Functional Characterization of Alternatively Spliced Human SECISBP2 Transcript Variants

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Functional characterization of alternatively spliced human SECISBP2 transcript variants

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ABSTRACT

Synthesis of selenoproteins depends on decoding of the UGA stop codon as the amino acid selenocysteine (Sec). This process requires the presence of a Sec insertion sequence element (SECIS) in the 3'-untranslated region of selenoprotein mRNAs and its interaction with the SECIS binding protein 2 (SBP2). In humans, mutations in the SBP2-encoding gene Sec insertion sequence binding protein 2 (SECISBP2) that alter the amino acid sequence or cause splicing defects lead to abnormal thyroid hormone metabolism. Herein, we present the first in silico and in vivo functional characterization of alternative splicing of SECISBP2. We report a complex splicing pattern in the 5'-region of human SECISBP2, wherein at least eight splice variants encode five isoforms with varying N-terminal sequence. One of the isoforms, mtSBP2, contains a mitochondrial targeting sequence and localizes to mitochondria. Using a minigene-based in vivo splicing assay we characterized the splicing efficiency of several alternative transcripts, and show that the splicing event that creates mtSBP2 can be modulated by antisense oligonucleotides. Moreover, we show that full-length SBP2 and some alternatively spliced variants are subject to a coordinated transcriptional and translational regulation in response to ultraviolet type A irradiation-induced stress. Overall, our data broadens the functional scope of a housekeeping protein essential to selenium metabolism.

INTRODUCTION

Selenocysteine (Sec), the 21st amino acid in the genetic code, is incorporated into a subset of proteins termed selenoproteins in response to an in-frame UGA codon (1). Since the UGA codon most commonly signals translation termination, its decoding as Sec relies on the presence of several unique, evolutionary conserved structures and protein factors. The major cis-acting determinant for Sec incorporation is the Sec insertion sequence (SECIS) element, a stem–loop RNA structure located within the 3'-untranslated region (UTR) of all eukaryotic selenoprotein mRNAs (2,3). This element acts by recruiting the specialized protein complexes required for the read-through of UGA and translation of selenoproteins. An additional RNA structure able to support UGA codon read-through, named the Sec redefinition element (SRE), has been recently identified within the coding region of selenoprotein N, a few nucleotides downstream of the UGA codon (4). While the SECIS element is absolutely required for Sec incorporation, the SRE appears to play only a fine-tuning role in determining the UGA decoding efficiency for some selenoproteins (5). Synthesis, delivery and incorporation of Sec into polypeptide chains is supported by selenocysteyl-tRNA[Ser]Sec(1) and by a set of specialized proteins [reviewed in (6)], including SECIS binding protein 2 (SBP2) (7,8), Sec-specific elongation factor eEFSec (9,10), ribosomal protein L30 (11),

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the 43 kDa RNA binding protein (SECp43) and Sec synthase (12). Although much progress has been made in delineating individual components required for selenoprotein synthesis, the overall mechanism that directs this process is not fully understood.

SBP2 is one of the most studied selenoprotein synthesis factors, initially shown to be required for this process in reticulocyte lysates and in vitro assays (8,13). Consistent with this, we have shown that SBP2 depletion in human cells leads to decreased selenoprotein synthesis (14). Hereafter, we refer to SBP2 as protein, whereas Sec insertion sequence binding protein 2 (SECISBP2) in italicized letters refers to gene or transcript. The first in vivo evidence showing that SBP2 is epistatic to selenoprotein synthesis was recently provided in a study that identified mutations in SECISBP2 in families presenting with clinical evidence of abnormal thyroid hormone metabolism (15). This was manifested through lack of functional selenoenzyme deiodinase 2 (DIO2) and dramatically reduced levels of selenoprotein P in affected individuals (15). Detailed biochemical and functional characterization of SBP2 has been carried out; however, its regulation at the gene and transcript level requires further studies.

Alternative splicing represents a functionally important and a major regulatory pathway of gene expression and ultimately protein function. Recent genomic studies have indicated that at least 60% of mammalian genes are subjected to alternative splicing (16), providing a significant contribution to protein diversity beyond that encoded in the genome sequence. Most alternative splicing events affect the coding sequence and it is believed that half of these alter the reading frame (17), and a third lead to nonsense mediated decay (NMD) of the mRNA product (18). Defects in alternative splicing and generation of aberrant ratios of mRNA transcripts from a single gene are now also recognized as major contributors to human disease and it is estimated that at least 15% of the mutations that cause hereditary disease affect pre-mRNA splicing (19). Splicing defects have also been associated with cancers and a genome wide analysis of human expressed sequence tags (ESTs) found strong evidence for cancer specific splice variants in 316 human genes (20–24). To date, this level of regulation has not been explored for any of the factors involved in Sec incorporation, including SBP2.

SBP2 is the only protein of the Sec incorporation machinery so far linked to a clinical condition (15). Interestingly, one of the mutations identified in patients alters the splicing of SECISBP2 by creating an alternative donor splice site, which produces a transcript with a 26 bp intron retention. This event alters the reading frame upstream of the SBP2 RNA-binding domain, giving rise to a truncated, non-functional protein. The regulation of SBP2 expression by alternative splicing thus appears to have significant implications for its function. Prompted by these findings, we herein carried out in silico, as well as functional analysis of alternative splicing of SECISBP2. We now provide evidence for a complex alternative splicing pattern in the 5’-region of human SECISBP2 that give rise to eight spliced variants generated through different exon combinations. All alternative splicing events are confined within the region of SBP2 that is dispensable for Sec incorporation in vitro, but may be involved in regulation of selenoprotein synthesis in vivo. Interestingly, one of the alternatively spliced isoforms contains a mitochondrial targeting sequence (MTS). We designated this transcript as mitochondrial Sec insertion sequence binding protein 2 (mtSECISBP2). First, using a minigene-based in vitro splicing assay we delineated the splicing events within the 5’-region of SECISBP2 and showed that splicing of mtSECISBP2 can be modulated by antisense oligonucleotides (ASOs). We furthermore demonstrated that the protein encoded by mtSECISBP2 does indeed localize to mitochondria and that transcription and translation of SBP2 is regulated in a coordinated manner in response to stress.

MATERIALS AND METHODS

In silico identification of alternatively spliced forms of SBP2

The previously characterized human full-length SECISBP2 gene (GeneBank ID: NM_024077) was used to search against both the EST and the non-redundant (NR) nucleotide databases to identify alternative forms of human SECISBP2 gene. Sequence analyses were performed using BLAST programs (available at http://www.ncbi.nlm.nih.gov/BLAST/) with default parameters. Tissue- and cell-type information of various ESTs was also retrieved from EST database. Identified sequences that were homologous to SECISBP2 were then mapped to human genomic sequences to analyze genomic structures of detected alternative forms. Cellular localizations of proteins were predicted by PSORT II (http://psort.ims.u-tokyo.ac.jp/form2.html).

Cell culture and treatments

The cell lines human embryonic kidney 293T, human cervical carcinoma C33A, human cervical carcinoma HeLa and normal foreskin fibroblast (NFF) cells, were maintained in RPMI 1640 medium supplemented with 10% fetal calf serum (Gibco-BRL, Gaithersburg, MD, USA) and 1% penicillin/streptomycin, in a humidified atmosphere containing 5% CO2. For Ultraviolet A (UVA) treatments, media was removed and kept at 37°C, and phosphate buffered saline (PBS) was added. Cells were subjected to a dose of 50 kJ/m2 of UVA irradiation. Control cells were maintained in PBS at room temperature, in the dark, for the duration of treatment. Following irradiation, the PBS was replaced with the media and cells were allowed to recover for the time indicated.

Generation of minigenes

SECISBP2 minigene splicing cassette was generated by amplifying genomic sequences starting from exon 1 through exon 4 of the SECISBP2 gene with high-fidelity Pfx polymerase (Invitrogen, Carlsbad, CA, USA) and genomic DNA (Clontech Laboratories, Inc. Palo Alto, CA, USA). Appropriate primers were used to reduce the size of intron 2 from ~5.6 kb to 356 nt that include 184 residues of the 5’-end of intron 2 and 172 residues of the...
3'-end of intron 2. An ~2.3 kb amplified fragment from genomic SECI SBP2 containing entire exon 1, entire intron 1, entire exon 2, partial intron 2 (only 356 nt), entire exon 3, entire intron 3 and entire exon 4 was cloned into pCI vector (Promega) between Xho I and Not I site. Subsequently, genomic sequences from the pCI vector were subcloned into a SBP2-GFP plasmid described previously (14). Here, appropriate primers were used to replace exon 1 through exon 4 of SBP2 cDNA sequence with ~2.3 kb genomic sequence described above (Figure 2A). The complete SBP2 minigene sequence is provided as supplementary data. Mutations were introduced using the Quick-Change site directed mutagenesis kit (Stratagene) as per manufacturer's instructions.

**Antisense oligonucleotides**

ASOs were synthesized by Dharmacon, Inc. The sequences of the oligonucleotides used are as follows: mG(mA)mU(mC)mG(mA)mU(mC)mG(mA)mU(mC)mG(mA)mU(mC)mG(mA)mU(mC)mG(mA)mU(mC)mG(mA)mU(mC)mG(mA)mU(mA)mA(mG)mU(mG)mA for the control ASO (GATC) and mCmUmGmCmCmUmAmAmA MGMUmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmAmA for the SBP2 specific ASO spanning the intron 2-exon 3a boundary (In2E3a). In these sequences, the letter m represents an O-methyl modification at the second position of a sugar residue and an asterisk represents a phosphorothioate residue and an asterisk represents a phosphorothioate modification of the backbone.

**Transfections and in vivo splicing assays**

All reagents were used according to the manufacturer's recommendations. Transient transfections of cells with plasmid DNA or antisense oligonucleotides were performed with Lipofectamine 2000 (Invitrogen). Cells were plated into 6-well plates 24 h prior to transfection so that their density on the day of transfection was 70%. 2.0 µg of plasmid DNA was used per well. For co-transfection experiments, cells were transfected with 1.0 µg of plasmid DNA and 100 nM of ASO per well. Total RNA was isolated 24 h after transfection with Trizol reagent (Invitrogen). To generate cDNA, reverse transcription was carried out with a SuperScript II reaction kit (Invitrogen) using oligo(dT) primer. Generally, 1.0 µg of total RNA was used per 20 µl of reaction mixture. Minigene-specific spliced products were subsequently amplified with forward primer annealing in the vector sequence (P1GFP) 5'-GCTAGGCATCCGGACTCA GAT-3', and the reverse SBP2-specific primer annealing in exon3b 5'-CTTAAACAGATCTTTCTTGGTG G-3 using Taq polymerase (Invitrogen). Analysis and quantifications of spliced products were performed with an FPL-5000 Image Reader and ImageGauge software (Fuji Photo Film Inc.). Results were confirmed by three independent experiments.

**Expression of endogenous SECI SBP2 transcripts**

For analysis of endogenous full-length SECI SBP2 and mtSECISBP2, C33A, HeLa and 239T cells were transfected with 100 nM ASOs per well of a 6-well dish. Total RNA was isolated 24 h after transfection with the RNeasy Mini Kit (Qiagen). Reverse transcription was carried out with oligo (dT) primers and SuperScript II (Invitrogen) as described above. Full-length SECI SBP2 and mtSECISBP2 transcripts were subsequently amplified by real-time RT-PCR with transcript-specific forward primers 5'-TCTTATACCTTGACTCCA CAC-3' for full-length SECI SBP2 and 5'-CCAGTGACAGAAATG TTACTCAG-3' for mtSECISBP2, and the same reverse primer 5'-TCTGTGCTGTGCTTGTTATGGG-3'. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as an internal standard (Fwd 5'-CTGCCACACCAACTGCTTAG-3'; Rev 5'-GCTCTCTGGGTCGCAGTGG AT-3'). Real-time RT-PCR was performed using Platinum SYBR Green qPCR SuperMix-UDG (Invitrogen) in a Rotor-Gene 6000 (Corbett Life Science) according to the instructions provided with the kit. Cycling conditions were used as suggested in the SYBR Green kit instructions. Results were analyzed using relative quantification software (Corbett Life Science).

**Cell lysis and western blotting**

Cells were lysed in universal immunoprecipitation buffer (UIP) as described previously (14). Proteins were separated on 4–12% gradient gels (Invitrogen) unless otherwise stated. Western blotting was performed using the following antibodies: anti-SBP2 and anti-HSP70 antibodies raised in house as described previously (14), anti-actin (Sigma), anti-GFP (Molecular Probes, Invitrogen) and anti-SBP2 antibodies (EC1) (Everest Biotech, Oxfordshire, UK). Except for Figure 4B, images were acquired using an LAS-3000 luminescent image analyzer (Fujifilm Life Science, Stanford, CT, USA). The western blot in Figure 4B was developed using traditional X-ray film.

**Fluorescence microscopy**

Cells, untransfected or transfected with GFP-tagged proteins, were washed in PBS twice and fixed with 4% paraformaldehyde in PBS for 30 min at room temperature. 4,6-Diamidino-2-phenylindole (DAPI) was used to stain the nuclei and MitoTracker CMXRos (Molecular Probes, Invitrogen) (50 nM) was used to stain mitochondria. For immunofluorescence, coverslips were blocked in 3% horse serum in PBS, incubated with anti-SBP2 antibody (EC1) at 1:250 dilution, followed by incubation with an Alexa fluor 488 dye-conjugated secondary antibody (Molecular Probes, Invitrogen). Colocalization of SBP2 with mitochondria was detected using a double immunofluorescent procedure. Coverslips were mounted with ProLong Gold (Molecular Probes, Invitrogen). Images were acquired in 20 z-sections by using a state-of-the art DeltaVision PD system microscope (Applied Precision, Washington, USA) with a 60× or 100×objective. Images were subsequently deconvolved with 10 cycles of the DeltaVision PD software.

**RESULTS**

**Human SBP2 is alternatively spliced**

In humans, the SECI SBP2 gene spans a 43 kb region on chromosome 9q22.1 and consists of 17 exons.
Following reverse transcription PCR (RT-PCR) of the 5′-end of SECISBP2 using mRNA isolated from 293T cells, we observed a second PCR product, shorter than the full-length transcript (data not shown). Sequence analysis of this band identified two alternatively spliced SECISBP2 variants: one lacking exon 2, and the second lacking part of exon 3, further designated exon 3a. To further examine whether additional SECISBP2 splice variants were present in humans, we searched EST and NR databases using known full-length SECISBP2 sequences and mapped and quantified the identified cDNAs onto the genomic sequence. This search confirmed that full-length SECISBP2 is indeed the most abundant transcript, currently represented by ∼120 ESTs and 5 complete mRNAs, and led to the identification of seven alternatively spliced SECISBP2 variants arising through different exon combinations. These variants are as listed in Table 1 along with their proposed nomenclature. A schematic representation of the genomic organization of human SECISBP2 is shown in Figure 1A, and the spliced variants for which sufficient sequence was available to determine their complete 5′-exon combination are presented in Figure 1B. The three functional domains of SBP2: the RNA binding domain, the Sec insertion domain and the ribosome interacting domain, are located within the C-terminal part of the protein (8,25), which corresponds to exons 12–16. Interestingly, all alternative splicing events occur upstream of exon 11, within the region dispensable for Sec insertion in vitro.

Sequence analysis of exon/intron boundaries showed that nearly all splice sites within the 5′-region of SECISBP2 conform to consensus sequences (AAG|GU or CAG|GU at the 5′-exon/intron boundary and CAG|G at the 3′-end) (26) with only a few deviations (Table 2). The majority of exons have one donor and one acceptor splice site; however, exons 3 and 7 have multiple acceptor sites, denoted as a, b, c or d. A very complex splicing pattern was noted between exons 6 and 7, with four possible splicing combinations. The most common acceptor site was the 7α site. The 6–7b splice variant appeared to be rare, however, an encoding mRNA derived from brain tissue (Table 1) was present in the EST database. The variants 6–7c and 6–7d were covered by several ESTs.

All SECISBP2 transcripts for which sufficient 5′-sequence information was available appear to begin with exon 1. This suggests the usage of a common promoter, located upstream of exon 1. As mentioned above, the overwhelming majority of SECISBP2 transcripts include all exons. However, the alternatively spliced SECISBP2 variants seem to be expressed in normal as well as in cancer-derived tissues (Table 1). The best represented alternatively spliced transcript lacked exon 3a as evidenced by 24 ESTs from normal and cancer-derived tissues and cell lines, and was also covered by three complete mRNAs (Table 1). Despite the presence of a large number of ESTs covering the 5′-region of SECISBP2 sequence, no alternative splicing events were detected downstream of exon 10.

**Alternative splicing of SECISBP2 creates several open reading frames**

We next examined the nucleotide sequences of the various transcripts for their potential to encode complete open reading frames (ORFs), and found that five SBP2 isoforms initiating from five different ATG start sites can be encoded (Figure 1C). As previously shown, the full-length SBP2 is translated using the first ATG codon in exon 1. This main ORF is however abrogated for some of the variants as premature termination codons (PTCs) are generated, suggesting a possibility of the use of alternative ATG start sites. As indicated in Figure 1B, these potential alternative translation initiation sites (referred by amino acid numbering in full-length SBP2) are methionine (Met) 69 within exon 3a for SBP2_Δ2, and Met 233 within exon 5 for SBP2_Δ3 and they are in the same frame as full-length SBP2. However, for the mtSECISBP2 and SECISBP2_6E transcripts, the first ATG codon downstream of the PTC is created in a different frame in exon 2 (Met 33) and in exon 6 (Met 283) respectively (Figure 1B). These reading frames create a short N-terminal amino acid composition different to full-length SBP2 (i.e., 27 aa for mtSBP2 MVRV1RSMCLPQLCSHILVSCGTSSDR, and 11 aa for SBP2E6 MP LIPLLHVQE), however, these reconnect with the full-length SBP2 reading frame at the next splice site. Interestingly, motif analysis using the PSORTII program predicted the existence of a classical MTS within the exon 3α-deleted variant (Figure 1C), and this form is further designated as mitochondrial SBP2, mtSBP2. The alternate reading frame for SBP2E6 did not seem to encode any targeting signals or motifs different to full-length SBP2. The complex splicing pattern between exon 6 and 7 was interesting as all splicing variations lead to changes in the amino acid composition of the encoded proteins. The splicing from exon 6–7c and 6–7d lead to deletion of a stretch of 38 or 39 amino acids (aa 294–331 or aa 294–332) from exon 7 (294ELS WTPMGYVVRQTLSTELSAAPK NVTS MN LKTIASS331), however, the reading frame starting in exon 1 is maintained throughout both isoforms. The ESTs covering the SECISBP2_Δ9 transcript did not have sufficient sequence upstream of the splicing event in order to determine its translation initiation sites; however, ORF prediction indicated that the reading frame in exon 1 can be maintained despite exon 9 skipping.

**Evolutionary aspects of splicing events within SBP2**

We next investigated the extent of alternative splicing events in SBP2 in other species. We thus analyzed the distribution of SECISBP2 homologs, the conservation of splicing events and evolution of the SECISBP2 gene in genomic and EST databases. As recently established, selenoprotein genes are widely distributed among eukaryotes including all vertebrates and most arthropods, nematodes, protozoa and lower plants (27–29). Selenoproteins were lost in fungi, land plants, some insects and most eukaryotic parasites. We found that SECISBP2 homologs are present in all selenoprotein-containing genomes, and absent in EST and genomic databases of organisms lacking Sec utilization, suggesting that SECISBP2 co-evolved...
Table 1. Alternatively spliced human SECISBP2 transcripts

<table>
<thead>
<tr>
<th>Transcript name</th>
<th>Exon combination</th>
<th>No. of ESTs</th>
<th>Normal tissue or cell line</th>
<th>Primary tumors</th>
<th>Cancer derived or transformed cell lines</th>
<th>Complete mRNAs</th>
</tr>
</thead>
<tbody>
<tr>
<td>SECISBP2</td>
<td>1–17</td>
<td>~120</td>
<td>Present in most tissues</td>
<td>Present in several tumors</td>
<td>Present in several cell lines</td>
<td>NM024077, AK090608, AK746532, BC036109, AF380995</td>
</tr>
<tr>
<td>mtSECISBP2</td>
<td>1.2–3b,4,5,6 ...</td>
<td>24</td>
<td>Pooled glandular (CB956376) Pancreas (BM315064) ES cell lines (CN256608, CN256604, CX870404) T-lymphocytes (CR994587) Liver Cho-CK cell line (CB121625) Thymus (DB160135) Small intestine (DA926236) Fetal brain (DA803510) Thalamus (DA403753) Corpus callosum (DA283160) Testis (DB459197, DC399547) Pooled mixed tissue (CV029893)</td>
<td>Retinoblastoma (BE252177) Choriocarcinoma (BG481218) Terratocarcinoma (DA754929, DA758978) Tongue tumor (DA450129)</td>
<td>Lymphoma (BQ049808) Osteosarcoma (BG113716) Neuroepithelioma (DA903910) Lymphoma (CR747151)</td>
<td>AL136881, AK290182, AM392812</td>
</tr>
<tr>
<td>SECISBP2_A2</td>
<td>1–3a,4,5 ...</td>
<td>2</td>
<td>ES cell line (CV811081)</td>
<td></td>
<td>Genitourinary tract high-grade tumor (AW630547) Mammary gland tumor (BP313796)</td>
<td>293T cell line (this study)</td>
</tr>
<tr>
<td>SECISBP2_A3</td>
<td>1.2–4,5 ...</td>
<td>3</td>
<td>Testis (DB459197)</td>
<td></td>
<td></td>
<td>293T cell line (this study)</td>
</tr>
<tr>
<td>SECISBP2_A7a</td>
<td>1–5,6b–7b ...</td>
<td>3</td>
<td>Uterus (AI129567, AI128470)</td>
<td></td>
<td>Genitourinary tract high-grade tumor (AW630547) Mammary gland tumor (BP313796)</td>
<td>AB208940</td>
</tr>
<tr>
<td>SECISBP2_c</td>
<td>3,4,5, 6a–7c ...</td>
<td>5</td>
<td>ES cell line (CN256603, CX787609)</td>
<td></td>
<td>Squamous cell carcinoma (BP352801) Large cell carcinoma (BQ430224)</td>
<td>AB208940</td>
</tr>
<tr>
<td>SBP2 _7d</td>
<td>3,4,5, 6a–7d ...</td>
<td>5</td>
<td>Pancreas (BU069273)</td>
<td></td>
<td>Retinoblastoma (BC001189, BE779955) Prostate cancer (EC508545)</td>
<td>AB208940</td>
</tr>
<tr>
<td>SECISBP2_A9</td>
<td>8–10 ...</td>
<td>2</td>
<td>Retinal pigment epithelium (CA389610)</td>
<td></td>
<td>Leiomyosarcoma (BU902304)</td>
<td></td>
</tr>
</tbody>
</table>

SECISBP2 transcripts that were identified experimentally or by EST database searches are listed according to the nomenclature proposed in the text. Information on exon combination, number of ESTs present, tissue of origin and corresponding GenBank accession numbers are given. ES = embryonic stem.
Table 2. Splice site boundaries of SECISBP2 transcript variants

<table>
<thead>
<tr>
<th>Donor exon (nt)</th>
<th>Acceptor exon (nt)</th>
<th>Intronsize(kb)</th>
<th>EXON/intron/EXON (splice site consensus: ...AGGuguau... (y)_{90,119}...yag...G...)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (116)</td>
<td>2 (146)</td>
<td>1.04</td>
<td>_AGCGAG_guaaggucaauuuuuuuuuuuucaag</td>
</tr>
<tr>
<td>1 (116)</td>
<td>*3a (121)</td>
<td>6.81</td>
<td>_AGGGG_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>*3a (121)</td>
<td>5.63</td>
<td>_GACAGA_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>*3b (129)</td>
<td>5.63</td>
<td>_GACAGA_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>4 (142)</td>
<td>5.63</td>
<td>_GACAGA_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>3 (250)</td>
<td>4 (142)</td>
<td>0.20</td>
<td>_UUUAAG_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>4 (142)</td>
<td>5 (227)</td>
<td>2.67</td>
<td>_AAUUCA_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>5 (227)</td>
<td>6 (78)</td>
<td>4.02</td>
<td>_UCAAAG_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>6 (79)</td>
<td>*7a (209)</td>
<td>1.53</td>
<td>_CAAAAG_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>6 (79)</td>
<td>*7b (171)</td>
<td>1.53</td>
<td>_CAAAAG_guaaggucauuuuuuuuuuucaag</td>
</tr>
<tr>
<td>6 (79)</td>
<td>*7c (95)</td>
<td>1.53</td>
<td>_CAAAAG_guaaggucauuuuuuuuuuucaag</td>
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<tr>
<td>6 (79)</td>
<td>*7d (192)</td>
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<tr>
<td>8 (123)</td>
<td>10 (132)</td>
<td>2.76</td>
<td>_AUUGAA_guaaggucauuuuuuuuuuucaag</td>
</tr>
</tbody>
</table>

The donor and acceptor exons are listed with their sizes in nucleotides (nt) in brackets. Introns sizes are given in kilobases (kb). Boundaries of splice sites was identified from the genomic DNA sequence (http://genome.ucsc.edu) and compared to the consensus of splice site motifs (16). Consensus nucleotides at the 5' and 3' splice sites are indicated in bold letters and splice sites are indicated with a vertical line. The polypyrimidine stretch is shown in italics.

*Exons with alternative donor or acceptor sites.
with the eukaryotic Sec-decoding trait. Several alternatively spliced transcripts were found in EST and genomic databases of different organisms, some of which were identical to human SECISBP2. Because the mtSBP2 is the most common isoform after full-length SBP2 in humans, we were particularly interested in its evolutionary conservation and existence in other species. Interestingly, sequence comparison between exon 2 of human SECISBP2 and other homologs revealed that the ATG codon is conserved in chicken, sheep, cow and monkey but not in mouse, rat and dog where it is present as GTG or CTG, which are possible weak translation initiation codons. However, we did not detect ESTs representing mtSECISBP2 in other organisms except for a distant homolog containing a strong predicted MTS (but low sequence similarity to human MTS) in chicken. It thus appears that the predicted mtSBP2 isoform may be specific to humans.

Characterization of SBP2 splicing in vivo and modulation with antisense oligonucleotides

The identification of alternative splicing within the 5′-region of human SECISBP2 prompted us to further characterize and quantify the occurrence of these events in vivo. We were particularly interested in the mtSECISBP2 variant since it appeared to be the best represented transcript after the full-length transcript. To gain a better insight into the expression pattern of the two transcripts, we first quantified their relative expression levels in a cDNA panel from various human tissues by real-time RT-PCR using isoform-specific primers spanning the exon 2–3a boundary for SECISBP2, and the exon 2–3b boundary for mtSECISBP2. As shown in Figure 2A, SECISBP2 and mtSECISBP2 were expressed in all tissues tested, with the highest expression levels for both transcripts in testis. The ratio between the SECISBP2 and mtSECISBP2 was on average ~4.4:1 in most tissues, which is consistent with the bioinformatics data presented in Table 1. However, colon, thymus and leucocytes had a ~2:1 ratio, indicating that mtSECISBP2 is most abundantly expressed relative to SECISBP2 in these tissues. We also confirmed the expression of mtSECISBP2 variant in a number of normal and cancer-derived cell lines including ones used in this study (data not shown).

As a second approach to characterize and potentially modulate SECISBP2 splicing in vivo, we generated a SECISBP2 minigene construct (WT minigene), schematically presented in Figure 2B. We also generated two mutant minigene constructs: one harbouring a point mutation at the exon 3a 3′ splice site 539AG>AA (named Ex3AG>AAΔT) which should abrogate the splicing at this site and hence deplete the production of mtSECISBP2; and a second construct harbouring a point mutation (69ATG>CTG) to abrogate mtSBP2 start codon in exon 2 (named Ex2ATG>CTG). The minigenes were transfected into C33A cells and products were analyzed by RT-PCR using primers specific to the minigene-derived transcripts as indicated in Figure 2B. The α-32P-DCTP labeled products were separated by native PAGE and verified by sequencing. As shown in Figure 2C, lane 1, full-length SECISBP2 was the predominant transcript expressed from the WT minigene, followed by mtSECISBP2 and SECISBP2Δ2. These results confirmed that mtSECISBP2 may indeed be the second most abundant SECISBP2 transcript. Notably, the Ex3AG>AA mutation indeed abrogated the exon 3a 3′ splice site responsible for the skipping of exon 3a, which is clearly evident by the absence of the mtSBP2 encoding transcript (Figure 2C, lane 2). This observation also conclusively confirmed the existence of an alternative acceptor site within exon 3, and shows that this site is required for production of the mtSECISBP2 transcript. As expected, the ATG mutant minigene showed no difference in splicing compared to the WT minigene (Figure 2C, lane 3).

ASO with a 2′-O-methyl modified ribonucleotide with phosphorothioate backbone have been used to manipulate pre-mRNA splicing in the spinal muscular atrophy gene, SMN2 (30). This backbone modification imparts a very high affinity for targeted mRNA, resistance to both exon- and endonucleases and does not support cleavage of hybridized mRNA by RNase H (31). We employed this technology to test whether splicing of the mtSECISBP2 can be enhanced using a 23-mer ASO complementary to the last 19 nt of intron 2 and the first four nucleotides of exon 3a (named In2E3a). This was expected to promote exon 3a skipping and thus block splicing of the full-length transcript and enhance the production of the mtSBP2-encoding transcript. An unrelated ASO was used as control. Resulting PCR products from cells co-transfected with the In2E3a, or control ASO, and the WT minigene are shown in Figure 2C, lanes 4 and 5. Notably, the In2E3a ASO efficiently blocked splicing at the exon 3a site, thus, promoting exon 3a skipping as shown by a dramatic reduction in full-length transcript levels and a corresponding increase in mtSECISBP2 transcript (lane 4), while the control ASO had no effect on the splicing pattern (lane 5 compared to lane 1). Similar results were obtained in HeLa cells (data not shown). The In2E3a ASO was also efficient in altering the splicing of the endogenous SECISBP2 transcript in several cell lines, as measured by real-time RT-PCR with isoform-specific primers. Generally, a 2- to 4-fold increase in exon 3a skipping with a corresponding 50–60% decrease in exon 3a inclusion was obtained in cell lines including C33A, HeLa and untransformed human fibroblast cells (NFF). Results from NFF cells are shown in figure 2D. Taken together, these findings demonstrated that the In2E3a ASO can be used as an efficient tool to promote SBP2 exon 3a skipping in vivo, and to generate predominantly the mtSBP2-encoding transcript from SECISBP2 gene.

Several SBP2 isoforms are expressed from the minigene

We next investigated the translation pattern of the alternatively spliced SBP2 isoforms using the minigene constructs. These were transiently transfected in several cell lines including 293T, C33A and HeLa, and the expressed proteins were analyzed by western blotting. Blots were probed with anti-GFP antibodies (which is tagged at the C-terminus of SBP2), and with anti-SBP2 antibodies raised against a central region of SBP2 (exon 6–8) to
ensure that the proteins detected are products that initiate at different ATG codons within the N-terminal region of SBP2 rather than degradation products. A representative example of the minigenes’ expression pattern in 293T cells is shown Figure 3A. Consistent with the data obtained from the splicing assay, full-length SBP2 initiating from the ATG in exon 1, was by far the highest expressed protein from the WT and Ex2ATG>CTG minigenes.
On the contrary, a small increase in expression of the mtSBP2 isoform expressed from the minigene by western blotting, its expression levels could be below the detection limit, but still responsible for regulating the expression of other downstream ATG-initiating isoforms (Figure 3A lane 1 compared to lane 2). However, this possibility remains to be investigated. We also noted that translation of the mtSBP2 isoform from the Ex3AG>AAΔT minigene did not increase significantly when a point mutation that abrogates the full-length SBP2 reading frame is introduced (Figure 3A lane 4). This suggests that the ATG codon context in exon 3b is rather weak, or that expression of this isoform is strictly regulated. The overall SBP2 splicing pattern was similar in other cell lines tested despite variations in transfection efficiency (data not shown).

We showed above (Figure 2B) that the In2E3a ASO is extremely efficient at increasing the levels of the mtSECISBP2 transcript both off the minigene and endogenously. We therefore tested if co-transfecting the WT minigene with the In2E3a ASO could induce the expression of the mtSBP2 protein. As shown Figure 3B, a band that corresponds to the predicted size of mtSBP2-GFP was indeed apparent in In2E3a ASO co-transfected cells, but not in control ASO transfeccted cells, demonstrating that this isoform can be translated in vivo, albeit very inefficiently. Although the In2E3a ASO proved efficient at inducing splicing of endogenous mtSECISBP2 transcript, we were unable to detect the endogenous mtSBP2 protein following In2E3a ASO transfection, despite extensive attempts in several cell lines. Overall, these results showed that full-length SECISBP2 is the most abundant and preferentially translated SBP2-encoding transcript. However, the alternatively spliced transcripts generated are also translated into protein, albeit far less efficiently.

The mtSBP2 isoform localizes to mitochondria

One of the main aims of the minigene splicing assay was to analyze the expression and localization of the protein encoded by the most common alternate SECISBP2 transcript-mtSBP2. Although the assay convincingly showed expression of the mtSECISBP2 transcript, it proved less amenable at analyzing the protein expression. Thus, in order to determine if the predicted mtSBP2 does indeed localize to mitochondria, we expressed the mtSBP2-encoding cDNA (commencing at the ATG codon in exon 2) fused N-terminal to GFP (mtSBP2-GFP) in C33A cells, and analyzed its subcellular localization by co-staining with the mitochondrial marker MitoTracker Red CMX-Ros. The full-length FLSBP2-GFP construct and a construct lacking the putative MTS encoded by the alternate reading frame in exon 2 (SBP2_Δ2-GFP) were used for comparison. Localization of the proteins was visualized using a Z-scanning
microscope followed by image deconvolution. Interestingly, mtSBP2-GFP expressing cells exhibited distinct cytoplasmic fluorescence, which overlapped significantly with the MitoTracker staining as indicated by the intense yellow staining in Figure 4A (Pearson coefficient 0.879). FLSBP2-GFP protein displayed a strong peri-nuclear punctate staining, however, this fluorescence did not overlap significantly with the MitoTracker staining (Figure 4A bottom panels, Pearson coefficient 0.264). Most likely, this pattern represents a ribosomal/endoplasmic reticulum (ER) staining which is the believed functional localization of SBP2 (14,32). Similar to FLSBP2-GFP, SBP2_Δ2-GFP localized throughout the cytoplasm and showed marginal co-localization with MitoTracker (data not shown). This data established that the MTS encoded by the alternative reading frame in exon 2 is functional, and required for targeting the mtSBP2-GFP protein to the mitochondria. It should be noted that only ~10% of cells transfected with the mtSBP2-GFP plasmid displayed strong mitochondrial localization as shown in Figure 4A, and some of the transfected cells also displayed a diffuse cytoplasmic fluorescence that did not co-localize with the MitoTracker staining (data not shown). Indeed, western blot of mtSBP2-GFP transfected cells showed the presence of additional proteins initiating in exon 3b and exon 5 (Figure 4B, lane 4), which explained the cytoplasmic

Figure 4. Localization of over-expressed mtSBP2-GFP and endogenous mtSBP2 isoform at the mitochondria. (A) The localization of GFP-tagged full-length (FLSBP2-GFP) and mitochondrial SBP2 isoforms (mtSBP2-GFP) in C33A cells was visualized by fluorescence microscopy. Mitochondria were stained with MitoTracker Red CMX-Ros. Single Z-layer deconvolution images show strong mitochondrial localization of mtSBP2-GFP (yellow) but not of FLSBP2-GFP. (B) Western blot of SBP2 isoforms expressed from cDNAs as GFP-fusion proteins. SBP2_Δ2-GFP and SBP2_Δ3a-GFP lack exons 2 and 3a respectively. mtSBP2-GFP cDNA begins at the ATG in exon 2. These proteins were resolved on a 6% SDS-PAGE gel, which yielded a higher level of separation compared to Figure 3. (C) High resolution single Z-layer deconvolution images show the localization of mtSBP2-GFP and endogenous mtSBP2 proteins at the mitochondria in C33A cells. 10% of cells display strong mitochondrial staining as shown by the yellow staining in the top panel enlargement, while in most cells only a few dots were detected within the mitochondria (middle panel). Immunofluorescence staining was performed with the anti-SBP2 antibody EC1. Enlargements show a similar punctated staining pattern along the mitochondria for both mtSBP2-GFP (bottom panel) and endogenous mtSBP2.
fluorescence observed. Notably, mtSBP2-GFP was poorly expressed in comparison to other isoforms and we consistently observed this in several cell lines tested. It is also interesting to note that cells transfected with a construct that lacks exon 2 (SBP2_A2-GFP) expressed high levels of proteins initiating in exons 3a, 3b and 5 (Figure 4B, lane 4), while lack of exon 3a (SBP2_A3a-GFP) did not seem to have a similar effect on proteins initiating in exons 3b and 5 (Figure 4B, lane 3). These results suggest that exon 2 might play a role in regulating the expression of some of the SBP2 isoforms by suppressing translation initiation at ATG start sites in exons 3a, 3b and 5. These results are also in agreement with the results from the minigene assay where mutation to the exon 2 ATG start site led to increased translation from exon 3b.

We also sought to determine whether the mtSBP2 isoform, or additional spliced variants could be detected endogenously in cells using our previously described anti-SBP2 antibody raised against an epitope in exons 6–8 (aa 279–378 in SBP2) (14) which should detect most isoforms, if expressed. However, we were unable to detect any SBP2 isoforms other than the full-length SBP2 by western blotting. Similarly, analysis of mitochondrial fractions of cells failed to reveal the existence of mtSBP2 by western blotting. This antibody was not suitable for immunofluorescence-based detection of mtSBP2 due to similar level of staining in SBP2-depleted and normal cells. Notably, a new anti-peptide antibody raised against the C-terminus of SBP2 (referred to as anti-SBP2 EC1) was shown to be very specific for SBP2 (data not shown). We used this antibody in immunofluorescence-based detection of mtSBP2 due to its ability to localize to the mitochondria, ~5–10% of cells displayed a clear mitochondrial staining (Figure 4C, middle panel). Interestingly, while most cells also showed some punctuated staining along the mitochondria, ~5–10% of cells displayed a clear mitochondrial staining (Figure 4C, middle panel). Collectively, these results provide evidence that mtSBP2 stains in a mitochondrial MTS that targets the mtSBP2-GFP protein to the mitochondria, and also that endogenous mtSBP2 localizes to the mitochondria. Although the EC1 antibody did detect full-length SBP2 by western blotting, we were unable to confirm the presence of mtSBP2 isoform in mitochondrial fractions of cells by this method.

**Coordinated transcriptional and translational regulation of SBP2 following UVA treatment**

We previously showed that SBP2 is regulated through redox-state and localization changes, and that these affect selenoprotein synthesis (14). In this study, we wished to investigate if oxidative stress may cause transcriptional changes in SECISBP2 expression, particularly in the full-length and mitochondrial transcripts. To complement our previous data, we used UVA irradiation, a physiologically relevant oxidative stress inducer that causes intracellular damage by production of oxygen singlet (O$_2^*$) molecules. To monitor the transcriptional response of SBP2, HeLa cells were exposed to 50 kJ/m$^2$ UVA irradiation and allowed to recover for the indicated amounts of time, and SECISBP2 and mtSECISBP2 transcript levels were measured by real-time RT-PCR. Interestingly, we found that both transcripts were induced by almost 3-fold immediately after UVA treatment, followed by a sharp decline at 2 h and subsequent stabilization of both transcripts for up to 24 h (Figure 5A). Importantly, these results show that both transcripts are regulated in a similar manner in response to oxidative stress. The response to UVA treatment at the protein level correlates well with the transcriptional response. We observed a rapid degradation of SBP2 with levels down to ~30% of mock-treated cells at 0 h after treatment (Figure 5B). Interestingly and as reported previously (33), the stress sensor HSP70 protein was stabilized in response to UVA treatment and remained elevated for 16 h post treatment (Figure 5B). We believe that the rapid degradation of SBP2 during the course of UVA irradiation is the trigger for the concomitant transcriptional induction seen in Figure 5A. Although, SBP2 protein levels recovered slightly at 2 h post treatment, they remained at only ~50% of the initial levels for up to 8 h and returned to the initial starting levels by 24 h post treatment. These results are consistent with our previous observations that selenoprotein synthesis is inhibited in response to oxidative stress and suggest that down regulation of SBP2 protein levels might provide additional mechanistic explanation for those observations (6,14).

We also investigated the UVA stress response pattern of the SBP2 isoforms expressed by the minigene constructs. We conducted a similar time course experiment in response to UVA treatment in HeLa cells expressing wild-type SBP2 protein (WT-SBP2GFP), the exon 2 ATG->CTG mutated SBP2 (ATGm-SBP2GFP) and the SBP2 mutated protein that initiates translation from exon 3b (E3b-SBP2GFP). As shown in Figure 5C, all minigene products showed a similar down-regulation pattern in response to stress, as seen for endogenous SBP2. Similar results were obtained in NFF cells (data not shown). From these experiments we thus conclude that mutation of the ATG codon in exon 2 and thus the lack of mtSBP2 expression does not affect the response of the full-length SBP2 to UVA-induced oxidative stress, and that the spliced variants E3b-SBP2GFP and E5-SBP2GFP (data not shown) have a similar pattern of regulation as full-length SBP2 in response to stress. Importantly, these experiments established a coordinated transcriptional and translational mechanism of SBP2 regulation in response to oxidative stress, and revealed that the alternatively spliced transcripts and the corresponding proteins have a similar pattern of regulation as the full-length SBP2.

**DISCUSSION**

SBP2 is a critical factor for selenoprotein synthesis, with roles in SECIS element binding, ribosome binding and Sec incorporation. Much of recent work has elaborated on
Figure 5. Coordinated transcriptional and translational regulation of SBP2 following UVA treatment. Transcriptional and translational response of full-length SBP2 (FLSBP2) and mitochondrial SBP2 (mtsBP2) following 50 kJ/m² of UVA irradiation was monitored in HeLa cells over 24 h. (A) Real-time RT-PCR using transcript specific primers shows a similar transcriptional induction of both transcripts in HeLa cells over 24 h. (B) Western blot using anti-SBP2 antibodies shows the translational response of endogenous SBP2 and HSP70 at different time points after UVA irradiation. Quantitation of FLSBP2 transcript and protein levels is presented in the graph below. Error bars represent the standard error of the mean (SEM). Transcript levels were normalized against GAPDH and protein levels were normalized against actin. (C) Western blots show the translational response of WT, Ex2ATG>CTG and Ex3AG>AA minigene-derived proteins to UVA treatment. HSP70 was used as a marker for UVA-induced stress and actin shows protein loading.
to a localization of the mtSBP2 isoform on the outer mitochondrial surface, in specific punctate clusters. This localization would indeed be in agreement with the functional localization of SBP2 at polysomes. The fact that we could not detect mtSBP2 in mitochondrial subfractions of cells by western blotting argues for a possible loose interaction between mtSBP2 and the organelle, which may be easily disrupted during the fractionation procedure. But if mtSBP2 is localized on the outer surface of the mitochondria, why would it require a classical type of MTS that generally targets proteins to the inner mitochondrial matrix? Although this question remains to be answered, our findings are relevant to a recent report showing that DAKAP1, a multifunctional protein with roles in cAMP dependent protein kinase (PKA) regulation and mRNA binding, can be targeted to the cytosolic side of the outer membrane of the mitochondria by use of a classical MTS. DAKAP1 contains a bi-functional targeting motif that switches to encode either an MTS, such as the one present in mtSBP2, or an ER targeting signal (41). Although the precise mechanism of how this protein attaches to the mitochondria outer membrane remains unknown at present, it is possible to reconcile the idea that proteins that localize on the cytosolic side of the mitochondrial membrane can be targeted there by classical MTs. The MTS in mtSBP2 may thus facilitate the localization of the protein to the cytosolic side of the mitochondria via active mitochondrial import. More detailed studies will be required to investigate this aspect of mtSBP2 localization as well as the precise role of this isoform in the cell. The low expression of mtSBP2 isoform in the cell lines tested indicates that its synthesis could be dependent on tissue-specific translation factors and may be maximized in tissues or organs with high demand for mitochondrial selenoproteins. A prime candidate would be testis, where PHGPx is the high demand for mitochondrial selenoproteins. A factors and may be maximized in tissues or organs with

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This study established that human SECISBP2 has an extensive alternative splicing pattern in the 5′-region. Some of the splicing events provoke ORF alterations, which lead to premature termination codons, thus promoting translation from downstream ATG start codons. Our in vivo splicing assay and treatment with ASOs showed that at least four additional ATG start codons in exons 2, 3a, 3b and 5 are used to produce proteins with different N-terminal amino acid sequence such as mtSBP2, or N-terminally truncated SBP2 isoforms. Because all alternative splicing events within SBP2 are confined within the region dispensable for Sec incorporation in vitro, it is reasonable to postulate that these events are unlikely to affect RNA binding per se, however, this level of regulation may play a fine-tuning or regulatory role in SBP2-dependent Sec incorporation function in vivo. The role of the N-terminal region of SBP2 is a puzzling, yet unanswered, question in the field. So far, the only characterized motif within this region is a nuclear localization signal (NLS) that enables SBP2 to shuttle between the nucleus and cytoplasm (14), however, its requirement for selenoprotein synthesis in vivo has not been determined. Interestingly, the NLS is located within exon 8, which is common to all alternatively spliced SBP2 isoforms suggesting that this motif may indeed play an important role in the function of SBP2 in the nucleus in vivo. Consistent with this, recent studies have suggested a new role of SBP2 in protection of selenoprotein encoding mRNAs from nonsense mediated decay by binding to these mRNAs in the nucleus (42,43).

The human selenoproteome consists of 25 selenoproteins (44) but the SECIS core element and the binding site for SBP2 are well conserved. As a result, Sec incorporation with regard to SECIS element binding would not require variability within the SBP2 RNA binding region which could explain the lack of alternate splicing in the C-terminal region of SBP2. In contrast, the hierarchy of selenoprotein synthesis is expected to involve specific factors that may dictate the differential binding of SBP2 to different selenoprotein mRNAs (25,43). The high sequence variability in the N-terminal region of SBP2 could thus serve as a protein–protein interaction domain and function in the recruitment of such factors prior to interaction with the SECIS element.

In a previous study we showed that acute oxidative stress caused by H2O2 and sodium selenite had an inhibitory effect on selenoprotein synthesis, and that this was mediated by oxidation of SBP2 redox-sensitive cysteine residues and its depletion from the ribosomes (14). In the current study, using UVA-irradiation as a cause of oxidative stress we found that SBP2 responded by coordinated transcriptional and translational changes following stress. Importantly, SECISBP2 and mtSECISBP2 transcripts were simultaneously and immediately induced during treatment, and stabilized during the recovery phase. At the protein level, SBP2 was degraded and levels remained approximately half of the initial levels for ∼16 h post-irradiation. The SBP2 isoforms that we could monitor using the minigene showed similar down-regulation as full-length SBP2, suggesting that their intracellular function is most likely related to the function of full-length SBP2 in SECIS binding and Sec incorporation. However, our data does not exclude the possibility that mtSBP2 or any other SBP2 isoforms may perform additional functions unrelated to selenium metabolism.

This is the first report validating the occurrence and significance of alternative splicing associated with SECISBP2, an essential gene linked to selenium metabolism. Although, we have focussed mainly on one spliced variant, mtSECISBP2, there remain other variants of significant interest. Having shown that an ASO-based approach could be used to generate specific spliced variants, future studies could be tailored to examine their functions. Recent years have seen a dramatic evolution in our understanding of translational regulation by microRNAs, a class of small RNA that could be synthesized by a stem-loop containing transcript generated from RNA Polymerase II (45). To a broader significance, it remains to be seen if some of the poorly translatable SECISBP2 spliced variants including mtSBP2 are meant
to generate microRNAs and/or serve as potential targets of microRNAs.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

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