TaqMan Fast PCR Universal master mix on an Applied Biosystems 7500 Fast real-time PCR system. For miRNA, a TaqMan miRNA reverse transcription kit was used to prepare the products for the TaqMan miRNA assays as described previously (Liu et al. 2015). RNA levels of PPP2CA and its isoform were measured...
using primers to detect either the standard (Forward1: 5-GAT CTT TCT ACA TGG TGG TCT C-3 and Reverse1: 5-ACA CAT TGG ACC CTC ATG GGG AA-3) or the novel isoform (Forward1 and Reverse2: 5-CCA GTT ATA TCC CTC ATG GGG AAC-3). GAPDH was used as an internal control (forward primer: 5-TGC ACC ACC AAC TGC TTA GC-3; reverse primer: 5-GGC ATG GAC TGT GGT CAT GAG-3).

**SUPPLEMENTAL MATERIAL**

Supplemental material is available for this article.

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Jian Wang, Zongcheng Li, Bailong Liu, et al.

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