Regulation and activity of the human ABCA1 gene in transgenic mice*

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Running Title: ABCA1 gene in transgenic mice

SUMMARY

The ABCA1 transporter is one of the limiting steps in cellular cholesterol efflux. To study the expression and activity of the human ABCA1 gene *in vivo* we have examined mice containing two human BAC transgenes with different 5' end. Mice containing a 255 kb BAC transgene, including 70 kb upstream of the previously defined exon 1, demonstrated a pattern of tissue specific expression mimicking that of the endogenous mouse gene. Compared to macrophages from control mice, macrophages from these transgenics had increases in apoA-I cholesterol efflux heightened in response to increases in cell cholesterol content. The observed increase in macrophage apoA-I mediated cholesterol efflux was not accompanied by alterations in plasma HDL in the transgenics. Mice containing a smaller 171 kb human BAC transgene, lacking the previously described exon 1 and ABCA1 promoter, while not expressing human ABCA1 in macrophages, did express the human transgene in liver at levels comparable to that of the orthologous mouse gene. Analysis by 5' RACE of liver mRNA from these animals revealed a new ABCA1 exon 1 (exon 1A) and a previously unrecognized promoter. Analysis of human tissue revealed that exon 1A containing transcripts accounted for a high proportion of the ABCA1 mRNAs present in human liver. This analysis of ABCA1 transgenics has shown that expression of human ABCA1 transgenes can result in increased cholesterol efflux from macrophages unaccompanied by changes in plasma HDL and has identified a new ABCA1 promoter in humans.

INTRODUCTION

A major mechanism postulated to contribute to the athero-protective effects of high plasma HDL is reverse cholesterol transport. This is a process whereby HDL participates in the transfer of excess cholesterol from peripheral tissues to the liver for catalysis (1,2). Specifically HDL is believed to protect against the accumulation of lipids in the vasculature by removing cholesterol and phospholipids through an active transport pathway (3,4). This pathway is impaired in Tangier disease (5-7), a rare recessive disorder characterized by the accumulation of lipids in peripheral tissues, dramatic reductions in plasma HDL, and an increased risk for cardiovascular disease (8,9). Recent studies have demonstrated that ABCA1, an ATP binding cassette transporter, plays a key role in the apolipoprotein mediated cholesterol transport (10) and that mutations in the ABCA1 gene are the underlying genetic defect in Tangier disease (11-15). These results imply that the ABCA1 transporter is a rate-limiting factor in reverse cholesterol transport and plays a key role in the protection against atherosclerosis.

Due to ABCA1's importance in HDL formation and cholesterol efflux, great efforts have been made in defining the genetic components and the cellular mediators determining ABCA1 expression levels. Various *in vitro* (10,16-18) and *in vivo* (19) studies of ABCA1 expression have shown that this gene is tightly regulated by the cholesterol status of the cell. Studies have defined the human ABCA1 promoter as spanning nucleotides –200 to –80, upstream of exon 1 (20). This promoter contains a DR-4 element that binds LXR and RXR hetero-dimers and transactivates gene expression

when bound to oxysterols and retinoic acid (21-23). This mechanism explains in part the tight regulation of ABCA1 gene by sterols and supports idea that the response of ABCA1 to increased cholesterol leads to an accelerated clearance of cholesterol by macrophages maintaining intracellular cholesterol homeostasis.

While both mice and humans with reduced ABCA1 have been characterized, and shown to have reduced HDL levels and decreased cellular cholesterol efflux (8,11,24-27), the *in vivo* effect of increased expression of this gene and its regulation have not been characterized. Accordingly, we have examined transgenic mice with two different human ABCA1 containing BAC transgenes. The mice with the human ABCA1 transgene with more human 5' DNA demonstrated largely appropriated regulation of the human ABCA1 transgene. Surprisingly, the increased cholesterol efflux in macrophages was not accompanied by changes in plasma HDL levels. Analysis of the mice with a 5' truncated ABCA1 transgene led to the discovery of a new ABCA1 promoter and alternatively spliced transcript that is present at high levels in the livers of humans.

EXPERIMENTAL PROCEDURES

Mice-The ABC1 transgenics examined in this study were created and maintained in a pure FVB background as described previously (28). The structure of the 2 BAC transgenes analyzed in this study is depicted in Figure 1. Both BAC1 and BAC2 encode the complete ABCA1 protein including the ATG methionine initiation site present in exon 2. The 255 kb BAC1 comprises the entire structural gene plus 70 kb of DNA upstream of the 5' initiation start site and at least 35 kb of DNA downstream of the polyadenylation

signal. The 171 kb BAC2 lacks exon 1 and the 5' initiation site, and contains 13 kb of DNA upstream of exon 2 and approximately 35 kb downstream of the polyadenylation signal. Studies of gene expression, cholesterol efflux, and plasma HDL were performed on at least two lines of BAC1 and BAC2 transgenic mice.

Diets and Plasma HDL measurements- Mice were fed either Purina mouse chow (no. 5001) or a western-type diet with 1.5g/Kg of cholesterol (Source-Harlan Teklad # TD 88137) for 2 and 4 weeks. Blood samples were collected following an overnight fast and HDL-cholesterol was measured by standard methods described previously (29).

Expression analysis of human and mouse ABCA1-Total murine RNAs from lung, liver, spleen, proximal, medial and distal small intestine and testis were extracted using the TRIZOL method (Gibco BRL, cat#15596). Total RNA from human tissues including liver, heart, lung, kidney, adrenal, intestine, brain and testis were purchased from Clontech. Reverse transcriptions were performed using 5 ug of total RNA, random hexamers (NE Biolabs) and Superscript II reverse transcriptase (Gibco BRL) at 42°C for 60 min. The amount of cDNA generated was measured using the TaqMan Syber-green quantitative PCR assay with a 7700 ABI PRISM Sequence Detector System (Perkin Elmer-Applied Biosystems). The primer pairs used to detect the mouse endogenous Abca1 gene (mouse exon 2F and mouse exon 4R), the human ABCA1 transgene (exon 3F and exon 4R), the human exon 1A transcript (exon 1AF and exon 2R), and the human exon 1 transcript (exon 1F and exon 2R) are listed in Table 1. The relative amount of ABCA1 transcript was normalized to 18S RNA amplification values retrieved from the

same sample. The control 18S RNA used to correct for total RNA amounts in each sample were purchased from AMBION and a ratio of 0.8/1.2 for primers/competimers was used for all the samples. PCR was performed with an initial hot start of 3 minutes at 94 °C followed by 40 cycles of 94 °C for 10 sec, 57 °C for 15 sec and 72 °C for 30 sec.

Isolation of peritoneal macrophages- Control and transgenic mice were injected intraperitoneally with 5 ml thioglycolate solution. On the fifth day after injection, the elicited cells were isolated by peritoneal lavage with 5 ml of sterile PBS. The cells were then pelleted by centrifugation for 10 min at 1000 rpm and recovered in RPMI-1640 with 10% FBS. 1 million cells were plated out on each well on 24 well plates. The cells were allowed to attach to the plates for 4 hours and then washed with RPMI-1640 with 1% FBS.

Cholesterol efflux- Peritoneal macrophages were labeled with 1 uCi/ml/well of ^{3}[H] cholesterol (48 Ci/mmol) for 24 h. At the same time, cells were incubated with 0.3 mM 8-(4-chlorophenylthio) adenosine 3':5'-cyclic monophosphate (cAMP), 50 ug protein/ml of acetylated LDL, or 1% FBS. Prior to cholesterol efflux measurements, cells were equilibrated (30 minutes at 37 °C) with 0.2% BSA in RPMI medium followed by brief rinses with serum-free RPMI. Cells were exposed to 25 ug/ml of lipid-free human apoA-I for 2, 4, 8, 14, and 22 hours. Medium recovered from cells was centrifuged (2000 x g, 10 min) to remove cellular debris and the supernatant was used to measure ^{3}[H]-cholesterol in the medium. Cell lipids were extracted using isopropanol and efflux results expressed as a % of initial cellular ^{3}[H] appearing in the medium at each time point.

5' Rapid Amplification of cDNA Ends (5' RACE)- 5' RACE was performed to determine the 5' end of the human ABCA1 transgene expressed in mouse liver. Total RNAs from the liver tissue of the BAC2 transgenic mouse were extracted using the TRIZOL method (Gibco, BRL). First-strand cDNA was generated from 1 ug of total RNA using Superscript reverse transcriptase (Gibco, BRL) at 42 °C for 60 min. An aliquot of the first strand cDNA was then amplified using a human ABCA1 specific primer Exon 4R (Table 1) and a universal primer (Clontech, CA). PCR was performed with 40 cycles of 94 °C for 10 seconds, 57 °C for 15 seconds, and 72 °C for 30 seconds. The amplified products were analyzed by agarose gel eletrophoresis and cloned into the TA cloning vector (Invitrogen) using conditions recommended by the manufacturer. Twenty-four single colonies were picked and sequenced from both ends using the ABI Prism BigDye Terminator Cycle Sequencing Kit (Applied Biosystems Division, Foster City, CA) with a 377 automated DNA sequencing instrument (Applied Biosystems Division, Foster City, CA).

RESULTS

Expression of human ABCA1 in mouse tissues- The tissue expression patterns of two human ABCA1 transgenes have been reported in Qiu et al. (2001). We have examined several additional tissues (Figure 2A), and the results support that BAC1 contains DNA necessary for appropriate tissue specific expression of ABCA1. BAC2 contains the entire coding sequence of human ABCA1 and 13 kb upstream of exon 2 (Figure 1).

Although this transgene lacks the previously described promoter (20), it is expressed in liver and testis, and at very low levels in all other tissues examined (Figure 2B).

To determine how the transgene is regulated in macrophages, we measured the transgene expression changes in cholesterol loaded and cAMP treated mouse peritoneal macrophages. Both cholesterol and cAMP analogs induce the apolipoprotein-mediated cholesterol efflux and ABCA1 expression (10,16-18,30). The BAC1 transgene was expressed in peritoneal macrophages and induced by acetylated LDL, in the same manner as the endogenous mouse gene (Figure 3). The response to cAMP treatment was different for the human transgene and the endogenous mouse gene. The human transgene was down regulated by the cAMP treatment while the endogenous mouse gene was highly induced (Figure 3). This may reflect differences in the kinetics of the response between the human and mouse ABCA1 genes in peritoneal macrophages. The response of ABCA1 to cAMP has previously been reported to differ between mouse and human cells, with mouse cells showing a high and immediate cAMP induction, and human cells showing no induction or requiring a longer cAMP incubation time (17).

Cholesterol efflux in peritoneal macrophages from BAC1 transgenics- To address the question of whether the expression of the human transgene confers functional activity, we measured the efflux of cholesterol to apoA-I using peritoneal macrophages from BAC1 and control mice. Apolipoprotein mediated efflux was approximately 2-fold greater in macrophages expressing human ABCA1 transgene compared to controls (Figure 4A). Macrophages from the transgenic and control mice responded similarly to acetylated LDL

exposures with nearly 4-fold increases in efflux compared to the non-exposure cholesterol efflux levels (Figure 4B). These findings are consistent with an up-regulation of ABCA1 gene expression with cholesterol loading of macrophages and demonstrate the human transgene mimicking the response of the endogenous mouse transporter.

Plasma HDL-cholesterol- Background for studying the effect of the increased ABCA1 expression on plasma HDL in the transgenics were studies demonstrating that decreased activity of ABCA1 results in dramatic reductions in plasma HDL in mice (25-27) and humans (8,11,24). The effect of the increased cholesterol efflux noted in isolated macrophages from the BAC1 transgenic mice on plasma HDL in these animals was assessed. Plasma HDL cholesterol in transgenic and control mice on chow and western diet was measured and no significant differences were noted on either diet (Figure 5).

5' RACE- To map the transcription start site of the liver transcript we performed 5' RACE on the total liver RNA extracted from BAC2 transgenics. The sequence of the 5' RACE product revealed a transcript with an alternative exon 1, and correctly spliced exons 2, 3 and 4 (Figure 6A). This newly discovered exon named exon 1A is located 2,210 bp upstream of exon 2. The exon 1 A is 136 bp in length (Figure 6B).

Analysis of the promoter sequence- Comparison of the sequence of exon 1A with the genomic sequence, identified a conserved 5' splice site located adjacent to this exon. Moreover, the sequence contains the classical TATA box and a CAAT site upstream of the initiation site, suggesting that it may be part of the promoter responsible for the transcriptional control of exon 1A (Figure 6B). Transfac searches (31) and visual analysis

of the promoter region have detected the presence of possible binding sites for several sterol sensing nuclear receptors including LXRs, SXR, LRH-1, and HNF3 (Figure 6B). These receptors have been shown to mediate transcriptional regulation of many genes implicated in cholestererol homeostasis, including the ABCA1 gene (32). These DNA motifs, although have not been proven to interact with the transcription factors, are likely targets for studying regulatory function of ABCA1 in liver and testis.

Expression of the exon 1A transcripts in human tissues- In the BAC1 transgenics, both exon 1 and exon 1A transcripts are present in all tissues with the highest exon 1A expression level in the liver (data not shown). The observation that BAC1 transgenic mice express both exon 1 and exon 1A transcripts suggested that exon 1A may not be a cryptic start site. To determine if the exon 1A transcripts present in human tissues and to examine their potential physiological relevance we investigated the expression of exon 1 and exon 1A in several human tissues (Figure 7). Exon 1A was found to be very abundant in human liver, while in other peripheral tissues such as lung or adrenals the exon 1 transcripts were found to be more abundant. These results indicate that exon 1A occurs naturally in human tissues and is the predominant ABCA1 transcript in liver.

DISCUSSION

The expression pattern of the BAC1 transgene, including 70 kb of DNA upstream of exon 1, suggests that this human transgene likely contains many of the necessary sequences required for the proper regulation of ABCA1 *in vivo*. While the observation that expression of this transgene was associated with increased apoA-I mediated

cholesterol efflux in peritoneal macrophages was predicted the finding that this was not associated with changes in plasma HDL on two different diets was surprising. An increase in plasma HDL was expected, given the fact that both human and mice with decreased ABCA1 expression have decreased HDL values (8,11,24-27) and that upregulation of the gene by rexinoids results in increased HDL plasma values (19).

One of the many possible explanations for the lack of changes in plasma HDL in the ABCA1 transgenics, is that the increased efflux in these animals may be too low to impact on plasma HDL. Induction of the ABCA1 gene by rexinoids which results in enormous increases in ABCA1 expression in macrophages is associated with only moderate increases in plasma HDL cholesterol levels (19). Another explanation for the absence of measurable increases in plasma HDL in BAC1 transgenics, relates to the fact that plasma HDL only measures the steady state level of this lipoprotein in plasma. The ABCA1 transgene may also affect HDL catabolism downstream of the efflux process, possibly in the liver, where it might compensate for the increased efflux occurring at peripheral tissue due to increased ABCA1 expression. Finally, it can be hypothesized that there are other limiting parameters necessary for HDL formation, such as apoA-I, which are not concomitantly up regulated upon ABCA1 over-expression. Through the analysis of higher expressing ABCA1 transgenics and the crossing of ABCA1 and apoA1 transgenics coupled with more in-depth metabolic studies should help elucidate the relationship between increased expression of ABCA1 and plasma HDL levels.

A surprising result of this study was the expression of the smaller human BAC2 transgene in liver and testis despite the absence of the previously defined ABCA1 promoter (20). The 5' RACE analysis of liver RNA from animals expressing this transgene identified a new ABCA1 exon (exon 1A) preceded by a sequence containing the hallmarks of a classical promoter. This new transcriptional start giving rise to a properly splice alternative variant, was noted to be the predominant ABCA1 form in human liver, supporting the physiological relevance of this transcript. Other alternative splice variants have been previously detected in HepG2 cells (21), but they do not correspond to the exon 1A variant identified in the present study, and although they change the amino acid sequence of the protein, their function has not been further characterized. The ABCA1 liver variant described in the present study has a different 5' UTR but no alterations in its protein sequence. This variant ABCA1 may confer a new level of regulation to the gene either at the transcriptional level, through the use of an alternate promoter, or the translational level with the new 5' UTR possibly affecting the intracellular site and efficiency of ABCA1 translation.

Several features of the newly identified exon 1A transcription variant suggest that it may contribute to tissue specific control of ABCA1 expression. This includes the detection of possible LXR/RXR and LRH-1/SF-1 binding sites at the 5' flanking region of exon 1A. LXRs are ligand-activated transcription factors and mediate the regulation of several genes implicated in cholesterol homeostasis (32,33). LRH-1 (Liver receptor homologue 1) is a monomeric nuclear receptor that functions as a tissue-specific

transcription factor and acts as a competence factor mediating the liver specific regulation of the cholesterol 7 α-hydroxylase gene by LXRα (34-36). SF-1 (Steroidogenic factor –1) has similar DNA binding requirements as LRH-1 and controls the oxysterol mediated transactivation of genes involved in steroidogenesis and gonad development (37). The presence of these DNA motifs in the 5' flanking region of exon 1A can potentially account for the expression of BAC2 in liver and testis. The putative exon 1A promoter might allow for an alternate regulation of ABCA1 by liver specific by-products of cholesterol catabolism and in that way contribute to the coordinate regulation of ABCA1 in the different steps of reverse cholesterol transport.

Modification of HDL metabolism has long been considered a target for therapeutic interventions in the prevention of atherogenesis (for a recent review, see (38)). With the discovery of ABCA1 and its impact on HDL metabolism effecting cholesterol efflux and intestinal absorption of dietary cholesterol (17,19,27), ABCA1 has become a major target for intervention. Due to ABCA1's expression in many tissues and its multiple apparent functions (25,39-41), only through *in vivo* studies can we begin to assess the relevant physiological effects of increasing its expression on lipid homeostasis and atherogenesis. Results of the present analysis of the *in vivo* effects of the human ABCA1 transgene illustrate the complexity of ABCA1 regulation and its impact on HDL formation and metabolism. Analysis of the atherogenesis susceptibility of these BAC transgenics with increases in cholesterol efflux, unaccompanied by measurable changes in plasma HDL

cholesterol, should provide important insights into the utility of altering the expression of ABCA1 expression on atherogenesis.

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FIGURE LEGENDS

FIG.1. **Map of the Human ABCA1 BACs.** Schematic representation of the exon/intron structure in the human ABCA1 gene is shown at the top. The newly identified exon (exon 1A or E1A) is located 2,210 bp upstream of exon 2. The ATG initiation codon and the sequence encoding for the first 21 amino acids of the ABCA1 protein is located in exon 2. The ESTs represent the open reading frames of two identified ESTs with unassigned function. BAC1 is 255 kb long and it contains 70 kb upstream of exon 1 and approximately 35 kb downstream of the 3'UTR. The 171 kb BAC2 lacks exon 1 and its promoter, but contains the new exon 1A and its promoter together with the complete coding sequence of ABCA1.

FIG. 2. **Expression of human ABCA1 genes in transgenic mice.** Total RNA was isolated from different tissues of (A) a BAC1 transgenic mouse and (B) a BAC2 transgenic mouse. RNA levels of the ABCA1 genes were measured using a Taqman quantitative assay using mouse Abca1 primers located in exon 2 and exon 4 and human ABCA1 primers in exon 3 and 4 (Table 1). The relative transcript amounts were obtained by normalizing the mouse and human ABCA1 signals to the 18S signals retrieved from the same tissues. The bars indicate the S.D. from the mean of four Taqman measurements. Similar results were obtained from at least two independent lines of BAC1 and BAC2 transgenic mice. SIP, SIM and SID are abbreviations for the proximal, medial and distal parts of the small intestine.

FIG. 3. **Expression of mouse and human ABCA1 in peritoneal macrophages from BAC1 transgenics.** Peritoneal macrophages isolated from 5 BAC1 transgenic mice were isolated as indicated in the "Experimental Procedures". 1 million cells/well were plated in 24 well plates and allowed to attach to the plates for 4 hours and then washed with RPMI-1640 with 1% FBS. Two wells were incubated for 24 hrs with 1% FBS, 50 ug protein/ml of acetylated LDL, or 0.3 mM 8-(4-chlorophenylthio) adenosine 3':5'-cyclic monophosphate (cAMP). RNA levels of the ABCA1 genes were measured using a Taqman quantitative assay using (A) mouse Abca1 primers located in exon 2 and exon 4 and (B) human ABCA1 primers in exon 3 and 4. The relative transcript amounts were calculated by normalizing the mouse and human ABCA1 signals to the 18S signal retrieved from the same RNA. Each column represents an average measurement of duplicate Taqman experiments.

FIG. 4. **^{3}[H] Cholesterol efflux in peritoneal macrophages from BAC1 transgenics.** A. ApoA-I mediated cholesterol efflux. Five BAC1 (□) and five control mice (O) were used to isolate the peritoneal macrophages as described in the "Experimental Procedures". The % of cholesterol was measured at the time intervals given after the addition of lipid-free human apoA-I. Each number represents an average measurement of two independent wells. B. ^{3}[H]-cholesterol efflux of cells incubated with or without acetylated LDL. Peritoneal macrophages were isolated from five BAC1 (gray column) and five control mice (white column). The efflux to apoA-I after 24 hrs was measured in the presence or

absence of acetylated LDL. Each column represents an average measurement of two independent wells for each treatment.

FIG.5. **Plasma HDL-cholesterol in BAC1 transgenics.** HDL cholesterol was measured in five 4-month old BAC1 transgenic mice (■; 3M and 2F) and 5 littermate control mice (□; 3M and 2F) on chow diet or on a western diet for two and four weeks. Error bars indicate the S.D. from the mean of the five samples in each group.

FIG. 6. **Alternative splice variant in BAC2 transgenics and the sequence of exon 1A and its putative promoter.** (A) Structure of the alternative splice variant found in the liver mRNA of BAC2 transgenics. The 5' RACE product contains exon 1A and a correctly spliced exons 2, 3 and 4. (B) Sequence of exon 1A and the upstream promoter region. The exon 1A sequence is underlined and in bold. The transcription initiation site mapped by 5' RACE PCR is indicated with +1. The putative CAAT site, TATA box and several possible transcription factors binding sites are given in bold capitals. The DNA motifs resembling DR-4 and DR-3 like elements are possible binding sites for LXR/RXR and SXR/RXR, respectively. The DNA motifs similar to the binding sites for the liver receptor homologue-1 (also called LRH-1; NR5A2) and for the steroidogenic factor-1 (SF-1) are indicated as LRH-RE/SF-1. The DNA sequences resembling the binding sites for hepatic nuclear factor-3 and sterol regulatory element binding-protein are indicated as HNF3 and SREBP, respectively.

FIG. 7. **Expression of exon 1 and exon 1A in human tissues.** The relative expression of (A) exon 1 and (B) exon 1A transcripts was measured from total RNA of different

human tissues (Clontech) in a Taqman PCR quantitative assay described in the "Experimental Procedures". The signals for each tissue were corrected for the total amount of RNA given by the 18S signal.

FOOTNOTES

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#Both authors have contributed equally to this work

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The abbreviations used are: HDL, high density lipoprotein; apoA-I, apolipoprotein A-I; ABCA1, ATP binding cassette transporter 1; Abca1, Mouse ATP binding cassette transporter 1; BAC, Bacterial Artifitial Chromosomes; PCR, polymerase chain reaction; bp, base pair(s); kb, kilobase(s); DMEM, Dulbecco's modified Eagle's medium; PBS, phosphate-buffered saline; BSA, bovine serum albumin; FBS, fetal bovine serum.

Acknowledgments- We thanks Dr. Trudy Forte for providing purified apoA-I for this study.

TABLE 1. Primers used in the Taqman system and 5' RACE PCRs.

Primer name	**Sequence (5'-3')**
Exon 1F	GGAGAAAGAGACGCAAACACA
Exon 2R	AGCGGCCAGAGCTCACAG
Exon 1AF	TCCACAGTAGAACACAGTTGAACA
Exon 3F	CAAACATGTCAGCTGTTACTGGAAG
Exon 4R	GAGCCTCCCCAGGAGTCG
Mouse Exon 2F	CATTAAGGACATGCACAAGGTCC
Mouse Exon 4R	CAGAAAATCCTGCAGCTTCAATTT

FIG. 1

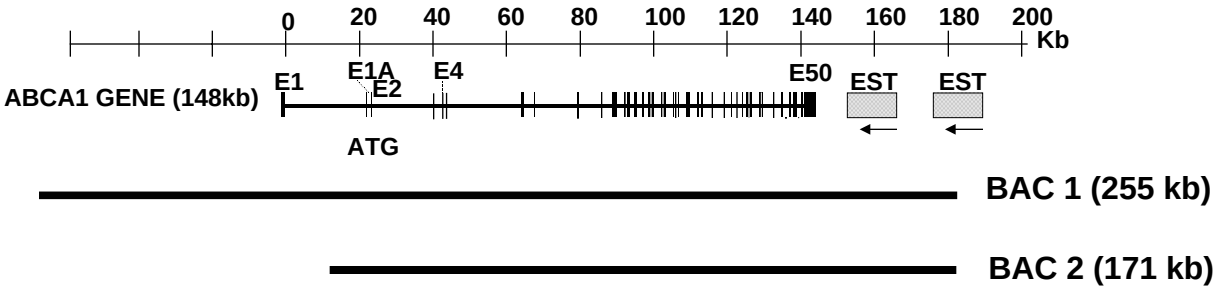

0
20
40
60
80
100
120
140
160
180
200
Kb
ABCA1 GENE (148kb)
E1
E1A
E2
E4
E50
EST
EST
ATG
BAC 1 (255 kb)
BAC 2 (171 kb)

FIG. 2A

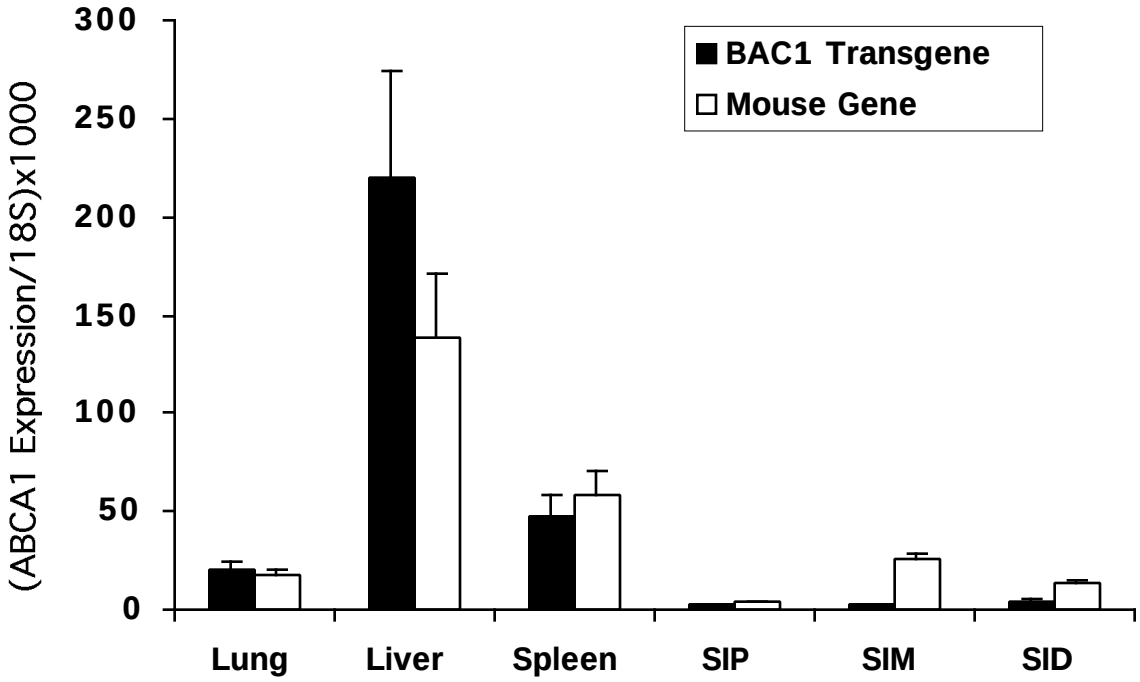

300
250
200
150
100
50
0
(ABCA1 Expression/18S)x1000
BAC1 Transgene
Mouse Gene
Lung
Liver
Spleen
SIP
SIM
SID

FIG. 2B

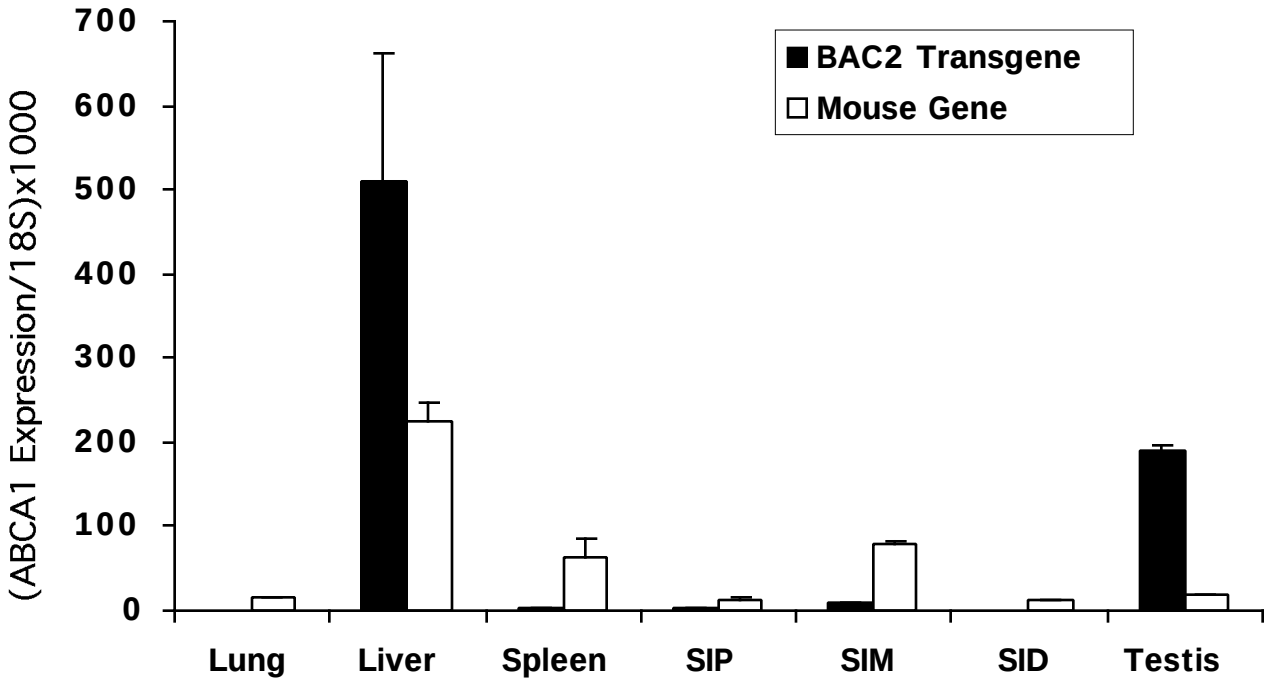

700
600
500
400
300
200
100
0
(ABCA1 Expression/18S)x1000
BAC2 Transgene
Mouse Gene
Lung
Liver
Spleen
SIP
SIM
SID
Testis

FIG. 3A

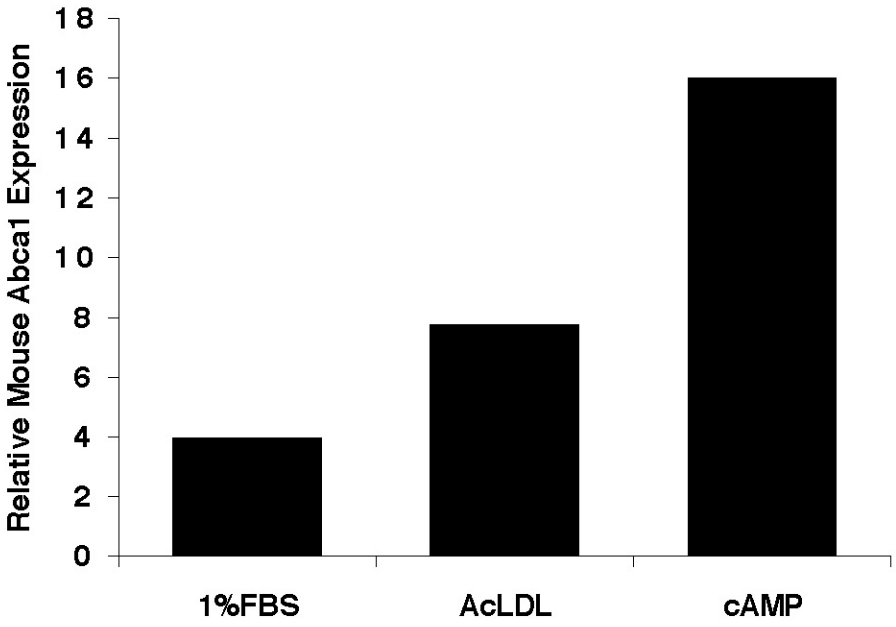

Relative Mouse Abca1 Expression
18
16
14
12
10
8
6
4
2
0
1%FBS
AcLDL
cAMP

FIG. 3B

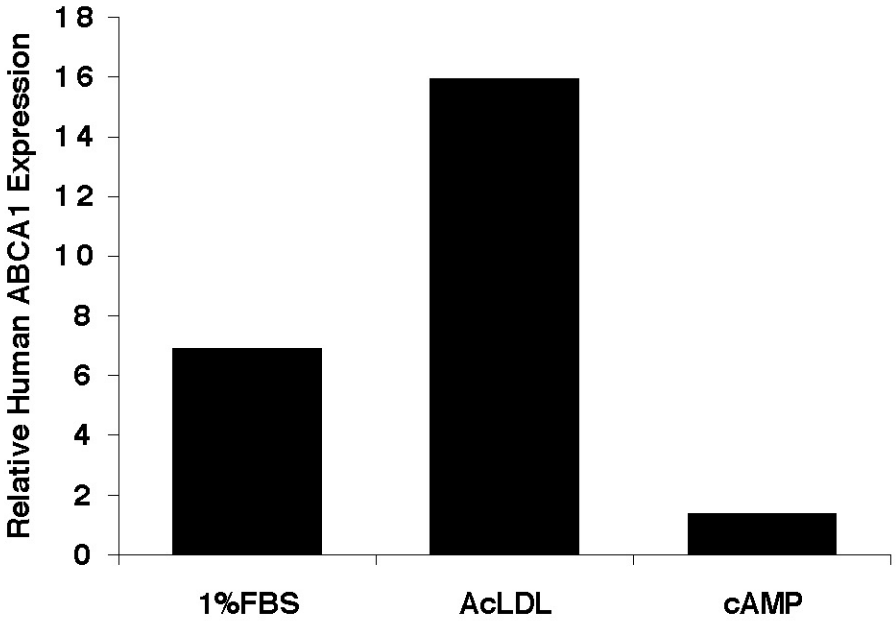

Relative Human ABCA1 Expression
18
16
14
12
10
8
6
4
2
0
1%FBS
AcLDL
cAMP

FIG. 4A

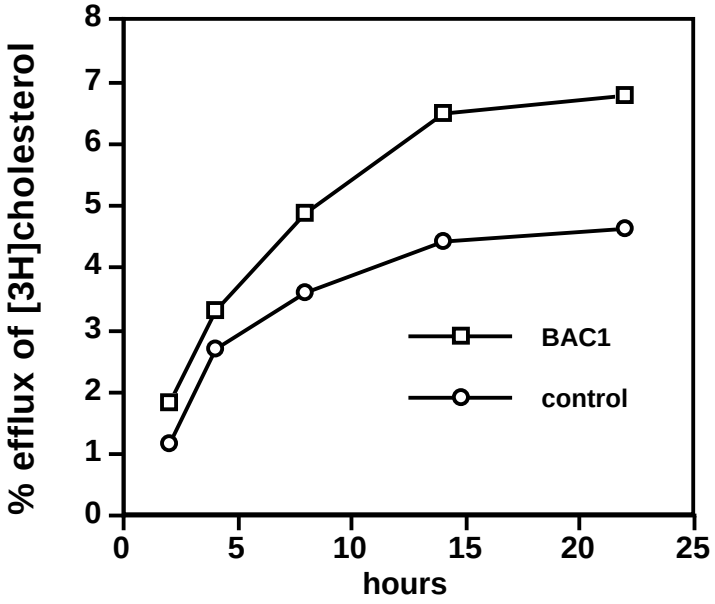

% efflux of [3H]cholesterol
0
1
2
3
4
5
6
7
8
0
5
10
15
20
25
hours
BAC1
control

FIG. 4B

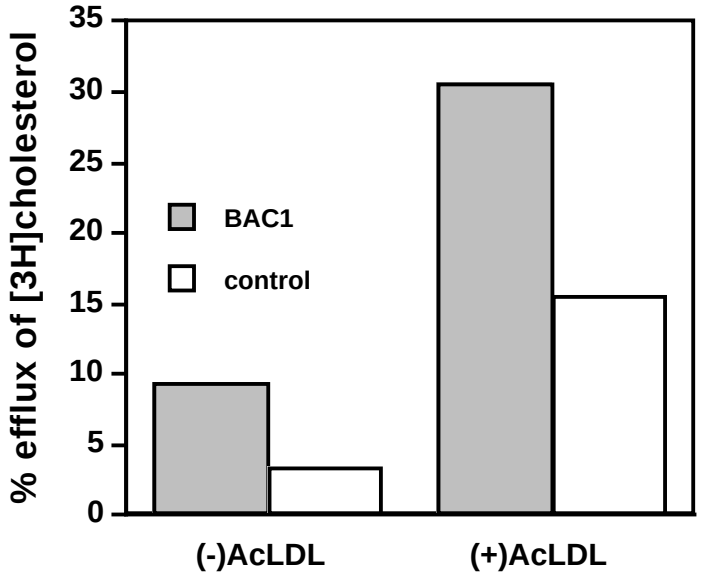

% efflux of [3H]cholesterol
0
5
10
15
20
25
30
35
BAC1
control
(-)AcLDL
(+)AcLDL

FIG. 5

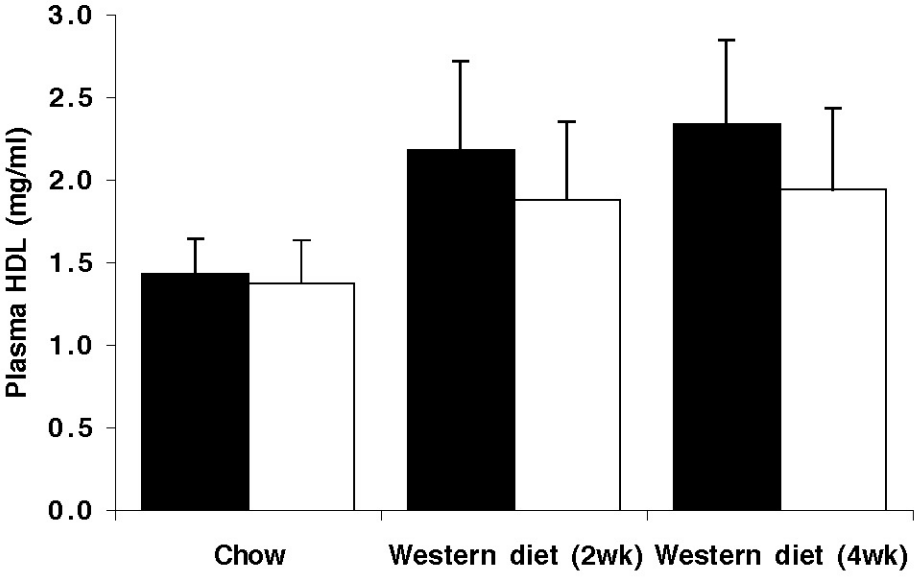

3.0
2.5
2.0
1.5
1.0
0.5
0.0
Plasma HDL (mg/ml)
Chow
Western diet (2wk)
Western diet (4wk)

FIG. 6A

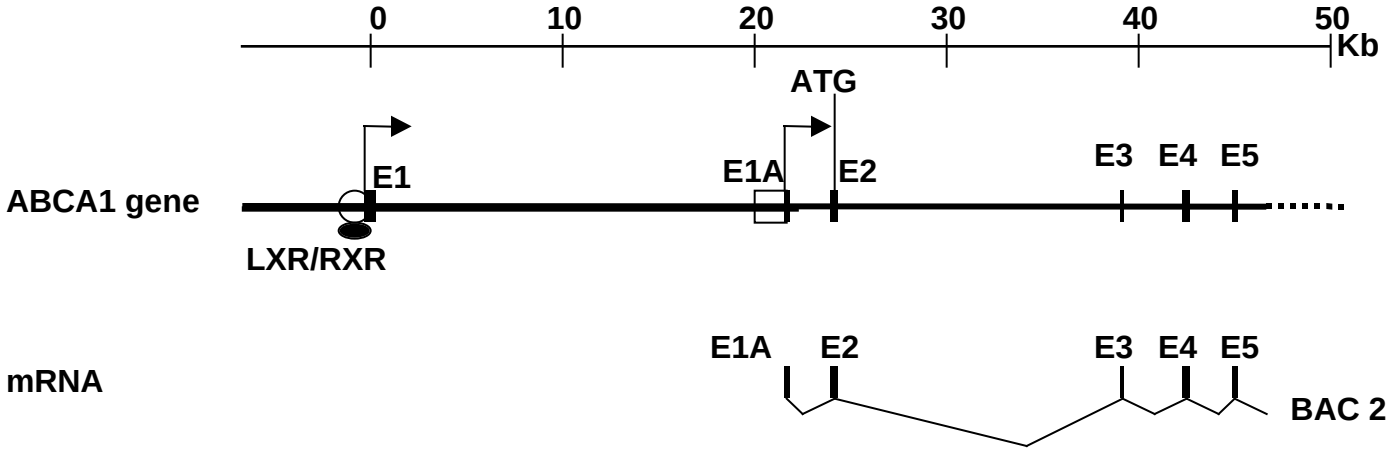


FIG. 6B

agagtaggctggagtcacagaagggaggccaggtagaccttggtgagcactggactctatgttcaggtgctgaggagctggcaaaaggttttaagtcgggg
agaggcatgttcagatatttggtctagctgagtaactttgggtgctctgtgacaaatggttgggagaccagtgaggtggcagttgcggtcatctaggagca
DR-3 like
ggatcagagtggcctat**TGACTG**gga**TGACTG**tgaagtgggatcctttccagccagtaactggaaatgtgtatgagggcagaagtgagtgtactgcatttg
HNF3
aaacattgagaaatctagtacatagtactgtctcttttatatctttttttttttttttttgatttt**GGTTTGTTTGTTCAC**taacttggaaaactgatgt
ggaaatgtccctttggcttcagttacctgagcagaaggggccgggcattgccaaactctcctcttaggacagaattgctcccagtattgatcattgtgttc
LRH-RE/SF-1
SREBP
tgagttgggggagcaaattgtgcaggaggccaggtcagtg**CCAAGGTGG**gtgggaggaattggagcaggaagcttgcctaag**TGTGCCCA**gcaaagccacg
DR-4 like
gtagaactttctactgtggctctatgctacttcttagcaaccttctccatgtg**CTTCCT**ggag**AGTCCT**tggagtcagaacctttttcttgaaacccagac

actttacttccaagaaaatgctgtccaagaaaactcatccttccttcttctcatgaacgttgtgatgaggtgtgtcttctcttcctttgagcttttccac
tcagggtttaggggaggtgatattctatatttgggtttggctctgggtactgcaacactaggctattaagatttcatccttactgctttgcccctcctatc

+1 Exon 1A
tttccagaaaccca**CAAT**ggatttgctagaaataatggaacgtcctgtttggacagga**TATAA**ccatttctcagctagaggatattgt**TGGAATGAAGAAA**
GATAAATGGGGAGAAGGGAACTCACATTGCTTTGGCACTTAAATTAAGCCATGTACTGTGTTGGGAAATTATTTATATTATCTCGTTGAATCCACAGTAGA
ACACAGTTGAACACCATACAAGgtaagtattgtcatcc

FIG. 7A

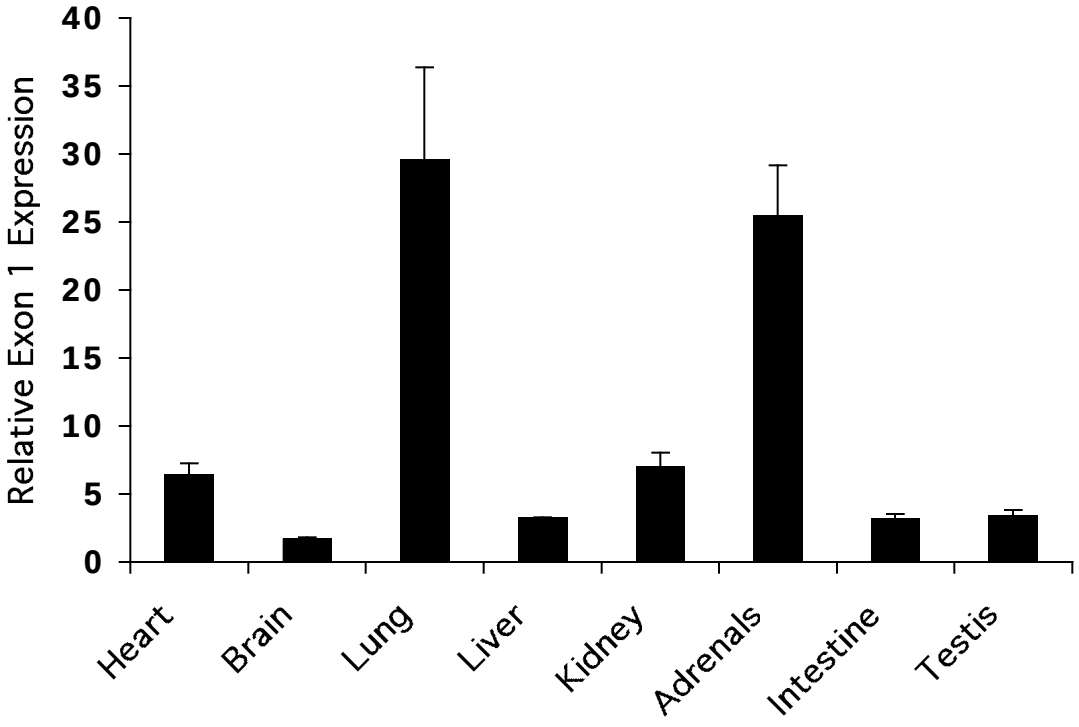
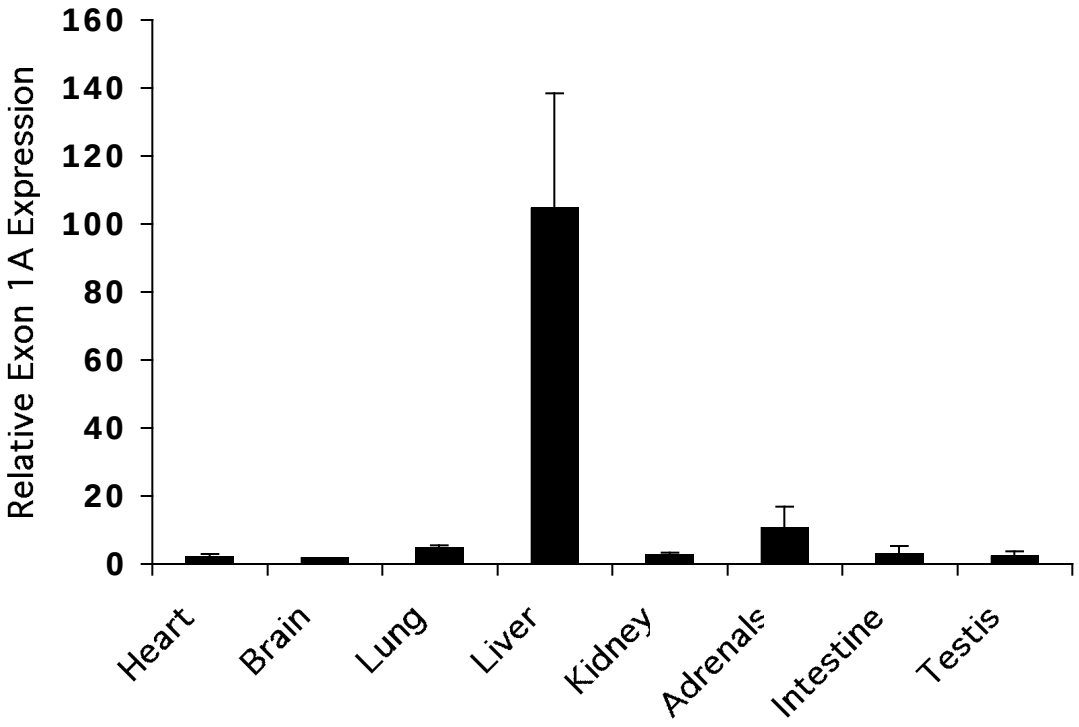

Relative Exon 1 Expression
40
35
30
25
20
15
10
5
0
Heart
Brain
Lung
Liver
Kidney
Adrenals
Intestine
Testis

FIG. 7B


Relative Exon 1A Expression
160
140
120
100
80
60
40
20
0
Heart
Brain
Lung
Liver
Kidney
Adrenals
Intestine
Testis