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(71) Demandeur/Applicant:
RIKEN, JP
(72) Inventeurs/Inventors:
NAKAMURA, YUSUKE, JP;
SEKINE, AKIHIRO, JP;
IIDA, ARITOSHI, JP;
SAITO, SUSUMU, JP
(74) Agent: SMART & BIGGAR

(54) Titre : DETECTION DE POLYMORPHISMES GENETIQUES

(54) Title: DETECTION OF GENETIC POLYMORPHISMS IN GENES ASSOCIATED WITH PHARMACOGENOMICS

(57) **Abrégé/Abstract:**

The present invention relates to genetic polymorphism data, compositions and methods for detecting genetic polymorphisms, methods for evaluating drugs using genetic polymorphisms and screening methods for drugs.



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(71) Applicant (for all designated States except US): **RIKEN**
[JP/JP]; 2-1, Hirosawa, Wako-shi, Saitama 351-0198 (JP).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **NAKAMURA, Yusuke** [JP/JP]; 1-17-33, Azamino, Aoba-ku, Yokohama-shi, Kanagawa 225-0011 (JP). **SEKINE, Akihiro** [JP/JP]; 1-11-8, Kita, Kunitachi-shi, Tokyo 186-0001 (JP). **IIDA, Aritoshi** [JP/JP]; 21, Tajiricho, Nakahara-ku, Kawasaki-shi, Kanagawa 211-0014 (JP). **SAITO, Susumu** [JP/JP]; 5-10-6-108, Higashiome, Ome-shi, Tokyo 198-0042 (JP).

(74) Agents: **HIRAKI, Yusuke** et al.; Toranomon No.5 Mori Building Third Floor, 17-1, Toranomon 1-chome, Minato-ku, Tokyo 105-0001 (JP).

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(57) Abstract: The present invention relates to genetic polymorphism data, compositions and methods for detecting genetic polymorphisms, methods for evaluating drugs using genetic polymorphisms and screening methods for drugs.



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DETECTION OF GENETIC POLYMORPHISMS IN GENES ASSOCIATED WITH PHARMACOGENOMICS

The present invention claims priority to Japanese Patent Application Ser. Nos. 2000-399,443 filed December 27, 2000, 2001-135,256 filed May 2, 2001, and 2001-256,862 filed August 27, 2001.

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FIELD OF THE INVENTION

The present invention relates to genetic polymorphism data, compositions and methods for detecting genetic polymorphisms, methods for evaluating drugs using genetic polymorphisms and screening methods for drugs.

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BACKGROUND

Human beings come in all shapes and sizes, and over three billion genetic codes are located in somewhat different sites in each human being. Individual DNA sequence variations in the human genome are known to directly cause specific diseases or conditions, to predispose certain individuals to specific diseases or conditions, and to affect responses of individuals to treatments such as drugs. Such variations also modulate the severity or progression of many diseases. Additionally, DNA sequences vary between populations. Therefore, determining DNA sequence variations in the human genome is useful for making accurate diagnoses, for finding suitable therapies, and for understanding the relationship between genome variations and environmental factors in the pathogenesis of diseases, the prevalence of conditions and the efficacy of therapies.

There are several types of DNA sequence variations in the human genome. These variations include insertions, deletions and copy number differences of repeated sequences. These differences in the genetic code are called genetic polymorphisms. The most common DNA sequence variations in the human genome are single base pair substitutions. These are generally referred to as single nucleotide polymorphisms (SNPs) when the variant allele has a population frequency of at least 1%. SNPs may be classified by where they appear in the genome. For example, a single nucleotide polymorphism may be classified as a coding SNP (cSNP) when it is in a region encoding a protein, or genome SNP (gSNP) when it is detected anywhere in a genome, without reference to

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whether it is in a coding region. Coding SNPs include silent SNPs (sSNP), and SNPs that may be in regions associated with coding sequences, such as regulatory regions or elements (*e.g.*, regulatory SNPs, or rSNPs) and introns (*e.g.*, intron SNPs, or iSNPs).

SNPs are particularly useful in studying the relationship between DNA sequence variations and human diseases, conditions and drug responses because SNPs are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. In addition, methods for detecting SNPs are more amenable to being automated and used for large-scale studies than methods for detecting other, less common DNA sequence variations.

Single nucleotide polymorphisms are useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. This is directly related in clinical medicine to diagnosing the risk for a disease and determining the proper pharmaceutical treatment. There is currently a worldwide effort going on to develop drugs based on the target genes that cause diseases. Individual patients also react differently when a drug is administered. In some patients, a drug may have a significant effect, in others a lesser effect and in still others no effect at all. In other words, there is a major difference in patient reactions to the same drug. Patients may also metabolize drugs at different rates. In addition to differences in therapeutic reactions among patients to drugs, there is also the possibility of strong and even fatal side effects due to genetically linked differences in, *e.g.*, drug metabolism, drug transport or drug receptor function. Analysis of genetic polymorphisms such as SNPs allows for the selection of drugs and the development of treatment protocols tailored to each individual patient (so-called "personalized" medical treatments). Instead of the using trial-and-error methods of matching patients with the right drugs, doctors may, for example, be able to analyze a patient's genetic profile and prescribe the best available drug therapy from the beginning. Not only would this take the guesswork out of finding the right drug, it would reduce the likelihood of adverse reactions, thus increasing safety.

SUMMARY OF THE INVENTION

The present invention identifies genetic polymorphisms relating to genes associated with drug metabolism. In some embodiments, the present invention provides

methods for determining variations in sequences and genes associated with drug-metabolizing enzymes. In preferred embodiments, the present invention provides methods for collecting genetic polymorphism data for use in evaluating the effectiveness and safety of a drug based on the data, and screening drugs using the data. In some preferred embodiments, the polymorphisms of the present invention are used to evaluate a causal relationship between the genetic make-up of a patient and a response to an administered drug.

The present invention relates to genes encoding enzymes associated with drug metabolism (drug metabolizing enzymes, or DMEs). In particular, the present invention relates to sequence variations associated with variations in DMEs. In some embodiments, variations occur in coding regions of DMEs, such as may alter a function of the DMEs, (*e.g.*, by increasing or decreasing its level of activity, or shifting its activity to an alternative target or function). In other embodiments, the variations occur in non-coding regions of the genome, such as may alter expression of a DME (*e.g.*, increasing or decreasing the amount of an enzyme produced in a cell) or processing of an RNA transcript encoding a DME (*e.g.*, by altering splicing).

In some embodiments, the present invention provides methods for detecting DME-related sequence variations. In some preferred embodiments, the methods of the present invention are used to create a profile of DME-related polymorphisms in a test subject.

In other embodiments, the present invention provides isolated nucleic acid sequences encoding variant DMEs. For example, the present invention provides a recombinant DNA vector comprising DNA having a nucleotide sequence encoding a variant DME, the nucleotide sequence comprising a sequence including, but not limited to, SEQ ID NOS:1-3360 and 3361-7669, and substantially similar sequences. In a preferred embodiment, the invention provides a host cell transformed with a recombinant DNA vector comprising DNA having a nucleotide sequence encoding a variant DME. The invention is not limited by the nature of the host cell employed. The art is well aware of expression vectors suitable for the expression of nucleotide sequences encoding variant DMEs that can be expressed in a variety of prokaryotic and eukaryotic host cells. In some preferred embodiments, the host cell is a eukaryotic cell grown in culture, such

as for use in *in vitro* drug screening (e.g., by monitoring the expression of genes associated with the pathways targeted by a particular test drug). In other preferred embodiments, the host cell is *in vivo*.

The present invention provides systems and methods for detection of
5 polymorphisms associated with genes encoding enzymes associated with drug
metabolism. The present invention is not limited in the nature of the detection assay used
for detection or identification of such polymorphisms. Such detection assays include, but
are not limited to, hybridization methods and array technologies (e.g., technologies
available from Aclara BioSciences, Haywood, CA; Affymetrix, Santa Clara, CA; Agilent
10 Technologies, Inc., Palo Alto, CA; Aviva Biosciences Corp., San Diego, CA; Caliper
Technologies Corp., Palo Alto, CA; Celera, Rockville, MD; CuraGen Corp., New Haven,
CT; Hyseq Inc., Sunnyvale, CA; Illumina, Inc., San Diego, CA; Incyte Genomics, Palo
Alto, CA; Motorola BioChip Systems; Nanogen, San Diego, CA; Orchid BioSciences,
Inc., Princeton, NJ; Applera Corp., Foster City, CA; Rosetta Inpharmatics, Kirkland,
15 WA; and Sequenom, San Diego, CA); polymerase chain reaction-based methods
(e.g., TAQMAN, Applera Corp., GENECODE system, EraGen, Middleton, WI);
branched hybridization methods; enzyme mismatch cleavage methods; NASBA;
sandwich hybridization methods; methods employing molecular beacons; ligase chain
reactions, and the like.

20 Methods of the present invention find application in improving the drug discovery
and approval processes. For example, the costs and risks of drug development may be
reduced if only those persons capable of responding to a drug are selected for clinical
trials. In addition, previously failed drug candidates may be revived as they are matched
with more appropriate patient populations. Decreases in the number of adverse drug
25 reactions, the number of failed drug trials, the time it takes to get a drug approved, the
length of time patients are on medication, the number of medications patients must take
to find an effective therapy, and an increase in the range of possible drug targets will
promote a net decrease in the cost of health care.

Thus, in some embodiments, the present invention provides a method of
30 identifying individuals having a polymorphism, comprising providing nucleic acid from a
subject; and detecting the presence of at least one polymorphism in said nucleic acid, said

at least one polymorphism including, but not limited to, polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669. In some embodiments, the method further provides the step of providing a prognosis (e.g., a genotype relative risk or a population attributable risk) to the subject based on the presence or absence of the at least one polymorphism. In some
5 embodiments, the detecting step is carried out using a detection assay including, but not limited to, a hybridization assay, a TAQMAN assay, an invasive cleavage assay, use of mass spectroscopy, a microarray, a polymerase chain reaction, a rolling circle extension assay, a sequencing assay, a hybridization assay employing a probe complementary to a polymorphism, a bead array assay, a primer extension assay, an enzyme mismatch
10 cleavage assay, a branched hybridization assay, a NASBA assay, a molecular beacon assay, a cycling probe assay, a ligase chain reaction assay, and a sandwich hybridization assay.

The present invention also provides a nucleic acid (e.g., a gene, a probe, a primer, etc.) comprising a sequence selected from the group consisting of SEQ ID NO:1-3360
15 and 3361-7669 or complements thereof. In some embodiments, the nucleic acid molecule comprises a label. In some embodiments, the nucleic acid is attached to a solid support (e.g., as part of a microarray). The present invention also provides vectors comprising the nucleic acid and host cell comprising the vector, as well as polypeptide encoded by the nucleic acid. Methods of producing and purifying polypeptides are well
20 known in the art.

The present invention further provides kits for detecting a polymorphism, comprising at least one reagent that specifically detects a polymorphism in a sequence including, but not limited to, SEQ ID Nos:1-3360 and 3361-7669. In some embodiments, the kit further comprising instructions for determining whether the subject is at increased
25 risk of having a drug metabolism disorder. In some embodiments, the at least one reagent comprises a nucleic acid probe. The kits can be configured for a variety of uses including, but not limited to, use as an in vitro diagnostic detection assay, an analyte specific reagent detection assay, and a research-use-only detection assay.

The present invention also provides a method for screening subjects for genetic
30 markers associated with drug metabolizing enzyme(s), comprising: a) providing a biological sample comprising a nucleic acid from a subject; b) testing the nucleic acid for

a polymorphism in a genetic marker associated with a drug metabolizing enzyme, said genetic marker comprising one or more nucleotide polymorphisms designated by n, said n selected from a base substitution, an insertion, or a deletion found in a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669. The present invention is not limited by the source of the nucleic acid. In some embodiments, the biological sample comprises blood, saliva, amniotic fluid, and tissue. In some embodiments, the subject is a human. In some preferred embodiments, the nucleic acid comprises DNA and/or RNA.

The present invention further provides a composition comprising an array of detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of detecting one or more nucleotide polymorphisms designated by n in SEQ ID Nos:1-3360 and 3361-7669, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.

The present invention also provides a composition comprising a detection probe for determining the presence or absence a single nucleotide polymorphism in a gene encoding a drug metabolizing enzyme, said gene comprising a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

The present invention further provides a method of determining the effectiveness of or side-effect of a drug or treatment protocol, comprising; a) administering a drug or treatment protocol to one or more subjects; b) obtaining nucleic acid from said one or more subjects; c) using a detection assay to detect the presence of at least one polymorphism in said nucleic acid from said one or more of subjects, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669; and d) assigning an effectiveness rating, side-effect rating, or score for said drug or treatment protocol based upon a result of one or more said detection assays (*See e.g.*, Toxicology Testing Handbook: Principles, Applications, and Data Interpretation, ed. Jacobson-Kram and Keller, 2001, herein incorporated by reference in its entirety).

The present invention also provides a method of prescribing a drug to or treatment protocol for a subject, comprising; providing nucleic acid from said subject; using a

detection assay to detect the presence of at least one polymorphism in the nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669; and, prescribing said drug or treatment protocol based upon the result of said detection assay.

5 The present invention further provides a method for generating assay data comprising: obtaining a sample from a subject containing nucleic acid; transferring said sample to a laboratory; and receiving data from said laboratory, wherein said data corresponds to the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in
10 SEQ ID Nos:1-3360 and 3361-7669. The present further provides data sets generated by this method.

DEFINITIONS

15 To facilitate an understanding of the present invention, a number of terms and phrases are defined below:

 As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (*i.e.*, a sequence of nucleotides such as an oligonucleotide or a target nucleic acid) related by the base-pairing rules. For example, for the sequence "5'-A-G-T-3'," is complementary to the sequence "3'-T-C-A-5'." Complementarity may be
20 "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection
25 methods that depend upon binding between nucleic acids. Either term may also be used in reference to individual nucleotides, especially within the context of polynucleotides. For example, a particular nucleotide within an oligonucleotide may be noted for its complementarity, or lack thereof, to a nucleotide within another nucleic acid strand, in contrast or comparison to the complementarity between the rest of the oligonucleotide
30 and the nucleic acid strand. Nucleotide analogs used to form non-standard base pairs, whether with another nucleotide analog (e.g., an IsoC/IsoG base pair), or with a naturally

occurring nucleotide (e.g., as described in U.S. Patent 5,912,340, herein incorporated by reference in its entirety) are also considered to be complementary to a base pairing partner within the meaning this definition.

5 The term "homology" and "homologous" refers to a degree of identity. There may be partial homology or complete homology. A partially homologous sequence is one that is less than 100% identical to another sequence.

As used herein, the term "hybridization" is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is influenced by such factors as the
10 degree of complementary between the nucleic acids, stringency of the conditions involved, and the T_m of the formed hybrid. "Hybridization" methods involve the annealing of one nucleic acid to another, complementary nucleic acid, *i.e.*, a nucleic acid having a complementary nucleotide sequence. The ability of two polymers of nucleic acid containing complementary sequences to find each other and anneal through base
15 pairing interaction is a well-recognized phenomenon. The initial observations of the "hybridization" process by Marmur and Lane, Proc. Natl. Acad. Sci. USA 46:453 (1960) and Doty et al., Proc. Natl. Acad. Sci. USA 46:461 (1960) have been followed by the refinement of this process into an essential tool of modern biology.

With regard to complementarity, it is important for some diagnostic applications
20 to determine whether the hybridization represents complete or partial complementarity. For example, where it is desired to detect simply the presence or absence of a foreign DNA sequence, it is only important that the hybridization method ensures hybridization when the relevant sequence is present; conditions can be selected where both partially complementary probes and completely complementary probes will hybridize. Other
25 diagnostic applications, however, may require that the hybridization method distinguish between partial and complete complementarity. It may be of interest to detect genetic polymorphisms. For example, human hemoglobin is composed, in part, of four polypeptide chains. Two of these chains are identical chains of 141 amino acids (alpha chains) and two of these chains are identical chains of 146 amino acids (beta chains).
30 The gene encoding the beta chain is known to exhibit polymorphism. The normal allele encodes a beta chain having glutamic acid at the sixth position. The mutant allele

encodes a beta chain having valine at the sixth position. This difference in amino acids has a profound (most profound when the individual is homozygous for the mutant allele) physiological impact known clinically as sickle cell anemia. It is well known that the genetic basis of the amino acid change involves a single base difference between the normal allele DNA sequence and the mutant allele DNA sequence.

The complement of a nucleic acid sequence as used herein refers to an oligonucleotide which, when aligned with the nucleic acid sequence such that the 5' end of one sequence is paired with the 3' end of the other, is in "antiparallel association." Certain bases not commonly found in natural nucleic acids may be included in the nucleic acids of the present invention and include, for example, inosine and 7-deazaguanine. Complementarity need not be perfect; stable duplexes may contain mismatched base pairs or unmatched bases. Those skilled in the art of nucleic acid technology can determine duplex stability empirically considering a number of variables including, for example, the length of the oligonucleotide, base composition and sequence of the oligonucleotide, ionic strength and incidence of mismatched base pairs.

As used herein, the term " T_m " is used in reference to the "melting temperature." The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. Several equations for calculating the T_m of nucleic acids are well known in the art. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41(\% G + C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (*see e.g.*, Anderson and Young, Quantitative Filter Hybridization, in Nucleic Acid Hybridization (1985). Other references (*e.g.*, Allawi, H.T. & SantaLucia, J., Jr. Thermodynamics and NMR of internal G.T mismatches in DNA. Biochemistry 36, 10581-94 (1997) include more sophisticated computations which take structural and environmental, as well as sequence characteristics into account for the calculation of T_m .

As used herein the term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds, under which nucleic acid hybridizations are conducted. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "weak" or "low" stringency are

often required when it is desired that nucleic acids that are not completely complementary to one another be hybridized or annealed together.

"High stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42 C in a solution
5 consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid
10 hybridization comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 1.0X SSPE, 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

15 "Low stringency conditions" comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5X Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharamcia), 5 g BSA (Fraction V; Sigma)] and 100 g/ml denatured salmon sperm DNA
20 followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

The term "gene" refers to a DNA sequence that comprises control and coding sequences necessary for the production of an RNA having a non-coding function (*e.g.*, a ribosomal or transfer RNA), a polypeptide or a precursor. The RNA or polypeptide can
25 be encoded by a full-length coding sequence or by any portion of the coding sequence so long as the desired activity or function is retained.

The term "wild-type" refers to a gene or a gene product that has the characteristics of that gene or gene product when isolated from a naturally occurring source. A wild-type gene is that which is most frequently observed in a population and is thus arbitrarily
30 designated the "normal" or "wild-type" form of the gene. In contrast, the term "modified," "mutant," or "polymorphic" refers to a gene or gene product that displays

modifications in sequence and or functional properties (*i.e.*, altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally-occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type gene or gene product.

5 The term "oligonucleotide" as used herein is defined as a molecule comprising two or more deoxyribonucleotides or ribonucleotides, preferably at least 5 nucleotides, more preferably at least about 10-15 nucleotides and more preferably at least about 15 to 30 nucleotides. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide. The oligonucleotide may be generated in
10 any manner, including chemical synthesis, DNA replication, reverse transcription, PCR, or a combination thereof.

Because mononucleotides are reacted to make oligonucleotides in a manner such that the 5' phosphate of one mononucleotide pentose ring is attached to the 3' oxygen of its neighbor in one direction via a phosphodiester linkage, an end of an oligonucleotide is
15 referred to as the "5' end" if its 5' phosphate is not linked to the 3' oxygen of a mononucleotide pentose ring and as the "3' end" if its 3' oxygen is not linked to a 5' phosphate of a subsequent mononucleotide pentose ring. As used herein, a nucleic acid sequence, even if internal to a larger oligonucleotide, also may be said to have 5' and 3' ends. A first region along a nucleic acid strand is said to be upstream of another region if
20 the 3' end of the first region is before the 5' end of the second region when moving along a strand of nucleic acid in a 5' to 3' direction.

When two different, non-overlapping oligonucleotides anneal to different regions of the same linear complementary nucleic acid sequence, and the 3' end of one oligonucleotide points towards the 5' end of the other, the former may be called the
25 "upstream" oligonucleotide and the latter the "downstream" oligonucleotide. Similarly, when two overlapping oligonucleotides are hybridized to the same linear complementary nucleic acid sequence, with the first oligonucleotide positioned such that its 5' end is upstream of the 5' end of the second oligonucleotide, and the 3' end of the first oligonucleotide is upstream of the 3' end of the second oligonucleotide, the first
30 oligonucleotide may be called the "upstream" oligonucleotide and the second oligonucleotide may be called the "downstream" oligonucleotide.

The term "primer" refers to an oligonucleotide that is capable of acting as a point of initiation of synthesis when placed under conditions in which primer extension is initiated. An oligonucleotide "primer" may occur naturally, as in a purified restriction digest or may be produced synthetically.

5 A primer is selected to be "substantially" complementary to a strand of specific sequence of the template. A primer must be sufficiently complementary to hybridize with a template strand for primer elongation to occur. A primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide
10 fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being substantially complementary to the strand. Non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize and thereby form a template primer complex for synthesis of the extension product of the primer.

15 The term "label" as used herein refers to any atom or molecule that can be used to provide a detectable (preferably quantifiable) effect, and that can be attached to a nucleic acid or protein. Labels include but are not limited to dyes; radiolabels such as ^{32}P ; binding moieties such as biotin; haptens such as digoxigenin; luminogenic, phosphorescent or fluorogenic moieties; and fluorescent dyes alone or in combination
20 with moieties that can suppress or shift emission spectra by fluorescence resonance energy transfer (FRET). Labels may provide signals detectable by fluorescence, radioactivity, colorimetry, gravimetry, X-ray diffraction or absorption, magnetism, enzymatic activity, and the like. A label may be a charged moiety (positive or negative charge) or alternatively, may be charge neutral. Labels can include or consist of nucleic
25 acid or protein sequence, so long as the sequence comprising the label is detectable.

The term "signal" as used herein refers to any detectable effect, such as would be caused or provided by a label or an assay reaction.

As used herein, the term "detector" refers to a system or component of a system, e.g., an instrument (e.g. a camera, fluorimeter, charge-coupled device, scintillation
30 counter, etc.) or a reactive medium (X-ray or camera film, pH indicator, etc.), that can convey to a user or to another component of a system (e.g., a computer or controller) the

presence of a signal or effect. A detector can be a photometric or spectrophotometric system, which can detect ultraviolet, visible or infrared light, including fluorescence or chemiluminescence; a radiation detection system; a spectroscopic system such as nuclear magnetic resonance spectroscopy, mass spectrometry or surface enhanced Raman
5 spectrometry; a system such as gel or capillary electrophoresis or gel exclusion chromatography; or other detection systems known in the art, or combinations thereof.

The term "sequence variation" as used herein refers to differences in nucleic acid sequence between two nucleic acids. For example, a wild-type structural gene and a mutant form of this wild-type structural gene may vary in sequence by the presence of
10 single base substitutions and/or deletions or insertions of one or more nucleotides. These two forms of the structural gene are said to vary in sequence from one another. A second mutant form of the structural gene may exist. This second mutant form is said to vary in sequence from both the wild-type gene and the first mutant form of the gene.

The term "nucleotide analog" as used herein refers to modified or non-naturally occurring nucleotides such as 7-deaza purines (*i.e.*, 7-deaza-dATP and 7-deaza-dGTP).
15 Nucleotide analogs include base analogs and comprise modified forms of deoxyribonucleotides as well as ribonucleotides.

The term "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different
20 forms, *i.e.*, two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

The term "polymorphic locus" is a locus present in a population that shows
25 variation between members of the population (*e.g.*, the most common allele has a frequency of less than 0.95). In contrast, a "monomorphic locus" is a genetic locus at little or no variations seen between members of the population (generally taken to be a locus at which the most common allele exceeds a frequency of 0.95 in the gene pool of the population).

30 A "non-human animal" of the invention can include mammals such as rodents, non-human primates, sheep, goats, horses, dogs, cows, chickens, amphibians, reptiles,

etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying drugs that can affect processes, *e.g.*, embryogenesis and tissue formation.

The term "operably linked" is intended to mean that the promoter is associated with the nucleic acid in such a manner as to facilitate transcription of the nucleic acid from the promoter.

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide which is produced by recombinant DNA techniques, wherein generally, DNA encoding the polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein.

A "regulatory element", also termed herein "regulatory sequence" is intended to include elements which are capable of modulating transcription from a basic promoter and include elements such as enhancers and silencers. The term "enhancer", also referred to herein as "enhancer element", is intended to include regulatory elements capable of increasing, stimulating, or enhancing transcription from a basic promoter. The term "silencer", also referred to herein as "silencer element" is intended to include regulatory elements capable of decreasing, inhibiting, or repressing transcription from a basic promoter. Regulatory elements are typically present in 5' flanking regions of genes. However, regulatory elements have also been shown to be present in other regions of a gene, in particular in introns. Regulatory elements may also be present downstream of coding regions. Thus, it is possible that DME genes have regulatory elements located in introns, exons, coding regions, and 3' flanking sequences. Such regulatory elements are also intended to be encompassed by the present invention and polymorphisms in such elements can be identified by any of the assays that can be used to identify polymorphisms in regulatory elements in 5' flanking regions of genes.

The term "regulatory element" further encompasses "tissue specific" regulatory elements, *i.e.*, regulatory elements that affect expression of a DME gene preferentially in

specific cells (*e.g.*, cells of a specific tissue). Gene expression occurs preferentially in a specific cell if expression in this cell type is significantly higher than expression in other cell types. The term "regulatory element" also encompasses non-tissue specific regulatory elements, *i.e.*, regulatory elements that are active in most cell types.

5 Furthermore, a regulatory element can be a constitutive regulatory element, *i.e.*, a regulatory element that constitutively regulates transcription, as opposed to a regulatory element that is inducible, *i.e.*, a regulatory element which is active primarily in response to a stimulus. A stimulus can be, *e.g.*, a molecule, such as a hormone, cytokine, heavy metal, phorbol ester, cyclic AMP (cAMP), or retinoic acid.

10 As used herein, the term "transfection" means the introduction of a nucleic acid, *e.g.*, an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. The term "transduction" is generally used herein when the transfection with a nucleic acid is by viral delivery of the nucleic acid. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of
15 exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the recombinant protein is disrupted.

As used herein, the term "transgene" refers to a nucleic acid sequence that has been introduced into a cell. Daughter cells deriving from a cell in which a transgene has
20 been introduced are also said to contain the transgene (unless it has been deleted). A transgene can encode, *e.g.*, a polypeptide, or an antisense transcript, partly or entirely heterologous, *i.e.*, foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome
25 in such a way as to alter the genome of the cell into which it is inserted (*e.g.*, it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). Alternatively, a transgene can also be present in an episome. A transgene can include one or more transcriptional regulatory sequence and any other nucleic acid, (*e.g.* intron), that may be necessary for optimal expression of a selected nucleic acid.

30 A "transgenic animal" refers to any animal, preferably a non-human animal, *e.g.* a mammal, bird or an amphibian, in which one or more of the cells of the animal contain

heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus.

5 The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of a protein, e.g. either agonistic or
10 antagonistic forms. However, transgenic animals in which the recombinant gene is silent are also contemplated. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more genes is caused by human intervention, including both recombination and antisense techniques.

The term "treating" as used herein is intended to encompass curing as well as
15 ameliorating at least one symptom of the condition or disease.

The term "sample" in the present specification and claims is used in its broadest sense. On the one hand it is meant to include a biological (*e.g.*, human) specimen. On the other hand, a sample may include a specimen of synthetic origin.

Biological samples may be animal, including human, fluid, solid (*e.g.*, stool) or
20 tissue, as well as liquid and solid food and feed products and ingredients such as dairy items, vegetables, meat and meat by-products, and waste. Biological samples may be obtained from all of the various families of domestic animals, as well as feral or wild animals, including, but not limited to, such animals as ungulates, bear, fish, lagamorphs, rodents, etc.

25 The term "source of target nucleic acid" refers to any sample that contains or is suspected to contain nucleic acids (RNA or DNA). Particularly preferred sources of target nucleic acids are biological samples including, but not limited to blood, saliva, cerebral spinal fluid, pleural fluid, milk, lymph, sputum and semen.

The term "polymerization means" or "polymerization agent" refers to any agent
30 capable of facilitating the addition of nucleoside triphosphates to an oligonucleotide. Preferred polymerization means comprise DNA and RNA polymerases.

The term "ligation means" or "ligation agent" refers to any agent capable of facilitating the ligation (i.e., the formation of a phosphodiester bond between a 3'-OH and a 5' P located at the termini of two strands of nucleic acid). Preferred ligation means comprise DNA ligases and RNA ligases.

5 The term "reactant" is used herein in its broadest sense. The reactant can comprise, for example, an enzymatic reactant, a chemical reactant or light (e.g., ultraviolet light, particularly short wavelength ultraviolet light is known to break oligonucleotide chains). Any agent capable of reacting with an oligonucleotide to either shorten (i.e., cleave) or elongate the oligonucleotide is encompassed within the term
10 "reactant."

 The term "nucleic acid sequence" as used herein refers to an oligonucleotide, nucleotide or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin that may be single or double stranded, and represent the sense or antisense strand. Similarly, "amino acid sequence" as used herein refers to peptide or
15 protein sequence.

 The term "peptide nucleic acid" ("PNA") as used herein refers to a molecule comprising bases or base analogs such as would be found in natural nucleic acid, but attached to a peptide backbone rather than the sugar-phosphate backbone typical of nucleic acids. The attachment of the bases to the peptide is such as to allow the bases to
20 base pair with complementary bases of nucleic acid in a manner similar to that of an oligonucleotide. These small molecules, also designated anti gene agents, stop transcript elongation by binding to their complementary strand of nucleic acid (Nielsen, *et al.* Anticancer Drug Des. 8:53 63 [1993]).

 As used herein, the terms "purified" or "substantially purified" refer to
25 molecules, either nucleic or amino acid sequences, that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated. An "isolated polynucleotide" or "isolated oligonucleotide" is therefore a substantially purified polynucleotide.

30 As used herein, the term "kit" refers to any delivery system for delivering materials. In the context of reaction assays, such delivery systems include systems that

allow for the storage, transport, or delivery of reaction reagents (e.g., oligonucleotides, enzymes, etc. in the appropriate containers) and/or supporting materials (e.g., buffers, written instructions for performing the assay etc.) from one location to another. For example, kits include one or more enclosures (e.g., boxes) containing the relevant
5 reaction reagents and/or supporting materials. As used herein, the term “fragmented kit” refers to a delivery systems comprising two or more separate containers that each contain a subportion of the total kit components. The containers may be delivered to the intended recipient together or separately. For example, a first container may contain an enzyme for use in an assay, while a second container contains oligonucleotides. The term
10 “fragmented kit” is intended to encompass kits containing Analyte specific reagents (ASR’s) regulated under section 520(e) of the Federal Food, Drug, and Cosmetic Act, but are not limited thereto. Indeed, any delivery system comprising two or more separate containers that each contains a subportion of the total kit components are included in the term “fragmented kit.” In contrast, a “combined kit” refers to a delivery system
15 containing all of the components of a reaction assay in a single container (e.g., in a single box housing each of the desired components). The term “kit” includes both fragmented and combined kits.

As used herein, the term “information” refers to any collection of facts or data. In reference to information stored or processed using a computer system(s), including but
20 not limited to internets, the term refers to any data stored in any format (e.g., analog, digital, optical, etc.). As used herein, the term “information related to a subject” refers to facts or data pertaining to a subject (e.g., a human, plant, or animal). The term “genomic information” refers to information pertaining to a genome including, but not limited to, nucleic acid sequences, genes, allele frequencies, RNA expression levels, protein
25 expression, phenotypes correlating to genotypes, etc. “Allele frequency information” refers to facts or data pertaining allele frequencies, including, but not limited to, allele identities, statistical correlations between the presence of an allele and a characteristic of a subject (e.g., a human subject), the presence or absence of an allele in a individual or population, the percentage likelihood of an allele being present in an individual having
30 one or more particular characteristics, etc.

The term "cleavage structure" as used herein, refers to a structure that is formed by the interaction of at least one probe oligonucleotide and a target nucleic acid, forming a structure comprising a duplex, the resulting structure being cleavable by a cleavage agent, including but not limited to an enzyme. The cleavage structure is a substrate for specific cleavage by the cleavage means in contrast to a nucleic acid molecule that is a substrate for non-specific cleavage by agents such as phosphodiesterases that cleave nucleic acid molecules without regard to secondary structure (*i.e.*, no formation of a duplexed structure is required).

10 DESCRIPTION OF THE DRAWINGS

Figure 1 shows sample embodiments of TAQMAN probes.

Figure 2 represents one embodiment of the TAQMAN PCR method.

Figure 3 shows examples of probes labeled with fluorescent dyes.

15 Figure 4 shows a sample embodiment of an invasive cleavage structure, *e.g.*, for an INVADER assay.

Figure 5 shows one embodiment of a FRET probe, *e.g.*, for an INVADER assay.

Figure 6 shows one embodiment of an INVADER assay.

Figure 7 shows a diagram of an INVADER assay probe in which the allele does not match the probe.

20 Figure 8 shows one embodiment of allele identification using a ligation reaction.

Figure 9 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 2 (ABCB2) gene.

Figure 10 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 4 (ABCB4) gene.

25 Figure 11 shows a drawing of the structure of and SNP position in the microsomal epoxide hydrogenase 1 (EPHX1) gene.

Figure 12 shows a drawing of the structure of and SNP position in the cytoplasmic epoxide hydrogenase 2 (EPHX2) gene.

30 Figure 13 shows a drawing of the structure of and SNP position in the guanidinoacetate-N-methyltransferase (GAMT) gene.

Figure 14 shows a drawing of the structure of and SNP position in the nicotinamide-N-methyltransferase (NNMT) gene.

Figure 15 shows a drawing of the structure of and SNP position in the phenylethanolamine-N-methyltransferase (PNMT) gene.

5 Figure 16 shows a drawing of the structure of and SNP position in the phosphatidylethanolamine-N-methyltransferase (PEMT) gene.

Figure 17 shows a drawing of the structure of and SNP position in the glutathione-S-methyltransferase 3 (GSTM3) gene.

10 Figure 18 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 5 (ALDH5) gene.

Figure 19 shows a drawing of the structure of and SNP position in the transglutaminase (TGM1) gene.

Figure 20 shows a drawing of the structure of and SNP position in the gamma glutamyltransferase (GGT1) gene.

15 Figure 21 shows a drawing of the structure of and SNP position in the NAD(P)H: quinone oxidotransferase (NQO1) gene.

Figure 22 shows a drawing of the structure of and SNP position in the p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue.

20 Figure 23 shows a drawing of the structure of and SNP position in the NRH: quinone oxide transferase 2 (NQO2) gene.

Figure 24 shows a drawing of the structure of and SNP position in the sulfotransferase 1A1 (SULT1A1/STP1) gene.

Figure 25 shows a drawing of the structure of and SNP position in the sulfotransferase 1A2 (SULT1A2/STP2) gene.

25 Figure 26 shows a drawing of the structure of and SNP position in the sulfotransferase-related protein 3 (SULTX3) gene.

Figure 27 shows a drawing of the structure of and SNP position in the tyrosyl protein sulfotransferase (TPST1) gene.

30 Figure 28 shows a drawing of the structure of and SNP position in the tyrosyl protein sulfotransferase (TPST2) gene.

Figure 29 shows a drawing of the structure of and SNP position in the sulfotransferase 1A3 (SULT1A3/ STM/HAST) gene.

Figure 30 shows a drawing of the structure of and SNP position in the cerebroside transferase (CST) gene.

5 Figure 31 shows a drawing of the structure of and SNP position in the sulfotransferase 1C1 (SULT1C1) gene.

Figure 32 shows a drawing of the structure of and SNP position in the sulfotransferase 1C2 (SULT1C2) gene.

10 Figure 33 shows a drawing of the structure of and SNP position in the thyroid hormone sulfotransferase (ST1B2) gene.

Figure 34 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 2 (CHST2) gene.

Figure 35 shows a drawing of the structure of and SNP position in the sulfotransferase 2A1 (SULT2A1) gene.

15 Figure 36 shows a drawing of the structure of and SNP position in the sulfotransferase 2B1 (SULT2B1) gene.

Figure 37 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 4 (CHST4) gene.

20 Figure 38 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 5 (CHST5) gene.

Figure 39 shows a drawing of the structure of and SNP position in the HNK-sulfotransferase (NHK-1ST) gene.

Figure 40 shows a drawing of the structure of and SNP position in the estrogen sulfotransferase (STE) gene.

25 Figure 41 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 1 (ADH1) gene.

Figure 42 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 2 (ADH2) gene.

30 Figure 43 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 3 (ADH3) gene.

Figure 44 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 6 (ADH6) gene.

Figure 45 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 7 (ADH7) gene.

5 Figure 46 shows a drawing of the structure of and SNP position in the short-chained alcohol dehydrogenase family (HEP27) gene.

Figure 47 shows a drawing of the structure of and SNP position in the L1 intracellular adhesion molecule (L1CAM) gene.

10 Figure 48 shows a drawing of the structure of and SNP position in the arylalkylamine-N-acetyltransferase (AANAT) gene.

Figure 49 shows a drawing of the structure of and SNP position in the N-actyltransferase homologue (ARD1) gene of *Saccharomyces cerevisiae*.

Figure 50 shows a drawing of the structure of and SNP position in the N-actyltransferase 1 (NAT1) gene.

15 Figure 51 shows a drawing of the structure of and SNP position in the N-actyltransferase 2 (NAT2) gene.

Figure 52 shows a drawing of the structure of and SNP position in the granzyme A (GZMA) gene.

20 Figure 53 shows a drawing of the structure of and SNP position in the granzyme B (GZMB) gene.

Figure 54 shows a drawing of the structure of and SNP position in the esterase D-formylglutathione hydrolase (ESD) gene.

Figure 55 shows a drawing of the structure of and SNP position in the dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene.

25 Figure 56 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase (MGST1) gene.

Figure 57 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 5 (ADH5) gene.

30 Figure 58 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M1 (GSTM1) gene.

Figure 59 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M2 (GSTM2) gene.

Figure 60 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M4 (GSTM4) gene.

5 Figure 61 shows a drawing of the structure of and SNP position in the glutathione-S-transferase Z1 (GSTZ1) gene.

Figure 62 shows a drawing of the structure of and SNP position in the glutathione-S-transferase P (GSTZPi) gene.

10 Figure 63 shows a drawing of the structure of and SNP position in the glutathione-S-transferase q1 (GSTT1) gene.

Figure 64 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 1L1 (MGST1L1) gene.

Figure 65 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 2 (MGST2) gene.

15 Figure 66 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 3 (MGST3) gene.

Figure 67 shows a drawing of the structure of and SNP position in the glutathione-S-transferase A1 (GSTA1) gene.

20 Figure 68 shows a drawing of the structure of and SNP position in the glutathione-S-transferase A4 (GSTA4) gene.

Figure 69 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 1 (NDUFA1) gene.

Figure 70 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 2 (NDUFA2) gene.

25 Figure 71 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 3 (NDUFA3) gene.

Figure 72 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 5 (NDUFA5) gene.

30 Figure 73 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 6 (NDUFA6) gene.

Figure 74 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 7 (NDUFA7) gene.

Figure 75 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 8 (NDUFA8) gene.

5 Figure 76 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a/b subcomplex 1 (NDUFAB1) gene.

Figure 77 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 9 (NDUFA9) gene.

10 Figure 78 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 1 (NDUFS1) gene.

Figure 79 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 3 (NDUFS3) gene.

Figure 80 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 4 (NDUFS4) gene.

15 Figure 81 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 5 (NDUFS5) gene.

Figure 82 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 6 (NDUFS6) gene.

20 Figure 83 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 8 (NDUFS8) gene.

Figure 84 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 3 (NDUFB3) gene.

Figure 85 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 5 (NDUFB5) gene.

25 Figure 86 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 7 (NDUFB7) gene.

Figure 87 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 1 (ABCA1) gene.

30 Figure 88 shows a drawing of the structure of and SNP position in the catechol-O-methyltransferase (COMT) gene.

Figure 89 shows a drawing of the structure of and SNP position in the vitamin-N-transferase (HNMT) gene.

Figure 90 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (aromatic compound-induced) polypeptide 1 (CYP1A1) gene.

5 Figure 91 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (aromatic compound-induced) polypeptide 2 (CYP1A2) gene.

Figure 92 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (dioxin-induced) polypeptide 1 (CYP1B1) gene.

10 Figure 93 shows a drawing of the structure of and SNP position in the arylacetamide deacetylase (AADAC) gene.

Figure 94 shows a drawing of the structure of and SNP position in the neuropathy target esterase (NTE) gene.

Figure 95 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C (CFTR/MRP) member 2 (MRP2) gene.

15 Figure 96 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 1 (ABCB1) gene.

Figure 97 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 3 (ABCB3) gene.

20 Figure 98 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 7 (ABCB7) gene.

Figure 99 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 8 (ABCB8) gene.

Figure 100 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 9 (ABCB9) gene.

25 Figure 101 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 10 (ABCB10) gene.

Figure 102 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 11 (ABCB11) gene.

30 Figure 103 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene.

Figure 104 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily XXVIIA polypeptide 1 (CYP27A1) gene.

Figure 105 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IVF polypeptide 1 (CYP4F2) gene.

5 Figure 106 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 4F polypeptide 3 (CYP4F3) gene.

Figure 107 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 4F polypeptide 8 (CYP4F8) gene.

10 Figure 108 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 (ALDH1) gene.

Figure 109 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 2 (ALDH2) gene.

Figure 110 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 7 (ALDH7) gene.

15 Figure 111 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 8 (ALDH8) gene.

Figure 112 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 9 (ALDH9) gene.

20 Figure 113 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 10 (ALDH10) gene.

Figure 114 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 7 (ABCC7) gene.

Figure 115 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 8 (ABCC8) gene.

25 Figure 116 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 9 (ABCC9) gene.

Figure 117 shows a drawing of the structure of and SNP position in the carboxylesterase 1 (CES1) gene.

30 Figure 118 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 4 (ABCC4) gene.

Figure 119 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 7 (ABCC7) gene.

Figure 120 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 1 (ABCG1) gene.

5 Figure 121 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 2 (ABCG2) gene.

Figure 122 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 4 (ABCG4) gene.

10 Figure 123 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily E member 1 (ABCE1) gene.

Figure 124 shows a drawing of the structure of and SNP position in the carbohydrate sulfotransferase 1 (CHST1) gene.

Figure 125 shows a drawing of the structure of and SNP position in the carbohydrate sulfotransferase 3 (CHST3) gene.

15 Figure 126 shows a drawing of the structure of and SNP position in the NADH:ubiquinone dehydrogenase flavoprotein 1 (NDUFV1) gene.

Figure 127 shows a drawing of the structure of and SNP position in the NADH:ubiquinone dehydrogenase flavoprotein 2 (NDUFV2) gene.

20 Figure 128 shows a drawing of the structure of and SNP position in the NADH:ubiquinone dehydrogenase flavoprotein 3 (NDUFV3) gene.

Figure 129 shows a drawing of the structure of and SNP position in the NADH:ubiquinone oxidoreductase A10 (NDUFA10) gene.

Figure 130 shows a drawing of the structure of and SNP position in the high-mobility group protein 17-like 1 (HMG17L1) gene.

25 Figure 131 shows a drawing of the structure of and SNP position in the UDP glycosyl transferase 2 family polypeptide A1 (UGT2A1) gene.

Figure 132 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 1 (hOATP1) gene.

30 Figure 133 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 2 (hOATP2) gene.

Figure 134 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 8 (hOATP8) gene.

Figure 135 shows a drawing of the structure of and SNP position in the human organic anion transporter 1 (hOAT1) gene.

5 Figure 136 shows a drawing of the structure of and SNP position in the human organic anion transporter 2 (hOAT2) gene.

Figure 137 shows a drawing of the structure of and SNP position in the human organic anion transporter 3 (hOAT3) gene.

10 Figure 138 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene.

Figure 139 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene.

Figure 140 shows a drawing of the structure of and SNP position in the formyltetrahydroforate dehydrogenase (FTHFD/ALDH1L1) gene.

15 Figure 141 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IIIA (aromatic compound-induced) polypeptide 4 (CYP3A4) gene.

Figure 142 shows graph of the results of typing performed on two different groups of subjects using the INVADER assay method.

20 Figure 143 shows a summary of genetic information.

Figure 144A shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein.

Accession No.: AF275948.1 and AL359846.11

25 Figure 144B shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein. (continuation of Figure 9A)

Accession No.: AF275948.1 and AL359846.11

Figure 145 shows a structure of ATP-binding cassette subfamily A member 4 (ABCA4) gene and the SNP location therein.

30 Accession No.: NT_019258.1

Figure 146 shows a structure of ATP-binding cassette subfamily A member 7 (ABCA7) gene and the SNP location therein.

Accession No.: NT_025194.1

Figure 147 shows a structure of ATP-binding cassette subfamily A member 8 (ABCA8) gene and the SNP location therein.

Accession No.: AC005922.1 and AC015844.5

Figure 148 shows a structure of ATP-binding cassette subfamily B member 1 (ABCB1) gene and the SNP location therein.

Accession No.: AC002457.1 and AC005068.1

Figure 149 shows a structure of ATP-binding cassette subfamily B member 4 (ABCB4) gene and the SNP location therein.

Accession No.: AC079591.1, AC079303.3 and AC005045.2

Figure 150 shows a structure of ATP-binding cassette subfamily B member 7 (ABCB7) gene and the SNP location therein.

Accession No.: AL360179.3 and AC002417.1

Figure 151 shows a structure of ATP-binding cassette subfamily B member 8 (ABCB8) gene and the SNP location therein.

Accession No.: AC010973.4

Figure 152 shows a structure of ATP-binding cassette subfamily B member 9 (ABCB9) gene and the SNP location therein.

Accession No.: AC026362.9 and AC073857.10

Figure 153 shows a structure of ATP-binding cassette subfamily B member 10 (ABCB10) gene and the SNP location therein.

Accession No.: AL121990.9

Figure 154 shows a structure of ATP-binding cassette subfamily B member 11 (ABCB11) gene and the SNP location therein.

Accession No.: AC008177.3 and AC069137.3

Figure 155 shows a structure of ATP-binding cassette subfamily C member 1 (ABCC1) gene and the SNP location therein.

Accession No.: AC026452.5 and AC025778.4

Figure 156 shows a structure of ATP-binding cassette subfamily C member 2 (ABCC2) gene and the SNP location therein.

Accession No.: AL392107.4

Figure 157 shows a structure of ATP-binding cassette subfamily C member 3 (ABCC3) gene and the SNP location therein.

Accession No.: AC004590.1 and AC005921.3

Figure 158A shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein.

Accession No.: AL356257.11, AL157818.12 and AL139381.12

Figure 158B shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein. (continuation of Figure 158A)

Accession No.: AL356257.11, AL157818.12, and AL139381.12

Figure 159 shows a structure of ATP-binding cassette subfamily C member 5 (ABCC5) gene and the SNP location therein.

Accession No.: AC068644.5

Figure 160 shows a structure of ATP-binding cassette subfamily C member 7 (ABCC7) gene and the SNP location therein.

Accession No.: AC000111.1 and AC000061.1

Figure 161 shows a structure of ATP-binding cassette subfamily C member 8 (ABCC8) gene and the SNP location therein.

Accession No.: AC000406.1

Figure 162 shows a structure of ATP-binding cassette subfamily C member 9 (ABCC9) gene and the SNP location therein.

Accession No.: AC084806.9 and AC008250.23

Figure 163 shows a structure of ATP-binding cassette subfamily D member 1 (ABCD1) gene and the SNP location therein.

Accession No.: U52111.2

Figure 164 shows a structure of ATP-binding cassette subfamily D member 3 (ABCD3) gene and the SNP location therein.

Accession No.: NT_019284.3

Figure 165 shows a structure of ATP-binding cassette subfamily D member 4 (ABCD4) gene and the SNP location therein.

Accession No.: AC005519.3

5 Figure 166 shows a structure of ATP-binding cassette subfamily G member 1 (ABCG1) gene and the SNP location therein.

Accession No.: AP001746.1

Figure 167 shows a structure of ATP-binding cassette subfamily G member 2 (ABCG2) gene and the SNP location therein.

Accession No.: NT_022959.2

10 Figure 168 shows a structure of ATP-binding cassette subfamily G member 4 (ABCG4) gene and the SNP location therein.

Accession No.: AP001315.3

Figure 169 shows a structure of ATP-binding cassette subfamily G member 5 (ABCG5) gene and the SNP location therein.

15 Accession No.: AC084265.2 and AC011242.8

Figure 170 shows a structure of ATP-binding cassette subfamily G member 8 (ABCG8) gene and the SNP location therein.

Accession No.: AC084265.2

20 Figure 171 shows a structure of ATP-binding cassette subfamily E member 1 (ABCE1) gene and the SNP location therein.

Accession No.: NT_006296.2

Figure 172 shows a structure of ATP-binding cassette subfamily F member 1 (ABCF1) gene and the SNP location therein.

Accession No.: NT_007592.3

25 Figure 173 shows a structure of organic anion transporter 1 (OAT1) gene and the SNP location therein.

Accession No.: AP001858.3, AJ249369.1, and AP000438.4

Figure 174 shows a structure of organic anion transporter 2 (OAT2) gene and the SNP location therein.

30 Accession No.: AC26532.3

Figure 175 shows a structure of organic anion transporter 3 (OAT3) gene and the SNP location therein.

Accession No.: AP001858.3

5 Figure 176 shows a structure of organic anion transporter polypeptide 1 (OATP1) gene and the SNP location therein.

Accession No.: AC022224.22

Figure 177 shows a structure of organic anion transporter polypeptide 2 (OATP2) gene and the SNP location therein.

Accession No.: NT_024399.2

10 Figure 178 shows a structure of organic anion transporter polypeptide 8 (OATP8) gene and the SNP location therein.

Accession No.: NT_024399.2

Figure 179 shows a structure of transporter 1 ATP-binding cassette subfamily B (TAP1) gene and the SNP location therein.

15 Accession No.: X66401.1

Figure 180 shows a structure of transporter 2 ATP-binding cassette subfamily B (TAP2) gene and the SNP location therein.

Accession No.: X66401.1

20 Figure 181 shows a structure of SLC22A4 solute carrier family 22 (organic cation transporter) member 4 (OCTN1) gene and the SNP location therein.

Accession No.: AC008599.6

Figure 182 shows a structure of SLC22A5 solute carrier family 22 (organic cation transporter) member 5 (OCTN2) gene and the SNP location therein.

Accession No.: AC023861.3

25 Figure 183 shows a structure of SLC22A1 solute carrier family 22 (organic cation transporter) member 1 (OCT1) gene and the SNP location therein.

Accession No.: AL35625.5

Figure 184 shows a structure of SLC22A2 solute carrier family 22 (organic cation transporter) member 2 (OCT2) gene and the SNP location therein.

30 Accession No.: AL162582.18

Figure 185 shows a structure of SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family) member 2 (NTCP) gene and the SNP location therein.

Accession No.: AL157789.6

5 Figure 186 shows a structure of SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1 (PEPT1) gene and the SNP location therein.

Accession No.: AL353574.8 and AL391670.6

Figure 187 shows a structure of microsomal epoxide hydrolase 1 (EPHX1) gene and the SNP location therein.

Accession No.: AC058782.8

10 Figure 188 shows a structure of cytoplasmic epoxide hydrolase (EPHX2) gene and the SNP location therein.

Accession No.: AC010856.3

Figure 189 shows a structure of catechol-O-methyl transferase (COMT) gene and the SNP location therein.

15 Accession No.: AC000080.2

Figure 190 shows a structure of guanidinoacetate N-methyl transferase (GAMT) gene and the SNP location therein.

Accession No.: NT_000879.1

20 Figure 191 shows a structure of phenyl ethanolamine N-methyl transferase (PNMT) gene and the SNP location therein.

Accession No.: AC040933.3

Figure 192 shows a structure of histamine N-methyl transferase (HNMT) gene and the SNP location therein.

Accession No.: AC019304.3

25 Figure 193 shows a structure of nicotinamide N-methyl transferase (NNMT) gene and the SNP location therein.

Accession No.: AC019290.3

Figure 194 shows a structure of phosphatidylethanolamine N-methyl transferase (PEMT) gene and the SNP location therein.

30 Accession No.: AC020558.3

Figure 195 shows a structure of aldehyde dehydrogenase 1 family member A1 (ALDH1A1) gene and the SNP location therein.

Accession No.: AC009284.2 and AL162416.3

5 Figure 196 shows a structure of aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene and the SNP location therein.

Accession No.: AC025431.7 and AC012653.8

Figure 197 shows a structure of aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene and the SNP location therein.

Accession No.: AC015712.7

10 Figure 198 shows a structure of aldehyde dehydrogenase 1 family member B1 (ALDH1B1) gene and the SNP location therein.

Accession No.: AL135785.9

Figure 199A shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein.

15 Accession No.: AC079848.6

Figure 199B shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein. (continuation of Figure 199A)

Accession No.: AC079848.6

20 Figure 200 shows a structure of aldehyde dehydrogenase 2 (ALDH2) gene and the SNP location therein.

Accession No.: AC002996.1 and AC003029.2

Figure 201 shows a structure of aldehyde dehydrogenase 3 family member A1 (ALDH3A1) gene and the SNP location therein.

Accession No.: AC005722.1

25 Figure 202 shows a structure of aldehyde dehydrogenase 3 family member A2 (ALDH3A2) gene and the SNP location therein.

Accession No.: AC005722.1

Figure 203 shows a structure of aldehyde dehydrogenase 3 family member B1 (ALDH3B1) gene and the SNP location therein.

30 Accession No.: AC004923.2

Figure 204 shows a structure of aldehyde dehydrogenase 3 family member B2 (ALDH3B2) gene and the SNP location therein.

Accession No.: AC021987.3

5 Figure 205 shows a structure of aldehyde dehydrogenase 5 family member A1 (ALDH5A1) gene and the SNP location therein.

Accession No.: AL031230.1

Figure 206 shows a structure of aldehyde dehydrogenase 6 family member A1 (ALDH6A1) gene and the SNP location therein.

Accession No.: AC005484.2

10 Figure 207 shows a structure of aldehyde dehydrogenase 8 family member A1 (ALDH8A1) gene and the SNP location therein.

Accession No.: AL445190.9 and AL021939.1

Figure 208 shows a structure of aldehyde dehydrogenase 9 family member A1 (ALDH9A1) gene and the SNP location therein.

15 Accession No.: AL451074.4

Figure 209 shows a structure of alcohol dehydrogenase 1 (ADH1) gene and the SNP location therein.

Accession No.: AP002027.1

20 Figure 210 shows a structure of alcohol dehydrogenase 2 (ADH2) gene and the SNP location therein.

Accession No.: AP002027.1

Figure 211 shows a structure of alcohol dehydrogenase 3 (ADH3) gene and the SNP location therein.

Accession No.: AP002027.1

25 Figure 212 shows a structure of alcohol dehydrogenase 4 (ADH4) gene and the SNP location therein.

Accession No.: AP002026.1

Figure 213 shows a structure of alcohol dehydrogenase 5 (ADH5) gene and the SNP location therein.

30 Accession No.: AC019131.4

Figure 214 shows a structure of alcohol dehydrogenase 6 (ADH6) gene and the SNP location therein.

Accession No.: AP002026.1

Figure 215 shows a structure of alcohol dehydrogenase 7 (ADH7) gene and the SNP
5 location therein.

Accession No.: AC027065.3

Figure 216 shows a structure of short-chain alcohol dehydrogenase family gene (HEP27) and the SNP location therein.

Accession No.: AL135999.3

10 Figure 217 shows a structure of UDP glycosyltransferase 1 family polypeptide A1 (UGT1A1) and the SNP location therein.

Accession No.: AC006985.2

Figure 218 shows a structure of UDP glycosyltransferase 2 family polypeptide A1 (UGT2A1) and the SNP location therein.

15 Accession No.: AC011254.3

Figure 219 shows a structure of UDP glycosyltransferase 2 family polypeptide B15 (UGT2B15) and the SNP location therein.

Accession No.: AC019173.4

20 Figure 220 shows a structure of UDP glycosyltransferase 8 (UGT8) and the SNP location therein.

Accession No.: U31353.1

Figure 221 shows a structure of glutathione S transferase A1 (GSTA1) gene and the SNP location therein.

Accession No.: AC021133.4

25 Figure 222 shows a structure of glutathione S transferase A4 (GSTA4) gene and the SNP location therein.

Accession No.: AC025085.4

Figure 223 shows a structure of glutathione S transferase M1 (GSTM1) gene and the SNP location therein.

30 Accession No.: AC000032.7

Figure 224 shows a structure of glutathione S transferase M2 (GSTM2) gene and the SNP location therein.

Accession No.: AC000031.5

Figure 225 shows a structure of glutathione S transferase Z1 (GSTZ1) gene and the
5 SNP location therein.

Accession No.: AC007954.7

Figure 226 shows a structure of glutathione S transferase Pi (GSTPi) gene and the SNP location therein.

Accession No.: X08058.1 and M24485.1

10 Figure 227 shows a structure of glutathione S transferase T1 (GSTT1) gene and the SNP location therein.

Accession No.: AF240786.1 and AP000351.3

Figure 228 shows a structure of microsomal glutathione S transferase 1 (MGST1) gene and the SNP location therein.

15 Accession No.: AC007528.5

Figure 229 shows a structure of microsomal glutathione S transferase 1-like 1 (MGST1L1) gene and the SNP location therein.

Accession No.: AC007936.2

Figure 230 shows a structure of microsomal glutathione S transferase T2 (MGST2)
20 gene and the SNP location therein.

Accession No.: AC019049.4

Figure 231 shows a structure of microsomal glutathione S transferase T3 (MGST3) gene and the SNP location therein.

Accession No.: AC064827.2

25 Figure 232 shows a structure of sulfotransferase 1A1 (SULT1A1/STP1) gene and the SNP location therein.

Accession No.: U52852.2

Figure 233 shows a structure of sulfotransferase 1A2 (SULT1A2/STP2) gene and the SNP location therein.

30 Accession No.: U33886.1, U34804.1 and AC020765.5

Figure 234 shows a structure of sulfotransferase 1A3 (SULT1A3/STM/HAST) gene and the SNP location therein

Accession No.: L34160.1 and AC012645.4

Figure 235 shows a structure of sulfotransferase 1C1 (SULT1C1) gene and the SNP
5 location therein.

Accession No.: AC019100.4

Figure 236 shows a structure of sulfotransferase 1C2 (SULT1C2) gene and the SNP
location therein.

Accession No.: AF186263.1

10 Figure 237 shows a structure of sulfotransferase 2A1 (SULT2A1) gene and the SNP
location therein.

Accession No.: AC024582.4, AC008745.5, NT_011190.1, and AC024582.4

Figure 238 shows a structure of sulfotransferase 2B1 (SULT2B1) gene and the SNP
location therein.

15 Accession No.: AC040922.2 and AC008403.6

Figure 239 shows a structure of sulfotransferase-associated protein 3 (SULTX3)
gene and the SNP location therein.

Accession No.: Z97055.1

Figure 240 shows a structure of tyrosyl protein sulfotransferase 1 (TPST1) gene and
20 the SNP location therein.

Accession No.: AC026281.5

Figure 241 shows a structure of tyrosyl protein sulfotransferase 2 (TPST2) gene and
the SNP location therein.

Accession No.: Z95115.1

25 Figure 242 shows a structure of cerebroside sulfotransferase (CST) gene and the
SNP location therein.

Accession No.: AC005006.2

Figure 243 shows a structure of thyroid hormone sulfotransferase (ST1B2) gene and
the SNP location therein.

30 Accession No.: AC027059.2

Figure 244 shows a structure of carbohydrate sulfotransferase 1 (CHST1) gene and the SNP location therein.

Accession No.: NT_008982.1

Figure 245 shows a structure of carbohydrate sulfotransferase 2 (CHST2) gene and
5 the SNP location therein.

Accession No.: AC055737.10

Figure 246 shows a structure of carbohydrate sulfotransferase 3 (CHST3) gene and the SNP location therein.

Accession No.: AC073370.3

10 Figure 247 shows a structure of carbohydrate sulfotransferase 4 (CHST4) gene and the SNP location therein.

Accession No.: AC010547.5

Figure 248 shows a structure of carbohydrate sulfotransferase 5 (CHST5) gene and the SNP location therein.

15 Accession No.: AC025287.3

Figure 249 shows a structure of HNK-sulfotransferase (HNK-1ST) gene and the SNP location therein.

Accession No.: AC012493.4

Figure 250 shows a structure of estrogen sulfotransferase (STE) gene and the SNP
20 location therein.

Accession No.: AC074273.1

Figure 251 shows a structure of NAD (P)H: quinone oxidoreductase 1 (NQO1) gene and the SNP location therein.

Accession No.: M81596.1

25 Figure 252 shows a structure of NRH: quinone oxidoreductase 2 (NQO2) gene and the SNP location therein.

Accession No.: AB050248.1

Figure 253 shows a structure of p53-inducible gene 3 (PIG3) in a quinone oxidoreductase homolog and the SNP location therein.

30 Accession No.: AC008073.3

Figure 254 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 1 (NDUFA1) gene and the SNP location therein.

Accession No.: AC002477.1

5 Figure 255 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 2 (NDUFA2) gene and the SNP location therein.

Accession No.: AB054976.1

Figure 256 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 3 (NDUFA3) gene and the SNP location therein.

Accession No.: AC009968.6

10 Figure 257 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 5 (NDUFA5) gene and the SNP location therein.

Accession No.: AC073323.5

Figure 258 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 6 (NDUFA6) gene and the SNP location therein.

15 Accession No.: AL021878.1

Figure 259 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 7 (NDUFA7) gene and the SNP location therein.

Accession No.: AC010323.6

Figure 260 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 20 8 (NDUFA8) gene and the SNP location therein.

Accession No.: AL162423.10

Figure 261 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 9 (NDUFA9) gene and the SNP location therein.

Accession No.: AC005832.1

25 Figure 262 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 10 (NDUFA10) gene and the SNP location therein.

Accession No.: AC013469.8

Figure 263 shows a structure of NADH-dehydrogenase(ubiquinone)1 α/β -subcomplex 1 (NDUFAB1) gene and the SNP location therein.

30 Accession No.: AC008870.6

Figure 264 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 3 (NDUFB3) gene and the SNP location therein.

Accession No.: AC007272.3

Figure 265 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 5 (NDUFB5) gene and the SNP location therein.

Accession No.: AC068361.2

Figure 266 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 7 (NDUFB7) gene and the SNP location therein.

Accession No.: AC010527.4

Figure 267 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 1 (NDUFS1) gene and the SNP location therein.

Accession No.: AC007383.4

Figure 268 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 3 (NDUFS3) gene and the SNP location therein.

Accession No.: AC067943.4

Figure 269 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 4 (NDUFS4) gene and the SNP location therein.

Accession No.: AC024569.3

Figure 270 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 5 (NDUFS5) gene and the SNP location therein.

Accession No.: AL139015.5

Figure 271 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 6 (NDUFS6) gene and the SNP location therein.

Accession No.: AC026443.2

Figure 272 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 8 (NDUFS8) gene and the SNP location therein.

Accession No.: AC034259.2

Figure 273 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 1 (NDUFV1) gene and the SNP location therein.

Accession No.: NT_009304.2

Figure 274 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 2 (NDUFV2) gene and the SNP location therein.

Accession No.: NT_011024.2

5 Figure 275 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 3 (NDUFV3) gene and the SNP location therein.

Accession No.: AP001748.1

Figure 276 shows a structure of gamma-glutamyl transferase 1 (GGT1) gene and the SNP location therein.

Accession No.: D87002.1

10 Figure 277 shows a structure of transglutaminase 1 (TGM1) gene and the SNP location therein.

Accession No.: M98447.1

Figure 278 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 1 (CYP1A1) gene and the SNP location therein.

15 Accession No.: X04300.1 and AC020705.4

Figure 279 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 2 (CYP1A2) gene and the SNP location therein.

Accession No.: AC020705.4

20 Figure 280 shows a structure of cytochrome P450 subfamily 1 (dioxin-inducible) polypeptide 1 (CYP1B1) gene and the SNP location therein.

Accession No.: AC009229.4

Figure 281 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 4 (CYP3A4) gene and the SNP location therein.

Accession No.: AF280107.1

25 Figure 282 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 5 (CYP3A5) gene and the SNP location therein.

Accession No.: AC005020.5

Figure 283 shows a structure of cytochrome P450 subfamily 3A polypeptide 7 (CYP3A7) gene and the SNP location therein.

30 Accession No.: AF280107.1

Figure 284 shows a structure of cytochrome P450 polypeptide 43 (CYP3A43) gene and the SNP location therein.

Accession No.: AC011904.3

5 Figure 285 shows a structure of cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene and the SNP location therein.

Accession No.: AL356793.10

Figure 286 shows a structure of cytochrome P450 subfamily IVF polypeptide 2 (CYP4F2) gene and the SNP location therein.

Accession No.: AC005336.1

10 Figure 287 shows a structure of cytochrome P450 subfamily IVF polypeptide 3 (CYP4F3) gene and the SNP location therein.

Accession No.: AD000685.1

Figure 288 shows a structure of cytochrome P450 subfamily IVF polypeptide 8 (CYP4F8) gene and the SNP location therein.

15 Accession No.: AC068845.3

Figure 289 shows a structure of cytochrome P450 subfamily XXVIIA polypeptide 1 (CYP27A1) gene and the SNP location therein.

Accession No.: AC009974.7

20 Figure 290 shows a structure of cytochrome P450 subfamily XXVIIIB polypeptide 1 (CYP27B1) gene and the SNP location therein.

Accession No.: AC025165.27

Figure 291 shows a structure of allylacetamide deacetylase (AADAC) gene and the SNP location therein.

Accession No.: AC068647.4

25 Figure 292 shows a structure of carboxyl esterase 1 (CES1) gene and the SNP location therein

Accession No.: AC007602.4

Figure 293 shows a structure of carboxyl esterase 2 (CES2) gene and the SNP location therein

30 Accession No.: AC027131.4

Figure 294 shows a structure of granzyme A (GZMA) gene and the SNP location therein.

Accession No.: AC091977.1

Figure 295 shows a structure of granzyme B (GZMB) gene and the SNP location therein.

Accession No.: AL136018.3

Figure 296 shows a structure of esterase D/formylglutathione hydrolase (ESD) gene and the SNP location therein.

Accession No.: AL136958.9

Figure 297A shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein.

Accession No.: AL138750.8, AL162417.20 and AF072711.1

Figure 297B shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein. (continuation of Figure 297A)

Accession No.: AL138750. , AL162417.20 and AF072711.1

Figure 298 shows a structure of interleukin 17 (cytotoxic T lymphocyte-associated serine esterase 8) (IL17) gene and the SNP location therein.

Accession No.: AL355513.11

Figure 299 shows a structure of ubiquitin carboxyl terminal esterase L3 (ubiquitin thiol esterase) (UCHL3) gene and the SNP location therein.

Accession No.: AL137244.28

Figure 300 shows a structure of dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene and the SNP location therein.

Accession No.: D89060

Figure 301 shows a structure of neuropathy target esterase (NTE) gene and the SNP location therein.

Accession No.: AC021153

Figure 302 shows a structure of L1 cell adhesion molecule (L1CAM) gene and the SNP location therein.

Accession No.: U52112

Figure 303 shows a structure of arylalkylamine N-acetyltransferase (AANAT) gene and the SNP location therein.

Accession No.: U40391

Figure 304 shows a structure of N-acetyltransferase homolog (ARD1) gene of
5 *Saccharomyces cerevisiae* and the SNP location therein.

Accession No.: U52112

Figure 305 shows a structure of N-acetyltransferase (NAT1) gene and the SNP location therein.

Accession No.: X17059

10 Figure 306 shows a structure of N-acetyltransferase 2 (NAT2) gene and the SNP location therein.

Accession No.: D10870

Figure 307 shows a structure of ATP-binding cassette subfamily B member 2 (ABCB2) gene and the SNP location therein.

15 Accession No.: X66401

Figure 308 shows a structure of ATP-binding cassette subfamily B member 3 (ABCB3) gene and the SNP location therein.

Accession No.: X66401

20 Figure 309 shows a structure of glutathione S transferase M3 (GSTM3) gene and the SNP location therein.

Accession No.: AF043105.1

Figure 310 shows a structure of glutathione S transferase M4 (GSTM4) gene and the SNP location therein.

Accession No.: M96233.1

25 Figure 311 shows a structure of aldehyde dehydrogenase 7 (ALDH7) gene and the SNP location therein.

Accession No.: AC004923

Figure 312 shows a structure of high-mobility group protein 17-like 1 (HMG17L1) gene and the SNP location therein.

30 Accession No.: Z97055.1

GENERAL DESCRIPTION OF THE INVENTION

The present invention provides a method of analysis of drug metabolizing enzymes by analysis of SNPs associated with their encoding genes. In some embodiments, the method of the present invention can be used in the selection of drugs based on, *e.g.*, particular characteristics of an individual patient or on characteristics of a target disease.

In some embodiments, the present invention provides a method for detecting a genetic polymorphism associated with a DME, wherein an oligonucleotide probe and/or oligonucleotide primer is created so as to include the genetic polymorphism site from genetic polymorphism data in a gene for encoding a drug metabolizing enzyme or so as to include the genetic polymorphism site in an amplified fragment when the gene encoding the drug metabolizing enzyme has been amplified, and wherein at least one genetic polymorphism in a gene for encoding the target drug metabolizing enzyme is detected using the oligonucleotide probe and/or oligonucleotide primer thus obtained.

The present invention further provides methods for evaluating a drug, wherein the effectiveness and safety of a drug metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by the detection method.

In some embodiments, the present invention provides a method for screening a drug, wherein the drug to be used is selected based on the results obtained in the evaluation method. In other embodiments, the present invention provides a method for screening a drug, wherein the genetic polymorphism data associated with the gene encoding a DME in a control subject is compared to the genetic polymorphism data associated with the same gene in a test subject, and wherein a drug to be used is selected from the results of an analysis of the effectiveness and/or safety of the drugs metabolized by the drug metabolizing enzyme.

The invention further features predictive medicines, which are based, at least in part, on determination of the identity of DME polymorphic regions that are associated with particular drug responses. For example, information obtained using the diagnostic assays described herein (alone or in conjunction with information on another genetic defect, which contributes to the same disease) is useful for determining if a test subject has an allele of a polymorphic region that is associated with a particular drug response.

Knowledge of the DME profile in an individual (the DME genetic profile), alone or in conjunction with information on other genetic defects contributing to the same disease (the genetic profile of the particular disease) allows customization of therapy for a particular disease to the individual's genetic profile, the goal of "pharmacogenomics."

5 For example, an individual's DME genetic profile can enable a doctor: 1) to more effectively prescribe a drug that will address the molecular basis of the disease or condition; and 2) to better determine the appropriate dosage of a particular drug.

The ability to target populations expected to show the highest clinical benefit, based on the DME genetic profile, allows: 1) the repositioning of marketed drugs with
10 disappointing market results; 2) the rescue of drug candidates whose clinical development has been discontinued as a result of safety or efficacy limitations, which are patient subgroup-specific; and 3) an accelerated and less costly development for drug candidates and more optimal drug labeling (e.g. since the use of DMEs as markers is useful for optimizing effective dose).

15

DETAILED DESCRIPTION OF THE INVENTION

Examples of genetic polymorphism data related to a DME, and useful in the detection, evaluation method and screening methods of the present invention are shown in Table 1. In some embodiments, a drug-metabolizing enzyme is at least one of the
20 following: epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone oxidoreductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and ATP-binding cassette.

The present invention relates to a method for detecting a genetic polymorphism in
25 a test subject using the genetic polymorphism data related to a drug metabolizing enzyme. The present invention analyzes the effectiveness, safety and strength of drugs metabolized by a drug metabolizing enzyme. The relationship between a disease and the drug to be evaluated is based on the results of the analysis. The genetic polymorphism data for the drug metabolizing enzyme is different for each patient with a given disease.
30 Therefore, the effectiveness and safety of a specific drug depends on drug metabolism in the presence of certain genetic polymorphism data and the side effects in the presence of

certain genetic polymorphism data. As a result, a physician can determine whether a certain drug should be used by a certain patient and can tailor drugs for use by a certain patient based on the genetic polymorphism data (so-called "made-to-order" treatments).

"Drug metabolizing enzymes" refer to a group of enzymes that catalyze *in vivo* structural changes in exogenous materials including drugs. When used for clinical purposes, the group of metabolizing enzymes includes some endogenous materials. Because drug-metabolizing enzymes absorb, metabolize and secrete drugs, the polymorphism of an enzyme depends on the amount of enzyme expressed (transcription and translation) and the amount of activity. As a result, there are blood serum concentrations of both unchanged materials and metabolites.

Drug metabolizing enzymes expressed by the genes that are targeted for genetic polymorphism analysis in the present invention include, but are not limited to the following classes of enzymes:

Epoxide hydrolases

Methyltransferases

N-acetyltransferases

Sulfotransferases

Quinone oxidoreductases

Glutathione S-transferases

UDP-glycosyltransferases

Aldehyde dehydrogenases

Alcohol dehydrogenases

Esterases

Ubiquinone dehydrogenases : NDUF

Cytochrome P450s (CYPs)

ATP-binding cassettes

ATP-binding cassettes / Transporters

Examples and descriptions of these enzymes are provided below.

(1) Epoxide hydrolases are enzymes that hydrolyze epoxide using a trans-cleavage mechanism to produce 1,2-glycol. Examples include microsomal epoxide hydrolase 1 and cytoplasmic epoxide hydrolase 2.

5 (2) Methyltransferases are enzymes that catalyze transmethylation in amino groups, hydroxyl groups and thiol groups. Examples include the following.

Catechol-O-methyltransferase

Vitamin-N-methyltransferase

Phenylethanolamine-N-methyltransferase

10 Phosphatidylethanolamine-N-methyltransferase

Nicotinamide-N-methyltransferase

Acetylserotonin-O-methyltransferase

Thiopurine S-methyltransferase

15 (3) N-acetyltransferases are enzymes that catalyze transacetylation in amino groups, sulfonamide groups and hydrazine groups. Examples include the following.

Arylamine-N-acetyltransferase 1, 2

Arylalkylamine-N-acetyltransferase

N-acetyltransferase homologues of *saccharomyces cerevisiae*

20 LI intracellular adhesion molecules

(4) Sulfotransferases are enzymes that contribute to sulfate conjugation and catalyzes trans-sulfonylation in phenols, steroids, arylamines and biliary acid. Examples include the following.

25 Sulfotransferase 1A1, 1A2, 1A3, 1C1, 1C2, 2A1, 2B1

Thyroid hormone sulfotransferase

Tyrosyl protein sulfotransferase 1, 2

Sulfotransferase-opening protein 3

Estrogen sulfotransferase

30 Cerebroside sulfotransferase

HNK-sulfotransferase 1

Carbohydrate sulfotransferase 2, 4, 5

Carbohydrate sulfotransferase 1, 3

5 (5) Quinone oxidoreductases are enzymes that catalyze the reduction of quinones such as o-quinone and p-quinone. Examples include the following.

NAD(P)H: Quinone oxidoreductase 1

NRH: Quinone oxidoreductase 2

Quinone oxidoreductase homologues

p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue

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(6) Glutathione S-transferases are enzymes that catalyze the conjugation of glutathione. Examples include the following.

Glutathione S-transferase Mu1, Mu2, Mu3, Mu4, Mu5

Glutathione S-transferase Z (zeta)

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Glutathione S-transferase P (pi)

Glutathione S-transferase 1 T1 (zeta)

Glutathione S-transferase 1 Theta 1, Theta 2

Microsomal Glutathione S-transferase 1

Microsomal Glutathione S-transferase 1-1

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Microsomal Glutathione S-transferase 2, 3

Microsomal Glutathione S-transferase Ha Subunit 1, 2

Microsomal Glutathione S-transferase A3, A4

Glutathione S-transferase A1, A4

Glutathione S-transferase M1, M2, M3, M4

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(7) UDP-glycosyltransferases are enzymes that catalyze the contribution of glucuronic acid to functional groups such as hydroxyl groups, carboxyl groups, amino groups and thiol groups after their introduction in the 1st drug metabolism route. Examples include the following.

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UDP-glycosyltransferase 1

UDP-glycosyltransferase 1 Family Polypeptide A1

UDP-glycosyltransferase 2 Family Polypeptide A1, B7, B10, B4, B11, B15, B17

UDP-glycosyltransferase 8

Dolichyl-diP-oligosaccharide protein glycosyl transferase

- 5 (8) Aldehyde dehydrogenases are enzyme that converts aldehydes into carboxylic acids. Examples include Aldehyde dehydrogenase 1 through 10.

Aldehyde dehydrogenase 1 family member A1, A2, A3

Aldehyde dehydrogenase 1 family member B1

Formyltetrahydroforate dehydrogenase

- 10 Aldehyde dehydrogenase 2

Aldehyde dehydrogenase 3 family member A1, A2

Aldehyde dehydrogenase 3 family member B1, B2

Aldehyde dehydrogenase 5 family member A1

Aldehyde dehydrogenase 6 family member A1

- 15 Aldehyde dehydrogenase 8 family member A1

Aldehyde dehydrogenase 9 family member A1

- (9) Alcohol dehydrogenases are enzymes that convert alcohols into aldehydes or ketones. Examples include the following.

- 20 Alcohol dehydrogenase 1 through 7

Hydroxy-CoA-dehydrogenase

Short-chain alcohol dehydrogenase family genes

- (10) Esterases are enzymes that hydrolyze some esters. Examples include the following.

Arylacetoamide deacetylase

Granzyme A

Granzyme B

Interleukin 17

- 30 Ubiquitin carboxyl-terminal esterase L1, 3

Carboxyl esterase 1

Lipase A

Esterase D-formylglutathione hydrolase

Carboxylester lipase

Dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

5 Neuropathy target esterase

(11) Ubiquinone dehydrogenases (NDUF) are enzymes that support energy metabolism, *e.g.*, as in the mitochondrial respiratory chain. Examples include NADH ubiquinone dehydrogenase 1a Subunit 1 through 10.

10 NADH-dehydrogenase (ubiquinone)1 α -subcomplex 1 through 3 and 5 through 10

NADH-dehydrogenase (ubiquinone)1 α / β -subcomplex 1

NADH-dehydrogenase (ubiquinone)1 β -subcomplex 3, 5, 7

NADH-dehydrogenase (ubiquinone) Fe-S protein 1, 3, 4, 5, 6, 8

NADH-dehydrogenase (ubiquinone) flavoprotein 1 through 3

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(12) Cytochrome P450s (CYPs) are enzymes that regulate 1st drug metabolism and introduce oxygen atoms to the drug. Examples include Cytochrome P450 (CYP) 1A1, CYP 1A2, CYP1B1, CYP 2A6, CYP 2B6, CYP 2C8, CYP 2C18, CYP 2C9, CYP 2C19, CYP 2E1, CYP 2D6, CYP 2E1, CYP 2F1, CYP 3A3, CYP 3A4, CYP 3A5, CYP 20 3A7, CYP 3A43, CYP 4A11, CYP 4B1, CYP 4F2, CYP 4F3, CYP 4F8, CYP 11B1, CYP 11B2, CYP 17, CYP 19, CYP 21A2, CYP 21A1, CYP 27B1 and CYP 27.

(13) ATP-binding cassettes absorb the drug and adjust the interstitial concentration with a transporter. Examples include the following.

25 ATP-Binding Cassette Subfamily A Members 1 through 6, 8

ATP-Binding Cassette Subfamily A Members 1, 4, 7, 8

ATP-Binding Cassette Subfamily B Members 1 through 11

ATP-Binding Cassette Subfamily B Members 1, 4, 7, 8, 9, 10, 11

ATP-Binding Cassette Subfamily C Members 1 through 6, 8 through 10

30 ATP-Binding Cassette Subfamily C Members 1, 2, 3, 4, 5, 7, 8, 9

ATP-Binding Cassette Subfamily D Members 1 through 4

ATP-Binding Cassette Subfamily D Members 1, 3, 4

ATP-Binding Cassette Subfamily E Members 1

ATP-Binding Cassette Subfamily F Members 1 through 3

ATP-Binding Cassette Subfamily F Member 1

5 ATP-Binding Cassette Subfamily G Members 1

ATP-Binding Cassette Subfamily G Members 1, 2, 4, 8

Organic anion transporters 1, 2, 3

Organic anion transporter polypeptides 1, 2, 8

Transporter 1 ATP-binding cassette subfamily B

10 Transporter 2 ATP-binding cassette subfamily B

SLC22A4 solute carrier family 22 (organic cation transporter) member 4

SLC22A5 solute carrier family 22 (organic cation transporter) member 5

SLC22A1 solute carrier family 22 (organic cation transporter) member 1

SLC22A2 solute carrier family 22 (organic cation transporter) member 2

15 SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family)
member 2

SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1

(14) Other enzymes include gamma glutamyl transferase 1, transglutaminase 1
20 and dihydropyrimidine dihydrogenase.

Genetic polymorphism data relating to DMEs can be obtained using any general
genetic polymorphism detection method. Examples include, but are not limited to, PCR
or other amplification methods, hybridization methods using an allele-specific
25 oligonucleotide matrix (e.g., TAQMAN PCR method, INVADER assay method), primer
extension reaction methods, sequencing methods, MALDI-TOF/MS methods and the
DNA chip methods (e.g., microarrays). Examples of detection methods that are
applicable to analysis of the DME associated polymorphisms of the present invention
include but are not limited to those listed below.

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1. Direct sequencing Assays

In some embodiments of the present invention, variant sequences are detected using a direct sequencing technique. In these assays, DNA samples are first isolated from a subject using any suitable method. In some embodiments, the region of interest is
5 cloned into a suitable vector and amplified by growth in a host cell (*e.g.*, a bacteria). In other embodiments, DNA in the region of interest is amplified using PCR.

Following amplification, DNA in the region of interest (*e.g.*, the region containing the SNP or mutation of interest) is sequenced using any suitable method, including but not limited to manual sequencing using radioactive marker nucleotides, or automated
10 sequencing. The results of the sequencing are displayed using any suitable method. The sequence is examined and the presence or absence of a given SNP or mutation is determined.

2. PCR Assay

15 In some embodiments of the present invention, variant sequences are detected using a PCR-based assay. In some embodiments, the PCR assay comprises the use of oligonucleotide primers that hybridize only to the variant or wild type allele (*e.g.*, to the region of polymorphism or mutation). Both sets of primers are used to amplify a sample of DNA. If only the mutant primers result in a PCR product, then the patient has the
20 mutant allele. If only the wild-type primers result in a PCR product, then the patient has the wild type allele.

3. Fragment Length Polymorphism Assays

In some embodiments of the present invention, variant sequences are detected
25 using a fragment length polymorphism assay. In a fragment length polymorphism assay, a unique DNA banding pattern based on cleaving the DNA at a series of positions is generated using an enzyme (*e.g.*, a restriction enzyme or a CLEAVASE I [Third Wave Technologies, Madison, WI] enzyme). DNA fragments from a sample containing a SNP or a mutation will have a different banding pattern than wild type.

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a. RFLP Assay

In some embodiments of the present invention, variant sequences are detected using a restriction fragment length polymorphism assay (RFLP). The region of interest is first isolated using PCR. The PCR products are then cleaved with restriction enzymes known to give a unique length fragment for a given polymorphism. The restriction-enzyme digested PCR products are generally separated by gel electrophoresis and may be visualized by ethidium bromide staining. The length of the fragments is compared to molecular weight markers and fragments generated from wild-type and mutant controls.

b. CFLP Assay

In other embodiments, variant sequences are detected using a CLEAVASE fragment length polymorphism assay (CFLP; Third Wave Technologies, Madison, WI; *See e.g.*, U.S. Patent Nos. 5,843,654; 5,843,669; 5,719,208; and 5,888,780; each of which is herein incorporated by reference). This assay is based on the observation that when single strands of DNA fold on themselves, they assume higher order structures that are highly individual to the precise sequence of the DNA molecule. These secondary structures involve partially duplexed regions of DNA such that single stranded regions are juxtaposed with double stranded DNA hairpins. The CLEAVASE I enzyme, is a structure-specific, thermostable nuclease that recognizes and cleaves the junctions between these single-stranded and double-stranded regions.

The region of interest is first isolated, for example, using PCR. In preferred embodiments, one or both strands are labeled. Then, DNA strands are separated by heating. Next, the reactions are cooled to allow intrastrand secondary structure to form. The PCR products are then treated with the CLEAVASE I enzyme to generate a series of fragments that are unique to a given SNP or mutation. The CLEAVASE enzyme treated PCR products are separated and detected (*e.g.*, by denaturing gel electrophoresis) and visualized (*e.g.*, by autoradiography, fluorescence imaging or staining). The length of the fragments is compared to molecular weight markers and fragments generated from wild-type and mutant controls.

4. Hybridization Assays

In preferred embodiments of the present invention, variant sequences are detected a hybridization assay. In a hybridization assay, the presence or absence of a given SNP or mutation is determined based on the ability of the DNA from the sample to hybridize to a complementary DNA molecule (*e.g.*, a oligonucleotide probe). A variety of hybridization assays using a variety of technologies for hybridization and detection are available. A description of a selection of assays is provided below.

a. Direct Detection of Hybridization

In some embodiments, hybridization of a probe to the sequence of interest (*e.g.*, a SNP or mutation) is detected directly by visualizing a bound probe (*e.g.*, a Northern or Southern assay; *See e.g.*, Ausabel *et al.* (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY [1991]). In a these assays, genomic DNA (Southern) or RNA (Northern) is isolated from a subject. The DNA or RNA is then cleaved with a series of restriction enzymes that cleave infrequently in the genome and not near any of the markers being assayed. The DNA or RNA is then separated (*e.g.*, on an agarose gel) and transferred to a membrane. A labeled (*e.g.*, by incorporating a radionucleotide) probe or probes specific for the SNP or mutation being detected is allowed to contact the membrane under a condition or low, medium, or high stringency conditions. Unbound probe is removed and the presence of binding is detected by visualizing the labeled probe.

b. Detection of Hybridization Using "DNA Chip" Assays

In some embodiments of the present invention, variant sequences are detected using a DNA chip hybridization assay. In this assay, a series of oligonucleotide probes are affixed to a solid support. The oligonucleotide probes are designed to be unique to a given SNP or mutation. The DNA sample of interest is contacted with the DNA "chip" and hybridization is detected.

In some embodiments, the DNA chip assay is a GeneChip (Affymetrix, Santa Clara, CA; *See e.g.*, U.S. Patent Nos. 6,045,996; 5,925,525; and 5,858,659; each of which is herein incorporated by reference) assay. The GeneChip technology uses miniaturized, high-density arrays of oligonucleotide probes affixed to a "chip." Probe arrays are

manufactured by Affymetrix's light-directed chemical synthesis process, which combines solid-phase chemical synthesis with photolithographic fabrication techniques employed in the semiconductor industry. Using a series of photolithographic masks to define chip exposure sites, followed by specific chemical synthesis steps, the process constructs

5 high-density arrays of oligonucleotides, with each probe in a predefined position in the array. Multiple probe arrays are synthesized simultaneously on a large glass wafer. The wafers are then diced, and individual probe arrays are packaged in injection-molded plastic cartridges, which protect them from the environment and serve as chambers for hybridization.

10 The nucleic acid to be analyzed is isolated, amplified by PCR, and labeled with a fluorescent reporter group. The labeled DNA is then incubated with the array using a fluidics station. The array is then inserted into the scanner, where patterns of hybridization are detected. The hybridization data are collected as light emitted from the fluorescent reporter groups already incorporated into the target, which is bound to the

15 probe array. Probes that perfectly match the target generally produce stronger signals than those that have mismatches. Since the sequence and position of each probe on the array are known, by complementarity, the identity of the target nucleic acid applied to the probe array can be determined.

In other embodiments, a DNA microchip containing electronically captured

20 probes (Nanogen, San Diego, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,017,696; 6,068,818; and 6,051,380; each of which are herein incorporated by reference). Through the use of microelectronics, Nanogen's technology enables the active movement and concentration of charged molecules to and from designated test sites on its semiconductor microchip. DNA capture probes unique to a given SNP or mutation are electronically

25 placed at, or "addressed" to, specific sites on the microchip. Since DNA has a strong negative charge, it can be electronically moved to an area of positive charge.

First, a test site or a row of test sites on the microchip is electronically activated with a positive charge. Next, a solution containing the DNA probes is introduced onto the microchip. The negatively charged probes rapidly move to the positively charged

30 sites, where they concentrate and are chemically bound to a site on the microchip. The

microchip is then washed and another solution of distinct DNA probes is added until the array of specifically bound DNA probes is complete.

A test sample is then analyzed for the presence of target DNA molecules by determining which of the DNA capture probes hybridize, with complementary DNA in the test sample (*e.g.*, a PCR amplified gene of interest). An electronic charge is also used to move and concentrate target molecules to one or more test sites on the microchip. The electronic concentration of sample DNA at each test site promotes rapid hybridization of sample DNA with complementary capture probes (hybridization may occur in minutes). To remove any unbound or nonspecifically bound DNA from each site, the polarity or charge of the site is reversed to negative, thereby forcing any unbound or nonspecifically bound DNA back into solution away from the capture probes. A laser-based fluorescence scanner is used to detect binding,

In still further embodiments, an array technology based upon the segregation of fluids on a flat surface (chip) by differences in surface tension (ProtoGene, Palo Alto, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,001,311; 5,985,551; and 5,474,796; each of which is herein incorporated by reference). Protogene's technology is based on the fact that fluids can be segregated on a flat surface by differences in surface tension that have been imparted by chemical coatings. Once so segregated, oligonucleotide probes are synthesized directly on the chip by ink-jet printing of reagents. The array with its reaction sites defined by surface tension is mounted on a X/Y translation stage under a set of four piezoelectric nozzles, one for each of the four standard DNA bases. The translation stage moves along each of the rows of the array and the appropriate reagent is delivered to each of the reaction site. For example, the A amidite is delivered only to the sites where amidite A is to be coupled during that synthesis step and so on. Common reagents and washes are delivered by flooding the entire surface and then removing them by spinning.

DNA probes unique for the SNP or mutation of interest are affixed to the chip using Protogene's technology. The chip is then contacted with the PCR-amplified genes of interest. Following hybridization, unbound DNA is removed and hybridization is detected using any suitable method (*e.g.*, by fluorescence de-quenching of an incorporated fluorescent group).

In yet other embodiments, a "bead array" is used for the detection of polymorphisms (Illumina, San Diego, CA; *See e.g.*, PCT Publications WO 99/67641 and WO 00/39587, each of which is herein incorporated by reference). Illumina uses a BEAD ARRAY technology that combines fiber optic bundles and beads that
5 self-assemble into an array. Each fiber optic bundle contains thousands to millions of individual fibers depending on the diameter of the bundle. The beads are coated with an oligonucleotide specific for the detection of a given SNP or mutation. Batches of beads are combined to form a pool specific to the array. To perform an assay, the BEAD ARRAY is contacted with a prepared subject sample (e.g., DNA). Hybridization is
10 detected using any suitable method.

c. Enzymatic Detection of Hybridization

In some embodiments of the present invention, hybridization is detected by enzymatic cleavage of specific structures (INVADER assay, Third Wave Technologies;
15 *See e.g.*, U.S. Patent Nos. 5,846,717, 6,090,543; 6,001,567; 5,985,557; and 5,994,069; each of which is herein incorporated by reference). The INVADER assay detects specific DNA and RNA sequences by using structure-specific enzymes to cleave a complex formed by the hybridization of overlapping oligonucleotide probes. Elevated temperature and an excess of one of the probes enable multiple probes to be cleaved for each target
20 sequence present without temperature cycling. These cleaved probes then direct cleavage of a second labeled probe. The secondary probe oligonucleotide can be 5'-end labeled with a fluorescent dye that is quenched by a second dye or other quenching moiety. Upon cleavage, the de-quenched dye-labeled product may be detected using a standard fluorescence plate reader, or an instrument configured to collect fluorescence data during
25 the course of the reaction (*i.e.*, a "real-time" fluorescence detector, such as an ABI 7700 Sequence Detection System, Applied Biosystems, Foster City, CA).

The INVADER assay detects specific mutations and SNPs in unamplified genomic DNA. In an embodiment of the INVADER assay used for detecting SNPs in genomic DNA, two oligonucleotides (a primary probe specific either for a SNP/mutation
30 or wild type sequence, and an INVADER oligonucleotide) hybridize in tandem to the genomic DNA to form an overlapping structure. A structure-specific nuclease enzyme

recognizes this overlapping structure and cleaves the primary probe. In a secondary reaction, cleaved primary probe combines with a fluorescence-labeled secondary probe to create another overlapping structure that is cleaved by the enzyme. The initial and secondary reactions can run concurrently in the same vessel. Cleavage of the secondary probe is detected by using a fluorescence detector, as described above. The signal of the test sample may be compared to known positive and negative controls.

In some embodiments, hybridization of a bound probe is detected using a TAQMAN assay (PE Biosystems, Foster City, CA; *See e.g.*, U.S. Patent Nos. 5,962,233 and 5,538,848, each of which is herein incorporated by reference). The assay is performed during a PCR reaction. The TAQMAN assay exploits the 5'-3' exonuclease activity of DNA polymerases such as AMPLITAQ DNA polymerase. A probe, specific for a given allele or mutation, is included in the PCR reaction. The probe consists of an oligonucleotide with a 5'-reporter dye (*e.g.*, a fluorescent dye) and a 3'-quencher dye. During PCR, if the probe is bound to its target, the 5'-3' nucleolytic activity of the AMPLITAQ polymerase cleaves the probe between the reporter and the quencher dye. The separation of the reporter dye from the quencher dye results in an increase of fluorescence. The signal accumulates with each cycle of PCR and can be monitored with a fluorimeter.

In still further embodiments, polymorphisms are detected using the SNP-IT primer extension assay (Orchid Biosciences, Princeton, NJ; *See e.g.*, U.S. Patent Nos. 5,952,174 and 5,919,626, each of which is herein incorporated by reference). In this assay, SNPs are identified by using a specially synthesized DNA primer and a DNA polymerase to selectively extend the DNA chain by one base at the suspected SNP location. DNA in the region of interest is amplified and denatured. Polymerase reactions are then performed using miniaturized systems called microfluidics. Detection is accomplished by adding a label to the nucleotide suspected of being at the SNP or mutation location. Incorporation of the label into the DNA can be detected by any suitable method (*e.g.*, if the nucleotide contains a biotin label, detection is via a fluorescently labelled antibody specific for biotin).

5. Other Detection Assays

Additional detection assays that are produced and utilized using the systems and methods of the present invention include, but are not limited to, enzyme mismatch cleavage methods (e.g., Variagenics, U.S. Pat. Nos. 6,110,684, 5,958,692, 5,851,770, 5 herein incorporated by reference in their entireties); polymerase chain reaction; branched hybridization methods (e.g., Chiron, U.S. Pat. Nos. 5,849,481, 5,710,264, 5,124,246, and 5,624,802, herein incorporated by reference in their entireties); rolling circle replication (e.g., U.S. Pat. Nos. 6,210,884 and 6,183,960, herein incorporated by reference in their entireties); NASBA (e.g., U.S. Pat. No. 5,409,818, herein incorporated by reference in its 10 entirety); molecular beacon technology (e.g., U.S. Pat. No. 6,150,097, herein incorporated by reference in its entirety); E-sensor technology (Motorola, U.S. Pat. Nos. 6,248,229, 6,221,583, 6,013,170, and 6,063,573, herein incorporated by reference in their entireties); cycling probe technology (e.g., U.S. Pat. Nos. 5,403,711, 5,011,769, and 5,660,988, herein incorporated by reference in their entireties); Dade Behring signal 15 amplification methods (e.g., U.S. Pat. Nos. 6,121,001, 6,110,677, 5,914,230, 5,882,867, and 5,792,614, herein incorporated by reference in their entireties); ligase chain reaction (Barnay Proc. Natl. Acad. Sci USA 88, 189-93 (1991)); and sandwich hybridization methods (e.g., U.S. Pat. No. 5,288,609, herein incorporated by reference in its entirety).

20 6. Mass Spectroscopy Assay

In some embodiments, a MassARRAY system (Sequenom, San Diego, CA.) is used to detect variant sequences (*See e.g.*, U.S. Patent Nos. 6,043,031; 5,777,324; and 5,605,798; each of which is herein incorporated by reference). DNA is isolated from blood samples using standard procedures. Next, specific DNA regions containing the 25 mutation or SNP of interest, about 200 base pairs in length, are amplified by PCR. The amplified fragments are then attached by one strand to a solid surface and the non-immobilized strands are removed by standard denaturation and washing. The remaining immobilized single strand then serves as a template for automated enzymatic reactions that produce genotype specific diagnostic products.

30 Very small quantities of the enzymatic products, typically five to ten nanoliters, are then transferred to a SpectroCHIP array for subsequent automated analysis with the

SpectroREADER mass spectrometer. Each spot is preloaded with light absorbing crystals that form a matrix with the dispensed diagnostic product. The MassARRAY system uses MALDI-TOF (Matrix Assisted Laser Desorption Ionization - Time of Flight) mass spectrometry. In a process known as desorption, the matrix is hit with a pulse from a laser beam. Energy from the laser beam is transferred to the matrix and it is vaporized resulting in a small amount of the diagnostic product being expelled into a flight tube. As the diagnostic product is charged when an electrical field pulse is subsequently applied to the tube they are launched down the flight tube towards a detector. The time between application of the electrical field pulse and collision of the diagnostic product with the detector is referred to as the time of flight. This is a very precise measure of the product's molecular weight, as a molecule's mass correlates directly with time of flight with smaller molecules flying faster than larger molecules. The entire assay is completed in less than one thousandth of a second, enabling samples to be analyzed in a total of 3-5 second including repetitive data collection. The SpectroTYPER software then calculates, records, compares and reports the genotypes at the rate of three seconds per sample.

In some embodiments, the present invention provides an oligonucleotide comprising a DME related sequence, or a complement of a DME-related sequence. In preferred embodiments, an oligonucleotide of the present invention comprises a sequence or a complement of a sequence selected from the group consisting SEQ ID NOs. 1-3360 and 3361-7669, or a substantially similar sequence.

In some embodiments, an oligonucleotide probe or oligonucleotide primer is created so the 5' terminus, 3' terminus or central base contains the genetic polymorphism site. In some preferred embodiments, an oligonucleotide is created comprising at least 13 contiguous bases of a sequence selected from SEQ ID NOs 1 through 3360 or the complement thereto, and further comprising the 21st nucleotide of the sequence selected from SEQ ID NOs 1 through 3360, or the complement thereto.

In some embodiments, an oligonucleotide of the present invention flanks or is adjacent to a polymorphic site, such that the presence of the polymorphism can be detected by modification of the oligonucleotide in a manner dependent on the presence or absence of the polymorphism.

In some embodiments, the present invention provides kits comprising one or more of the components necessary for practicing the present invention. For example, the present invention provides kits for storing or delivering the enzymes of the present invention and/or the reaction components necessary to practice a cleavage assay (e.g., the INVADER assay). The kit may include any and all components necessary or desired for the enzymes or assays including, but not limited to, the reagents themselves, buffers, control reagents (e.g., tissue samples, positive and negative control target oligonucleotides, etc.), solid supports, labels, written and/or pictorial instructions and product information, inhibitors, labeling and/or detection reagents, package environmental controls (e.g., ice, desiccants, etc.), and the like. In some embodiments, the kits provide a sub-set of the required components, wherein it is expected that the user will supply the remaining components. In some embodiments, the kits comprise two or more separate containers wherein each container houses a subset of the components to be delivered. For example, a first container (e.g., box) may contain an enzyme (e.g., structure specific cleavage enzyme in a suitable storage buffer and container), while a second box may contain oligonucleotides (e.g., INVADER oligonucleotides, probe oligonucleotides, control target oligonucleotides, etc.). In some embodiments one or more the reaction components may be provided in a predispensed format (*i.e.*, pre-measured for use in a step of the procedure without re-measurement or re-dispensing). In some embodiments, selected reaction components are mixed and predispensed together. In preferred embodiments, predispensed reaction components are predispensed and are provided in a reaction vessel (including but not limited to a reaction tube or a well, as in, *e.g.*, a microtiter plate). In particularly preferred embodiments, predispensed reaction components are dried down (*e.g.*, desiccated or lyophilized) in a reaction vessel.

Examples of genetic polymorphism data (especially the SNP data) that can be used in the method of the present invention are shown in Table 1.

Table 1

1 / 161

GENE	number	position	SEQ.	SEQ ID.No
ABCB2	1	5'flanking - 673	agctaagagtcaaagcacc G/C cttttccaccagcctcg	1
ABCB2	2	5'flanking - 646	ccaccagcctcgctgctg T/G tcccttcacggacactotag	2
ABCB2	3	5'flanking - 563	ttgcaagcgtggctgtac A/C ggcgacctccctgcgtccc	3
ABCB2	4	5'flanking - 236	gctttgogcggcgctaac G/T tgttagggcagatctgccc	4
ABCB2	5	Intron3 + 408	aaggaaactgaggccaagac C/T ctaaagtctgaaactgcaca	5
ABCB2	6	Exon4 + 153	ccctcaccatggcaccctg A/G tcaccctgctctgctttc	6
ABCB2	7	Intron4 + 289	gtattcttttagcatccaag G/T ggcatagctgtctctttc	7
ABCB2	8	Intron4 + 291	attcttttagcatccaagg C/G catagctgtgtctctttc	8
ABCB2	9	Intron5 - 63	ttccttcaggtaagtactg C/T ggctcttctgtctccctcca	9
ABCB2	10	Intron7 - 185	gtctctgcccctgtcttgc C/T gcttctctatctctactcc	10
ABCB2	11	3'flanking + 71	agcgcacttttcagctgagg G/A tgtctctcttttatcatcc	11
ABCB2	12	3'flanking + 129	aactgcataccttttccct T/C aagcttttaattctatga	12
ABCB2	13	3'flanking + 459	cattcagggaggcccaggc G/A tgtgacgtcgacagttgctg	13
ABCB4	1	exon3 + 3	aacaccctattttatagat C/T caatgactgagtcaagaatt	14
ABCB4	2	intron3 + 45	cagcatctctactatacca T/C gctctgcttaaggctctct	15
ABCB4	3	intron3 + 498	actcaaataggtggtaggag C/T agagacaattcaatacagac	16
ABCB4	4	intron3 + 515	gagcagagacaattcaatac A/G gacagaagtcttagatgaga	17
ABCB4	5	intron6 + 1030	tagttttgccatgtagaatt G/C aaaaagttagatgggtgt	18
ABCB4	6	intron6 + 1437	gttaagcctgcttcaatcaa G/A ttagttatattctgttcta	19
ABCB4	7	intron6 + 2449	ttgacttagcgacactgtta G/A catactatctttcctgtgt	20
ABCB4	8	intron7 + 451	ccttgctgcacctgtgtgt A/C taagttggcttattatagt	21
ABCB4	9	intron7 + 530	agtagagacaggctggcgat C/G acaccggacagagctaactg	22
ABCB4	10	intron7 - 152	aacagaatcatgaaattaag T/C tgttaatgattgaaggcct	23
ABCB4	11	exon8 + 40	aggataaattgtttatgtc C/T ctgggtaccatcatggccat	24
ABCB4	12	intron8 + 130	ctgggtgactccagatatca T/C agaaggagttgaaaattct	25
ABCB4	13	intron8 + 248	aatacacaggaagcttctaa A/G taaagtaaggaagtcactct	26
ABCB4	14	intron8 + 531	ctaaagagtgaatggattca A/G tacgtcccttggaaactcacc	27
ABCB4	15	intron8 + 4240	ctgaggttccagcttatctc T/A tagagatgtttacttagct	28
ABCB4	16	intron8 + 4343	tgttagaagaaaaaagggt C/T atattacaagagggtctgac	29
ABCB4	17	intron8 + 4677	cccaagatatcttcataact G/C tccatagtgccatgggtgcc	30
ABCB4	18	intron9 + 113	tttaccagattcacctatt A/G ttatcattttgctcccaaa	31
ABCB4	19	intron9 + 982	tgtcctatacagttttgt T/A taagtttagtaaatgatta	32
ABCB4	20	intron11 + 457	tccagcttgggtgacagagt A/G agacttcactcaaaaaaa	33
ABCB4	21	intron11 + 1337	tactcttggggagcctatca C/G cagggtgggtcagatatagc	34
ABCB4	22	exon12 + 3	tgttcttttctgtccagat A/T ctctcgccatttagtgaaa	35
ABCB4	23	intron12 + 1288	cagaccacactaacctcag T/C tggacctcaggatgtcagtg	36
ABCB4	24	intron13 + 206	tgtggataagaaaatagcat G/A tggtagaccatttgtgaaa	37
ABCB4	25	intron13 + 988	cagtcgggttgaagcttgc T/C acccttcttcacttctca	38
ABCB4	26	intron13 + (1413-1414)	ttatcttcacttatgttt (T) ctcagttaagttatgcta	39
ABCB4	26	intron13 + (1413-1414)	ttatcttcacttatgttt ctcagttaagttatgcta	40
ABCB4	27	intron13 + 1931	cttgcaaatgtgtctctcc A/G caaaaaaaaaggaaaggat	41
ABCB4	28	intron23 + 784	agtatctcctaaactcttgc T/C atgcaggaaaaattattta	42
ABCB4	29	intron25 + 158	gaaatatttactgtattaa T/C gtctagaacttaaatataag	43
ABCB4	30	intron25 + 2920	ctgagtcttctatacatct T/A ttccattctcggatgctgt	44
ABCB4	31	intron29 + 411	cttctctacctgaattct A/C ggctctcgaacttgacttt	45
ABCB4	32	intron32 + 458	agaaaatgaaattgccctac T/C gagctaactctgaaagcaca	46
EPHX1	1	intron1 + 110	tgcaaaatgtgtctactag C/T ttctagtgcataaaatattg	47
EPHX1	2	intron1 + 143	aaatattgttgagctctc G/A ctgtgctgggcccagtcacca	48
EPHX1	3	intron1 + 1097	aatccagagagggagataga T/G tggagttcaagggtggaca	49
EPHX1	4	intron1 + 1717	ttccaagacagagcagggg T/C gctgctggggcgtggttgc	50
EPHX1	5	intron1 + 1772	aactcgatgctttctctcc G/T totgggtcctaactgcagt	51
EPHX1	6	intron1 + 2054	gaaatgtaacaggcaacact A/G tggacacagaaagtagatta	52
EPHX1	7	intron2 + 1414	atttccaaaatctgttggg G/T gtaactgaaacacttgggaa	53
EPHX1	8	exon3 + 174	taccctcacttcaagactaa G/A attgaaggtagtttgcaaa	54
EPHX1	9	intron3 + 6583	ctgtcaataccatgaagggg G/C ggcgggggcactaagggtgg	55
EPHX1	10	intron4 + 34	agaggttccataactgcccc G/A tctcggccaagggtggggcc	56
EPHX1	11	intron4 + 63	aagggtgggcccgggtgtcc C/T accaggctctcttccggcg	57
EPHX1	12	intron5 + 154	gcagtgcctgaggcacgtt G/A cttggatcctcctgtctgta	58
EPHX1	13	intron5 + 276	tgctggaccaagctctggga T/C agccctgagcagaactcccc	59
EPHX1	14	exon6 + 130	gatgtggagctgtgtatccc C/T gtcaaggagaagggtattota	60

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GENE	number	position	SEQ.	SEQ ID.No
EPHX1	15	intron8 + 206	ggcgctggctcccgggcgg C/A cctcagtaccgctcccagt	61
EPHX1	16	intron8 + 353	tggccctcccagaaaagaga A/G ggccctcagtgggggagag	62
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagaggtgagagag	63
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc (C) tccccgccccccaacacgg	64
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc tccccgccccccaacacgg	65
EPHX2	2	5'flanking - 522	aaagtcactggatagcccc T/C cccccgccccccaacacggt	66
EPHX2	3	5'flanking - 521	aagtcactggatagcccc C/T ccccgccccccaacacggtc	67
EPHX2	4	5'flanking - 516	actggatagcccccccc G/C ccccccaacacggttattg	68
EPHX2	5	5'flanking - 515	ctggatagcccccccc G/C ccccccaacacggttattgt	69
EPHX2	6	Intron1 - 74	tggctgctctcaatgaata T/C gaacagtgtctgttccatg	70
EPHX2	7	Intron3 + 72	gagcattaggtcagaatcca T/C tgaagtggctttgagatca	71
EPHX2	8	Intron4 + 473	gtgtgtctctactttaattc A/G caaaagggtgattgaatggag	72
EPHX2	9	Intron5 + 276	caagagtgggatgttcaagg C/T catcctgacctcacttttga	73
EPHX2	10	Intron8 + 8	tctgctcctcccggtgggtg T/C gctgtcttgagctgtotta	74
EPHX2	11	Intron9 + 1573	atgtctgaagactgatgaa C/T gatggacggctgcactgctc	75
EPHX2	12	Intron10 + 207	gaacaggatggagatgagct T/C gtttattgtcttttaatga	76
EPHX2	13	Intron12 + 911	tgaagagacctcgacatgtc G/T catccacatactacaggga	77
EPHX2	14	Intron12 + 2425	atcttctcagctgagcaaac C/T gaggctcagagggttaacc	78
EPHX2	15	Intron12 + 2460	taaccccaactggccaag G/A ccaggtagatgattgggtca	79
EPHX2	16	Intron12 - 281	aagtccttcaagagattat T/C ataagtagtaccttctcatt	80
EPHX2	17	Intron12 - 268	agattattataagtagtacc T/G tctcattataggaatattga	81
EPHX2	18	Exon13 + 50	cctgagtcggactttcaaaa G/T cctcttcagagcaagcgtg	82
EPHX2	19	Intron13 + 1739	ttgtogtaacagggttttca G/T atgagcatatttcctttgta	83
EPHX2	20	Exon14 + 33	atgcataaagtctgtgaagc G/A ggtaagagacatgcttggga	84
EPHX2	21	Intron14 + 314	ggattgagagcttacctcta T/C gggggtcacctcgtgtatgc	85
EPHX2	22	Intron14 + 878	attcccttattccttcacac C/T gtctgtcactcattcattca	86
EPHX2	23	Intron14 + 948	gcacaggctgggtatgaagc T/C ggggctgcactgcagctac	87
EPHX2	24	Intron15 + 259	agagggttttactactttt C/T agtcatggctcctcagagaa	88
EPHX2	25	Intron16 + 459	tcctcatttgcgaagcagaa G/C atgagtttcaatctctggg	89
EPHX2	26	Intron16 + 645	gtaagtgaacacactgctac G/A tgccagacttctgcccagac	90
EPHX2	27	Intron16 + 985	gtcattatcatcatatgacc G/A atgaaaatgaccaaactgca	91
EPHX2	28	3'flanking + 12	aggtggccttacacacatct T/C gcatggatggcagcattgtt	92
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atggggtgaaccctttccc	93
EPHX2	30	3'flanking + 544	tagccacctgcctttctccc G/A gcttccctagcagagtttgc	94
GAMT	1	intron1 + 429	ctcggaagctgagctcagg G/A agacagctgtccccgggggtg	95
GAMT	2	3'flanking + 626	cactgacctccttgccctga G/A agaaggcggctcctgtgct	96
NNMT	1	5'flanking - 228	ataatttctcagcagctc A/T agtgcctcctctggtctaca	97
NNMT	2	intron1 + 44	cccactaatgtgagtcata T/C agatggagtctcagggcacg	98
NNMT	3	intron1 + 149	ggataaaaaacgaatattgtt A/G tagcgattccacagtttaca	99
NNMT	4	intron2 + 158	agataggcccatgtgtgtgc G/A tgttagtaaatgtgtatg	100
NNMT	5	intron2 + 433	gctgtagccatccaagccta T/C agaacttggctgtgagtgtg	101
NNMT	6	intron2 - 3064	atcactgactggtaagttc C/T agttctgtgtaactcaagt	102
NNMT	7	intron2 - 260	atttcatggagggaagtcca T/C ggtagaagcaggctgctagg	103
NNMT	8	3'flanking + 71	ggctcagtggttggggccca A/G tgggtcatctaggacgggac	104
PNMT	1	5'flanking - 390	aagaggtgaatggctgcggg G/A ggctggagaagagagatggg	105
PEMT	1	exon2 - 4	agctcagcagacctcctggc C/T gtgggtggtagctccttcc	106
PEMT	2	intron4 + 39	actgtccagacgggagtatc C/T cactgcttggtagccccac	107
PEMT	3	intron4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggcctctg	108
PEMT	4	intron4 + 1355	ctggagccaggctgcagccg A/C agtgctggccatcctggcg	109
PEMT	5	intron4 + 5925	gtccaggcactgtggcccta C/T gtgggagtctccagtctcca	110
PEMT	6	intron4 + 6028	ggcagtggtccaaggaccag G/C atggactccctcttctcacc	111
PEMT	7	intron4 + 6078	atctgtaccctgcggactc C/T acctggcttctgtccatcac	112
PEMT	8	intron4 + 6089	cgcggactctacctggcttc A/G tgccatcacccccgccagat	113
PEMT	9	intron4 + 6379	tcagggtgtccctccctcat G/A cctcctcaccctgccctctc	114
PEMT	10	intron4 + 7339	tgttaaggaatcctgccaaga C/T ggcagatgcacacggggtca	115
PEMT	11	intron4 + 7619	ctcctgcacatgtgtccag A/G gaggaaggcatttgacagg	116
PEMT	12	intron4 + 8858	ggcatgtgtgtgtgtgtgta T/G gtgtgtgagtgtgtcatgt	117
PEMT	13	intron4 + 9029	tttctggaccagaaagcgtc G/A tctctgccagggcctcttg	118
PEMT	14	intron4 + 9056	gccagggcctcttgacttg C/T gggaaagctgagctgagctg	119
PEMT	15	intron4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgtgtgtggcact	120

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GENE	number	position	SEQ.	SEQ ID.No
PEMT	16	intron4 + 9523	agcagcattactctgtgtgc T/C gctggcactggcctggtggg	121
PEMT	17	intron4 + 9622	gacaaagtgtacaacaaggt G/A tctogaactgggtcagctca	122
PEMT	18	intron4 + 10776	ccattcctgggtcttctttg G/A aggctgaatgaaattccatg	123
PEMT	19	intron4 + 10912	tctgccccactttgtctcaga G/C gtgcaacaaggccttcagga	124
PEMT	20	intron4 + 11590	ggacactggcctgatgcaga G/C gtgtggtctctctcctgcag	125
PEMT	21	intron4 + 12090	ggccagggcaccctaccag G/C ctgagtcccacctgtccagc	126
PEMT	22	intron4 + 12263	taccgccttcccagatgga G/A cgggtgctcatgggactta	127
PEMT	23	intron4 + 12448	tctggtcccctctcctgctt G/A tagttcctgggctaaaatc	128
PEMT	24	intron4 + 12730	tgggaccagtgcggccacca C/T ggcccaaggacctggtgttc	129
PEMT	25	intron4 + 13240	gggctccaggcacacagcgg T/C ccagtacacctgtcgttt	130
PEMT	26	intron4 + 13494	tccgtggaactcagagatgg T/C acctccctgcgagggtggggc	131
PEMT	27	intron4 + 13817	aactotcccctgctgctgag A/G cagatcttgagcctcggcc	132
PEMT	28	intron4 + 14773	cggcctgtgttcctatgccc C/T ctatgcctctcactgcctgg	133
PEMT	29	intron4 + 14951	gtcctgaggccccctcccacc G/A gagcctggggtgcctcaca	134
PEMT	30	intron4 + 16896	gctgtgactgtcttgagac T/C gggcttggcgggcctggtg	135
PEMT	31	intron4 + 19439	ccaggagcctctgaggcagc G/A ggggttctcaaccacacac	136
PEMT	32	intron4 + 19559	atthtgcagcatgtcacgt C/T ccttcataatgaagcaagg	137
PEMT	33	intron4 + 20051	acagcactgcgggagccacg A/G catctgcagacgcatttgat	138
PEMT	34	intron4 + 20816	tggactctctggcgtccatc C/T agccacttcagtgcgacgtg	139
PEMT	35	intron4 + 21196	ggctggctgggcccctgggat C/G atcgtgacaggcttagtg	140
PEMT	36	intron4 + 21528	acaggtgggagccgaggctc G/T ggaggtgggcccggctgagc	141
PEMT	37	intron4 + 21596	ccgcttcccctgtctctggc C/T gtacgagaaagtgtcccact	142
PEMT	38	intron4 + 22672	agcctcccactgccttgtgg C/T tgaggggagggggccgggtc	143
PEMT	39	intron4 + 22713	tctaacgtgtcttctttgt A/T ctgaaaaccaaacccttct	144
PEMT	40	intron4 + 23010	tgccgggcagcggggaggga G/A ggogagtgttcccccaagt	145
PEMT	41	intron4 + 23588	gtgcaggcgcctcgtcatccc C/T gcagccaagtcttgggcgga	146
PEMT	42	intron4 + 23627	gacactgccctgagccagga C/T ggtgaggtgggacgccttc	147
PEMT	43	intron4 + 23941	tgagggttgggactctaca G/A aggagagtggactcacgggg	148
PEMT	44	intron4 + 24091	gacacctcttactgtcagc G/T ctgagacacgccctgcct	149
PEMT	45	intron4 + 25348	caggccagttggaatctac G/A tagagtgaagcatctcagc	150
PEMT	46	intron4 + 25603	taagcagttaacactgatgc G/A tgatgaaaattccaacagca	151
PEMT	47	intron4 + 31540	cctccagggtggcaggaacac T/C gtgaggagcatgcaacgtgc	152
PEMT	48	intron4 + 31637	gtgggttgggacgccaggac G/A gtgagggttcaagggtgtg	153
PEMT	49	intron4 + 31642	ctgggacgccaggacgggtga G/A gggcttcaagggtgtttgt	154
PEMT	50	intron4 + 35593	ggaggagctgaaagagctgg G/A gctcgggatcaggtggttca	155
PEMT	51	intron4 + 35647	actttgaggcaccaccgcac C/A tgcctgtcgtgaggagac	156
PEMT	52	intron4 + 35862	tcccagtgtgtgtctgtcc C/T cgtctcagccgagcactcag	157
PEMT	53	intron4 + 35882	ccgtctcagccgagcactca T/G cggccagggtgtgtgactc	158
PEMT	54	intron4 + 37141	ccacaggccggatgccttga T/C acttctcagctgcagggtg	159
PEMT	55	intron4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgccatgg	160
PEMT	56	intron4 + 38872	acctcagacagcaaggacgg G/T catgccatgggtcccggcag	161
PEMT	57	intron4 + 39140	atgtctcaaatctccctccc C/T gggaaatctaggcacaggtc	162
PEMT	58	intron4 + 39635	caggcccaggagcagggtggg G/T cctcctcacaggagcagggc	163
PEMT	59	intron4 + 39713	actctgagcatgctggctcc C/T tcttcttccagggcagca	164
PEMT	60	intron4 + 40436	cctggttgtgtctcggaccc G/A gaggcagacagaggagcct	165
PEMT	61	intron4 + 47485	acaatgactgttgagccct C/T gagcaggctgtgtcacgtgg	166
PEMT	62	intron4 + 48131	actgggggatcctgaatccc G/A cctcctgatgccagtggagc	167
PEMT	63	intron4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttgcggag	168
PEMT	64	intron4 + 48702	gagatggggcggttcggga G/A gcaaaagcaggaaggcagaa	169
PEMT	65	intron4 + 50302	gcatgtgcatgggcagaggc T/C gttcccatctgagtgggacc	170
PEMT	66	intron4 + 54102	ggccgogtgcctcagacc A/T tgggctcctctggcagttct	171
PEMT	67	intron4 + 54220	cccaggacagatcttctcc G/A ccagacgtctcttctgcct	172
PEMT	68	intron4 + 54371	gcagataatgtcagctggg G/A tgcagtgtgttgtgtccc	173
PEMT	69	exon5 + 79	tggcctgctactctctaagc G/C tcaccatctgctcctgaac	174
PEMT	70	intron5 - 6796	ggaggaagtcagcttcttac A/C gatggtggctcccagotttc	175
PEMT	71	intron5 - 6636	ttttctcctctcacctttg T/C gttcagaggcagaggtgtgc	176
PEMT	72	intron5 - 6448	gttgggcccaggctctgacag G/A acctcgggaccagctcctg	177
PEMT	73	intron5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	178
PEMT	74	intron5 - 4824	ggacaggccgggggttgagc G/A gctgcatgaaggaggagg	179
PEMT	75	intron5 - 4249	tcaccagagtatttctctog C/A ggcagggtgcctggggtagcc	180

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GENE	number	position	SEQ.	SEQ ID.No
PEMT	76	intron5 - 4230	gaggcaggtgcctgggtag C/T cactgggoggggtccatgag	181
PEMT	77	intron5 - 4182	ggagagtaaggggtggggg G/A cacttaggacaggaagctg	182
PEMT	78	intron5 - 3369	ccaggtggggccgtgtgcct G/C tggcctggtgtgtggcccag	183
PEMT	79	intron5 - 2625	cagggaagctgggcccctgaa C/T gagctgggcttttgggccac	184
PEMT	80	intron5 - 1200	attattgtgagcatgggaag A/T gcacatttggtoacacatgt	185
PEMT	81	intron6 + 606	gcctggctagacgcccacca A/G tgacctgatgatggcagca	186
PEMT	82	intron6 + 1229	tttgggtccaggaagggggac G/A gcagccaggagcgtctggat	187
PEMT	83	intron7 + 716	atggagatgtgctccccgg C/G gggtcagaggacctgoggtc	188
PEMT	84	intron7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	189
PEMT	85	intron7 + 1718	gggcttccaggtgtctgagc T/C ccccgcatgtaggaccca	190
PEMT	86	intron7 + 2695	ggctttgggggacctggac C/T cattctagaaaacagcctt	191
PEMT	87	intron8 + 140	ccagggtctccaggtcagag C/T ggccatggtagcttacaatg	192
PEMT	88	3'flanking + 179	tacttaggaggcgtcagggg C/T tcacctggccatggccatgg	193
PEMT	89	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggccttgtgtgacc	194
GSTM3	1	5'flanking - 144	ccaacgccggcattagtcgc G/T cctgcgcacggccctgtgga	195
ALDH5	1	5'flanking - 2808	cgttgcactgtaggactctc C/T ccacgtcccctaataccatc	196
ALDH5	2	5'flanking - 2575	gcagttcccgcggatagaga A/G ggtccggtccttcccgctgt	197
ALDH5	3	5'flanking - 2537	tgtgggtgaactgtaaaaaa C/T tgccgtattcaggaggata	198
ALDH5	4	5'flanking - 940	cttcaactaatctgggaaca C/T tacactctgtttaatttca	199
ALDH5	5	5'flanking - 785	tgggaaagctgaaaaggat G/T ctgagacctgtggttggggg	200
ALDH5	6	exon1 + 183	ccgacggtcaaccctaccac T/C ggggaggtcattgggcacgt	201
ALDH5	7	exon1 + 257	cgtgaaagcagcccgggaag C/T ctccgcctggggtcccat	202
ALDH5	8	exon1 + 320	gcggggcccggtgtgaacc G/T cctggcagacctagtggagc	203
ALDH5	9	exon1 + 605	acttccccggcactcgcca C/T agccaacactgtggttatga	204
ALDH5	10	3'flanking + 1527	aaagtgaactgtaagacc G/A tagagaaaaactctggttc	205
TGM1	1	Exon2 + 179	tgccgaaatgcggcagatga C/T gactggggacctgaaccctc	206
TGM1	2	Intron9 - 611	acttaccactctgtcctctc C/T tgccaggcctcttctgtca	207
TGM1	3	Intron9 - 272	ccgcacatctgtacctgoc C/G ccactctccagcagagcagc	208
TGM1	4	Intron10 + 54	tcagtcatgggttctctgtt C/T ccaacttcaccgctgactga	209
TGM1	5	Intron10 - 51	aggaggccgggagtcaggcc A/G ccctoagacctctggtca	210
TGM1	6	Intron12 - 47	gggagtcctgggggaagcc T/G catgtagggaagcaggcctc	211
TGM1	7	Intron13 + 72	ggataaggacatcagaggtg G/A gcgctaagccagcagcaggc	212
TGM1	8	Intron14 + 1671	atctcttaccacacccccca C/G catggtggggagggttctca	213
TGM1	9	Intron14 + 1691	ccatggtggggagggttctc G/A tcctaagggtatccgcagagc	214
TGM1	10	Intron14 - 1634	tcctgcctccctccttcag G/A gagctcagaaacacctcaa	215
TGM1	11	Intron14 - 1459	ggaaacctctcagaaccagg T/C tccaagccaaatgctttgcc	216
TGM1	12	Intron14 - 801	cagaatacaaaaagtggtatg G/C gaggcaaggagtccgtag	217
TGM1	13	Exon15 + 233	ctcgaggtggagcttagccc T/C gtgccaggagcaatgggact	218
TGM1	14	Exon15 + 369	ggagtcagtcttcaacttga C/A tgggggaacagatgctaata	219
GGT1	1	intron1 + 85	ttatccagtaaggtggctcc G/A tcaccttttctctgttggg	220
GGT1	2	exon3 + 68	gacggccaggtccggatggt G/T gtgggagctgtgggggcac	221
NQO1	1	1 intron 1 80	aggaggtttaggggcttgg C/A ctgaatttgttcttctgact	222
PIG3	1	5'flanking region -47	gggaaggaggaaaggaaaga G/A ggggagggtgttctgttta	223
PIG3	2	intron 2 243	taacaccggacgcccagcag A/C agtcccagcttottagaatc	224
PIG3	3	3'flanking region 282	agcaggccccagccctgccc G/A ctactcacctgggccccacc	225
NQO2	1	5'flanking region -434	tttctgttcaccacggacc C/G tcattctgtaaccgggatac	226
NQO2	2	5'flanking region -406	gtaaccgggataccagccag A/G gatggggagcgggaggcgca	227
NQO2	3	5'untranslated region -102	tcctgcggtcctactgggg A/C gtgcgtggtcggaaggtga	228
NQO2	4	intron 1 1919	tcaactcaaataagactgagt T/C agtcaactcagctcttgacc	229
NQO2	5	intron 1 2004	acaaactcacatgccaccag C/G catatgatgtaaacatgtaa	230
NQO2	6	intron 1 3391	aaagcagagggtgtgcagg C/T gcccctgcccctaggctagg	231
NQO2	7	intron 1 3456	caaaggcctcatcctcagg C/A ggccaactcttctgttttag	232
NQO2	8	intron 1 3595	actgcccagctttaggttca T/C tottgtaagtgttctgtgtg	233
NQO2	9	intron 1 3596	ctgcccagctttaggttcat T/C cttgtaagtgttctgtgtg	234
NQO2	10	intron 1 3598	gcccagctttaggttcatc T/C tgtaagtgttctgtgtgtca	235
NQO2	11	intron 1 3651	ccctgcgtttgaaggatg A/G atgtgacctctccacattc	236
NQO2	12	intron 1 6036	tggtgtggcggttcaactgat C/T cccagccttctgtctgatc	237
NQO2	13	intron 2 14	atggcaggtaatgattcact A/G ttgtggagtaagacttttt	238
NQO2	14	intron 2 192	gccacgtggaagtgtataaa C/T tatctggaattatctgttt	239
NQO2	15	intron 2 635	cacctgtttagcacctagc A/C ccactcctggcctctgcca	240

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GENE	number	position	SEQ.	SEQ ID.No
NQO2	16	intron 2 685	agtagcaccctccccacc G/A gctgtgacaaaccaaagt	241
NQO2	17	exon 3 139	ctgatttgatgccatgaac T/C ttgagccgagggccacagac	242
NQO2	18	intron 3 36	aatgctctattataaaaac T/C atctttatgtttttacttt	243
NQO2	19	intron 3 728	aacgtgggcataaaccacca T/C ctagtgcacaaaagcaggtg	244
NQO2	20	intron 4 1577	tgcctctgcacacccttcc C/T gacaccagccctttctttac	245
NQO2	21	intron 4 1832	tcggccggccacgtggagcc C/T gctttctctctgcacccac	246
NQO2	22	intron 4 2583	tggtgttacgcacagctcct C/T gtccctccctgcctgccc	247
NQO2	23	exon 5 330	ctgtactgggtcagcgtgcc A/G gccatcctgaagggtggat	248
NQO2	24	exon 5 405	atcccaggattctacgattc C/T gggttgctccaggtatgtgc	249
NQO2	25	intron 5 21	gtatgtgctcttgataagg A/T tcactatggatagttggagg	250
NQO2	26	intron 5 253	atggcaacaaggagtgagg T/C caggtgtcaggtgacggggg	251
NQO2	27	intron 6 2435	cccccttaaatcatttaac T/C gaatggtatgtaacaggtgt	252
SULT1A1	1	5'flanking region -1597	gcagagtaaagggaactcaact C/G aagaagaggaacgtgggggt	253
SULT1A1	2	5'flanking region -1491	gaggggtatattcatgaaga G/T tccaggaaggttaagatt	254
SULT1A1	3	5'flanking region -1376	cggttcatatgttactgat C/T atacaatgagatcctaggtg	255
SULT1A1	4	5'flanking region -1375	ggtttcataatgttactgatc A/G tacaatgagatcctaggtga	256
SULT1A1	5	5'flanking region -1370	catatgttactgatcataca A/G tgagatcctaggtgaaacct	257
SULT1A1	6	exon 1B -65	aacctgcattccccacaca G/A caccacaatcagccactgc	258
SULT1A1	7	intron 1B 442	gagccaccctgccttaggcct G/A tgcctttgctgagtcacag	259
SULT1A1	8	exon 1A -197	gctgggggtcccagcaggaa A/G tggtagacaaaggcgctg	260
SULT1A1	9	exon 1A -159	ctggctggcagggagacagc A/G caggaaggtcctagagcttc	261
SULT1A1	10	exon 1A -95	gagacctcacacaccctga T/C atctgggccttgcccagca	262
SULT1A1	11	intron 1A 60	ctggtttcagccccagccc C/T gccactgactggctttgtga	263
SULT1A1	12	intron 1A 69	agccccagccccgccactga C/G tggctttgtgagtcgggca	264
SULT1A1	13	intron 1A 174	tgtgatgggtgtaagggaac G/A ggcttggtcttgccccctga	265
SULT1A1	14	intron 6 11	catgaaggaggtgagaccac C/G tgtgaagcttcctccatgt	266
SULT1A1	15	intron 6 17	ggaggtgagaccacctgtga A/T gcttccctccatgtgacacc	267
SULT1A1	16	intron 6 35	gaagcttccctccatgtgac A/T cctgggggcgggcacctcac	268
SULT1A1	17	intron 6 71	ctcacagggaccaccaggg T/C caccagccccctccctgg	269
SULT1A1	18	intron 6 108	ttggcagccccacagcagg C/A ccgattccccatcctgcct	270
SULT1A1	19	intron 6 111	gcagccccacagcaggccc G/A gattccccatcctgcctct	271
SULT1A1	20	intron 6 270	ctccctgccaaagggtgtgc C/T acccagggccacagtcatgg	272
SULT1A1	21	intron 6 488	tttacttttctgaatcag C/T aatccgagcctccactgagg	273
SULT1A1	22	intron 6 509	aatccgagcctccactgagg A/G gccctctgctgctcagaacc	274
SULT1A1	23	exon 7 600	ccctctgctgctcagaacc C/G aaaaggagattcaaaagat	275
SULT1A1	24	exon 7 645	gagtttggtgggcactccct G/A ccagaggagaccgtggactt	276
SULT1A1	25	exon 8 902	gctgtgagaggggctcctgg G/A gtcactgcagagggagtg	277
SULT1A2	1	5'flanking region -547	tgttctttcttggttctatg G/C atccatgctctgctccacc	278
SULT1A2	2	5'flanking region -425	tgtgggttgactgggcccag G/A acccctggcacctcaagac	279
SULT1A2	3	5'flanking region -358	cttccagggcctgcctatc C/T cagctttctccttcttgcct	280
SULT1A2	4	5'flanking region -355	tccagggcctgcctatccca G/T ctttctccttcttgcctggg	281
SULT1A2	5	5'untranslated region -28	actcggggcaggaggggcac A/G agggcaggttcccaagagct	282
SULT1A2	6	intron 1A 85	ctgactggccttgtagtg G/A ggcaagtcaactcagcctccc	283
SULT1A2	7	exon 2 24	gagctgatccaggacatctc T/C cggccgcccactggagtaagt	284
SULT1A2	8	intron 2 34	gccaccaccctctcccagg T/C ggagctcccccacttgcca	285
SULT1A2	9	intron 5 77	cagcaaccctgtgtcggcac T/C ccctggccgcttctccagt	286
SULT1A2	10	intron 6 684	actgggggtcccaggggtcga G/C gagctggctctatgggttt	287
SULT1A2	11	3'untranslated region 895	gctctgagctgtgagagggg T/C tctggagtcactgcagagg	288
SULT1A2	12	3'flanking region 98	cctccccgctccagctcctc A/T acttgccctgttgagagg	289
SULT1A2	13	3'flanking region 817	ccactgactcggggcttgcc A/C aggtgccagggctggcaaa	290
SULT1A2	14	3'flanking region 1006	cctctccctggaggctgct T/C taccgctgtgggggcgat	291
SULT1A2	15	3'flanking region 1464	tccgtagcccaggcaagtt C/T ggtgaccagagagcagcccc	292
SULTX3	1	intron 1 332	cctgcttctccctttacctg G/T ctggctgtgtgacctggac	293
SULTX3	2	intron 1 1167	taggaatggctaagcgtgtc G/A ttggcttctgtggcactca	294
SULTX3	3	intron 1 2872	cattctcactgatgcagacg G/A aagcttctgggcctggcggt	295
SULTX3	4	intron 1 6242	cacccttggttttaccagc A/G tggaaacattttacctaagt	296
SULTX3	5	intron 1 6601	gcgtgggcttctggaggag C/T gagaggagagtgaggggccc	297
SULTX3	6	intron 1 6768	agcttgaaatgagccagact C/T tctgggacctgtgacccc	298
SULTX3	7	intron 1 6905	agtactttgtttatcctcc C/T catcctcacaactttgcat	299
SULTX3	8	intron 1 7464	gccaggatcccttgagagac G/A acatgaacacagccaggagc	300

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GENE	number	position	SEQ.	SEQ ID.No
SULTX3	9	intron 1 7833	tgcttcgggctgggcttggc G/A ggggcagctgtgtccaggc	301
SULTX3	10	intron 1 8189	caaaactggggcccttaatgc C/T gcacaccagagcctccttcc	302
SULTX3	11	intron 1 8316	ctctcacacaaggcgaggc C/G tcttccccttgaggcagagc	303
SULTX3	12	intron 1 8617	agacagaggctggggccaag C/T cagggttgccggagcttct	304
SULTX3	13	intron 1 8631	gccaagccagggttgcogga G/T cttcctggactggcaggcc	305
SULTX3	14	intron 1 9493	ttttcctcttagagcttccc G/A tctgtctctgtgtcagggc	306
SULTX3	15	intron 1 10306	caggcggggagcctgaatgc C/T gcagtcgtgagggtggccag	307
SULTX3	16	intron 1 11987	tcataaaataatgatcag T/C acaacttttggaaatttgag	308
SULTX3	17	intron 1 13085	ctctgtgcccgggtgttga C/A aggccatgccctagagctct	309
SULTX3	18	intron 1 13108	gccatgccctagagctcctgg G/A gagttccaccccagaacagc	310
SULTX3	19	intron 2 700	gaaccatctgggagctgttc C/T gtactgccgtgccgaggggcc	311
SULTX3	20	intron 2 818	agccatagtagctagccagc G/A atcagcgtgggaggggagc	312
SULTX3	21	intron 2 1677	actccacttcccctgaaccc C/T accccttccctcctcctctg	313
SULTX3	22	intron 4 4954	gcgtgccgaaggcgaggagg C/T tgggatggctcaagacgtga	314
SULTX3	23	intron 5 3632	ccagctgactcccacaccag C/T ggtcagagaacattgtcttt	315
SULTX3	24	intron 5 3662	acattgtcttttaagggttc C/T gaagtgtcgaataaagaaa	316
SULTX3	25	intron 6 1874	tctgatctcagagagctgac A/G atggaaagaattctaaacga	317
SULTX3	26	intron 6 2133	agaccgggtgcctgcagtta T/G cccacagctcagccctccct	318
SULTX3	27	intron 6 2524	ggaagggccagggtgcctg T/C gatgccagagcagtgcaact	319
SULTX3	28	intron 6 2573	agatcatactgctcctggg A/G tgtttattaaacacctgcc	320
SULTX3	29	3'flanking region 12	gttcccggtgtgcgtcag C/G gttctgtctgtggggtag	321
SULTX3	30	3'flanking region 445	tccaaagcctgtcttctga T/G ttctgtggaaggagagctcc	322
TPST1	1	5'flanking region -298	accgcgccacatgccagct A/C atttttttgtattttttt	323
TPST1	2	intron 1 3520	agaaaagcagattaatgta C/G agtgacgcttagacaacaag	324
TPST1	3	intron 1 3610	ggcagaaagagaatatagca A/G ctattaaacacaaataaatt	325
TPST1	4	intron 1 20828	tattgtgtccacctgggtca A/G tgtgtcctgtgataagtgc	326
TPST1	5	intron 1 -6761	aatacaataactattctgta T/C aattctagagggccagaga	327
TPST1	6	intron 1 -544	tagaacaagtgaatatttta C/T gttcttagtggtttatggtt	328
TPST1	7	intron 1 -526	tacgttcttagtggttatg G/T ttggcagtttcccccaaca	329
TPST1	8	intron 1 -234	tcaagacatttaataatgca C/T atgtttcagctaaccctttt	330
TPST1	9	intron 1 -48	ttatagtgggttaagcatg A/G ttctaaaaaatttaataa	331
TPST1	10	intron 2 -18944	aaaacattagaactgggaag G/A ttaaaaaatotttagtcttt	332
TPST1	11	intron 2 -18687	tatgtgcaccctaataacat A/G ttctctaaaaactagtacta	333
TPST1	12	intron 2 -18501	ttggaaggtaacttaatgta A/G gtgcctgaaaaacagggata	334
TPST1	13	intron 2 -159	gaatggggatttccctcagt C/G ctgccactggctgctcttg	335
TPST1	14	intron 2 -19	acctgttgccctaaactcac G/A cctgctttgttttccaggt	336
TPST1	15	intron 3 158	tgctggggaagaaagatcag C/G gctcgggactgttgatttt	337
TPST1	16	intron 3 3779	agcagggcacgtcacccctcc C/T ggcacacccatgtgttcacc	338
TPST1	17	intron 4 292	ttgttattttcattatgaac C/T atgaaatatttcagctgaaa	339
TPST1	18	3'untranslated region 1518	gttgtctgtacatgttctaa T/G gttttgtagaacacgtgtgc	340
TPST1	19	3'flanking region 264	acgggtgcttgccctgcatta C/T cattttgtagtgaagttct	341
TPST2	1	intron 2 578	tcacctatcatcctcactgc G/A aggatgccaggatacctccc	342
TPST2	2	intron 2 789	cttaagccatcgtgcaggtc A/G ttgctgtcttctgctcactt	343
TPST2	3	intron 3 2009	cccaggctggagtgtagtgg T/C gtgatctcggctcactgcaa	344
TPST2	4	intron 3 2017	ggagtgtagtgggtgtgatct C/T ggctcactgcaacctccgcc	345
TPST2	5	intron 3 2035	ctcggctcactgcaacctcc G/A cctcccggttcaagcagtt	346
TPST2	6	intron 4 104	aatgttcagtcctcctcaattc C/T tggcatctgatttctcct	347
TPST2	7	intron 4 379	taaataaataaactatttgt C/T cctttctgttattataaggt	348
TPST2	8	intron 4 588	tactgcagcctgatacttct C/T ggcttaagccatcctctcac	349
TPST2	9	intron 4 626	caccccaggctcctgagtag C/T taggactgcagggtgcagcc	350
TPST2	10	intron 4 718	cccaggctgggtctagaactc C/G tggccgtaagggtgcccct	351
TPST2	11	intron 4 873	gttgatggccttatttatac G/A ttccattacagcttctagt	352
TPST2	12	intron 4 949	caaatatttgaaaatgggac C/G caggcctgaggaagagcttt	353
TPST2	13	intron 4 1033	taagctcagcatttctgagc G/A tgtgtctgattttaggaaata	354
TPST2	14	intron 4 1051	gcgtgtgtgattttaggaa A/G taaacagttatcgtattgaa	355
TPST2	15	intron 4 1356	gattcaacgtacataccagc C/T gacattgacaggtgaatggc	356
TPST2	16	intron 4 1707	gtctccttaaaagggtggctc G/T ctgcccctggcttggcccag	357
TPST2	17	intron 5 215	aagaccagcctgacaaaac G/A gtgaaaccccgctctacta	358
TPST2	18	intron 5 341	tgggaggcagaggtgcagct G/A agctgagatcacgccgttgc	359
TPST2	19	intron 6 31	ggacttcaactgggggttccc G/A ctgcttctgggtggcccgg	360

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GENE	number	position	SEQ.	SEQ ID.No
TPST2	20	intron 6 273	gtttgtctgacactggggac A/G gggcaggaagcaccactatg	361
TPST2	21	intron 6 693	aaagggattttttgaactt G/C gtaattcaaagatttaagat	362
TPST2	22	intron 6 1635	tcctgggtacagagttggcc T/G tgaacaaacatgagtccttc	363
TPST2	23	3'untranslated region 1147	cttccccactttcagatctc C/T gcaaatgacttcattgccaa	364
SULT1A3	1	exon 8 843	cgcttogatgaggactatgc G/A gagaagatggcaggctgcag	365
CST	1	intron 1b 6302	agagctccccagagaggact A/G tgaggctgcatgatgcata	366
CST	2	intron 2a 1004	gagtgagacccccatctcta C/T aaaatttttttaaaaagta	367
CST	3	intron 2a 1395	atgcctaagttacagtagc T/C aggcaggaaaggcacaacca	368
CST	4	intron 1d 473	ccagagcctgaggttggtgc T/A ggggccccctccatggctgcc	369
CST	5	intron 2b 726	ctatctctccagtgcctctc T/C gtccctgtctggaccctgct	370
CST	6	intron 2b 745	ctgtccctgtctggaccctg C/A tggggggccacagagcaggc	371
CST	7	exon 3 85	tcactagtttctgctgctg G/A tgtactcctatgccgtgcc	372
CST	8	intron 3 308	tcgtctgaggtcaggagttc G/A agaccagcctggccaacatg	373
CST	9	intron 3 853	ttttgtcctataaaatggca G/A ttcatgtggcccaagctga	374
CST	10	exon 4 198	gaggcagtgatcggggccaa C/T ggctcggcgggggagtgcca	375
SULT1C1	1	intron 3 2280	gcaaattttggattttta G/T tacagtcagggttttaccat	376
SULT1C1	2	intron 3 3742	gcagatctcactttctggca G/A attccctgaatttgcctccc	377
SULT1C1	3	intron 3 4453	ttcatagggcttttccctca C/T ttgttttgaattttgtata	378
SULT1C1	4	intron 3 5234	gaaaagagactagaggcagg A/G gagctttgcagttcttctaa	379
SULT1C1	5	intron 3 6175	tggctggcaggaaggtagg G/C agtcctctctctctgtgtcc	380
SULT1C1	6	intron 4 205	acatgaaggcaggatccaga T/C tgaatgtttggagggaacta	381
SULT1C1	7	intron 4 408	ggctcacgcctgtaatcca G/C cactttgggaggccgaggcg	382
SULT1C1	8	intron 4 429	cactttgggaggccgaggcg G/C gtggatcacaaagtcaggag	383
SULT1C2	1	5'flanking region -110	tcctgttaactcacagagaa C/T ggaagggtggaacgggacc	384
SULT1C2	2	exon 1 15	acactaatggccttacacga C/G atggaggattttacatttga	385
SULT1C2	3	intron 1 297	gtagactgtttattatttc A/C ttcccaatctaggcccttat	386
SULT1C2	4	intron 1 363	gagtggtgtagctagaaagg T/G gatcctgagctctgatttggg	387
SULT1C2	5	intron 1 2300	gggctaactatcagcagccac C/T acctcaggaaggatgacttc	388
SULT1C2	6	intron 2 455	aagacttgaagcaaataga T/G aaaaaaaaaatcgtagaat	389
SULT1C2	7	intron 4 55	caaaatctccaaacacctta G/A aaggaaagaatcttttctt	390
SULT1C2	8	intron 4 111	ctgccttcttaaatggaaca T/C tctcactctcttcaggaat	391
SULT1C2	9	intron 5 1657	ctttgtgttactttgttt T/C acttggtaaaaaagtgtgt	392
SULT1C2	10	intron 5 2082	tctgtcctagagatggagg C/A gtcccacagccacagtgtg	393
SULT1C2	11	intron 6 933	agctactgaacctctccac A/G taactgtatttcaggggcag	394
ST1B2	1	intron1 80	actgttcataaaatcatta C/T cattctaaataaagttaata	395
ST1B2	2	intron 2 -352	aacatttaaatagtcattta T/C agcaatgcacagggtataata	396
ST1B2	3	intron 2 -85	attacataatgctcaaaaat G/A tcttgaaaaactggttgga	397
ST1B2	4	intron 4 460	gtacttgacattaaaaata T/C ctgatgtttatatatccata	398
ST1B2	5	intron 4 470	ttaaaaaatatctgatgttt A/G tatatccataaatagcta	399
ST1B2	6	intron 4 518	tttaagattgtcctcatatt C/G ttacttcttgggttactaa	400
ST1B2	7	intron 4 616	aatgtttatgaaaatagact T/C ttatctggttttagtggcct	401
ST1B2	8	intron 5 58	ctgcatcatgctgtaaaagg G/A ttgatatttgccttccaact	402
ST1B2	9	exon 6 612	taatagaatccaaaggagga A/C atcaagaagatcattagatt	403
ST1B2	10	intron 6 582	aatacattacttccatttaa G/A tagtctgtttattgtggctt	404
ST1B2	11	intron 6 3130	agatgtaaaaaattattcaa A/T ttttaaaagcctgaaaaatt	405
ST1B2	12	3'untranslated region 907	tttaaaagtgtctaaatcaca C/A atctgaagaaataagagatt	406
ST1B2	13	3'flanking region 50	tcagatcccagttttgtcc T/G ttgattctgagtttccaaat	407
ST1B2	14	3'flanking region 328	tttgaccaggacactgtgt T/G ccactgctgtctaccgagtt	408
ST1B2	15	3'flanking region 446	gtagttcagattttggaaat C/A tttttctatatcataccta	409
CHST2	1	5'flanking region -260	agccggacagtccgcccggc G/A gtgatccgggggcccgtccc	410
CHST2	2	5'flanking region -56	gogctggggaccagccgccc C/T gcccgccctggagtcgccc	411
CHST2	3	3'flanking region 218	aggagtgaacacatctttg T/A attotaaaggcagaaaccaa	412
CHST2	4	3'flanking region 383	gcagagaccaatgttttgg G/C ctgaggctggttcagaaaaa	413
CHST2	5	3'flanking region 952	tactgaaacattctgcagaa T/C gttatactatgagaagaaat	414
SULT2A1	1	intron 2 478	ggactgggctctgtacacac T/C togtcttactgtgtgtaaat	415
SULT2A1	2	intron 3 382	caaaacctcttaatatct G/A ttctatctgtctcagaact	416
SULT2A1	3	intron 3 409	tctgtctcagaactgattgc A/G tgactctaggatcgctatat	417
SULT2A1	4	intron 5 249	agctggaaattacaggcaca C/T gccaccacaccagctaatt	418
SULT2A1	5	intron 5 395	aggcatgagccacggcgccc G/A gccaatattatcagctttaat	419
SULT2A1	6	3'flanking region 33	ttccttgttaaaagttacca G/C gggtggccaggcacgggtgt	420

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GENE	number	position	SEQ.	SEQ ID.No
SULT2A1	7	3'flanking region 46	gttaccagggttggccaggc A/G cgggtggttcattgcctgtaat	421
SULT2A1	8	3'flanking region 199	ttagccaggogcattggctc A/G tgtctgtaatcccagcactt	422
SULT2B1	1	intron 2 4162	ttotcccctctcctcaccat C/T cgcacacaggatgatctacat	423
SULT2B1	2	intron 3 879	gagggcatccagctctgggg G/A ctggacctgggggtttgtgg	424
SULT2B1	3	intron 4 3882	ttccacgctccttcccttggc C/T gactgacctccctccgctga	425
SULT2B1	4	intron 5 1780	cctgcagaaggggggtccctt C/T catgtccaagcagtaatggc	426
SULT2B1	5	intron 5 1814	taatggctgcagcatggagc G/A ttgtgggggcattgagacag	427
SULT2B1	6	exon 6 789	ccctcttctccagggtctg C/T ggcgactggaagaaccactt	428
CHST4	1	5'flanking region -1092	atgaagccttgtgccatctc G/A ctgtgtcgtgccagcacctg	429
CHST4	2	5'flanking region -941	ctgccagagagaaacaggaa G/A ggaggaagagccacacaatt	430
CHST4	3	intron 1 -150	caggaaatgatttggaag G/T actggtgccattgttggcac	431
CHST5	1	intron 1 -144	ggcctcttaggtttcagcca A/C gacaggtagctcttagcacc	432
CHST5	2	intron 2 17	caacgtaagagcgcttctca T/A tgtccagctcctttgtttot	433
CHST5	3	intron 2 139	aatcccagcactttggagg C/A ggagatgtgcggatggatca	434
CHST5	4	intron 3 1829	gactgtatgtctgtattca T/C ataggaacaaataattcatg	435
CHST5	5	intron 3 2037	aatgaaaccaacaccaaca C/G tgcagagaagcaaaacaaag	436
CHST5	6	intron 3 2134	aagcagctaaattgtgttc G/A tacagggtgcaattaggcagg	437
CHST5	7	intron 3 2528	atggtaaagtgcctgggt G/A cagtatgtcagcatcctgct	438
CHST5	8	intron 3 2674	gcacttatcctagaaaggcc A/G ttctgaagactcagcagga	439
CHST5	9	intron 3 7039	ctggctcccgcggccaccc T/C gggaccgcagccacgtctga	440
CHST5	10	intron 3 7211	gtagccccaggacacccccca T/G cctcaacatcccattctggg	441
CHST5	11	intron 3 7294	ggagcttccagtggcttggg T/C acccccgactcttctgcat	442
CHST5	12	intron 4 108	gcagggtcctgcactctgca G/A ggggcaatcacagggtgggag	443
CHST5	13	intron 4 402	agcactggaaaaagtacagt T/C gcactttagcggagggtggg	444
CHST5	14	intron 4 547	ctcctgtcccgcattgagg C/G gaaggagcagagggtgagatc	445
CHST5	15	intron 4 1142	gccccagggtctcatagctcc C/G cattggcagtgtctgggattt	446
CHST5	16	intron 5 1187	cactgggcagtaattggggc A/G tgggatgggcagaggggccc	447
HNK-1st	1	intron 1 139	gtgttttggcgacttgaaga C/T ctccctagtctgcgggagta	448
HNK-1st	2	intron 1 1020	acctgagcagaaaaattctct T/C ctctgctgaaatgaaaattg	449
HNK-1st	3	intron 1 1091	aagaatttgtaaacatcaca G/A gcaacttgcaattatattog	450
HNK-1st	4	intron 1 1971	ctataactatttcaaacata C/T gaaacaggcataattggatt	451
HNK-1st	5	intron 1 2096	atttagaatattcatttacc A/C agaaatccaaatataacctg	452
HNK-1st	6	5'untranslated region -91	ctatccagtgcagaaggaa C/A caagaacctcagttcagggg	453
HNK-1st	7	intron 2 -530	agtgggcggaggcgagaagc G/A tcagtgttcattcctttgct	454
HNK-1st	8	intron 2 -466	gctacatcttgcagccagt C/T agaattttaaacacagccag	455
HNK-1st	9	intron 2 -92	acggaaatatttgtgtgat A/T ctactgactgaaatcacct	456
HNK-1st	10	intron 3 152	catggcctccgttccctcat G/A ttacagagggtgtgaggggag	457
HNK-1st	11	intron 3 312	cacagtggccttatgccttg C/T agcagggcgcctctcagggt	458
HNK-1st	12	intron 3 1948	tcctttgatgtatcaagttt T/C gtgtgtaattgtttcagtgt	459
HNK-1st	13	intron 3 2140	ttacacctggagaggagcac C/T gcagcggtccttaatactgc	460
HNK-1st	14	exon 4 187	agaagcacattcctgaggaa C/T tgaagggtggcacagccagg	461
HNK-1st	15	intron 4 581	cctgatcattccctagctgg G/A atgaggggtgcactctggaa	462
HNK-1st	16	intron 4 615	tctggaaggcctctcacttc G/C taacccccattctggatcta	463
HNK-1st	17	intron 5 7	gattgttctaaatgggtgtg G/A tgggtctactgaatgtccac	464
HNK-1st	18	intron 5 123	acctgaagggtactggggc G/T tccagacaggcctgttttg	465
HNK-1st	19	intron 5 721	ataattatgggctctgttta T/C gaaatttagcttcagacagg	466
HNK-1st	20	intron 5 867	tgctgcccacagagtgggtg G/A tcaactcctggcactgtttg	467
HNK-1st	21	exon 6 444	ccaggagcattttcttccat T/C gaggagatccccgaaaacgt	468
HNK-1st	22	intron 6 94	ctgagtctgtacttggcag A/G ttgatcggaggaccacagag	469
HNK-1st	23	intron 6 247	catgaaggtagacatcatttt G/A ttaatagaaattagcaggca	470
HNK-1st	24	exon 7 696	aggaggaaccggacagagac C/G cgggggatccagtttgaaga	471
HNK-1st	25	exon 7 870	gagacctggaggacgatgc C/T ccatacatottaaaaggagc	472
HNK-1st	26	3'untranslated region 1110	tcaaatactttattagacc T/C ggggctaaccagggtgaagat	473
HNK-1st	27	3'untranslated region 1178	ccacacccctccttgagga C/T gcccggtgtctccacaggc	474
HNK-1st	28	3'untranslated region 1393	ggaagcatcacacagcgtta G/A gagccgtttccttcaggtgt	475
HNK-1st	29	3'untranslated region 1452	tgaggttctcctggctagtc A/G ggggtgcttcacccatcact	476
HNK-1st	30	3'untranslated region 1540	gcaagggggtgctgaaatc G/C cagagacttttgacagcatca	477
HNK-1st	31	3'untranslated region 1696	gggtggtgtggtgtccaggg G/A tccatctttccagaatccat	478
HNK-1st	32	3'untranslated region 1829	aggggaggcttttctacct G/A agaaggggagtgtctttgag	479
HNK-1st	33	3'untranslated region 2211	tccagcagtgcggcttctg G/T caacaaggtaggacctgggtg	480

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GENE	number	position	SEQ.	SEQ ID.No
HNK-1st	34	3'untranslated region 2212	ccagcagtgccggcttcctgg C/T aacaaggtagggccctgggtgc	481
HNK-1st	35	3'flanking region 1016	cacacgaagggtgtgcactca C/T ggctgcagggcaccaggt	482
HNK-1st	36	3'flanking region 1152	gcattgcttgcctcatctgga A/G tctccagaagcaggaacag	483
HNK-1st	37	3'flanking region 1291	gccgagaccctcagcaggat A/G gtgcagttacagggctgagc	484
STE	1	5'flanking region -605	caggtttctaaaataataat C/T gaaaggtagtgatgtttac	485
STE	2	5'flanking region -536	taaaattttcaggtctgctt A/G agagttaaaggcaaagagtt	486
STE	3	5'flanking region -231	ccttcttccccaaccctga C/T ggcagacttgggaatttgaa	487
STE	4	5'untranslated region -64	tgcagcttaagatctgctt G/A gtatttgaagagatataaac	488
STE	5	intron 1 69	aaatatagaatgaaaattat G/A tattacaaagctcttaaaaa	489
STE	6	intron 1 311	caatgagaaaaataagcaag C/G aggttagaaggaggtagaat	490
STE	7	intron 1 655	tctaagaaagtagggactat G/A agaaccctatgtatctata	491
STE	8	intron 1 671	ctatgagaaccctatgtat C/T tatatccaccatagttatt	492
STE	9	intron 1 772	aaaaggcaggttggaagatg C/A aggagggagtagtcagaaa	493
STE	10	intron 1 1715	taaccatotttgcttaacctt A/G tcatttttagccaagtcatt	494
STE	11	intron 1 1928	aaatgatacatattcaggaa A/G tcaaaaatctctgacttaga	495
STE	12	intron 1 1953	aaatctctgacttagatacc C/T ggcaataataatcaaatgta	496
STE	13	intron 1 2087	aattttgaaagaaattgaag T/G tctgtggtttttatttca	497
STE	14	intron 1 2323	taggtatgtaggaggtccc G/C ttatatacatagttgttaat	498
STE	15	intron 2 165	tctattccatgaccacaatt T/G ttacctgtaactgaatagt	499
STE	16	intron 2 1707	cctaggacccaacatgagac A/G taatataccatcagtaaaat	500
STE	17	intron 3 850	ggtgtccattccctcaagaa T/G ttatactttgtttacacac	501
STE	18	intron 4 1653	agtaacaggctagtagataa T/C ataaataactgaggccaacg	502
STE	19	intron 4 1899	tacatgaacttagagaatca A/G gtagatcacacaccaaca	503
STE	20	intron 4 1930	cacaccaacaataaaattac A/G cagaatgataaaagaatttg	504
STE	21	intron 5 666	ttctgatcatgtagtaaaa T/C tataaagaaaataataatgt	505
STE	22	intron 5 982	aggcaaaagcagaacctttg A/C ctacacacacattatattat	506
STE	23	intron 7 369	agattttattcctctctctt T/C ttgagttgaagaaataagtt	507
STE	24	intron 7 447	caccttcaagggttaagtgg C/A aaaaaatagaaattcaaata	508
STE	25	intron 7 672	aatcttgcctttgaacctt A/T ctgtcagtgagagtcaggga	509
STE	26	intron 7 856	tgttacagaggacttaaaac A/G gttgtcttgccttgcaaacgg	510
STE	27	3'flanking region 218	cagcctcccaagtagctagg A/G ctacagacatgtgcaacct	511
ADH1	1	5'flanking region -55	atcatgtgtggaactggaat C/T ggtgttattcaagcaaaaa	512
ADH1	2	intron 1 268	acatttgcggtaaagcgata A/G ttattccaagctaattcatg	513
ADH1	3	intron 3 442	aaatggaggctacatggcta C/A ggctgaatgagcatgacctt	514
ADH1	4	intron 6 56	tacaacttggaggatgcatt T/G aggtgcagaatatatgttt	515
ADH1	5	intron 8 74	gtctagcagaaaaatgaaaag G/A tggaaggatgagaaaaatta	516
ADH2	1	intron 2 340	ctatttttaaaagcgtgcat T/C ctacataagacttaaatat	517
ADH2	2	intron 3 91	aaggcaatgagagacgaaag T/G gcttgacacagggtcaccgog	518
ADH2	3	intron 3 205	atgtattgtaccttcaacc A/G ttatgtaccgagtatctact	519
ADH2	4	intron 7 108	acaattgacaaggcaagatt T/C tgaaaacaaatcaaaaataa	520
ADH3	1	5'flanking region -254	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	521
ADH3	2	intron 2 355	tatgcattctctatattat A/G caagacaaaaatttaggat	522
ADH3	3	intron 3 32	acactcagggaaacatgcctt G/A gttcaccatcacaagattag	523
ADH3	4	intron 4 6	ctgcttgaaaaaatgagtaag C/T ttctgatgctttctttgcac	524
ADH3	5	exon 5 453	agcaccttctccagtagac A/G gtggtgatgagaatgcagt	525
ADH3	6	exon 6 815	ttcgtttgaagtcatcggtc A/G gcttgacaccatggtatgat	526
ADH6	1	intron 3 249	tgaacttgacttgaaagta C/A aaatgagacaaaaatttatg	527
ADH6	2	intron 6 1072	taaccctatactgtattgc A/G tcaacttctaacaggcagct	528
ADH6	3	exon 7 885	gtctgtgtggtgttgggt G/A ttgcctgccagtggtcaact	529
ADH6	4	intron 7 1292	gttgagaaacactgcctagt C/A ccgtctgtggtcctagaatt	530
ADH6	5	intron 7 1616	ctatcacagaataatcogca T/C agaactaagcagattacg	531
ADH7	1	5'flanking region -528	tgtgcagacacagaaagttt T/C acttaactttctacacctaa	532
ADH7	2	intron 1 361	tcagtagcatgtgctgact C/T gctgcagtagttcaatggga	533
ADH7	3	intron 3 183	aacctcaacctttagaaggc A/G aaccttacggtgtttataaa	534
ADH7	4	intron 4 76	tgaattgaattaattaatac G/A tgtatttgatgtatcaaaca	535
ADH7	5	intron 6 615	tggcatagcgtaaagagact T/A ggaaaaatggaataaagcca	536
ADH7	6	intron 8 532	aagtctaaccatatacacia T/C ttagtatgccattgtactat	537
ADH7	7	intron 8 651	gctgctattttttcaagta G/A gccacaaaaatttccttattt	538
ADH7	8	intron 8 760	catttttagatgaagaccaa T/G gttgtgaaagcaataaata	539
ADH7	9	intron 8 1207	tctccacatttggctagcc T/C acaggatcatcatattatga	540

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GENE	number	position	SEQ.	SEQ ID.No
ADH7	10	intron 8 1691	tccctcatctcattgcccac G/A ctcattgctttaattcagtc	541
ADH7	11	3'untranslated region 1364	atttacattttgtaaggcta T/C aattgtatcttttaagaaaa	542
ADH7	12	3'untranslated region 1498	gatatagtaaatgcatctoc T/C agagtaatattcacttaaca	543
ADH7	13	3'untranslated region 1584	aaacacttggtatgagttaa C/G ttggattacattttgaaatc	544
ADH7	14	3'untranslated region 1818	aatataaacatagagctaga A/G tcattatcatacttatca	545
ADH7	15	3'flanking region 865	tacatcaaaagaaataaatc C/T aagaaggaataaacacattt	546
HEP27	1	5'flanking region -191	tcagcactctgtgtctagct A/T aaggtttgtaaagcaccaa	547
HEP27	2	5'untranslated region -163	gaacccatcaattccgtaca C/A attttggtgactttgaagag	548
HEP27	3	intron 1 1941	aaatttacccctaaccagcct G/C actctctgccactttctgtt	549
HEP27	4	exon 3 289	ttgtgtgccacgtgggaag G/A ctgaggaccgggagcagctg	550
HEP27	5	intron 4 1070	tgtctcagttcacaggatca T/C gactctttttctcgaaactg	551
HEP27	6	3'flanking region 362	ggctttgtgtgtgtccatt A/G tctgaactgggcctgtctggg	552
L1CAM	1	intron 1 + 767	tttgacttccttacatgggt G/A actgtgtgagtcactctgtt	553
L1CAM	2	intron 1 + 862	gcattgggtcatgtgtatgt G/C tgagtggggtgaatgtaag	554
L1CAM	3	intron 1 + 1332	cagggatgaaggagcagagc C/T gctgagaggccacacaggtg	555
L1CAM	4	intron 4 + 502	ttccctggggttttccott T/C gcattccatccctccctgagc	556
L1CAM	5	intron 18 + 147	agcgacgttatgaaattccc C/A acattcacattttctataat	557
L1CAM	6	intron 24 + 221	ctccttagccccccagaggg C/T cccaactttaagagcactact	558
AANAT	1	5'flanking-542	aggggtgcaggatgggtgt G/T agctggagggcaggggtag	559
AANAT	2	5'flanking-263	ccccccacataagaggtggg C/G ttgtccaagactccgaggga	560
AANAT	3	intron3 39	cgcccagctccaggaggcc T/A ctgaagacagaggtcagcca	561
AANAT	4	exon4 150	cagccggccgtgcgccgggc C/T gcgtcatgtgcgaggacgc	562
ARD1	1	intron1 + 317	ccgtcgggtctgtcggcccc C/G ctccctcggggtgggcagg	563
ARD1	2	intron6 + 322	gtctctcagcatctgtcac G/A ccagggaccacacctctct	564
ARD1	3	intron6 + 1095	aaggctccatcctgagacaa A/C aagtccagtgtgacctgcc	565
ARD1	4	intron6 + 1179	aggaggaagacctgtatccc A/G gggacaccctcctccactcc	566
ARD1	5	intron7 + 159	cctccaggctgctaggcaga C/T ggctcctctaaagcccagc	567
ARD1	6	intron7 + 295	tgaccagccctgccaccga G/T gagccttgggcagaaacctg	568
ARD1	7	intron7 + 416	actaccatggaggccccac G/A acagagcgtgcccttgac	569
NAT1	1	3'UTR 215	aataataataataataaa A/T aaatgtattttaagatggc	570
NAT2	1	exon2 867	cgtgcccaaacctggtgatg G/A atcccttactatttagaata	571
NAT2	2	3'flank 521	ccatccatactttgccacaa G/A agaaggaacatgagctttat	572
NAT2	3	3'flank 573	gatttgaaatcctgtggaca C/T ggggtgaattacttttaaaa	573
NAT2	4	3'flank 918	attttctgtttgtaattcc A/G gtatcagggtatagtttaa	574
NAT2	5	3'flank 979	actattctccctcttcgact C/T gtgatgactataataatctt	575
NAT2	6	3'flank 1958	tacctattgaagtaagccta C/T gtcatatccacctatttgtt	576
NAT2	7	3'flank 2034	ccactgattcccagagctag T/G tcattaagaagacagtcct	577
NAT2	8	3'flank 2201	cagattactggagggtact G/A ttgtctaccaatgcaaatg	578
NAT2	9	3'flank 2818	gggatatttgtctcctttct C/G ccagtgcatgttggaacc	579
NAT2	10	3'flank 3237	atatatattccaattaaaa A/Δ caaaataaatttcgaaact	580
NAT2	11	3'flank 3386	caacaaagagatttttaaa G/A ctttttaaaacaccagacag	581
NAT2	12	3'flank 3660	cagcactattcgcaatagca A/G agatgtggaatcaatctaaa	582
NAT2	13	3'flank 3973	agcagaaaaataaataatg C/T gtactaggcttactacctgc	583
NAT2	14	3'flank 4029	caaaacaaacccccatgaca T/C gagttatctatataacaaa	584
NAT2	15	3'flank 4118	ataagattaatatctgcata C/A aaatctttgtttacagcttg	585
NAT2	16	3'flank 4146	tgtttacagcttggtatata C/T tgaattatgtctgtcccc	586
NAT2	17	3'flank 4279	ttaatctgataggattgtg G/C ctttataagaaaaagaaaag	587
NAT2	18	3'flank 4323	ttgtctctccccagtcag T/G taccaaggaaaggccatgtg	588
NAT2	19	3'flank 4446	tcaattggctttatctgcga T/C tctggaatcaggcaatactc	589
NAT2	20	3'flank 4462	gcgattctggaatcaggcaa T/C actccatttcataaaacaga	590
GZMA	1	5'-flanking -462	cctcagcttgcaattggcct A/G ctaattcttatataatccaa	591
GZMA	2	5'-flanking -172	agcctgcctgtgtggcagtga G/C ccacatccaccattctcac	592
GZMA	3	intron1 1949	gacataaggttctctctatc A/T gcatgtatggtttgccttgt	593
GZMA	4	intron2 + 683	gactgcgtgaccaggtggaa C/T tagcctcagcatggaagggt	594
GZMA	5	intron2 + 1250	gttggtgtagtttatactag G/A ttatgaatgatagccttaat	595
GZMA	6	exon4 + 105	tgccaagttgcagggtgggg C/G aggactcacaatagtgcac	596
GZMA	7	intron4 + 696	atagagccttacctgaagaa A/G ggtgtgcagtatgcattgtt	597
GZMA	8	intron4 + 1141	ctgttcaggaggatccgg G/A ttccaacatggttctttatt	598
GZMB	1	5'flanking + 529	gcctccgtctcacaccaaca A/G gcagatttccccaccacggc	599
GZMB	2	intron3 + 141	gagggaagattgtgcagccc C/T atcactgttcggggcccag	600

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GENE	number	position	SEQ.	SEQ ID.No
GZMB	3	3'flanking + 448	ttttcagggcctgtccctcc G/A atgggggcaggcttctccca	601
ESD	1	5'-flanking -333	gtcttgggacagaggagtg G/A gggagttgaaattaggccct	602
ESD	2	intron 1 603	gtcatttctgatggggtcat C/T agggaaatgggattgagcgc	603
ESD	3	intron 1 717	tgtgtggtagaagcagcatt C/T taagcactacgtgaattaac	604
ESD	4	intron 1 1864	gctttcatgcaggattgatc G/C tagtgggatgtattaggaag	605
ESD	5	intron 1 2389	ttttgggaacacctgtctag G/A tgtaagagccagtgggaata	606
ESD	6	intron 2 21	taaaactgttttattgttta T/C atgttactctgaacattgaa	607
ESD	7	intron 2 588	taaaattagtagtctctct G/A taagttcattatttaagata	608
ESD	8	intron 2 1498	tagaaaaatgtgtatcacac C/T gtaagtgttcagtaattgta	609
ESD	9	intron 3 92	ctttatctagatattatagt C/A cctcattttacttttaact	610
ESD	10	intron 3 422	gtaaagagattaaacacaca C/T gcacacatacatatacctat	611
ESD	11	intron 3 581	agaaaacctgagaaatgaca C/T aatttatttaagccatagt	612
ESD	12	intron 3 2270	gccagtaattacatgtagcc G/A ttacatcaaattagctaatt	613
ESD	13	intron 3 2951	taatgaaagtaaattgttca A/G ctccctaacaaaagttaa	614
ESD	14	intron 3 3001	aaatgtcagaaatttttgt G/A ccgtcagtcacacaagaa	615
ESD	15	intron 3 3096	aaggagcatacagaaaactt G/C ccatgatggggcctttgtgg	616
ESD	16	intron 4 2611	tctaatagtccccagtatta A/G tgggtcacatcttcatgtcc	617
ESD	17	intron 5 390	tctttttcatctctgttaa C/T atcaaccatacagttaaaca	618
ESD	18	intron 7 107	ttagtattggaactaaactt T/C tctagtgttgagaactttgg	619
ESD	19	intron 8 1090	aaattctaactaattaaagg G/T ttcactcttagtaactaga	620
ESD	20	intron 8 1651	tataaagtgtgttaataa A/G tatatatgaataagaattat	621
ESD	21	intron 8 2047	agaaggaaaaaggccatttt G/C ttaagaatccctgagatag	622
ESD	22	intron 9 -3490	atagaaggagaggctatact A/G cctccttaagtctcaggacc	623
ESD	23	intron 9 -2596	actaaggataaaaatatggc A/G tactcagtcacattggaact	624
ESD	24	intron 9 -666	aggccttaatgacatatttc T/C cctcacataaagatacaaca	625
ESD	25	intron 9 -660	taatgacatatttccctca A/C ataaagatacaacatgcttt	626
ESD	26	intron 10 799	tatggtaactgaagaaatg A/G cattaagttcctaaagttat	627
DDOST	1	intron2 629	attctgttaagaagttctta T/C attaagaaattgtctcct	628
DDOST	2	intron2 3125	gagaatataggagcttctgc G/A tatgcoctgaaagtcagtcag	629
DDOST	3	intron2 3920	attactcatttaataaataa A/G tggattactgagcactgtct	630
DDOST	4	intron3 189	actgctgtccaggggtccat C/T tggggctgagcccagctgga	631
DDOST	5	intron6 185	ctgtcctctgttcgggagg C/T gtggcagcttttcccttact	632
DDOST	6	exon8 37	aactatgaactagctgtggc C/T ctctcccgctgggtgttcaa	633
DDOST	7	intron9 37	tcctgccccagaatgctgcc A/Δ aaaaacggccccaggcctca	634
MGST1	1	5'flanking - 5	tctggaccctgaacaggagg G/C gacatcgtgacaaagcaaat	635
MGST1	2	intron1A+330	atcagcaggcgatgtgttact C/G tgggogggtaaatcagggtga	636
MGST1	3	intron1C+1428	gtaaagggaaagggcggtcc T/A caactgagaagtgaagattc	637
MGST1	4	repeat	attatttgcctacctcagg G/A ttttcgggtcaagcgagat	638
MGST1	5	intron1C+2914	ctcatcagggtgtgtgcaga G/T ggcttgggtgctggccagtct	639
MGST1	6	intron1C + 4274	attgtaatagattaacaaag G/T tgatgaaagtagtgacata	640
MGST1	7	intron1C+4276	tgtaatagattaacaaagtt T/G atgaaagtagtgacataat	641
MGST1	8	intron1C+4306	gtgtacataatgtacatagt A/G tagttgaacacatagcaagc	642
MGST1	9	intron1C+4406	gatggctatatgaccaataa T/A gatacatataaatgtataga	643
MGST1	10	intron1C+4464	agaaagattgcagctgatag A/G tgcaggctaataaggacac	644
MGST1	11	intron1C+4683	aatggcagaggactggaaat G/T tacattttaagctttaccc	645
MGST1	12	intron1C+4767	gccttcctcttcagcacatt C/T ccaattatacttccaattcc	646
MGST1	13	repeat	atttcaatttttttttgg G/A gggggagacagagtctcact	647
MGST1	14	repeat	aattacctcccaaaggcctc A/T tatccagatactatcacat	648
MGST1	15	intron2+2379	ttctcaaatttcattatata C/G tattcttcaacccaaagttt	649
MGST1	16	intron2+2767	tttaactatagatgccttct T/G ctctcttgtgtttgattta	650
MGST1	17	repeat	tcactgcagcctcaacctct C/T gggctcagggtgatcctcaa	651
MGST1	18	repeat	aaaaaaattttagatatgg T/G tactccctatgttgccagg	652
MGST1	19	repeat	ctccctatgttgccaggct A/G atcttgaattcttgggctca	653
MGST1	20	intron3+1495	gtcagacaatggccttcagc G/A tctctctttgcagaatatg	654
MGST1	21	intron3+2528	ttttggagacacttttcaga G/C agagcgtttccagcatcttc	655
MGST1	22	intron3+2567	tccctttccatttttaagtt A/Δ gacttttttttccacctct	656
MGST1	23	intron3+2731	atacacatatggaacaatta A/C ctaaaaacttaaggtaatat	657
MGST1	24	intron3+3288	gggtttatagtttcccccc C/Δ tccccgcccccaaaagaccc	658
MGST1	25	intron3+4288	ccattctatttgcactgc G/A taacacaggcgtagaagtg	659
MGST1	26	intron3+4378	aaatgtctgtccttttggca T/C gttgtgaaggagaacactaa	660

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GENE	number	position	SEQ.	SEQ ID.No
MGST1	27	intron3+4429	attggaggtgacgatatctc T/C gtgatgctgggggagaaatc	661
MGST1	28	intron3+4817	attgctatagaagagagtaa C/T gtaaagcagaaatagttttc	662
MGST1	29	intron3+6077	tttgaaattagtgtctttaa T/C agttatctttttccacagag	663
MGST1	30	exon4+304(3'UTR)	aagaattctgtacttccaat T/G tataatgaatactttcttag	664
MGST1	31	3'flanking+1581	tctgtgtgcatgaacatgca C/T gcggtgcacgcgcacacacac	665
MGST1	32	3'flanking+1729	tatgtggagcaatttgaaaa A/T agtatattctaagccattaa	666
MGST1	33	3'flanking+3407	ggatcactgctaaagatccc G/A gagtcaactccatgtcccagt	667
MGST1	34	intron1B+36	ggagaaggggaccgcacatgca G/A aggggtggcaggcaggaggagg	668
MGST1	35	3'flanking+25	gggtaaaccattttgaata T/C tagcattgccaatatcctgt	669
MGST1	36	exon4+266(3'UTR)	aaagaaaatcatacaactca G/A catccagttggctttttaag	670
SULT1A2	1	intron 4 1728	tcagcttctctctttgccaa A/Δ ccaagagatgagctggcctg	671
SULTX3	1	intron 1 6415	tgacctctccctgttagtgt G/Δ ggggcagctctttccagtgt	672
SULTX3	2	intron 5 2457	gcccttaaagggaagttcat C/Δ cttctctgccttccaggctc	673
PIG3	1	5'untranslated region-93	tcogcogaggatacagcggcc (CCTGY)n cagacaatatgttagccgtg	674
ADH2	4	intron 7 + 108	acaattgacaaggcaagatt T/C tgaaaacaaatcaaaaaataa	675
ADH2	5	intron 3 +(1721-1723)	actgcatagaaatttaagaa GAA/ Δ cttgtttattcctctccag	676
ADH2	6	3' untranslated +(2305-2306)	gttaatgctttccactctc AG/Δ gggaaggatttgcattttga	677
ADH5	1	5' flanking - 115	taactgctgtaaagttacac G/A gggaagcccttcccgcacaa	678
ADH5	2	5' flanking - 114	aactgctgtaaagttacac G/A ggaagcccttcccgcacaa	679
ADH7	16	intron 8 + 727	ttcagatccctgtaagccag G/A tattatttttaccattttta	680
GSTM1	1	5' flanking - 694	tacgaagtggctaatttaca C/T agtacttagccagatgaccg	681
GSTM1	2	5' flanking - 661	gatgaccgaaggactcagta C/T ccgagggcccctaacagaaaa	682
GSTM1	3	5' flanking - 658	gaccgaaggactcagtaccc G/A agggcccctaacagaaaaaca	683
GSTM1	4	5' flanking - 656	ccgaaggactcagtaccca G/A ggcccctaacagaaaaacaca	684
GSTM1	5	5' flanking - 537	tagaggggagactaagccct G/C ggagtagctttcggtacaga	685
GSTM1	6	5' flanking - 525	taagccctgggagtagcttt C/G ggatcagaggaagtcctgct	686
GSTM1	7	5' flanking - 465	aattaaattcccaggttggg G/A ccaccacttttagctgtac	687
GSTM1	8	5' flanking - 383	gocgagagaaggctgaggga C/T accgcgggcaggaggaggagaa	688
GSTM1	9	5' flanking - 382	cggagagaaggctgaggga C/T ccgcgggcaggaggaggagaa	689
GSTM1	10	5' flanking - 378	gagaaggctgagggaacccg C/T gggcaggaggaggagaaggag	690
GSTM1	11	5' flanking - 343	agggagaagagctttgctcc G/A ttaggatctggctggtgtct	691
GSTM1	12	intron 2 + 118	tgctggagctgcaggctgtc T/C ctccctgagccccgggtgag	692
GSTM1	13	intron 3 + 233	agtgagtgcccggtctctc T/C ctgctcttgcttatgggaag	693
GSTM1	14	intron 4 + 26	tgtgggtggctgcaatgtgt G/A gggggaaggtggcctcctcc	694
GSTM1	15	intron 5 + 140	actatcagcagttattctca C/T gactccaatgtcatgtcaac	695
GSTM1	16	intron 5 + 577	ctgccacccattagaagga A/G ctttctactttccctgagct	696
GSTM1	17	intron 5 + 645	gctggtctggatccagaggc T/A gccaggtgcttggcgctcc	697
GSTM1	18	exon 7 + 519	caccgtatatttagcccaa G/C tgcttggacgccttcccaaa	698
GSTM1	19	exon 7 + 528	tttagcccaagtgttggga C/T gccttccaaatctgaagga	699
GSTM1	20	intron 7 + 2421	cagcaccgttagaatcttc A/G taagtgttagctgttactgt	700
GSTM1	21	3' flanking + 42	atttgcctctggccatctac C/T cagactgtctgtctgtctgt	701
GSTM2	1	intron 1 + 7	ggaacatccgcggggtgagc C/G agggccgctggcggtggg	702
GSTM2	2	intron 1 + 45	gggacgggggtgcgtggggg C/T ggggaagtgtggagcagctg	703
GSTM2	3	intron 3 + 70	gactgcatctcctctcccca G/C cttagaggtgttaagatcag	704
GSTM2	4	intron 3 + 224	agcaggccctggtctcctct T/C tgccctgcatatgggaagg	705
GSTM2	5	intron 5 + 100	ttgattcctctggtgagtt C/A ttggtcttgctgactctaag	706
GSTM2	6	intron 5 + 341	tcctcttggtgggttcattg T/C ctggctggcttcaggagtga	707
GSTM2	7	intron 5 + 696	accttagctagacacagag C/T gctgatttgcatttaca	708
GSTM2	8	intron 5 + 723	ttgtgcatttacaatccttt A/G gctaggcagaaaaagttctcc	709
GSTM2	9	3' untranslated + 1006	ctcagccccgagctgtcccc G/A tgttgcataaggagcagca	710
GSTM2	10	3' flanking + 139	ttctgctggcatagtaagg C/T gottgagaattcttgcctcc	711
GSTM3	2	5' flanking - 144	ccaacgccgcatagctgc G/T cctgcgcacggccctgtgga	712
GSTM3	3	intron 7 + 165	agcctaacttctataccttg A/G aggcactgtctacaaaaaaa	713
GSTM3	4	intron 7 + 257	ctgttgactgggtgggtgc T/G ttataagattggtgtatttt	714
GSTM3	5	exon 8 + 91	cccagtggggcaacaagcct A/G tatgctgagcaggaggcaga	715
GSTM4	1	intron 4 + 67	ttggctggattgggtgcta T/C gctcagagtgtgtgtgtt	716
GSTM4	2	intron 7 + 77	gatgotttcccagtcctgga T/G ctgcataaagaataacttgc	717
GSTM4	3	intron 7 + 80	gctttcccagtcctggatct G/A cataaagaataacttgcatt	718
GSTZ1	1	5' flanking - 546	agcaggggcccaccagccgac C/A gcctcgaagcgccgtgagcc	719
GSTZ1	2	5' flanking - 321	tgtctgaccagccgccccgc T/C aaggagtcacaagagggcag	720

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GENE	number	position	SEQ.	SEQ ID.No
GSTZ1	3	intron 1 + 2890	aaaatactgcatcaaaacca G/A gccacgctctgttggggga	721
GSTZ1	4	intron 1 + 2896	ctgcatcaaaaccaggccac G/A ctctgttggggggacaccaa	722
GSTZ1	5	intron 2 + 255	tctcccaacactgctctcca A/G agccccttggcaaccatgtt	723
GSTZ1	6	intron 2 + 1560	caccactgtttaaggccctg G/C gggggcagagttaaacacaa	724
GSTZ1	7	exon 3 + 94	ccttgaaaggcatcgactac G/A agacggtgcccatcaatctc	725
GSTZ1	8	intron 4 + 297	agaaggaggagtttctggc C/T ctgtccctctgttccaggg	726
GSTZ1	9	intron 6 + 94	tatctgaaccagcctccag G/A ctgcttgggcctgacagt	727
GSTPi	1	intron 1 + 269	ctccccgggctccagcaaa C/G ttttcttgttctgtcagt	728
GSTPi	2	intron 2 + 134	ccccgggcctccttctgtt C/T cccgcctctcccgccatgcc	729
GSTPi	3	intron 5 + 438	gtgtgtgcgctgcgtgtgc G/A tgtgtgtgcgtgtgtgtg	730
GSTPi	4	intron 6 + 162	cccgctggctgagtcctag C/T cccctgcccctgcagatctc	731
GSTT1	1	5' flanking - 103	taaagagtgtccaggcgtc C/T gtgccgccaatggggcaca	732
MGST1L1	1	5' flanking - 105	tgctgccgctgccgtggggc G/A gggcgtgggcgggtgctggct	733
MGST1L1	2	intron 1 + 277	agtgtctgtgagagaagcag G/A ttctggagggtggagtgtgg	734
MGST1L1	3	intron 2 + 8030	ggggttatacagagccctc C/G gccccaccacacatatgca	735
MGST1L1	4	intron 2 + 8499	gtatggcaggagtggggctc C/T ggcaagccatagaggtatgg	736
MGST1L1	5	3' untranslated + 468	cgccacctgtgaccagcagc T/G gatgcctccttggccaccag	737
MGST2	1	5' flanking - 46	ggtcagcattcaaaagtcaag A/T agcgccatttatcttccgt	738
MGST2	2	intron 1 + 176	ggtcacccatgccgcctgct A/C cctccttcccaggggcaag	739
MGST2	3	intron 1 + 204	tcccaggggcaagcagagac T/C gagaacattccagagattag	740
MGST2	4	intron 1 + 373	ttacaagtgttccaaaggaa A/T cgtgcctgcttctaaacctg	741
MGST2	5	intron 2 - 3245	cctcgtgattgcccacctc G/A gcctcccaaagtgtgggat	742
MGST2	6	intron 2 - 1998	aggccgaggtgggcggatca T/C gaggtcaggagatcgagacc	743
MGST2	7	intron 2 - 1640	tgtttattccttgcatagcc A/G taatataaagtatgaatttt	744
MGST2	8	intron 3 + 41	actgtgttctaattgatgact A/G tgatgcttaaacgattaagg	745
MGST2	9	intron 3 + 453	atcagagtgtctatgttgacag A/G tatatgaactttggcttcat	746
MGST3	1	5' flanking - 520	acaaaaaggccctaacagcg A/C taaatccattcacttcggga	747
MGST3	2	5' flanking - 355	cgccataaacgcctacggtg G/A ctctgctggggacaaattat	748
MGST3	3	5' flanking - 234	ctgggggagtagatatatgt T/A ttgagaatgagaggagtaa	749
MGST3	4	intron 1 + 74	agcctttgcgcaggcactcc C/T atattcagcctatgcgagc	750
MGST3	5	intron 1 + 682	agaaaatgcccttctttat G/C tgggtggcagcacggagcc	751
MGST3	6	intron 1 + 832	cgagtttacaagctacataa T/C agcgtcgggggcaagtaagt	752
MGST3	7	intron 1 + 1919	aataaaattcctgagtttct G/C tcaactgctcttacagtacc	753
MGST3	8	intron 1 + 1991	tgtaattaggcaacaggaaa A/G ttgtactatcttcaaatgc	754
MGST3	9	intron 1 + 4458	tcttccatcctcctaacata T/C agttagcttccactctccaa	755
MGST3	10	intron 1 + 4676	tgaatatgcaatgcaattgt C/G gggggatagttacttttcat	756
MGST3	11	intron 3 + 278	cagcatgacctatctaaacc G/C atgtgactctcccaggcct	757
MGST3	12	intron 4 + 423	cttgcccttttgttgggg T/G gtgggtggtcacagagaag	758
MGST3	13	intron 4 + 506	gtgcagagaagaaaaaaaag T/C ggggaagggtggaaggggat	759
MGST3	14	intron 4 - 162	tcacagatattttatttcc C/T gactgaaactaacttaattc	760
MGST3	15	intron 4 - 130	acttaattctacctaattg C/G gtggggagtagttggccaaa	761
MGST3	16	intron 4 - 105	ggagtagttggccaaatcat C/G aaattgttaacttttgcta	762
MGST3	17	intron 4 - 65	aacatattgttaatacaacc C/T taggtgttaaaaaaggtttg	763
MGST3	18	intron 5 + 105	atcccagcactttgggagggc G/C aaggcaggcagattgcttga	764
MGST3	19	intron 5 + 197	aaaaaatacaaaaattagcc G/A gatgtgtggtgcacacctg	765
MGST3	20	intron 5 + 222	tgggtgtgcacacctgtagt C/T ccagctacttgggaggctga	766
MGST3	21	intron 5 + 374	tcttatgctactatattttt T/C ttcttgggaatttgagaaaa	767
MGST3	22	3' untranslated + 517	atgaactacctttatttcca G/T ttacattttttctaaata	768
MGST3	23	3' flanking + 166	agtctgattgtggtgatgta G/T gtatagtcacacagtgta	769
GSTA1	1	5' flanking - 266	ttgcaaaaagagcaaaatct C/A ggtgaaatgtattgtgtaaa	770
GSTA1	2	intron 2 + 1220	gagacacaggctttcctaag A/C tatgacaacaccataactag	771
GSTA1	3	intron 4 + 1813	aaaggcaccactggagggtg A/C attattttgccatcacctga	772
GSTA1	4	intron 5 + 732	gaagagtgttgcatagaagg T/C ggagtcactgcccaaggag	773
GSTA1	5	intron 6 + 333	ttatcccatatgtgccaca A/G tgagccggtctgagcagagc	774
GSTA1	6	3' flanking + 412	ctttcttatgcatttgcaaa A/C caatgattctgtctgtgtg	775
GSTA4	1	intron 1 + 280	gcattggtggaagggtgggt C/T ggatcgtccccgggcctggc	776
GSTA4	2	intron 3 + 176	ggaaatcacttctattcaa T/C agttccataaaagctggccg	777
GSTA4	3	intron 4 + 94	acaccacatttactttatgt C/G ttacatagttagttagatca	778
GSTA4	4	intron 5 + 1062	cacactgtgcacatgcaga C/T acccatggcatccaagagt	779
GSTA4	5	exon 6 + 487	cagatgtgattttactocaa A/G ccattttagctctagaagag	780

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GENE	number	position	SEQ.	SEQ ID.No
GSTA4	6	intron 6 + 595	tgagctctgagagcaaatga G/A agatgttagcacccctaaaca	781
GSTA4	7	intron 6 + 630	taaacatcaccocaaaggat T/A cctaccattctccttctgag	782
GSTA4	8	intron 6 + 3943	tcttcgtatgtatctaatacc T/C ttttggtagccttaaagtt	783
GSTA4	9	3' untranslated + 1099	taataacaaccgaatgtcta G/A taaatgactctcctctgagc	784
GSTA4	10	intron 5 +(370-371)	gttgtcgaacagctgtctca (TA) gctgacatcctccctgataa	785
GSTA4	10	intron 5 +(370-371)	gttgtcgaacagctgtctca gctgacatcctccctgataa	786
NDUFA1	1	5' flanking - 1437	agggtctaaaaatcctgatta T/A acctaccttgaagcttttaa	787
NDUFA1	2	intron 2 + 3071	aataaaagtacatggcatat C/A ttgtatgggaacagacttgt	788
NDUFA1	3	3' flanking + 1218	aactccatgtgtataaagca A/G caccacagatgacacttcca	789
NDUFA1	4	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgaccttttactttt	790
NDUFA1	5	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgaccttttactttt	791
NDUFA2	1	intron 2 + 1087	aacatacaaaaaattagccgg A/G tatggtggcgggcacctgta	792
NDUFA2	2	intron 2 + 1089	catacaaaaaattagccggat A/G tggtggcgggcacctgtaat	793
NDUFA2	3	intron 2 + 1356	ttccctgaaacaaccattg T/C ggccatccagaatcagccaa	794
NDUFA2	4	3' flanking + 467	cacagcctcatgggtcagcc C/T actccagagggtgcattccc	795
NDUFA2	5	3' flanking + 744	ggaagcagggggcctggcca C/T agccgctggcagtaagcagg	796
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa (ACAC) aaagatcataacaatagcta	797
NDUFA2	6	3' flanking +(844-845)	tatagtctacaaagaatgaa aaagatcataacaatagcta	798
NDUFA3	1	intron 2 + 2656	tccctgctgccctccctgc G/A cactttatcttcccttgcc	799
NDUFA3	2	exon 4 + 241	aggggcccagcctggagtgg C/G tgaagaaactgtgagcacct	800
NDUFA3	3	3' flanking + 1019	tccttacctgcactggcacc A/G gctctggagccccagtcct	801
NDUFA5	1	intron 3 + 2155	agactctagcatggtacctg G/C aacataaggctccttagaaa	802
NDUFA5	2	intron 3 + 2493	ggcatattgctagttttctc G/T gtctcaatttcacatctat	803
NDUFA5	3	intron 3 + 2712	acaaattttgaactgttcac C/T taacacaggctttttctgaa	804
NDUFA5	4	3' flanking + 1296	aggtatctaaaaggattgac A/C atttggtcattggttcttc	805
NDUFA5	5	intron 3 +(30-31)	aagtcagttttgtgtcttg (GATTTGTGGTATCCAG) tgtaa catttaaccaaaaaa	806
NDUFA5	5	intron 3 +(30-31)	aagtcagttttgtgtcttg tgtaa catttaaccaaaaaa	807
NDUFA5	6	intron 3 +(427-428)	attaagtagcagtaataaa AG/Δ tctagactgctgattcatac	808
NDUFA5	7	intron 3 +(4733-4734)	tataggaattttaaaatata TA/Δ ggatattgaaacattcagtt	809
NDUFA6	1	5' flanking - 1148	tttataatttatatgtta C/T gtgctttctttgtatagct	810
NDUFA6	2	5' flanking - 363	actaccaaggagcgcgggg G/A cagcggatagcaggacgct	811
NDUFA6	3	exon 1 + 26	ggggagcggcgctccgccaag C/T tacttctaccgccagcacct	812
NDUFA6	4	intron 1 + 1318	attcagcagtttgaaaacat A/G atgtttgctggcagaatac	813
NDUFA6	5	intron 2 + 562	agttaaagaatctgaaaagt G/C tcagaaatgattaccctga	814
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatggggatgctga (T) ggtacctacctgacctatga	815
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatggggatgctga ggtacctacctgacctatga	816
NDUFA7	1	5' flanking - 731	accaaccaaaaggcttatcaa A/G ggggtgtcctctttgcaccc	817
NDUFA7	2	5' flanking - 434	aaagggaaaccatcagaaccc C/T gtgatgaaatgagaatcggc	818
NDUFA7	3	5' flanking - 395	gctcccggttccggctggc A/G ggggttagggcagggttagag	819
NDUFA7	4	5' flanking - 100	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	820
NDUFA7	5	intron 1 + 92	tcacctccctcctaagccgg G/A acccttcgctctcccgaaat	821
NDUFA7	6	intron 1 + 133	ctccctgggaacccccagct A/C gtcaccccttcagccgggga	822
NDUFA7	7	intron 1 + 136	cctgggaacccccagctagt C/G accccttcagccgggaccc	823
NDUFA7	8	intron 2 + 89	tccttagaccctgaaacg G/C agggctgacatcctgccacc	824
NDUFA7	9	exon 3 + 196	gccgccgggaatctgtgccc C/G? cttccatcatcatgtctcg	825
NDUFA7	10	intron 3 + 4203	gcctccacccctggggcgcc T/G cctccatcacccacccctcc	826
NDUFA7	11	intron 3 + 4604	gggcottgtgtacgtggag A/G ccaaaagtgggaaggaggga	827
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtcccctgct (CAGAGGCT) aacactggccg aagagaaag	828
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtcccctgct aacactggccgaagagaaag	829
NDUFA7	13	5' flanking - (1240-1239)	tgatagagccctgatccacc CA/Δ ctctctgaaacttcttctgct	830
NDUFA7	14	intron 2 +(4142-4143)	cattttgtgactgaggtagc AG/Δ gggcccacagcggggccatg	831
NDUFA8	1	intron 1 - 75	tttgtttctctattctgac C/T cgcattgaggtaaagctgaga	832
NDUFA8	2	intron 2 + 790	caaacctagacaaagtgtgc C/T ctttatccagaagtgagcag	833
NDUFA8	3	intron 2 + 900	ttcaggagataaaaagctct G/A attgctcaggcctgagatgg	834
NDUFA8	4	intron 2 + 3837	gaagttgtcttgaagttag A/G taagaatatgtactacata	835
NDUFA8	5	intron 2 + 3942	tcattgttttgcaaagagat G/T cccctaaccagctttctt	836
NDUFA8	6	intron 3 - 66	gaggagacaccaggaggcgc A/G ttgatggttacagattctc	837

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GENE	number	position	SEQ.	SEQ ID.No
NDUFA8	7	3' untranslated + 520	tttatttctggaccaagtaa A/G gatgggtcogtggcccacac	838
NDUFA8	8	3' flanking + 367	gtcatacaaggggagcctcc A/G ggatagaagtgcagaaactt	839
NDUFA8	9	3' flanking + 777	attcttttttcaactactagg C/T tgttctccacatctgact	840
NDUFA8	10	3' flanking + 1053	aaagaaaaagcactgtgtga T/A ctgccatggcgcgttctgca	841
NDUFA8	11	3' flanking + 1190	gattctctaataaaaaataa G/T acttttttttgcattttttt	842
NDUFA8	12	intron 2 +(449-453)	ggtoattgtgcatgatacttaa (GTAAA) aaaaaactaagctgtgtaat	843
NDUFA8	12	intron 2 +(449-453)	ggtoattgtgcatgatacttaa aaaaaactaagctgtgtaat	844
NDUFA8	13	intron 2 +(707-708)	ctcattttggaaagactctc (A) acottgctgtaccaaaaatg	845
NDUFA8	13	intron 2 +(707-708)	ctcattttggaaagactctc acottgctgtaccaaaaatg	846
NDUFAB1	1	intron 1 + 8451	cagcaccctgtagaggcctc G/A ggatgctgaagatgccatga	847
NDUFAB1	2	intron 1 + 8495	gacacaggcattctgcagac G/A ctgacaatttttagtggcag	848
NDUFA9	1	5' flanking - 807	gatggctctttgtagaacaa T/G gcagattctcaaagggtgacc	849
NDUFA9	2	5' flanking - 769	accacagttaaagaaaaaat T/C acaagccattgcgctagaga	850
NDUFA9	3	5' flanking - 353	cacaccctattttggtttct C/G ttctccacttttcccctcgt	851
NDUFA9	4	5' flanking - 322	ttcccctcgtttctgtcccc C/T ctttctctctcctgggccc	852
NDUFA9	5	intron 1 + 447	attcatatgagcacaatgga A/G atgataatattacaatacca	853
NDUFA9	6	intron 1 + 1039	ggcttgatgttcagcctgag G/A caagaattaggagtgttttag	854
NDUFA9	7	intron 1 + 4010	aatgtatccaaaagagattc T/G cattcctgccatgaagaa	855
NDUFA9	8	intron 3 + 49	gacaaatataaattactaag G/A tcatttttaggagtgtatagg	856
NDUFA9	9	intron 3 + 107	aatttcttcccagaatggac C/T aaaggcatcctctgttccca	857
NDUFA9	10	intron 3 + 1183	atctctggtaattattcatac A/G gattatttgaatcccttta	858
NDUFA9	11	intron 3 + 1395	attcctagttctttgtccct C/T aagttgttggtcacottgt	859
NDUFA9	12	intron 3 + 2363	agaaaatagtcataatggc C/T ccaactaacactagtcttta	860
NDUFA9	13	intron 3 + 2608	gtcatttgattacctgagta A/C agtgtactgttacctgtttg	861
NDUFA9	14	intron 4 + 561	attttataaattctttgatg A/C ctgggggtcttattcaact	862
NDUFA9	15	intron 4 + 860	attgtgtagagtaatgacag C/T agagctgtcaacttttttaa	863
NDUFA9	16	intron 4 + 879	gcagagctgtcaactttttt A/T aaaaaataatttttagcttaa	864
NDUFA9	17	intron 4 + 893	tttttaaaaaaataatttt A/G gcttaaaaaaattaaaaatt	865
NDUFA9	18	intron 4 + 1090	atcattgctgtttaaaagt T/C aagtagtgtgaatttcagta	866
NDUFA9	19	intron 4 + 1188	aaccaatccttttattttt A/T tcttcagaaactttgattt	867
NDUFA9	20	intron 5 + 161	gggtgtgtgtgatgtttga C/T gttttgattgattgccttct	868
NDUFA9	21	intron 5 + 373	ctttctacccccttgactg C/T agtggttttgtgccactctt	869
NDUFA9	22	intron 5 + 457	gccagggaagatgcctattc A/C cacagtgccttatgctcctt	870
NDUFA9	23	intron 5 + 3113	gatttttctccttcttcaat G/A taagcttcccttaaaataaa	871
NDUFA9	24	intron 5 + 3339	tctaaactcaaaacagggtt G/A ttgggtattgtttaggctg	872
NDUFA9	25	intron 6 + 414	tatagttttgccttttccag G/C atattacatatatggttaga	873
NDUFA9	26	intron 6 + 518	ctttcatttcttttcatagc T/C tgatagctcatttctttata	874
NDUFA9	27	intron 7 + 974	ggattatgcgtacttggaaa A/G tacttggatagcgggtgatta	875
NDUFA9	28	intron 8 + 368	acattaattttagtgagta T/G cacaatgcctccagaggctg	876
NDUFA9	29	intron 8 + 954	gcatgcaatcagttatata T/C ctgataagaattacaattc	877
NDUFA9	30	intron 8 + 1253	tcctcttgaaattgtagata G/T gtatctacacatttctcatc	878
NDUFA9	31	intron 8 + 11608	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	879
NDUFA9	32	intron 8 + 11930	ctacaaatatattctaaatg C/T gtaatcatggataagtacaa	880
NDUFA9	33	intron 9 + 1998	tgtttttcaagcctttaaac G/A gctgtggaacctgtgtotca	881
NDUFA9	34	intron 9 + 2238	ccagctacttgggaggctga A/G gtgggaggatcacttgagcc	882
NDUFA9	35	intron 9 + 2885	acagcggctgtcttctctgc A/G gttctcataggctagcttac	883
NDUFA9	36	intron 10 + 801	tacactaaagtgtctcttac G/A ttatacttgagaaagtgtt	884
NDUFA9	37	intron 10 + 910	tgcagactttcagggtggta G/C gatgagggtgtgtgtgtgt	885
NDUFA9	38	intron 10 + 1180	aaaactgagtcagaacgccc G/A tgctcagaaaaacaggggct	886
NDUFA9	39	3' flanking + 554	gtgccagcacttaggaatta T/G gaccttctaataagttctt	887
NDUFA9	40	5' flanking - (1129-1128)	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	888
NDUFA9	40	5' flanking - (1129-1128)	taaacagtaggggcaagata gagtggaaacagccaagatt	889
NDUFA9	41	5' flanking - 341	tggtttctcttctcacttt T/Δ cccctcgttttgtcccccc	890
NDUFS1	1	5' flanking - 3	tcctagggggtcgtgtgtgt C/G cagacagtttagcagaacag	891
NDUFS1	2	intron 1 + 445	gtgttagcaatggctcacgc T/C totgtttgtgtccttgttt	892
NDUFS1	3	intron 1 + 470	tttgtgtccttgtttgttt G/T gtccattgaccacgttggac	893
NDUFS1	4	intron 1 + 502	acgttggacagcattttttt A/G ttctttaactaacgggaaa	894
NDUFS1	5	intron 1 + 557	tttgaaaagtttagcccagg A/G ttgcattgcaaataacaaaa	895
NDUFS1	6	intron 1 + 5218	tatctcagaatatctcagga A/G catttagtagacagctatgc	896
NDUFS1	7	intron 3 + 1371	aagccctaaaatagatagtg T/G caatgggaatgaaaacaaga	897

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GENE	number	position	SEQ.	SEQ ID.No
NDUFS1	8	intron 5 + 414	ttttgaaacgaggtctcact A/G tgttgtccaggctgggcttg	898
NDUFS1	9	intron 10 + 812	gagtgcgggtggcgcgatctc G/A atctcgggtcactgcagcct	899
NDUFS1	10	intron 11 + 233	ggaggccaaggcaggcagat C/T gcctaagtgcaggagtttga	900
NDUFS1	11	intron 11 + 283	ggccaacatggcgaaacccc G/A tctctactaaaaatacaaaa	901
NDUFS1	12	intron 11 + 585	ctgtatgtcttaattttaaa G/T taaatttgcattttatata	902
NDUFS1	13	exon 12 + 1251	gcaccactgtttaatgctag A/G attcgaaagagggttgtaat	903
NDUFS1	14	intron 13 + 5159	attacttttagaaaacgtgt T/C ttagctgatactcaggoata	904
NDUFS1	15	intron 14 + 250	aaaaattgttatattagtta C/T accttgggtcaaaaattgca	905
NDUFS1	16	intron 14 + 550	gataaagtctcactatgttg C/T ccagggtgatctcaaaactcc	906
NDUFS1	17	intron 14 + 2429	ctgaaaatacaaaaattagc C/T ggggtgtgtggcatgtgcct	907
NDUFS1	18	intron 14 + 2530	ttacagtgcagccagatcac G/T ccactgcgctccagcctggg	908
NDUFS1	19	intron 14 + 2659	acacatttaattttttacat T/C gaaaatactgcagttatgtt	909
NDUFS1	20	intron 16 + 150	agaaaacatgtattcagaaa C/T aggaattcaagggttacagt	910
NDUFS1	21	intron 18 + 279	cactgtgtagcaatttatgg T/C gaattttccaaagtggcaaa	911
NDUFS1	22	3' flanking + 182	tctaggataattataattaa T/A aataatcatagtaacaatgg	912
NDUFS1	23	intron 11 + 3226	aatgtattgtctgtgcttt T/ Δ aacattttgtaatagtaaat	913
NDUFS3	1	5' flanking - 194	tctgccacaaggagctagga C/T cagctcacctcacgatttc	914
NDUFS3	2	intron 1 + 46	cgggggtcaggcgcagcggcg T/C gccagtgagagagctcct	915
NDUFS3	3	intron 6 - 439	aaagctgtgtcaaatgtact G/A cttagatctggactgtgaa	916
NDUFS3	4	intron 6 - 280	gggtgggtgagcagtcagttc G/A gagctcctgatgtgggagt	917
NDUFS4	1	5' flanking - 439	aactgaatacagccctgtcc T/A gagggcttgcaaagtgaatc	918
NDUFS4	2	intron 1 + 1829	gaaaaaaaaatcttaatgcca G/T ggaagacgttttttaatac	919
NDUFS4	3	intron 1 + 2057	attaatgggaaaaatctacat C/G taaaattcattttattgtaa	920
NDUFS4	4	intron 1 - 521	ttcatttttaactaattttat T/G tctcccattttgtgaatggg	921
NDUFS4	5	intron 3 - 1259	ataaaattatgatattatta G/A tactaatatagccagccata	922
NDUFS4	6	intron 3 - 1174	aatatatataattataggaa T/C ctacagtagcaaccatggt	923
NDUFS4	7	intron 4 + 10682	cacaatataggcacaaaactt A/C ctaccaaaagcactaacaagt	924
NDUFS4	8	intron 4 + 12299	ttactatatagatatatgg A/T atagactatagagtatctct	925
NDUFS4	9	intron 4 + 12560	accaaaataaggtattatgca G/A gctcatctttttatataaga	926
NDUFS4	10	intron 4 + 18801	ggaaagacttgotttgccag T/C gtatccgaaacctctgttat	927
NDUFS4	11	intron 4 + 19888	tcgcacagctgagaagagca A/G ggggctggttttcagtaccc	928
NDUFS4	12	intron 4 + 20178	agaaaagatgagtataatto G/A tctaacttaccattotttaa	929
NDUFS4	13	intron 4 + 23016	ctactctgtgaaagtaaggt T/A atgttgaaacaagtaaat	930
NDUFS4	14	intron 4 + 23124	actttctttggagatggagt T/A ccagcagttgggaatgtaat	931
NDUFS4	15	intron 1 + 766	tgtgatgatttttttttt T/ Δ ggctgtattaaccttcatt	932
NDUFS4	16	intron 1 + 1261	tttctttctcttttttttt T/ Δ gagatacattctcactctga	933
NDUFS5	1	intron 1 + 388	ccaaacatagccagcacttc C/T ggctgtaactccgggctgtt	934
NDUFS5	2	intron 1 - 13082	agtgcagccagattgcacca G/A tgcattccagcctgggcaac	935
NDUFS5	3	intron 1 - 12905	gttttcaacaaaggactcca G/T agtagtagagaagttctgt	936
NDUFS5	4	intron 1 - 12564	attttcatcacacctcaact T/G aaggataacagccttaaga	937
NDUFS5	5	intron 1 - 12561	ttcatcacacctcaacttaa G/A gtataacagcottaagaatg	938
NDUFS5	6	intron 1 - 10561	aacaatgtggtatagtgagg C/G ggggtgtgagcaggtgtcat	939
NDUFS5	7	intron 1 - 9065	cctgatgctcctggctccag G/A gtagacctttcccttaga	940
NDUFS5	8	intron 1 - 8871	tcaccacgtgtctgtagata T/C aggaccgcagaccttcgctt	941
NDUFS5	9	intron 1 - 7312	aatccttggcttctagaat G/T ggtcactgatggtatataat	942
NDUFS5	10	intron 1 - 6827	aacctctgcctccccgattc A/G cgccattctcctgctcagc	943
NDUFS5	11	intron 1 - 6725	agtagagacggggttccacc G/A tgttagccagcatggtctcg	944
NDUFS5	12	intron 1 - 6631	aggcgtgagccactgcgccc G/A gcctagaccttcttattata	945
NDUFS5	13	intron 1 - 6531	cccaacagctcccaatgtaa A/G acagatottattaatattctg	946
NDUFS5	14	intron 1 - 6346	gcaacagatcttgacctata T/C cccatagggtacagctgagg	947
NDUFS5	15	intron 1 - 6327	atcccatagggtacagctga G/C gactttaatcagaaaaggag	948
NDUFS5	16	intron 1 - 6122	tagccttgcttttactctac T/C gttcctcccaatcacacc	949
NDUFS5	17	intron 1 - 2512	acaaactottaatgcgaatt T/C tgcagatcaaagtgggotta	950
NDUFS5	18	intron 1 - 1945	tttaatctcctttaaatttc G/A caatttcacaacctagggtta	951
NDUFS5	19	intron 2 + 75	tttttttttttttttgagac G/A aagtctcactcttgcctcct	952
NDUFS5	20	intron 2 + 148	ctgtagcctctgcctccag G/A ttcaggcgattcgctacct	953
NDUFS5	21	3' flanking + 150	cagattcaagtgggtctcct G/C cctcagcctcccaagtagct	954
NDUFS5	22	intron 1 - (10682-10681)	attataaacactaaacaaac AT/ Δ gtgtggtctcttttagagggg	955
NDUFS5	23	intron 1 - 10272	aggaacaagtgactaccctg A/ Δ aaaaagaagagatgaaacaa	956
NDUFS5	24	intron 1 - 2069	accagacagagttcccttta C/ Δ ttgttttctgtggcaaga	957

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GENE	number	position	SEQ.	SEQ ID.No
NDUFS6	1	intron 1 + 26	ggccgctgggtacaggatgc A/C ccttctccagccgcacctc	958
NDUFS6	2	intron 2 + 1076	ggatcatgggtggaggagg G/A gottgtgtctgggtgggttg	959
NDUFS6	3	intron 2 + 1260	cagttgtcgagtaagtgggtg T/C atagggttaagtgtctttct	960
NDUFS6	4	intron 2 + 1413	caaaggagctcatggcattg C/T gaatgggacattttcttcgt	961
NDUFS6	5	intron 2 + 1568	tggagaaggggagggtttctc T/C tagtgtggatgoggtatggt	962
NDUFS6	6	intron 2 + 1692	gaccgtgggtgacggaggttt C/T ctgggcatcgatgggtggtt	963
NDUFS6	7	intron 2 + 6488	tagcttaaataattattggc A/G ttcattgtcagaatgcctga	964
NDUFS6	8	intron 2 + 6563	tttaaactttatttttaa G/A tccatgaatgggtcggtat	965
NDUFS6	9	intron 2 + 6740	aaagatttaaacctacatat C/T ttatgccaatcatttgat	966
NDUFS6	10	intron 2 + 6832	gcgagggactcattttacag A/T ggttgacacttcaactgtgt	967
NDUFS6	11	intron 2 + 7054	ttcactgccggagccttggcc G/A tgtgaaccggagccgggct	968
NDUFS6	12	intron 2 + 7186	ggtcagggtcacccttgagc T/C gcgcacactaaatgacggga	969
NDUFS6	13	intron 2 + 7225	gagggcatcccgctcagtc G/A ccagtgtcaggcgtcagca	970
NDUFS6	14	intron 2 + 7810	cttcactctggggcgggga C/T gctgtagaaggagcacaaag	971
NDUFS6	15	intron 2 + 11080	gtaactgttcagtgtttct C/T ctttgatttcattgtaa	972
NDUFS6	16	intron 2 + 11657	gggacagaacgatgtgtgg G/A gagaagaggcgtggcagag	973
NDUFS6	17	intron 3 + 208	cgaaaacccctttcaactg T/C gaagtgtggcgcatgtt	974
NDUFS6	18	intron 3 + 1031	ctagagtgggactgggcacc C/T ggcatgtccctctctgggt	975
NDUFS6	19	3' flanking + 270	gcttcagagagccaaggtgg G/C tcttgaggtgcatagtgaag	976
NDUFS8	1	5' untranslated - 45	agtgtagcctccgctcccg A/C ttgactggcctgcttggca	977
NDUFS8	2	intron 1 + 163	aggtgcagcggggagccggc T/C ctacgggcgcagcgcggcc	978
NDUFS8	3	intron 3 + 123	tctctgagcctgtttccact T/C ttaaaatgattatggtgatg	979
NDUFS8	4	intron 6 - 505	aggcaaggcaggccgggcac G/A gtggctcacgcttgaatcc	980
NDUFS8	5	3' flanking + 491	ggccctgagctggcctgct C/A cagccacatcctcttctctg	981
NDUFS8	6	3' flanking + 693	ttcacttcatttgcagttag G/A aaaccagctccgagaggtga	982
NDUFS8	7	3' flanking + 1267	tttccagacgtaaccgcc G/A tcagagcgtggcatggagcc	983
NDUFS8	8	3' flanking + 1362	cgtgtgggtttttcccttac C/T gtggtctccaggcacttac	984
NDUFS8	9	3' flanking + 1449	tgtcagaacaggcctatggc G/A cccaaccacaagtccccaa	985
NDUFS8	10	3' flanking + 1572	cagccccacaggcctgtgt C/A gctgtgtgggcttagggat	986
NDUFS8	11	3' flanking +(783-784)	cagagaccttgaccccccc (C) atctaccatcatttccaaa	987
NDUFS8	11	3' flanking +(783-784)	cagagaccttgaccccccc atctaccatcatttccaaa	988
NDUFB3	1	5' flanking - 1439	ttaaaagttagctttttct G/A ccgggcacggtggctcacgc	989
NDUFB3	2	5' flanking - 1436	aaagttgactttttctgcc G/A ggcacggtggctcacgcctg	990
NDUFB5	1	5' flanking - 213	ggcggatgaaactctctac A/C aagaaggccaaaccggccg	991
NDUFB5	2	intron 1 + 6288	ggggatgttgattacctagg T/C cagtaaagtaagaaggcat	992
NDUFB5	3	intron 1 - 1581	ctctggggcactgtatct A/G ttctttccctgtttaccct	993
NDUFB5	4	intron 1 - 1487	ccctcttagaccgtatatag T/G tctagcataggatctgcaca	994
NDUFB5	5	intron 2 + 556	ttgtctggaccatctgccac G/A gtagataaagctctgaatca	995
NDUFB5	6	intron 3 + 467	ggcgccatcgactccagcc C/T gggcaacagagtgaactct	996
NDUFB5	7	intron 3 + 497	agtgaactctgtcccccc C/G caaaaaaaaaactataatcct	997
NDUFB5	8	exon 5 + 397	atgatagtcctgaaaagata T/C atgaaagaacaatggccgtc	998
NDUFB5	9	intron 1 +(231-215)	attagcatttctaaaacgtt GTT/Δ attcaccatcccaattaatg	999
NDUFB7	1	intron 1 + 68	cctgaacacctggcacccca G/A ggctggcaccacagggtgg	1000
NDUFB7	2	intron 2 + 266	gggctctctaggggcctgtt T/C gatggggacagggcaggtgg	1001
ABCA1	1	5' flanking - 278	gggcccggggggggaagg G/C acgcagaccgggaccctaa	1002
ABCA1	2	5' flanking - 99	acataaacagaggccgggaa G/C gggcggggaggaggagag	1003
ABCA1	3	intron 1 + 159	gcggtgttaaatgggagac G/T atgtcctagtacgagctctg	1004
ABCA1	4	intron 1 + 506	gaattggctatatgtcccc G/C ggactggagcggcacagtcc	1005
ABCA1	5	intron 1 + 5897	gtacaaaacccttttagcttt T/G gcaaacctccttaagacc	1006
ABCA1	6	intron 1 + 5929	ttaagaccogatttaaatgc C/T tccctctcatgaagctctt	1007
ABCA1	7	intron 1 + 5962	aagctcttctggatccactc T/C ttccatcactaagttgaaa	1008
ABCA1	8	intron 1 + 5985	cccatcactaagttgaaagt A/C agatcccttctctttactt	1009
ABCA1	9	intron 1 + 11416	ttacagtgcctttatagga G/A agaaagaagaattgtgtct	1010
ABCA1	10	intron 1 + 11935	tctctgtggagcaaatagag G/A gctgtctgacacttggttcc	1011
ABCA1	11	intron 1 + 12281	gaatgtttgatttggaaaa T/A cttaataacagtagttttt	1012
ABCA1	12	intron 1 + 12924	gtgctgacaattttatactc T/C aggttgaacctccggggaag	1013
ABCA1	13	intron 1 + 13002	gagcctcaatcacagattct C/G tctagctcacatgaagttaa	1014
ABCA1	14	intron 1 + 17715	ggagcatgactttgtggaag C/T ctctctcttccaccagag	1015
ABCA1	15	intron 1 + 17848	gagggctgactgtcaccctt T/C gataggagcccagcactaaa	1016
ABCA1	16	intron 1 + 21384	gtgggtgggaggaattggag G/C aggaagcttgccctaagtg	1017

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GENE	number	position	SEQ.	SEQ ID.No
ABCA1	17	intron 1 + 22145	gtagcttctaatacaacgaa C/G tgattcctggagagcagctt	1018
ABCA1	18	intron 1 + 23063	ggaggcacctgtgacaccca G/A cggagtagggggcggtgtg	1019
ABCA1	19	intron 1 + 23131	agtgtgcatatgtgctgacc G/A tgggagcttgtttgtcggtt	1020
ABCA1	20	intron 2 + 156	ggacacaggactgtgtggtc T/C ggatatggcatgtggcttat	1021
ABCA1	21	intron 2 + 384	gctgtgggtgaagtgtgta A/G tggccccactcttagagatc	1022
ABCA1	22	intron 2 + 1081	agtgcagccaaaattgcaaa G/A tcataccattcaaattaata	1023
ABCA1	23	intron 2 + 2801	aagaaaagtgtattattca A/G gttgctgatgcttagattgt	1024
ABCA1	24	intron 2 + 2830	tgcttagattgttagagttg C/G aaagatctggcttgcattctt	1025
ABCA1	25	intron 2 + 2856	tctggcttgcattctgtaca A/G ctgacagaactggggctcag	1026
ABCA1	26	intron 2 + 3187	tgatagctgttgcctgcagc A/G tacggacgttcattgcgcag	1027
ABCA1	27	intron 2 + 3190	tagctgttgcctgcagcata C/T ggacgttcattgcgcagttc	1028
ABCA1	28	intron 2 + 3194	tgttgctgcagcatacggc C/T gttcattgogcagttcctgt	1029
ABCA1	29	intron 2 + 3204	agcatagggacgttcattgc G/A cagttcctgtctcctgagat	1030
ABCA1	30	intron 2 + 3401	acataaagcctgtgtgctgc T/C gccaggaagactagaaacgc	1031
ABCA1	31	intron 2 + 13927	gtcaccacatacctggcact A/G tgctaaggctgggaatgcag	1032
ABCA1	32	intron 3 + 4163	ccagcccacttcatcttacc G/A tagttacctccttagagtat	1033
ABCA1	33	intron 3 + 4262	tgtcaaagaggaactaagga T/C gccagggactttctgcttag	1034
ABCA1	34	intron 3 + 4306	ccctctcatcacttctccaa C/T gctggtatcatgaacccat	1035
ABCA1	35	intron 5 + 240	gacagaagaaaagtccccag G/A gaagaatactacagacttg	1036
ABCA1	36	intron 5 + 490	gatgggcatttgaactgtt G/A totttaaaaagtgaatctt	1037
ABCA1	37	intron 5 + 583	tatctggggagtgggcattt T/G ctgactgaggcattggctgc	1038
ABCA1	38	intron 5 + 1051	ggctacaaaactgtgcttcc C/T ttgggcagtaaaagaggcaa	1039
ABCA1	39	intron 5 + 3051	tagagaacaagtctaatct G/A ttttcttgaaatagtcgaa	1040
ABCA1	40	intron 5 + 3127	aagtccatgatttttaggc A/G aaatggcctccttctctt	1041
ABCA1	41	intron 5 + 5924	ctttcttccacaaaattgcc C/T cccagagctttctggaaggg	1042
ABCA1	42	intron 5 + 6831	ccagtcctcagccttgcca T/C tgcttatgctggtctgaaa	1043
ABCA1	43	intron 5 + 12678	gctcaccgctctgctcacc G/C accctctggccatctcctot	1044
ABCA1	44	intron 5 + 14214	cagcttggctccagaggcct G/A gacctgggtccagaggtcc	1045
ABCA1	45	intron 5 + 14257	gctggttccccggcttggtc C/T cagaggcctggatgtgtggc	1046
ABCA1	46	intron 5 + 18078	cctaccacaccatgcacgtg C/T acagccaagggttgttgact	1047
ABCA1	47	intron 5 + 18795	ctgggctcttctggacctg G/A ccagctaaaaggaaatctcc	1048
ABCA1	48	intron 5 + 18948	gcattggtgtactaagaac G/A catattccctatcctatagg	1049
ABCA1	49	intron 5 + 19053	ctccccaacattaaaagt T/C aagggtgcttattcaaatg	1050
ABCA1	50	intron 5 + 19148	ggcccaagaaactgcattt C/A gcatgctccctaaatgaagc	1051
ABCA1	51	intron 5 + 19229	atgctaacagttagagtca C/T atgtgatgggaagcatcagg	1052
ABCA1	52	intron 5 + 19405	cttgotcaatttattctgtc T/C atataactcaatattactga	1053
ABCA1	53	intron 5 + 19534	catgtgacctcttagctcc G/A cggattaactcctgtcctca	1054
ABCA1	54	exon 6 + 474	gaaaccttctctgggttct G/A tatcacaacctctctctccc	1055
ABCA1	55	intron 6 + 210	gcaacctggcgtcatgggcc A/C gctggttaaaataaaattga	1056
ABCA1	56	intron 6 + 334	acagttctgaggcaataacc G/A tggtaagggttattgatct	1057
ABCA1	57	intron 6 + 2288	cttcttcaaaagcttgggt C/T cactggaccacgtatgaagt	1058
ABCA1	58	intron 6 + 2322	atgaagtagaatagtttag T/C ccagaaaggcaattaagtaa	1059
ABCA1	59	intron 6 + 2820	gtgcttgatacattotgag T/G ttcagtaaagagacctgatg	1060
ABCA1	60	exon 7 + 656	tgagcttgtggcctaccaa G/A ggagaaactggctgcagcag	1061
ABCA1	61	intron 7 + 416	catcataaagatgacattgt G/A ggctgtcacagttggaaggc	1062
ABCA1	62	intron 7 + 471	agaccacactatttagctta C/T ttagtaataacattgcaaag	1063
ABCA1	63	intron 7 + 504	ttgcaaagaaaaattccgac G/A aagtttttcagcctaggaa	1064
ABCA1	64	intron 7 + 679	gctctggtgaaattcctctc G/C ctaccccaaacatcatcatt	1065
ABCA1	65	intron 7 + 1740	acaaatgctcacccttcag C/T tggatgattgaaattttgg	1066
ABCA1	66	intron 7 + 2122	tgattaagggtggctactacc A/G ggtgcttctgcatatctcg	1067
ABCA1	67	intron 7 + 7753	taggaattccaagctgtgaa T/C ttttactgaagctcttgg	1068
ABCA1	68	intron 7 + 8973	atggaaattgtttatattg A/T ctacagattgccaatattat	1069
ABCA1	69	intron 7 + 8976	gaaattgtttatattgact A/G cagattgccaatattattag	1070
ABCA1	70	intron 7 + 11327	ctaacaatcttattccatt G/C agtccctataaaagaagtgg	1071
ABCA1	71	intron 7 + 11738	ctgacgtttaaggagaccg C/T gtaggctcctttaggactg	1072
ABCA1	72	intron 7 + 12295	agtctgtaaattattgttct T/A tttttctttagcttatgct	1073
ABCA1	73	intron 8 + 387	tagcaaggccaatcatttta C/G caacacacatgcttgctaac	1074
ABCA1	74	intron 8 + 697	ggaactgtctggtgtcccc A/T gcataggaagctgagccagg	1075
ABCA1	75	intron 8 + 1312	attgtctgcagatccctc G/A cagccctctgtccctgttc	1076
ABCA1	76	intron 8 + 3036	cttatgtgggaagaaattt T/G ttttttgattggggagtgg	1077

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GENE	number	position	SEQ.	SEQ ID.No
ABCA1	77	intron 8 + 3176	aatggcctggttctctgtc C/A cctttctgtctgtatgcctc	1078
ABCA1	78	intron 8 + 3364	ggcagaaggcaaagcttagg A/T cctagagagtgtctggaccac	1079
ABCA1	79	intron 8 + 3373	caaagcttaggacctagaga G/A tgotggaccacgccactcac	1080
ABCA1	80	intron 8 + 3561	cagggatttattaatgattt C/A ttgtgaaatgtttggaaata	1081
ABCA1	81	intron 8 + 3654	agtgcoggaatacatttgca T/C gtaagacagaacgctgcctg	1082
ABCA1	82	intron 8 + 4715	ggcagaggggtctcagaatc C/T gcatttccaacaatgtctcc	1083
ABCA1	83	exon 9 + 936	cgtattgtctcgggcatcc C/T gagggaggggggctgaagat	1084
ABCA1	84	intron 9 + 2309	cccctcaagagtcagtttaa A/G tgttggtcatgttagttgtc	1085
ABCA1	85	intron 9 + 2392	atgggagggccttgcttca T/C gaaaacattttccagatca	1086
ABCA1	86	intron 10 + 228	tggggatggggaggactggc A/G cagggctgctgtgatgggt	1087
ABCA1	87	intron 10 + 319	ttctcgggtccctggctccc C/T acctgactccaggtgaacaa	1088
ABCA1	88	intron 11 + 377	gaaagaagtgtggagcaaa A/C gcattgatgtacatgtagac	1089
ABCA1	89	intron 11 + 521	agtgtctagagacaattgg G/A ttcaaatgtggagcaggctg	1090
ABCA1	90	intron 11 + 2850	ctctatacaatcattatgct G/C ccattgaaataataataca	1091
ABCA1	91	intron 11 + 2976	ctccaattcggtagaaccag A/G gcttcatcttctctgtcgaa	1092
ABCA1	92	intron 11 + 3056	gtttgcagctgctgttttc C/T ggcagcacatctgtgcaggc	1093
ABCA1	93	intron 12 + 340	ggcattatttgtgaaactta T/C ctaaaatcgaattcgggtcc	1094
ABCA1	94	intron 12 + 381	aattaaattttgaaattt A/G tattaataattatattagta	1095
ABCA1	95	intron 14 + 1728	caggctcagaggccttggcc C/T atcaccctggctcacgtgtg	1096
ABCA1	96	exon 15 + 2040	atgggcctggacaacagcat C/A ctctggttagctggttcat	1097
ABCA1	97	intron 15 + 1382	cttttagacagaaaagttac G/A tgggatattatctccacag	1098
ABCA1	98	intron 15 + 1453	tatataaggagaaaccagtt G/A aaattacctattgaagaaac	1099
ABCA1	99	intron 15 + 1567	ttctgcgtagtttgggtaa G/A tcacttatcttctttaggat	1100
ABCA1	100	intron 15 + 1617	cagttgcctcatcagaaaga T/A gaacagcattacgcctctgc	1101
ABCA1	101	intron 16 + 95	agttgagaacagaagatgat T/A gtctttccaatgggacatg	1102
ABCA1	102	intron 16 + 452	tgggttttgccttgagtaat G/A ttttctgaactaagcacac	1103
ABCA1	103	intron 16 + 657	ctgttgctcagctctgggt T/C cataggcatcagcagcccca	1104
ABCA1	104	exon 17 + 2473	gottcaatctcaccacttgc G/A tctccatgatgctgtttgac	1105
ABCA1	105	exon 18 + 2649	ggttccaaccagaagagaat A/G tcagaaagtaagtgtgttg	1106
ABCA1	106	intron 18 + 1730	tgaagttcaagcgcagtgc C/G ctgtgtccttacactccact	1107
ABCA1	107	intron 19 + 426	aggaccttacagtgggtagt A/G tcaggaggggtcaggggctg	1108
ABCA1	108	intron 19 + 468	aaagcaccagcgttagcctc A/G gtggcttcagcagcattcc	1109
ABCA1	109	intron 20 + 876	ccctcctcatctaaagtga C/T acatggggctcatgtgcagg	1110
ABCA1	110	intron 22 + 118	catgggatactcttctgtta T/G cacagaagagataaaggga	1111
ABCA1	111	intron 22 + 560	aaagctttgccattotaggg G/A tcatagccatacagggtgaa	1112
ABCA1	112	intron 23 + 102	acctcttttgccatgttgaa A/G ccaccatctccctgctctgt	1113
ABCA1	113	intron 23 + 287	gtcaaagaaaagagacttgt C/T aagaggtgaagccttggct	1114
ABCA1	114	intron 23 + 1063	accttcaccctcaggaagc G/A aggtgttcacacggcacac	1115
ABCA1	115	intron 25 + 321	ctctttacttaagtacagt T/G gaggaacagcggcatcagga	1116
ABCA1	116	intron 25 + 376	gttagaaattcagcaacttg G/C gccagctcagacctactga	1117
ABCA1	117	intron 25 + 478	catacataggaaatgacaaa C/T gtttatggatggatagtcta	1118
ABCA1	118	intron 25 + 579	tcatttaattctcaaaaaa G/T atgaaaaaatgaacactcag	1119
ABCA1	119	intron 27 + 153	aatggtaaaagccacttgtt C/T ttgacagcatcgtcatgtg	1120
ABCA1	120	intron 28 + 1058	actatcatgggagataatga C/T tatggttgccatgattgga	1121
ABCA1	121	intron 28 + 1317	caggacctcagttctgagt C/T acctgaatgtgagcactat	1122
ABCA1	122	intron 30 + 372	tatatgatttttaggtttg T/C ttatcagcttcttgccttt	1123
ABCA1	123	intron 30 + 506	ccttttaaaaagtaagcagt A/G gataaataaattcagtgag	1124
ABCA1	124	intron 30 + 1033	ctggatttcaggtgccttt G/C attttccacatgaaggttgt	1125
ABCA1	125	exon 31 + 4281	tcttccctttgcagagacac G/A cctgccaggcaggggagga	1126
ABCA1	126	intron 33 + 626	ggctcctgttactgatttc C/T gtctttctctctgccttt	1127
ABCA1	127	intron 33 + 719	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	1128
ABCA1	128	intron 33 + 726	cctcatgctagaaggagcc G/A gagcctgtgtataaggccag	1129
ABCA1	129	intron 33 + 889	ctttcctcaatgtctcagct A/G tctaactgtgtgtaatca	1130
ABCA1	130	intron 33 + 1097	ctgtgcacccactgtctgg G/C ttttaatgtcaggctgttct	1131
ABCA1	131	exon 35 + 4760	tatgacaggactggacacca G/A aaataatgtcaaggtaaacc	1132
ABCA1	132	intron 35 + 234	aacctatctaaacctcagtt T/C cctcatctgtgaaatggaga	1133
ABCA1	133	intron 37 + 411	aactctgtacattttatcag C/T agcttatccatccattgcaa	1134
ABCA1	134	intron 37 + 1224	caggcataggtgattcagag A/G tgaaggtcaagtcctgaa	1135
ABCA1	135	intron 37 + 1720	aaattaaaattactctgact G/T ggaatccatcgttcagtaag	1136
ABCA1	136	intron 40 + 251	tgaaggtaaggaaaatagt T/G tatttgcttggatccactgg	1137

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GENE	number	position	SEQ.	SEQ ID.No
ABCA1	137	intron 40 + 252	gaaggtaaggaaaatagtgt T/C atttgcttggatccactggc	1138
ABCA1	138	intron40 + 319	agcactggaaaagtcaaacc A/G taactttgagaattaggtga	1139
ABCA1	139	intron 40 + 957	cttggtactcttttttcctt G/C tcatgggtgatagccatttg	1140
ABCA1	140	intron 41 + 146	tgatgtgggcatcccgcagc G/T ccctccctgcccacccctgga	1141
ABCA1	141	intron 42 + 239	cattggttttatatgcttac A/C tttatgtgttagttattaaa	1142
ABCA1	142	intron 42 + 321	aataaatgggtgattttgag T/A ttgagtttcatagtccaaaa	1143
ABCA1	143	intron 42 + 322	ataaatgggtgattttgagt T/C tgagtttcatagtccaaaa	1144
ABCA1	144	intron 42 + 533	agatgaaaaattatgtagat G/A ataataatgatacgggtct	1145
ABCA1	145	intron 42 + 546	tgtatgataatgaatgat A/G cggttctaaaaagacaggtt	1146
ABCA1	146	intron 43 + 739	tacagccacacttaaaatgg T/A cccattatgaaatacatatt	1147
ABCA1	147	intron 44 + 18	taggtgagaaaagaagtggc T/C tgtattttgctgcaaagact	1148
ABCA1	148	intron 44 + 264	acaatataatttgctgttt T/C ttaagagtataatttagtga	1149
ABCA1	149	intron 44 + 279	tgtttttaagagtataatt T/C agtgatttttggtaaattga	1150
ABCA1	150	intron 44 + 508	ttacattgctacataaaat C/T cccctatgtacatgtacct	1151
ABCA1	151	intron 44 + 1477	gatctcctctcctgtctctt A/T catttttgcagtagcaatgt	1152
ABCA1	152	intron 44 + 1665	tggttgtaagaactgatttg G/A ttggtatagctgtgagggcc	1153
ABCA1	153	intron 44 + 1956	gtgttgctcacactcaaaat T/G totgggccttctcatttgg	1154
ABCA1	154	intron 45 + 68	aatatataccttatggcttt T/C ccacacgcattgacttcagg	1155
ABCA1	155	intron 46 + 608	ttatactgacttcaatagag G/C ttacagacaaaaagttgtt	1156
ABCA1	156	intron 47 + 336	ttcacaattgtaaacaccac T/C acactgaacagcatcatccc	1157
ABCA1	157	intron 49 + 55	agggtgtggattcctgcccc G/C acactcccgcccataggtcc	1158
ABCA1	158	3' UTR(exon 50)+7949	aacaaaaatgtgggtgtctc C/T aggcacgggaaacttgggtc	1159
ABCA1	159	3' UTR(exon 50)+8226	aggagcccactgtaacaata C/T tgggcagccttttttttt	1160
ABCA1	160	3' UTR(exon 50)+8682	aactctctccactttttcca G/A aatttgaatattaacgctaa	1161
ABCA1	161	3' UTR(exon 50)+8697	ttcagaatttgaatattaa C/T gctaaagggtgaagacttca	1162
ABCA1	162	3' UTR(exon 50)+9097	aactattttgaagaaaacac A/G acattttaatacagattgaa	1163
ABCA1	163	5' flanking - (1033-1032)	tgacttaaatatttagacat (AT) ggtgtgtaggcctgcattcc	1164
ABCA1	163	5' flanking - (1033-1032)	tgacttaaatatttagacat ggtgtgtaggcctgcattcc	1165
ABCA1	164	intron 5 + 6368	ttctgatggggtgtgtgtg C/Δ tgagaatcatgactgggtgg	1166
ABCA1	165	intron 5 + 9709	cattttctgtctgaaccccc T/Δ caccattcaggcagctgct	1167
ABCA1	166	intron 5 + 13816	tcctactctcctttttt T/Δ catttgccctcctccaccac	1168
ABCA1	167	intron 10 +(270-271)	cttttcaggaggaggagccaaa (G) cgctcattgtctgtgcttct	1169
ABCA1	167	intron 10 +(270-271)	cttttcaggaggaggagccaaa cgctcattgtctgtgcttct	1170
ABCA1	168	intron 20 +(611-612)	tttagcccatcctctcccc (C) gccaccctccttattgaggc	1171
ABCA1	168	intron 20 +(611-612)	tttagcccatcctctcccc gccaccctccttattgaggc	1172
ABCA1	169	intron 32 +(391-392)	gagtgccttgggtactctct (T) gatgggggactccatgataa	1173
ABCA1	169	intron 32 +(391-392)	gagtgccttgggtactctct gatgggggactccatgataa	1174
ABCA1	170	intron 37 + 847	gotgtatatttgaatgtcc C/Δ gtttcaaaaagcaaagccaa	1175
COMT	1	5'flanking - 1287	cgtatgatattccccattct G/A agtcagaaatacctagaat	1176
COMT	2	5'flanking - 1217	tgtgatgatgggaaggggaa G/A cttttctgtctgtgtcccc	1177
COMT	3	5'flanking - 503	caggggctccaggaggacga G/A tgtgtatcctccattgtct	1178
COMT	4	5'flanking - 425	gagaagttgggaagtctggc C/T agtggggccggtgcctgggtg	1179
COMT	5	5'flanking - 277	cccagccccagttccccac C/T tgggaagggggctacttgtg	1180
COMT	6	intron1 + 12058	ctggcccatggaagggagg G/A agggggcccgacggggcca	1181
COMT	7	intron1 + 12070	agggaggggaggggggcccg A/G cggggccacagtaaaggagt	1182
COMT	8	intron1 + 18831	tgtgtatgttctgtgtaaac C/T agcccttgggtttacacatc	1183
COMT	9	intron2 + 832	cctctcctttggccaccct G/C actacccccaactccggggc	1184
COMT	10	intron3 + 90	ggagaagctgttatcaccac A/G ttccagggggctgggaacc	1185
COMT	11	intron3 + 425	ccccaaaggtggcggttogg T/G gattcagagagggcagctct	1186
COMT	12	intron3 + 671	ggctcctgtcttttgggaga G/A gtggggggcctgcctgggg	1187
COMT	13	intron3 + 676	ctgctctttgggagaggtgg G/T gggccgtgcctggggatcca	1188
COMT	14	intron5 + 75	tcagcctcagcctctccaaa G/C agccaggcattccagtagag	1189
COMT	15	intron5 + 310	accagacaccaggggcagaaa C/T ggcacaggaccaaggagatg	1190
COMT	16	intron5 + 346	agatgggtggggaagggcc G/A ctctggggccagcctgctct	1191
COMT	17	intron5 + 3023	aaggcagccgcccgtctcaa G/A gcttaggccattgtcctct	1192
HNMT	1	5'flanking - 211	cagaggcagatgacagtctt C/T cgttaaagatttactgtg	1193
HNMT	2	intron1 + 5409	aatataactgatataattgg A/G acatttcatgttggcctagt	1194
HNMT	3	intron2 + 2561	cacttgtgcttggacaagaa A/G agaaggcctacaagaaaaag	1195
HNMT	4	intron2 + 2895	caatcagaaatgaagaaaa A/C ctccaagaaaaatttaagtt	1196
HNMT	5	intron2 + 3977	accaaacttgggaagtgtaaa G/A ttatgcatgtatgttcatgt	1197

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GENE	number	position	SEQ.	SEQ ID.No
HNMT	6	intron2 + 5296	ttaacatagtgagttggag T/C cccaggattttatttcctt	1198
HNMT	7	intron2 + 13317	caaccctcatgaattcttag C/T tgggatgggtccctataaca	1199
HNMT	8	intron2 + 14682	gtagatgagcaaatgagttc A/Δ ggagagatttaaatacccta	1200
HNMT	9	intron2 + 15406	gtctatgcattcatgcaccc G/A tctaaccagctgtctaccta	1201
HNMT	10	intron2 + 28943	atgtgacttaaaacttcaggt A/G tatcaatatccctgaatgt	1202
HNMT	11	intron4 + 49	cagaaagaagacttttcaga A/G tatatatataatgaatatct	1203
HNMT	12	intron4 + (1942-1943)	tttgagaaaaatttaaggta (A) tcttctatggcccacttcca	1204
HNMT	12	intron4 + (1942-1943)	tttgagaaaaatttaaggta tcttctatggcccacttcca	1205
HNMT	13	intron4 + 2405	ccctgtgaccaagcagataa C/A ctcatgctttatttagtcca	1206
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatattttgtcttcattat	1207
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt atatattttgtcttcattat	1208
HNMT	15	intron5 + 235	ctttcttttgggaaaatag T/C ctttgtcttctatatatgaa	1209
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag (AT) acacagcagactctgtcttc	1210
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag acacagcagactctgtcttc	1211
HNMT	17	intron5 + 749	ttacaccagaccccatatt T/G aacaccatattgcacaaaat	1212
HNMT	18	intron5 + 1101	gtaggcagcctattcttgat T/G atattcatcaatcatacaga	1213
HNMT	19	intron5 + 1137	acagaaaaagttattgtagac G/A gaaataacaattcattgaga	1214
HNMT	20	intron5 + 1348	aaggagcatgaatagttcca C/G aagtaactgagaactgatta	1215
HNMT	21	intron5 + 1673	caaaagaaagggagtaaaga C/G tcaacaatcagtttagctttt	1216
HNMT	22	intron5 + 2022	attttatttggggctttota C/T gtctctctctoctaagccta	1217
HNMT	23	intron5 + 2285	tgctactacttaactctaaa G/C atccagagtaaattgatggag	1218
HNMT	24	intron5+4159	taccagttgaccagcaacc C/T tcttatagagtagtttaa	1219
HNMT	25	intron5 + 4501	aatgatccacaaaattacta C/G tcattgtttctttcaatga	1220
HNMT	26	intron5 + 5251	cacacacacacacacacaca C/G caaatggaagcagccagaca	1221
HNMT	27	intron5 + 5802	gaaaaagaaaatctggctta C/T atcatgttgaaaacaaaagt	1222
HNMT	28	intron5 + 6189	tccaattccaccttctccta G/C agcatatctgcagttacct	1223
HNMT	29	intron5 + 6297	gtcttggttcatctcttgag T/A taaattagatctgggaactt	1224
HNMT	30	3'flanking + 458	tatgtcactctcaagaactc C/T tataagaccaagagtcact	1225
HNMT	31	3'flanking + 993	ctgaaatgaacactgaacc G/A ttaatcatactgatattgac	1226
HNMT	32	3'flanking + 1793	gtggagcacagcatttttagg G/A cttgatatttgcttattata	1227
GAMT	3	intron5 + 1411	ggtagcctgggtgccatccc G/A accaggagacgcaggtgcc	1228
PNMT	2	intron1 + 35	ctgaggcagcaggggacaaga G/T gtcgtcggggagtgaagca	1229
CYP1A1	1	intron 1+1590	ccactcttcaaaaaggaggta C/T atgtgacagcagctggaaat	1230
CYP1A1	2	exon2+160	gaatccaccagggccatggg G/A ctggcctctgattgggcaca	1231
CYP1A2	1	5'flanking-731	gcctgggctaggtgtagggg T/G cctgagttccgggcttggct	1232
CYP1A2	2	intron1+371	cttccctgtgttcacactaa C/T ctttctctctttgaaattg	1233
CYP1A2	3	intron3+44	atagccaggagaagccttga G/A acccaggtgtttgttcagt	1234
CYP1A2	4	intron5+81	tccctgctaggaactgttta T/C ataataagaggaggggacct	1235
CYP1A2	5	exon6+181	ctggccatcctgctacagca A/T ctggagttcagcgtgccgcc	1236
CYP1A2	6	exon6+295	cggctgcgcttctccatcaa C/T tgaagaagacaccaccattc	1237
CYP1B1	1	5'flanking-3669	tgtatcctgtgaagcatcac G/A gttatccttctctgcacatg	1238
CYP1B1	2	5'flanking-3149	tgacagcacttaccaccta G/C ttctctgatttttgagtca	1239
CYP1B1	3	5'flanking-1222	gggggaagccacccccgcc G/A aggcctccggcttccctta	1240
CYP1B1	4	5'flanking-376	ttccgggaagcaagctcaag T/C cgcggagaggggaaggaggt	1241
CYP1B1	5	5'flanking-265	ctggggacaccgtgcggcct C/T gattggaggtggctgtgatg	1242
CYP1B1	6	intron1+129	tgcccgagcgtgttcccca G/A attgcaggaaccgttacgcg	1243
CYP1B1	7	intron1+379	tgagtgtcagccttctcct C/T tctgtccccagcatgggcac	1244
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt (T) gagtcaaagacttaaagggc	1245
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt gagtcaaagacttaaagggc	1246
CYP1B1	9	exon3+1284	agtatagtggggttccatga G/T ttatcatgaattttaaagta	1247
CYP1B1	10	3'flanking+2226	ttctttttcttttttttt T/Δ aaaatttattcctatttct	1248
CYP1B1	11	3'flanking+(2226-2227)	ttctttttcttttttttt (T) aaaatttattcctatttct	1249
CYP1B1	11	3'flanking+(2226-2227)	ttctttttcttttttttt aaaatttattcctatttct	1250
CYP1B1	12	3'flanking+2230	ttttcttttttttttttaa A/Δ ttattcctatttcttaca	1251
PEMT	90	intron1 + (297-299)	attgtgtgagactcagaggt TGT/Δ ccgtgttagtctttgggatt	1252
PEMT	91	intron1 + 817	tcatgaagcctgtaaggcac A/G tctctgccccagcagcttc	1253
PEMT	92	intron1 + 830	aaggcacatctctgccccaa G/A cagcttctaattccagttct	1254
PEMT	93	intron1 + 1035	gagttctctgaaggagctaa T/C accagttagttttgaaga	1255
PEMT	94	intron1 + 1573	agtgggcaggggagactaac C/T ggggtgtgaggggtgggct	1256
PEMT	95	intron1 + 1759	gatttttcttaaagaaagaa A/G gaaagaaacatacaacatac	1257

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GENE	number	position	SEQ.	SEQ ID.No
PEMT	96	intron1 + 2768	gcaccttgctgtccacaggg C/A ggggcacctccaggattcag	1258
PEMT	97	intron1 + 2785	ggcgggggcacctccaggat T/C cagaagatgactccagtagg	1259
PEMT	98	intron2 + 4598	ccgtgggttttttttttt T/Δ cttcatttcttgggtgtg	1260
NAT2	21	exon2 + 288	atgttaggaggggtatttta C/T atccctccagttaacaaata	1261
NAT2	22	5'flank - 2053	ctggattgcaacattttaat T/C ccagggtgcaggtttccaac	1262
NAT2	23	5'flank - 1299	gaatcaccagtgccggagggt A/G taacagtgaaccaagacac	1263
NAT2	24	5'flank - 1145	ctgtagaacacaaggatatt C/T ggaggcagttgtacatgcc	1264
NAT2	25	5'flank - 1036	ccttcccacagagtcccag T/A tcatgtggcagcatgccaga	1265
NAT2	26	5'flank - 94	aaagatttgctaagagattc G/A cagaggcaacctgaggccct	1266
NAT2	27	5'flank - 643	atgtttatattttatattaa T/C attaatgtataaaaaattt	1267
AADA	1	5'UTR + 29	attaaagtacactattcagg C/T atatcatgtaggtttacttt	1268
AADA	2	intron1+138	gctgtggcctttgacaatgt G/A ttacttagaaatgtgtttg	1269
AADA	3	intron1+142	tggcctttgacaatgtgtta C/T ttagaaatgtgtttgtttt	1270
AADA	4	intron1+1033	ttccagcagagacaccaaca A/G gtaaaaacaccccagctaca	1271
AADA	5	intron1 + 1253	ttttttccctcatatttgc T/C gtctgtgtacatatgtga	1272
AADA	6	intron1+1366	ctctggtagccttttaatta A/G ttaattcattcattactta	1273
AADA	7	intron1+1369	tggtagccttttaattaatt A/C attcatcatttacttacat	1274
AADA	8	intron1+2501	ggttacagaaagaatgggtg C/A ttggccaaaaatgatatgg	1275
AADA	9	intron2+1971	aatgagagtttaagtaggag A/C attttctttatttttgtgc	1276
AADA	10	intron2+1988	gagaattttcttttatttt A/G tgcaggagaaatataaaca	1277
AADA	11	intron2+2341	aggtgcctttctattgtcc C/T atgcagacttaggtgatcct	1278
AADA	12	intron2+2546	gtctgacacagaaggatcaa T/A ggcaaaatgtgcaagacaaa	1279
AADA	13	intron2+2609	taggaggttccactgggaaac T/C tgaattccactgagtcata	1280
AADA	14	intron2+2663	tataaatacagtggttaaatt T/C gtctctcgtattttaaggta	1281
AADA	15	intron4 + 605	tgtgtcagtaaaatattata T/C taagtaggtgaatgagatca	1282
AADA	16	intron4 + 621	tatattaagtaggtgaatga G/T atcatgtaattgtgagacta	1283
AADA	17	intron4 + 679	ttagagattcagacgaattc A/G tataatcttcgatgggtgat	1284
AADA	18	intron4+1680	gttaaaatgtggataaatac C/T acaatttgcaaaatatttgg	1285
AADA	19	intron4+1748	atttagaagttctatacatc T/C tttatagtattattacacact	1286
AADA	20	intron4+1771	tatagtattattacacacttc G/A aaaacacaaaattattttt	1287
AADA	21	exon5 + 238	caagtcactcttccaaattt A/G ttaattggagttccctgctc	1288
AADA	22	3'UTR + 121	ttagaaattggtcttttta A/G aatggtctagtttaagttcca	1289
NTE	1	5'flanking - 535	caagatctgtctccgattc C/T tgttaactctagactttctg	1290
NTE	2	5'flanking - 15	gtaaatccccggcaaaaacc A/G gcagcgcttgcaagccac	1291
NTE	3	5'flanking - 748	agcatggcgcggggaggagg G/T gtgggagggtcgggaggagc	1292
NTE	4	5'flanking - 690	tgaataatttaaaggggccc T/C gcctgcggagccgggaggaa	1293
NTE	5	intron6 + 605	tcttgccatatacttagtgg A/G ggggtctacatcaggggttt	1294
NTE	6	intron6 + 748	agcctccagcctctcttctc C/T ggggggttatctcaggcatct	1295
NTE	7	intron6 + 987	gggtctggctctgggatccc C/T gtgcgtcatgtagtctacot	1296
NTE	8	intron6 + 1882	tggcctcaagcaatcctccc G/A cctcggcctcccaaagtgtc	1297
NTE	9	intron6 + 2222	gaatgttatgtagaacaga G/A agactgtatctcgggtcttc	1298
NTE	10	intron12 + 166	tatctggtaccgaggaagct C/G tggcctcgtccccaaggggcc	1299
NTE	11	intron13 + 69	atccagggtccaccgctgcc C/T gtcttgattgtttaatctg	1300
NTE	12	intron14 + 8	agccccgcctcgggtaaggc C/T tgggacctgcccgggtgtg	1301
NTE	13	intron16 - 113	gccaccgcgccttgcgcctt T/C atatttttcttaaccttcc	1302
NTE	14	intron21 + 34	agagccggccggcccagagc A/G tgctgggagatgtagtccgg	1303
NTE	15	intron21 + 128	gaagaaatcgtgccctgag G/A gtttcaaaccctaagtagga	1304
NTE	16	intron21 + 151	ttcaaaccctaagtaggacc C/G aggtgcagagcattctgggg	1305
NTE	17	intron21 + 651	ccactgtactccagccggga C/T gacagagctagaacctgttt	1306
NTE	18	intron21 + 737	tggaaaatagtctgtggatt G/T ttgttaggactctgggcac	1307
NTE	19	intron21 + 1752	acagctgggtctaggctgtta G/C tggagaaaactgggaagcaac	1308
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/Δ gtagcttttctttcttggc	1309
NTE	21	intron21 + 1907	cactgcaacctctgcctccc A/G ggttcaagtgttctctctgc	1310
NTE	22	intron21 + 2065	ctgcctcgttttatgttcag G/T tccccattagacagaggaa	1311
NTE	23	intron21 + 2336	agtctgggagcacaggagca G/A gaatttcagataaggaggaa	1312
NTE	24	intron23 + 41	tggggagggtgggtgggtggg G/C ctggagcctcaaatctttc	1313
NTE	25	intron23 + 71	caaattcttccagacctgag T/C tcaagttctcggcttccaac	1314
NTE	26	intron23 + 81	cagacctgagttcaagtct C/T ggcttccaaccacggagcct	1315
NTE	27	intron24 + 150	gtggggcggtgtgtaccto A/C gccgtcgtattccgcagct	1316
NTE	28	intron29 + 37	gcctgcagcaaccgctgacg T/C cacgtggggtggggggatg	1317

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GENE	number	position	SEQ.	SEQ ID.No
NTE	29	intron29 + 370	cgtcccaggtcagcgagccc G/A tcgggcccggctgggootccg	1318
NTE	30	intron30 + 56	acctcccgaccacacacac G/A cacacgcgtgggcacacaca	1319
NTE	31	intron30 + 358	aaaaatacaaaaaattaacc A/G ggctgggtgggtgtgcctgt	1320
NTE	32	intron30 + 372	ttaaccaggctgggtgggtg T/C gcctgtaatcccagctactc	1321
NTE	33	intron30 + 430	aatcaacttgaacctgggag G/T tggaggttgagtgagctga	1322
NTE	34	intron30 + 655	gtgtgcacaccagctatata T/C gcaaatgtttctctcaggg	1323
NTE	35	intron30 + 659	gcacaccagctatataatgca A/C atgtttctctcaggggcag	1324
NTE	36	intron30 + 760	tgaatatgggcatttgccaa C/T gcatgccagtctgtcccgtt	1325
NTE	37	intron30 + 835	gcacacacgtagataggatg T/C ggacacctgtaccgagttaa	1326
NTE	38	intron31 + 40	tggctgctgcataggtggc T/C ggctaagctttgctacttaa	1327
NTE	39	intron31 + 41	ggctgctgcataggtggc T/C ggctaagctttgctacttaa	1328
NTE	40	intron31 + 1329	gtctgtcaagggcaggacag G/A ggatgtgtaggcgagtgctg	1329
NTE	41	intron35 + 31	aatggcttctgtcgttttc G/A gactggggaccacacctctg	1330
DDOST	8	intron2 + 1299	atcttctgatgactgggtt C/T ggtgcagtaactggtgtttg	1331
DDOST	9	intron2 + 1581	gatactgttgggtgggagaaa T/C gacagagagtgtaaaacagt	1332
DDOST	10	intron2 + 2822	gtttctcaacagggtgcattc T/G tgacgtttcagactggataa	1333
DDOST	11	intron2 + 3392	cagaaggcgtggaggcctgc C/T gcgcctccctctgttgctgc	1334
DDOST	12	intron5 + 495	attgcttgaacccaggaggc G/A gaggttgagtgagccaagg	1335
DDOST	13	intron6 + 226	ggaactgcttgggtcacagc C/T tcgttttgtcccagtatcc	1336
DDOST	14	intron8 + 303	aagagaaataggtcattagg A/T tgaattttaggcaagaga	1337
DDOST	15	3'flanking + 40	cacagcgtggagacggggca G/A ggaggggggttattaggatt	1338
MRP2	1	exon 1 + 77	catattaatagaagagtctt C/T gttccagacgcagtcaggga	1339
MRP2	2	intron2+192	atcaaagtggctttgatttt T/G gcataagaatggtgactctt	1340
MRP2	3	intron 1 + 413	gataagttotagaactggca A/C ctaatgatatggactagaag	1341
MRP2	4	intron2+3639	gtcatatcccacccccaaat C/A gacccaataggtacaatgaa	1342
MRP2	5	intron2+3989	agttatgaaaccgatttttc C/T gggactggttgttctagtct	1343
MRP2	6	intron2+4078	aggtttccagatgtgttccc T/C aggcattctgtgtgtagga	1344
MRP2	7	intron2+4171	cttattcttggctcagttgg C/T tttctaccacctcttagctt	1345
MRP2	8	intron 2 + 5373	gttaaggatatgtgaactca A/G aatttttatacacagtgcaa	1346
MRP2	9	intron2+4436	ggactagtgaagaattaga C/G ctttctgaataaatagatc	1347
MRP2	10	intron 2 + 3930	aaaactggcaggagaatttc A/G ctggagctgcatgcaggact	1348
MRP2	11	intron 2 + 4257	gggtatttgaaagtcttgc G/A gctgctggaggctgcggtgt	1349
MRP2	12	intron 3 + 772	ggtataaggcaagattttt A/T aaaaaattaattgcttaatc	1350
MRP2	13	intron 7 + 1658	ggactcttaccagcttagtt G/T cctggttttctaatactaaaa	1351
MRP2	14	exon 10 + 40	tggccaggaaggagtagacc G/A ttggagaaacagtgaacctg	1352
MRP2	15	intron 11 + 1672	aactttttaagtottaagac T/A ggaaggcctgtgtcctaggg	1353
MRP2	16	intron 12 + 148	ccctctcaccgccccatgcc A/G ctttctccttctgtaccat	1354
MRP2	17	intron 2 + 1020	agtgtctgcgattacaagcct G/C agccacctgcacagcctctg	1355
MRP2	18	intron 2 + 5227	taccataatttatgtgtcct A/G tatgacatgaatttcattgg	1356
MRP2	19	intron 2 + 5373	gttaaggatatgtgaactca A/G aatttttatacacagtgcaa	1357
MRP2	20	intron 2 + 5538	ttaatgaggttaagcacatg G/T tcatatgtttaaaagccttt	1358
MRP2	21	intron 13 + 180	catgagttttotgagcccca G/C ttatcttaactataaaatga	1359
MRP2	22	intron 13 + 1497	gtgcagggtccccctgatgc T/C atagccagttcctctttaga	1360
MRP2	23	intron 15 + 169	atgagctgaaagcaaagggt T/C tcagccccttcccctgataa	1361
MRP2	24	intron 15 + 949	ttccagggtgacacatttagt A/G cctaatttgggaaatgttaa	1362
MRP2	25	intron 15 + 984	tgtaatctagtccaatccc A/C tttagtaagaaaggagggtgc	1363
MRP2	26	intron 16 + 4059	catcctgatgcacagttatt C/T aaatttaagctccatttgtt	1364
MRP2	27	intron 19 + 10899	atgtatggagtatttatgga G/A taaagtattccatgctgtat	1365
MRP2	28	exon 22 + 51	caagcaataggattgttttc G/A atattcttcatcatccttgc	1366
MRP2	29	intron23+56	tatactgaggatctttctga C/T agggaggaattattatgtcc	1367
MRP2	30	intron 23 + 734	tgagccaactactgtactag G/A cactggggcactcaatgaat	1368
MRP2	31	intron 23 + 801	atgggcccagacccaactcac T/G gattttttagtgtatctgag	1369
MRP2	32	intron 27 + 124	gggtccctaaagtcttctt C/G ctctaactcaaaaggacctaa	1370
MRP2	33	exon 28 + 52	cagattggcccagcaaaaggc A/C agatccagtttaacaactac	1371
MRP2	34	exon 28 + 84	aacaactaccaagtgcggta C/T cgacctgagctggatctggt	1372
MRP2	35	exon 28 + 129	agagggatcacttgtgacat C/T ggtagcatggagaaggtagg	1373
MRP2	36	intron 29 + 154	ttccctaggatggacacgtc A/G ttccagaaactttgaaatgt	1374
MRP2	37	intron 30 + 91	gtgttaggtgatgcctggca T/C agaattttcatccaggtctg	1375
MRP2	38	intron 31 + 170	gcaaaaattttacatcacgc A/G aatgaaaacgaacaaggtta	1376
MRP2	39	intron 26 + 154	ctggctccatcttttaccga T/C ggacgtattccttactcttc	1377

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GENE	number	position	SEQ.	SEQ ID.No
MRP2	40	3'-flanking + 739	gtgaattttattataagct C/T gttctccttaaaactttatc	1378
MRP2	41	intron 3 + 1145	acatccttctcccctcagtc C/T tcggttagtggcagttct	1379
MRP2	42	intron23+432	tggcagtagagcagggtgag G/A aggattattctgcagaggaa	1380
ABCB1	1	5'flanking-196	gcttggagccatagtcacg T/C actcaaaattttttatct	1381
ABCB1	2	5'flanking-16	tactctttacctgtgaagag T/C agaacatgaagaaatctact	1382
ABCB1	3	intron1+71660	cttgctggaggaagggtgct A/C gaaaatataccaaatccaag	1383
ABCB1	4	intron1+80091	gaaataatattcaagttctg A/C aataatatcatgacctatag	1384
ABCB1	5	intron1+103126	gatatgaatcagaattcatc T/C gtgtctcaagaaaaggctcat	1385
ABCB1	6	intron1+103148	tgtctcaagaaaaggctcatg C/T gataaattaagttctgctag	1386
ABCB1	7	intron1+108428	aattaatttatcatcatctg A/G tcaccatttcacacaactca	1387
ABCB1	8	intron1+112042	cataagttgaaatgtcccca A/G tgattcagctgatgcgcgtt	1388
ABCB1	9	intron2+491	gctctctggcttcgacgggg G/Δ actagaggtagttctacct	1389
ABCB1	10	intron4+36	attaactattcaaaatactt C/T ggaaatttgacatctcctta	1390
ABCB1	11	intron5+1596	ttagctctcttactgcttca T/C agtggagaatcaaatactt	1391
ABCB1	12	intron8+1789	aaacactctgaatattaaac C/T gctcctggaaccacagctca	1392
ABCB1	13	intron14+24	agttgtccttgcccttgcc T/C ttctagagggtgcaaaaaata	1393
ABCB1	14	intron14+81	tgcaggaagttaggaaacta C/T tataaatcggaagaagggaa	1394
ABCB1	15	intron15+38	caaaccaacctgattataa A/G cataagaacattctactact	1395
ABCB1	16	intron17+73	gtttgggtgggctagggtac A/G gtaggagtgggaacaagaga	1396
ABCB1	17	intron18+564	caacagtaaagttacaatct G/A aaaggaatgctctctgttta	1397
ABCB1	18	intron18+2062	tttccttgaggaaatggttat C/T ctctgtgtccttgagtcca	1398
ABCB1	19	intron18+2293	ccacatcaggttttcccag A/G caccttgggacagtttgaaa	1399
ABCB1	20	intron20+557	aaaaccctaaccattgacac G/A tgtgaatgtttcctgggga	1400
ABCB1	21	intron21+24	cgtgcctcctttctactggt G/A ttgtcttaattggccattt	1401
ABCB1	22	intron21+2725	ctgacctgttttggctgac A/G ggttttagttcctcccctca	1402
ABCB1	23	intron21+4725	tcttggtattaaaagatcca A/G agagataggaatatgtaatt	1403
ABCB1	24	intron22+8507	tgcacttaggaaaaaaacaa T/C atggaaatgtgtaaaatata	1404
ABCB1	25	intron22+8537	tgtaaaatatacttttttt T/A aaaaaaaaggacacatttat	1405
ABCB1	26	intron22+8565	aggacacatttattcagcat T/C atgatcagactattacattt	1406
ABCB1	27	intron22+8952	caccttggtttcatggtttg G/A caaagtactggcctgtacca	1407
ABCB1	28	intron22+9520	caccaacaaatatcttttc A/G cagttgggtgggcatctggt	1408
ABCB1	29	intron22+9836	agactctgacttagacatga C/T ggcaggggaaagagagactt	1409
ABCB1	30	intron24+377	taaaatacagatgtgttgta C/A taagttctgcaagcctttgg	1410
ABCB1	31	intron24+1493	ggggaggtgtccaggcacga A/Δ catggagagctggacttgat	1411
ABCB1	32	intron24+1495	ggaggtgtccaggcacgaac A/T tggagagctggacttgatac	1412
ABCB1	33	intron25+342	tgcagccttgatctctggtg C/T tcaagcatcctcctgcctc	1413
ABCB1	34	intron26+134	cttgataaagtctgagagc C/G taaatatggtctccaagtgg	1414
ABCB1	35	intron26+1272	gtccttcaattttgtggtga A/G cttaaaaacaggactctaaa	1415
ABCB1	36	intron26+1394	tattaagtgtgtgttaaag A/G ttgtctataatgaattgta	1416
ABCB1	37	intron26+(1987-1988)	aagggtctggaagagtgaag (AAAG) gaggtatttgcctccagac	1417
ABCB1	37	intron26+(1987-1988)	aagggtctggaagagtgaag gaggtatttgcctccagac	1418
ABCB1	38	intron27+59	gcagcctctctggcctatag G/T ttgatttataaggggctggt	1419
ABCB1	39	intron27+80	ttgatttataaggggctggt T/C tcccagaagtgaagagaaat	1420
ABCB3	1	intron3+8	tctcctttggcaggtaggtg G/A tgggcagctgggtccatttg	1421
ABCB3	2	intron4+104	cttcacccgatgccaggac C/T tggggatgctttctcttctg	1422
ABCB3	3	intron10+219	gcagcagtggtgctccctcc A/G tgggcagccccgtcaggtcc	1423
ABCB3	4	intron11+(317-319)	atggtgccaggtggatgtg GTG/Δ tccatctcattcctgtcttt	1424
ABCB3	5	exon12+19	agctgcaggactggaattcc T/C gtggggatcgcacagtgtg	1425
ABCB3	6	exon12+(356-357)	aggtgggtgggtgggtg GG/TGGTGGGGTGGA ggctg tctgtgtccagga	1426
ABCB7	1	intron1+220	acggggcaggaggttctggg C/A agaggacacctggagcgtg	1427
ABCB7	2	intron1+480	agttaactcccttctgaca G/A gcgtgcttcttgataggcca	1428
ABCB7	3	intron1+(512-513)	gataggccaaaaccgtaact AT/Δ ctttccaaaacatagaccgc	1429
ABCB7	4	intron1+1690	agttotccaataaggcagat G/A aagttaagataaaatttga	1430
ABCB7	5	intron1+5309	aattaatatcatttattgct G/A tattgtgtcagtgttatct	1431
ABCB7	6	intron1-11274	tgcttctttcaagccagcc A/G gctttaaaaaaagttagct	1432
ABCB7	7	intron1-11085	caggtttccagggtcatgt A/G gacctgaagaaaaatgagag	1433
ABCB7	8	intron1-10037	attctactttctcaactct T/C ttattacattatctcatcat	1434
ABCB7	9	intron1-21	ccactctgaaacttccccct G/A cttttttccttgcagcag	1435
ABCB7	10	intron3+(135-136)	ttctctaataaaaaaaaaa (A) catattaattgaccatagtt	1436

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GENE	number	position	SEQ.	SEQ ID.No
ABCB7	10	intron3+(135-136)	ttctotaatgaaaaaaaaa catattaattgaccatagtt	1437
ABCB7	11	intron3+333	aaaacaatttggtgtgtgc G/A tgtgcttcaagggttaattgtt	1438
ABCB7	12	intron12+524	taaccactctgocctcagta C/T gaaacacagtgcogaaccca	1439
ABCB7	13	intron13+1543	atcctgtgaggtggggaagc G/A tatggctagcataaataaa	1440
ABCB7	14	intron13+2400	tgttaccttactgocctcatt C/G tcattcttcccacctgctat	1441
ABCB7	15	intron15+2201	ctccttcttaaccttagcaa G/C agtctggagatttacttato	1442
ABCB8	1	5'flanking-2272	ggcttaggcctaagggtga T/C gttggggccagtagccctga	1443
ABCB8	2	5'flanking-2070	agctatgaaaaacaagacct G/A tccttctagaggtagcaaaa	1444
ABCB8	3	intron1+25	aaacggaaaaacctactcag A/C gcgggccattgaccggccgg	1445
ABCB8	4	exon2+308	tgtgtgctcctggggtagcc G/A tcgtggtgaggctttcccca	1446
ABCB8	5	intron2+334	cccccaacttaaacatttgt C/G ccctctgtctccccattcca	1447
ABCB8	6	intron4+12	cctgtcctcggtactgccagc C/T gcagggtgcagagttggggt	1448
ABCB8	7	intron5+547	agttcatagcattctcgtc G/A gccccctcaggcctgctgct	1449
ABCB8	8	exon7+57	ggcaatgtgcggactgtgcg A/T gccttogccatggagcaacg	1450
ABCB8	9	intron9+1231	ttccgcagctgcattggaca C/T cctcgcgtgccccgtttctg	1451
ABCB8	10	intron9+2164	cctcttgagggtccttctag C/T gctgcctatgtggagattct	1452
ABCB8	11	intron9+2645	ttcctgcctggtgcctcccc C/Δ ggtgccttagcaagtgtct	1453
ABCB8	12	intron9+2646	tcctgcctggtgcctcccc G/A gctgccttagcaagtgtct	1454
ABCB8	13	intron9+3229	caggcccgagcaggaggtcc G/A tgggtcagctgggctccctt	1455
ABCB8	14	intron12+(113-114)	tcctccactgccacaagggg (GG) ccttcttctcctgggacaatc	1456
ABCB8	14	intron12+(113-114)	tcctccactgccacaagggg ccttcttctcctgggacaatc	1457
ABCB8	15	intron13+128	tgctctcgggagaccctggc C/T gtcttcacatgtcctcagct	1458
ABCB8	16	intron13+305	atccagggtctagagaagcct A/G tagtggaggtgctgagctgc	1459
ABCB8	17	intron14+135	acagttgtgtcagggaagac C/G agaaccacagccaaagggga	1460
ABCB8	18	intron14+159	accacagccaaaggggacag A/T gtcgttgtgtggggacaggg	1461
ABCB8	19	intron15+747	gttggagccttgggctctgt A/G agggggacagagggaatcat	1462
ABCB8	20	3'flanking+333	cctatcccctggctcaccoc G/A ggaccacagtcctccatctt	1463
ABCB8	21	3'flanking+1168	ccctcttcagggggtgtgat G/A cagtgcattgatggagcagc	1464
ABCB8	22	3'flanking+(1719-1721)	tagaccgcaggagccgcgcc GTC/Δ ttctaacctgcctcggcc	1465
ABCB9	1	intron1+ 69	agggtgccaggccaggcagc G/C gttggggggcgtctgggcac	1466
ABCB9	2	intron1+8873	tgggcccagcacgtggggcc T/C ggaactacctcaaaggcttc	1467
ABCB9	3	intron1+8940	accagctcagcctgccagc G/A tgcacacggcaccacagctgg	1468
ABCB9	4	intron1+11410	agatccaaggatccagagg T/C tggaatgtgacctccgtgc	1469
ABCB9	5	intron1+12863	gggaagccagatgccacaa G/A gctctgtgacttcaattcca	1470
ABCB9	6	intron1+19731	gccaagtgtcaagatcgagc G/A aggggagggcctgacgaggg	1471
ABCB9	7	intron1+29649	cagaatccagatcccgtaa T/C gttgttaagaagcctgcaca	1472
ABCB9	8	intron1+31793	ggccaggcggggagggttac C/T ggccagaccggtgggcaaaa	1473
ABCB9	9	intron1+37537	agagtcacagggttggggtg C/A ccccggaagggtggcatcta	1474
ABCB9	10	intron1+38293	taccagccctgtgcttccag G/A gacctgtgacctgtcaact	1475
ABCB9	11	intron1+44661	cccagggtgcctggcttcac A/G gcaggattgccgtcctgcag	1476
ABCB9	12	intron1+49576	aaagtggccccgtgcttgt C/T ccctgaagccctaaagcacc	1477
ABCB9	13	intron1+64669	ccacagacaagccgggtagc C/A cacctgcagctcaacacac	1478
ABCB9	14	exon2+448	cctggttttggccctgttc G/A tgtggacgtacatttcaactc	1479
ABCB9	15	intron7+3364	ggtaccaggagtcgggtatc A/G gtgggacaggaacgcgtgtc	1480
ABCB9	16	intron11+113	gggccccaggagctctccca G/T actatcagcctcctgggctg	1481
ABCB9	17	exon12+370	cccaggcctgcagcactgaa A/G gacgacctgccatgtccat	1482
ABCB10	1	5'flanking-424	tcgcgtctgcgcgtccgcc C/T ggtctgccggcgtgagaaag	1483
ABCB10	2	exon1+491	acaaggggagggtgcgcccc G/T cagcggccggactcccgag	1484
ABCB10	3	intron1+37	ccacttccctccgcggggcc T/G ctcttctccacacggggg	1485
ABCB10	4	intron1+217	actcgtttgcagatttaca C/T ttgtttcttgttgacacac	1486
ABCB10	5	intron1+405	gcgtttatactttttttt T/Δ aacaaaaaacattatttg	1487
ABCB10	6	exon3+185	agggccggggcccaggcttc C/T gtaggcacagtatgatggt	1488
ABCB10	7	intron6+1269	caaattcacaactgtgcctt C/G cacagaatgggttgaaaaac	1489
ABCB10	8	intron9+632	ccccactccacttgggtgag G/A gcagggtgaggtgatgggt	1490
ABCB10	9	intron10+2373	tacctcagggcactcagaca G/C cctcaccaatcagaggctca	1491
ABCB10	10	intron11+108	tccttttctgtttttttt T/G ttttttttttggagtgg	1492
ABCB10	11	intron11+2379	cattggttttagtgatttc T/A gtgttgatccatcatca	1493
ABCB11	1	5'flanking-(2596-2595)	tgtggttagagctttctct (TT) gagacattttgctaagggt	1494
ABCB11	1	5'flanking-(2596-2595)	tgtggttagagctttctct gagacattttgctaagggt	1495
ABCB11	2	5'flanking-1746	agctgaagtgaattaagcac G/A atcaactcagtactcacact	1496

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GENE	number	position	SEQ.	SEQ ID.No
ABCB11	3	5'flanking-(326-314)	agggggaaagttaaaggta (T)9-12 gtcttggtatgttttaagt	1497
ABCB11	4	5'flanking-135	agagggttcccaagcacac T/C ctgtgttgggttattgct	1498
ABCB11	5	intron1+511	aaatatagatgcaaaaaaa A/Δ tgagctgtggatgcatgttt	1499
ABCB11	6	intron1+581	aatttcagtttttaggtcac C/T caagccagtgggagtcacat	1500
ABCB11	7	intron1+(1938-1951)	aaagacgttttaagggttt (A)10-13 gaaagaaaagaaaactgtag	1501
ABCB11	8	intron1+4517	ggtttcccaacatctcatct G/A ataaaaaaataatttgcca	1502
ABCB11	9	intron1+5651	aaagagaataggtagtgga T/C tagtattcctgtgcttaatg	1503
ABCB11	10	intron1+(12200-12201)	aagagatggctctagcccc CT/Δ gtttgattggggcacttac	1504
ABCB11	11	intron1+13023	gtttggctactttgattaaa G/A aagaaagaagagataataat	1505
ABCB11	12	intron2+739	cctgcacatattctgaccta C/T actggggaaaacagtatgtg	1506
ABCB11	13	intron2+(921-922)	tattttgtagttcaaaaaagt (GAGATCTTCTTCAGCT AATTTAGAAATGT) tgctgtccatttgatattca	1507
ABCB11	13	intron2+(921-922)	tattttgtagttcaaaaaagt tgctg tccatttgatattca	1508
ABCB11	14	intron3+644	agccacacgtttctatttgc G/A tgggaagtttaaaaaatggg	1509
ABCB11	15	intron3+2231	agtgaacctgagattgagct A/G tactgaaatctctagaagag	1510
ABCB11	16	intron3+2406	aaagggtggtctttaaatcc T/C tatgttttctcatcaggtt	1511
ABCB11	17	exon4+10	tttctcatcaggttacaaga T/C gagaagaaaggtagtgccgt	1512
ABCB11	18	intron4+434	acaatttatagtatttctca A/G tgccccacacagtttatota	1513
ABCB11	19	intron4+518	gtagatgagtagctaaaaac G/T aaagtcagctcctgaaataa	1514
ABCB11	20	exon5+120	ggcacaatgacagatgtttt T/C attgactacgacgttgagtt	1515
ABCB11	21	intron5+320	gggaggtgacccatgaattt T/C acttgagtatcatctccaag	1516
ABCB11	22	intron5+16076	agaagaggtaacagtaagcc T/G cctgattacagcacacatc	1517
ABCB11	23	intron6+303	atttgcaggtgtgttttag G/C gggcagttgagtagcttgaa	1518
ABCB11	24	intron7+1141	aaaggattcagcaggcatga A/G gaaagaaaagcctttgcaaga	1519
ABCB11	25	intron8+2463	ccattggctaataagcaatga A/C ctatgacatggtctaactta	1520
ABCB11	26	intron8+2677	tcaatgatgttacagtgaga A/C tctaattattgtattaaaccc	1521
ABCB11	27	intron8+2699	ctaattattgtattaaaccca T/A gccacatgttaaatgaatct	1522
ABCB11	28	exon9+24	gtgtccaagtttacggacta T/C gagctgaaggcctatgccaa	1523
ABCB11	29	intron9+108	caccttggtctgtggcctcc A/G gaggaagtacttgttcaaga	1524
ABCB11	30	intron10+2475	taatcattccaaaccacgga C/A ttatttcattaagaacatg	1525
ABCB11	31	intron10+2478	tcattccaaaccacggactt T/A atttcattaagaacatgata	1526
ABCB11	32	intron10+2711	tttacagattggaaaagcca C/T tgaagtattgcaggtccaga	1527
ABCB11	33	intron10+3539	agtgactgtaattagatca C/G ttgtgcacagagaaaaaatg	1528
ABCB11	34	intron10+3623	tgcagaaggtgttctttca T/C gaccttctgagtttcagaa	1529
ABCB11	35	intron10+3661	gaattcattaataaaaaataa A/T cacataatggagcgtgacat	1530
ABCB11	36	intron10+5100	gggccactctttggcttggc A/G atagactgtggccaatgaaa	1531
ABCB11	37	intron10+5292	gotatttggtaggaacatct G/A ggcattgatcaggtagccttc	1532
ABCB11	38	intron10+5912	gagtaatttcagtaaaaaa A/Δ taaagtggatttttaataca	1533
ABCB11	39	intron12+116	tgtttcagtaatagggaat G/A gaggtgtctttctctgaaag	1534
ABCB11	40	intron12+326	gataaatgacaaggcaatta G/C aacaatcaggaagcacaggt	1535
ABCB11	41	intron12+335	caaggcaattacaacaatca A/G gaagcacaggttcttcccaa	1536
ABCB11	42	intron12+2572	cctcatccttgccaatgttt C/T cttttactggtttttgatgg	1537
ABCB11	43	exon13+23	tctaaatgacctcaacatgg T/C cattaaaccaggggaaatga	1538
ABCB11	44	intron13+70	atggcagtatattgatcaaa C/T agaaagggttagcatacatt	1539
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttt (C) tgccattgggtcaagtatga	1540
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttt tgccattgggtcaagtatga	1541
ABCB11	46	intron14+32	catacattcctgggagaaac C/T aagaggatcatagaaggaaaa	1542
ABCB11	47	intron14+80	cacaattatacacatttctt C/T tcgtatgattcccaagtcac	1543
ABCB11	48	intron14+439	tattgtgtcaaaaacaattc A/G ttgtatatctcatttotaag	1544
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatatttt (T) gctgtgtgtctaacaggag	1545
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatatttt gctgtgtgtctaacaggag	1546
ABCB11	50	intron14+1283	gctgtgtgtctaacaggag A/C aaagagacacggatttgctc	1547
ABCB11	51	intron14+1339	tgagatagatatttaggacc G/A tgaccaattttatttttgg	1548
ABCB11	52	intron14+1359	gtgaccaattttattttgg T/C tgaaaaatcttatttgaagt	1549
ABCB11	53	intron14+1480	tattgattagacaataaccc G/A tctggggaaggatatttct	1550
ABCB11	54	intron15+370	ccttttctaattgtctgcaca G/A cctatttaagaatattccca	1551
ABCB11	55	intron16+(550-559)	aaagtttagtgtttctatca (T)9-12 gctacttctgatggacttct	1552
ABCB11	56	intron17+188	tttctctcccaattcatgg T/G tttttggttagcttctcatc	1553
ABCB11	57	intron17+194	tccccaattcatgggtttt T/G gttagcttctcatctcttg	1554

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GENE	number	position	SEQ.	SEQ ID.No
ABCB11	58	intron17+(197-198)	caattoatggggttttgggt (T) agcttctcatcttcttgggg	1555
ABCB11	58	intron17+(197-198)	caattoatggggttttgggt agcttctcatcttcttgggg	1556
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)7G(A)4 tctgtgttagtgttctct	1557
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)12 tctgtgttagtgttctct	1558
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)10 tctgtgttagtgttctct	1559
ABCB11	60	intron17+1070	tcagacttgggttttctat C/T tttcttcttgagaacaagtt	1560
ABCB11	61	intron17+1651	tgttaaaatatctcattgta T/C atgctgacggatttttcttg	1561
ABCB11	62	intron17+2226	ccttaagtctcctctatca T/A gcacctgttctcaccagct	1562
ABCB11	63	intron17+2979	ctctctcttcttctcagc T/Δ ctactatttactgttggt	1563
ABCB11	64	intron17+3288	aatccccatatcctacctta T/G ccctctcatccatgaatctt	1564
ABCB11	65	intron17+3289	atccccatatcctaccttag C/T catctcatccatgaatcttg	1565
ABCB11	66	intron18+97	aatatgagttttctaggtat A/G tatctagcagtggttcaagt	1566
ABCB11	67	intron18+98	atatgagttttctaggtata T/C atctagcagtggttcaagtc	1567
ABCB11	68	intron18+892	ctctgaaagtagtgatata C/T cttatttgtgttgatcaa	1568
ABCB11	69	intron18+2681	atgtatgagatcaagtcagg A/G tcaaatattagacaccata	1569
ABCB11	70	intron18+3780	ggaccatctgtggggcaat C/G gttccagaaaatgctggtat	1570
ABCB11	71	intron18+5741	ctcacgggtataaatacaac C/T gtagcaaagggttttctttt	1571
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttcag (C) ttttattcaagccacagca	1572
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttcag ttttattcaagccacagca	1573
ABCB11	73	intron19+10022	tggctaagttaaaaaaaaaa A/Δ gagattcaactataattgct	1574
ABCB11	74	intron21+322	caagattcaatactgcccc C/Δ aggggggtgggtgaacagggc	1575
ABCB11	75	intron22+257	ctgttcaatttctctcgca T/C agtgattcattccacattcc	1576
ABCB11	76	intron22+552	taattaatatcttgccttg G/C ggggtaaatgagggatggtta	1577
ABCB11	77	intron22+569	ttgggggttaaagaggat G/A gtacataaacacttctcaa	1578
ABCB11	78	3'flanking+243	aaacaccacagaatgacata G/A aactaaaggcggcaggaatc	1579
CYP4B1	1	5'flanking-333	gaaacattcagagtgctgt A/T tgagaagacagtggttatta	1580
CYP4B1	2	5'flanking-18	gagcagctgaaggcaggtca G/T atgaaggctaggtggctgga	1581
CYP4B1	3	intron1+341	tccaaaacctctggatagta C/T atagaagtaggcaatccatt	1582
CYP4B1	4	intron1+542	cctatgggtggctcaggagc C/T gtgacaccttcccaggttca	1583
CYP4B1	5	intron1+2856	gaggactttgcacatagtag G/A tgctcagctatattgttggc	1584
CYP4B1	6	intron1+6086	tttgaatctaaagactggg G/T cacgatgctagtgtgtgac	1585
CYP4B1	7	intron1+6598	ttttgggtgtggggagagg G/A cccatagtagggagacagct	1586
CYP4B1	8	intron1+6660	acctaagggtgtccatctg A/G aggagagcagtcctaggggg	1587
CYP4B1	9	intron1+7242	ccctgtctcccttaactca T/C gctggactgttcccttgggt	1588
CYP4B1	10	intron2+107	gcctgtgtactaagtctg G/C agctgaggttcccacctac	1589
CYP4B1	11	intron3+361	atggtgtgtggttaggacca C/T ggctgtgaccagaggctgt	1590
CYP4B1	12	intron4-492	aaaggctttcacatctaaaa C/A gtgtctctcattttctgtc	1591
CYP4B1	13	intron4-315	ggattacttacatatacacc A/G tgcgggggagctcaccacct	1592
CYP4B1	14	intron4-157	ctaccaccttatctgata T/C tccagcaggatggagggcag	1593
CYP4B1	15	exon5+22	acaagtgggaagagaaagct C/T gggagggttaagtccttgac	1594
CYP4B1	16	intron5+125	cccaggagccttagcttgc G/A gggagacaggacctgctcat	1595
CYP4B1	17	intron5+(287-289)	tgtctaagccaatccctct CCT/Δ accctctgcttagcaggagc	1596
CYP4B1	18	intron6+54	gcctgggttctctctctgg C/T ccctctatgccccctccat	1597
CYP4B1	19	intron7+(99-100)	agctottaagcatttcccc (TC) tttctcagcaaatataacc	1598
CYP4B1	19	intron7+(99-100)	agctottaagcatttcccc tttctcagcaaatataacc	1599
CYP4B1	20	exon8+114	tctgtgttctctactgcat G/A gccctgtacctgagcacca	1600
CYP4B1	21	exon8+139	tgtacctgagcaccagcat C/T gttgtagagaggaggtcgc	1601
CYP4B1	22	intron8+247	agaaagttgtcaacaagagg C/T tgatatttgtgtgtaact	1602
CYP4B1	23	intron8+366	tgtgggggtgaacagagctg A/G gacagctgggagagccagtt	1603
CYP4B1	24	intron8+650	cctttgcttgtgtgcagaca C/A cctgccttctctctgggt	1604
CYP4B1	25	intron8+844	tcatatgtgagaatcccc C/A ccacgggtatccagacaca	1605
CYP4B1	26	intron8+1767	tccattccaagaatgttct G/T gttgtgtgctggcagggat	1606
CYP4B1	27	exon9+53	tgtgcatcaaggagagcttc C/T gcctctaccacctgtgcc	1607
CYP4B1	28	intron9+652	agtggatgtggtcatgaac G/T ctctgtcactggcagtggtc	1608
CYP4B1	29	intron9+774	cctggtcaccaacctctgtt C/T tgcccacaggaagcctgatc	1609
CYP4B1	30	intron10+33	tgggctgggagatcagacag G/T gtgggggactgggagggtca	1610
CYP4B1	31	exon12+224	ccagatggctcaggctgtga C/A ctccctgggcaccacctcc	1611
CYP4B1	32	exon12+270	ctgggtgtggaggagttggg G/A cccctgccttcaggaggct	1612
CYP4B1	33	3'flanking+129	tctgtgtctcacagtcacgt G/A gtgtccaggcattcagggt	1613
CYP27A1	1	intron1+295	aggaggagctgtcttggga A/G gagagtggcagaggcaaatg	1614

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GENE	number	position	SEQ.	SEQ ID.No
CYP27A1	2	intron1+17503	cagtgcataaagcctctgat C/T ctcttagagaaggaggac	1615
CYP4F2	1	intron1+(145-146)	ccaagccctggcaacctca CA/Δ gtgattcaggctgggccttt	1616
CYP4F2	2	intron1+193	tttaatcagtctctctct C/T ttccattctaagtgtta	1617
CYP4F2	3	intron1+324	ccctgctctacctcggcac T/C gcccgctcctgcctctcac	1618
CYP4F2	4	intron1+367	tccttgagggtccctgggcc G/C ttctctgggcctcaggatct	1619
CYP4F2	5	intron1+402	ggatctcaccgtccatcccg T/C ctgcctgcaggatgtcca	1620
CYP4F2	6	exon2+35	gcctgtcctggctgggcctc T/G ggccagtggcagcatccct	1621
CYP4F2	7	exon2+166	cgggtgttccacaaccccc A/G agacggaactggtttgggg	1622
CYP4F2	8	intron2+125	ggcagagaagcagaggaggc A/G tottactcattcctctgctt	1623
CYP4F2	9	intron2+440	gggccgtctccacttcac T/C acaccgaaggcacctttct	1624
CYP4F2	10	exon3+48	gttctgactcagctggtggc C/T acctacccccagggtttaa	1625
CYP4F2	11	intron3+701	agactccacccagcttggg T/A cccttctctgacctgtg	1626
CYP4F2	12	intron3+742	cttcccatcgttgacgggc G/A aggtgagcagggggaatgg	1627
CYP4F2	13	intron3+1020	gctttagctttctccatgc G/A ctttctctatcaagggtggc	1628
CYP4F2	14	intron3+1039	cgttttctctatcaagggtg C/A ctttctctatgatgtcaac	1629
CYP4F2	15	intron3+1040	gcttttctctatcaagggtg C/G ttttctctatgatgtcaacg	1630
CYP4F2	16	intron3+1920	ccacctgtctaacctctgtt G/C ctgttgctcatgtctgggg	1631
CYP4F2	17	intron3+1945	ttgctcatgtctggggcgtg T/A ctctacaatggctgttatat	1632
CYP4F2	18	intron3+2621	agcattctgtagaatgtga G/A ctgtgctcaggggttgogga	1633
CYP4F2	19	intron3+2665	tgttgatcgttaggaggc A/G tgtcaaggcatgtggaacc	1634
CYP4F2	20	intron6+194	gggtttgaactggtgggtgt G/T gtcagagctcttaggggac	1635
CYP4F2	21	intron7+67	tgtgaaatgtcagatgaaag G/A atttgaactgattaagagg	1636
CYP4F2	22	intron7+2811	ttccaagggaattgccatt T/G aattctctgttaactcaggt	1637
CYP4F2	23	intron7+(3096-3097)	gggggtgggggttggggggg (G) ttactgccttctctccagga	1638
CYP4F2	23	intron7+(3096-3097)	gggggtgggggttggggggg ttactgccttctctccagga	1639
CYP4F2	24	intron8+145	ggtgctgtctacctcgggt G/A ctgaagcagcccagagaccc	1640
CYP4F2	25	exon9+44	ctctcctgggtcctgtacca C/T ctgcaaagcaccagaata	1641
CYP4F2	26	exon11+48	gaaccatcacaccagct G/A tgtggccggaccctgaggtg	1642
CYP4F2	27	intron12+108	tggtccaagttccagctctc C/T ttccctcacctcctctggag	1643
CYP4F2	28	intron12+285	gcattgggatccaggcacgg A/T taccctctctctattctc	1644
CYP4F2	29	exon13+238	aagtgaagcctagaattacc C/A taagaccctgtccacagtc	1645
CYP4F2	30	exon13+342	tgtgcgtgaatgtcatggc G/A gccctattcagtagccaa	1646
CYP4F2	31	exon13+563	tagtgactgtcctttata T/C gaaattccagaacaggcca	1647
CYP4F2	32	exon13+707	aaatgtccggacctagata G/C tgacgaaggtagcacgacac	1648
CYP4F3	1	intron2+258	cattaatgcacctctcgggg G/T ctcttgggcagggggttggg	1649
CYP4F3	2	intron2+916	ttagggacatgtcctgagtc C/T aactgctccccacaaacct	1650
CYP4F3	3	intron2+3417	atccagggtctcacacagtgt C/T acttctctcttggcttag	1651
CYP4F3	4	intron2+4090	gagagcatgaattgggtcct G/A tgtcttctctccagattca	1652
CYP4F3	5	intron3+89	tgtgctgcctccagcgggtc G/A cgtgccatgtgcagacagg	1653
CYP4F3	6	intron3+243	tcaagtctgctgtacggcta C/T gtctgtcacctgtatattt	1654
CYP4F3	7	intron3+502	aggtctgggacccagggtcc G/C taagtgaactgtctgagaca	1655
CYP4F3	8	intron3+755	ttttgtggccatgtcaggac A/T tgtgaacacatgtcagtgtc	1656
CYP4F3	9	intron3+855	gggacagacagggtgtcta G/A gtcctgtgaaggcattctg	1657
CYP4F3	10	intron3+970	cctgacatagctcctacgtg C/T catgttaggcagtgtcattg	1658
CYP4F3	11	intron6+122	gaggagttgttatacctgat C/T gttgaaggactggtatgaat	1659
CYP4F3	12	exon7+159	ggtgcacgacttcacagatg C/A cgtcatccaggagcggcgcc	1660
CYP4F3	13	intron7+2107	cagggtgocagtgttttt T/Δ ctcaaaaagtttcatcaag	1661
CYP4F3	14	intron7+2255	gaccaagaagggtctaggag T/A gcaagatgggcttgggttc	1662
CYP4F3	15	intron8+132	cctcaatgcaagggtgtgt A/C caccctcgggtgctgaagca	1663
CYP4F3	16	exon9+59	taccacctgcaaagcacc G/A gaataccaggagcgtgtcg	1664
CYP4F3	17	intron9+13	attgaatggtgagtgcaggt G/A ctggtgccctgttctgagc	1665
CYP4F3	18	intron9+36	ggtgccctgttctgagcct G/C tctcattggctctgttccc	1666
CYP4F3	19	intron9+167	acctcctgactgtctggg C/G aaaggttataggcccttagg	1667
CYP4F3	20	intron9+369	tcctaattctacccttc G/A tccagtccagggtattataa	1668
CYP4F3	21	intron9+458	tcattcatccatccagtcct T/C gttcagcaatactctcata	1669
CYP4F3	22	intron10+46	ctcctgggttaggaagagggg A/C ccctcaggcaggagcattg	1670
CYP4F3	23	intron10+63	gggcccctcaggcaggggagc C/A ttgtcctgactgcccccttc	1671
CYP4F3	24	intron11+14	ccctgagggtcggggccccc C/G tctctgttttgtcattcc	1672
CYP4F3	25	intron11+84	gatcaggagaatccaacatc G/A cctccctccaagacacacac	1673
CYP4F3	26	intron11+113	caagacacacaccactgtct T/C tccaaggctggcggactggg	1674

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GENE	number	position	SEQ.	SEQ ID.No
CYP4F3	27	intron11+164	cggcaacccttcttgggtctc T/G cctccaggtctatgaccct	1675
CYP4F3	28	intron11+165	ggcaacccttcttgggtctcg T/C ctccaggtctatgaccctt	1676
CYP4F3	29	intron12+156	gaaaaggccacagagtagg G/A ttgggttggctcctagaagga	1677
CYP4F3	30	intron12+253	gagctcggctaggctcgag G/T atatgcaagccacatgggg	1678
CYP4F3	31	intron12+346	tgggtgtccaggccaggtt A/C ccggcttgatggggccagga	1679
CYP4F8	1	5'flanking-61	accatgtttaccatcattg G/T tcttgagctcccagcccc	1680
CYP4F8	2	exon1+67	gtggcagcatcccgtggct G/T ctctgtgtgtggctggggc	1681
CYP4F8	3	intron1+707	tacgcagcaggattcacca T/G tattccacattatccactg	1682
CYP4F8	4	intron1+857	acacccctaccctcacatc G/A tgacacagctgggcccagaag	1683
CYP4F8	5	intron1+907	tgccatctccacccctcccc G/A tgcagggcatcttctttat	1684
CYP4F8	6	intron2+668	tgtggcacttccaccatag T/C tcattgccctcttgcctcag	1685
CYP4F8	7	intron2+818	gccacagagaccatggctca G/A gcccacaaatgctgagtgc	1686
CYP4F8	8	intron2+1079	tatgcttgggtgttgagaa C/T atgttgaccatgtaggagc	1687
CYP4F8	9	intron2+1194	coggtcccccttatgcccc C/A accctccttcttctctgc	1688
CYP4F8	10	intron5+45	aacatgggtgaggtgggg G/T gtgggtgtggggagagcaaa	1689
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag (GCCAG) tggcctctcctgggtcttgt	1690
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag tggcctctcctgggtcttgt	1691
CYP4F8	12	intron8+222	tttattccccactaactg C/G tatgcaagcttagtaaaatc	1692
CYP4F8	13	intron8+334	cttgagaattaacggcaaa A/T accgcaatgacttttgacc	1693
CYP4F8	14	intron8+1999	ttctaagtacatttattctc T/C tgcttttagctatgatctag	1694
CYP4F8	15	intron8+4184	caggagggccgtgtatgctc C/T ctggataattgttgggtgtt	1695
CYP4F8	16	exon9+119	acgtggtgctcccagacagc C/T gagtcatcccaaagggtcc	1696
CYP4F8	17	intron11+282	gggttgggggttcgggcct G/C gttcctggcgagtggggc	1697
CYP4F8	18	intron11+340	tgcagtcagacctccacct C/T ggccccaggaactgcatcg	1698
CYP4F8	19	3'flanking+35	atcacctacctttgaccaa T/C tacctttcagatttcoggt	1699
CYP4F8	20	3'flanking+83	ctgtgttggccctgtgcct G/C agtcccgcgatggccagta	1700
CYP4F8	21	3'flanking+90	ggccccgtgcctcagctccc A/G cggatggccagtagggggcg	1701
ALDH1	1	intron1+564	cattattcttcagccaagt T/C tgttgccattggagcagatg	1702
ALDH1	2	intron1+710	gttctgagagtaactctgaa C/T ttgacctgttccactgct	1703
ALDH1	3	intron1-3868	cccttttatatccagaata C/G agcctaaactcttctctg	1704
ALDH1	4	intron2+2933	taagtatgctatactatatt T/C gatagatactatactata	1705
ALDH1	5	intron2-1646	caatgtgattaactgaatgc C/T gcaaatatgcaactgtatag	1706
ALDH1	6	exon3+54	caggctttcagattggatc C/T ccgtggcgtactatggatgc	1707
ALDH1	7	intron3+157	taggccccttaacattgaac T/G attotcaaatagtaatctgc	1708
ALDH1	8	intron3+339	tgagtctcctagaatgatag G/A ttaggtttattcaagcattt	1709
ALDH1	9	intron3+655	agcagttagatgagtcagag C/A ataataagttgggggaggg	1710
ALDH1	10	intron3+735	gaagccaatttaacataaac C/A aataccaagatcaggttca	1711
ALDH1	11	intron3+863	gcaagtatggttaatacaag G/A accatttattactcaaatat	1712
ALDH1	12	intron3+1757	agatgacaagattctctata T/A ttcaaaaattccctagcaca	1713
ALDH1	13	intron5+90	ttctctaaaacagatggatg C/A ttatgtattgttaaatgtg	1714
ALDH1	14	intron6+213	caggaagccaaacacaaagg T/C ttggtgtcaaacagtcact	1715
ALDH1	15	intron6+1323	tttgaattaaattcttata C/T tgaacttttaactttta	1716
ALDH1	16	intron7+638	gcaaaagaaagtgggtgaag C/A atactgtaccatgcaaaaaa	1717
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttt (T) gttgtgattatttatctatc	1718
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttt gttgtgattatttatctatc	1719
ALDH1	18	intron9+1757	tgatctagaatttagtttt A/G taaatgaatagaatccagtg	1720
ALDH1	19	intron12-1383	aatcccacttattactctcc T/G gagagctcaagtgcctata	1721
ALDH1	20	3'flanking+40	tttaagtacaagttttgt T/C acagtatttcttctgtca	1722
ALDH2	1	intron3+1766	aaattggtggctcatcctgc C/Δ tggcccccttctcctctc	1723
ALDH2	2	intron8+52	gaaggtagccctggccacct G/C tgtgtggctccagccgatc	1724
ALDH2	3	intron8+69	cctgtgttggctccagcc G/A atcctgtcgccccccagtg	1725
ALDH2	4	intron9+5197	gctttcttatgaccttggtc C/A atttccagttgtcttgtg	1726
ALDH2	5	intron11+114	gagctgggctcagttctcc T/C gggtcaggtgtgatgtga	1727
ALDH2	6	3'flanking+411	ggatatgatttctgcccctc T/C tctgtgtgggtaaacagct	1728
ALDH2	7	3'flanking+(432-433)	tctgtgtgggtaaacagct TC/Δ tgttcatgcatttactttt	1729
ALDH2	8	3'flanking+488	ccaataagaatgtgottgaa G/T gttcatgcatttaattgt	1730
ALDH7	1	5'flanking-1455	ctgcctgtccaccccacag C/T agcttgacatcatcccccac	1731
ALDH7	2	intron1+464	catgaatgactctgggaaag A/G atcattcttagcaatggact	1732
ALDH7	3	intron1+2269	aaatggaatccaaacagaa G/C agacctccccctaccggtca	1733
ALDH7	4	intron2+1349	actgagcttctgccaccggc C/T gcctgcccgccttcatgaga	1734

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GENE	number	position	SEQ.	SEQ ID.No
ALDH7	5	intron2+1820	tccgtgtggaaggcaccttc C/G cccagcctcagtggctagga	1735
ALDH7	6	intron2+2046	aacctcaggcgtgcctcag C/G cagggagccagcctggcccc	1736
ALDH7	7	intron2+2939	aagcacgcactgaacatgga G/A tgagtgagtgaacgaatgaa	1737
ALDH7	8	intron3+7	tgcccaagaacctggtgagc C/T ggccgggctgaggcgggcag	1738
ALDH7	9	intron4+36	gccccctccggtcacccttc T/C ccgctcgaggcctcagggcc	1739
ALDH7	10	intron6+(116-117)	attctcctctctctctctct CT/Δ ggaccaggctgggagcagtc	1740
ALDH7	11	intron6+263	cagaccctcatacgtgacct T/C gctgccccccaggctcttag	1741
ALDH7	12	intron6+1298	gtagacagagctggactcca T/G ccttgggtgataaggatcc	1742
ALDH7	13	intron6+1411	gccagggtcacaagcagagg C/T gggaggagccaagggtttg	1743
ALDH7	14	exon7+185	acctcgctggcccccgacta C/T gtcctatgcagccctgagat	1744
ALDH7	15	exon7+339	tgcgggcattgctgggctgc G/A gctgtggccattgggggcc	1745
ALDH7	16	intron7+249	ccagggtccaggggtcagc G/A tgctaagatgaactcccatc	1746
ALDH7	17	intron7+277	atgaactcccatcccaccac C/T ggctatcctgaaaggctgta	1747
ALDH7	18	intron7+498	gaccaaggctcgggggattct C/T tgtgtcccacaggccctgag	1748
ALDH7	19	intron8+14	cagccagggtgggggtgctgc C/T gggctgggcagggtcaggag	1749
ALDH7	20	intron8+49	caggagcccgcagtgggcag C/T acaagtgtggcagcagggg	1750
ALDH7	21	intron8+111	tcaggactttgggatgtgtg A/T cctcttggctctgtctctgc	1751
ALDH7	22	intron8+3219	atcctgatggggctcaaggc A/G gcctcacgcacatcctgttc	1752
ALDH7	23	exon9+33	gtgctgacctcagaccagcag C/T gggggcttctgtgggaacga	1753
ALDH7	24	intron9+946	tcccaggcccccgagctgac C/A cttcttgggtggcgtggccc	1754
ALDH7	25	intron9+1067	aggctccccaagcctgggtc C/T ctcttggcccccaacctct	1755
ALDH7	26	exon10+137	ccgcaatcgccgcgcgcct G/A aggatgctgctgggtggccat	1756
ALDH7	27	exon10+397	cgctcccaacctagagagcc G/A aggtgggaggcatgggaaac	1757
ALDH7	28	exon10+1198	ctcttccccatgctgctcat C/T ctcttggcccccatccactc	1758
ALDH7	29	exon10+1475	caggggtggacctgagtttc G/A tctcctgtctctctggctga	1759
ALDH7	30	3'flanking+15	cctggcaatacttacatctc A/G gtgatttgcttctgtgcat	1760
ALDH7	31	3'flanking+60	caacaggactctggaccaag G/C ccttggcgttgggtaacaat	1761
ALDH8	1	intron1+98	aggggaaggggatgtgtgcc G/A tggcccggtgggtcagggggc	1762
ALDH8	2	intron1+157	atggctgcaggggcatggg T/C acggggcttgcctcaggagag	1763
ALDH8	3	intron1+354	tctgtggacagacaaggatt C/G ggtcgggggcaccagggtg	1764
ALDH8	4	intron1+851	tatgacaggctccatcaggcc T/G caccttctgtgtgtcttat	1765
ALDH8	5	intron1+894	ctcagcatctgccccacag T/G gcttttgacacgttggttc	1766
ALDH8	6	intron1-463	aaagaacctccgagtcct C/G gtttagtcccagaaggagg	1767
ALDH8	7	exon2+61	gccttcaactgagggcgcc G/A cggccggccgagttccgggc	1768
ALDH8	8	intron2+8	ggacctgcataagggtgggcc A/G tggagagtgggccccggcag	1769
ALDH8	9	intron2+23	gggccgtggagagtggggccc G/C ggcaggggctggagcagcgt	1770
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca (A) gccacctgtgatgcaggct	1771
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca gccacctgtgatgcaggct	1772
ALDH8	11	exon3+72	gactacgctctcaagaacct T/G caggcctggatgaaggatga	1773
ALDH8	12	intron8+375	ctgcagcatcctaacctcac C/T gtcgcgactcaaggctgccg	1774
ALDH8	13	intron8+463	aatcaacccccatggcacc G/A accgtcactgagagggtgct	1775
ALDH8	14	exon9+33	atgctggagoggaccagcag C/A ggcagcttggaggcaatga	1776
ALDH8	15	exon10+428	aggtgtcctcactcaccoca C/T cctccccaattccagccctt	1777
ALDH9	1	exon1+121	actgtgtggggtatggcggg G/A tgggtgggagaatgtggtgt	1778
ALDH9	2	intron1+67	cggcgatttccggccagcc C/G ccgttctctgtgtctgcag	1779
ALDH9	3	intron1+103	tgacagcttgactgagcac A/G agacagtgcagtgagagt	1780
ALDH9	4	intron1+1818	gaatttttgagaaaaaaaa A/Δ tgttcttttagggttgcctt	1781
ALDH9	5	intron2+5891	tcaggaacaggaagtaaaga G/A gtttacatttctaaattct	1782
ALDH9	6	intron2+6398	atcaaaaaaactgtctgat T/G atogtgcctgaacctgcct	1783
ALDH9	7	intron2+9677	atgacgctgagtttgggtgt A/G ttcttttgttttcttgcct	1784
ALDH9	8	intron2+9991	gggagaagtgaggacctac C/T cttggcttctaattcttcat	1785
ALDH9	9	intron2+10198	ttgtcagagacatctttgat A/G atccttacgtactatatcag	1786
ALDH9	10	intron2+10256	ttagtagataacttttttt T/Δ gtaaggatggagaataatag	1787
ALDH9	11	intron2+11382	catattcaattcttttatgt T/C ctttagaccaaaagaaaggca	1788
ALDH9	12	intron2+11455	taaacctttaagctcatcat C/T ggaccatctattgaatttct	1789
ALDH9	13	intron2+12044	atttaaagtgaagctattt C/T tagttttaaaaattgagcag	1790
ALDH9	14	intron3+334	ctatttagcaaacctttttt T/Δ gacagtgtataaagttttoa	1791
ALDH9	15	intron3+368	gttttcaacaattgatattg G/Δ aaggttgtagggcctagga	1792
ALDH9	16	intron4+191	ccctcaaggagcttatagtt T/A aggtgtacacaatcatgtc	1793
ALDH9	17	intron4+557	tagaaaaaattgtaattgta A/G aaagcattactgttaggaca	1794

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GENE	number	position	SEQ.	SEQ ID.No
ALDH9	18	intron5+830	agttcaagatgatttttag G/C ttcagggcctagttgaactta	1795
ALDH9	19	intron5+838	atgatttttaggttcaggg C/T ctagttagcttagcatgcaa	1796
ALDH9	20	intron6+120	agaaaagttgcacaaatagt A/C caaagaattcccatgtacct	1797
ALDH9	21	intron6+2569	attaaaaatctgctttaata T/C tttttgggggagaggacac	1798
ALDH9	22	intron8+1414	cggatcttcaaaaaattagc T/C gggggtggtggtgcacactg	1799
ALDH9	23	intron9+664	aaagttcacatttttttt T/Δ ataactcatggtcaagagc	1800
ALDH9	24	intron9+2170	taatgcacacatttttttt T/Δ cttcataggacatccaacg	1801
ALDH9	25	exon11+587	aaaacaaaaaacaaaaaaa A/Δ ccttggtcctttataggttc	1802
ALDH10	1	intron1+39	gggtgtggggaaactggccc C/T cgccgcgcacttgtggactg	1803
ALDH10	2	intron3+2491	tgccgcgaagaaattggcac T/A gctgagttctacatgcagtt	1804
ALDH10	3	intron3+2595	ttctgtacatcaacttgtga T/A ggattgaggccagttctggt	1805
ALDH10	4	intron3+2775	taccgctttgccctgacca G/A gggtaaattcttcaataact	1806
ALDH10	5	intron3+3424	aggcactctgcacacacccc G/A cgtctcatgcattttccctg	1807
ALDH10	6	intron3+3676	atgttgaagagattgctgat G/A ttgacgttaggattttatt	1808
ALDH10	7	intron4+481	tagaaaaataagaggtttcag G/T ttctctctgctaaatccggt	1809
ALDH10	8	intron4+769	atcctgctttatacctgaac G/A tcttgaggcagagccaaaa	1810
ALDH10	9	intron4+796	aggcagagccaaaagccaca A/G ccaggagagtctgtaccgaa	1811
ALDH10	10	intron5+254	attagttgtggcatatactt T/G ttttaaaaaagttaaataat	1812
ALDH10	11	intron6+137	aatcctgctttctgtgtac T/C gtacctgtagcttttgttat	1813
ALDH10	12	intron6+923	aggctaataaatggtaagag G/A aagggctatcctgattagc	1814
ALDH10	13	intron7+331	tgctttctgtatgttaatcc A/Δ cagggcattgctgaataaca	1815
ALDH10	14	intron8+643	tttagaacatgacctgcctg C/T ctctcccatgtgagatga	1816
ALDH10	15	intron8+666	ctcccacatgtgagatgact G/A actcagctttttatttctcc	1817
ALDH10	16	intron9+2129	tgttttcatttttaaaaaaa G/T gtttgactttggaattcatg	1818
ALDH10	17	exon10+(1894-1895)	ttggctgtctactaataca CA/Δ tctgctcaaaatgaacata	1819
ALDH10	18	3'flanking+31	gtatttgcactttttttt T/Δ ctcattttaaaattcttagc	1820
ALDH10	19	3'flanking+106	gtgtgttgggggtggtggt G/A gtgctatagtaaataaggtt	1821
ALDH10	20	3'flanking+1630	aaaagcacgtgggaaacaca A/G ttaatcatgtcttaccgtat	1822
ABCC7	1	5'flanking-834	gctaaaacactccaaagcct T/G ccttaaaaatgcgcactggg	1823
ABCC7	2	5'flanking-729	cctccttgacagattttttt T/Δ ctcttcagtagctgtccta	1824
ABCC7	3	exon1+125	tagcagggaccccagcgccc G/C agagaccatgcagaggtcgc	1825
ABCC7	4	intron1+6200	ctatgtgagacgttaagaag G/A tagaggtggccaagaaggaa	1826
ABCC7	5	intron1+7538	agttctctttcttagcatgg C/A ctacagaggtgcaactacct	1827
ABCC7	6	intron1+13519	gaaacttaaatcttgagtoa T/C acaattgtgtctacatactg	1828
ABCC7	7	intron1+14110	attacacagtatttttttt T/Δ aattttggggaaagtogatt	1829
ABCC7	8	intron1+14293	gccaggcagattcctgactc C/Δ tatacccagagcttatcag	1830
ABCC7	9	intron1+14316	taaccagagcttatcagag C/G atttatgtcccaaagagaa	1831
ABCC7	10	intron1+14433	cagaataacaatgatggctc G/A gaaaaatatgggtattctg	1832
ABCC7	11	intron1+14824	acgttttgacagttgcacaa G/C ttcttttcttaagctttaa	1833
ABCC7	12	intron1+23401	aatatttttgaatatcacta C/G ggtatcctgcatagtgattt	1834
ABCC7	13	intron3+879	gaaaaatttcagttcataca C/A ccccatgaaaaatacattta	1835
ABCC7	14	intron3+922	acttatcttaacaaagatga G/C tacacttaggccagaatgt	1836
ABCC7	15	intron3+933	caaagatgagtacacttagg C/T ccagaatgtctctaatgct	1837
ABCC7	16	intron3+13704	ttttccaaataaaaaaaaa A/Δ tcaggtgatctctgtaaatg	1838
ABCC7	17	intron3+13758	tattaaagaacatgatgctt A/G aaacagattagggaaaacta	1839
ABCC7	18	intron4+240	ctctgtgtagtttttttt T/Δ ctctaatcatgttatcatt	1840
ABCC7	19	intron4+376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	1841
ABCC7	20	intron4+586	tgtccagacaagagacccaaa T/C tgccgaggaatcatttaggt	1842
ABCC7	21	intron4+1089	tttcaatctgaacattttac G/A taagtgaagactttgttaga	1843
ABCC7	22	intron4+1615	aaagttaggtggtattgtat C/T tgccttcctttctcaatgtt	1844
ABCC7	23	intron4+1946	aatacaaaacaaactgagct T/C tgcctatacttttcaagaat	1845
ABCC7	24	intron6+783	tatctaagttttggagtcaa A/G tagcactttgtttgaatccc	1846
ABCC7	25	intron6+(1128-1131)	gattgattgattgattgatt GATT/Δ tacagagatcagagagctgg	1847
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt (T) cttcagttgagctccatgtt	1848
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt cttcagttgagctccatgtt	1849
ABCC7	27	intron7+1434	gaatgtttggtgtgaacctg T/C ataactgtggcatgaaattgt	1850
ABCC7	28	intron8+752	catgctctctctcagtcac A/G ttcttcattatatcaccta	1851
ABCC7	29	intron8+1109	tatggccaagacttcagtat G/A cgtggacttaattcttctt	1852
ABCC7	30	intron8+1312	atgaagacattcatttttt T/Δ ctccgtccaatgttggatta	1853
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgt (GT) ttttttaacagggtattggg	1854

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GENE	number	position	SEQ.	SEQ ID.No
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt tttttaacagggatttggg	1855
ABCC7	32	intron10+2119	gaacactttatagtttttt T/G ggacaaaagatctagctaaa	1856
ABCC7	33	intron11+3867	ttttcttcaagaaattaga A/Δ gaggggagaaattggttaa	1857
ABCC7	34	intron11+11844	tgaatcaaaatcatctaaaa A/Δ gcttcagaaaccagacttt	1858
ABCC7	35	intron11+12144	atattaaacagagttacata T/C acttacaacttcatacatat	1859
ABCC7	36	intron11+20975	gtgtggatagtaaagccag G/A gtaaatcacatagcatctaa	1860
ABCC7	37	intron11+27057	atggaagagaagtttttagta G/A aggggaggaaggaggaggtg	1861
ABCC7	38	intron11+27131	gagagagacttttttttt T/Δ aaggcgagagtttactacct	1862
ABCC7	39	intron13+152	gtattaactcaaactgatc T/A gccctactgggccaggattc	1863
ABCC7	40	intron13+287	tttcagtatcattgccttg T/C gatataattactttaatta	1864
ABCC7	41	intron15+(85-86)	atacatatatatgcacacac AT/Δ aaatatgtatatatacacat	1865
ABCC7	42	intron15+106	taaatatgtatatatacaca T/A gtatacatgtataagtatgc	1866
ABCC7	43	intron15+3341	ggaagtataaattttaaata A/C actgagacccaaacttacia	1867
ABCC7	44	intron15+5556	tgctattgactaatagtaata A/T attttagggcagctttatga	1868
ABCC7	45	intron15+5919	tggtagttctatgtggaaac C/A gtgaggaaataattttatat	1869
ABCC7	46	intron17+2479	caaaaagggtatggaagtcag A/C ggagaaggagaccctatgt	1870
ABCC7	47	intron18-81	aagtatgcaaaaaaaaaa A/Δ gaaataaatcactgacacac	1871
ABCC7	48	intron19+751	cattaataaaataacaaatc A/G tatctattcaaagaatggca	1872
ABCC7	49	intron19+820	tgacatttgtgatatgatta T/C tctaatttagtctttttcag	1873
ABCC7	50	intron21+1532	ttacotttaactttttttt T/Δ agtttgatcagctctcttta	1874
ABCC7	51	intron21+1607	atgcttttggagttgggtct C/T ataatgtatagaaatgttt	1875
ABCC7	52	intron21+11260	atgtggaacaatcatgacta T/C atgccttttactttctctat	1876
ABCC7	53	intron22+(130-131)	agaatcaatattaacacac AT/Δ gttttattatatggagtcot	1877
ABCC7	54	intron23+1828	ctgtcctaaagtttaaaaag A/Δ aaaaaaaaaaggaagaaggaa	1878
ABCC7	55	intron24+(7100-7112)	cctttacaaactcttagaca (T)12-14 agtttaacatgttacaac	1879
ABCC7	56	intron25+237	actcttcccccttgcaaca C/T atgatgaagcttttaatac	1880
ABCC7	57	exon27+115	gggtgaagctctttccccac C/T ggaactcaagcaagtgcag	1881
ABCC7	58	exon27+334	ggatgaattaagttttttt T/Δ aaaaaagaaacatttggtaa	1882
ABCC8	1	5'flanking-1099	aaaggggtcgaaggggtctt T/C cttttgtgtccctgactg	1883
ABCC8	2	5'flanking-(424-422)	caccaccaccaccaccac CAC/Δ aaggtaacgttctgccccac	1884
ABCC8	3	intron1+1212	agcctgggcaacatagtgag A/G cccccccgcccctttctaca	1885
ABCC8	4	intron2+1003	aggaggactgtgaatcccag C/A ctgcatgtttgggtcggatt	1886
ABCC8	5	intron2+1253	catctcactaaggaagaatc C/T agtaaccagcaaggatgaga	1887
ABCC8	6	intron2+1382	cccagactgcaactcctgcag T/C gctgcctggctcctgtagtt	1888
ABCC8	7	intron2+2371	tttcagagctgtctggaaat T/A tagggggcaggtgggagggg	1889
ABCC8	8	intron3+1957	ccctaccctagcccagggg C/T ccccatagtagtatgaatgg	1890
ABCC8	9	intron3+(2088-2089)	agagaacccttcattaacca (CCA) gggcgtggctgaccagtgtc	1891
ABCC8	9	intron3+(2088-2089)	agagaacccttcattaacca gggcgtggctgaccagtgtc	1892
ABCC8	10	intron3+2204	taaagcacaagttatcacc C/A tggatggatttgccttttc	1893
ABCC8	11	intron3+2286	ttatctcccttgaaaggac A/G ctccacagagccagaaatc	1894
ABCC8	12	intron3+2312	cagagccagaaattctagaa C/G agggaaaagtggaggggagg	1895
ABCC8	13	intron3+2356	ctgtgaactgcagggacaga A/G ggaaatgggtattgggagaa	1896
ABCC8	14	intron3+2359	tgaactgcagggacagaagg A/C aatgggtattgggagaatgg	1897
ABCC8	15	intron3+2370	gacagaaggaaatgggtatt G/A ggagaatggccagccctcca	1898
ABCC8	16	intron3+2382	tgggtattgggagaatggcc A/G gccctccaaggggctgatgt	1899
ABCC8	17	intron3+4910	ggggacagccttcagctgtg G/A aattcctccagtcctagaga	1900
ABCC8	18	intron3+4969	cattattccagtcctgaggc A/G tgagagcagaaggccgatgc	1901
ABCC8	19	intron3+5003	ccgatgcttctgccctccat C/G ctaatgtcctcctgcagggg	1902
ABCC8	20	intron3+5019	ccatcctaattgtcctcctgc A/C gggacccaaggtggatggca	1903
ABCC8	21	intron4+14	ggtgagggttaagcaggccac C/T tgggccagggtggggtggga	1904
ABCC8	22	intron4+187	agacactgcatctggccac G/A tgtgtctaccccagggtcc	1905
ABCC8	23	intron4+204	cacgtgtgctctaccccagg G/C tcccagagggagaggggggt	1906
ABCC8	24	intron4+254	gttcgctgaggttggcggat G/A acttccgtagaaagggaag	1907
ABCC8	25	intron4+357	tgtattcatatcgtacgct G/C gtaaatgaatgagtaagtgt	1908
ABCC8	26	intron5+92	ggcattaggtcaaaatcctg G/A tgggacaaaaggggaaactg	1909
ABCC8	27	intron6+4205	tctgtagaaagtacatgggg G/A catgaagatcattggcttga	1910
ABCC8	28	intron6+5519	gattcccagggaatgttaaa A/C aggaccgggtcttccctaac	1911
ABCC8	29	intron6+5575	tctgaccagtagaccagccag G/C ggggcaagtttccatcccc	1912
ABCC8	30	intron6+6587	gttgccatctgagatcttgc C/T ggaagtacacaagagaccct	1913
ABCC8	31	intron6+6747	ttccactggccttttctgct C/T agtaattgtacattacagg	1914

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GENE	number	position	SEQ.	SEQ ID.No
ABCC8	32	intron9+191	gaggaagctgcctcccggtg A/G ggacaggaagcgggcatggc	1915
ABCC8	33	intron10+1963	cccaggagtccaacctccct T/G tgtccagctagaccatgggtg	1916
ABCC8	34	intron10+2724	cctgggacatgttttcttat A/G taaacagcatcaaaagatgt	1917
ABCC8	35	intron10+2938	gcccgccaggactcctcac G/C tgtccaagtcacctagggag	1918
ABCC8	36	intron10+3094	tccgaggatgtgtttttt T/Δ cctccgttagtcagcagt	1919
ABCC8	37	intron10+3368	tcctgctcatatgcggcacc A/G tcagactcttgggcaggcaa	1920
ABCC8	38	intron10+8897	ggtattgattaaaagcctca C/T gggcagagaaattcgccatc	1921
ABCC8	39	intron11+308	tgtgtattgtagaagtgtg G/A gaaatccagaacagaaagct	1922
ABCC8	40	intron11+1171	gcctctcatttcccttcca G/A tgctgagcgtttccagtgtg	1923
ABCC8	41	exon12+7	gcctctgtccacagacttcc G/A tgggccacgtcagcttcttc	1924
ABCC8	42	intron12+356	accaagaatgaggccatccc G/T tccccacgtggctgccccat	1925
ABCC8	43	intron12+934	tgggttcaaagatggaatgg G/T gcataactcagcaaaattat	1926
ABCC8	44	intron12+1370	gggagggaggctggacaggg C/G atgaaggcagagcctgtgtg	1927
ABCC8	45	intron15+412	ggaggtgggaccagcatgg C/T gttcttgggaccacaagga	1928
ABCC8	46	intron15+688	actccccggccccactcac A/G tctgccaccttccctccctg	1929
ABCC8	47	intron16+4464	actcattccaagtattgatc G/A agaagagaggttaggtactgg	1930
ABCC8	48	intron16+4574	ttgaagatcttaagttgtt T/C tggttcactcatttcgcaa	1931
ABCC8	49	intron16+5011	agctaaaagcaaacagcct C/T tgacctggcaagcattccca	1932
ABCC8	50	intron16+7608	tgctacttttcttttgac C/G cttataacttctgacttcg	1933
ABCC8	51	intron16+7730	ccagctcctagtgggctgga G/A ggaaggacatcggttgggg	1934
ABCC8	52	intron16+8369	ttgcaactgagttagggcc T/C ggagagcttactgtgtgtg	1935
ABCC8	53	intron16+9708	tgcacttgccgcctacttat T/G ccagaccatgattgggtc	1936
ABCC8	54	intron17+651	tatagattaatgaggctctg A/G gtccctcaaaaccttcctc	1937
ABCC8	55	intron17+692	cccttacctctccaaaaaac A/G cttgagataccctagaggtg	1938
ABCC8	56	intron17+1541	ctcaggatcttctggagga C/T atggttcaactccatgagag	1939
ABCC8	57	intron18+580	actaagcagattctaccaa C/T tgcacctcccatccccttg	1940
ABCC8	58	intron18+658	gaacaagcccctgagaatgc C/T ttccgcacccccctactcccg	1941
ABCC8	59	intron18+660	acaagcccctgagaatgcct T/C ccgcacccccctactccgcc	1942
ABCC8	60	intron19+93	gcccttccatcgatcaccca T/C acccagccatctcactcccc	1943
ABCC8	61	intron19+123	tctcactccccagggtotta T/C ctgcactccagcctctocat	1944
ABCC8	62	intron19+219	cataggggagagggcaggaa C/T ggaggggaaggagagagccc	1945
ABCC8	63	intron19+845	tagtatttaacctgccaaa C/T gctgtgtgaagtgtgacct	1946
ABCC8	64	intron20+338	tccctccacaagcttagac A/G aacaggattctcctgtgact	1947
ABCC8	65	exon21+10	tttgggtgacagggcatcaac C/T tgtotgggtgtcaacgccag	1948
ABCC8	66	intron21+192	caaggatagcacaatgacc C/Δ attgcagacttcagatggag	1949
ABCC8	67	intron23+17	gaaggtgggtatatccagg A/G tggccaagcagccaccctg	1950
ABCC8	68	intron23+67	gttctgctagaacctgaact C/T ataaaggtcttctgtcctt	1951
ABCC8	69	intron26+268	gtgagcgtctgcacatcaa G/C taaagattgtttctctcc	1952
ABCC8	70	intron26+308	cgataagtgggtgtaatttg C/T ccatccccacccatgagttc	1953
ABCC8	71	intron26+348	cagctccctgccctccctc A/G ctctctctccctcagccagc	1954
ABCC8	72	intron26+807	gacagctgtgagtcaggcc G/A agccggcagctgagaaaggc	1955
ABCC8	73	intron26+834	cagctgagaaaggcggcagt G/C gtcagatgggcttgagaaac	1956
ABCC8	74	intron28+(118-121)	cctccaaaaataaaaacaa AAAA/Δ cagaaatgaaggaaatagaa	1957
ABCC8	75	intron28+1348	tggggtaaaggaagacggg G/A ttgaacgcttgagtttgt	1958
ABCC8	76	intron29+1253	ctcttagggatcttgtctaa G/T taaagaagagcagagcaaag	1959
ABCC8	77	intron29+1589	cagatcccagcttctgtaa A/G cagcctcagatcaggccaaa	1960
ABCC8	78	intron29+2322	gogcctcacactcctataac G/A cgcacatgccctgatgcaca	1961
ABCC8	79	intron29+2348	atgccctgatgcacacacat T/C ttcaacacgcacttactcta	1962
ABCC8	80	intron29+2418	agacacgtcacctcccaca C/T gtctccacctgggggtgtg	1963
ABCC8	81	intron29+2494	tcagtcacctcagacacatg C/A cctctctccacgcagagaca	1964
ABCC8	82	intron29+2735	gcgccaaggagagtgtga C/T ggcagcccaggttgatcaga	1965
ABCC8	83	intron30+386	gctcctggggctccagcctt C/T gcagccctgtgtgtgtgtg	1966
ABCC8	84	intron33+93	ggcttcgagtcacctcgtg G/T cctccagggccgaggcctc	1967
ABCC8	85	intron33+358	agggacctgggggcagacag C/T gaggccaccttgattgag	1968
ABCC8	86	intron38+54	cccagggacaggactggcct G/C ttgtggcgtcatcagtga	1969
ABCC8	87	intron38+466	aggacattctggccacatgc C/Δ tcctcctcctcctccaagcc	1970
ABCC8	88	intron38+529	tggcccccaccgagggtgtg A/G ttcccaccatcctgaccgc	1971
ABCC9	1	intron3+38	tgtgtttctcctaaagag C/A tattgttttccccccaaa	1972
ABCC9	2	intron3+305	gctggccttctggcttgag T/A agttgtattttaagaatcag	1973
ABCC9	3	intron3+320	tgcagaagtgtattttaag A/G atcagagctctgtgaggag	1974

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GENE	number	position	SEQ.	SEQ ID.No
ABCC9	4	intron3+631	ttctgtggaaatcagaggct G/C tctaaaatattcctaatttt	1975
ABCC9	5	intron3+8644	tggacgcactcaacattttc A/G agttattactccttcaactc	1976
ABCC9	6	intron4+757	aggatatcatgaaacactga A/C tcttagtaaaaaactatcttt	1977
ABCC9	7	intron4+1022	tactgtggaaatttttcttgc A/C acagagatatgtatttttca	1978
ABCC9	8	intron5-1217	cagtggtagatgtgtttct A/G ttgccatcatctacaaatat	1979
ABCC9	9	intron6+(106-107)	tatgagttgttcaaataggc (T)7-9 cagagaattgaatgctttct	1980
ABCC9	10	intron6+1347	tcagtcgtattcctactaaa A/Δ caaaattttgtaagttatgt	1981
ABCC9	11	intron6+1618	ctttttatttgctgcttacc G/A ttttactaagggttgatata	1982
ABCC9	12	intron6+1835	cttttaataaatgcaaaactg C/T acacctggtctataaaaaaga	1983
ABCC9	13	intron7+407	cctatagaatttttcttttc T/G tttttctcaaaaaaattaaa	1984
ABCC9	14	intron7+423	ttcttttttctcaaaaaaa C/T taaatgtttgtatttttt	1985
ABCC9	15	intron8+743	ttctgtagatgaagcttaag A/T gctagatcttatttgaaaaa	1986
ABCC9	16	intron8+850	ttttaacttattgtttgcc T/G tttcattttttaatagaaaa	1987
ABCC9	17	intron9+585	cgaatttgctgcttttagag A/T aatctttgcaaataataaaa	1988
ABCC9	18	intron9+1394	atttttcttctgtaagtat G/C agtgatagagctgactgcag	1989
ABCC9	19	intron12+1167	atttgtaagacttttaaaat G/A agataattgtgctggtgtct	1990
ABCC9	20	intron12+1195	tgtgctggtgtctatatctt A/G ctgagaaaaactagaatttat	1991
ABCC9	21	intron12+2123	ataagtgtctcccagtggt G/A attggacttagagcattttc	1992
ABCC9	22	intron12+(2653-2656)	caaaacagaataatgaaaag TAAC/Δ tattatctaaaataataaaa	1993
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct (CTCTTT) aagtcaaaatatattagtat	1994
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct (CT) aagtcaaaatatattagtat	1995
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct aagtcaaaatatattagtat	1996
ABCC9	24	intron14+85	ttctgtgaaagtgtcccaaa T/A tgtgcctttaaattgttttt	1997
ABCC9	25	intron14+275	agtgtcacatgtatttttc T/C ggtattcctatgtttatcaa	1998
ABCC9	26	intron14+453	ctcatttcaaacttggtat T/C tggactctccccaggcattg	1999
ABCC9	27	intron14+3709	atccccctagtgtgtacact G/A agcttgctccatctttcct	2000
ABCC9	28	intron14+3813	ctgatttatattagtctga C/T ttccaagtccagacatcta	2001
ABCC9	29	intron14+4000	ttcttttacttcaatgtagc A/Δ ccaaatcagaagggtgacatt	2002
ABCC9	30	intron16+1466	atcccactggatttaattac A/C ttgtgtagctgtacaacca	2003
ABCC9	31	intron16+5357	attttggaagagaaattata T/G aaccttccacaactgaattt	2004
ABCC9	32	intron17+1368	aatcctggtgttttttttt T/Δ ctttttcatttttcagtagg	2005
ABCC9	33	intron20+98	aagtaactcaaggaaagatg G/A ttaactgtgaaatcgtaa	2006
ABCC9	34	intron22+28	ctcatagttcagaagagttc A/C gagcccaattcagaagagtt	2007
ABCC9	35	intron22+194	tgaacctataaaattcta G/Δ ccatctttggatgaggtgca	2008
ABCC9	36	intron22+1370	ccagggacaaaagaagatga C/T gtaaacttaaggattgggac	2009
ABCC9	37	intron22+1487	agcaagccaggaagaaagtc C/G attagttgtatttagaaat	2010
ABCC9	38	intron23+(455-462)	atagccatgaaggataagaa AATTAGAA/Δ tgccatttgt tatgtttcag	2011
ABCC9	39	intron24+(460-465)	aactctttctcttcatctgc TTTAAAA/TTTTAA gcaagccttg aaggagagtg	2012
ABCC9	40	intron24+595	gcatgcaaaataatgaagaa A/G acaatctgtctgacattga	2013
ABCC9	41	intron28-926	aaatatttcagaatttgggg G/A ttagagcatttgccgtcat	2014
ABCC9	42	intron29+2692	cttgtaagtcttttttttt T/Δ aaagtaatgaaaatttctaa	2015
ABCC9	43	intron29+5464	agacaacactgctttttgt G/A tgttcacaattcaacgacag	2016
ABCC9	44	intron29-1830	aactggctgaaaggaaaaaa A/T tcatattgtgtaaatattt	2017
ABCC9	45	intron31+102	tgcttttgctttocacttca G/A tatccagaaaactctctcat	2018
ABCC9	46	intron33+877	aacatggaactatagtaaat A/G tagttttttggggttcaga	2019
ABCC9	47	intron36+1281	aatttacactttttttttt T/Δ gcaggagaatattttgcaaa	2020
ABCC9	48	3'flanking+197	aatggagctcatgcatgtgt T/G ttcaaatatatacatgcaaa	2021
CES1	1	5'flanking-983	tatttcocttagccagcggtat T/C cacagtgtgttagtgaatt	2022
CES1	2	5'flanking-814	tcacattgccttgacatcac A/C cctactgctcctccacccta	2023
CES1	3	5'flanking-248	agtctgcaagggtgacacc G/Δ ttatgccacaagcagttggg	2024
CES1	4	intron1+22	tgagtccttctgaagtcaaa T/Δ atgcggggcactttttgaaa	2025
CES1	5	intron1+30	tctgaagtcaaatatgcggg G/T cactttttgaaatccttggt	2026
CES1	6	intron1+1662	aagggaatccctgagctgag C/A atgaccagcccagtggttc	2027
CES1	7	intron1+1726	cctccctgaagtcctcagca A/C tottagctggttctctgccc	2028
CES1	8	intron1+2716	tgcttccaaggaagttcatc T/G cagtattatttgaattagc	2029
CES1	9	intron1+(2747-2749)	tgtaattagcaacaacaaca AAA/Δ gaaaagaagctaaatattga	2030
CES1	10	intron1+3288	ttatttgcattaaagaaa A/Δ ctcaagcgttagcctggca	2031
CES1	11	intron1+3691	gagaatatgggacaccctt T/G ttcatctctcatccagcat	2032

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GENE	number	position	SEQ.	SEQ ID.No
CES1	12	intron1+3819	tccttcttgcatttattttt A/G gctggatgtttttatgcctc	2033
CES1	13	intron1+3880	aaccagctcaatgggttagg G/A aggacattgatcgtcatccc	2034
CES1	14	intron2+74	gagtcaggcagctcccctga T/C gggctgatcctttgctctgg	2035
CES1	15	intron2+552	atggaagggtgtgtcattca C/A cctggccaagctgggaagaa	2036
CES1	16	intron2+885	cagtattttagatggtaaag T/C attatgatgtaatatattgt	2037
CES1	17	intron2+2001	ttggcatgtcagggtgcaa G/A actcatgtagaaatcactcc	2038
CES1	18	intron3+2119	cgctgagtgcatgaatagtc T/C aggttgagggtgatgggag	2039
CES1	19	intron4+127	taaggcatccaagccccttc G/A taattggacactacctacc	2040
CES1	20	intron4+347	ctgtcatgacacttagcag T/G cagcccagcaggtgaaggtt	2041
CES1	21	intron4+(1984-1985)	tgtggtcctgaaggctctgc (C) tgacatctctgctccccacc	2042
CES1	21	intron4+(1984-1985)	tgtggtcctgaaggctctgc tgacatctctgctccccacc	2043
CES1	22	intron5+766	gaggtgggcagagggtcagc T/C cactactggattcctcagtc	2044
CES1	23	intron5+825	ggagtagatctagcctggaa T/G agcgagtgaagtactgaccc	2045
CES1	24	intron5+828	gtagatctagcctggaatag C/T gaggtagtactgacccac	2046
CES1	25	intron5+868	ctcctgagcatgaactctcc T/A cccctccactctgctgtcag	2047
CES1	26	intron7+68	acttcttcatttcagctgtc C/G tcttgcccaggacagtttc	2048
CES1	27	intron7+681	cctccaaaatcaacaatcca A/G ttatgcctgtctgctagtt	2049
CES1	28	intron7+885	aggaaactatccaaagagaaa T/C acattcatatacttcgcagg	2050
CES1	29	intron7+2151	gtcgtgtaaaactgaaaatct C/G aggagttgatggcttcaggc	2051
CES1	30	intron7+2470	atatagatatacgaattcac G/A gaggtagtgcgggaagaacct	2052
CES1	31	intron8+128	cgtgtttgtttctgaggccc A/C gagagggtagtgactcacc	2053
CES1	32	intron8+2618	cctgatggcaacacatgagt T/C gggctctctctaactgtga	2054
CES1	33	intron8+2665	aaaaattattcatcaaaggt G/A aaacctaaaattaagacatg	2055
CES1	34	intron8+3785	ccatggcgcatggccatgcc G/A gtctatggtagtggctcac	2056
CES1	35	intron8+3791	cgcattggccatgccgtcta T/C ggtactggtctcacctcag	2057
CES1	36	intron10+222	gtgggctggagaagctgcat C/T gctcaccoggggctggtgt	2058
CES1	37	intron10+230	gagaagctgcatcgtcacc A/C ggggctggtggtcactttt	2059
CES1	38	intron11+1177	ctagcaggtgccctgacaca C/G ctttgacaggaaggggcag	2060
CES1	39	intron11+1311	gccctatgctctgcgtctga A/G ctatatatagagttccatc	2061
CES1	40	intron11+2025	ttctcatttgggatgctaag A/G ttaaaaattagcataacact	2062
CES1	41	intron11+2029	catttgggatgctaagatta A/C aaattagcataacacttcca	2063
CES1	42	intron11+2317	cattcacaaaagctctttct T/C ctatggttggctctgagtt	2064
CES1	43	intron11+3887	caaatatttggctctaattc C/T gcttcacactcagacagcta	2065
CES1	44	intron12+2311	gcgcctctgggcatctcact G/A tgcattgcttaggcgccttgc	2066
CES1	45	intron12+2331	gtcatgcttaggcgccttg C/G ggctctgtgtttttcagaa	2067
CES1	46	3'flanking+71	aacggtgatgaaagaggoga T/C gtgagaaggaagggtgcttt	2068
CES1	47	3'flanking+362	ttgcatggcacttactgacc G/A ttgcacaggcctgcaacacc	2069
CES1	48	3'flanking+581	atttctggattctgttagta C/T gtagaaagctctaaagcatg	2070
CES1	49	3'flanking+1348	aatctgctgctgggagaga G/C agcaaagcatgcagatcaac	2071
ABCB4	33	intron22+767	acagtgggctgatgcataga A/Δ cctgtagcaatccaccagca	2072
AADA	23	intron2+46	tgtcactgaggtagttcgca A/G acattttactaagtcttcag	2073
AADA	24	3'flanking+208	aatgctaaaaaaaaaaaaa A/Δ tcaactgtgtactttgggga	2074
ABCA4	1	5'flanking - 1005	tgccatcataagcagaaaact A/C tctctctctcttgggaagct	2075
ABCA4	2	5'flanking - 819	gtctagagcttttcaaagag A/T acacattctgagatttgagg	2076
ABCA4	3	5'flanking - 680	agcaccaccccatgacagg G/A tggaaatgacagtaatgggco	2077
ABCA4	4	intron1 + 208	tgcccttcccagggaagatgt G/A tttctctgtcctcagccaca	2078
ABCA4	5	intron1 + 234	ctgtcctcagccacatgaaa A/G tcttttgctaccgtgcctg	2079
ABCA4	6	intron1 + 510	agctcagatcaagtcacag T/C ttaactggacacattttt	2080
ABCA4	7	intron1 + 1527	gcttaacaaccagcataaaa G/A agagcagcatgggacacgct	2081
ABCA4	8	intron1 + 2077	caggactgtagctgctggcc T/C aaaatgagcccattcctgtg	2082
ABCA4	9	intron1 + 2174	ccctctcaatctggcctttc G/C ctggcatgggtgggcgactc	2083
ABCA4	10	intron1 + 2246	gtcccaggagatggagcc A/G ctgggctgagggccttggc	2084
ABCA4	11	intron1 + 2364	ttctgtotggcacgcctccc G/A atggctcccacctgctacc	2085
ABCA4	12	intron1 + 4243	ctccctggggtatgcctgta C/G gcagttaagcgtcaaggaca	2086
ABCA4	13	intron1 + 4287	atgcgctctggggaggggga A/C gctgagcatgattttggaag	2087
ABCA4	14	intron1 + 4309	ctgagcatgattttggaagc C/T ggcagaagaggctattgtga	2088
ABCA4	15	intron1 + 4416	tgcagcaaccgccccgccc C/T ccgcaaaaaacaaacacact	2089
ABCA4	16	intron1 + 4996	tttaccctggacaggcag G/A ccaagctggctggtcccctc	2090
ABCA4	17	intron1 + 5007	aacaggcaggccaagctggc T/C ggtcccctccctgatacaca	2091
ABCA4	18	intron1 + 5080	gtgtgtggctggtttcttag C/G aagcaccatggttccaagtt	2092

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GENE	number	position	SEQ.	SEQ ID.No
ABCA4	19	intron1 + 5152	gggagatgaacgtaagtggg G/A ggcaggcctacaaggttgca	2093
ABCA4	20	intron1 + 7110	ccactggatctgcttttggg A/G tcaagagtccttaagctcca	2094
ABCA4	21	intron1 + 7290	gatttttgggtgctttgcaa T/A ggatcacagtcatttattca	2095
ABCA4	22	intron1 + 7483	tctgagcctctttccttaac T/C gcagagtgaagggtacaga	2096
ABCA4	23	intron1 + 7497	cttaactgcagagtgaagg C/T tacagagaaatctttactac	2097
ABCA4	24	intron2 + 1067	tcaagcagcagcagcaactg C/A gtggagtcttctgaactaa	2098
ABCA4	25	intron2 + 1106	aacactcctatgccctctc G/A gcacaaaatgacgtgtcccc	2099
ABCA4	26	intron2 + 1119	ccctctcggcacaaaatgac G/A tgtcccccttgcttccct	2100
ABCA4	27	intron2 + 1243	caccagcagcagggactggc A/T cacatgagatgctcctgctt	2101
ABCA4	28	intron3 + 26	tggtgagatccctaccatgc A/G ggggaggaagttgcacaccc	2102
ABCA4	29	intron3 + 101	agcatggagcactgaagg C/T ttgtggctttgctgagcccc	2103
ABCA4	30	intron3 + 330	tgcttgggtggagtgaatca T/C ttaggagaaaaactcagtt	2104
ABCA4	31	intron3 + 470	tgaagtcaggtttacaaagt C/G aagtttactcttgggagaa	2105
ABCA4	32	intron3 + 634	tgaaaaccaatgacctct T/C ccaagaaaaatggccacata	2106
ABCA4	33	intron3 + 1016	ccttgggggagctcagtatg A/G ttctccaggagaagcctgc	2107
ABCA4	34	intron3 + 1554	gaaagttgggtttcatgtt T/C gcactcacattatgagtga	2108
ABCA4	35	intron3 + 1686	ctagacattctcacagagcc A/G agggcagcaaggcggggctc	2109
ABCA4	36	intron3 + 1823	ttcacctctctccatggacc A/G gtctccctgctcctcaatg	2110
ABCA4	37	intron3 + 1938	caaattcctgggaacaaatc G/A ggttgacctcagctttattct	2111
ABCA4	38	intron3 + 1951	acaaatcgggttgacctcagc T/G ttattctccctgtcccatca	2112
ABCA4	39	intron3 + 2063	ggctgtcagagcctacctgc G/T tgaatgggtggaaggcagg	2113
ABCA4	40	intron3 + 2079	ctgcgtgaatgggtggaagg G/A caggtctcagagaattgggt	2114
ABCA4	41	intron3 + 2186	agacacacagagcatgggac C/T gagaggcagcagaccctgc	2115
ABCA4	42	intron3 + 2214	gagcagaccctgccaaaact G/A ggagactgaatagatcgtc	2116
ABCA4	43	intron4 + 2717	cgtgcttctgcacagccacc T/C gggaaggtatgccgatggt	2117
ABCA4	44	intron4 + 2802	attctcagcagggaggatta A/G tggtaaaagcccaggaatgg	2118
ABCA4	45	intron4 + 3182	ccccagagccacagcagcc C/G tgtctcctgggtggtcttgt	2119
ABCA4	46	intron4 + 3515	agtataataaaagcaggagc C/T atagccccaactctcaaga	2120
ABCA4	47	intron4 + 3907	aggggagtgacagtgggcac C/A actctcaggaacccattac	2121
ABCA4	48	intron4 + 3923	gcaccactctcaggaaccc A/G ttactgtgagagaagccact	2122
ABCA4	49	intron4 + 3952	agagaagccactgtgccact G/C tgtgttgaacttcaagacc	2123
ABCA4	50	intron4 + 4125	ggctgtccagcacacagggg C/A aggcctcttgccactgggg	2124
ABCA4	51	intron4 + 4637	aatcacttgcccaagggtca C/T cttaactgttaggtgttctt	2125
ABCA4	52	intron4 + 5319	acctctaggggctccagag A/G cccaagaacagaaccttc	2126
ABCA4	53	intron6 + 2266	caccttgacagacctcagac G/A ggtcctgggggcttgcttc	2127
ABCA4	54	intron6 + 2857	ccagaggagaaagctctgcc G/A tagtcggcctcagttaacca	2128
ABCA4	55	intron6 + 2861	aggagaaagctctgcctag T/C cggcctcagttaaccacgga	2129
ABCA4	56	intron6 + 3078	gcaggcattaaaatgggact T/G tgcctttattgctcctgggc	2130
ABCA4	57	intron6 + 3375	ttaaatgocaaatgagttct C/G attaacaagaagaggga	2131
ABCA4	58	intron6 + 3412	ggaaaatctcagtaaacac C/T gtgacggcatctaccactt	2132
ABCA4	59	intron6 + 4635	ctttcgggtggatattgcta C/T gtcaagtgtctgggaagcc	2133
ABCA4	60	intron6 + 5576	ccactaatatgcattcttta G/C taagcgtctcaatatacac	2134
ABCA4	61	intron6 + 5925	aaaaagcattttgctcttat A/G aaagcacagcctcttttgag	2135
ABCA4	62	intron6 + 6916	cccagacaaccaagcagag A/G cctcttagggccggaatcat	2136
ABCA4	63	intron6 + 6993	agcacagatcaaggcctaa A/G ggccccttagactgacctca	2137
ABCA4	64	intron6 + 7242	ttgccattttgatctgtgac T/C tttttccagaaatagttt	2138
ABCA4	65	intron6 + 7454	atggagggtcctcctgggac T/C aggcagtattcagagatgta	2139
ABCA4	66	intron6 - 264	aaacagcaattagaatcact T/C tgaaatagttagatattta	2140
ABCA4	67	intron6 - 86	aggagggggggagtttcaa A/G catataggagatcagactgt	2141
ABCA4	68	intron6 - 32	tatactacaaacatatata T/C atttaaaaaattgtttact	2142
ABCA4	69	intron7 + 828	gatgtgggaaagtagagaa G/C agccattgtactaatgctc	2143
ABCA4	70	intron7 + 1019	aggctcttgactgtctaga T/C agcaagtctaattcattgtg	2144
ABCA4	71	intron8 + 374	gtaaacacggctgtgggatg C/T ttttacaacacaatatcgt	2145
ABCA4	72	intron8 + 874	tgatgagcttgtattgtg G/A ggtacagcctattaatttag	2146
ABCA4	73	intron9 + 605	tcgtgtctctgtctgtatct C/T tgtctgggtttaggccaact	2147
ABCA4	74	exon10 + 1268	aacttttgaagaactggaac G/A cgttaggaagttggtcaaag	2148
ABCA4	75	exon10 + 1269	acttttgaagaactggaacg C/T gtttaggaagttggtcaaagc	2149
ABCA4	76	intron11 + 5236	ggcctggcacagatgaaata C/T tattcagagttcacagtgt	2150
ABCA4	77	intron11 + 5270	cagtgtattttcatttcata A/G tatatttgattttcaggtct	2151
ABCA4	78	intron11 + 5687	atcatgtaattgtactttaga C/G tcagatatataaatattgt	2152

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GENE	number	position	SEQ.	SEQ ID.No
ABCA4	79	intron11 + 7136	gacttcccaacttaccttag T/C ggagctgtagtcacatagaa	2153
ABCA4	80	intron11 + 7180	acgctcataaatgcttctct G/A ggctgtaaagggtgaatttt	2154
ABCA4	81	intron11 + 7701	gttagacgcaggcattacct C/T gtggctttgccccagtgga	2155
ABCA4	82	intron11 + 8073	gggatgtttgccacatcca T/C tggcattttcctcaaaaggaac	2156
ABCA4	83	intron11 + 8586	cagctgcctgcgctggagag G/A gctcaaacctctccgccag	2157
ABCA4	84	intron11 + 8893	agcaaagatgcccttgact C/T cttttccactagtgggtgt	2158
ABCA4	85	intron11 + 9257	gaatgagggtcacttgctgca T/A ggcagggtggcttcccatga	2159
ABCA4	86	intron11 + 11234	cccaaataatttgttttc G/A ttttaggaattaaatttcag	2160
ABCA4	87	intron11 + 11641	aagaaacaaacatttattga C/G aacttttgggtgtgacctg	2161
ABCA4	88	intron11 + 11808	tggatattcttaaagaaata C/T caattccatttccctttaac	2162
ABCA4	89	intron11 + 11923	aagatcattattaatatctc A/G tcagcgtgggtgcacttaag	2163
ABCA4	90	intron11 + 12055	tgagaacattacatgggacc T/C gccccagggtcatggaggct	2164
ABCA4	91	intron12 + 305	tcacctgtggctgggaggt G/A tgagtgcctatccaagccc	2165
ABCA4	92	intron13 + 1461	ttgggtttcagtgtcagcat G/A tagctgtctactcagatccc	2166
ABCA4	93	intron14 + 1237	aagggcaccaaagtctaag A/G gatgaggggaggagctgagc	2167
ABCA4	94	intron14 + 1268	ggagctgagcccccttgcct T/C atctaggtttcccttgttct	2168
ABCA4	95	intron14 + 1309	ttccatccctcagctgtct T/C cttttccagtaccaacatg	2169
ABCA4	96	intron14 + 2979	tcacctgtgtgggtagcaaa C/T ctcaaaaaatcaagtataga	2170
ABCA4	97	intron17 + 23	gagtcctttaaacaacaaat C/G ttaatgtttgaaatcaactc	2171
ABCA4	98	intron17 + 204	tgctgggcccctgtgtgatca T/G gaatggctgatcatggatga	2172
ABCA4	99	intron17 + 715	gggactccccctagagctgaa G/A tactctcccatctgtttgtt	2173
ABCA4	100	intron18 + 1282	ggaagatgaagaacctaac C/T gcttcagaaattcatgagg	2174
ABCA4	101	intron18 + 1531	gtctacccccttaggaccatt G/A taagagtacattgaggtaat	2175
ABCA4	102	intron19 + 1802	actgctcaccaggaggcaa C/A gcctcagtcacatgcaccgaa	2176
ABCA4	103	intron20 - 195	acagattattccattgtatg C/A atgaactatgtaagccatcc	2177
ABCA4	104	intron23 + 755	ctggctgcogctggggtttc C/T tatgtccatccacggggagg	2178
ABCA4	105	intron26 + 497	ctgagttaggtctagatggg G/A acactttggatgaatgagga	2179
ABCA4	106	intron26 + 702	tatcaaatataactcagacg T/G cagtctcctggcccccttga	2180
ABCA4	107	intron27 + 156	cctgctttccaaacccttat C/T ttgattcttggtaacatgaa	2181
ABCA4	108	intron27 + 385	tttaaagaacagtgcac G/A tgacttgcctttgaaatgc	2182
ABCA4	109	intron28 + 299	gacatgccatcagaccactg C/T gagtgtcaggcagcctacc	2183
ABCA4	110	intron29 + 168	ctccttcacactgtgtgc A/G gggacattcactacctcta	2184
ABCA4	111	intron29 + 497	gctgtcaataaggacaaaa C/T agactaatttcaaattctc	2185
ABCA4	112	intron29 + 567	agctgctaggaataaaaagg G/A agacaaaacgatccacaagc	2186
ABCA4	113	intron29 + 577	aataaaaaggagacaaaac G/A atccacaagctagagatggt	2187
ABCA4	114	intron30 - 2494	aatcacagctcatctgtgc A/G tcatagggatcccaaaagaa	2188
ABCA4	115	intron30 - 2169	aatgtaacagccaaagtct A/G gaaaaaggcaagccagtcc	2189
ABCA4	116	intron31 + 535	ctaactgtgaattatctct T/G tgatcactgccctttgagat	2190
ABCA4	117	intron31 + 957	gagttctcagcagcaaatct C/A cagtatgaaattttggattt	2191
ABCA4	118	intron32 + 445	tccagaggtttagaacctca C/T caagtgggactctaggagcc	2192
ABCA4	119	intron33 + 48	aggatttttgaacttgcttaa C/T taccatgaatgagaaactct	2193
ABCA4	120	intron35 + 129	tgtttagtcaggcacatatg A/C acatccgactttcaaataag	2194
ABCA4	121	intron35 + 209	tctccccaacatttatgtgg C/A aagtaagtttacatttgggt	2195
ABCA4	122	intron36 + 3209	ttgaggcctccacacccac G/A gcaggttgcacctgaggaa	2196
ABCA4	123	intron36 + 3542	cttggcagggttagggca T/C ggggtgggtaggaggacta	2197
ABCA4	124	intron37 + 304	ctgggggcagccattcccca A/G cccctcaccagctctgact	2198
ABCA4	125	intron37 + 525	taaatttgatgagtaattc A/G tccatctcgccctcagtttc	2199
ABCA4	126	intron37 + 766	tgttcaggctggagaaccc T/G cctatgaattgtacagggt	2200
ABCA4	127	intron37 + 856	aaaaccccatgaagtgtca A/G ggcaggcatcattatctcca	2201
ABCA4	128	intron38 + 62	tagtagagtatgtttggct G/A agcagagccaggggcaagca	2202
ABCA4	129	intron38 + 761	tccttgggcaagttaattt G/A atgaagagactgggtgttct	2203
ABCA4	130	intron38 + 1315	cagagtcagactctggaaag G/T cggggggataagaacacagc	2204
ABCA4	131	intron38 + 1316	agagtcagactctggaaagg C/A ggggggataagaacacagcc	2205
ABCA4	132	intron38 + 1526	ccaacatttctaagcacc G/A ccttcaaaaacctggtattt	2206
ABCA4	133	intron38 + 1561	gtattttcatgtaaattatc C/A gatacacagctgctatggaa	2207
ABCA4	134	intron38 + 1562	tattttcatgtaaattatcc G/A atacacagctgctatggaaa	2208
ABCA4	135	intron38 + 1674	ccagctgaacaccacgtgcc G/A ggtgtgtgctgatataaaca	2209
ABCA4	136	intron38 + 2867	tgctggctagacaaagggg A/C agctcccggccactagaaac	2210
ABCA4	137	intron38 + 2874	ctagacaaaggggaagctcc C/T gccactagaaactgcagg	2211
ABCA4	138	intron39 + 123	gaggggacctgttgggctg G/A aggtgtcctgccagctggag	2212

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GENE	number	position	SEQ.	SEQ ID.No
ABCA4	139	intron40 + 1904	gacactgtacagccagccca A/C tctgaccccttttctcat	2213
ABCA4	140	exon41 + 5814	ggaaataaaactgacatctt A/G aggtacatgaactaaccaa	2214
ABCA4	141	intron41 + 122	atttggttcccagttttatg T/G agggcatcatccctgtgtt	2215
ABCA4	142	intron41 + 287	tctgcagagcatgggtcagc C/T tcgagatgtctcagtactca	2216
ABCA4	143	intron41 + 411	cctcttcccctccttgcctt C/A accctgtctcagttctcagt	2217
ABCA4	144	intron41 + 443	gttctcagtcoggtttcttc G/A tatcttgagatttatccag	2218
ABCA4	145	exon42 + 5844	cgtatcttgagatttatcc A/G ggcacctccagcccagcagt	2219
ABCA4	146	intron43 + 328	ttttagcctattctataa A/G aatgcaccattgcttcccat	2220
ABCA4	147	intron43 + 345	taaaaatgcaccattgcttc C/G cattacctccctccacacat	2221
ABCA4	148	intron43 + 370	acctccctccacacattttt A/G caaacggttcagggagttt	2222
ABCA4	149	intron43 + 376	ctccacacatttttataaaa C/T gtttcagggagtttactgag	2223
ABCA4	150	intron43 + 670	ttaaacagactgggtcccta T/C gggcaggacagagaggatga	2224
ABCA4	151	intron43 + 701	gagaggatgagctctcactc A/G tctgcctcttctcgtgctgc	2225
ABCA4	152	intron43 + 822	gttaggtgctgctgacatct G/A tccagcatctgcttgactgg	2226
ABCA4	153	intron43 + 915	ggcaggacagagctctgagca C/T gcttactggctcagacagg	2227
ABCA4	154	intron43 + 1242	actgagctggacgctagaaa G/T aaactataggcttaagacac	2228
ABCA4	155	intron43 + 1671	tagagaagtttacttccatc G/A ggacacatgcattcttcta	2229
ABCA4	156	intron43 + 2036	ttgaaggatactcagtaatt G/A cttttttcttgagatttt	2230
ABCA4	157	intron45 + 176	gtgtttgggtcacacagctc C/T ggagaaaaacaagtcacggc	2231
ABCA4	158	intron45 + 193	ctccggagaaaaacaagtca C/T ggcacagccttgactggga	2232
ABCA4	159	intron47 + 238	cccaagtctctggatggggc A/G tctgatcaggatgcattgcag	2233
ABCA4	160	intron47 + 269	atgcattgcagagcctggctg G/A gatgagggagggtgctacc	2234
ABCA4	161	intron47 + 326	accacttatctcaacagatc C/G gggacctgtggcctatttac	2235
ABCA4	162	intron47 + 715	aagtcactaagctgggttgt G/A ggaggaacagcacataaccc	2236
ABCA4	163	intron47 + 734	tgggaggaacagcacataac C/T caccttatctatgctgaggt	2237
ABCA4	164	intron47 + 931	ggacactgcattagatatcta T/C agaatagcagcatgtcagg	2238
ABCA4	165	intron47 + 1260	acactctctgtggaccatc A/C ctcatccaagagagggtaac	2239
ABCA4	166	intron48 + 1663	tctgcctcttctcttacctc T/C aggtgtttgtaaattttgct	2240
ABCA4	167	intron49 + 127	agagagccccaccacacca C/T ggtccctaccaagtcccccac	2241
ABCA4	168	intron49 - 1545	gcagttaattccaaactttt C/A tccctattggatgagatca	2242
ABCA4	169	5'flanking - (1441-1400)	gtaaattcagttgaatcag (TCA)14-16 atttttcagctctggttcctg	2243
ABCA4	170	intron1 + (4712-4720)	gaggggaggggactataggc (A)8-10 cagcctaattcaaggatgag	2244
ABCA4	171	intron1 + (7295-7304)	ttgttgctttgcaatggat CACAGTCAT/Δ ttattcactc attcattcac	2245
ABCA4	172	intron2 + (951-952)	cctgtccatcagactctttt TT/Δ acctctccccgaggagccca	2246
ABCA4	173	intron3 + (2642-2653)	cctgggtgacagagcagat (A)10-12 tagcatgagatattattact	2247
ABCA4	174	intron4 + 5202	cacaaagcatctgacacccc C/Δ atccagccctggctaacttt	2248
ABCA4	175	intron6 + (3029-3044)	cactaaaaacaaaaatttac (A)16-18 cctgaaagaaattgcaggca	2249
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt (G) cttttatggattacaaaga	2250
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt cttttatggattacaaaga	2251
ABCA4	177	intron6 + 5985	ttcctcttcaaaccccc C/Δ agactaggagaaggtctgtc	2252
ABCA4	178	intron6 + 6094	gggacggacagaaaaagacc T/Δ agttctgttgagccaaaga	2253
ABCA4	179	intron6 - 161	tattttttcaattaaataaa A/Δ gagtttttgtttctaaaag	2254
ABCA4	180	intron7 + (809-810)	gggcccagatgacacactga (TG) tgtgggaaagttagagaaga	2255
ABCA4	180	intron7 + (809-810)	gggcccagatgacacactga tgtgggaaagttagagaaga	2256
ABCA4	181	intron8 + (472-484)	atcttccccaccttcaacta (T)10-13 ggtctctatggggtaaagg	2257
ABCA4	182	intron9 + (48-71)	gtacctggacctccagaa (GT)11-13 gagagagatgtgccttctg	2258
ABCA4	183	intron9 + 554	ataggggcagaaaaagacaca A/Δ ccaaaagtctctctcactt	2259
ABCA4	184	intron10 + 11	catgatcagagtaagggggg G/Δ ttggaggatggggaggggag	2260
ABCA4	185	intron11 + 4242	ggagaggaaatgatgttagt G/Δ cctcctgtaaataggcccag	2261
ABCA4	186	intron11 + (13743-13753)	tgctcttttgggttaattg (T)9-11 cctcttcaggagaagaaaa	2262
ABCA4	187	intron13 + (636-637)	cggggtggagggttgggagg (G) ctcatgttcattatagatg	2263
ABCA4	187	intron13 + (636-637)	cggggtggagggttgggagg ctcatgttcattatagatg	2264
ABCA4	188	intron18 + (569-570)	tgctgcctcatctctctc TT/Δ aaactagtctgtatttctc	2265
ABCA4	189	intron20 - (304-297)	tataacctgactttttttc (A)7-9 ggattgcttttttaacata	2266
ABCA4	190	intron22 + (1236-1246)	gctgaattagtcccttggg (T)9-11 agttaactcctgattttgc	2267
ABCA4	191	intron26 + (4626-4635)	gataatcaatgctgtaagg (A)9-10 tggcattagagatccagacc	2268
ABCA4	192	intron33 + (115-116)	taaaaccgtctgtttgttt GT/Δ ttacatggtttttagggccc	2269
ABCA4	193	intron36 + 1078	taagcagctatcacttaaca A/Δ tacaaaaccagagattatca	2270
ABCA4	194	intron37 + (290-291)	ccttgaccaaagcctggggg (T) cagccattcccaaccctc	2271

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GENE	number	position	SEQ.	SEQ ID.No
ABCA4	194	intron37 + (290-291)	ccttgaccaaagcctggggg cagccattccccaacccctc	2272
ABCA4	195	intron38 + 896	ataaaaagaggggggaaaaaa A/ Δ gaaggcagtcgctgcagggc	2273
ABCA4	196	intron38 + (1209-1210)	gtggacccctgagactgact CT/ Δ ttccagatcttgttaggggt	2274
ABCA4	197	intron38 + 1322	actctggaaaggcggggg G/ Δ ataagaacacagccccagca	2275
ABCA4	198	intron38 + 3107	gggccccacctgtgaagag A/ Δ gggggggtggggtttgcgcc	2276
ABCA4	199	intron40 + 152	ttttctccaataatacaagt A/ Δ gaggatcgggttaaaatagg	2277
ABCA4	200	intron43 + 330	tgtagcctattcctataaaa A/ Δ tgcaccattgcttccatta	2278
ABCA4	201	intron43 + 1354	tttaattggcccagccatgc C/ Δ ttgggtggctttgtcattg	2279
ABCA4	202	intron47 + (1305-1308)	catcctgctgaaggagaaag AAAG/ Δ caccaatggcccaagcccta	2280
ABCA7	1	5'flanking - 1598	agaatgttggccccctcccc C/T tctgcatcctctgcagaag	2281
ABCA7	2	5'flanking - 1594	aatgttggccccctccccct C/T ctgcatcctctgcagaagcc	2282
ABCA7	3	5'flanking - 1180	ggccagtgagtgacgggcag G/A tcgccc aaatagcagcgtgc	2283
ABCA7	4	5'flanking - 460	agagctggggctgtgcctcc A/G gctgggcaactgcctgtctc	2284
ABCA7	5	5'untranslated - 9	ctctgtcccgtcccctgccc A/G gtctcaccatggccttctgg	2285
ABCA7	6	intron5 + 91	ccccgggccaaggacctccc G/A ttccaggcatccaggctgtc	2286
ABCA7	7	exon6 + 563	cagcttgttggaggcgcgtg A/G ggacctggcccaggaggtag	2287
ABCA7	8	intron8 + 103	gccggagggtcacggaaact A/G ttgaagaagtaggagttag	2288
ABCA7	9	intron8 + 166	tgcggaggatcagaggcaca C/T gcaggagcaaggcagagggg	2289
ABCA7	10	exon9 + 955	accggaccttcaggagctc A/G ccctgctgagggatgtcgg	2290
ABCA7	11	intron9 + 421	tttttttttttttttt T/A taagagatggagtctcactc	2291
ABCA7	12	intron9 + 463	gttgcccaggctggactgca G/A tggcagatcttggctcact	2292
ABCA7	13	intron9 + 467	cccaggctggactgcagtg C/T gagatcttggctcactgcaa	2293
ABCA7	14	intron9 + 488	gagatcttggctcactgcaa C/T ctccgcctcctggattcaag	2294
ABCA7	15	exon10 + 1184	cgcacacgctgatgtggggc A/G cctggtgggcacgctggggc	2295
ABCA7	16	intron10 + 10	gagtgcaggaggtgagggcc T/C gtccacctcgggggtctgtt	2296
ABCA7	17	exon11 + 1388	cctgggcccccgccacgtgc G/A catcaaaatccgcatggaca	2297
ABCA7	18	intron12 + 115	caggctgcgaactttgcacc T/G ttacaccactccacgtgacc	2298
ABCA7	19	exon13 + 1824	ccctcctgtctcagcgccgc A/G ctgctggttctggtgctcaa	2299
ABCA7	20	intron13 + 55	ggtgcgctggagggtgacag A/G caggggcccggccacgtggg	2300
ABCA7	21	intron13 + 78	ggggcggccccacgtgggtg C/A gcgccccaggccaatccag	2301
ABCA7	22	exon14 + 1851	cgttgctctcagcagctggg A/G gacatctcccctacagcca	2302
ABCA7	23	exon15 + 2153	caggggcgcgcagtggcaca A/C cgtgggcacccggcctacgg	2303
ABCA7	24	intron15 + 34	ggcggggctcggggcgggt C/G gcacctgcttgcgggaggc	2304
ABCA7	25	intron16 + 8	ctggacccaaagggtgaggc A/C ctacgaggcttaatagctgg	2305
ABCA7	26	intron16 + 161	tcccgagcttttataggcc C/T cggcccagcaggtcccggat	2306
ABCA7	27	exon17 + 2385	caccccatctctgcagtgct G/A gtagaagaggcacccggccgg	2307
ABCA7	28	exon17 + 2421	ccggcctgagtcctggcgt C/A tccgttcgcagcctggagaa	2308
ABCA7	29	intron20 + 166	cagacagtaagagtgggg A/G tagacagaggttcccctgga	2309
ABCA7	30	exon21 + 3027	ctgctgggagaccgtgtggc C/T gtggtggcaggtggccgctt	2310
ABCA7	31	intron22 + 1386	gggtggggcgtgagccggg C/T tccctgaagcaccctttgt	2311
ABCA7	32	exon23 + 3417	gggatctccgacaccagcct C/G gaggaggtgtgaggcctggg	2312
ABCA7	33	intron23 + 147	ggagctctgttgctcagat G/A tcccttggaaggcctgggg	2313
ABCA7	34	exon25 + 3528	gctggcctagacgtaaccct A/G cggctcaagatgcggccaca	2314
ABCA7	35	exon29 + 4046	cccagcctgccagtgtagcc G/A gcccggtgccggcgccctgc	2315
ABCA7	36	intron30 + 81	ccccctgggagctctcccg C/A cccccggccctcagctccc	2316
ABCA7	37	exon31 + 4239	ctgcctgcatggccccacag A/G tacggaggcttctcgtggg	2317
ABCA7	38	intron32 + 1	caaggagcagctgtctgagg G/C tgcactgtgagtcctccac	2318
ABCA7	39	intron33 + 54	ccactgcttgcactgccct G/A totggccccctttaggcagg	2319
ABCA7	40	intron34 + 245	cagtacttgggaggccgag G/A caggaggactgcttgtggcc	2320
ABCA7	41	exon36 + 5057	ggtgagccgatcttgaac A/G ggtcttcttatcttcccc	2321
ABCA7	42	intron38 + 65	ggccactcaccttctgaa A/G gacctgcactctcccagta	2322
ABCA7	43	intron40 + 154	ctctacctcccacacggga C/G caggccctgagacaccctg	2323
ABCA7	44	intron40 + 277	ctgagcccccgccgccccca T/C cccagcgtggcccgggaac	2324
ABCA7	45	exon41 + 5592	gtggcccgggaaccagtg C/T gcgcacctcagcatgggata	2325
ABCA7	46	intron41 + 286	ctccttgactctgccttctg T/C ggccctgcccacttgcctct	2326
ABCA7	47	intron41 + 389	tggccgttcccagtttgcag C/T cgttctactgcctcttccat	2327
ABCA7	48	intron41 + 991	cacactatggccctgcccc C/T acccatcccagctccaccca	2328
ABCA7	49	intron41 + 994	actatggccctgccccacac C/T catcccagctccacccacac	2329
ABCA7	50	intron41 + 998	tggccctgccccacacccat C/G ccagctccacccacacccatg	2330
ABCA7	51	intron41 + 1001	ccctgccccacacccatccc A/G gctccacccacacccatggcc	2331

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GENE	number	position	SEQ.	SEQ ID.No
ABCA7	52	intron41 + 1051	actcatgctggctccacca C/T accatggccccgccccatac	2332
ABCA7	53	intron41 + 1131	tgccctgccccatgccatt A/G tgccctgctccacactcaa	2333
ABCA7	54	exon44 + 5985	gaagcgctctgctcgccct G/A gccatcatggtgaatggcg	2334
ABCA7	55	intron44 + 201	ggcgaggaccaggaggcgt G/C agcgggggctctgggtgga	2335
ABCA7	56	intron44 + 233	ctgggtggatttagaagaca C/T aatcagggtgtgcgttgagt	2336
ABCA7	57	intron44 + 313	agttaggggaggcctggtt A/G gtggcgggggccataggaaa	2337
ABCA7	58	intron44 + 337	ggcgggggccataggaaagt G/C ggcggggggtatttattgt	2338
ABCA7	59	exon45 + 6133	tggcgccgagttccctggg G/T cggagctgcgcgaggcacat	2339
ABCA7	60	exon45 + 6159	ctgcgcgaggcacatggagg C/T cgctgcgcttccagctgcc	2340
ABCA7	61	intron45 + 27	acggcgccggggtcgggctg G/C gggaggcaggctgggggcca	2341
ABCA7	62	3'untranslated + 6580	aaggctggagagaagccgtg G/C tggtaaacccgtgtgcatgt	2342
ABCA7	63	3'flanking + 108	caagctgagtgtgcacatac G/A ggccaagtggcgattcatag	2343
ABCA7	64	3'flanking + 376	cttacaggagcccggtgtcc C/T ggagcacaggccaggggccgg	2344
ABCA7	65	3'flanking + 687	cagcaggagagacttggggag G/A ggggagagagttcacactgc	2345
ABCA7	66	3'flanking + 688	agcaggagagacttggggagg G/A gggagagagttcacactgcg	2346
ABCA7	67	3'flanking + 1169	cctcgacctgaccttca C/T ggggctgcaggggcgggtgat	2347
ABCA7	68	intron9 + (398-422)	cgtgaactaccacgtcctgc (T)22-26 aagagatggagtctcactct	2348
ABCA7	69	intron12 + (175-184)	ggggactctgagggtctggt (G)8-10 actctgagggtctgggggcc	2349
ABCA7	70	intron30 + (81-87)	ccccctgggagctctccgg (C)6-7 ggccctcagctcccttccc	2350
ABCA7	71	intron34 + (349-361)	agaaagagaaagagagaaag (A)12-14 cagaaatgtgcttgggtga	2351
ABCG1	1	5'flanking - 1772	cctgggcttcagcaggggcc T/C cacacctgcaatgggtgcct	2352
ABCG1	2	5'flanking - 1754	cctcacacctgcaatgggtg C/T ctgggagagggtgcagatg	2353
ABCG1	3	5'flanking - 1450	tccaaagcccagatttggtg T/C ttttgggctcttttggat	2354
ABCG1	4	intron1 + 4	ctggtggaggaagaaaggta G/A ggaggcggtgcttctgtgt	2355
ABCG1	5	intron1 + 576	agctcaggaggtgtctggaa C/T gccacacagtgcaggagttt	2356
ABCG1	6	intron1 + 1426	aattctcttctcaactaa A/G gaaatattttatagaaaaat	2357
ABCG1	7	intron1 + 2342	agagcctgcaatgggccc G/A agggacctgcccagactca	2358
ABCG1	8	intron1 + 2399	gaggggttgacagacaggat A/G tgtctgctgtgtccagctg	2359
ABCG1	9	intron1 + 2406	tgacagacaggatatgtctg C/G tgtgtccagctgctggtt	2360
ABCG1	10	intron1 + 2911	ccctctctgtcccactgtt G/C tcccaacaccagcctgttct	2361
ABCG1	11	intron1 + 4363	tataatagattcctagcaga A/G aacataattgtgagaggac	2362
ABCG1	12	intron1 + 4752	gctttcagagcccattcaca C/T aagggtctcattttattagg	2363
ABCG1	13	intron1 + 5026	ccaggtctgtgggattcag G/A ccaaaaaggagcgtagcaag	2364
ABCG1	14	intron1 + 5532	gggttaaattattccgggcag C/T gccaaagtcagattatctga	2365
ABCG1	15	intron1 + 5681	gctaaagtgcaggaaggca T/C catgaataaatcctttcagg	2366
ABCG1	16	intron1 + 6290	tcacagcagattcatgagag T/A tgaatgttagccgcatgt	2367
ABCG1	17	intron1 + 6386	agatgctcccctccagccag C/T acattttctcctgtgagca	2368
ABCG1	18	intron1 + 6758	acctgcatgtgggtgcccc C/G ctgccttctctactgcctt	2369
ABCG1	19	intron1 + 7029	tgggtcagattaaatatatc C/T tgaaggactaaaccgtaaaa	2370
ABCG1	20	intron1 + 7176	ttgctcacattgtgaaaaaa C/G gcaaaaagatgggttttcag	2371
ABCG1	21	intron1 + 9243	gcctgagagcgctggcagta G/A gaagggtcgccagtgtggac	2372
ABCG1	22	intron1 + 11224	tctggttagagaggaaaat G/A ggcagcatcattttgtacc	2373
ABCG1	23	intron1 + 11371	gggctctcttgagccctt T/G tctctccagccctgcgtct	2374
ABCG1	24	intron1 + 12420	gggatttogaatctcaacac T/C ctgagctctgtgcttcccc	2375
ABCG1	25	intron1 + 12484	gagttgtcctccaagagaat C/T ttgtatggttcctttctg	2376
ABCG1	26	intron1 + 12955	ctggggttggtgggagccac A/G gtctcacacctattggcagg	2377
ABCG1	27	intron1 + 12985	ctattggcaggctgtgaaca T/C tgttcttgatttgcaata	2378
ABCG1	28	intron1 + 20041	acatggccggttcccttct T/C cctcggaatggcctggaatt	2379
ABCG1	29	intron1 + 20046	gccggcttcccttctctc G/A gaatggcctggaattogac	2380
ABCG1	30	intron1 + 21058	acaagacttagaattgacc G/A tgattttaaaactattctaa	2381
ABCG1	31	intron1 + 26189	ttcttgatgtggccatgca C/T gggggcaagggttgatgag	2382
ABCG1	32	intron1 + 27453	atcatgtggttgggggaaa G/C ctgggaccccaacttggtaca	2383
ABCG1	33	intron1 + 28098	caggaaggagacagctgtg G/C tgctgcttagagtaggcgc	2384
ABCG1	34	intron1 + 29670	ccttcagttgtaataggcag A/G aggagcgcacaggaggctg	2385
ABCG1	35	intron1 + 29810	attgtttctcctggtttgt T/C tgtgtgactttcccttaa	2386
ABCG1	36	intron1 + 36220	cagatcccttggttctggg C/T aggtagtaggagaggtttt	2387
ABCG1	37	intron1 + 36341	aaacagggttgagtctcc G/A taaggacaggagaccttcc	2388
ABCG1	38	intron1 + 36370	aggagacctccacatcct G/A gcaagaattcttctttttc	2389
ABCG1	39	intron1 + 36662	cagactaaatgcacaattct G/A gattgagctgactgtattga	2390
ABCG1	40	intron1 + 36914	tgtaaaagatggagaagaac A/G cagtagtcgctgtgtgag	2391

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GENE	number	position	SEQ.	SEQ ID.No
ABCG1	41	intron1 + 37029	tgtgactcatggcctctgcc A/G ggggactgggctggccctgc	2392
ABCG1	42	intron4 + 1196	tgaaaagaaaatggatgagt G/A gaaacaaaagagagaaaat	2393
ABCG1	43	intron4 + 1200	aagaaaatggatgagtggaa A/C caaaagagagaaaatgtgg	2394
ABCG1	44	intron4 + 2041	aagcagaggctttccaccc G/A gagactcaagaagctgctcc	2395
ABCG1	45	intron4 + 2490	gtggtgaagtagagctgagc A/T cacgggggagccctccatcc	2396
ABCG1	46	intron4 + 2552	atggccttgggccactgcct G/A ctgtgccccgagccgagctt	2397
ABCG1	47	intron4 + 2822	cagcaggctccgtgctgaag T/C cacagcaagccaggcccttg	2398
ABCG1	48	intron4 + 2850	agccaggcccttggcctgcc G/A gagctggaagaccagaaca	2399
ABCG1	49	intron4 + 2919	gcctcccaggagtagctaca C/T gggacccgaaggcagatggc	2400
ABCG1	50	intron4 + 3506	ggcagcctgggctgccgaga T/C cctccctggagcgcccgccg	2401
ABCG1	51	intron4 + 3538	cgccccgcccgaagccccag G/A ggggctggagctacaagtgg	2402
ABCG1	52	intron4 + 3554	ccaggggggctggagctaca A/G gtggccttgacagtttttg	2403
ABCG1	53	intron4 + 3721	ccagctcatgggcaggggtg C/T ggagggaaaggcaccacag	2404
ABCG1	54	intron4 + 3852	caccagagccactcagtcgg C/T caagagcgtcgccagtggt	2405
ABCG1	55	intron4 + 3921	gaagaccagcagtcgatgcc A/G gctgggaagagggtctgcc	2406
ABCG1	56	intron4 + 3979	accaccagcctttccaga C/T agccttcagaagctgtttc	2407
ABCG1	57	intron4 + 4291	gagccgtggagtaggggtcc G/A cttgctatggctcccagggg	2408
ABCG1	58	intron4 + 4922	gaaaccaccagaaattgtgc A/G tcctctcatgtgtccattca	2409
ABCG1	59	intron4 + 4968	tattgactggacaccttctc C/T gtatggggcactgggctagg	2410
ABCG1	60	intron7 + 672	atcagtaacgggtcactaac G/A gatgctgctgagtggggcag	2411
ABCG1	61	intron7 + 840	atttcatttcctaatgtcg T/C ctgaccagagagcgggaggt	2412
ABCG1	62	intron7 + 891	tggcccactgttgagggtgt G/A ggtgaccagaggggcctgga	2413
ABCG1	63	intron7 + 997	tgtgtcctggtttgtggctt C/G atctaggaggtgtggtggcc	2414
ABCG1	64	intron9 + 1616	ctggaggagaagacaggata A/C agtctaagacgtgctgtcac	2415
ABCG1	65	intron9 + 1630	aggataaagtctaagacgtg C/T tgtcacagagttcagggtcc	2416
ABCG1	66	intron9 + 1674	gcttccaaaggccgcacccg G/T gttgttctctgagccgagga	2417
ABCG1	67	intron9 + 1689	atccgggtgttctctgagc C/T gaggacggccttgcgaacgc	2418
ABCG1	68	intron10 + 446	tggctgacagtgaacacagc G/A gctgcttctccagaacttta	2419
ABCG1	69	intron10 + 581	atgcagagtttcagaagagg C/G agactcaggaagagtaaggc	2420
ABCG1	70	intron13 + 243	accggagagccatggcagg A/C ccaagtgttctggacgttgc	2421
ABCG1	71	3'untranslated + 2370	gcctctcagctgatggctgc A/G cagtcagatgtctggtggca	2422
ABCG1	72	3'flanking + 1124	ctcagaactacatcgagtga G/A gtcagtggtgaaaacgcca	2423
ABCG1	73	3'flanking + 1252	atggggcccacagccctgcc T/C cagaagcagcttgggtctcg	2424
ABCG1	74	3'flanking + 1433	gggggaagagcttgggaacc A/G tgagggtgttaggtgcaa	2425
ABCG1	75	3'flanking + 1513	tgaagggtgaactggagtag G/C tgaggattctgcagttgacg	2426
ABCG1	76	intron1 + (19909-19944)	ccgatgaggaggggatgggg (CACCAGGCAGCAGACTCTGA TGAGGAGGGGAGGGGG)caccaggcagcagactctga	2427
ABCG1	77	intron1 + (19909-19944)	ccgatgaggaggggatgggg ca ccaggcagcagactctga	2428
ABCG1	78	intron1 + (25136-25137)	catgaacttgctgaccata (G) ccctgtgaggagctagggt	2429
ABCG1	79	intron1 + (25136-25137)	catgaacttgctgaccata ccctgtgaggagctagggt	2430
ABCG2	1	intron1 + 152	tcatttgaaagtgggtatgc G/A gtttaaaactgacagttcaa	2431
ABCG2	2	intron1 + 614	agctagtcataaataaatac G/A ccagagtagtaaggaagaga	2432
ABCG2	3	intron1 + 10002	cctcatgaatgggtatacatg T/A cccaacatatctcttcgat	2433
ABCG2	4	intron1 + 10123	acagtggtcccttgggtgc G/A tatacccaaatccctgcata	2434
ABCG2	5	intron1 + 10768	ataggaataattgagaacag G/A gtctgaagaactctgcagga	2435
ABCG2	6	intron1 + 10791	ctgaagaactctgcaggaaa T/C gaaaatagttccctgctttt	2436
ABCG2	7	intron1 + 10792	tgaagaactctgcaggaaat G/A aaaatagttccctgctttta	2437
ABCG2	8	intron1 + 14183	tcacttaaggcttgcagg T/G gtctaggacacagaaagaga	2438
ABCG2	9	intron1 + 14934	aaagtgtctttaaattcc A/G tcttgagtcagtgagctatt	2439
ABCG2	10	intron1 + 14955	tcttgagtcagtgagctatt G/T aaattcaagcaataagttat	2440
ABCG2	11	intron1 + 17251	ctgtttgggaacagcaactc A/C atcataggcagagagaaagt	2441
ABCG2	12	intron1 + 17347	atttcaaacctgtttcaca G/A ttgttaagctcatcttaagg	2442
ABCG2	13	intron1 + 17626	gaaggtgcataacaactcc T/G acataaagtctggagctata	2443
ABCG2	14	intron1 + 18271	aatgaagctgctcattgcc A/G cacatttaaaaatggacttg	2444
ABCG2	15	intron1 + 18369	ctattgctttctgtctgca G/T aaagataaaaactctccaga	2445
ABCG2	16	exon2 + 34	atgtcgaagttttatocca G/A tgtcacaaggaaacaccaat	2446
ABCG2	17	intron2 + 36	tgtaaaaagacagctttta A/G ttacctacagtgaacctca	2447
ABCG2	18	intron2 + 4230	caaccctaaattggagggcc C/T gggcgtgggtgattgagaaag	2448
ABCG2	19	intron2 + 4518	gttgacagacttttatagtg A/C gggacactgacctgcacgca	2449

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GENE	number	position	SEQ.	SEQ ID.No
ABCG2	20	intron2 + 6278	atgtatgtaccacgtcttca T/C attcttaaaggatgacccta	2450
ABCG2	21	intron3 + 10	ggcaaattcttctgtgagtata A/G gagagtataagtaagcgttt	2451
ABCG2	22	exon5 + 421	tgacggtagagagaaaactta C/A agttctcagcagctcttcgg	2452
ABCG2	23	intron6 + 3158	actattctagttgattctag A/G ttgtcaatacaacacactga	2453
ABCG2	24	intron6 + 3203	tcctattctgttttaataaa A/G gcattgaatttaggtttgct	2454
ABCG2	25	intron6 + 3287	gtcaggctgaactagagcaa A/G caatctaaaggcaagaatag	2455
ABCG2	26	intron7 + 179	ttcattttttagtagcaccagc T/C tgttatttaggtatctttct	2456
ABCG2	27	intron9 + 5677	gcacttggactttgctttgc T/C acatactgcattgctctgc	2457
ABCG2	28	intron9 + 5974	tatactaataaatgggtgtgt A/T taagtttttatctotaattg	2458
ABCG2	29	intron10 + 1908	gacgcttatgtgcagcctat G/T ttgatgtctggaaaggctga	2459
ABCG2	30	intron10 + 2094	ccctgagggctgaggtatct G/A gattattccagacttgcta	2460
ABCG2	31	intron11 + 20	tgtgagtaggtctttgttct A/G ggaacggggctgtccagcag	2461
ABCG2	32	intron11 + 1447	tggtcttcaaggaaagcccc C/T gtcaaaagaaggaaaagaagc	2462
ABCG2	33	intron12 + 49	atgtcttagtcttgccat G/T ggtgaagtcagttgcacctt	2463
ABCG2	34	intron12 + 1566	tatgcagttacatggacaga C/T acaacattggagaccgaggg	2464
ABCG2	35	intron13 + 40	gctctgataagggaattgtt C/T ttctctcatttcttctgc	2465
ABCG2	36	intron13 + 1823	ttactcaagcaggcctgact C/T ttagtatttgcctttttag	2466
ABCG2	37	intron14 + 497	ctaataaaaacaacaagaa T/C gaaagattgtcactgtaaat	2467
ABCG2	38	intron14 + 815	taactcttggaaactctt A/G aaatttaaaactgtttacct	2468
ABCG2	39	intron15 + 110	ccaggggcaactgaattttc C/T gagcctacgttttctcatcc	2469
ABCG2	40	intron15 + 566	gccgcatagtcatgtgtgt T/A gtttttaaatgaacttgga	2470
ABCG2	41	intron15 + 639	aacaagaaacactgaataa G/A ttgagaaaaaaccccgttt	2471
ABCG2	42	intron15 + 1197	tgagtagctgggattacagg C/T gccaccaccacacotggct	2472
ABCG2	43	intron16 + 520	catcaattcaggtaagaaa T/C agaagattgtagcacacaaa	2473
ABCG2	44	5'flanking - (998-995)	gttgggatggctacactcac TCAC/Δ aaagcctgatggcccgttc	2474
ABCG2	45	intron13 + 405	ctgctagtttattttttt T/Δ aacatttttaatttatgtt	2475
ABCG2	46	intron13 + (692-702)	tcaatatgtttctgcttato (T)9-11 aatggtacttaatoctaat	2476
ABCG2	47	intron15 + (645-650)	aaacactgaataagttgag (A)7-8 ccccgttttcacataatgtt	2477
ABCG4	1	intron1 + 84	ggcctgggtgtccatgttc G/A gaaagtcctgcaccagtggg	2478
ABCG4	2	intron2 + 77	gaacacagaaggattctga A/G agggcattgacccccatcct	2479
ABCG4	3	exon6 + 679	tggtgtccctcatgaagtc C/T tggcacagggggccgtacc	2480
ABCG4	4	intron7 + 95	ggcctcctagggtagagat C/T tcaccgtcgcctgccttccc	2481
ABCG4	5	intron7 + 158	cttgcccttgggaagtgtg G/A tgaatctaaactgagctctc	2482
ABCG4	6	intron8 + 106	ccccagaggcattgcaacca A/G tgggtgctaggaagaacctta	2483
ABCG4	7	intron8 + 1089	aggtacacaacttaattgta C/G aagattctctgtagacctgg	2484
ABCG4	8	intron11 + 1113	acgtgagacgagataagtga T/C ggtcatatggccagggagga	2485
ABCG4	9	intron11 + 1120	acgagataagtgtgtcat A/G tggccagggagggaaggggac	2486
ABCG4	10	intron11 + 1173	gggggacagctgaacaaga A/G tgtggaggcaggatggacac	2487
ABCG4	11	3'untranslated + 2758	gagtgcaggcacatacatg A/C gaacaggccatctcagccct	2488
ABCE1	1	5'flanking - 158	aactcagattctcggcacct C/T cagcagctggcttcgccaac	2489
ABCE1	2	intron9 + 237	ctgaaattatatgcaaatc C/T ttagctttataggaagcaga	2490
ABCE1	3	intron9 + 4203	ttgtgtaggaagtgtatca T/G taatttgacatatgagatgt	2491
ABCE1	4	intron10 + 1811	ccaagaaactcagctttct C/T ttcacttaaatataggaaac	2492
ABCE1	5	intron17 + 2301	atatccagaaacagatggtta T/C gtgcagaacaggtgtacag	2493
ABCE1	6	3'untranslated + 1810	tggatgattagactgactct G/C agaatttgataagccattt	2494
ABCE1	7	intron1 + (5349-5363)	tttgtctgggttgggtggg (T)13-16 gagactgggtctgactctca	2495
ABCE1	8	intron1 + (5845-5854)	tacatttgcataaattata (T)9-10 gcagataatcatttcatctc	2496
ABCE1	9	intron5 + (836-851)	taaattcacatgattctgta (T)14-16 aggtcctcctgactggcag	2497
ABCE1	10	intron8 + (1153-1169)	tccttcaaacttatattgc (T)13-17 catagtttcatgtttgatga	2498
ABCE1	11	intron9 + (1023-1024)	ttgctctgtttcaaatctct (T) attcatgggccagcagctog	2499
ABCE1	11	intron9 + (1023-1024)	ttgctctgtttcaaatctct attcatgggccagcagctog	2500
ABCE1	12	intron9 + (2338-2346)	agttagatggacctgggg (A)8-9 ctagttaaggaaaagtaata	2501
ABCE1	13	intron9 + (3213-3221)	ttccaattttcattgttac (T)8-9 ctggccagattactcctgaa	2502
ABCE1	14	intron10 + (284-299)	tcctctgcattttggcttct GCAGTATTACTGTAGT/Δ atttg	2503
ABCE1	15	intron10 + (840-853)	tttttgggttctttcttct (T)13-14 aatcttggaggaatctttt	2504
ABCE1	16	intron16 + (1163-1172)	gattagaaatccaggttaaa (T)9-10 gttttgcacaaaaatattac	2505
ABCE1	17	intron16 + (1372-1382)	taaaatttaatacaaaattga (T)10-11 ctcttagtcctcaaacctt	2506
CHST1	1	intron1 + 2475	taaatggagaaaaataacacc G/A acctgatagcattgtgtga	2507
CHST1	2	intron1 + 2612	aaactcccaagcatgtctca C/A ctatgccttaccctaggtc	2508

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GENE	number	position	SEQ.	SEQ ID.No
CHST1	3	intron1 + 3900	gccctgccccactcccaga C/G ttgcgccctccagccccctt	2509
CHST1	4	intron1 + 6520	cctccccagaggagctggg C/T acactggggccttgtgtgt	2510
CHST1	5	intron1 + 7534	atttgtgttgccatactgc T/C cacatggaaggatgctctag	2511
CHST1	6	intron1 + 7911	tttcccttaggaagaaaaac G/A ccttgcctgtttatgcattt	2512
CHST1	7	intron1 + 7963	aaaacattcatgggggatta G/C tgctggctaogtcagagtca	2513
CHST1	8	intron1 + 9173	gcgctgccacagatcaggcc G/A aggtgggggacagaaatgcc	2514
CHST1	9	intron1 + 9701	cccagaattctgaatacagc A/G gcgatgacgggactacgagg	2515
CHST1	10	intron1 + 12132	aacagatccacaggaccaga C/A agcaaaggggaggaacatgc	2516
CHST1	11	intron1 + 12465	atgcagggaaggggcttggc G/A caaaactgtcaactgagata	2517
CHST1	12	intron1 + 12561	atgctccctgggtccactttc G/A ctttgagtttcaggtagctg	2518
CHST1	13	intron3 + 529	ccatggtctgcaggggtcct T/G catgctcaggggattggggt	2519
CHST1	14	intron3 + 617	agaggacagaggaaagagga C/A cacctggagaactgggcgcc	2520
CHST1	15	intron3 + 796	aagaggcttcgcagctgtc C/T gcaggttaaatoctggggtg	2521
CHST1	16	intron3 + 818	caggtaaatoctggggtgc A/G aggaatgtttgttcagctcc	2522
CHST1	17	3'flanking + 762	ataactggtacaggtttact G/C gtgtctacactggcagagaa	2523
CHST1	18	intron1 + 7874	gttttcccttgcccttgcct T/Δ cattttcatcacctcattt	2524
CHST1	19	3'flanking + (335-349)	cacactgccacacctggota (T)12-15 ggatttttagtagagacgggg	2525
CHST3	1	5'untranslated - 294	tccagcgtgccgaccggccc C/G gcagcgccctccatccctccg	2526
CHST3	2	intron1 + 96	gcgtccaggcgccgcgcgcca G/A actttggaggagagaaggggg	2527
CHST3	3	intron1 + 4467	agagaagaatggggcagagc C/G ggagcagccaggggaggtga	2528
CHST3	4	intron1 + 4853	ggatgagcactgccagctg A/G tccctgccaccttccacag	2529
CHST3	5	intron1 + 4965	tccactgcagagggggacaca G/C tgaccaggacggaagtggg	2530
CHST3	6	intron1 + 5046	gggctgtccatctttgtacc C/T ctggttccatcccagtgct	2531
CHST3	7	intron1 + 5300	ccttttctctctaaggcct A/G aagagatgacagaatgctgc	2532
CHST3	8	intron1 + 5354	agcgcgtggactccacagcg G/A ggtgtggggtggccctggc	2533
CHST3	9	intron1 + 5428	gacacgcttcagccctctgt C/G tctattgccccaaatctggc	2534
CHST3	10	intron1 + 5621	ctgtggcttccctgggccc A/G ggaaatttatcactgaggtt	2535
CHST3	11	intron1 + 6555	gagtggggcactgtggaag G/C ttctggttctgtctttgtc	2536
CHST3	12	intron1 + 6990	aaacacactgggccaccccc G/A tccccgactgtgactacac	2537
CHST3	13	intron1 + 7133	ctgagggcctgtcctgcagg T/G ttgatgtgtctgaagaggcc	2538
CHST3	14	intron1 + 7161	gtctgaagaggccccagaa T/C agaaatctagaacctgccag	2539
CHST3	15	intron1 + 7199	cagtcacgaagcagtgctac C/T caccagaggatgaagaactg	2540
CHST3	16	intron1 + 7316	cttgcatctggtgtaggtgc C/T tggggtagcgtgccagga	2541
CHST3	17	intron1 + 7967	gacaggaacccccaccccgag T/G gatgtctggccctgtgacct	2542
CHST3	18	intron1 + 11412	gcttgcaactctgattcatt C/T tgcagtcactggctctttgt	2543
CHST3	19	intron1 + 11591	ccctggaagggcctcactgc G/A gtgactcattaccagcatg	2544
CHST3	20	intron1 + 12541	accacacagcatgaatggg G/C ccagccccagcctgcccgct	2545
CHST3	21	intron1 + 12672	gtagccacagctggggctgt G/C gggcagggcatggcaaggg	2546
CHST3	22	intron1 + 14809	ggatgtgtagggtttgggt C/T ggccctaagggatgggtgga	2547
CHST3	23	intron1 + 16161	gatgctggtcaggcattgtc G/A ttgggatotttaacaccacc	2548
CHST3	24	intron1 + 16385	tatttagcatgtgggtttca A/C ctttctgtttttcaaaggg	2549
CHST3	25	intron1 + 33638	gacttgggccacgtccttgg G/C catgaatcttggctatgtc	2550
CHST3	26	intron1 + 33878	agcaagaaagtgtgtcccc C/T acagccccactcaggcataa	2551
CHST3	27	intron1 + 34690	agcacacatggagctttccc G/A cagtgggttcagcgtccc	2552
CHST3	28	intron1 + 35145	aggggaagccgaagcctcact T/C gctggggcttgccctggcctc	2553
CHST3	29	intron1 + 35340	tgtgaagttttcccacagt T/C ggtggccatggttcgcacog	2554
CHST3	30	intron1 + 35436	gccactcatgtatggagcaa T/C tgcctttttttcttctctt	2555
CHST3	31	intron1 + 36150	ccatagaagaggctgggcct G/T aggaagccagggaagcagga	2556
CHST3	32	intron1 + 36194	ggtgtggggaggccagcagg G/A gtgtgggcctcagcggggag	2557
CHST3	33	intron1 + 36561	ctctggtgtttgtgtcaat A/G tgcagagtgtggacaaaac	2558
CHST3	34	intron1 + 37602	ctggaacagcaacttaaaaa A/T agaaatagtccctggaaggg	2559
CHST3	35	intron1 + 37725	gggtagccagggcagctccc C/T gaccgcacctgcctttt	2560
CHST3	36	intron1 + 37734	gcagctccccgaccogca C/G ctgcttttcacccctctcc	2561
CHST3	37	intron1 + 38208	gccattctagatgogagtcc C/T gactttggggtgcttga	2562
CHST3	38	intron1 + 38219	cgagtcccgactttgggg T/C gcttgcatctgtggaagggga	2563
CHST3	39	intron2 + 255	ctacagctgtgaaaggttag A/G caagatacttaacattctg	2564
CHST3	40	3'untranslated + 2202	acacctcagaggagcctgtg C/A ttaacattttaggattatt	2565
CHST3	41	3'untranslated + 2569	aggcctcatctgggtaggg G/G caagaggaaagtacagagtg	2566
CHST3	42	3'untranslated + 2717	ctggaattctccttagggc C/T ctgggaagagtattgcttaa	2567
CHST3	43	3'untranslated + 2753	cttaacgcaggatgtgctgg G/A tgtttgtttcgggctttta	2568

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GENE	number	position	SEQ.	SEQ ID.No
CHST3	44	3'untranslated + 2800	gcttggtgtctttcttgttt C/T atggctgtgttttgccttt	2569
CHST3	45	3'untranslated + 3283	ccgagggtctgccagctctg C/T ttctggttctctggacaatt	2570
CHST3	46	3'untranslated + 3327	ctgtcagatacggccattg T/C aaaccagagggtgcattt	2571
CHST3	47	3'untranslated + 3787	gttcccatgtggaggctgg A/G ggggtctggactggggaggg	2572
CHST3	48	3'untranslated + 3860	ggccctgctaattgtggacag T/C agactttatccctccttctt	2573
CHST3	49	3'untranslated + 4915	ccagatgtgcatagaagcca G/A tctctgtcacatacaccgca	2574
CHST3	50	3'untranslated + 4993	taaagcaaatttaggtttt G/A tccttctgcaatacatgcac	2575
CHST3	51	3'untranslated + 5223	ggaaggagcttcagcaggag G/A tccttccagaagggtgatt	2576
CHST3	52	3'untranslated + 5370	tcatacctgtaatcccagca G/T ttggggaggccaagggtggga	2577
CHST3	53	3'untranslated + 5545	ccattcccaaagtcagaaag T/C gaagccagatctcaagggtct	2578
CHST3	54	3'untranslated + 5859	caaaagcacaaagcagaatt G/C gcaacttcacttgtctca	2579
CHST3	55	3'untranslated + 5870	cagaattggcaacttcac T/A tgtctcaagagctccaagat	2580
CHST3	56	3'untranslated + 5971	ttccaaggctacagacatgg C/T gccatcctcacaggcctagc	2581
CHST3	57	3'untranslated + 6208	atttcatgtctgcatggtac G/A agacacccttcacggca	2582
CHST3	58	3'untranslated + 6223	tacgagacacccttcac G/A gcatacactgccatggtatg	2583
CHST3	59	3'flanking + 281	agacaggagtgttggccag C/T ggtcagggggcctggggatg	2584
CHST3	60	3'flanking + 997	acctottaagattttgagc C/T ggtgcctgtcatcccaacct	2585
CHST3	61	intron1 + 22595	cgggagcaggaaaaaaaaa A/ Δ gaataagaagaaaagggtct	2586
CHST3	62	intron1 + (35423-35424)	gctcatgtctcacagccactc AT/ Δ gtatggagcaattgcctttt	2587
NDUFV1	1	intron3 + 670	ctgggtggagtgggggtggca T/C ggagtgaagaccagtcct	2588
NDUFV1	2	intron6 + 160	tgtgccggccccagccctga C/G catgcaccccttggggacc	2589
NDUFV1	3	intron9 + 27	accacccttctgcgtagcac G/A gagggtgggtggcatcaagg	2590
NDUFV1	4	3'flanking + 1111	tgtaggctgaggctcagcccc A/C atccagtccaaagcccacc	2591
NDUFV1	5	3'flanking + 1658	gaatgcggaagtgtctctg G/A gcacccaccatgtccgggc	2592
NDUFV1	6	3'flanking + 1713	gatctggggcggagggtaca C/T ggggtctggcgctgggtgaag	2593
NDUFV1	7	intron4 + 214	tgggttaaattttttttt T/ Δ gottcaaaaatatagtattt	2594
NDUFV1	8	3'flanking + (772-774)	tgaactcggggttcagggtc TTC/ Δ ctgtgaacactggtttgaa	2595
NDUFV2	1	intron1 + 526	ggaaatgtctggctaaataaa C /T ggtatcaaaactaactctgaa	2596
NDUFV2	2	intron1 + 6689	tcgttggatggtagtattgt T/G tgaacaacagaagaaattca	2597
NDUFV2	3	intron1 + 14767	ccaaatgcatgccagcagag C/T gtggcaggaaggtagacaaag	2598
NDUFV2	4	exon2 + 86	aaggaaattgcataagacag T/C tatgcaaaatggagctggag	2599
NDUFV2	5	intron2 - 29	cagaagatcttactctctaa T/G gaagctggataacacttttt	2600
NDUFV2	6	intron2 - 168	ttacttttggaatcact T/C atcaaatgtgtgttagaca	2601
NDUFV2	7	intron4 + 677	aaaccacatactatttgatt C/A tgatgagaatcacataacca	2602
NDUFV2	8	intron4 + 2295	tatgattcaactttcaaaag A/T gtattgtgatgaaataga	2603
NDUFV2	9	intron5 + 102	caacttctgcoactctattg G/A atctgtacttacctagtaat	2604
NDUFV2	10	intron7 + 5466	tggtaaagggtttaagata A/C caaatgtcagctttcagga	2605
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattaatcctt (CTT) ttattataagtatacagtct	2606
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattaatcctt ttattataagtatacagtct	2607
NDUFV3	1	5'flanking - 606	aattacgactaacgttgggg A/G cgaactctttgctaaataaa	2608
NDUFV3	2	5'flanking - 222	cgcgcgcgcgcgcgcacagc G/A ccaggcgccgcagggcac	2609
NDUFV3	3	5'flanking - 111	tggccccaaggagggaactt A/G gccctactggggatgcgogc	2610
NDUFV3	4	intron1 + 137	ttgggcccgtgaccccgctc C/T ctgggcccaggactgaccgc	2611
NDUFV3	5	intron2 + 152	tatacaagacacaagatcta T/C aacagatttagaccaaaaca	2612
NDUFV3	6	intron2 + 6304	ttcacagatgaagggttcc G/A aaattttgtcaagaaagac	2613
NDUFV3	7	intron2 + 6433	tcgccttctcttctatctc T/G tccagctcctctgattctga	2614
NDUFV3	8	intron2 + 6563	cctttgaaaacagagccccc C/T gattacagtatcagcaaaa	2615
NDUFV3	9	intron2 + 9619	actatcttctgtgcgcatgc G/A cagagcccaccttgacagc	2616
NDUFV3	10	intron2 + 9858	aggatgccagctctttaaag G/A agacatogttttgtttaac	2617
NDUFV3	11	intron2 + 11673	cttggttaggtaagcgctgt A/G tgtgagccaagtcattcata	2618
NDUFA10	1	5'flanking - 1734	tgcacctgaactgtttact T/C tcctgtaaccatttaccctt	2619
NDUFA10	2	5'flanking - 1492	aaaacatccacgcaaacagg T/C tgtgagaagttacgtctgcg	2620
NDUFA10	3	intron3 + 370	aagactgtgcatgtgccatg C/A agacagagatgtggatgcca	2621
NDUFA10	4	intron3 + 2485	ttgtattttctttctctg G/A aatgcagtgtacgttgaca	2622
NDUFA10	5	intron4 + 236	ctgtgaaagcagattggagc C/T ctggacctcaaacacacgca	2623
NDUFA10	6	intron4 + 1742	tgtggcatctgtgagtgt C/T tgctgaagtctgaggactgg	2624
NDUFA10	7	intron4 + 2090	ggctgggggaaagcagatca T/C gttggctaaaggacaggtgg	2625
NDUFA10	8	intron4 + 3054	cagctgattatactactgaa A/C cgggataaatgcagcttgat	2626
NDUFA10	9	intron4 + 3066	ctactgaaacgggataaatg C/T agcttgatgattttcagctg	2627
NDUFA10	10	intron4 + 3377	gtcacagtttaaatgtctgt G/A ttttactctgtgaagtagc	2628

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GENE	number	position	SEQ.	SEQ ID.No
NDUFA10	11	intron5 + 46	aagcatctctatTTTgaatg T/C agatcagcactaaaagccct	2629
NDUFA10	12	intron8 + 1465	gcaacgcccagttcctggta C/T aggcctcatatccagcgtgc	2630
NDUFA10	13	intron8 + 1809	cctggaggcacaaggatggc C/A ggggcactcaacttccctct	2631
NDUFA10	14	intron8 + 11226	gttggtgactgtgtggggc A/G tctcacctctgggctgcag	2632
NDUFA10	15	intron8 + 11319	atcttgccctccctcctgcc G/A tctgttcaggcttgaatcct	2633
NDUFA10	16	intron8 + 11386	ccataatcctagcttgaacc C/T tctttttccctgctgaccc	2634
NDUFA10	17	intron8 + 12301	acataattattgtaaacatg C/T cgcttaccagtgcattcat	2635
NDUFA10	18	intron8 + 13361	ccaggccactgattgctttc G/A cattttctagcattttctta	2636
NDUFA10	19	intron9 + 183	ttctgtgtggaaagctgat G/A aagtcctcagatgacagccc	2637
NDUFA10	20	intron9 + 6669	aataataatgaccatttctg G/T aaattcatagaattcctttt	2638
NDUFA10	21	intron9 + 8028	gaggacattccacagaacgt G/A tgactattagagcagaaggt	2639
NDUFA10	22	intron9 + 10742	ctggaggagaggggtggagc C/G agttcagccagcactgggggt	2640
NDUFA10	23	intron9 + 10985	agaaaggggttacacaggagc A/G cacttctcaggagtggtgt	2641
NDUFA10	24	intron9 + 10989	agggttacacaggagcacac T/C tctcaggagtggtgtgacg	2642
NDUFA10	25	intron9 + 12601	ctgtgaatcctctcacctgc G/A tgaagggcctggctgcctct	2643
NDUFA10	26	intron9 + 13908	cacattgttatgtaaccaag C/T ctggaattgcagtgtgaaga	2644
NDUFA10	27	intron9 + 13911	attgttatgtaaccaagcct G/T gaattgcagtgtgaagaact	2645
NDUFA10	28	intron9 + 14064	tcttgactattagaaacct A/G tcagataaattttaaacag	2646
NDUFA10	29	intron9 + 14184	tggctttggttgggaacagc G/A agagatacagaaccgacggt	2647
NDUFA10	30	intron9 + 16487	cttgaagctgatcgttccct C/A cttgaagctgatcgttccct	2648
NDUFA10	31	intron9 + 16779	gccagacgtgactgctttag G/A ttctcatgacattcagacc	2649
NDUFA10	32	intron9 + 17663	ttccaaatcaccacagaact T/G tgcagtattttgaagctcct	2650
NDUFA10	33	5'flanking - (1668-1659)	gtaaaattgttttaactaga (C)9-11 ttctaaaccaaggtataaa	2651
NDUFA10	34	5'flanking - (1355-1334)	ctgtatccattggaaggcac (A)15-21 tgcaaaggaaacaaggcaaa	2652
NDUFA10	35	intron1 + (46-61)	tggcgggggtggcagggtggc GGGGTGGCGGGGTGGG/ Δ gag cagttccacatctcccc	2653
NDUFA10	36	intron4 + 2486	ctcactggaaactTTTTTTT T/ Δ aatttaatttttaaaatttt	2654
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta (A) cgggtgtgattcttctgcca	2655
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta cgggtgtgattcttctgcca	2656
NDUFA10	38	intron9 + 1054	gcgctgtgttttctccctt A/ Δ tctgtcctgtacacgtgtg	2657
NDUFA10	39	intron9 + (8161-8172)	ttctcgtcttctgggagac (T)10-12 aatgttgaaaatatgtgttt	2658
NDUFA10	40	intron9 + (8646-8647)	aattccccattgcttctct (TT) ctgtagacattttaaaccta	2659
NDUFA10	40	intron9 + (8646-8647)	aattccccattgcttctct ctgtagacattttaaaccta	2660
NDUFA10	41	intron9 + (16503-16523)	ccctccttgaagctgatcgt TCCCTCCTTG AAGCTGATCGT/ Δ gtccaagatagttgctagga	2661
NDUFA10	42	intron9 + (17905-17936)	caaataatgtatacatgta (CA)12-18 tcttcatgaaaaactotttc	2662
MGST1	37	5'flanking - 1376	ttaataaatgtttattcaat T/G aaaccaactgctaatttct	2663
MGST1	38	intron1A + 147	cctggagatttttaactttct G/A cgaagtttttaaaaacaact	2664
MGST1	39	intron1B + 36	ggagaaggggaccgcacatgca A/G aggggtggcaggcaggagg	2665
MGST1	40	intron1C + 456	ccccttgggacgggttctcac C/T tgtccccacttcccagtc	2666
MGST1	41	intron1C + 719	gcccgcgaagcattgctgtat A/G gcaccagggcctccagttag	2667
MGST1	42	intron1C + 985	cgagtaaaattttctaccg C/G ttgttttagagtgggtctct	2668
MGST1	43	intron2 + 3083	aaaaaattttagatatggg T/G actccctatgttgcccaggc	2669
MGST1	44	intron2 + 3106	tccctatgttgcccaggctg A/G tcttgaattottgggctcaa	2670
MGST1	45	intron3 + 1703	ttctcttctaagaagaagtc T/C gtgcagatacttagcacaaa	2671
MGST1	46	intron3 + 2557	tccagcatcttccctttcca T/C ttttaagttagactttttt	2672
MGST1	47	intron3 + 3032	agagacatttagaatatatt C/A cctttaaggtagagaataa	2673
MGST1	48	intron3 + 3045	atatattccctttaaaggta G/C agaataacccttcaactgaga	2674
MGST1	49	intron3 + 3289	ggtttatagtgttccccccc T/A cccgcccccaaaagaccca	2675
MGST1	50	intron3 + 3885	gaagctgcgctccaggaag G/C agtctgtcgttgagaagag	2676
MGST1	51	intron3 + 3976	ggaaagctggggaactgttt G/T cctggaacagagtctcaaaa	2677
MGST1	52	intron3 + 4298	gtcaactgcgtaacacagg C/T gtagaagtggacattgtttt	2678
MGST1	53	intron3 + 4519	tttaatagaaaatggatttc C/T tgtttttctttcccatctc	2679
MGST1	54	3'untranslated + 603	gggtaaaccattttgaata T/C tagcattgccaatatcctgt	2680
MGST1	55	3'flanking + 147	tatttgcttctctctctct C/T tgttttcttttctctgaaa	2681
MGST1	56	3'flanking + 237	cagcacgttttctctatgaa C/T aagacattctccaaataact	2682
MGST1	57	3'flanking + 1318	tggctctgtgtcatgaaca T/C gcacgctgcacgcgcacac	2683
MGST1	58	3'flanking + 1331	atgaacatgcacgctgcac G/A cgcacacacacacacaca	2684
MGST1	59	intron1C + (904-923)	tgogattatcttggtaatt (A)18-20 ggcaaatcagtcacaaatttg	2685
MGST1	60	intron1C + (3433-3434)	ccccttcaataactagaacaa (AA) gcagacacattaaatgttac	2686

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GENE	number	position	SEQ.	SEQ ID.No
MGST1	61	intron1C + (3433-3434)	ccccttcaataactagaacaa gcagacacattaaatgttac	2687
MGST1	62	intron1C + 5146	actatttcaattttttttt T/ Δ ggagggggagacagagtctc	2688
MGST1	63	intron2 + (552-563)	cccagcattataagaatgac (T)9-13 aagtgcagatgtggggaggg	2689
MGST1	64	exon3 + (172-173)	tagcatttggcaaaggagaa AA/ Δ tgccaagaagtatcttcgaa	2690
MGST1	65	intron3 + (152-158)	agaaaactggatgtctgaaa TTGACA/GTCCAATAT cactg cacttgtatgtgtg	2691
MGST1	66	intron3 + (2198-2200)	ggattttagattcctcccta CTA/ Δ ttotttcogaccttccacco	2692
MGST1	67	intron3 + (2571-2580)	tttccatttttaagtttagac (T)9-10 cacctctctcgttacttcag	2693
MGST1	68	intron3 + (4682-4683)	tcctcttcatgtctctatgt (GAGATGTTG TGGCTCACAT) agtcatcctctttgtgagac	2694
MGST1	69	intron3 + (4682-4683)	tcctcttcatgtctctatgt agtcatcctctttgtgagac	2695
MGST1	70	3'flank + (1359-1360)	acacacacacacacacacac CC/ Δ tgctctggagttgggcaact	2696
MGST1	71	3'flank + (1889-1891)	ttagaatagtttctaactat ACT/ Δ ttactcccaagagaagcctt	2697
HMG17L1	1	3'untranslated + 864	ctttotgatttttgatagtc G/C gttgaagaaggagtttgaa	2698
UGT2A1	1	5'flanking - 1602	ataacatcttctgcagagaa A/C cttcaatggaaatacactca	2699
UGT2A1	2	5'flanking - 1480	tacagattatctttggtgat G/C ggagagcttagaagagacat	2700
UGT2A1	3	5'flanking - 1406	atttcagaagatttattaac A/T tgaaaaggatcactctgctt	2701
UGT2A1	4	5'flanking - 1388	acatgaaaaggatcactctg C/T ttattcagacatatgcac	2702
UGT2A1	5	5'flanking - 935	aaattattcaatctctttgg G/A cagtgtttctttttcttg	2703
UGT2A1	6	5'flanking - 287	cctgaatgtagagttgagat G/A tacagaagctttatccaatt	2704
UGT2A1	7	5'flanking - 128	gagaagtaagacacattacc C/T ataaatctgtaatatccta	2705
UGT2A1	8	intron1 + 535	cattgatcagggtgatttat C/T catgctaagcttatttaatt	2706
UGT2A1	9	intron1 + 642	tatattgatcatgttgatac A/C ttatacacatatttgccta	2707
UGT2A1	10	intron1 + 1221	ttttaatctaataagcaatt C/G aggaccatctaaagggaat	2708
UGT2A1	11	intron1 + 1448	agggtgcttacaggcaacatc C/T acatagcagctgtggctgg	2709
UGT2A1	12	intron1 + 2000	gacacattagcttctttct A/G cagatctctgttctaaaaca	2710
UGT2A1	13	intron1 + 3118	cttaaaattctttaatgaaa T/G cattgcaacaaatttatatc	2711
UGT2A1	14	intron1 + 3191	ataaatagaacaactcccta A/T gtttacttctctgcagtga	2712
UGT2A1	15	intron1 + 3770	atcaccagataatttactat C/T cattaaggagtaggtcatca	2713
UGT2A1	16	intron1 + 4584	tgattggtagaatcttga A/C aaatcttctagtatcattcc	2714
UGT2A1	17	intron1 + 4854	tactctgtgcattgttaata G/A cctatcacttgtggtctgcc	2715
UGT2A1	18	intron1 - 19146	ctgtttaaattctcattcaa C/T ggccacatggttaaaataaa	2716
UGT2A1	19	intron1 - 18346	atggcaatatttttagaaat G/A ttaactccaataatgaata	2717
UGT2A1	20	intron1 - 18218	tatatcattattttaactta T/G agatagcactagccctaatt	2718
UGT2A1	21	intron1 - 17937	ctcctaataatttgactca C/T catacttattcagcactatc	2719
UGT2A1	22	intron1 - 12585	ttccacacagggaagca A/G cagaggaaattttcttgot	2720
UGT2A1	23	intron1 - 11430	aacaaaggttttttctta C/G agttctgatggctagacgtc	2721
UGT2A1	24	intron1 - 10761	tttaaaatgcatgtattt T/G ccacttttaaaaactatatac	2722
UGT2A1	25	intron1 - 381	aaatcctccctccttcttc C/T ttcccaggccccactctac	2723
UGT2A1	26	intron1 - 329	ttocctttctccttttctcc A/G tctctctcttctctctctc	2724
UGT2A1	27	intron1 - 41	ttttctcctcagcaaacata T/A aagctaatttctccatcca	2725
UGT2A1	28	intron2 + 263	caccttgatactggacttgg T/C gggacagaaaaccagatcat	2726
UGT2A1	29	intron2 + 454	agaaagcccatgaaataag G/C cagggttttaggttttaatt	2727
UGT2A1	30	intron2 + 554	aaaaacttttttgagttgac A/T atggtgagtttagtttctga	2728
UGT2A1	31	intron2 + 1113	ctgcaggcaagctctagtga A/T tgtttattataggaaataat	2729
UGT2A1	32	intron2 + 1304	gacaaatcagccatgtttta C/T aatagcagacattatgccat	2730
UGT2A1	33	intron2 + 1305	acaaatcagccatgttttac A/G atagcagacattatgccatt	2731
UGT2A1	34	intron2 + 1367	atcgatataggctttgggaa A/C tatgaataccaaccatgggt	2732
UGT2A1	35	intron2 + 2074	aaatttttcttagacctat G/T aatcaaaggaggcatacagt	2733
UGT2A1	36	intron2 + 2164	attttattagatataactgg A/C atgctaacaattttaaaagc	2734
UGT2A1	37	intron2 + 2298	taacaatttcagtttagcatg A/C gaagagttgtcccttattta	2735
UGT2A1	38	intron2 + 2346	tttctgtaatggttttgctt T/C catgcttggacttgaatca	2736
UGT2A1	39	exon3 + 922	gtgttggtgttttctctg G/A gatcaatggtcaaaaacctt	2737
UGT2A1	40	intron3 - 217	aagcttagaagtataaata T/C caaaacaataatactatact	2738
UGT2A1	41	intron3 - 194	aaacaataatactatactgg G/A tagactattagtacaagact	2739
UGT2A1	42	exon5 + 1171	acggagtccctatggtggga G/A ttcccatgtttgctgatcag	2740
UGT2A1	43	intron5 + 1546	tttttaaaattcagaaactc A/G gttatggtgtattcttataa	2741
UGT2A1	44	intron5 + 1547	tttttaaaattcagaaactca G/A ttatggtgtattcttataa	2742
UGT2A1	45	intron5 + 2013	atcatattcattaccctccc G/T ctattattgtatttgaatc	2743
UGT2A1	46	intron5 + 2318	aatttagtgctttttcttaa C/T ggaagtaacctgcttaaaaa	2744

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GENE	number	position	SEQ.	SEQ ID.No
UGT2A1	47	intron5 + 2505	taattgacttttattaatac G/A tacatgttgataagtcata	2745
UGT2A1	48	intron5 + 2639	tagactattacaaagttgtt A/G gttgctgacaattttgttca	2746
UGT2A1	49	intron5 + 4009	gaatccaggctggaactttt C/A ttccagacacaaaccaaata	2747
UGT2A1	50	intron5 + 4311	atacagacactgtccttttc G/A tcacaaacatacagatgtgt	2748
UGT2A1	51	intron5 + 4545	agctcacacagtatcaaaat T/C atttttgaaaaattatgct	2749
UGT2A1	52	intron5 + 4616	actttttatgtctacattt G/C atcatactgtgttaagcata	2750
UGT2A1	53	intron5 + 4717	tgcaagaattatattttctc C/A acgtaactatggccttaaac	2751
UGT2A1	54	exon6 + 1524	gctatatttttggtcataca A/G tggttgtttgttctgtca	2752
UGT2A1	55	3'untranslated + 1683	aaggagttaacaaaaaacac G/A tctcccatcctgtttccaaa	2753
UGT2A1	56	3'flanking + 685	aatctagaaaaataattatca T/C tttataaaatttttagtca	2754
UGT2A1	57	intron1 - (18967-18965)	ctcccaattagattgattag TAT/Δ gagttcctgggggttactggt	2755
UGT2A1	58	intron1 - (18862-18803)	aatacattotcccccttca (AC)14-17 atgcttactggcctatttat	2756
UGT2A1	59	intron1 - (17463-17447)	aaacttagaaacctctattc (A)16-27 gtaaagaaaatggcagagaa	2757
UGT2A1	60	intron1 - 10860	attcaatgcaactttttttt T/Δ gtaatggcagaattagaaca	2758
UGT2A1	61	intron2 + (528-538)	ctgttaggaaacaattggtt (A)8-10 ctttttgagttgacaatgg	2759
UGT2A1	62	intron2 + (1514-1533)	ttgtgtgtatgtatgttt (GT)9-11 tattttaatgaattaatato	2760
UGT2A1	63	intron5 + (916-917)	gcttagtatattatataat AA/Δ gtctatatatatagcttagt	2761
UGT2A1	64	intron5 + 1163	caatatttatgtcatttttt T/Δ ctacacattactctgtttcc	2762
UGT2A1	65	intron5 + (3819-3838)	agacagacagacacacaaaac (AC)8-12 tcaacacatgtaaactactc	2763
UGT2A1	66	intron5 + 4785	tatcttcaatgaaaaataaaa A/Δ caaaaattgtctaatttctg	2764
OATP1	1	5'flanking - 916	acagagtagatgttcaataa G/A tatttgtgtatctgtgaga	2765
OATP1	2	5'flanking - 843	tagtgcagcgactatgcctt G/A atgtgtgtgtgtttgggatt	2766
OATP1	3	5'flanking - 526	aaatgtgtgcctgtatgtta T/C acatctgtacatatatttcc	2767
OATP1	4	5'flanking - 172	acaaacacaactcaaagtat G/A tgtgttattaaaagtagcta	2768
OATP1	5	intron1 + 206	ttgattcaggcaagtttagtc C/G taaatggccttgagagactt	2769
OATP1	6	intron1 + 454	caacataacaataatttctt G/A taagaaaaatggcattttg	2770
OATP1	7	intron1 + 999	gttagcaaggttagatatt A/G atgtggatgttaagacaaaa	2771
OATP1	8	intron1 + 1223	ttgctagaagctagtaggac C/T agctttataaatacagagat	2772
OATP1	9	intron1 + 1326	aactagttaggcaacccatg T/C gtttaggggaaaagcaatg	2773
OATP1	10	intron1 + 1336	gcaacccatgtgttttaggg G/A aaaagcaatgaggtcatgat	2774
OATP1	11	intron1 + 1498	atagtttgccttaagaata C/T actctgagaaggtttatagt	2775
OATP1	12	intron1 + 5041	ttatgtctcccgaggagttag C/T totctaaatgcataaggaga	2776
OATP1	13	intron1 + 9532	aaagactgggagcacttccc A/G atgacaaatactagactaga	2777
OATP1	14	intron2 + 198	ttacctcatattaacaccta A/C atattgccacatatcctacc	2778
OATP1	15	intron2 + 961	aaaaagttatatagaaatat A/G agtgtcactcctttctagtt	2779
OATP1	16	intron2 + 1110	gtctactagtgttcaactcc T/C ttgatcttagcctgtatca	2780
OATP1	17	intron2 + 1419	aaagcctaagaaggatgcag T/C gcaatagcctatgtgagaag	2781
OATP1	18	intron2 + 3339	tatggtttgcaaaaaactta T/C tcgtatattgttttttca	2782
OATP1	19	intron3 + 66	caggaaatgaagttgcactt T/C cctctctaggagcaatgctt	2783
OATP1	20	intron3 + 205	tcagttttgtcaatttacac A/G atggggatttgggacctttt	2784
OATP1	21	intron3 + 6377	aatgaatagactttgagttta C/T tggatttttagtgataaat	2785
OATP1	22	intron3 + 7238	tgaatgtcacattttttaa G/A tttgtgttccttatctcata	2786
OATP1	23	intron4 + 1016	ttttattctggattcatgtt T/C gtggaaattgcagtagtcca	2787
OATP1	24	intron5 + 110	tccacaatgatgagtagagt A/G tottggcacagttggccttc	2788
OATP1	25	intron6 + 496	agtgtctgaattataagcca A/G ttttatagttggttgggacc	2789
OATP1	26	intron7 + 1934	aaagtgaaggaaattaaaa G/C tgagaacttgagcctgaatg	2790
OATP1	27	intron7 + 2140	tagaatgtaccaaataaatc A/G gcactctgaggatgggacc	2791
OATP1	28	intron7 + 2365	tgaaatcttctttatcaact C/T gattttccctccagactttac	2792
OATP1	29	intron8 + 88	gcaaactcctaagttgaagt G/C ttttaggatatttttgact	2793
OATP1	30	intron9 + 534	tcatatattgtattttaaag G/A ttatctgggttttactgaaa	2794
OATP1	31	intron9 + 1286	tattcttctgagataaatca T/C tgaaggagtggctatgtgtt	2795
OATP1	32	intron11 + 215	ttcactcctattcctcgtta C/T ttttctccttatttcttag	2796
OATP1	33	intron11 + 663	ttcttcttcttttgagctc T/A aaagtagagttcagttaatc	2797
OATP1	34	intron11 + 999	atcatcactgcagtagagtt A/G gaattatctaactttgtgat	2798
OATP1	35	intron11 + 16727	tttcttttatttacaactt A/G tttacttttcaggtgtatga	2799
OATP1	36	intron12 + 48	ctatcagaacaatattatta T/G tattattttttattacactt	2800
OATP1	37	intron12 + 686	tatgttttgataaactttgc C/A gtacaaataaagaaaattga	2801
OATP1	38	intron12 + 708	tacaaataaagaaaattgaa A/G tatttccaaataaatcaagt	2802
OATP1	39	intron13 + 418	tctctggtctccaaatcat A/G tattttctccctctttacat	2803
OATP1	40	intron13 + 436	atatattttctccctcttta C/A attttgctgaacaatcttc	2804

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GENE	number	position	SEQ.	SEQ ID.No
OATP1	41	3'untranslated + 2130	gtctttaagaacctaataaaaa C/A ctottaactcaaaataataa	2805
OATP1	42	3'flanking + 57	agtgactaaagtttttctta C/A aaacaagtgtctgaatcaaa	2806
OATP1	43	3'flanking + 572	aatacactatgggtattttat G/A tgtactataaatggagttag	2807
OATP1	44	3'flanking + 788	atttcctaaatgatcagatg C/T atcatatgaaaaaagaaagc	2808
OATP1	45	3'flanking + 1356	aggtagactgacataaatggg G/A gcagaggacataatgaggtt	2809
OATP1	46	5'untranslated - (189-188)	attttctaactctgtattaaa (A) gcgttccagggtatttttga	2810
OATP1	47	5'untranslated - (189-188)	attttctaactctgtattaaa gcgttccagggtatttttga	2811
OATP1	48	intron4 + (725-726)	tgatctttaatagcggggaa AA/Δ caggcaagtacgctatagtt	2812
OATP1	49	intron4 + (1082-1083)	attgagtcaggaaacccaaaa CA/Δ gttcaaaaatttgaaaaat	2813
OATP1	50	intron4 + 2301	aatgtcatgtctttttttt T/Δ aatgcagagtgtacaaagga	2814
OATP1	51	intron9 + (241-246)	attgtatgtcatgtgggtg TGTGTG/Δ catgattgtctttgtgat	2815
OATP2	1	5'flanking - 2574	ggataaggcaaccctatgt A/G tcaactgtgcaggagaggga	2816
OATP2	2	5'flanking - 2366	aacataggaatgtgcagagc C/T ctgtggggattagagaagag	2817
OATP2	3	5'flanking - 2244	tgatgatgccagagctttga T/G cattgggtgggtatagaaaca	2818
OATP2	4	5'flanking - 1723	tcttcagacttcaaaggcc A/G tgatatttcacagagctgt	2819
OATP2	5	5'flanking - 1180	tgctttttaacaggcataa T/G ctttggtctcctgagccaga	2820
OATP2	6	5'flanking - 811	tatgtcatatgtgtataca G/A gtaaaagtgtgtatatatgt	2821
OATP2	7	intron1 + 7188	aatcatttgaaatttaagaa A/G aaaatatgttcagagaaaaa	2822
OATP2	8	intron1 + 7331	gtgaaatgaggaacaaagt T/C ccaccttttttctgaata	2823
OATP2	9	intron1 + 7391	agagagatgtgaaatagtag T/G tttctggggaagtaggggaa	2824
OATP2	10	intron1 + 7886	ttgttagtagaaagaaatc G/A aagcctaaaactaaaggaag	2825
OATP2	11	intron1 + 7958	ttgctattatataattttt T/A aaaaaaagatttcctaata	2826
OATP2	12	intron1 + 7959	tgctattatataattttt A/T aaaaaagatttcctaata	2827
OATP2	13	intron1 + 8036	ggaaaaaatgggtgaaatt A/T atcaaagggcagcttattac	2828
OATP2	14	intron1 + 9164	acattatattctatataaaa G/T agtcagttgaagtaaaagt	2829
OATP2	15	intron1 + 10123	tctgtcttctacttttgt T/G tccagcattgacctagcaga	2830
OATP2	16	intron2 + 193	tgattaagtatttctttggc G/A aaatttttgatgcttaatag	2831
OATP2	17	intron2 + 1020	ttgagtaacatttaggcca G/A tggcagtcataaggaaaaag	2832
OATP2	18	intron2 + 14865	agaggaattaatcataagag G/T tttatttggttaaagtgaca	2833
OATP2	19	intron2 + 14931	gtagttaataacagaaaaa A/T tatcagaaattttaaaaaat	2834
OATP2	20	intron2 + 15417	ttctaaaataagtaagctaa A/T tattctatattataactacta	2835
OATP2	21	intron2 + 20823	ttgtataagagatacaaaaac A/C aattcctactaggggaaata	2836
OATP2	22	intron2 + 20852	ctaggggaaataaagcttca G/C taaggaggtggcattaagct	2837
OATP2	23	intron2 + 20930	atggagagaagcagcagtg A/G ccacagataaatgaagttag	2838
OATP2	24	intron2 + 21360	ttcaaaagctgtatttctca T/C tagtgctttttgtgaataaa	2839
OATP2	25	intron2 + 21467	tatatacacataacctgtcc A/G gaagatgtggtataagccaa	2840
OATP2	26	intron2 + 21621	tatcaatacttatgaagaga A/G ctaactattctaactaggga	2841
OATP2	27	intron2 + 22760	ttccccacctctgttggtt C/G tctcttaaacttctccttg	2842
OATP2	28	intron2 + 23199	cctatctgcacataacatta C/T aaacttatggcaattataaa	2843
OATP2	29	intron2 + 23218	acaaacttatggcaattata A/G aactcaatacatattatact	2844
OATP2	30	intron2 + 23330	gcccttgctcctgttctct G/A tacctgcctcaactacatag	2845
OATP2	31	intron2 + 23673	ctggagacggtagctcaaac T/C gaggatgaaaatagacattt	2846
OATP2	32	intron3 + 89	ggttatcaactggggtaaat T/G tatctctcacaggcaatttg	2847
OATP2	33	intron3 + 224	tgctaaatattctataatgc A/G caaagaatgatgtaactgaa	2848
OATP2	34	intron4 + 97	ccctttaaataggcagttac C/A ttttgagaagatacccacta	2849
OATP2	35	intron4 + 568	ttcatgatccaaattgtggc A/G acgtatttcaggcaacaag	2850
OATP2	36	intron4 + 599	aggcaacaagatagaagaag A/G aaagaataagaagcaacaaa	2851
OATP2	37	intron4 + 753	aaaatagacattattccaag T/A taccaagttcccggttaaaa	2852
OATP2	38	intron4 + 781	ttcccggttaaaaatcccaa G/C tataattactgtggaaggaa	2853
OATP2	39	intron4 + 1196	aaggaccacaatctagatca G/T cattgtctaaatagccat	2854
OATP2	40	intron4 + 1229	tatgccataatatgtgacac T/C ttgacacctggtattttctac	2855
OATP2	41	intron4 + 1623	catctagttaaagtgatta G/C attttatttttactacattt	2856
OATP2	42	exon5 + 388	attctaaagaaactaatatc A/G attcatcagaaaattcaaca	2857
OATP2	43	exon5 + 452	taatcaaattttatcaactca A/G tagagcatcacctgagatag	2858
OATP2	44	intron5 + 165	ttatatacacagttcgccc A/T ttaacaacacaggtttaaac	2859
OATP2	45	intron5 + 189	acaacacaggtttaaacac G/A cgttttcacttctatgcaaa	2860
OATP2	46	intron5 + 191	aacacaggtttaaacacgc G/A ttttcacttctatgcaaat	2861
OATP2	47	intron5 + 507	atataactttgctttcattg C/T aaaaggcaaacgtttatatac	2862
OATP2	48	intron5 + 520	ttcattgcaaaaggcaaac A/G ttatatcatttaagacttt	2863
OATP2	49	intron5 + 856	agtcatgataaacctaataag A/G ataaaacaacaaaaagaaa	2864

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GENE	number	position	SEQ.	SEQ ID.No
OATP2	50	intron5 + 1157	acagataattttacttgtt T/C gtgcttttctgtatgatg	2865
OATP2	51	intron5 + 1226	ccttgattgtaataatctcc A/C catgccaagagtggggccag	2866
OATP2	52	intron5 + 1228	ttgattgtaataatctccac A/C tgccaagagtggggccaggt	2867
OATP2	53	intron5 + 1304	actgttctcgtggtaatgaa G/T aagtctcacaagatctgatg	2868
OATP2	54	intron5 + 1348	ttataaatgagagttccct G/A caaaagctctcttgctgcc	2869
OATP2	55	intron5 + 1407	ttgctcttctcatcttcc G/A ccatgatttgaggccccc	2870
OATP2	56	exon6 + 521	gtcatatcatgtggatatatg T/C gttcatgggtaatatgcttc	2871
OATP2	57	exon6 + 571	gggagactcccatagtaacca T/C tggggctttcttacattgat	2872
OATP2	58	exon6 + 597	ctttcttacattgatgattt C/T gctaaagaaggacattcttc	2873
OATP2	59	intron7 + 33	agaacaaggtaccatgataa C/T gtctttctaagcacacatgc	2874
OATP2	60	intron7 + 267	caaaataaccaaagttaaaa T/A gtctccctccaaactgact	2875
OATP2	61	intron7 + 1260	gtaatctcacatttctctgc A/G ttacacttggtaaaacttt	2876
OATP2	62	intron7 + 1386	agtctcaaattaatagccaa G/A agcatgcctttattgtaacc	2877
OATP2	63	intron7 + 1472	ctttaccacatgacagaatg G/A catgttcttagcaaataata	2878
OATP2	64	intron7 + 1697	ttacatgttcaattttaga C/A atatgccttagagtagctac	2879
OATP2	65	intron7 + 2273	ttctcagctctatctagcg C/T gattatgacccttagttact	2880
OATP2	66	intron8 + 207	gtggaagagaattaggttg T/C actttttagcagggagaaac	2881
OATP2	67	intron8 + 546	tggggagaagtttctcccta T/C gtaattagagtaatatattat	2882
OATP2	68	intron8 + 565	atgtaattagagtaatat A/C ttttgtaattatctatcta	2883
OATP2	69	intron8 + 668	taagtaatgtaaattaggt G/T catcagcatttgacagtgc	2884
OATP2	70	intron8 + 739	tggagaaccattgagagtca A/G taaacaaagagaatgacttg	2885
OATP2	71	intron8 + 2193	tgatcacagatccaaatgac A/G taattttaccatgaacaga	2886
OATP2	72	intron9 + 112	attttagtaatacaggataa G/C tataattttctgtattott	2887
OATP2	73	intron9 + 266	ttagaggtagtatctgtata A/G ttggatottataatttagtg	2888
OATP2	74	intron9 + 305	tgctaagatctgagacaaac C/G cttttgtaattataatcatt	2889
OATP2	75	intron9 + 888	aggttctgtatgtttttta T/C aaatgacaaagatatattaa	2890
OATP2	76	intron11 + 10224	tacactgttccataaaaaa T/C tcctotatattattcctagt	2891
OATP2	77	intron11 + 10359	attaatagattcaacgtgag G/C ttcccttaaactttagccta	2892
OATP2	78	intron11 + 10916	cttatatagaaagaaatoca C/G aaaactattttaccttttat	2893
OATP2	79	intron11 + 10997	aatatattagtttgaacaag T/C gagacttcactaaatataat	2894
OATP2	80	intron11 + 11018	gagacttcactaaatataat G/A caatgtatttgcagcactgt	2895
OATP2	81	intron12 + 442	aacattccaaaactttta C/T gactcacagcatgactttta	2896
OATP2	82	intron12 + 445	attccaaaacttttaatcga C/T tcacagcatgacttttataa	2897
OATP2	83	intron12 + 447	tcctaaaacttttaatogact C/A acagcatgacttttataata	2898
OATP2	84	intron12 + 907	aatgaaaagaagctggcaga T/C tgaacatactgaatgagag	2899
OATP2	85	intron13 + 65	tatatatatatatatata C/T acacacacatacatatatta	2900
OATP2	86	intron13 + 870	aattctgagtatcttatttc G/A atgtatccaatctgtggcac	2901
OATP2	87	intron13 + 1935	taaaaaaaaaaaagtctgc T/C ttacagcaattgagccaag	2902
OATP2	88	intron13 + 2261	aacgaatcctccaaatttt G/C aacttttttaatacaaat	2903
OATP2	89	intron14 + 248	tcaaggataataaccaactt G/A tcaaaaatcagagataatag	2904
OATP2	90	intron14 + 2463	attgtttactaatatggaa C/G cttcttcaagacatatttt	2905
OATP2	91	intron14 + 2857	tcacatgtatttccaggac A/T cctggcaagatgctcctcag	2906
OATP2	92	intron14 + 11458	atctccagaggctctgtgt C/T tccccaaagtcactgacct	2907
OATP2	93	3'untranslated + 2243	ataataaaaacaaactgtagg T/C agaaaaatgagagtactca	2908
OATP2	94	3'untranslated + 2404	tttaataaaaacaaatgagt A/G tcatacaggtagagggttaa	2909
OATP2	95	3'untranslated + 2515	cagagtttgaactataatac T/G aaggcctgaagtctagcttg	2910
OATP2	96	3'untranslated + 2539	gcctgaagtctagcttgat A/G tatgtacaataatatctgt	2911
OATP2	97	intron1 + 457	taattggcaaacataaaaaa (A) caggtgtctcaaagtcacat	2912
OATP2	98	intron1 + 457	taattggcaaacataaaaaa caggtgtctcaaagtcacat	2913
OATP2	99	intron1 + (7537-7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	2914
OATP2	100	intron1 + (7537-7538)	gatcagcattacaaccaaga atggagaatgacattcagga	2915
OATP2	101	intron1 + (10032-10035)	tgtgtgattctatattactt ACTT/ Δ gtttcaaatttctctccaca	2916
OATP2	102	intron1 + (10058-10061)	ttcaaatttctctccacaaa TTTA/ Δ tttttctattaaattgtaat	2917
OATP2	103	intron2 + (413-423)	acttatttaaaaattctttt (A)11-13 caaaaaacaggatttaaaaa	2918
OATP2	104	intron3 + (1595-1603)	ttgccaagtaattcaagtgc (T)8-10 gtatttaaaacaacttttca	2919
OATP2	105	intron4 + (10-23)	ttcatgggatagtaagtgtt (A)12-14 cctctgtgccactatcagta	2920
OATP2	106	intron5 + (1567-1572)	gtgaatataaattacttcta CTTGTA/ Δ aattaaaaaaaataagtag	2921
OATP2	107	intron5 + (1577-1585)	attacttgacttgtaaat (A)9-10 taagtagaataattaagagt	2922
OATP2	108	intron8 + (1939-1941)	ttctctaactccttctactc CTT/ Δ atttcaagcagatgcaactg	2923
OATP2	109	intron10 + (3077-3078)	aaattctttatctactttt (CTT) ttccctctttctctgcttcc	2924

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GENE	number	position	SEQ.	SEQ ID.No
OATP2	110	intron10 + (3077-3078)	aaattctttatctacttttt ttccctctttctctgcttc	2925
OATP2	111	intron11 + 11011	aacaagtgcagacttcactaa A/ Δ tataatgcaatgtatttgca	2926
OATP2	112	intron12 + (1160-1169)	agcatgacatggttagatg (A)9-11 gcatttttaacatttgtaa	2927
OATP2	113	intron12 + (1310-1312)	tccatcttaataataaatgt TGT/ Δ ctactcaaaaggagaagtct	2928
OATP2	114	intron13 + (9-34)	tacgagcactaggtatgatg (A)24-27 tatatatatatatatata	2929
OATP2	115	intron13 + (35-64)	aaaaaaaaaaaaaaaaaaaaa (TA)10-21 cacacacacatacatatt	2930
OATP2	116	intron13 + (1379-1387)	aaaattattcaccacaatac (A)8-10 caaagtaaagttatgaacac	2931
OATP2	117	intron13 + (1916-1928)	aattctcttaaaataatgtt (A)11-13 gtctgcttttacagcaattg	2932
OATP2	118	intron14 + (588-596)	caattatactttacctcttt (A)8-10 ctaatttcaaattcatatat	2933
OATP8	1	5'flanking - 1413	aataggggcttaataactct G/C aaacttatgattttctcatat	2934
OATP8	2	5'flanking - 1345	gaatttatctacagatatg A/G ccacacagaaatgacatat	2935
OATP8	3	intron1 + 38962	atgaaattagtttaaaaaa G/A caaccttaactataactctc	2936
OATP8	4	intron2 + 253	acagacttaccaacaaagaa T/G tatccttccaaaatgtcta	2937
OATP8	5	intron2 + 329	actcatggtttgcaaatata C/G ttttaggaaactttatctc	2938
OATP8	6	intron2 + 2568	ccattctggtgctttctttc G/A tgaactattttccatcagt	2939
OATP8	7	intron2 + 2679	ctctattgctctctctcca T/C gtttaatactaaataattta	2940
OATP8	8	intron2 + 2753	caggaaactttcacaagcc C/A ctaattaatttaagctccct	2941
OATP8	9	intron2 + 3132	tggtttaattgtaggagatt T/C acctcacagttaaattaca	2942
OATP8	10	intron2 + 3193	aatgtcttgggcatatttgc A/G ttcatttggggcattcagtt	2943
OATP8	11	intron2 + 3207	atttgcattcatttggggca T/C tcagtctactagatacaaa	2944
OATP8	12	exon3 + 334	gaactggaagtattttgaca T/G ctttaccacattttctcatg	2945
OATP8	13	intron3 + 76	agaattttatttttataactt G/A taagtgggcagttacotttt	2946
OATP8	14	intron4 + 2443	tcaatttcatgttctctta C/T agttataggattctaaaga	2947
OATP8	15	intron4 + 67	taatcacgtctataaagttt C/G tgatattctttaacaaaatt	2948
OATP8	16	intron4 + 91	tattctttaacaaaattgat T/A taagaacaaataggaagaac	2949
OATP8	17	intron4 + 197	ggtttgaactgcacctgttc G/A cttatatgcagctttgtcc	2950
OATP8	18	intron4 + 813	tttaacagaataaaaaaaaa T/A attttgtaacgacaaaagaa	2951
OATP8	19	intron4 + 974	atatgcaccttaaaaaataac C/G tggatttttaaatatgtaat	2952
OATP8	20	intron4 + 1003	taaatatgtaatgtacataa G/T gaattatgtcatatttgt	2953
OATP8	21	intron6 + 155	cattaataatcagaataaaa A/G agaaatttagctctattta	2954
OATP8	22	intron6 + 750	atccaactggggttagatt T/G cctctttctgctctctctcc	2955
OATP8	23	intron6 + 780	gcctctctccatctgcacc C/T tctcttttctcagcaaaaca	2956
OATP8	24	intron6 + 1248	ctatgcctgtaatctcaca C/T ttccctttatttaaaattgg	2957
OATP8	25	intron6 + 1500	togtgtctgtttagcatat A/G ataactcatcagggttgtg	2958
OATP8	26	intron6 + 2008	ataacataaatgagtaaaga A/G tatcaagggcaggaaattag	2959
OATP8	27	intron6 + 2087	actactctccccatacacac T/C aaaactcatgtctccccag	2960
OATP8	28	intron6 + 12305	tcatctatggaggactgcaa T/C cattatcattatttccaga	2961
OATP8	29	intron7 + 363	taacaaatgataccagccat C/G atactattctctggtaatag	2962
OATP8	30	intron7 + 411	cctttatttttgagaacct G/A gtggatgatattaagacgta	2963
OATP8	31	intron7 + 428	cctgggtggatgatattaaga C/A gtatatagatcactgtaata	2964
OATP8	32	intron7 + 634	aaaattatataatacatat A/G taattacctaagtattca	2965
OATP8	33	intron7 + 1791	tgttttttaagggttagtga T/C gtgaatagtaaagcgaattt	2966
OATP8	34	intron7 + 2000	agttgagcaaattgctctca G/A gtagcataatgtcacttgaa	2967
OATP8	35	intron7 + 2043	gtttattgatccatttttta A/G tggatcaacattgtagttag	2968
OATP8	36	intron7 + 2171	atttattttgagcaaaggctc G/A cgactctcttagaaagcctc	2969
OATP8	37	intron7 + 2173	ttattttgagcaaaggctgc G/A actctcttagaaagcctcac	2970
OATP8	38	intron7 + 2179	tgagcaaaggctcgcgactct C/T ttagaaagcctcacaatca	2971
OATP8	39	intron7 + 2219	atttgaactttaagtctta T/G ataacttatattacaaaat	2972
OATP8	40	intron7 + 2261	cagatattaatatatatttt A/T ttattgaaatatgttatttt	2973
OATP8	41	intron8 + 150	acaaaatttctccatcttgt T/C atatcatcgttgttctgcat	2974
OATP8	42	intron8 + 154	aatttctccatcttgttaata A/T catcgttgttctgcatttga	2975
OATP8	43	intron8 + 1303	tttttttgagatggagtct C/T gctctgttggccaggctggg	2976
OATP8	44	intron8 + 1372	aagctccgctccaggttc T/G ccacccttctcttaagaaa	2977
OATP8	45	exon9 + 1272	tccttcttgtttcaacttct A/G tatttccctctaactctgca	2978
OATP8	46	intron10 + 63	tcacagatttgatttaataa A/T taattatcaaactctctcat	2979
OATP8	47	intron10 + 911	cttgcccaatatcctaccaa C/T gtattattaaacggcatgga	2980
OATP8	48	intron10 + 972	tcctagtttcttgaagata G/A gctacaactttagtaaactt	2981
OATP8	49	intron10 + 1101	tcctgtgtctgtgtgtcc A/T gtagtgaagacctgaaagag	2982
OATP8	50	intron10 + 1103	cctggtcctgtgtgtccag T/C agtgaagacctgaaagagag	2983
OATP8	51	intron10 + 2027	cccatttcatgagtggcta A/G gtttgtcccgtttcaaact	2984

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GENE	number	position	SEQ.	SEQ ID.No
OATP8	52	intron10 + 2028	ccattttcatgagtggtctaa G/A tttgtcccgtttcaaaacta	2985
OATP8	53	intron10 + 2148	gtattttggaaagaaaatgt A/G ggtggaagagaaatatttta	2986
OATP8	54	intron10 + 2214	atatacagaatttcatacac T/C aatttcttaaattcoctaaat	2987
OATP8	55	intron10 + 2316	taaataatttagtttgagac T/G tctttaaatataatggaatg	2988
OATP8	56	intron10 + 2372	tgtatttggcaaatgtattt G/T ttaataatttcaaaaactatt	2989
OATP8	57	exon11 + 1557	cagaacagaaattactcagc A/G cacttgggtgaatgcccaag	2990
OATP8	58	intron11 + 147	tttcttagaattattttgat A/C tttcaataacatcattaata	2991
OATP8	59	intron11 + 10339	aaaaaactgcatttttagtgg G/C ttagctagaaaagatttgc	2992
OATP8	60	intron11 + 10358	ggtagctagaaaagatttg T/G ctcatacacacaataaatta	2993
OATP8	61	intron11 + 10538	caacagaggatcaatgtaaa T/G gaaatctcttaaattaaaca	2994
OATP8	62	intron12 + 55	ataaatattaatgttaaata C/T taaagactgaatgcaattaa	2995
OATP8	63	intron12 + 1802	taaaatgaatcggtaaaaca T/G tcatgtataaatcactgtca	2996
OATP8	64	intron12 + 2612	ataggcatataatactcttt C/A ttccctctgtatataggag	2997
OATP8	65	exon13 + 1833	aacagctgtggagcacaagg G/A gctttaggatataataatc	2998
OATP8	66	5'flanking - (1590-1587)	atatacataacatataccta TATC/Δ tatgttatgtgtctgtctat	2999
OATP8	67	5'untranslated - (11-28)	agcatcagcaacaattaaaa ATATTCAT TGGTATCTG/Δ tagtttaataatggaccaac	3000
OATP8	68	5'untranslated - (4-7)	tattcacttggatctgttag TTTA/Δ ataatggaccaacatcaaca	3001
OATP8	69	intron4 + (213-214)	cctgttcgcttatatgcagc (T) tttgtccaaccaaacagaa	3002
OATP8	70	intron4 + (213-214)	cctgttcgcttatatgcagc tttgtccaaccaaacagaa	3003
OATP8	71	intron4 + 505	tataactttctctttataaa G/Δ atgcaaaatgttatagcatt	3004
OATP8	72	intron4 + 616	aaaaataaatgaagtggagg A/Δ aaaaaaatgatttcaagttt	3005
OATP8	73	intron4 + (804-812)	acatccatgtttaacagaat (A)9-11 tattttgaacgacaaaaga	3006
OATP8	74	intron4 + 855	gagattgtttaaccaaaatta G/Δ gaaactattattcaacacac	3007
OATP8	75	intron7 + (619-628)	tttatatatgaattaaaa (AT)4-5 catatataatcttacctaag	3008
OATP8	76	intron7 + (1773-1779)	attttctatattatgaactg (T)7-8 aagggtagtgatgtgaatag	3009
OATP8	78	intron8 + (1270-1290)	tagtgtgccaccctctctc (T)19-23 gagatggagtctcgtctgt	3010
OATP8	79	intron10 + 665	ttctttcttaactcaaaggc T/Δ tttttttccatgtgacac	3011
OATP8	80	intron11 + (247-250)	aaaaatcttaaggcacacac TGAT/Δ tgacagttgcottgattgta	3012
OATP8	81	intron12 + (1622-1630)	aaataaatgttggcatcta (T)8-10 atttttctaagggtcgtctgt	3013
OATP8	82	3'untranslated + (2464-2465)	gagaaaagcctgatgccttt A/Δ aaaaaaatgaaacactttg	3014
OAT1	1	5'untranslated - 127	gcagctcggactcagctccc G/A gagcaaccagctcggagg	3015
OAT1	2	5'untranslated - 20	gaaggcctcagccccagcc A/G ctgggctgggcctggcccaa	3016
OAT1	3	intron3 + 150	caatagaacaaccttttctc G/A ggctcatgcgcctgaccc	3017
OAT1	4	intron4 + 211	ttctotggcttccccactc A/C gttctccagcctgcctgctc	3018
OAT1	5	intron5 + 33	gagacttcccatgataacct C/T ccagggttcacccccaaac	3019
OAT1	6	intron6 + 168	gaaccagatgccccagcct C/T gactcagtcctcagctccac	3020
OAT1	7	intron1 + (58-71)	ggaagatgggggcctttgtt (A)13-15 gtacatggagaaattaactg	3021
OAT1	8	intron3 + (1306-1319)	aataggttgaggaggagcag (A)12-15 tcaagagtgtggagggggca	3022
OAT2	1	intron4 + 842	ttgacctccaaaagtgttg G/A attacaggcatgggcatg	3023
OAT2	2	intron5 + 33	gtgtgtgtgagcatgcatat C/A tgtgtgtgggtgggagtg	3024
OAT2	3	intorn5 + 183	ccacatccatcattcgagac A/C aactcgtctcagctgccatg	3025
OAT2	4	intorn5 + 184	cacatccatcattcgagaca A/C actcgtctcagctgccatga	3026
OAT2	5	exon7 + 1269	actagactgctagtgtcctc C/T ggtgagcccagtcocatagg	3027
OAT2	6	3'untranslated + 1792	ataaatgtgtacatgagtgt A/G tgaacacaaatacataaggt	3028
OAT2	7	3'flanking + 1386	tgtagcagcccacatcgcca G/A tgttcacacctgagagagag	3029
OAT3	1	5'flanking - 580	ctgtgtcagagacacagaca C/G ggaggtcctggctgccccag	3030
OAT3	2	5'flanking - 463	ttcctgagaggcaaattccc T/C tcccctactcgggaggtgcc	3031
OAT3	3	5'untranslated - 16	cctgccacagctctggctc G/A tcttgccccagtgccatgac	3032
OAT3	4	exon2 + 153	cctgtccaccactgtcggcc G/A ccccaaatgcctccacagg	3033
OAT3	5	intron2 + 177	gcaccaagacccttggttc T/C tcccactcagagtccaagca	3034
OAT3	6	intron2 + 6201	gctcatcctctctgtcctt T/G tgccccagcacaggttctc	3035
OAT3	7	intron3 + 79	tctgtccacccgtgcaccc G/C caaagaggcaaagagctggg	3036
OAT3	8	exon5 + 723	tggcgttggctgcagtaac T/A gtgtccattcccttctctgt	3037
OAT3	9	intron5 + 524	tcgaagtacaaaggaaagt T/C aaagagaagcctgagcctgg	3038
OAT3	10	intron7 + 386	gaccaatgggtttcagactc G/A aagacaaaaattatgtttat	3039
OAT3	11	intron7 + 754	gcccacgtcagacatgacca G/A tcaatcacagcactttctcc	3040
OAT3	12	intron9 + 81	attgtcctgtcctctaccca G/A gggagccatcctttatgaac	3041
OAT3	13	5'flanking - (661-660)	tacatttgggtcccaggggg (G) agcggctgatcaggagagaa	3042
OAT3	14	5'flanking - (661-660)	tacatttgggtcccaggggg agcggctgatcaggagagaa	3043

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GENE	number	position	SEQ.	SEQ ID.No
OAT3	15	intron8 + (211-212)	tctgacttgactgggcaaa AA/ Δ gtatgggtgtatctggatag	3044
ALDH1A2	1	5'flanking-716	cagggatcctcattctgagc C/G cgaggcgagggggactcgca	3045
ALDH1A2	2	intron1+314	cggtcccgactgcccgggg G/ Δ aaggogtcggaaccgcttag	3046
ALDH1A2	3	intron1+(664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaacgttgacatctt	3047
ALDH1A2	4	intron1+1370	gcattgcagcttagaagttt A/G tttatgagggtctctaaac	3048
ALDH1A2	5	intron1+1557	ggtagctttttcagaattta A/ Δ ttggaagctcttcagttc	3049
ALDH1A2	6	intron1+1934	tcagctcttttagtgagactt C/G taaattttctaagacaagca	3050
ALDH1A2	7	intron1+(1971-1980)	agcatagtggacaagcagta (T)9-11 aaacgtgaagagcagaagct	3051
ALDH1A2	8	intron1+2295	tactgtaagacaatatgtta T/C tgtttttgtcttgctaaac	3052
ALDH1A2	9	intron1+2387	ttgggacccacatagagtca C/T tacttaaaataaatgaccag	3053
ALDH1A2	10	intron1+2841	aggaatgtgctttttaaac T/ Δ agatgggttagtcaaggag	3054
ALDH1A2	11	intron1+3035	gacttttataattttgtata A/G ctgatattataggaatacac	3055
ALDH1A2	12	intron1+3319	aaagagttatgtttttttt T/ Δ ctgcatctgatattatatgg	3056
ALDH1A2	13	intron1+3474	ttgtcttttatttattcat T/C taaactctgttttctgggg	3057
ALDH1A2	14	intron1+4186	ccttccaaacctttacttaa G/C attgtctgttttggtcataa	3058
ALDH1A2	15	intron1+4222	cataaattgtcagctaaact A/G catgttaatagaggacttca	3059
ALDH1A2	16	intron1+4254	aggacttcaggtttttttt T/ Δ aaatacttttcataactat	3060
ALDH1A2	17	intron1+4397	cccttccactacatgggcct A/G tgttaccatgtggaattatc	3061
ALDH1A2	18	intron1+5935	aactccaggttgcaaataga T/C gtttctggtattttaagtag	3062
ALDH1A2	19	intron1+6206	tttgaaagccctcctagca T/G ttctttaatttctttattga	3063
ALDH1A2	20	intron1+9559	agataaattgatgaattatt C/T actctgtctgctgatagat	3064
ALDH1A2	21	intron1+(9631-9632)	taaaaagaatttctaaaaga (AAGA) cctttttttgaataactct	3065
ALDH1A2	21	intron1+(9631-9632)	taaaaagaatttctaaaaga cctttttttgaataactct	3066
ALDH1A2	22	intron1+12731	ctgaaatagaaacctttcag T/A gtacctgcagagcagtgaa	3067
ALDH1A2	23	intron1+13442	cagtgctcataaagatccagc G/A gaaatcaaaatgtttcatat	3068
ALDH1A2	24	intron1+(14173-14176)	tctaaaaaaataataata AAAA/ Δ gagaaaattaagttaagat	3069
ALDH1A2	25	intron1+14586	actcatttattggttcaaag C/G cttcttcaaccttaggat	3070
ALDH1A2	26	intron1+14595	ttggttcaaagccttcttca A/G ccttaggatatgcattgagg	3071
ALDH1A2	27	intron1+14711	gtttgagacattaacttcta A/G ttcaactgaagatgctagtt	3072
ALDH1A2	28	intron1+(15327-15337)	gaagagcacagtagaaagac (T)9-11 aacctagcaatactattga	3073
ALDH1A2	29	intron1+17258	atcagtacaatgtgtgggc A/G tacaacacttaatttaaat	3074
ALDH1A2	30	intron1+18277	taatacaaatcatttgaagc A/G ttactattaaaaaaacaaa	3075
ALDH1A2	31	intron1+18734	ctttgagcacctactgcatt T/A taagtctgttaagatgtgg	3076
ALDH1A2	32	intron1+19081	ttaatcacctcaatctttaa C/T gaatttcttgattttcttt	3077
ALDH1A2	33	intron1+21514	aatcaggatatggggggttc G/A ttctttattctgccacaaat	3078
ALDH1A2	34	intron1+21732	cattttaaaatagtgcttta A/G taggacttggtgttaaagt	3079
ALDH1A2	35	intron1+21865	tggcatagggttaaaaatgt C/T tggtaggactcttttcca	3080
ALDH1A2	36	intron1+26282	taaagaaggagaaaaaaa A/ Δ ctaatctgagactttgcagg	3081
ALDH1A2	37	intron1+27805	ggatgatgctacccaaggaa T/C tgcacacttccagacagtac	3082
ALDH1A2	38	intron1+28204	tcactccatttttaactgt C/G cttcctaaatgtgtggttaa	3083
ALDH1A2	39	intron1+28521	tctttgttacacttcttaa T/C cggggtatcagataatcttc	3084
ALDH1A2	40	intron1+49478	gaataaaaggataggacat G/T ggtaagaccacttttccct	3085
ALDH1A2	41	intron1+49834	gcctctcaattttctcatgt G/T taatagagagaaaacctgc	3086
ALDH1A2	42	intron1+50351	gactgactggttcataagtt C/G agaaatttactgtggtgtct	3087
ALDH1A2	43	intron1+51181	tgttattaccatagtagttc C/T gtaacacttggccgttgact	3088
ALDH1A2	44	intron3+654	ttaacctctcttgagtaaaa G/A gaatccttcagaaccagagg	3089
ALDH1A2	45	intron3+668	gtaaaaaggaatccttcagaa C/T cagaggggatggtacggacc	3090
ALDH1A2	46	intron3+712	catacacttctgctccgttt G/T ccctgtcattctgtgagcca	3091
ALDH1A2	47	intron3+1273	tattcatactgtgaaaaagg T/A gtttcatggtgaagaaattc	3092
ALDH1A2	48	intron3+1743	ccacacctaaatgagattcc C/T gttttaaacactctcaagct	3093
ALDH1A2	49	intron3+2891	tgcacatatatactcattgt A/G gtttttactaggaactagac	3094
ALDH1A2	50	intron3+2919	ctaggaactagacaaaactg G/A cagtactagaaatctttta	3095
ALDH1A2	51	intron4+290	cattgtgctagattaggtgc T/C ggggtaggtatgaaggggca	3096
ALDH1A2	52	intron4+380	ctccttgccctcctgaaaca T/C ataagatctactctttggaa	3097
ALDH1A2	53	intron4+461	gattatggctgattttcagt G/T tcttttaaatattttctct	3098
ALDH1A2	54	intron4+506	tctatatttctcgaaaggcc G/A tgaattactttcataatcta	3099
ALDH1A2	55	intron4+1952	ttggtcccaactccactgt C/G atttcattattaaaacaaca	3100
ALDH1A2	56	intron4+2079	ctctatttggcctaacggta C/T cttggttttcttttacttcc	3101
ALDH1A2	57	intron4+2519	ttgggtcataagagctctct C/G catggtgtctcaaacagatg	3102
ALDH1A2	58	intron4+(2840-2851)	ttgtctctgcatacttggc (T)11-13 cacagtgaagtctggaatat	3103

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GENE	number	position	SEQ.	SEQ ID.No
ALDH1A2	59	intron4+7231	aataggatacaatacacaa A/T gatagtgattcagatcctaa	3104
ALDH1A2	60	intron4+7958	taaaatcgtttttattgtta C/T taggtatataaaatttgcta	3105
ALDH1A2	61	intron4+8090	tctgattttatcactgttta C/T agattgcttagtcatactca	3106
ALDH1A2	62	intron4+12823	tgtagcctgtagctaaatg C/T ttttcaaataatgtgaacggt	3107
ALDH1A2	63	intron4+12939	atgagggtccgacttttaaga T/C tttgtctacattttcttcc	3108
ALDH1A2	64	intron4+14935	tattgatggagttcttttta T/G aaatggacttttacottctt	3109
ALDH1A2	65	intron4+15321	gcatttgggtgtctgagaga C/T atatccagaaatagctatg	3110
ALDH1A2	66	intron4+15412	tttcaagttattttctgttt T/G tttttttttttttttttg	3111
ALDH1A2	67	intron5+1888	aatccaaacatctgtacttt G/T tagtggacaagatttatgtc	3112
ALDH1A2	68	intron7+9166	gaaaagctactttattcaaa G/A ataaaagtattttaagaaaa	3113
ALDH1A2	69	intron7+9914	aagctggagaaaatactagg C/T tttcctcaacagtgtttcc	3114
ALDH1A2	70	intron7+18942	tttggagggaactaatccc G/A tgacttctaggttatctctt	3115
ALDH1A2	71	intron7+19820	ttcaccctcattttaggtt A/G ggggaggtggcttgctacag	3116
ALDH1A2	72	intron7+19826	cctcatttttaggttagggga G/A gtggcttgctacagtttag	3117
ALDH1A2	73	intron7+19913	cgtgaatcattcagttttt A/G tttaaaaataaccagtttgaa	3118
ALDH1A2	74	intron7+(20110-20111)	catgatttattctctaacta (ACTA) tgctaagtcaaagattotgc	3119
ALDH1A2	74	intron7+(20110-20111)	catgatttattctctaacta tgctaagtcaaagattotgc	3120
ALDH1A2	75	intron7+21857	acaatgaaaattaagaaagg A/T gaagagggaagaagcagaga	3121
ALDH1A2	76	intron7+21929	tacaagacacaggcatcttt A/G actagtttactgggatctct	3122
ALDH1A2	77	intron7+23308	ggctttgacttcggaaacct G/T tgggtataacaaagtactg	3123
ALDH1A2	78	intron7+23554	gacattgtgaaaaccaggg C/T tgttaggagtgctcgtcc	3124
ALDH1A2	79	intron7+(23701-23703)	catctgagatttgccttgtg GTG/Δ ttaccgagttagtggtgc	3125
ALDH1A2	80	intron7+26479	gatacatgaacaatttgttt T/C atcctcatgatattcttcaa	3126
ALDH1A2	81	intron7+26561	taaaggccacaatgcagtga T/C tgaatctccagttacatt	3127
ALDH1A2	82	intron7+26662	ttccttagtccttccatca C/T gaaactaaagctgtctcca	3128
ALDH1A2	83	intron8+76	tttatctctccacttttgat G/A ggacactagcaaaagatatt	3129
ALDH1A2	84	intron8+(700-711)	accatctcattcagtgatc (T)11-12 ccctccactgttgccaggc	3130
ALDH1A2	85	intron8+724	ttttttccctccactgt T/C gccaggcagagctgcttcc	3131
ALDH1A2	86	intron8+800	cagattgctgaatttcagc C/A ccagcttgaatttgccagag	3132
ALDH1A2	87	intron8+1251	gatttctgtgaaattgaga G/A gatctggcaacctggggctc	3133
ALDH1A2	88	intron8+1627	ggccctcccccaggcaaagc G/A gtgagaacatggctgttcc	3134
ALDH1A2	89	exon9+141	tggagcgggccaagaggcgc G/A tagtggggagtcctttgac	3135
ALDH1A2	90	intron9+778	aaccagtctggacagatccc T/C ttagcttgtgaaagttag	3136
ALDH1A2	91	intron9+801	tagcttgtgaaagttagga A/G gtgaagggtggctcacttc	3137
ALDH1A2	92	intron9+868	tctgaaggcctcgtgtactt T/C agtggggtggggaggggccac	3138
ALDH1A2	93	intron9+1338	aatttttgctcttttact A/G tcaatacaacttgctaagt	3139
ALDH1A2	94	intron10+(227-229)	ctatgtgcttatgattatta TTA/Δ gccaacagaacaatcagaat	3140
ALDH1A2	95	intron10+316	ctaatgtgggtcactggga T/C gttaccaggagagagaatc	3141
ALDH1A2	96	intron10+368	ctttacatctgtgcaagaga G/A ggacaaggagcaaatoagcc	3142
ALDH1A2	97	intron10+660	gtaacttgcattgaaatgt G/A gaaagcaggtaaaggaatga	3143
ALDH1A2	98	intron11+104	tggggaataccaaaagcaac C/T aaagttcaccagaaaagggg	3144
ALDH1A2	99	intron11+229	aaacttctaaaagaaatacc A/G tgccagtcagattatgtgt	3145
ALDH1A2	100	intron12+117	catacatcaacaaacattt C/T gtggagcacatgtactata	3146
ALDH1A2	101	intron12+691	gatagggaagatcactgtga A/G ctggaaaaatctgggaacc	3147
ALDH1A2	102	intron12+1934	catcttgtctagattgcatg T/C ttgtttgtttgtttgtct	3148
ALDH1A2	103	intron12+1973	ctactacccccaaaacatg T/A tttctctttcttaaatgacc	3149
ALDH1A2	104	intron12+2722	ccagagtactccagtatac C/A tcaactgccaggaccacag	3150
ALDH1A2	105	intron12+3855	cacttgaaagcaaccataat T/C gtgaggttctgatgctga	3151
ALDH1A2	106	intron12+4185	ttgttttaagcgaaatgaac T/C atacggacaggagaacagcc	3152
ALDH1A2	107	intron12+4991	acaggaacacttagacatgc A/G acccactcccaccctccgtc	3153
ALDH1A2	108	intron12+(5018-5019)	cccaccctccgtcttggggg (G) aggaaagcacactactgtcc	3154
ALDH1A2	108	intron12+(5018-5019)	cccaccctccgtcttggggg aggaaagcacactactgtcc	3155
ALDH1A2	109	intron12+(5051-5052)	actgtcccaaagaactaata (A) ctgaaccagtgtgccttgt	3156
ALDH1A2	109	intron12+(5051-5052)	actgtcccaaagaactaata ctgaaccagtgtgccttgt	3157
ALDH1A2	110	intron12+(5300-5302)	ttaaagttttaaaaaaactt CCT/Δ taaaaactactcatgagatg	3158
ALDH1A2	111	intron12+5405	catcccaggacttgctgttc G/C caggtgataaactgcacctc	3159
ALDH1A2	112	intron12+5435	aactgcacctccccaggact C/A ccgctgcactcacatgcagc	3160
ALDH1A2	113	3'flanking+449	tttgggcgggaacaatttt T/C caaggttgtaaagccaaatt	3161
ALDH1A2	114	3'flanking+597	acctgggatattcctgacct A/C atctggtttcttttaccca	3162
ALDH1A2	115	3'flanking+669	atagagactggaagtcac T/C gtgcagttcacgccttctga	3163

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GENE	number	position	SEQ.	SEQ ID.No
ALDH1A2	116	3'flanking+1122	cgtgctccactgagctcctc T/G gtcacaccccattcttgccc	3164
ALDH1A2	117	3'flanking+2214	tgcagctgtaaaaagaaatc T/C gtaaatggtagccgtactac	3165
ALDH1A3	1	5'flanking-1425	cagtgttagccagccgatat C/T ggtcaaggctgccccgctcg	3166
ALDH1A3	2	5'flanking-1379	ccattatcccctttccccgg C/T ctcagctgtgactccaggc	3167
ALDH1A3	3	5'flanking-1270	aaactacccctctatccagc T/A ctatccagaaggacaccagg	3168
ALDH1A3	4	5'flanking-(1214-1213)	acggaggcctcaaaacagga (GGA) aaataaggagacccctcccc	3169
ALDH1A3	4	5'flanking-(1214-1213)	acggaggcctcaaaacagga aaataaggagacccctcccc	3170
ALDH1A3	5	5'flanking-1103	gcacagctttgtcaggagt C/T cgtgcctccggtctttgttc	3171
ALDH1A3	6	intron1+986	gccttaactttcccacctt T/G ggctctcttatttttgc	3172
ALDH1A3	7	intron1+1462	gtacaggatttcaaaatact G/A tatatagaaccagacagta	3173
ALDH1A3	8	intron1+1661	cctgttgtcttgggtggc G/A caaccttggcagttaaagg	3174
ALDH1A3	9	intron1+2360	agaggatagaagtcccttct A/G atttagaggcctctttctt	3175
ALDH1A3	10	intron1+2516	tgaacacatattcttttga G/A ttagctgagtggcctgttg	3176
ALDH1A3	11	intron1+2624	cctgagacaccttacagctc C/T gtcctgcttccatgtcatc	3177
ALDH1A3	12	intron1+3255	ttcatctttctacaaatgg G/C cccctcttctggctgcact	3178
ALDH1A3	13	intron1+(3643-3656)	gcttcagaggtttttgtggg (T)12-14 aacattctatcaactttta	3179
ALDH1A3	14	intron1+4265	ccaaaagccctctcttttaa T/C atgacattaataagacaatt	3180
ALDH1A3	15	intron1+5187	caagatggataagacgtcac C/T taaggctcttagcatgttga	3181
ALDH1A3	16	intron2+43	ctctaagtaattcaattatg G/T atgaccaaaggataaggaaa	3182
ALDH1A3	17	intron2+127	cagggcctgggctagctgcg T/C gaattggcatgtggtctca	3183
ALDH1A3	18	intron2+(285-300)	aggaaaggttttctttttc (T)16-17 atcaattattggacctgga	3184
ALDH1A3	19	intron2+778	cgtgtgcagagtaggcttgg A/G tttatcttggccatgagtt	3185
ALDH1A3	20	intron2+1216	actcggtagagtcactcctg A/C ctggtgtccacatccactc	3186
ALDH1A3	21	intron3+81	accatggggtatgggaaaa A/C gatcacggctcctggtttgt	3187
ALDH1A3	22	intron3+236	gctcagcttctgaccaagt T/G gttgtctataggcagttgag	3188
ALDH1A3	23	intron3+1467	ggcccgtttagggggagga G/T atctcctttctggccttga	3189
ALDH1A3	24	intron3+1725	ccacatgtccccgggtgag A/G gtagctccctcccagggtaa	3190
ALDH1A3	25	intron3+3777	gccagaagtagatgccccca A/G ttcagctgctgcattactgg	3191
ALDH1A3	26	intron3+3829	caagtcaactgggcccgttagc G/C tccgtgcctgcacctgaag	3192
ALDH1A3	27	intron3+4299	tcactttccacagccacact G/A gccagcctggccgagaagga	3193
ALDH1A3	28	intron4+84	agagccccccctgactgtt C/G cctaaggcaccattcccaac	3194
ALDH1A3	29	intron4+126	ccactccctctccaaatggt A/G ctgccaattcttcttctaag	3195
ALDH1A3	30	intron6+(290-291)	tagagaattttcaggggggg (G) tcaaccaagaggagccaaa	3196
ALDH1A3	30	intron6+(290-291)	tagagaattttcaggggggg tcaaccaagaggagccaaa	3197
ALDH1A3	31	intron6+705	aacagctggtgatgagccaa T/G tttccactttcctttggtga	3198
ALDH1A3	32	intron7+56	ggggcgtgttatttgacacc C/T gtgagcttttctttgacag	3199
ALDH1A3	33	intron7+1107	gatgctgttactctccttgg A/G gacagacactgcctgtgga	3200
ALDH1A3	34	intron7+1610	aagagccacacagaaccacc C/G ccctactgggctgttggat	3201
ALDH1A3	35	intron7+1820	cacctgtaagtggagcggct T/C agaccaaggatcccaggatg	3202
ALDH1A3	36	intron8+963	gagaaaggacaggaggagga C/T acaggctctcaggaaggaaa	3203
ALDH1A3	37	intron8+1824	accattcttatccactaagc G/A tgtccccaagatcttattc	3204
ALDH1A3	38	intron8+2384	cgcctccctcgccccctccc C/A tccagtggacttggcagtg	3205
ALDH1A3	39	intron9+24	atccccctggtgtgtgtgaa A/C ccatggtgcttcttagggg	3206
ALDH1A3	40	intron9+91	gcctacagggtccctctccg T/C gaaaggaatgctgacctgc	3207
ALDH1A3	41	intron9+219	actgaggcatgggaggagg C/G gctattcccagggcagaagg	3208
ALDH1A3	42	intron9+435	ccagacggagagagcctggg G/A caggagaatgtatctccagg	3209
ALDH1A3	43	intron9+1472	ttgacttttagggccagata C/T accgattcttccaagagaa	3210
ALDH1A3	44	intron9+2038	taaacaatgtttctctacgg G/A ctctccaggagtggtggagt	3211
ALDH1A3	45	intron9+2124	caaacagggtctgccagatg G/A catatgccagcagccaggg	3212
ALDH1A3	46	intron9+2154	agcagccaggaggacctgc G/C gttggcggaagcccctgtgt	3213
ALDH1A3	47	intron9+2197	cttttggccctcaggagg G/A gaagagcagctcagcagcat	3214
ALDH1A3	48	intron9+2466	ttcttagttcctcatgttcc C/T ctctagaatgtttctgtg	3215
ALDH1A3	49	intron9+3655	gattggtcaagtggcatgca C/T gggttatgccctctctcctg	3216
ALDH1A3	50	intron9+3954	gggtgcgcttttgacaactg C/G tcagtagcgtgttcacaagc	3217
ALDH1A3	51	exon10+88	tggaaatcgggggctcagcc A/G tggaagacaagggctcttc	3218
ALDH1A3	52	intron10+8	tgccaaagaggaggtacaag G/A gggctgtggcaaggctacga	3219
ALDH1A3	53	intron10+307	ctctctgattttctaacaca A/C ccggtccccgagtcagtc	3220
ALDH1A3	54	intron10+378	gtgggttttgcaggaaatca G/A ttcaagaacotgtggattca	3221
ALDH1A3	55	intron10+975	aatattgtgtattccttcc C/G ctggtagtattatggaaac	3222
ALDH1A3	56	intron10+1088	cagtgcaggagccaggggg C/T cttctccagatgactctgag	3223

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GENE	number	position	SEQ.	SEQ ID.No
ALDH1A3	57	intron11+105	ttgtttacattgtatattat A/G taccaagccctgtctcagtg	3224
ALDH1A3	58	intron11+274	agggctccagtagctgtgcc T/G gtggccctgtgtgtactg	3225
ALDH1A3	59	intron11+1088	cagtgcaggagccaggggg T/A cttctccagatgactctgag	3226
ALDH1A3	60	intron12+96	ctccaatctgtgacacccc G/A tccccccacacccgcccctc	3227
ALDH1A3	61	intron12+5642	totgtgctaacgtctgtctc T/C ctcatgccccctaggctggc	3228
ALDH1A3	62	exon13+104	gggtccttctcacaacatc G/C gacggcggaatgtggcagat	3229
ALDH1A3	63	exon13+281	ataggttgtctgtgaaatog C/T agtctgtcctggggaggag	3230
ALDH1A3	64	3'flanking+743	gtgagcaggaaactgttagga G/A aaggatatttccctcattt	3231
ALDH1A3	65	3'flanking+1145	gcctcccagctacccccacc A/G cctcaggaggggtcattcca	3232
ALDH1A3	66	3'flanking+1185	aacctagggtgtgagaatc T/C ggggtgggattaccagcaaaa	3233
ALDH1A3	67	3'flanking+1600	acaccacgccctgcaaattg T/C tgggaactgtcgggtggcaa	3234
ALDH1A3	68	3'flanking+1847	caggagccctgcccgtgccc C/G ggttctgtgaaatggcagtg	3235
ALDH1L1	1	intron1+252	cgcagcgcaggactggccc G/C ccaggatctggccggccgc	3236
ALDH1L1	2	intron1+544	ctcaggggctgctgtggagt C/T ccagctccagccactgogct	3237
ALDH1L1	3	intron1-6596	cagattttcttaagtgca C/G tagccactgaggatattttt	3238
ALDH1L1	4	intron1-6513	caattatggtttatcttagg G/A acatgtttatagagatagta	3239
ALDH1L1	5	intron1-6478	atagtattcttacttagctt G/A cattctaaattttgttccct	3240
ALDH1L1	6	intron2+240	gtggcattagggtcctggag A/G agggctatagagaagcccag	3241
ALDH1L1	7	intron2+1326	gaggaggagaccggagagga G/C agccagtcagtcaggggccc	3242
ALDH1L1	8	intron3+386	gtcctactctaactccact G/A ccgtgtcttgggcagcaca	3243
ALDH1L1	9	intron4+271	gggcccgtcaatagacaag G/C aaggctaaaggcagggactg	3244
ALDH1L1	10	intron4+356	taggattctatttctctctc C/T ttactcgttgattctcctt	3245
ALDH1L1	11	intron4+608	gtgtctgtataggctgtctc A/C gtcacatgcttctgtctggg	3246
ALDH1L1	12	intron4+664	ggtcacatggcctgagcggc A/G gggcggctcagtcacctggg	3247
ALDH1L1	13	intron4+785	gagggtcgttggccctgcc C/G gaggacaggctggcaggggac	3248
ALDH1L1	14	intron4+874	ccctggggagcccttctgt T/G tgggcgcagcaggaagagca	3249
ALDH1L1	15	intron4+1349	tcctcaggctcttctctcac G/A tgggcccagactccttggct	3250
ALDH1L1	16	intron4+1799	ctggggctgggaaggaggca G/A ggtcctattgctggggatag	3251
ALDH1L1	17	intron4+1815	ggcagggtcctattgtctggg G/A atagcaaccactggatctc	3252
ALDH1L1	18	intron5+272	aaagcccacaggagagataag A/G gtgggagttagggggcaaaa	3253
ALDH1L1	19	intron5+301	tagggggcaaaaacgtcagcc G/A tagtgcgagcagtcctcaag	3254
ALDH1L1	20	intron5+343	caaggtgtgaggggacagtgc G/A ggtctctggagcaatagcca	3255
ALDH1L1	21	intron6+926	cctgcctgggctactggctt C/T gggggcttctctcaccac	3256
ALDH1L1	22	exon7+41	aacgctgaacacttcaggcc T/C ggtgcccaggaggagacgctt	3257
ALDH1L1	23	intron7+305	cctagaatcagagagaagcc C/T tcccaggagcctgggttca	3258
ALDH1L1	24	intron7+837	gtccggacaaaaccccatggg C/T gtgtacccccagccgtgtt	3259
ALDH1L1	25	intron7+866	cccagccgtgtgtgtgtc C/T ggcctaccagagtgaggcgt	3260
ALDH1L1	26	intron7+884	tccggcctaccagagttagg C/T gtggcagtatggggcctggc	3261
ALDH1L1	27	intron7+1118	aatgttcagaaaatcatgc G/C aggcagtaagggcagaggaa	3262
ALDH1L1	28	intron7+1168	aaagtaaagggttcaggagaa G/A tctagcctggggctgtccc	3263
ALDH1L1	29	intron7+1451	cagggcacccacagcatctg T/C ccagagacctgcaaagacag	3264
ALDH1L1	30	intron7+1489	caggaatgcaaagaaggcaa T/C taagtgtcttaagaggaagc	3265
ALDH1L1	31	intron7+1579	tcagggtgggaggggagtga G/A gagagaccagctgagcacac	3266
ALDH1L1	32	intron7+1691	ctggctgggcttttagcttc A/C gaaagctccagaacatcttt	3267
ALDH1L1	33	intron8+2627	aaagaggagagccgggggtg C/T ttgtgccagggttggggga	3268
ALDH1L1	34	intron8+2646	gcttgtgccagggttgggg G/A aactggttctgattgggcct	3269
ALDH1L1	35	intron8+2925	ctgtgccctcataggtcc C/G agactgaatccttcagagga	3270
ALDH1L1	36	exon9+4	caggtcttgccttcagagt G/T ttggcagcggatcctcccc	3271
ALDH1L1	37	exon10+109	cagctgttagtgaggagct G/T cgaggggacgatgaggaggg	3272
ALDH1L1	38	intron10+(671-672)	tggcattttcctctgtctga (AG) gtctcttagcccaccctaa	3273
ALDH1L1	38	intron10+(671-672)	tggcattttcctctgtctga gtctcttagcccaccctaa	3274
ALDH1L1	39	intron11+8	caccgatggaagtgtgagt G/A agggccagcacccttctcc	3275
ALDH1L1	40	intron11+447	atgagccaaagcacgcctat G/A gtagatacacacgtgaacat	3276
ALDH1L1	41	intron11+601	ctcaaatgagtcatttgag A/G ggagttaatgaaagactcat	3277
ALDH1L1	42	intron11+639	catctgcaaaggagaggga G/A ggggtaggacacagacagg	3278
ALDH1L1	43	intron12+684	tcctgggagaagagagggtg C/T ggccagatgagccgagaaca	3279
ALDH1L1	44	intron12+767	cgtctagggtgcgaagcca A/G gttatggcgtggtcccaacg	3280
ALDH1L1	45	intron12+1014	tcataggttcagtcctctt C/T gcaagccctcaattctaga	3281
ALDH1L1	46	intron12+1359	ctggttctgcctcagctcag C/T acagcagaggctgggtctag	3282
ALDH1L1	47	intron12+1734	ggtgtccaggctgctggtg G/T tcagtagggccggccgagcc	3283

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GENE	number	position	SEQ.	SEQ ID.No
ALDH1L1	48	intron12+1901	ttcagcagcctaactgaatt G/A acaatagaatagtcctgcaa	3284
ALDH1L1	49	intron12-470	gggatggggccacctctcca T/C ctctggagatgccaggctca	3285
ALDH1L1	50	intron12-334	aagggcagcctcttggggcca T/C gacccctttgctgtctgcag	3286
ALDH1L1	51	intron12-325	ctcttggggccatgacccctt T/C gctgtctgcagcaagtgggt	3287
ALDH1L1	52	intron12-221	gaaggaagcagagggaagatc G/C aggaaaggagagaggacag	3288
ALDH1L1	53	intron12-4	cccgttcccctcaccctgg T/C caggttggcagatctcatgg	3289
ALDH1L1	54	intron13+34	tcccaccagtgtagcaca T/C gcagactggcccagccatat	3290
ALDH1L1	55	intron13+58	gactggcccagccatatagg A/G gaactccaagggcagcacag	3291
ALDH1L1	56	intron13+125	ccacaactgggtggcttgaa T/C gacacctgtttattagcttg	3292
ALDH1L1	57	intron13+126	cacaactgggtggcttggaat G/A acacctgtttattagcttg	3293
ALDH1L1	58	intron13+281	acctgcattccagacagagttc T/G ggtgttgacagagttcagtt	3294
ALDH1L1	59	intron13+299	tcgggtgttgacagagttca A/G ttccgtgtggatgcagggt	3295
ALDH1L1	60	intron14+121	catttatcaaacagccatcc A/G tgtgcttcttgacacctgc	3296
ALDH1L1	61	intron14+167	gccaggaattgttgtaagga C/T ttgaggacaattgtatttaa	3297
ALDH1L1	62	intron14+205	taatctcccagtaacactgg A/C tcagtcaggtcacagggtggg	3298
ALDH1L1	63	intron14+219	cactggatcagtcaggttcca C/G ggtgggaaacaagagtaaac	3299
ALDH1L1	64	intron14+2275	tctcatctgtgatgcacgc T/C cagacctctgctcccagcct	3300
ALDH1L1	65	intron14+2431	agaatgactgagtgatcaga C/G ctagagagccccagccccgg	3301
ALDH1L1	66	intron14+2660	agccaagcatttcttggggga C/T accaagaaaccttgcttgg	3302
ALDH1L1	67	intron14+2740	aactccaccctcaccgtcca T/C gcagctccccaggagcgtca	3303
ALDH1L1	68	intron14+2756	tccatgcagctccccaggag T/C gtcagagggcagaggagggg	3304
ALDH1L1	69	intron14+2805	ccgcacagcaggagaatggc T/C ccaaggaggaggaggacggg	3305
ALDH1L1	70	intron14+(3636-3637)	tctcctgggtgtgtgtgggg (G) tgtggggcagctcccctatc	3306
ALDH1L1	70	intron14+(3636-3637)	tctcctgggtgtgtgtgggg tgtggggcagctcccctatc	3307
ALDH1L1	71	intron14+4347	tccaggacagaaacagcagg C/T gtgagctgcctctcagaggg	3308
ALDH1L1	72	intron15+380	atgtcccttatgtggcttcc A/G agaccagaagtcctggagag	3309
ALDH1L1	73	intron15+(1055-1056)	gccacaatctgcagctactc (C) tcccagcttgcctgtgggt	3310
ALDH1L1	73	intron15+(1055-1056)	gccacaatctgcagctactc tcccagcttgcctgtgggt	3311
ALDH1L1	74	intron17+15	gaaaaggtgcgtggctgggg G/C tggagcagaggaggggctgc	3312
ALDH1L1	75	intron17+44	aggaggggctgctgtgagtg C/T gcctgggacatggcagtgct	3313
ALDH1L1	76	intron17+51	gctgctgtgagtgccctgg G/A acatggcagtgctgtccaca	3314
ALDH1L1	77	intron17-(2224-2223)	ctggtgtcatctcccagact CT/Δ gtcactaaaccacaatatga	3315
ALDH1L1	78	intron18+140	agcgtcatcacaagcatagc G/A tggcaggcagcaggcttagg	3316
ALDH1L1	79	intron19+(51-52)	tggttcactgggacagcagc GC/Δ ctggctggagggggttgag	3317
ALDH1L1	80	intron19+399	tcaggtcagcctgggcctga C/A catggacaggggcccctggag	3318
ALDH1L1	81	intron19+1794	gtcctgtctgggggtcttaa G/C ggagtcagagacttccaca	3319
ALDH1L1	82	intron19+1969	tgatcgggggtgcggtttggg G/T cgacaggacaggagcagaga	3320
ALDH1L1	83	intron19+1972	tcgggggtgcggtttggggcg A/G caggacaggagcagagaata	3321
ALDH1L1	84	intron19+2083	tgagaagagcagagggtgt G/T ccgggtgctcaggtcacacc	3322
ALDH1L1	85	intron19+2119	acacctgtgtctgattaggg C/T tgattaggggtgcagagttt	3323
ALDH1L1	86	intron20+1388	ttacctcttcccactcccg C/T tggactgtgagttccatgag	3324
ALDH1L1	87	intron20+1564	cccaggaaccaggaacagtg G/A ggagccatcaccocgcccctg	3325
ALDH1L1	88	intron20+1873	tcagtgttaaacatcattt G/A tgtatgtatgaaaaatattg	3326
ALDH1L1	89	intron20+2427	actaggattggatggacttg G/C gatcaggctcagctctgtc	3327
ALDH1L1	90	intron20+2458	cagctctgtcacctgccaac C/T ggcggccccatttccctcaa	3328
ALDH1L1	91	intron20+2544	ccaggtgggagagccatctg C/T agcgtggtgacaccatcac	3329
ALDH1L1	92	intron20+2573	gacacccatcacacgggtgc C/T gtgaccgggtgcttatgtcg	3330
ALDH1L1	93	intron20+2574	acacccatcacacgggtgcc G/A tgaccgggtgcttatgtcgg	3331
ALDH1L1	94	exon21+33	agccaaactgttttcacagac G/A tggagaccacatgttcata	3332
ALDH1L1	95	exon21+87	ccttcgggcctgtcatgac A/G tctctogggttgcctgatggg	3333
ALDH1L1	96	intron21+323	ccatgcattaaaccaccccc C/G aactgagtggttggaata	3334
ALDH1L1	97	intron21+361	ataatcagagattttttta C/G tcacggtctaggttcaatga	3335
ALDH1L1	98	intron21+478	gtcttgcgggaggcttctc C/A gcgtggcagcctcgggggttg	3336
ALDH1L1	99	intron21+1086	caacccaactcttggccccgg C/T gctgcagccggcacatttt	3337
ALDH1L1	100	intron22+235	gggocctggaggagacactcc A/C gccaggaggcactgggggccc	3338
ALDH1L1	101	intron22+313	atagcagggaggaggtggcc G/A tgaagaccaggggcccgtg	3339
ALDH1L1	102	intron22+1214	tgggcccacttatgaatcct G/C ccgagttccctcagctccc	3340
ALDH1L1	103	intron22+1226	tgaatcctccccagttccc T/C cagctccctcctaaccctag	3341
ALDH1L1	104	intron22+1623	ggggcttcccactgtccaga C/G aaggcgggtgggagctgggga	3342
ALDH1L1	105	intron22+1698	attctggggagtcctggccc A/G ctatccactgocagggataa	3343

Table 1

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GENE	number	position	SEQ.	SEQ ID.No
ALDH1L1	106	3'flanking+145	gagagacaggaggaaatggg C/T gtgggtcatctcaggcccca	3344
ALDH1L1	107	3'flanking+239	tgggaaacaggtgggaagac G/A gggattgagctgggtgagcc	3345
ALDH1L1	108	3'flanking+288	ggaagcagctcagactccct C/T agcagatggggccgggcccct	3346
ALDH1L1	109	3'flanking+1513	agggtcggctcagaccccgg A/C gtgctcctggcatgtccagc	3347
ALDH1L1	110	3'flanking+1707	cgggtgggacttgccctagca C/T gtgccacttataccagaaca	3348
ALDH1L1	111	3'flanking+1709	gtgggacttgccctagcaac C/T gccacttataccagaacaga	3349
ALDH1L1	112	3'flanking+1745	acagatgagtcctatgtaac C/T gcttcttgagttccctttgt	3350
ALDH1L1	113	3'flanking+1843	ctgcctctcagcccacagcc G/A ggccgctcacactcctccca	3351
CYP3A4	1	intron2+(754-763)	cacaaaatgagtttgtgggg (T)9-11 acacaaaggcgggaatcacat	3352
CYP3A4	2	intron7+258	accactaatcaactttctgc C/T tctatggatttgcctattct	3353
CYP3A4	3	intron7+894	tgctgatctcactgctgtag C/T ggtgctccttatgcataagac	3354
CYP3A4	4	exon9+(32-33)	ttccttcagctgatgattga (A) ctctcagaattcaaaagaaa	3355
CYP3A4	4	exon9+(32-33)	ttccttcagctgatgattga ctctcagaattcaaaagaaa	3356
CYP3A4	5	intron10+12	cccaataagggtgagtggatg G/A tacatggagaaggagggagg	3357
CYP3A4	6	intron10+459	agacatgtgactttttttt T/ Δ gaaaggtaacaatcactttc	3358
CYP3A4	7	intron10+608	agccgtctcgaatgtctccc C/T acttcataactcctccacac	3359
CYP3A4	8	intron12+2467	ttttttgccattactccat A/G gagatcagaatatcactctg	3360

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA1	1	(5' flanking region -99)	acataaacagagggccgggaa G/C gggcggggaggaggagagag	3361
ABCA1	2	(intron 1 159)	gcggtgttaaatggggagac G/T atgtcctagtagcagctctg	3362
ABCA1	3	(intron 1 506)	gaattggctatatgtctccc G/C ggactggagcggcacagtc	3363
ABCA1	4	(intron 1 5897)	gtacaaaaccctttagcttt T/G gcaaacctcctttaagaccc	3364
ABCA1	5	(intron 1 5929)	ttaagacccgatttaaatgc C/T tccctcctcatgaagctctt	3365
ABCA1	6	(intron 1 5962)	aagctcttctggatccactc T/C tcccatcactaaagttagaa	3366
ABCA1	7	(intron 1 5985)	cccatcactaaagttgaaagt A/C agatcccccttctcttactt	3367
ABCA1	8	(intron 1 11416)	ttacagtccctttatagga G/A agaaagaagaaattgtgtct	3368
ABCA1	9	(intron 1 11935)	tctctgtggagcaaatagag G/A gctgtctgacacttgggtcc	3369
ABCA1	10	(intron 1 12281)	gaatgtttgatattgtgaaaa T/A cttaataacacagtagttttt	3370
ABCA1	11	(intron 1 12924)	gtgctgacaatcttatactc T/C aggttgaaacctccggggaag	3371
ABCA1	12	(intron 1 13002)	gagcctcaatcacagattct C/G tctagctcacatgaagttaa	3372
ABCA1	13	(intron 1 17715)	ggagcatgactttgtggaag C/T ctctcctcttccaccagag	3373
ABCA1	14	(intron 1 17848)	gagggctgactgtcacctt T/C gataggagcccagcactaaa	3374
ABCA1	15	(intron 1 21384)	gtgggtgggaggaattggag G/C aggaagcttgcctaaagtgtg	3375
ABCA1	16	(intron 1 23063)	ggaggcacctgtgacaccca G/A cggagtagggggcgggtgtg	3376
ABCA1	17	(intron 1 23131)	agtgtgcatagtgtgctgacc G/A tgggagcttgtttgtcggtt	3377
ABCA1	18	(intron 2 2801)	aagaaaagtgtattatttca A/G gttgctgtagcttagattgt	3378
ABCA1	19	(intron 2 2830)	tgcttagattgttagagttg C/G aaagatctggcttgcattct	3379
ABCA1	20	(intron 2 2856)	tctggcttgcattcttgtaca A/G ctgacagaaactgggctcag	3380
ABCA1	21	(intron 2 3187)	tgatagctgttgcctgcagc A/G tacggacgttctattgcgcag	3381
ABCA1	22	(intron 2 3190)	tagctgttgcctgcagcata C/T ggacgttctattgcgcagttc	3382
ABCA1	23	(intron 2 3194)	tgctgcctgcagcatacggg C/T gttcattgcgcagttcctgt	3383
ABCA1	24	(intron 2 3204)	agcatcggacgttctcattgc G/A cagttcctgtctcctgagat	3384
ABCA1	25	(intron 2 3401)	acataaagcctgtgtgctgc T/C gccaggaagactagaaacgc	3385
ABCA1	26	(intron 2 13927)	gtcaccacatacctggcact A/G tgctaaggctgggaatgcag	3386
ABCA1	27	(intron 3 4163)	ccagcccacttcatcttacc G/A tagttacctccttagagtat	3387
ABCA1	28	(intron 3 4262)	tgtcaaaagaggaaactaaagga T/C gccagggacttctgcttag	3388
ABCA1	29	(intron 3 4306)	ccctctcatcacttcttccaa C/T gctggatcatgaaccccat	3389
ABCA1	30	(intron 5 490)	gatgggcatttgaacttgtt G/A tctttaaaaaagtgaatctt	3390
ABCA1	31	(intron 5 583)	tatctggggagtgggcattt T/G ctgactgaggcattgggtgc	3391
ABCA1	32	(intron 5 1051)	ggctacaaaactgtgtgttcc C/T ttgggcagtaaaagagggcaa	3392
ABCA1	33	(intron 5 3051)	tagagaacaagtctaattct G/A tttccttgaaaaatagtcgaa	3393
ABCA1	34	(intron 5 3127)	aagtcctatgatttttttaggc A/G aaatggcctccttctcctct	3394
ABCA1	35	(intron 5 5924)	ctttctttcacaaaaattgcc C/T cccagagctttcttggaagg	3395
ABCA1	36	(intron 5 6831)	ccagtcctcagccttgcca T/C tgcttatgctggctctggaag	3396
ABCA1	37	(intron 5 12678)	gctcaccgctctgctcacc G/C acctctggccatctcctct	3397
ABCA1	38	(intron 5 14214)	cagcttggtcccagaggcct G/A gacctgggtcccagaggctcc	3398
ABCA1	39	(intron 5 14257)	gctggttccccggcttggtc C/T cagaggccttgatgtgtggc	3399
ABCA1	40	(intron 5 18078)	cctaccacaccatgcacgtg C/T acagccaaagggtgtgtgact	3400
ABCA1	41	(intron 5 18795)	ctgggctcttctcctggacctg G/A ccagctaaaaggaaatctcc	3401
ABCA1	42	(intron 5 18948)	gcattgggtggtactaagaac G/A catattccctatcctatagg	3402
ABCA1	43	(intron 5 19053)	ctcccccaacattaaaagt T/C aagggtgcttatttcaaatg	3403

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA1	44	(intron 5 19148)	ggcccaagaaactgcatttt C/A gcatgctccctaaatgaagc	3404
ABCA1	45	(intron 5 19229)	atgctaacagtgtaggtca C/T atgtgatgggaagcatcagg	3405
ABCA1	46	(intron 5 19405)	cttgctcaatttattctgtc T/C atataactcaatattactga	3406
ABCA1	47	(intron 5 19534)	catgtgaccctcttagctcc G/A cggattaaactcctgtcctca	3407
ABCA1	48	(coding region 474 (Leu 158 Leu))	gaaaccttctctgggttctt G/A tatcacaacctctctctctccc	3408
ABCA1	49	(intron 6 210)	gcaacctggcgtcatgggcc A/C gctgggttaaaaaataaattga	3409
ABCA1	50	(intron 6 334)	acagttctgagggaataacc G/A tgggttaagggttattgatctt	3410
ABCA1	51	(intron 6 2288)	cttctttcaaaagcttgtggt C/T cactggaccacgtatgaagt	3411
ABCA1	52	(intron 6 2322)	atgaagtagaatagttagg T/C ccagaaaggcaattaaagtaa	3412
ABCA1	53	(intron 6 2820)	gtgcttgatacattcttgag T/G ttcagtaaagagacctgatg	3413
ABCA1	54	(intron 7 416)	catcataaagatgacattgt G/A ggctgtcacagtttggaagcc	3414
ABCA1	55	(intron 7 471)	agaccacactatttagctta C/T ttagtaataaacatttgcaag	3415
ABCA1	56	(intron 7 504)	ttgcaaaagaaaaattccgac G/A aagttttttcagccctaggaa	3416
ABCA1	57	(intron 7 679)	gctctggtgaaattcctctc G/C ctaccccaaaacatcatcatt	3417
ABCA1	58	(intron 7 1740)	acaaatgctcacccctttcag C/T tggaaatgattgaaaattttgg	3418
ABCA1	59	(intron 7 2122)	tgattaaaggtggctactacc A/G ggtgctttctgcatatctcg	3419
ABCA1	60	(intron 7 7753)	taggaattccaagctgtgaa T/C tttttactgaagctcttttg	3420
ABCA1	61	(intron 7 8973)	atggaaatttgttttatattg A/T ctacagatttgccaatattat	3421
ABCA1	62	(intron 7 8976)	gaaattgttttatattgact A/G cagatttgccaatattattag	3422
ABCA1	63	(intron 7 11327)	ctaacaatcttatttccatt G/C agtcttataaaaagaagtgg	3423
ABCA1	64	(intron 7 11738)	ctgacgttttaaggagaccg C/T gtaggtccctttgaggactg	3424
ABCA1	65	(intron 7 12295)	agtctgtaaaattattgttct T/A tttttcttttagcttatgct	3425
ABCA1	66	(intron 8 387)	tagcaaggccaatcatctta C/G caacacacatgcttgctaaac	3426
ABCA1	67	(intron 8 697)	ggaactgtctgtgtgtccccc A/T gcataggaaagctgagccagg	3427
ABCA1	68	(intron 8 3036)	ctttatgtgggaagaaatttt T/G ttttttttgattggggagtgg	3428
ABCA1	69	(intron 8 3176)	aaatggcctggttctctgtc C/A cttttctgtctgtatgcctc	3429
ABCA1	70	(intron 8 3364)	ggcagaaggcaaaagcttagg A/T cctagagagtgctggaccac	3430
ABCA1	71	(intron 8 3373)	caaaagcttaggacctagaga G/A tgctggaccacgccactcac	3431
ABCA1	72	(intron 8 3561)	cagggatttattaatgattt C/A ttgtgaaatgttttggaata	3432
ABCA1	73	(intron 8 3654)	agtgcgggaatacattttgca T/C gtaagacagaacgctgcctg	3433
ABCA1	74	(intron 8 4715)	ggcagaggggtctcagaatc C/T gcatttccaacaatgtctcc	3434
ABCA1	75	(coding region 936 (Pro 312 Pro))	cgtattgtctcggggcatcc C/T gagggagggggggctgaagat	3435
ABCA1	76	(intron 9 2309)	ccctcaagagtcagtttaa A/G tgttggtcatgttagttgtc	3436
ABCA1	77	(intron 9 2392)	atgggagggtctgtgtctca T/C gaaaacatttttccagatca	3437
ABCA1	78	(intron 10 228)	tggggatggggagggaactggc A/G cagggctgctgtgatgggt	3438
ABCA1	79	(intron 10 319)	ttctggtggtccctggctccc C/T acctgactccaggtgaacaa	3439
ABCA1	80	(intron 11 377)	gaaagaagtgtgggagcaaaa A/C gcatgatgttacatgtagac	3440
ABCA1	81	(intron 11 521)	agtgtcttagagacaattgg G/A ttcaaatgtggagcaggctg	3441
ABCA1	82	(intron 11 2850)	ctctatacaaatcattatgct G/C ccattgaaataataataaca	3442
ABCA1	83	(intron 11 2976)	ctccaaattcggtagaaccag A/G gcttcatcttctctgtcgaa	3443
ABCA1	84	(intron 11 3056)	gttgcagctgctgtttttc C/T ggcagcacatctgtgcaggc	3444

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA1	85	(intron 12 340)	ggcattattgtgaaactta T/C ctaaaatcgaattcgggtcc	3445
ABCA1	86	(intron 12 381)	aattaaaattttgaaatttt A/G tattaataattatattagta	3446
ABCA1	87	(intron 14 1728)	caggctcagaggccttgccc C/T atcacccctggctcacgtgtg	3447
ABCA1	88	(coding region 2040 (Ile 680 Ile))	atgggcctggacaacacagcat C/A ctctggtttagctggttcat	3448
ABCA1	89	(intron 15 1382)	cttttagacagaaaaagttaac G/A tgggatattatctccccacag	3449
ABCA1	90	(intron 15 1453)	tataaaggagaaaaaccagtt G/A aaattacctattgaagaaac	3450
ABCA1	91	(intron 15 1567)	ttctgcgtagtttttggttaa G/A tcacttatcttctttaggat	3451
ABCA1	92	(intron 15 1617)	cagttgcctcatcagaaaaa T/A gaacagcattacgcctctgc	3452
ABCA1	93	(intron 16 95)	agttgagaacagaaagatgat T/A gtcttttcccaatgggacatg	3453
ABCA1	94	(intron 16 452)	tggtgttttgcttgagtaat G/A ttttctgaaactaagcacaac	3454
ABCA1	95	(intron 16 657)	ctgttgccctcagttctgggt T/C cataggcatcagcagcccca	3455
ABCA1	96	(intron 18 1730)	tgaagttcaagcgcagtg C/G ctgtgtccttacactccact	3456
ABCA1	97	(intron 19 426)	aggaccttacagtggttagt A/G tcaggagggtcaggggctg	3457
ABCA1	98	(intron 19 468)	aaagcaccagcgttagcttc A/G gtggcttcacgacgattcc	3458
ABCA1	99	(intron 20 876)	ccctcctcatctaaaagttaa C/T acatggggtcatgtgcagg	3459
ABCA1	100	(intron 22 118)	catgggatactcttctgtta T/G cacagaagagataaaaggca	3460
ABCA1	101	(intron 22 560)	aaagctttggcattcttaggg G/A tcataggccatacaggggtgaa	3461
ABCA1	102	(intron 23 102)	accccttttgccatgttgaa A/G ccaccatctccctgctctgt	3462
ABCA1	103	(intron 23 287)	gtcaagaaaaagagacttgt C/T aagaggtaagagccttggct	3463
ABCA1	104	(intron 23 1063)	acctttcacccctcaggaaagc G/A aggtgtttcacacgggcacac	3464
ABCA1	105	(intron 25 321)	ctctttacttaagtacagt T/G gaggaacagcggtcatcagga	3465
ABCA1	106	(intron 25 376)	gttagaaattcagcaacttg G/C gccagctcagacactactga	3466
ABCA1	107	(intron 25 478)	catacataggaaatgacaaa C/T gtttatggatggatagtcta	3467
ABCA1	108	(intron 25 579)	tcatttaattctcaaaaaa G/T atgaaaaaatgaacactcag	3468
ABCA1	109	(intron 27 153)	aatggtaaaaagccacttgtt C/T tttagcagcatcgtgcattgtg	3469
ABCA1	110	(intron 28 1058)	actatcatgggagagataatga C/T tatggtgttccatgattgga	3470
ABCA1	111	(intron 28 1317)	caggaccagtggttcttgagt C/T acctgaatgtgagcaactat	3471
ABCA1	112	(intron 30 372)	tatatgattttttaggttttg T/C ttatcagcttcttcgctttt	3472
ABCA1	113	(intron 30 506)	cccttttaaaaagtaagcagt A/G gataataaaattcagtggaag	3473
ABCA1	114	(intron 30 1033)	ctggatttcagtggtgccttt G/C attttccacatgaaggttgt	3474
ABCA1	115	(coding region 4281 (Thr 1427 Thr))	tcttccctttgcagagacac G/A ccctgccaggcaggggagga	3475
ABCA1	116	(intron 33 626)	ggctccttggttactgatttc C/T gtcttttctctctgcctttt	3476
ABCA1	117	(intron 33 719)	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	3477
ABCA1	118	(intron 33 726)	cctcatgctagaaggaggcc G/A gagcctgtgtataaagggccag	3478
ABCA1	119	(intron 33 889)	cttctcctaattgtctcagct A/G tctaactgtgtgtgtaatca	3479
ABCA1	120	(intron 33 1097)	ctgtgacccccactgtctgg G/C ttttaatgtcaggctgttct	3480
ABCA1	121	(intron 35 234)	aacctatctaaacctcagtt T/C cctcatctgtgaaaatggaga	3481
ABCA1	122	(intron 37 411)	aactctgtacatttttatcag C/T agcttatccatccattgcaa	3482
ABCA1	123	(intron 37 1224)	caggcataggtgatttcagag A/G tgaagggtcaagtccttgaa	3483
ABCA1	124	(intron 37 1720)	aaattaaaaattactctgact G/T ggaatccatcgttcagtaag	3484
ABCA1	125	(intron 40 251)	tgaaggttaaggaaaaatagt T/G tatttgcttggatccactgg	3485

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA1	126	(intron 40 252)	gaaggtaaggaaaaatagtg T/C atttgttggtggtccactggc	3486
ABCA1	127	(intron 40 319)	agcactggaaaaagtcaaac A/G taactttgagaattagtgga	3487
ABCA1	128	(intron 40 957)	cttgttactcttttttctct G/C tcatgggtgatagccatttg	3488
ABCA1	129	(intron 41 146)	tgatgtgggcatcccgagc C/T cctccctgcccacccctgga	3489
ABCA1	130	(intron 42 239)	cattggttttatatgtcttac A/C tttatgtgttagttattataa	3490
ABCA1	131	(intron 42 321)	aataaatgggtgatttttgag T/A ttgagttttcatagtcacaaa	3491
ABCA1	132	(intron 42 322)	ataaatgggtgatttttgag T/C tgagttttcatagtcacaaa	3492
ABCA1	133	(intron 42 533)	agatgaaaaattatgttagat G/A ataataatgatacggttct	3493
ABCA1	134	(intron 42 546)	tgtagatgataaatgaatgat A/G cggttctaaaaagacaggtt	3494
ABCA1	135	(intron 43 739)	tacagccacacttaaaatgg T/A cccattatgaaatacatatt	3495
ABCA1	136	(intron 44 18)	taggtgagaaaaagaagtggc T/C tgtattttgtgcaaaagact	3496
ABCA1	137	(intron 44 264)	acaataaatgtgtgtgttt T/C ttaagagataaatatttagtga	3497
ABCA1	138	(intron 44 279)	tgttttttaagagtataatt T/C agtgatttttggtataattga	3498
ABCA1	139	(intron 44 508)	ttacattgctacataaaat C/T cccctatgtacatgtaccta	3499
ABCA1	140	(intron 44 1477)	gatctcctctcctgtctctt A/T catttttgcagtagcaatgt	3500
ABCA1	141	(intron 44 1665)	tggttgtaagaaactgatttg G/A ttggtatagctgtgagggcc	3501
ABCA1	142	(intron 44 1956)	gtgtgtcgcacactcaaaat T/G tctgggcttctcatttgggt	3502
ABCA1	143	(intron 45 68)	aatatatacctttatggcttt T/C ccacacgcatgtgacttcagg	3503
ABCA1	144	(intron 46 608)	ttatactgacttcaatagag G/C tttcagacaaaaaagtgtttt	3504
ABCA1	145	(intron 47 336)	ttcacaaattgtaaaacaccac T/C aactgaacagcatcatccc	3505
ABCA1	146	(3' untranslated region 7479)	aacaaaaatgtgggtgtctc C/T aggcacgggaaacttggttc	3506
ABCA1	147	(3' untranslated region 8226)	aggagcccactgtaacaata C/T tgggcagccttttttttttt	3507
ABCA1	148	(3' untranslated region 8697)	ttccagaatttgaatatata C/T gctaaagggtgtaagacttca	3508
ABCA1	149	(3' untranslated region 9097)	aactattttgaagaaaaaac A/G acattttaatacacagattgaa	3509
ABCA1	150	(5' flanking region (-1033)~(-1032))	tgacttaaatatttagacat (AT) ggtgtgtaggcctgcattcc	3510
ABCA1	150	(5' flanking region (-1033)~(-1032))	tgacttaaatatttagacat ggtgtgtaggcctgcattcc	3511
ABCA1	151	(intron 5 6368)	ttctgatgggggtgtgtgtg C/ Δ tgagaatcatgactgggtgg	3512
ABCA1	152	(intron 5 9709)	cattttctgtctgaacccc T/ Δ caccattcaggcagctgct	3513
ABCA1	153	(intron 5 13816)	tccctacttctccttttttt T/ Δ catttgcctcctccaccac	3514
ABCA1	154	(intron 10 270~271)	cttttcaggaggagagccaaa (G) cgctcattgtctgtgtctct	3515
ABCA1	154	(intron 10 270~271)	cttttcaggaggagagccaaa cgctcattgtctgtgtctct	3516
ABCA1	155	(intron 20 611~612)	tttagcccatcctctcccc (C) gccacctccttatttaggc	3517
ABCA1	155	(intron 20 611~612)	tttagcccatcctctcccc gccacctccttatttaggc	3518
ABCA1	156	(intron 32 391~392)	gagtgccttgggtactctct (T) gatgggggactcccatgataa	3519
ABCA1	156	(intron 32 391~392)	gagtgccttgggtactctct gatgggggactcccatgataa	3520
ABCA1	157	(intron 37 847)	gctgtatatgtgaatgtcc C/ Δ gtttcaaaagcaaaagccaa	3521

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA4	1	(5' flanking region -1005)	tgccatcataagcagaaaaact A/C tctctctctcttcttgaagct	3522
ABCA4	2	(5' flanking region -819)	gtctagagtctttcaaagag A/T acacattctgagatttgagg	3523
ABCA4	3	(5' flanking region -680)	agcaccacccattgcaggg C/A tggaatgacagtaaatgggccc	3524
ABCA4	4	(intron 1 208)	tgccttcccaggaagatgt G/A tttctctgtctcagccaca	3525
ABCA4	5	(intron 1 234)	ctgtcctcagccacatgaaa A/G tcttttgctaccgtgctg	3526
ABCA4	6	(intron 1 510)	agctcacgatacaagtcacag T/C ttaactggacacattatttt	3527
ABCA4	7	(intron 1 1527)	gcttaacaaccagcagcataaaa G/A agagcagcatgggacacgct	3528
ABCA4	8	(intron 1 2077)	caggactgtagctgctggcc T/C aaatgagccattcctctgtg	3529
ABCA4	9	(intron 1 2174)	ccctctcaatctggcctttc G/C ctggcatgggtgggagctc	3530
ABCA4	10	(intron 1 2246)	gctcccaggagatggagcc A/G ctgggctgagggccttggc	3531
ABCA4	11	(intron 1 2364)	ttctgtctggcacgcctccc G/A atggctccccacctgctacc	3532
ABCA4	12	(intron 1 4243)	ctccctgggtatgcctgta C/G gcagttaaagcgtcaaggaca	3533
ABCA4	13	(intron 1 4287)	atgccgctctggggagggga A/C gctgagcatgattttggaag	3534
ABCA4	14	(intron 1 4309)	ctgagcatgatattttggaagc C/T ggcagaagaggctattgtga	3535
ABCA4	15	(intron 1 4416)	tgcagcaaccgccccccccc C/T ccgcaaaaaaacaacacact	3536
ABCA4	16	(intron 1 4996)	tttacccttggaacacaggcag G/A ccaagctggc t/c ggtccctc	3537
ABCA4	17	(intron 1 5007)	aacaggcag g/a ccaagctggc T/C ggtccctcctcctgatacaca	3538
ABCA4	18	(intron 1 5080)	gtgtgtggctggtttcttag C/G aagcaccatggttccaagtt	3539
ABCA4	19	(intron 1 5152)	gggagatgaacgtaagtga G/A ggcaggcctacaagggtgca	3540
ABCA4	20	(intron 1 7110)	ccactggatctgcttttga A/G tcaagagtccttaagctcca	3541
ABCA4	21	(intron 1 7290)	gatttttggctggctttgcaa T/A ggatcacagtcatttattca	3542
ABCA4	22	(intron 1 7483)	tctgagcctcttctccttaac T/C gcagagtgaagg c/t tacaga	3543
ABCA4	23	(intron 1 7497)	cttaac t/c gcagagtgaagg C/T tacagagaaatctttactac	3544
ABCA4	24	(intron 2 1067)	tcaagcagcagcagcaactg C/A gtggagtcttcttgaaactaa	3545
ABCA4	25	(intron 2 1243)	caccagcacaggagactggc A/T cacatgagatgctcctgctt	3546
ABCA4	26	(intron 3 26)	tgttgagatccctaccatgc A/G ggggaggaagtggcacaccc	3547
ABCA4	27	(intron 3 101)	agcatggagcactgagtgtt C/T ttgtggctttgctgagcccc	3548
ABCA4	28	(intron 3 330)	tgcttgggtggagtgaatca T/C tgtaggagaaaaaactcagtt	3549
ABCA4	29	(intron 3 470)	tgaagtcagggtttacaaaagt C/G aagtttacttcttgggagaa	3550
ABCA4	30	(intron 3 634)	tgaataaccaatgacccctct T/C ccaagaaaaatggccacata	3551
ABCA4	31	(intron 3 1016)	ccttgggggagctcagtatg A/G ttcttcaggagaagcctgc	3552
ABCA4	32	(intron 3 1554)	gaaagtgggttttcatgttt T/C gcactcacattatgagtga	3553
ABCA4	33	(intron 3 1686)	ctagacattctcacagagcc A/G agggcagcaaggcgggctc	3554
ABCA4	34	(intron 3 1823)	ttcacctctctccatggacc A/G gtctccctgctcctcaatg	3555
ABCA4	35	(intron 3 1938)	caaatctctgggaacaaaatc G/A ggttgaccagc t/g ttattct	3556
ABCA4	36	(intron 3 1951)	acaaatc g/a ggttgaccagc T/G ttattctcctgtcccatca	3557
ABCA4	37	(intron 3 2063)	ggctgtcagagcctacctgc G/T tgaatgggtggaagg g/a cagg	3558
ABCA4	38	(intron 3 2079)	ctgc t/g tgaatgggtggaagg G/A cagggtcagagaattgggt	3559
ABCA4	39	(intron 3 2186)	agacacacagagcatgggac C/T gagaggcagcagacccctgc	3560
ABCA4	40	(intron 3 2214)	gagcagaccctgccccaaact G/A ggagactgaatagatcgctc	3561

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA4	41	(intron 4 3182)	ccccagagccacagcagcc C/G tgtctcctgggtggtcttgt	3562
ABCA4	42	(intron 4 3515)	agtataataaaagcaggagc C/T atagcccccactctcaaga	3563
ABCA4	43	(intron 4 3952)	agagaagccactgtgccact G/C tgtggtcgaaacttcaagacc	3564
ABCA4	44	(intron 4 4637)	aatcaactgccccaaaggtca C/T cttaactgttaggtgttctt	3565
ABCA4	45	(intron 4 5319)	acctctaggggctcccagag A/G ccccaagaacagaaccttc	3566
ABCA4	46	(intron 6 2266)	caccttgccagacctcagac G/A ggctctggggcttgccttc	3567
ABCA4	47	(intron 6 2857)	ccagaggagaaagctctgcc G/A tag t/c cggcctcagtttaacca	3568
ABCA4	48	(intron 6 2861)	aggagaaagctctgcc g/a tag T/C cggcctcagtttaacca	3569
ABCA4	49	(intron 6 3078)	gcaggcatataaatgggact T/G tgcctttattgctcctgggc	3570
ABCA4	50	(intron 6 3375)	ttaaatgccaaaatgagttct C/G attaacaagaaagaggaa	3571
ABCA4	51	(intron 6 3412)	ggaaaatctcagtaaacac C/T gtgacggcatctaccactt	3572
ABCA4	52	(intron 6 4635)	ctttcgggtggatattgcta C/T gtcaagtgtctgggaaagcc	3573
ABCA4	53	(intron 6 -264)	aaacagcaattagaatcact T/C tgaatagttagtagtattta	3574
ABCA4	54	(intron 7 828)	gatgtgggaaagttagagaa G/C agcccatgttactaatgctc	3575
ABCA4	55	(intron 7 1019)	aggcttcttgactgtctaga T/C agcaagtctaatcatttgtg	3576
ABCA4	56	(intron 8 374)	gtaaacacggctgtgggatg C/A ttttacaacacacaatatcgt	3577
ABCA4	57	(intron 8 874)	tgatgagcttgttattgggtg G/A ggtacagcctattaaatttag	3578
ABCA4	58	(intron 9 605)	tcgtgtctctgtcttgatct C/T tgtctgggttttagggccaact	3579
ABCA4	59	(coding region 1268 (Arg 423 His or His 423 His))	aacttttgaagaactggaac G/A c/t gtttaggaagtgtggtcaaaag	3580
ABCA4	60	(coding region 1269 (Arg 423 Arg or His 423 His))	acttttgaagaactggaac g/a C/T gtttaggaagtgtggtcaaaagc	3581
ABCA4	61	(intron 11 5687)	atcatgtaatgtacttttaga C/G tcagatatataataatttgt	3582
ABCA4	62	(intron 11 7136)	gacttcccaacttaccttag T/C ggagctgtagtcacatagaa	3583
ABCA4	63	(intron 11 7180)	acgctcataaatgcttctct G/A ggctgtaaagggttgaatttt	3584
ABCA4	64	(intron 11 7701)	gttagacgcaggcattacct C/T gtggctttgccccagtggtga	3585
ABCA4	65	(intron 11 8073)	gggatgtttgccccacatcca T/C tggcatattctcaaaaggaac	3586
ABCA4	66	(intron 11 8586)	cagctgcctgcgctggagag G/A gctcaaacctcttccgcccag	3587
ABCA4	67	(intron 11 11234)	cccaataaattttgtttttc G/A ttttaggaattaaatttcag	3588
ABCA4	68	(intron 11 11641)	aagaaacaaacattttattga C/G aacttttggtgtgtgacctg	3589
ABCA4	69	(intron 11 11808)	tggattttcttaaaagaata C/T caattccatttcccttttaac	3590
ABCA4	70	(intron 11 11923)	aagatcattatataatctc A/G tcagcgtggtgtcacttaag	3591
ABCA4	71	(intron 12 305)	tcacctgtggtcgaggaggt G/A tgagtgcgtatccaagccc	3592
ABCA4	72	(intron 13 1461)	ttgggtttcagtgctcagcat G/A tagctgtctactcagatccc	3593
ABCA4	73	(intron 14 1268)	ggagctgagcccccttgtcct T/C atctaggtttcccttgttct	3594
ABCA4	74	(intron 17 23)	gagtcctttaaaacacaaaat C/G ttaatgtttgaaatacaactc	3595
ABCA4	75	(intron 17 715)	gggactcccctagagctgaa G/A tacttcccactctgtttgtt	3596
ABCA4	76	(intron 18 1282)	ggaagatgaagaacctaagc C/T gcttccagaaaattcatgagg	3597
ABCA4	77	(intron 20 -195)	acagattattccattgtatg C/A atgaactatgtaagccatcc	3598
ABCA4	78	(intron 23 755)	ctggctgccgctgggtttc C/T tatgtccatccacggggagg	3599
ABCA4	79	(intron 26 702)	tatcaaatatacaactcagacg T/G cagtctcctggcccccttga	3600
ABCA4	80	(intron 27 156)	cctgctttccaaaccccttat C/T ttgattcttggtaacatgaa	3601
ABCA4	81	(intron 27 385)	tttaagaacagtgagtcac G/A tgacttgctctttgaaatgc	3602

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA4	82	(intron 28 299)	gacatgccatcagaccactg C/T gagtgttcaggcagcctacc	3603
ABCA4	83	(intron 29 168)	ctcttccacacttgtgtgc A/G gggacattcactacctccta	3604
ABCA4	84	(intron 29 497)	gctgtcaataaggaccacaaa C/T agactaatttcaaatctctc	3605
ABCA4	85	(intron 29 567)	agctgctaggaataaaaaagg G/A agacaaaa g/a atccacaagg	3606
ABCA4	86	(intron 29 577)	aataaaaaagg g/a agacaaaa G/A atccacaagctagagatggt	3607
ABCA4	87	(intron 30 -2494)	aatcacagctcatctgtgc A/G tcatagggatcccaaaagaa	3608
ABCA4	88	(intron 30 -2169)	aatgtaacagccaaagtctt A/G gaaaaaggcaagccagtctc	3609
ABCA4	89	(intron 31 535)	ctaactgtgaattatcatct T/G tgatcactgccctttgagat	3610
ABCA4	90	(intron 35 209)	tctcccaacatttatgtgg C/A aagtaagtttacatttgggtt	3611
ABCA4	91	(intron 37 525)	taaatgtgaatgagtaattc A/G tccatctcgccctcagtttc	3612
ABCA4	92	(intron 37 766)	tgttgaggctggagaacc T/G cctatgaattgtacagggct	3613
ABCA4	93	(intron 37 856)	aaaacccatgaagtgttca A/G ggcaggcatcattatctcca	3614
ABCA4	94	(intron 38 62)	tagtagagtatgtgtgtgc G/A agcagagccaggggcaagca	3615
ABCA4	95	(intron 38 761)	tccttgggcaagttaattctt G/A atgaagagactgggtgttct	3616
ABCA4	96	(intron 38 1315)	cagagtcagactctggaaag G/T c/a ggggggataagaacacagc	3617
ABCA4	97	(intron 38 1316)	agagtcagactctggaaag g/t C/A ggggggataagaacacagcc	3618
ABCA4	98	(intron 38 1561)	gtattttcatgtataattatc C/A g/a atcacagctgctatggaa	3619
ABCA4	99	(intron 38 1562)	tattttcatgtataattatc c/a G/A atcacagctgctatggaaa	3620
ABCA4	100	(intron 38 2874)	ctagacaaaagggg a/c agctcc C/T gccactagaaaacttgcagg	3621
ABCA4	101	(intron 40 1904)	gacactgtacagccagccca A/C tctgaccccttttcttcat	3622
ABCA4	102	(coding region 5814 (Leu 1938 Leu))	ggaaaataaaactgacatctt A/G aggtacatgaactaaacaa	3623
ABCA4	103	(intron 41 122)	atttggttcccagttttatg T/G agggtcacatccctgtgtt	3624
ABCA4	104	(intron 41 411)	cccttcccctccttctctt C/A accctgtctcagttctcagt	3625
ABCA4	105	(intron 41 443)	gtctcagtcctgggtttcttc G/A tatcttgagattttatcc a/g g	3626
ABCA4	106	(coding region 5844 (Pro 1948 Pro))	c g/a tatcttgagattttatcc A/G ggcacctccagccagcagt	3627
ABCA4	107	(intron 43 328)	ttttagcctattcctataa A/G aatgcaccatttgcttc c/g cat	3628
ABCA4	108	(intron 43 345)	taa a/g aatgcaccatttgcttc C/G cattacctccctccacacat	3629
ABCA4	109	(intron 43 370)	acctccctccacacattttt A/G caaaa c/t gttcagggagttt	3630
ABCA4	110	(intron 43 376)	ctccacacattttt a/g caaaa C/T gtttcagggagtttactgag	3631
ABCA4	111	(intron43 670)	ttaaacagactgggtcccta T/C gggcaggacagagaggatga	3632
ABCA4	112	(intron43 822)	gttaggtgctgctgacatct G/A tccagcatctgcttgactgg	3633
ABCA4	113	(intron 43 915)	ggcaggacgagtccttgagca C/T gcttactggctcagacagg	3634
ABCA4	114	(intron 43 1242)	actgagctggacgctagaaa G/T aaactataggcttaagacac	3635
ABCA4	115	(intron 43 1671)	tagagaagtttacttccatc G/A ggacacatgcattcttttcta	3636
ABCA4	116	(intron 43 2036)	ttgaaggatactcagtaatt G/A cttttttcttgcagtattt	3637
ABCA4	117	(intron 45 176)	gtgtttggttcacacagctc C/T ggagaaaaaacaagtca c/t ggc	3638
ABCA4	118	(intron 45 193)	ctc c/t ggagaaaaaacaagtca C/T ggcacagccttgactggga	3639
ABCA4	119	(intron 47 238)	cccaagtctctggatggggc A/G tctgatcaggatgcatgcag	3640
ABCA4	120	(intron 47 269)	atgcatgcagagcctggctg G/A gatgagggagggtgctacc	3641
ABCA4	121	(intron 47 326)	accacttatctcaacagatc C/G gggacctgtggcctatttac	3642
ABCA4	122	(intron 47 715)	aagtcactaagctggttgggt G/A ggaggaaacagcacataac c/t c	3643

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA4	123	(intron 47 734)	t g/a ggaggaacagcacataac C/T caccttatctatgtctgaggt	3644
ABCA4	124	(intron 47 931)	ggacactgcataagatatcta T/C agaaatagcagcatgtcagg	3645
ABCA4	125	(intron 47 1260)	acactctctgtgtggaccatc A/C ctcatccaagagagggtaac	3646
ABCA4	126	(intron 48 1663)	tctcgtctctctcttaccctc T/C aggtgtttgttaaatcttctg	3647
ABCA4	127	(intron 49 127)	agagagccccacccacacca C/T ggtccctaccaagtccccac	3648
ABCA4	128	(5' flanking region (-1441) ~ (-1400))	gtaaatctcagttgaatcag (TCA)14-16 atttttcagtcctggttcctg	3649
ABCA4	129	(intron 1 4712-4720)	gaggggcggggactataggg (A)8-10 cagcctaattcaaggatgag	3650
ABCA4	130	(intron 1 7295-7304)	ttgttggcttttgcaa t/a ggat CACAGTCAT/Δ ttattcactcattcattcac	3651
ABCA4	131	(intron 2 951-952)	cctgtccatcagactcttct TT/Δ acctctcccgaggagccca	3652
ABCA4	132	(intron 3 2642-2653)	cctgggtgacagagcgagat (A)10-12 tagcatgagatattattact	3653
ABCA4	133	(intron 4 5202)	cacaaagcatctgacacccc C/Δ atccagocctggctaacttt	3654
ABCA4	134	(intron 6 3029-3044)	cactaaaaacaaaaatttac (A)16-18 cctgaaagaaattgcaggca	3655
ABCA4	135	(intron 6 5138-5139)	ttcatgacagatcagatggt (G) cttttatggattttacaaaaga	3656
ABCA4	135	(intron 6 5138-5139)	ttcatgacagatcagatggt cttttatggattttacaaaaga	3657
ABCA4	136	(intron 6 5985)	tttcctcttctcaaaccccc C/Δ agactaggagaaggtctgtc	3658
ABCA4	137	(intron 6 6094)	gggacggacagaaaaagacc T/Δ agtttctgttgagccaaaaga	3659
ABCA4	138	(intron 6 -161)	tattttttcaattaaataaa A/Δ gagttttttgtttcttaaaag	3660
ABCA4	139	(intron 7 809-810)	gggcccagtagtgacacactga (TG) tgtgggaaaagttagagaa g/c a	3661
ABCA4	139	(intron 7 809-810)	gggcccagtagtgacacactga tgtgggaaaagttagagaa g/c a	3662
ABCA4	140	(intron 8 472-484)	atcttccccacctttcacta (T)10-13 ggtcttctatggggttaaagg	3663
ABCA4	141	(intron 9 48-71)	gtaccctggacctcccagaa (GT)11-13 gagagagatgtgccttctctg	3664
ABCA4	142	(intron 9 554)	ataggggcagaaaaagacaca A/Δ ccaaaagtctctctcactt	3665
ABCA4	143	(intron 10 11)	catgatcagagtagtaaggggg G/Δ ttggaggatggggaggggag	3666
ABCA4	144	(intron 11 4242)	ggagaggaaatgatgttagt G/Δ cctcctgtataataggccccag	3667
ABCA4	145	(intron 11 13743-13753)	tgtctctttgtgggtaattgg (T)9-11 cctcttcaggagaagaaaa	3668
ABCA4	146	(intron 13 636-637)	cggggtggaggggttggagg (G) ctcatgtgtcattatagatg	3669
ABCA4	146	(intron 13 636-637)	cggggtggaggggttggagg ctcatgtgtcattatagatg	3670
ABCA4	147	(intron 18 569-570)	tgtgcccctcatcttctctc TT/Δ aaactagttctgtatttctc	3671
ABCA4	148	(intron 20 (-304) ~ (-297))	tataacctgacttttttttc (A)7-9 ggattgctttttttaacata	3672
ABCA4	149	(intron 22 1236-1246)	gctgaattagttcccttggg (T)9-11 agttaactcctgatttttgc	3673
ABCA4	150	(intron 26 4626-4635)	gataatcaatgctgtaagg (A)9-10 tggcattagagatccagacc	3674
ABCA4	151	(intron 33 115-116)	taaaaccgtcttgtttgttt GT/Δ ttacatggttttttagggccc	3675
ABCA4	152	(intron 36 1078)	taagcagctatcacttaaca A/Δ taaaaaccagagattatca	3676
ABCA4	153	(intron 37 290-291)	ccttgaccaaaagcctggggg (T) cagccattcccca a/g cccctc	3677
ABCA4	153	(intron 37 290-291)	ccttgaccaaaagcctggggg cagccattcccca a/g cccctc	3678
ABCA4	154	(intron 38 896)	ataaaaaagagggggaaaaaa A/Δ gaaggcagtcgctgcaggcc	3679
ABCA4	155	(intron 38 1209-1210)	gtggaccctgagactgact CT/Δ ttccagatcttgttaggggtt	3680
ABCA4	156	(intron 38 1322)	agactctggaaag g/t c/a ggggg G/Δ ataagaacacagccccagca	3681
ABCA4	157	(intron 38 3107)	gggccccacctgtctgaagag A/Δ gggggggtggggtttgcccc	3682
ABCA4	158	(intron 40 152)	ttttctccaataatacaagt A/Δ gaggatcggttataaataagg	3683
ABCA4	159	(intron 43 330)	tgtagcctattcctataa a/g a A/Δ tgcaccattgcttc c/g catta	3684
ABCA4	160	(intron 43 1354)	tttaattggcccagccatgc C/Δ ttgtgtggcctttgtcattg	3685

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA4	161	(intron 47 1305~1308)	catcctgctgaaggagaaag AAG/△ caccaatggcccaagcccta	3686
ABCA7	1	(5' flanking region -1596)	agaatgttgcccccctccc C/T t c/t ctgcatcctctgcagaag	3687
ABCA7	2	(5' flanking region -1594)	aatgttgcccccctccc c/t t C/T ctgcatcctctgcagaagc	3688
ABCA7	3	(5' flanking region -1180)	ggccagtgaagtacggggcag G/A tcgcccataatagcagcgtgc	3689
ABCA7	4	(5' flanking region -460)	agagctgggtcgtgcctcc A/G gctgggcaactgcctgtctc	3690
ABCA7	5	(5' untranslated region -9)	ctctgtccctccctccc A/G gtctaccatggcctctctgg	3691
ABCA7	6	(intron 5 91)	ccccggccaaggacctccc G/A ttccaggcatccaggctgtc	3692
ABCA7	7	(coding region 563 (Glu 188 Gly))	cagcttgttgaggcccgctg A/G ggacctggcccaggaggtac	3693
ABCA7	8	(intron 8 103)	gccggagggtcacggaaact A/G tttaagaagtaggagtttag	3694
ABCA7	9	(intron 8 166)	tgcggaggatcagaggcaca C/T gcaggagcaaggcagagggg	3695
ABCA7	10	(coding region 955 (Thr 319 Ala))	acgggaccttcgaggagctc A/G ccctgctgagggatgtccgg	3696
ABCA7	11	(intron 9 421)	tttttttttttttttttttt T/A taagagatggagtctcactc	3697
ABCA7	12	(intron 9 463)	gttgcccaggctggactgca G/A tgg c/t gagatcttggctcact	3698
ABCA7	13	(intron 9 467)	ccaggctggactgca g/a tgg C/T gagatcttggctcactgcaa	3699
ABCA7	14	(intron 9 488)	gagatcttggctcactgcaa C/T ctccgcctcctggattcaag	3700
ABCA7	15	(coding region 1184 (His 395 Arg))	cgcacacgtgatgtggggc A/G cctggtgggcaacgctggggc	3701
ABCA7	16	(intron 10 10)	gagtgaaggagggtgagggcc T/C gtccacctgagggtctgtt	3702
ABCA7	17	(coding region 1388 (Arg 463 His))	cctgggccccggccacgtgc G/A catcaaaaatccgcacatggaca	3703
ABCA7	18	(intron 12 115)	caggctgcgaactttgcacc T/G ttacaccactccacgtgacc	3704
ABCA7	19	(coding region 1824 (Ala 608 Ala))	cccttccctgctcagcgccgc A/G ctgctggtttctgtgtctcaa	3705
ABCA7	20	(intron 13 55)	ggtgcgctggagggtgacag A/G cagggggcgccccacgtggg	3706
ABCA7	21	(intron 13 78)	ggggcgccccacgtgggtg C/A gcgccccaggcccaatccag	3707
ABCA7	22	(coding region 1851 (Gly 617 Gly))	cgttgccctctcacagctggg A/G gacatcctccccctacagcca	3708
ABCA7	23	(coding region 2153 (Asn 718 Thr))	cgagggcgcgagtggcaca A/C cgtgggccccggccctacgg	3709
ABCA7	24	(intron 15 34)	ggcggggctccgggcccgggt C/G gcacctgctttgaggaggc	3710
ABCA7	25	(intron 16 8)	ctggacccaaaagggtgaggc A/C ctacgaggcttaatagctgg	3711
ABCA7	26	(intron 16 161)	tcccgcagcttttataggcc C/T cggccccagcaggtcccggat	3712
ABCA7	27	(coding region 2385 (Leu 795 Leu))	caccccatctctgcagtgtc G/A gtagaagaggcacccggcccg	3713
ABCA7	28	(coding region 2421 (Val 807 Val))	cccgccctgagtcctggcgt C/A tccgttcgcagcctggagaa	3714
ABCA7	29	(intron 20 166)	cgagacagtaagagttgggg A/G tagacagaggttccccctgga	3715
ABCA7	30	(coding region 3027 (Ala 1009 Ala))	ctgctgggagaccgtgtggc C/T gtggtggcaggtggccgctt	3716
ABCA7	31	(intron 22 1386)	gggtggggcgtgagccgggg C/T tcctgaagcaccctttgt	3717

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA7	32	(coding region 3417 (Leu 1139 Leu))	gggatctccgacacaccagcct C/G gaggaggtgtgagggcctggg	3718
ABCA7	33	(intron 23 147)	ggagctctgtgtggctcagat G/A tcccttggaaggcctgggg	3719
ABCA7	34	(coding region 3528 (Leu 1176 Leu))	gctggccctagacgtaaccct A/G cggctcaagatgccgcacaca	3720
ABCA7	35	(coding region 4046 (Arg 1349 Gln))	ccagcctgccagtgtagcc G/A gcccggtgcccggcgcctgc	3721
ABCA7	36	(intron 30 81)	ccccctgggagctctccgg C/A cccccggccctcagctccc	3722
ABCA7	37	(intron 32 1)	caaggagcagctgtctgagg G/C tgcactgtgagtcctccac	3723
ABCA7	38	(intron 33 54)	ccactgcttgcactgccct G/A tctggcccttctgtaggcagg	3724
ABCA7	39	(intron 34 245)	cagtactttgggagggccgag G/A caggaggactgcttctggcc	3725
ABCA7	40	(coding region 5057 (Gln 1686 Arg))	ggtgagccggatcttgaac A/G ggtcttctcttatcttcccc	3726
ABCA7	41	(intron 38 65)	ggcccaactcacctttctgaa A/G gacctgcactctctcccaggta	3727
ABCA7	42	(intron 40 154)	ctctacctccacacagcgga C/G caggccctgagacacccctg	3728
ABCA7	43	(intron 40 277)	ctgagccccccggcgcccca T/C cccacgcgtggccccgggaac	3729
ABCA7	44	(coding region 5592 (Ala 1864 Ala))	gtggccccgggaacccagtcg T/C gcgcacctcagcatgggata	3730
ABCA7	45	(intron 41 286)	ctccttgactctgccttctg T/C ggccctgcccacttgcctct	3731
ABCA7	46	(intron 41 389)	tggccgttcccagtttgag C/T cgttctactgcctcttccat	3732
ABCA7	47	(intron 41 991)	cacactatggccctgcccc C/T ac c/t cat c/g cc a/g gctccaccca	3733
ABCA7	48	(intron 41 994)	actatggccctgcccc C/t ac C/T cat c/g cc a/g gctccaccca	3734
ABCA7	49	(intron 41 998)	tggccctgcccc C/t ac c/t cat C/G cc a/g gctccaccca	3735
ABCA7	50	(intron 41 1001)	ccctgcccc C/t ac c/t cat c/g cc A/G gctccaccca	3736
ABCA7	51	(intron 41 1051)	actcatgctggctccacca C/T accatggcccccccatatg	3737
ABCA7	52	(intron 41 1131)	tgcctgcccccatgcccatt A/G tgcctctgctccacactcaa	3738
ABCA7	53	(coding region 5985 (Leu 1995 Leu))	gaagcgctctgctgcgcct G/A gccatcatggtgaatgggcg	3739
ABCA7	54	(intron 44 201)	ggcgaggaccaggaggcgt G/C agccgggggctctggtgga	3740
ABCA7	55	(intron 44 233)	ctgggtggatttagaagaca C/T aatcaggtgtgcttggagt	3741
ABCA7	56	(intron 44 313)	agttaggggaggccctggtt A/G gtggggggggccataggaaa	3742
ABCA7	57	(coding region 6133 (Ala 2045 Ser))	tggcgccgaggttccctggg G/T cggagctgcgcgaggcacat	3743
ABCA7	58	(coding region 6159 (Gly 2053 Gly))	ctgcgcgaggcacatggagg C/T cgcctgcgcttccagctgcc	3744
ABCA7	59	(intron 45 27)	acggcgccggggtcgggctg G/C gggaggcaggctgggggcca	3745
ABCA7	60	(3' flanking region 108)	caagctgagtggtgcacatac G/A ggccaagtggcgattccatag	3746
ABCA7	61	(3' flanking region 376)	cttacaggagcgcgggtgtcc C/T ggagcacaggccaggccgg	3747
ABCA7	62	(3' flanking region 687)	cagcaggagagacttggggag G/A g/a gggagagagttcacactgc	3748
ABCA7	63	(3' flanking region 688)	agcaggagagacttggggag g/a G/A gggagagagttcacactgcg	3749
ABCA7	64	(3' flanking region 1169)	cctcgacctgacccacttca C/T ggggctgcaggcggtgtgat	3750
ABCA7	65	(intron 9 398~422)	cgtgaactaccacgtcctgc (T)22-26 aagagatggagtctcactct	3751
ABCA7	66	(intron 12 175~184)	ggggactctgagggtctggt (G)8-10 actctgagggtcttgggggccc	3752

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA7	67	(intron 30 81~87)	ccccctgggagctctccgg (C)6-7 ggccctcagctccccctccc	3753
ABCA7	68	(intron 34 349~361)	agaaagagaaagagagaaag (A)12-14 cagaaatgtgctttgggtga	3754
ABCA8	1	(intron 1 204)	ctggtaattaattatagata A/G ataaaaacattgagttagaa	3755
ABCA8	2	(intron 1 266)	aacattatgttgttttaaac A/G taactgagtgtagaaaataag	3756
ABCA8	3	(intron 1 733)	ttgccatatgtataataaaag T/A attcatgttttttgcctagcct	3757
ABCA8	4	(intron 1 861)	agactggagtttgcctgcta C/T ctaagactgtagctgattcc	3758
ABCA8	5	(intron 1 907)	gaggagatcatcctctcttggc C/T aatgtctattaaacttcgcca	3759
ABCA8	6	(intron 1 1262)	cagaaacttttgccctctct G/A taggctagctcactgtgaaa	3760
ABCA8	7	(intron 1 1537)	agctctcttaaaagtatcca T/C gctgaatttttctgcacctta	3761
ABCA8	8	(intron 1 7622)	tcgttaacagcaatgataat T/C tagccatcctttatcc c/t a	3762
ABCA8	9	(intron 1 7639)	t t/c tagccatcctttatcc C/T agaaacaacaggctcataag	3763
ABCA8	10	(intron 1 7720)	tcctatgtttacaaaactgcc C/T tggagaacagaaaaagagaa	3764
ABCA8	11	(intron 1 9397)	cataatatatacatatgc G/A cacacacacacatatataca	3765
ABCA8	12	(intron 1 9519)	agtagttcatgttggaaaca T/C atgcttgagaaatgcagaaa	3766
ABCA8	13	(intron 1 12973)	ttgataacagggcacagggca T/C cacaataaataatgatggaaca	3767
ABCA8	14	(intron 1 13100)	cattggagtataggctacg T/C tttttgttggtttgcaggat	3768
ABCA8	15	(intron 1 13128)	ttgtttgcaggatatttctt T/C tcttaagaacttcatatta	3769
ABCA8	16	(intron 2 420)	caattagttttcttcaaaaa A/G gtagaaaagtgggaattgta	3770
ABCA8	17	(intron 2 505)	catataaaaaatcttgatta A/T actttgttatatttttaaaaa	3771
ABCA8	18	(intron 2 819)	gcaatgccttggaaactatct C/T ttaaaacacattgactttca	3772
ABCA8	19	(intron 3 915)	ttgtgttcgatagatcagta G/A ggtgactagtttaacaaatgat	3773
ABCA8	20	(intron 3 1539)	aaagggaaaatctgtggtgat C/T gccctgtcattcattcatag	3774
ABCA8	21	(intron 3 2341)	ttcctttcttgtcaacttc C/T gtccaaaattccactcaagct	3775
ABCA8	22	(intron 3 2882)	tattctatatctgtactct A/G ttaatatcttataataataa	3776
ABCA8	23	(intron 3 3314)	atttaaatatctatctctct A/G tatttaccatttcaaaattta	3777
ABCA8	24	(intron 4 89)	gaggttagtatgccaaaatta G/A agcatcactatctgtcataa	3778
ABCA8	25	(intron 4 3264)	ttccattggcctattatgcc C/T gtgttatatccagtggttaga	3779
ABCA8	26	(intron 4 3403)	aagagaccaacaaaaattctt C/G atcagcagaaaaagcacagga	3780
ABCA8	27	(intron 5 389)	gcttactgaatatataaaatt G/C agaaaagccatgccaaagcaa	3781
ABCA8	28	(intron 5 479)	tgagagtggtgagtaactca A/G aatgcctggactcc g/a aggtc	3782
ABCA8	29	(intron 5 494)	actca a/g aatgcctggactcc G/A aggtcccagcaggtcaatga	3783
ABCA8	30	(coding region 792 (Ala 264 Ala))	atgggtcttcgggattcagc G/A ttctggtgagtcaaaacgcag	3784
ABCA8	31	(intron 6 200)	cctcccaagtagctgggact G/A caggtgccg a/g ccaccatgcc	3785
ABCA8	32	(intron 6 210)	agctgggact g/a caggtgccg A/G ccaccatgcctggataattt	3786
ABCA8	33	(intron 6 1751)	gtgagttattattgtgttgg C/T ttgacagctgtttgtttttt	3787
ABCA8	34	(intron 6 1808)	atttcattatagttttcaaa G/T aatatgttaaaaaacaaaagaa	3788
ABCA8	35	(intron 6 2412)	tattcctaattctaaagaat T/C ctgccccaaaacttttacctt	3789
ABCA8	36	(intron 6 2506)	tggatgaataaagtgaatgaa G/A agttatcttaga a/g tccattt	3790
ABCA8	37	(intron 6 2519)	gaatgaa g/a agttatcttaga A/G tccatttgcaggtcttcttt	3791
ABCA8	38	(intron 7 28)	agtgaattaaatatcttcc A/G tccacctatagcctaaaaat	3792
ABCA8	39	(coding region 991 (Gly 331 Ser))	taaagaaaatctttcctcacc G/A gcctggctcgtgttctctctc	3793

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA8	40	(intron 8 74)	tggatccataggctgtaac C/T atttacaactcagcattgt	3794
ABCA8	41	(intron 9 1417)	acacatacttaaatatattt T/C ctctgttctacttttgtttt	3795
ABCA8	42	(intron 9 2504)	agaggaattatggtttgg G/A aatgaataaaagcagaaata	3796
ABCA8	43	(intron 10 2013)	tggccaaagatctttccaac C/T tgtccagtggttcacagga	3797
ABCA8	44	(intron 10 2378)	ctgaagaaaattgtcacttt G/A aagtatcttttcttttttc	3798
ABCA8	45	(intron 11 -697)	aaaaaaaaaaaaaagagag A/G gagaagaaaaatatgtta	3799
ABCA8	46	(intron 11 -528)	tataaagttagaaaaaat G/T a a/g tatgttttagaaaatagat	3800
ABCA8	47	(intron 11 -526)	taaaagttagaaaaaat g/t a A/G tatgttttagaaaatagatgt	3801
ABCA8	48	(intron 11 -342)	ctcaaggagtttttagccat G/A taataactttactattaatct	3802
ABCA8	49	(coding region 1632 (Asn 544 Asn))	ggttcagtcaccatctataa C/T aataagcttttcagaaaatggc	3803
ABCA8	50	(intron 14 252)	cttattgcaaaaataagtga G/A ttgagtttctaagagatcaa	3804
ABCA8	51	(intron 15 130)	ttttgttttgagacggagt A/C tcatcatctcggctcactg	3805
ABCA8	52	(intron 16 534)	acatacatcttcatcctaaat A/G cacattttatggtgacaaca	3806
ABCA8	53	(intron 16 588)	gaatcatcaggaaaagtgtta C/T gcaaatcttgatttagtactt	3807
ABCA8	54	(intron 16 645)	atttaagaaaaattttaga C/T gtttttaggtggaatgaagaa	3808
ABCA8	55	(intron 17 431)	tgtcaggtttttctttttttt T/A ttctttatgttagaaaattgg	3809
ABCA8	56	(intron 17 1390)	gctgtaaaactcgttttttga C/A ttaggtaacctcatgattcta	3810
ABCA8	57	(intron 17 2452)	cacgttatacctatagtaac G/A cggaaga g/c tctaactcatgag	3811
ABCA8	58	(intron 17 2460)	acctatagtaac g/a cggaaga G/C tctaactcatgagat g/c cttag	3812
ABCA8	59	(intron 17 2475)	gaaga g/c tctaactcatgagat G/C cttagcagagccaatctcta	3813
ABCA8	60	(intron 18 152)	gaagaagcacaggagagagg C/T agaattcttgacatccaaagg	3814
ABCA8	61	(intron 19 7477)	aaaatctattttgaaagaca C/T ttggaactaaaaaaatcttt	3815
ABCA8	62	(intron 21 196)	ttgttttaagtaaaaaataaaa T/C g/c acaaaaacatttttcaaag	3816
ABCA8	63	(intron 21 197)	tgttttaagtaaaaaataaaa t/c G/C acaaaaacatttttcaaaga	3817
ABCA8	64	(intron 21 287)	actgtgtgtgtgtgtgtgtgt G/T gggggagggatagcattggg	3818
ABCA8	65	(intron 21 403)	cctgcacaaatgtgcacatgt A/G ccctaaaacccataaagtataa	3819
ABCA8	66	(intron 21 1207)	ccagcc g/a gagtgcagtggc A/G ggatcatagctcactgtaac	3820
ABCA8	67	(intron 24 692)	ctctagatatagacaaaaa A/C caagggtgcacaaatggccatg	3821
ABCA8	68	(intron 25 212)	cctgatttaatatatgggaag G/A aagggttaagggttagtgga	3822
ABCA8	69	(intron 26 67)	ataaattttcagttctgtac A/G cactgtgaaaacttcttttat	3823
ABCA8	70	(intron 27 515)	gtgtctcccaaacccacatca G/T ttctatctttttgctattaca	3824
ABCA8	71	(intron 27 661)	cctggatattatcagactta G/A aatggagaggaagaaagtcaat	3825
ABCA8	72	(intron 30 1967)	caaaaattagatacaagggg G/C tgaattgacttttaattgta	3826
ABCA8	73	(intron 31 112)	ctctaaatgctgacccaggt C/G aactgggttagattttacaac	3827
ABCA8	74	(intron 33 401)	cttctcactaggtgtgtgaga C/T gctgtgtttaaaatttttatgt	3828
ABCA8	75	(intron 35 484)	taacagcatcatcctg a/t tgt A/G tttattttcatagacagaaa	3829
ABCA8	76	(intron 36 258)	tttgcagtgtatgttggttaa A/G cctaagtcaaaactcagtta	3830
ABCA8	77	(intron 36 375)	atattattttactgtcttag C/G ctgtatattaaagaaactgac	3831
ABCA8	78	(3' flanking region 674)	gcgggtggacatagaaaagccc G/A gaagcttcttctgtgtgctta	3832
ABCA8	79	(intron 1 56-57)	ttttgctttttgtgtgtgagt TT/ Δ gtttcagaggtttttgtcttt	3833
ABCA8	80	(intron 1 1180-1191)	taaagtataataataaaaag (A)9-11 gaaattcctcctgtacagag	3834
ABCA8	81	(intron 1 9877-9885)	ctcctgcaaatagggtatgac (A)8-12 tcaactgagtacaaaaagct	3835

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCA8	82	(intron 1 12588)	gtactagagtgcactccttt T/ Δ gcaacaggacggccaaagga	3836
ABCA8	83	(intron 6 78)	tcaatgcacatcttttttttt T/ Δ gaaatggagtcctcgtctgt	3837
ABCA8	84	(intron 9 265)	gtatatggatatttttttttt T/ Δ agacctcttagaaaagctagt	3838
ABCA8	85	(intron 9 2666)	atTTTTTaaaggatatcca A/ Δ tagtcattctcaatttcttc	3839
ABCA8	86	(intron 11 -447)	ggatatctctgggtttttttt T/ Δ ctacaaactcaagttttttg	3840
ABCA8	87	(intron 15 8407)	gtggaataatttttgactta T/ Δ gcatttgggtcaataaaatt	3841
ABCA8	88	(intron 15 9458~9470)	tatgtcgagtaacatatgtc (T)11-15 ctgaatgccagcttgcagtt	3842
ABCA8	89	(intron 16 54~56)	tgaataatagtcacatcat CAT/ Δ aattattatcattacaacta	3843
ABCA8	90	(intron 17 433)	tcaggTTTTTctttttttt t/a t T/ Δ ctttatgttagaaattggac	3844
ABCA8	91	(intron 24 1462)	actccatctcaaaaaaa A/ Δ gagagaaaaaaattctgcat	3845
ABCA8	92	(intron 33 155)	caatactttgcaaaaaaa A/ Δ gatctttccctgatgatatt	3846
ABCA8	93	(intron 34 184)	atactgaatgggtttttttt T/ Δ ctctttctcatatgacctc	3847
ABCA8	94	(3' flanking region 1240)	atccttggaccacaaaaaa A/ Δ ctttatctgtgtcttgcgtg	3848
ABCB1	1	5'flanking - 196	gctttggagccatagtcatg T/C actcaaaatttatttttatct	3849
ABCB1	2	5'flanking - 16	tactctttacctgtgaagag T/C agaacaatgaagaaatctact	3850
ABCB1	3	intron 1 + 71660	cttgctggagggaagggtgct A/C gaaaataataccaaatcccaag	3851
ABCB1	4	intron 1 + 80091	gaaataatttcaagttctg A/C aataataatcatgacctatag	3852
ABCB1	5	intron 1 + 103126	gatatgaatcagaatttcac T/C gtgtctcaagaaaagggtcat	3853
ABCB1	6	intron 1 + 103148	tgctcaagaaaagggtcatg C/T gataaattaaatttctgctag	3854
ABCB1	7	intron 1 + 108428	aattaatttatcatcatctg A/G tcaccatttcacacaaactca	3855
ABCB1	8	intron 1 + 112042	cataaagtgaatgtcccca A/G tgattcagctgatgcgcgtt	3856
ABCB1	9	intron 2 + 491	gctctctgcttcgacgggg G/ Δ actagaggttagtctcacct	3857
ABCB1	10	intron 4 + 36	attaactattcaaaataactt C/T ggaaatttgacatctcctta	3858
ABCB1	11	intron 5 + 1596	ttagctctcttactgcttca T/C agtggagaatcaaaactt	3859
ABCB1	12	intron 8 + 1789	aaacaactctgaataattaaac C/T gctcctggaaccacagctca	3860
ABCB1	13	intron 14 + 24	agttgtccttgcccttttgc T/C ttctagaggtgcaaaaaata	3861
ABCB1	14	intron 14 + 81	tgcagggaagttaggaaacta C/T tataaatcggaagaagggaa	3862
ABCB1	15	intron 15 + 38	caaaccaacctgatttataa A/G cataagaacattctactact	3863
ABCB1	16	intron 17 + 73	gtttgggtgggctagggtac A/G gtaggagtgagggaacaagaga	3864
ABCB1	17	intron 18 + 564	caacagtaaaagttacaaact G/A aaaggaatgctctctgttta	3865
ABCB1	18	intron 18 + 2062	tttccctgaggaatgggttat C/T ctctgtgttctcttgagtcca	3866
ABCB1	19	intron 18 + 2293	ccacatcaggttttccccag A/G caccttgggacagtttgaaa	3867
ABCB1	20	intron 20 + 557	aaaaccctaaccattgacac G/A tgtgaatgttttctctgggga	3868
ABCB1	21	intron 21 + 24	cgtgcctccttctactaggt G/A ttgtcttaatttgccattt	3869
ABCB1	22	intron 21 + 2725	ctgacctgtttttggctgac A/G ggttttagttctctccctca	3870
ABCB1	23	intron 21 + 4725	tcttggatttaaaagatcca A/G agagatagggaatatgttaatt	3871
ABCB1	24	intron 22 + 8507	tgcacttaggaaaaaaacaa T/C atggaaatgtgtaaaaata	3872
ABCB1	25	intron 22 + 8537	tgtaaaaataactttttttt T/A aaaaaaaggacacacatttat	3873
ABCB1	26	intron 22 + 8565	aggacacatttatcagcat T/C atgacagactattacattt	3874
ABCB1	27	intron 22 + 8952	caccttgggttcatgggttg G/A caaagtactggcctgtacca	3875
ABCB1	28	intron 22 + 9520	caccaacaaatatcttttc A/G cagttgggtgggcatctggt	3876
ABCB1	29	intron 22 + 9836	agactctgacttagacatga C/T ggcaggggaaagagagactt	3877
ABCB1	30	intron 24 + 377	taaaaacacagatgtgttgta C/A taagtctgcaagcctttgg	3878

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCB1	31	intron 24 + 1493	ggggaggtgtccaggcacga A/ Δ catggagagctggacttgat	3879
ABCB1	32	intron 24 + 1495	ggaggtgtccaggcacgaac A/T tggagagctggacttgat	3880
ABCB1	33	intron 25 + 342	tgcagccttgatcttctggg C/T tcaagcgatcctcctgcctc	3881
ABCB1	34	intron 26 + 134	cttgataaaagtctgagagc C/G taaatatggtctccaaagtgg	3882
ABCB1	35	intron 26 + 1272	gtccttcaattttgtgtgga A/G cttaaaaaacaggactctaaa	3883
ABCB1	36	intron 26 + 1394	tattaagtgtgtgttaaag A/G ttgtgctataatgaattgta	3884
ABCB1	37	intron 26 + (1987-1988)	aagggctggaagagtgaaag (AAAG) gaggcattttgtccccagac	3885
ABCB1	37	intron 26 + (1987-1988)	aagggctggaagagtgaaag gaggcattttgtccccagac	3886
ABCB1	38	intron 27 + 59	gcagcctctctggcctatag G/T ttgatttataaggggctgggt	3887
ABCB1	39	intron 27 + 80	ttgatttataaggggctgggt T/C tcccagaagtgaagagaaat	3888
ABCB4	1	exon 3 + 3	aacaccccttattttatagat C/T caatgactgagtcagaat	3889
ABCB4	2	intron 3 + 45	cagcatctctacttatacca T/C gctctgctttaagggttctct	3890
ABCB4	3	intron 3 + 498	actcaaataggtggtaggag C/T agagacaattcaatacagac	3891
ABCB4	4	intron 3 + 515	gagcagagacaattcaatac A/G gacagaagtcttagatgaga	3892
ABCB4	5	intron 6 + 1030	tagttttgcccattgtagaatt G/C aaaaagttagatgggtgtt	3893
ABCB4	6	intron 6 + 1437	gttaagcctgcttcaatcaa G/A ttagttatatcttcttcttcta	3894
ABCB4	7	intron 6 + 2449	ttgacttagcgacactgtta G/A catacttatcttcttcttctgt	3895
ABCB4	8	intron 7 + 451	ccttgctgcacctgtgtgt A/C taagtttggcttattatagt	3896
ABCB4	9	intron 7 + 530	agtagagacagggtggcgat C/G acacggacagagactaactg	3897
ABCB4	10	intron 7 - 152	aacagaatcatgaaattaaag T/C tgttaaatgatttgaaggcct	3898
ABCB4	11	exon 8 + 40	aggataaattgtttatgtcg C/T ctgggtaccatcatgggcat	3899
ABCB4	12	intron 8 + 130	ctgggtgactccagatatca T/C agaaggagtgttaaaaattct	3900
ABCB4	13	intron 8 + 248	aatacacaggaaagcttctaa A/G taaagtaaggaagtcactct	3901
ABCB4	14	intron 8 + 531	ctaaagagtgaatggattca A/G tacgtcccttgggaactcac	3902
ABCB4	15	intron 8 + 4240	ctgaggttccagcttatctc T/A tagagatgtttacttagtct	3903
ABCB4	16	intron 8 + 4343	tgtagaagaaaaaaagggt C/T atattacaagagggtctgac	3904
ABCB4	17	intron 8 + 4677	cccaagatatcttcataact G/C tccatagtcctagggtgccc	3905
ABCB4	18	intron 9 + 113	tttaccagattccactatt A/G ttatcatttttctcccaaa	3906
ABCB4	19	intron 9 + 982	tgctctataacagtttttgggt T/A taagtttagtaaatgatta	3907
ABCB4	20	intron 11 + 241	gcactttgggaggcccaagggt A/G cataaatcacttgaggtcag	3908
ABCB4	21	intron 11 + 457	tccagcttgggtgacagagt A/G agacttcatctcaaaaaaaa	3909
ABCB4	22	intron 11 + 1337	tactcttggggagcctatca C/G cagggtgggtcagatatagc	3910
ABCB4	23	exon 12 + 3	tggttcttttctgtccagat A/T ctctcggcatttagtgacaa	3911
ABCB4	24	intron 12 + 1288	cagaccacactaaacctcag T/C tggacctcaggatgtcagtg	3912
ABCB4	25	intron 13 + 206	tgtagataagaaaaatagcat G/A tggtagaccattttgtgaaa	3913
ABCB4	26	intron 13 + 988	cagtcgggttggaaagcttgc T/C acccttcttctcacttccctca	3914
ABCB4	27	intron 13 + (1413-1414)	tttatcttctcacttatgtttt (T) ctcaagtttaagttatgcta	3915
ABCB4	27	intron 13 + (1413-1414)	tttatcttctcacttatgtttt ctcaagtttaagttatgcta	3916
ABCB4	28	intron 13 + 1931	cttgcaaatgttgctctctcc A/G caaaaaaaaggaaggat	3917
ABCB4	29	intron 22 + 767	acagtgggctgtagcataga A/ Δ cctgtagcaatccaccagca	3918
ABCB4	30	intron 23 + 784	agtatctcctaaactcttgc T/C atgcaggaaaaattatttta	3919
ABCB4	31	intron 25 + 158	gaaatattttactgtattaa T/C gtctagaacttaaatataag	3920
ABCB4	32	intron 25 + 2920	ctgagttcttctatacatct T/A ttccattctcctcggtgctgt	3921

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCB4	33	intron 29 + 411	cttctctacattgaattct A/C ggctctcgaactttgacttt	3922
ABCB4	34	3'flanking + 458	agaaatgaaattgccctac T/C gagctaaactctgaaagcaca	3923
ABCB7	1	intron 1 + 220	acggggcaggaggttcttggg C/A agaggacacctggagcgctg	3924
ABCB7	2	intron 1 + 480	agttaactcccttgctgaca G/A gcgtgcttcttgataggcca	3925
ABCB7	3	intron 1 + (512-513)	gtagggccaaaaccgtaact AT/Δ ctttccaaaacatagaccgc	3926
ABCB7	4	intron 1 + 1690	agttctccaaataaggcagat G/A aagtttaagataaaaatttga	3927
ABCB7	5	intron 1 + 5309	aattaatatcatattattgct G/A tattgtgtcagtggttatct	3928
ABCB7	6	intron 1 - 11274	tgcttcttttcaagccagcc A/G gctttaaaaaaaagttagct	3929
ABCB7	7	intron 1 - 11085	caggttttcagggtcatgt A/G gacctgaagaaaaaatgagag	3930
ABCB7	8	intron 1 - 10037	attctactttctcaacttct T/C ttattacattatctcatcat	3931
ABCB7	9	intron 1 - 21	ccactctgaacttccccct G/A ctttttttcttctgtcagcag	3932
ABCB7	10	intron 3 + (135-136)	ttctctaataaaaaaa (A) catatttaattgaccatagtt	3933
ABCB7	10	intron 3 + (135-136)	ttctctaataaaaaaa cattaattgaccatagtt	3934
ABCB7	11	intron 3 + 333	aaaaaatttgtgtgtgc G/A tgtgtttcaaggtttaattgtt	3935
ABCB7	12	intron 12 + 524	taaccactctgccctcagta C/T gaaacacagtgccgaacca	3936
ABCB7	13	intron 13 + 1543	atcctgtgaggtggggaagc G/A tatggctagcataaaataaa	3937
ABCB7	14	intron 13 + 2400	tgttaccttactgcctcatt C/G tcatttcttccccacctgctat	3938
ABCB7	15	intron 15 + 2201	ctccttcttaaccttagcaa G/C agtctggagatttactttatc	3939
ABCB8	1	5'flanking - 2272	ggcttaggcctaagggtga T/C gttggggccagtacccctga	3940
ABCB8	2	5'flanking - 2070	agctatgaaaaacaagacct G/A tccttcttagaggtagcaaaa	3941
ABCB8	3	intron 1 + 25	aaacggaaaaaacctactcag A/C gcgggccattgaccgcccgg	3942
ABCB8	4	exon 2 + 308	tgtgtgtcctgggggtagcc G/A tcgtgtgtgaggttccccca	3943
ABCB8	5	intron 2 + 334	ccccacttaaaaacatttgt C/G cctctgtcttccccattcca	3944
ABCB8	6	intron 4 + 12	cctgtccgggtactgccagc C/T gcagggtgcagagttggggt	3945
ABCB8	7	intron 5 + 547	agttcatagcattctcgtc G/A gccccctcaggcctgctgct	3946
ABCB8	8	exon 7 + 57	ggcaatgtcggactgtgcg A/T gccttcgccatggagcaacg	3947
ABCB8	9	intron 9 + 1231	tttccgcagctgcattggaca C/T cctcgcgtgccctgttctg	3948
ABCB8	10	intron 9 + 2164	cctcttgagggtccttcttag C/T gctgcctatgtggagattct	3949
ABCB8	11	intron 9 + 2645	ttcctgcctggtgcctcccc C/Δ ggctgccttttagcaagtgtc	3950
ABCB8	12	intron 9 + 2646	tcctgcctggtgcctcccc G/A gctgccttttagcaagtgtg	3951
ABCB8	13	intron 9 + 3229	cagggccgagcaggaggagtc G/A tgggtcagctgggctccctt	3952
ABCB8	14	intron 12 + (113-114)	tcctccactgccacaagggt (GG) ccttcttctcctgggacaatc	3953
ABCB8	14	intron 12 + (113-114)	tcctccactgccacaagggt ccttcttctcctgggacaatc	3954
ABCB8	15	intron 13 + 128	tgctctcgggagaccctggc C/T gtcttcacatgtcctcagct	3955
ABCB8	16	intron 13 + 305	atccagggtctagagaagcct A/G tagtggaggtgctgagctgc	3956
ABCB8	17	intron 14 + 135	acagttgtgtcaggggaagac C/G agaaccacagcccaaggga	3957
ABCB8	18	intron 14 + 159	accacagccaaaggggacag A/T gtctgtgtgtggggacaggg	3958
ABCB8	19	intron15+747	gttggagccttgggctctgt A/G agggggacagaggggaatcat	3959
ABCB8	20	3'flanking + 333	cctatccccctggctcacc G/A ggaccacagtcctccatctt	3960
ABCB8	21	3'flanking + 1168	ccctctttcaggggtgtgat G/A cagtgcattgatggagcagc	3961
ABCB8	22	3'flanking + (1719-1721)	tagaccgagcagcccgcc GTC/Δ ttcctaacctcgcctcggcc	3962
ABCB9	1	intron 1 + 69	aggggtgccaggccaggcag G/C gttggggggcgctctgggac	3963
ABCB9	2	intron 1 + 8873	tggggccagcacgtggggcc T/C ggaactacctcaaggcttc	3964

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCB9	3	intron 1 + 8940	accagctcagcctgcccagc G/A tgcacagggcaccagctgg	3965
ABCB9	4	intron 1 + 11410	agatccaaggatccagagg T/C tggaatgtgacctccgtgc	3966
ABCB9	5	intron 1 + 12863	gggaagccagatgcccaca G/A gctctgtgacttcacttcca	3967
ABCB9	6	intron 1 + 19731	gccaagtgtcaagatcgagc G/A agggaggggcctgacgaggg	3968
ABCB9	7	intron 1 + 29649	cagaatccagatgcccgtaa T/C gttgtaagaagcctgcaca	3969
ABCB9	8	intron 1 + 31793	ggccaggcggggagggtac C/T ggcagacccgggtggcaaaa	3970
ABCB9	9	intron 1 + 37537	agagtcacaggggttgggtg C/A cccgggaagggtggcatcta	3971
ABCB9	10	intron 1 + 38293	taccagcctgtgctttcag G/A gaccatgtgacctgtcaact	3972
ABCB9	11	intron 1 + 44661	ccgaggtgcctggcttcac A/G gcaggattgccgtcctgcag	3973
ABCB9	12	intron 1 + 49576	aaagtggccccgtggcttgt C/T cctgaagccctaaagcacc	3974
ABCB9	13	intron 1 + 64669	ccacagacaagccgggtagc C/A cacctgcagctcaacacac	3975
ABCB9	14	exon 2 + 448	cctggtttgggcccctgttc G/A tgtggacgtacatttcactc	3976
ABCB9	15	intron 7 + 3364	ggtaccaggagtcgggtatc A/G gtgggacaggaacgcgtgtc	3977
ABCB9	16	intron 11 + 113	gggccccaggagctctccca G/T actatcagcctcctgggctg	3978
ABCB9	17	exon 12 + 370	ccaggcctgcagcactgaa A/G gacgacctgacctgtcccat	3979
ABCB10	1	5'flanking - 424	tcgcgtctgcgcgtccgcc C/T ggtctgccggcgtgagaaaag	3980
ABCB10	2	exon 1 + 491	acaagggcggttgccgcc G/T cagcggccggactcccgag	3981
ABCB10	3	intron 1 + 37	ccacttccctccgcgggcc T/G ctcttctccacacgcgggg	3982
ABCB10	4	intron 1 + 217	actcgttgcagattttaca C/T ttgttttcttctgttgacacac	3983
ABCB10	5	intron 1 + 405	gcgtttatacttttttttt T/ Δ aaccataaacacattatttg	3984
ABCB10	6	exon 3 + 185	agggccggggcccaggcttc C/T gtaggcacagtagatggt	3985
ABCB10	7	intron 6 + 1269	caaatcacaaactgtgcctt C/G cacagaaatgggttggaac	3986
ABCB10	8	intron 9 + 632	ccccactccacttggttgag G/A gcagggtggatggtgatgggt	3987
ABCB10	9	intron 10 + 2373	tacctcagggcactcagaca G/C cctcaccaatcagaggctca	3988
ABCB10	10	intron 11 + 108	tccttttccctgttttttt T/G ttttttttttcttcttgagtg	3989
ABCB10	11	intron 11 + 2379	cattggtttttagtgatttc T/A gtgttgtgcacatccatcatca	3990
ABCB11	1	5'flanking - (2596-2595)	tgtggttttagagctttctct (TT) gagacatttttctgtaagggt	3991
ABCB11	1	5'flanking - (2596-2595)	tgtggttttagagctttctct gagacatttttctgtaagggt	3992
ABCB11	2	5'flanking - 1746	agctgaagtgaattaagcac G/A atcaactcagtaactcacact	3993
ABCB11	3	5'flanking - (326-314)	agggggaaaagtttaaaggta (T)9-12 gtcttgttatgtttttaagt	3994
ABCB11	4	5'flanking - 135	agagggtttcccaagcacac T/C ctgtgtttggggttattgct	3995
ABCB11	5	intron 1 + 511	aaataatagatgcaaaaaaa A/ Δ tgagctgtggatgcatgttt	3996
ABCB11	6	intron 1 + 581	aatttcagtttttaggtcac C/T caagccagtgaggatcacat	3997
ABCB11	7	intron 1 + (1938-1951)	aaagacgttttaagggtttt (A)10-13 gaaagaaaaaactgtag	3998
ABCB11	8	intron 1 + 4517	ggtttcccaacatctcatct G/A ataaaaaaataatttgcca	3999
ABCB11	9	intron 1 + 5651	aaagagaatagggttagtgga T/C tagtattcctgtgcttaatg	4000
ABCB11	10	intron 1 + (12200-12201)	aagagatggtctctagcccc CT/ Δ gtttgatttggggcacttac	4001
ABCB11	11	intron 1 + 13023	gtttggctactttgattaaa G/A aagaaaagagagataataat	4002
ABCB11	12	intron 2 + 739	cctgcatctattctgacctc C/T actggggaaaaacagtatgtg	4003
ABCB11	13	intron 2 + (921-922)	tattttgtagttcaaaaagt (CAGATCTTCTTCAGCTAATTAGAAATGT)	4004
ABCB11	13	intron 2 + (921-922)	tgctgtccatttgatttca	4005

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCB11	14	intron 3 + 644	agccacacgttttcttattgc G/A tgggaagtttataaaatggg	4006
ABCB11	15	intron 3 + 2231	agtgaacctgagattgagct A/G tactgaaatctctagaagag	4007
ABCB11	16	intron 3 + 2406	aaagggtggtctttaaattcc T/C tatgttttctctcatcaggtt	4008
ABCB11	17	exon 4 + 10	tttctcatcaggtttacaaga T/C gagaagaagggtgatggcgt	4009
ABCB11	18	intron 4 + 434	acaattatagtagtatttctca A/G tgccccacacagtttatcta	4010
ABCB11	19	intron 4 + 518	gtagatgagtagtagctaaaaac G/T aaagtcagctcctgaaataa	4011
ABCB11	20	exon 5 + 120	ggcacaatgacagatgtttt T/C attgactacgacgtttgagtt	4012
ABCB11	21	intron 5 + 320	gggaggtgaccccatgaattt T/C acttgagtatcatctccaag	4013
ABCB11	22	intron 5 + 16076	agaagaggtaacagtagaac T/G cctgattttacagcacacatc	4014
ABCB11	23	intron 6 + 303	atttgcaggtgtgtttgttag G/C gggcaggttagtagcttgaa	4015
ABCB11	24	intron 7 + 1141	aaaggattcagcagggcatga A/G gaaagaaaagcctttgcaaga	4016
ABCB11	25	intron 8 + 2463	ccattggctaataagcaatga A/C ctatgacatgggtctaactta	4017
ABCB11	26	intron 8 + 2677	tcaatgatgtttacagtgaga A/C tctaataattgtattaaaccc	4018
ABCB11	27	intron 8 + 2699	ctaataattgtattaaaccca T/A gccacatgtttaaataaatct	4019
ABCB11	28	exon 9 + 24	gtgtccaaagtttacggacta T/C gagctgaaggccttatgccc	4020
ABCB11	29	intron 9 + 108	caccttgggtctgtggcctcc A/G gaggaagtagtctgttcaaga	4021
ABCB11	30	intron 10 + 2475	taatcattccaaaaccacgga C/A ttatttcttaataagaacatg	4022
ABCB11	31	intron 10 + 2478	tcattccaaaccacggactt T/A atttcattaaagaacatgata	4023
ABCB11	32	intron 10 + 2711	tttacagattggaaaaagcca C/T tgaagtattgcaggtccaga	4024
ABCB11	33	intron 10 + 3539	agtactgttaattagtagtaca C/G ttgtgcacagagaaaaaatg	4025
ABCB11	34	intron 10 + 3623	tgcaagaaggtgttcttctca T/C gacctcctgagtttcagaa	4026
ABCB11	35	intron 10 + 3661	gaattcattataataaaaaataa A/T cacataatggagcgtgacat	4027
ABCB11	36	intron 10 + 5100	gggccactctttggccttggc A/G atagactgtggccaatgaaa	4028
ABCB11	37	intron 10 + 5292	gctatttggtaggaacatct G/A ggcatgatcaggtagccttc	4029
ABCB11	38	intron 10 + 5912	gagtaataattcagtaaaaaa A/Δ taaagtgggtatttttaaatca	4030
ABCB11	39	intron 12 + 116	tgtttccagtaataagggaat G/A gaggtgtctttctctgaaag	4031
ABCB11	40	intron 12 + 326	gataaatgacaagggaat G/C aacaatcaggaagcacaggt	4032
ABCB11	41	intron 12 + 335	caaggcaattacaacaacatca A/G gaagcacaggttcttcccaa	4033
ABCB11	42	intron 12 + 2572	cctcatccttgccaatgtttt C/T cttttactgtgtttttgatgg	4034
ABCB11	43	exon 13 + 23	tctaaatgacctcaacatgg T/C cattaaaccagggggaaatga	4035
ABCB11	44	intron 13 + 70	atggcagtagtattgatcaaa C/T agaaaggtgtagcatacatt	4036
ABCB11	45	intron 13 + (1578-1579)	ttattggcctctatttttttc (C) tgccatttggtcaagtatga	4037
ABCB11	45	intron 13 + (1578-1579)	ttattggcctctatttttttc tgccatttggtcaagtatga	4038
ABCB11	46	intron 14 + 32	catacattcctggggagaaa C/T aagaggtcatagaaggaaaa	4039
ABCB11	47	intron 14 + 80	cacaattatacacattttctt C/T tcgtatgatccccaaagtc	4040
ABCB11	48	intron 14 + 439	tattgtgtcaaaaaacaattc A/G ttgtatatctcctcattctaag	4041
ABCB11	49	intron 14 + (1262-1263)	cagccttgcattatatttt (T) gctgtgtgtgtctaacaggag	4042
ABCB11	49	intron 14 + (1262-1263)	cagccttgcattatatttt gctgtgtgtgtctaacaggag	4043
ABCB11	50	intron 14 + 1283	gctgtgtgtgtctaacaggag A/C aaagagacacggatttgctc	4044
ABCB11	51	intron 14 + 1339	tgagatagatatttaggacc G/A tgaccaatttttatttttgg	4045
ABCB11	52	intron 14 + 1359	gtgaccaatttttatttttgg T/C tgaataatcttattttgaagt	4046
ABCB11	53	intron 14 + 1480	tattgattagacaataaacc G/A tctggggaaggatatttct	4047
ABCB11	54	intron 15 + 370	ccttttctaattgtctgcaca G/A cctatttaagaatatattccca	4048

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCB11	55	intron 16 + (550-559)	aaagtttagtggtttctatca (T)9-12 gctactttctgatggacttct	4049
ABCB11	56	intron 17 + 188	ttctctccccaattcatgg T/G tttttggttagcttctcatc	4050
ABCB11	57	intron 17 + 194	tccccaattcatgggttttt T/G gttagcttctcatcttcttg	4051
ABCB11	58	intron 17 + (197-198)	caattcatgggtttttggtt (T) agcttctcatcttcttgggg	4052
ABCB11	58	intron 17 + (197-198)	caattcatgggtttttggtt agcttctcatcttcttgggg	4053
ABCB11	59	intron 17 + (289-296)	ggggacttcttttaaaaaa G/A(A)4 tctgtgttagtgttctctct	4054
ABCB11	60	intron 17 + 1070	tcagacttgggttttctctat C/T tttcttcttgagaacaagt	4055
ABCB11	61	intron 17 + 1651	tgttaaaatatctcattgta T/C atgctgacggatttttcttg	4056
ABCB11	62	intron 17 + 2226	ccttaagtctctctctatca T/A gcacttgttctcaccagct	4057
ABCB11	63	intron 17 + 2979	ctctctctcttctctcagc T/Δ ctactatttctactgttggct	4058
ABCB11	64	intron 17 + 3288	aatccccatatctctaccta T/G ccatctcatccatgaatctt	4059
ABCB11	65	intron 17 + 3289	atccccatatctctaccttag C/T catctcatccatgaatcttg	4060
ABCB11	66	intron 18 + 97	aatatgagtttcttaggtat A/G tatctagcagtgtttcaagt	4061
ABCB11	67	intron 18 + 98	atatgagtttcttaggtata T/C atctagcagtgtttcaagt	4062
ABCB11	68	intron 18 + 892	ctctgaaagtttagtgataca C/T cttatttgtgtttgaatcaa	4063
ABCB11	69	intron 18 + 2681	atgtatgagatcaagtcagg A/G tcaaatatttagacacccata	4064
ABCB11	70	intron 18 + 3780	ggaccatcctgtggggcaat C/G gttccagaaaaatgctggtat	4065
ABCB11	71	intron 18 + 5741	ctcacccgtataaaatacaac C/T gtagcaaaagttttctttt	4066
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag (C) tttttattcaagccacagca	4067
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag tttttattcaagccacagca	4068
ABCB11	73	intron 19 + 10022	tggctaagttaaaaaaaaa A/Δ gagattcaactataattgct	4069
ABCB11	74	intron 21 + 322	caagattcaatactgcccc C/Δ aggggtggtgaaacagggc	4070
ABCB11	75	intron 22 + 257	ctgttcaatttctctctcgca T/C agtgattcatctccacattcc	4071
ABCB11	76	intron 22 + 552	taattaataatcttctctctg G/C ggggtaaatgaggatggta	4072
ABCB11	77	intron 22 + 569	ttggggggttaaatgaggat G/A gtagcataaacacttctcaa	4073
ABCB11	78	3'flanking + 243	aaacaccacagaatgacata G/A aactaaaggcggcaggaatc	4074
ABCC1	1	5'flanking - 1661	cattcaccccttgggggaccc A/G ggccaataaaaaaatcacag	4075
ABCC1	2	intron 2 + 635	gatgtgccctacctgaccct T/C ggctcggggcagacttgggg	4076
ABCC1	3	intron 2 + 4769	gggcaggagtgagctcagg G/Δ ttcctggtccaaatgggttc	4077
ABCC1	4	intron 2 + 10069	tatggaggttttctctctct T/C tctgtgagtttctctctga	4078
ABCC1	5	intron 2 + (11965-11984)	taaaagccaatcaaatcaac (T)18-20 aaacaagccacgcatgtgcc	4079
ABCC1	6	intron 4 + 4302	caactgtaatcccagcacct T/G gggaggccaaggcgaagtga	4080
ABCC1	7	intron 4 + 4394	gtctttactaaaaatacaaa A/C attagctaggcatgggtggcg	4081
ABCC1	8	intron 4 + 4524	ccactgcgctccagcctggg T/C gacaagagtgaactctgtc	4082
ABCC1	9	intron 6 + 9045	aggctcttaaaactacccctgc G/A ctccaagaatcagtgccctgg	4083
ABCC1	10	intron 7 + (3059-3071)	agtcttttgtatgcaccact (A)11-13 gccattttctcctgcacgacc	4084
ABCC1	11	intron 8 + (886-889)	ttctatgtaacagtaagaaa GAAA/Δ agcagctgcccaattaaacaa	4085
ABCC1	12	intron 11 + 198	tgaattgtcaggttgatgtt C/A tcttgggtggcagtcgcttt	4086
ABCC1	13	intron 11 + 784	tgtggattgatccaggagat C/G aagcaatgttgcagtactc	4087
ABCC1	14	intron 12 + 122	agccttgcctgccagttgga C/G tcacttggggagccttaaca	4088
ABCC1	15	intron 12 + (3138-3148)	accccatctctattgaaaag (A)10-12 tcaatataaaaaacatttac	4089
ABCC1	16	intron 12 + 3227	tggatgtgttagtgatggg C/T tgatcccagggtcgccccag	4090
ABCC1	17	intron 13 + 2060	tgtcattacaactattcct T/C cttggtcaggttgggcaatt	4091

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactattccttc (C) ttggtcaggttggcacaatta	4092
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactattccttc ttggtcaggttggcacaatta	4093
ABCC1	19	intron 13 + 11776	gccacctggggaggggcccaa G/A cgggtctccaggggcctgtca	4094
ABCC1	20	intron 14 + 179	aaagaaagaaaaacacatttg A/T cttcttgacagagaaactcgc	4095
ABCC1	21	intron 16 + 219	ctagcacagaggggtccctg G/T gattgtaagttacagcagcc	4096
ABCC1	22	intron 16 + 310	ggaagtctctactttcaggtg C/T ggtgtgatccagggaactctg	4097
ABCC1	23	intron 16 + 890	ctctccagagaaaaacaattct G/T tagaaggcctgcattgaaaa	4098
ABCC1	24	intron 17 + 1171	aacccagggtcctcaagaagc G/A tgggaaataatgcatactcc	4099
ABCC1	25	intron 17 + 1332	cacctcttagtgtctgtgc A/G actgcacattttgtctcttgg	4100
ABCC1	26	exon 18 + 53	gattcagaatgattctctcc G/A agaaaaacatccttttttggat	4101
ABCC1	27	intron 19 + (3373-3379)	ccaagctaggcagctctaca CA/Δ tgtgactcactggtgcccggg	4102
ABCC1	28	intron 20 + 2730	gcgtgaggtctgtctctcta C/T ccttccgtccaggtgagcaa	4103
ABCC1	29	intron 20 + 2789	cttggccccagataggttcc G/C caccocccgttcttcttccc	4104
ABCC1	30	intron 20 + 2919	gatgcaaatgcgcgccacca C/T cctggcacctcgtgcgttca	4105
ABCC1	31	intron 20 + 3024	cttacatcaaaactggggcac C/T cccctctctcaccaccacc	4106
ABCC1	32	intron 20 + 9718	gtggctgcgtcagtgacga A/C caggagaagtgaaggctgag	4107
ABCC1	33	intron 20 + 9733	gacgaacaggagagaagtgaag G/C ctgaggtctatagggggtg	4108
ABCC1	34	intron 20 + (9895-9896)	gctgggtcccagtgctcacac AT/Δ gtgtgtgaggacaggtgca	4109
ABCC1	35	intron 20 + 9952	gggtatcattcttcttctctg G/A gtgtgtgggtatttgtgtt	4110
ABCC1	36	intron 20 + 11120	gcggagtgggggcagtagtc A/G tcatcactcactgagttattg	4111
ABCC1	37	intron 20 + 11147	tcaactgagttattgtgaacc G/A ggaagagatatgatctgtg	4112
ABCC1	38	intron 20 + (11629-11631)	tattttgaatatcacttctt CTT/Δ tcaatgcttgggaatcacgg	4113
ABCC1	39	intron 20 + 11864	gagctccagataccaccctgc C/T ccacaaaccagacagcctgtt	4114
ABCC1	40	intron 21 + 3860	tggagagtgcacatgggtggg G/Δ tgtgtgtcatatattcatat	4115
ABCC1	41	intron 22 + 878	ttaaagatcgtctctatttttg G/A caagtgttaataattctcca	4116
ABCC1	42	intron 22 + (4445-4446)	gtggggctggggctggggct (GGGGCT) ggggtgcgtgcatgtgctaag	4117
ABCC1	42	intron 22 + (4445-4446)	gtggggctggggctggggct ggggtgcgtgcatgtgctaag	4118
ABCC1	43	intron 23 + 62	gttgtggcttctgtctaatta T/C agaaatggatccttagagtc	4119
ABCC1	44	intron 24 + 3171	aacctgagggctcaccatat C/T tcaaacacagctgcacagct	4120
ABCC1	45	intron 24 + (3349-3368)	ctcttgaattgggtgccagc (T)19-22 ccctgcatttaccaaaatag	4121
ABCC1	46	intron 24 + 3369	tttttttttttttttttttt T/C ccctgcatttaccaaaatag	4122
ABCC1	47	intron 24 + 3584	ccaaggatttttatttttca A/G caacaaaggaaatgatttta	4123
ABCC1	48	exon 25 + 60	gagtcggtcagccgctcccc G/A gtctattccccatttcaacga	4124
ABCC1	49	intron 27 + 4539	tcttttttactcactgcagc G/A tgaggaaacaaatcacattta	4125
ABCC1	50	intron 30 + (1708-1714)	gacccaacactatctcctgg (T)6-7 ctccgggtcaagtgcgggc	4126
ABCC1	51	exon 32 + 652	tggagaaaaatcattttctcc C/T cttggcagtggtcccaggcc	4127
ABCC1	52	3'flanking + 158	ctgatgctcttccaggacac G/A aaagaacccatctttgaat	4128
ABCC1	53	3'flanking + (187-199)	ccatctttgaatatcaatga (T)11-13 aagtactgttccggggagaa	4129
ABCC1	54	3'flanking + 2227	cattagaataggtagtatca G/A ccagccgggcatggtggctc	4130
ABCC2	1	exon1+77	catattaatagaagagctctt C/T gttccagacgcagctccagga	4131
ABCC2	2	intron1+413	gataagttctagaactggca A/C ctaatgatattggactagaag	4132
ABCC2	3	intron2+192	atcaaaagtggctttagatttt T/G gcataagaatggtgactctt	4133
ABCC2	4	intron2+1020	agtgtgcgattacaagcct G/C agccacctgcacagcctctg	4134

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC2	5	intron2+3639	gtcatatccaccccccaaat C/A gacccaataggtacaatgaa	4135
ABCC2	6	intron2+3930	aaaactggcaggagaatttc A/G ctggagctgcatgcaggact	4136
ABCC2	7	intron2+3989	agttatgaaacccgatttttc C/T gggactggtgttcttagtct	4137
ABCC2	8	intron2+4078	aggtttccagatgtgttccc T/C aggcattcctcgtggttagga	4138
ABCC2	9	intron2+4171	cttattctttggtcagttgg C/T tttctaccacctcttagctt	4139
ABCC2	10	intron2+4257	gggtattggaaaagtctcttc G/A gctgctggaggctgcggtgt	4140
ABCC2	11	intron2+4436	ggactagtgaagaattaga C/G ctttcctgaataaaatagatc	4141
ABCC2	12	intron2+5227	taccataatttatgtgtcct A/G tatgacatgaatttcattgg	4142
ABCC2	13	intron2+5373	gttaaggatatgtgaactca A/G gtgtgtctataggataaaatt	4143
ABCC2	14	intron2+5538	ttaatgaggttaagcacatg G/T tcatatgttttaaaagccttt	4144
ABCC2	15	intron3+772	ggtataaggcaagatttttt A/T aaaaaattaatgtccttaatc	4145
ABCC2	16	intron3+1145	acatccttctccctcagtc C/T tcggttagtggcagtatctt	4146
ABCC2	17	intron7+1658	ggactcttaccagcttagtt G/T cctgggttttctaatactaaaa	4147
ABCC2	18	exon10+40	tggccaggaaaggagtacacc G/A ttggagaaacagtgaaacctg	4148
ABCC2	19	intron11+1672	aacttttttaagtctttaagac T/A ggaaggcctgtgtccttaggc	4149
ABCC2	20	intron12+148	ccctctcaccgcccccatgcc A/G cttttcctccttctgtaccat	4150
ABCC2	21	intron13+180	catgagttttctgagcccca G/C tttatctaactataaaatga	4151
ABCC2	22	intron13+1497	gtgcagggtccccctgatgc T/C atagccagttcctctttaga	4152
ABCC2	23	intron15+169	atgagctgaaagcaaaaggtt T/C tcagcccttccccctgataa	4153
ABCC2	24	intron15+949	ttccagggtgacacacatttagt A/G cctaatttgggaaatgttaa	4154
ABCC2	25	intron15+984	tgttaattctagtccaatccc A/C ttagtaagaaggagggggtc	4155
ABCC2	26	intron16+4059	catcctgatgcacagttatt C/T aaatttaagctccatttgtt	4156
ABCC2	27	intron19+10899	atgtatggagtatattatga G/A taaagtattcccatgctgtat	4157
ABCC2	28	exon22+51	caagcaataggattgttttc G/A atattcttcatcactccttgc	4158
ABCC2	29	intron23+56	tatactgaggatctttctga C/T agggaggaaattattatgtcc	4159
ABCC2	30	intron23+432	tggcagtagagcagggtgag G/A aggtattattctgcagaggaa	4160
ABCC2	31	intron23+734	tgagccaaactactgtactag G/A cactgggacactcaaatgaat	4161
ABCC2	32	intron23+801	atgggccagaccccaactcac T/G gatttttttagtgtatctgag	4162
ABCC2	33	intron26+154	ctggctccatcttttaccca T/C ggacgtattccttactcttc	4163
ABCC2	34	intron27+124	gggtccctaaagttttccttt C/G ctctaactcaaaaggacctaa	4164
ABCC2	35	exon28+52	cagattggcccagcaaaaggc A/C agatccagtttaacaaactac	4165
ABCC2	36	exon28+84	aacaaactaccaagtgcggtta C/T cgacctgagctggatctggt	4166
ABCC2	37	exon28+129	agagggatcacttgtgacat C/T ggtagcatggagaaggtagg	4167
ABCC2	38	intron29+154	ttccctaggatggacacgtc A/G ttccagaaactttgaaatgt	4168
ABCC2	39	intron30+91	gtgttaggtgatgcctggca T/C agaatttttcatccagggtctg	4169
ABCC2	40	intron31+170	gccaaaattttacatcacgc A/G aatgaaaaacgaacaaggtta	4170
ABCC2	41	3'flanking+371	gtgaattttttattataagct C/T gttctccttaaaactttatc	4171
ABCC3	1	5'flanking - 1064	tccttctgagcccccaacaag C/T ggtgctgagttggcgtctgg	4172
ABCC3	2	5'flanking - (827-820)	ctggggcttcacctgtcctt (C)7-8 aacctgatcaggctgaagc	4173
ABCC3	3	intron 1 + 1226	tattgtacatatatgacct T/G tgtgtgtgtacgcacacacg	4174
ABCC3	4	intron 1 + (1389-1399)	aaacttggggcaatggaggt (A)10-12 ctgtaaaaaggcataattgg	4175
ABCC3	5	intron 1 + 2070	gcgcacttctccttgatgct C/T gtgagctatacacacacctcct	4176
ABCC3	6	intron 1 + 4477	gcctgtagtccccagacagg G/A aaatggtcttgaacactgg	4177

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC3	7	intron 1 + 6189	agtaccatgaagtctgcc T/C gagggggcctctgccacgtg	4178
ABCC3	8	intron 2 + 268	ttgtatttttagtagagatg G/A ggtttgccatttttggcagg	4179
ABCC3	9	intron 2 + 376	tgtgccagccagcattctg G/C tttaatgagccctctccc	4180
ABCC3	10	intron 2 + 446	ctcacctgacctgcttgggg C/T catgggaatctgacaaactga	4181
ABCC3	11	intron 8 + 2323	gaggctgggtgagagcgt C/G atcgataggcgtgagcagcag	4182
ABCC3	12	intron 12 + 85	ctcattggactctacctga C/Δ accacctccacgctgctcag	4183
ABCC3	13	intron 19 + 1581	ttctgttgccctttcaatc C/T cctcattttatttttcacgc	4184
ABCC3	14	exon 22 + 180	aacacttccctgaggctggg C/T gtctatgctgcttttaggaat	4185
ABCC3	15	intron 30 + 1979	cctctgtctgttccatccct C/G tctacctcaccctccct	4186
ABCC3	16	intron 30 + 2340	atgcaccagccagcctgaa A/C gaatgagtaagagttggagg	4187
ABCC3	17	3'flanking + (555-558)	ttttcttgagcaagccaaca AAGA/Δ gtttcttttctgcaggtcag	4188
ABCC3	18	3'flanking + 1455	aacccctatgattagaact G/A tagtctgttttaggaagcca	4189
ABCC3	19	3'flanking + (1650-1659)	aattcacagttaacaaagct (A)9-11 tcttgtttataaaattacaca	4190
ABCC4	1	5'flanking - 644	attcatctgggtcactactct C/T gatttaccggctttcttga	4191
ABCC4	2	exon 1 + 67	ggagcggagcccgccggccac C/T gccgctgatacagcgcgacc	4192
ABCC4	3	intron 1 + (864-865)	ctttgaccagcttcttctcc C/T/Δ gtttccaatactttcacttc	4193
ABCC4	4	intron 1 + 21255	ggatggaatggtgagcaca A/G acctggcattttaaggaccg	4194
ABCC4	5	intron 1 + 21503	ctgttttctacccactgggg T/C cagcaaatcagccctttta	4195
ABCC4	6	intron 1 + 21900	tgatgctcaagcaatacaaa C/G tagaaaaatagaggctgg	4196
ABCC4	7	intron 1 + 22005	aaggggagtcatactactccag C/T gtgcatttttagtttctgtctt	4197
ABCC4	8	intron 1 + (22256-22264)	tttgtgtgttatttgcgtc (T)8-9 cctggaaggaagtgtggc	4198
ABCC4	9	intron 1 + 27784	ccagggaaactggtggcacac C/G ctgagtctgtaggtgggt	4199
ABCC4	10	intron 1 + 27821	ggctaaagactcacaacctg A/T gggaaaggccaggaagaa	4200
ABCC4	11	intron 1 + 27837	cctgagggaaaggccaggga A/G agaaaggaaagccatggccta	4201
ABCC4	12	intron 1 + 27880	gggtgttatttgggaccca C/T gccatccagccgacagag	4202
ABCC4	13	intron 1 + 40310	accaagcaggggaggtgaga A/T ttgtgcagactggggatat	4203
ABCC4	14	intron 1 + 40372	ttgcttgaataaaaggatgc G/A agtcaactgtattgtgaagt	4204
ABCC4	15	intron 1 + 40413	ttctttcaaatcccaattcct G/A actgatttcccttgcctcca	4205
ABCC4	16	intron 1 + 40958	gaagtttaccgaaaaaaca A/G caagaaactccccagtaaaa	4206
ABCC4	17	intron 1 + 50060	tgtggctatggggaacatga G/A gctcatagaaactgaagact	4207
ABCC4	18	intron 2 + 181	gcctgggggaaactcctgtt G/T cctgtgctccgtagaggtc	4208
ABCC4	19	intron 2 + 254	gaggtctgtccctctaggtg G/A aagtgttgtggttgaggag	4209
ABCC4	20	intron 2 + 290	aggaggttgtctggcttctc T/C gtgctactgatggggcttca	4210
ABCC4	21	intron 2 + 543	ttacgaagctttttcctcat T/C gtaggttctgggataaagaa	4211
ABCC4	22	intron 3 + 557	ggccttgcaactgggctggc G/A gtggtgccccagaggctgga	4212
ABCC4	23	intron 3 + 718	gtgtgtcttcttctgttctg G/A agtggattgctggttggag	4213
ABCC4	24	intron 3 + 801	acattccatgaaaaaatcaaa G/A acagccagaaggccaataac	4214
ABCC4	25	intron 3 + 1022	aggggtggatgttgtgtgtg T/C taaaaagggtggctttaa	4215
ABCC4	26	intron 3 + 1471	tgctgggggtgtccacagcga A/G gtgtttccacatggccccga	4216
ABCC4	27	intron 3 + 1490	tagtgtttccacatggcccc G/A atcagtttccagttggaaaga	4217
ABCC4	28	intron 3 + (1833-1834)	gggctgccagccacttgggg (G) tggggctcttaaccacaga	4218
ABCC4	28	intron 3 + (1833-1834)	gggctgccagccacttgggg tggggctcttaaccacaga	4219
ABCC4	29	intron 3 + 1870	cagatggtgactggactaca G/A tgagatttgggtaagctttt	4220

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Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC4	70	intron 8 + 5212	tcagggaattgtggtccaat A/T tgcagctagggaagaaatcc	4264
ABCC4	71	intron 8 + 5444	gaaccttaatttccctca T/G gtacatagtcttctggtggga	4265
ABCC4	72	intron 8 + 8969	tcacctcctgagtactag A/G gaaagtcagctagccctc	4266
ABCC4	73	intron 8 + 9106	ccagtgtcctaattaggtttac T/C gtgtgcatagttttttattt	4267
ABCC4	74	intron 8 + 9412	tgtttgtaagtgcaggatgg G/A ggacacatctctgcctgta	4268
ABCC4	75	intron 9 + 116	tggcttgcttatttactgaa A/G ctatgttacaaaagattctca	4269
ABCC4	76	intron 9 + 1384	cacggcaggaaagctgcaccc T/C ggggtctctctgagatggtctg	4270
ABCC4	77	intron 9 + 1459	agatttgggagcagagggcg A/G ggggtctctctgaggggtact	4271
ABCC4	78	intron 9 + 1632	agcagcactcctgcccagcc C/A cactgcctccgtccctccct	4272
ABCC4	79	intron 9 + 3630	gtaaatttttcatatttgaag G/A ttatcttgatctctcttattcc	4273
ABCC4	80	intron 9 + 3830	ggtgtccacccttcaggga C/T gccagattcatttttgaagaa	4274
ABCC4	81	intron 9 + 3940	gagcatttaccaaaagtgtgt C/T gtgcagaagaatagccactt	4275
ABCC4	82	intron 10 + 1504	gggcaaggctgcattgcagt G/A gcttattcttctgctcagtg	4276
ABCC4	83	intron 11 + 1817	ttttaggggagttgagaaaca G/C atggcaaatcttctgctagttt	4277
ABCC4	84	intron 11 + 3342	actggaattattctggtcttg T/C aggtacagagattgcatgtg	4278
ABCC4	85	intron 11 + 3377	catgtgtaatacaaaacctgc T/C ggacagaaaatggtccctgagc	4279
ABCC4	86	intron 11 + (3610-3625)	tcctggccaccctcccccgc (A)15-17 gtcttagaggaaaaatagg	4280
ABCC4	87	intron 11 + 3737	ataagttcatcgagctaaaa A/G tataattgagataaaaaaat	4281
ABCC4	88	intron 11 + 6953	agagtagagacaaaagaaatg C/A caccttgatctgttaagaggg	4282
ABCC4	89	intron 13 + 442	ctatgacaggttagaagtga G/C gtctctgggaccacaacatagg	4283
ABCC4	90	intron 13 + 459	tgacgtccttgggaccaca T/C agggcttctcttgggaaggct	4284
ABCC4	91	intron 13 + 633	tgaacacttaaaacccacag G/A catgtaggcctggccttgct	4285
ABCC4	92	intron 13 + 645	accacagggcatgtaggcct G/T gcttgcccttgaaactagtt	4286
ABCC4	93	intron 13 + 3306	aatgttctcaacgagttaga A/C aattggattgaacaatatgc	4287
ABCC4	94	intron 14 + 252	taatttagaaactttttgttt A/G cctctccatgacttaattc	4288
ABCC4	95	intron 15 + 124	tggattctgtggttttcaggg C/T tctattccatgatattggta	4289
ABCC4	96	intron 15 + 1552	tttggacttctgcctgtttc C/T ccacagctttgtcaacagag	4290
ABCC4	97	intron 16 + 157	cctactggtgttccatgtcc G/A ttacaaagacctgcgaaaaa	4291
ABCC4	98	intron 17 + 329	cccaaatgtgtgttcatttt T/C aaaaaatgtattttatctaa	4292
ABCC4	99	exon 18 + 56	atggaggaggaaaatgtaacc G/A agaagctagatcttaactgg	4293
ABCC4	100	intron 19 + 7202	aattaaaaataatgtttttt T/A cacataacaatgggttatatg	4294
ABCC4	101	intron 19 + 7445	ttttggcataaatttttaac T/C actagaatgttctgattcat	4295
ABCC4	102	intron 19 + 9018	tacgtgatggcctgaagaga A/G aaaccgtacattgggtctttt	4296
ABCC4	103	intron 19 + 11388	aagagttcagagatttttggg A/G gttggaggaaaaaaatagcat	4297
ABCC4	104	intron 19 + 11646	cattatttttaatttttttt T/A cctcctgttgggtgcagaat	4298
ABCC4	105	intron 19 + 13517	gagaaacttacattattttt A/T aaaaaatgctataactagtc	4299
ABCC4	106	intron 19 + 21033	tgggagtgccctgggctagc G/A ctgaaacttcagggttttcag	4300
ABCC4	107	intron 19 + 21095	agacttttgggaagaagcaga A/T ctgaaggtaagactgagtaa	4301
ABCC4	108	intron 19 + 21634	gtgctatttctgagcactca C/T ggccccattgggcatgggct	4302
ABCC4	109	intron 19 + 21715	tgttttgcacccccctaca C/T agcttgcctcatgcttctc	4303
ABCC4	110	intron 19 + 23090	agcaacagacttgagagactt G/A agcttctaaaaagtttcatta	4304
ABCC4	111	intron 19 + 24297	cgaatgtgatgaatgtggga A/G cctttttgagatagcagcac	4305
ABCC4	112	intron 19 + 25947	gagtctaaattaaatatgag C/A aaaactagaaaccatttaaa	4306

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC4	113	intron 19 + 30193	acagatttgcaagagtctac A/C aaagtataataattctgtca	4307
ABCC4	114	intron 19 + 36938	aagccgagtcattctcttgg C/G tatcttctgtggactacttt	4308
ABCC4	115	intron 19 + 37322	gttcccatgagggctgacct C/T gctcaccctggttaaccgc	4309
ABCC4	116	intron 19 + (38361-38362)	cggttagcttccctagct (T) gcggaggggtttctgagaaaa	4310
ABCC4	116	intron 19 + (38361-38362)	cggttagcttccctagct gcggaggggtttctgagaaaa	4311
ABCC4	117	intron 19 + 38746	taaagacatgctggtaatta T/C gtaaaataaagataaagtcac	4312
ABCC4	118	intron 19 + 42343	tgtaaggccagaaatcagcag C/T aacgattggatgttcccgga	4313
ABCC4	119	intron 19 + 44733	agcaggctggggaataaaaa A/ Δ tacagaggttatcattatgt	4314
ABCC4	120	intron 20 + (405-419)	aagggcaataacttaggcac (T)13-15 ggatagaaccaggtgtggtt	4315
ABCC4	121	intron 20 + (637-648)	ctaagtcttaagctgtcttt (A)12-13 ccaacaatcctacagaaaa	4316
ABCC4	122	intron 20 + 842	caagctggggcacttttttt T/ Δ tcccaagtgtttattttgga	4317
ABCC4	123	intron 20 + 843	aagctggggcacttttttt T/C cccaagtgtttattttgga	4318
ABCC4	124	intron 20 + 1347	ggacctctgatttttttttt T/ Δ cttttgcaaacatttttaaa	4319
ABCC4	125	intron 20 + (14553-14567)	tcctacacacccctcatct (A)13-15 tcagcagcttgactgagctt	4320
ABCC4	126	intron 20 + 15487	ggtttttccagtggtgatag C/T acatgtagaaagcagctactg	4321
ABCC4	127	intron 20 + 16161	gcgttgagtcataagccga T/C agtgccgcttgtgcacgcga	4322
ABCC4	128	intron 20 + 30891	acgtcccccactgttctatc C/T ttctcaagaagcaagcgttg	4323
ABCC4	129	intron 20 + 31180	ccttgacgtgctcatacat G/A tcatttgctattgtttatcat	4324
ABCC4	130	intron 20 + 31283	gtgttaaagctaaaaaaaa A/ Δ cctgttagacattttgact	4325
ABCC4	131	intron 21 + 4204	ttgaacctgacctgaataccc A/T gttggagataaaaaacagtgcc	4326
ABCC4	132	intron 22 + 1026	gtgccctactccacgttaaaa A/C tcttctgtagctcaactgag	4327
ABCC4	133	intron 23 + 377	gcctgggtgcatgaggttgag A/G aaaattctcagcaggagagt	4328
ABCC4	134	intron 25 + 4122	cccttttgattaaaaattgca C/G/T tgggacaagaaccaccccca	4329
ABCC4	135	intron 25 + 6418	ttgcactgaggttaattggctg C/A agaaattaaagtgaggggtat	4330
ABCC4	136	intron 25 + (8765-8775)	tgcactcctgtgatttttttc (T)5-11 aatcctgcgcctggatctc	4331
ABCC4	137	intron 26 + 67	tatgtttaattgctttttact G/C ttattgcttttttttaattgg	4332
ABCC4	138	intron 26 + (101-109)	taattggatgaagagattgt (T)8-9 caccacaatagagcattgttt	4333
ABCC4	139	intron 28 + 391	tagatatgatcttttttttt T/ Δ aaatctctattgtgaagtag	4334
ABCC4	140	intron 29 + 2569	atcctcttttttctataacg C/T accactatctccacattaaa	4335
ABCC4	141	intron 29 + 7820	gaaaaacaaacctgtgtcctg C/T ttggaggttcagcatattct	4336
ABCC4	142	intron 30 + 6269	tagatgttcttttgggcattg A/G aaagatgggttattctgttt	4337
ABCC4	143	intron 30 + 6320	gtttaataagggtttaattag C/T tctactttgtttaattacatt	4338
ABCC4	144	intron 30 + 6474	ctttgatgctatgggttttca A/G tccacagatgttcataactt	4339
ABCC4	145	intron 30 + 6519	ttccactatgaattatattt C/T ctgccatttttaacacacctt	4340
ABCC4	146	intron 30 + 6574	aatgggttttgggtcctaaatc C/T aactgggttcaaaaactagac	4341
ABCC4	147	intron 30 + 6680	aggtgtgtctcctgtatatg A/G cgtgggttaggttttactctg	4342
ABCC4	148	intron 30 - 704	acgtttatcagaaaaacctgt A/C tctcttctagttcagctaga	4343
ABCC4	149	intron 30 - 228	atctatgaatcagagtgatc A/G gaactaaaaatggatctacag	4344
ABCC4	150	intron 30 - (14-5)	acattcttttatgcttacc (T)9-10 ctaggatatacttcaaaagaa	4345
ABCC4	151	exon 31 + 146	agtcctgtccgaaggcattt G/T ccactagtttttggactatg	4346
ABCC4	152	3'flanking + 173	atthtttaaggagtaggaca A/G agttgtcacagggtttttgtt	4347
ABCC4	153	3'flanking + (430-440)	tgtaccccttactccccatc (A)10-11 tggatcacatggttaaggat	4348
ABCC4	154	3'flanking + 556	aaaggtgctttgatactgaa G/A gacacaaatgtgaccgtcca	4349

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC4	155	3'flanking + 1144	cctccctgaaattgcatata T/C gtatatagacatgcacacgt	4350
ABCC4	156	3'flanking + 1426	tttagtgactgaaattgca A/T cagtgatcataatgaggttt	4351
ABCC5	1	intron 1 + 628	tttgccacacagagccgcg G/C gtggctttgtgtttatcaca	4352
ABCC5	2	intron 1 + 1834	tgagttccagtgacctctc C/T gtttcaaaactgctcaccgcc	4353
ABCC5	3	intron 1 + 3055	agaaagtcttttaaaaaaaa A/ Δ ccaacctttctatgtatag	4354
ABCC5	4	intron 2 - 20280	gaatgcacgcgtactactaagta T/C ttttgtaagttcagacacca	4355
ABCC5	5	intron 2 - 20260	tttttgtaagttcagacacc A/T tctagaatctgtcttgacctg	4356
ABCC5	6	intron 2 - 19204	tgaataaaagcattcgcaca C/T ctaccacatttcttcgggac	4357
ABCC5	7	intron 2 - 19043	ttggctggcattaggctggc G/A ttacttcagctaacatgaag	4358
ABCC5	8	intron 2 - 18824	ttgaacactcttcaagatgc A/G tgcacagcactgaaccgagt	4359
ABCC5	9	intron 2 - 18807	tgcattgcacagcactgaacc G/A agtggctgtggtgcagataaa	4360
ABCC5	10	intron 2 - (18735-18734)	atagaagccttaaaactcaca (A) cactactctacatagatga	4361
ABCC5	10	intron 2 - (18735-18734)	atagaagccttaaaactcaca cactactctacatagatga	4362
ABCC5	11	intron 2 - 15903	taccaaagcctgtctcatgga G/A gtagaaagcaagactgacat	4363
ABCC5	12	intron 2 - 15901	ccaaagcctgtctcatgagg C/T agaaagcaagactgacatgt	4364
ABCC5	13	intron 2 - 15847	tgatggaaacctcaaaaggcc G/A tcttgcccagtcctccattta	4365
ABCC5	14	intron 2 - 15605	aggagacgccacagacactga C/T agctgtacctgacctgaggg	4366
ABCC5	15	intron 2 - 13571	ccgatttgtgccccagatacc G/A ctttatttgagggtgtgtgcc	4367
ABCC5	16	intron 2 - 13402	tacctgtgtgtgtccggcc G/T ccaggaaagggtgtgtgtgt	4368
ABCC5	17	intron 2 - 13325	ccagagggcctccgtgcagg G/C gaaaagcccttgggttgcct	4369
ABCC5	18	intron 2 - 7293	tttgttaggataaaaattgca C/T tgagtgcctgttcttaaacca	4370
ABCC5	19	intron 5 + 374	ccgggtgtgtgagccagcac C/T gggaacataccaagtgcctg	4371
ABCC5	20	intron 5 + (2212-2213)	cgcctcctgcagtgctctct CT/ Δ tggtagtgtaactctgtct	4372
ABCC5	21	intron 5 + 3283	accagagagagtgctgggtt C/T tggaaattcagcgtagctacc	4373
ABCC5	22	intron 5 + 3469	ttggctttctttgtgtgtgg C/T tttttgttttattttttgtca	4374
ABCC5	23	intron 7 + 443	cacttttattaaagacagta C/T gattacataaacatttggccc	4375
ABCC5	24	intron 7 + 458	cagtacgattacataacatt T/G ggcctcctctagcaagcagg	4376
ABCC5	25	intron 9 + 176	caaaaacaaaacaaaacaa A/G acaaaaaaaaataaccacat	4377
ABCC5	26	intron 9 + 214	catatggagatgatgtgtg G/T tctctccttacttggacctg	4378
ABCC5	27	intron 10 + 703	tgtgggctggaattccttga T/C gttgccactgcataagattag	4379
ABCC5	28	intron 10 + 3580	catggggctggagctgtgaa A/G accagtaggtactggcatgt	4380
ABCC5	29	intron 10 + 3655	atcctttgaataaactcttta G/A gggagagaaaatgatggaaaat	4381
ABCC5	30	intron 10 + 3854	gaagtttagaatcatgcacac T/C tcggggaagataggatcagg	4382
ABCC5	31	intron 10 + 5040	ctttgaagacatgagagttt C/T ttggcaagaagatgttctct	4383
ABCC5	32	intron 10 + 5316	cagttaaatgtcattaggtc C/T gctttaggctggctgagggg	4384
ABCC5	33	intron 12 + 234	tgactgttgtcccagctgga G/A ccatttggtctcatgacctc	4385
ABCC5	34	intron 12 + 300	tgcacaggtatgccctgtgt A/G ttgaaaaatgtcagagataag	4386
ABCC5	35	intron 12 + 318	gtattgaaaaatgtcagagat A/G agagatgagcagacacacctta	4387
ABCC5	36	intron 12 + 1545	gtagcatccctaaacccaaga C/T aaatgtctactatcagtcctc	4388
ABCC5	37	intron 13 + 20	ggcaaggaatgtttggcttc T/C gtcattgctttccatcttggc	4389
ABCC5	38	intron 14 + 278	ttctatccagatatatttttaa A/G actacaagtaagcgtgtgca	4390
ABCC5	39	intron 16 + 1663	tgactggagactttttttttt T/ Δ aaatattatagatcaattc	4391
ABCC5	40	intron 16 + 1664	gactggagactttttttttt A/T aatattatagatcaattca	4392

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC5	41	intron 17 + 20	ggtaatggccttttttggaa T/G ttttagatttgatcaaaag	4393
ABCC5	42	intron 18 + 232	ggacacctgcaggctatctg C/T tctcatccgttggtattag	4394
ABCC5	43	intron 19 + 249	ggaccagtaggaacacagacc G/A tccctggccctgaccactc	4395
ABCC5	44	intron 20 + 846	ttaaccagaagaaaaaaggc G/A gtgggtg99ggagacagcca	4396
ABCC5	45	intron 20 + 1154	tcttgagacgaaaaaataa A/Δ tcagagcatccagggtttcta	4397
ABCC5	46	intron 22 + (1424-1425)	gaggaatgcagcggaatat (AT) caactctgggttttaacaggg	4398
ABCC5	46	intron 22 + (1424-1425)	gaggaatgcagcggaatat caactctgggttttaacaggg	4399
ABCC5	47	intron 24 + 132	atccacagaatctccagca A/G tctctcaaccgtgcttgga	4400
ABCC5	48	intron 24 - 874	gtgctggagaggttaggatt A/G cggtcagtggtggtacaaa	4401
ABCC5	49	intron 24 - 630	tgatgataaaaaattaccaa G/A cagttatatcacagcatttt	4402
ABCC5	50	intron 24 - 102	acaggtggcagctacctc G/C tgggtactatggtgtgtcc	4403
ABCC5	51	exon 25 + 120	taccgagaaaaacctccctct C/T gtcttaaaagaagtatcctt	4404
ABCC5	52	intron 26 + 263	ctgggcccagggtctctgctc C/T gtgacttcggacaagtatt	4405
ABCC5	53	intron 26 - 3257	ccgaggtgaattgtgtgt T/C gtctcacactttggggagata	4406
ABCC5	54	intron 27 + 873	gtttttctctctgctctatc G/A ggattcttctcatttgaaga	4407
ABCC5	55	intron 29 + (2733-2734)	gtgtccaaaagggaaggacacg (TGTCCAAAGGAAGGACACG) cttatgttctctcttgtggcc	4408
ABCC5	55	intron 29 + (2733-2734)	gtgtccaaaagggaaggacacg cttatgttctctcttgtggcc	4409
ABCC5	56	intron 29 + 2959	acatgattttccacggctac A/G tagaagtcctcataggaat	4410
ABCC5	57	intron 29 + 4020	aataaaaaataaaggggga G/A gtgcacgcagggttagtga	4411
ABCC5	58	exon 30 + 684	ccctctgccgctctccccc G/A gccgtccagggttggtgtg	4412
ABCC5	59	exon 30 + 947	agtctatccacagagagtcc C/T actgcctcagggttccctatgg	4413
ABCC5	60	exon 30 + (1145-1160)	tcaccgcagtcgtcgcacag (TC) 6-8 ccctcaaaagtctgcaacttt	4414
ABCC5	61	3'flanking + 4	attattttggattttgtaaa A/C ctcttcgtgtatcaaaacaat	4415
ABCC5	62	3'flanking + 2008	ccgcagacctggcacagcc C/Δ tgttctcaaaagggtgagctcc	4416
ABCC5	63	3'flanking + 2052	ccagctaggacagggccagc A/G ccaggcagttaggaccgtgg	4417
ABCC7	1	5'flanking - 834	gctaaaaacactccaaagcct T/G ccttaaaaaatgcgcactggg	4418
ABCC7	2	5'flanking - 729	cctccttgccagatttttttt T/Δ ctctttcagtcagtggtccta	4419
ABCC7	3	exon 1 + 125	tagcaggggaccccgccgccc G/C agagaccatgcagaggtcgc	4420
ABCC7	4	intron 1 + 6200	ctatgtgagacgttaagaag G/A tagaggtggccaagaaggaa	4421
ABCC7	5	intron 1 + 7538	agttctctttcttagcatgg C/A ctacagaggtgcaactacct	4422
ABCC7	6	intron 1 + 13519	gaaacttaaatctttagtca T/C acaattgtgtctacatactg	4423
ABCC7	7	intron 1 + 14110	attacacagttatttttttt T/Δ aattttggggaaagtgcatt	4424
ABCC7	8	intron 1 + 14293	gccaggcagattcctgactc C/Δ tataaccagagcttatcag	4425
ABCC7	9	intron 1 + 14316	taaccagagcttatcagag C/G atttatgtcccccagaagaa	4426
ABCC7	10	intron 1 + 14433	cagaataacaatgatggctc G/A gaaaaatatgggtattttctg	4427
ABCC7	11	intron 1 + 14824	acgttttgacagttgacaaa G/C tttctttctttaaagctttaa	4428
ABCC7	12	intron 1 + 23401	aataattttgaaaaatcacta C/G ggtatcctgcatagtgattt	4429
ABCC7	13	intron 3 + 879	gaaaaatttcagtttcataca C/A ccccatgaaaaatacatatta	4430
ABCC7	14	intron 3 + 922	acttatcttaacaaaagatga G/C tacacttagggccagaatgt	4431
ABCC7	15	intron 3 + 933	caaagatgagtacacttagg C/T ccagaatgttctctaatgct	4432
ABCC7	16	intron 3 + 13704	ttttccaaaataaaaaaaa A/Δ tcaggtgatattctgtaaatg	4433

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC7	17	intron 3 + 13758	tattaaagaacatgatgctt A/G aaacagattagggaaaacta	4434
ABCC7	18	intron 4 + 240	ctctgttagttagttttttt T/ Δ ctctaatcatgtttatcatt	4435
ABCC7	19	intron 4 + 376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	4436
ABCC7	20	intron 4 + 586	tgccagacaagagacacaaa T/C tgccgaggcatcatttaggt	4437
ABCC7	21	intron 4 + 1089	tttcaatctgaacattttac G/A taagtgaagactttttagga	4438
ABCC7	22	intron 4 + 1615	aaagttaggtggtattgtat C/T tgtcttccctttctcaatgtt	4439
ABCC7	23	intron 4 + 1946	aatacaaaaacacttgagct T/C tgcctatacttttcaagaat	4440
ABCC7	24	intron 6 + 783	tatctaagttttggagtcac A/G tagcactttgtttgaatccc	4441
ABCC7	25	intron 6 + (1104-1131)	gattgattgattgattgatt (GATT)6-7 tacagagatcagagagctgg	4442
ABCC7	26	intron 7 + (731-732)	gtagcaatgagaccattttt (T) cttcagttgagctccatgtt	4443
ABCC7	26	intron 7 + (731-732)	gtagcaatgagaccattttt cttcagttgagctccatgtt	4444
ABCC7	27	intron 7 + 1434	gaatgtttggtgttaacctg T/C ataactgtgcatgaaattgt	4445
ABCC7	28	intron 8 + 752	catgctctcttctcagtcacc A/G ttccttcatttatatcaccta	4446
ABCC7	29	intron 8 + 1109	tatggccaagacttcagtat G/A cgtggacttaattcttccct	4447
ABCC7	30	intron 8 + 1312	atgaagacattcattttttt T/ Δ ctccgtccaatgttggatta	4448
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgtgt (GT) ttttttaacagggatttggg	4449
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgtgt ttttttaacagggatttggg	4450
ABCC7	32	intron 10 + 2119	gaacactttatagttttttt T/G ggacaaaaagatctagctaaa	4451
ABCC7	33	intron 11 + 3867	tttttcttcaagaaaattaga A/ Δ gaggggagaaaattggttaa	4452
ABCC7	34	intron 11 + 11844	tgaatcaaaatcatctaaaa A/ Δ gcttcagaaaaccagacttt	4453
ABCC7	35	intron 11 + 12144	atattaacagagttacata T/C acttacaacttcatacatat	4454
ABCC7	36	intron 11 + 20975	gtgtggatagtaaatgccag G/A gtaaatcacatagcatctaa	4455
ABCC7	37	intron 11 + 27057	atggaagagaagtttttagta G/A aggggaggaaggaggaggtg	4456
ABCC7	38	intron 11 + 27131	gagagagacttttttttttt T/ Δ aaggcgagagtttactacct	4457
ABCC7	39	intron 13 + 152	gtattaaactcaaatctgac T/A gccctactgggccaggattc	4458
ABCC7	40	intron 13 + 287	tttgcagtatcatgtgccttg T/C gatataattacttttaatta	4459
ABCC7	41	intron 15 + (85-86)	atacatatatatgcacacac AT/ Δ aaatatgtatatatacacat	4460
ABCC7	42	intron 15 + 106	taaaatatgtatatatacacac T/A gtatacatgtataaagtatgc	4461
ABCC7	43	intron 15 + 3341	ggaagtataaaatttgtaaat A/C actgagaccccaacttacaa	4462
ABCC7	44	intron 15 + 5556	tgctattgactaaatagtaat A/T atttttagggcagcttttatga	4463
ABCC7	45	intron 15 + 5919	tggtagttctatgttggaac C/A gtgaggaataaatttttatat	4464
ABCC7	46	intron 17 + 2479	caaaaagggtatggaaagtcag A/C ggagaaggagacccctatgt	4465
ABCC7	47	intron 18 - 81	aagtatgcaaaaaaataaaaaa A/ Δ gaaataaatcactgacacac	4466
ABCC7	48	intron 19 + 751	cattaataaaaaataacaaatc A/G tatctattcacaagaatggca	4467
ABCC7	49	intron 19 + 820	tgacattttgtgatattgatta T/C tctaatttagtcttttttcag	4468
ABCC7	50	intron 21 + 1532	ttacctttaacttttttttt T/ Δ agtttgatcagctctcttta	4469
ABCC7	51	intron 21 + 1607	atgcttttggagttgggtct C/T ataaatgtatagaaaatgttt	4470
ABCC7	52	intron 21 + 11260	atgtggaacaatcatgacta T/C atgcttttacttttctctat	4471
ABCC7	53	intron 22 + (130-131)	agaatcaaatattaaacacac AT/ Δ gttttattatatggagtcac	4472
ABCC7	54	intron 23 + 1837	ctgtcctaagaagtttaaaaaag A/ Δ aaaaaaaagggaaggaa	4473
ABCC7	55	intron 24 + (7100-7112)	cctttacaactcttttagaca (T)12-14 agtttaacatgttacaac	4474
ABCC7	56	intron 25 + 237	actcttcccccttgtcaaca C/T atgatgaagcttttaaatat	4475
ABCC7	57	exon 27 + 115	gggtgaagctcttttccccac C/T ggaactcaagcaagtgaag	4476

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC7	58	exon 27 + 334	ggatgaattaagtattttttt T/ Δ aaaaaaacaacatttggtaa	4477
ABCC8	1	5'flanking - 1099	aaaggggctgaaggggtctt T/C cttttgtgttccccctgactg	4478
ABCC8	2	5'flanking - (424-422)	caccacaccaccaccacac CAC/ Δ aaggtaacgttctgccccac	4479
ABCC8	3	intron 1 + 1212	agcctgggcaacatagttag A/G cccccccccccttttctaca	4480
ABCC8	4	intron 2 + 1003	aggaggactgtgaatcccag C/A ctgcatgtttgggtcggatt	4481
ABCC8	5	intron 2 + 1253	catctcaactaaggagaatc C/T agtaaccagcaaggatgaga	4482
ABCC8	6	intron 2 + 1382	cccagactgcactcctgcag T/C gctgcctggctcctctgtagtt	4483
ABCC8	7	intron 2 + 2371	tttcagagctgtctggaat T/A tagggggcaggtgggagggg	4484
ABCC8	8	intron 3 + 1957	ccctacccctagcccagggg C/T cccacatgagtatgaatgg	4485
ABCC8	9	intron 3 + (2088-2089)	agagaaccccttcattaaaca (CCA) gggcgtggctgaccagtgtc	4486
ABCC8	9	intron 3 + (2088-2089)	agagaaccccttcattaaaca gggcgtggctgaccagtgtc	4487
ABCC8	10	intron 3 + 2204	taaagcacaagtattatcccc G/A tggatggatttgccttttc	4488
ABCC8	11	intron 3 + 2286	ttatctcccttgaaaggac A/G ctccacagagccagaaaattc	4489
ABCC8	12	intron 3 + 2312	cagagccagaaaatttctagaa C/G agggaaaaagtggaggggagg	4490
ABCC8	13	intron 3 + 2356	ctgtgaactgcaggagacaga A/G ggaatgggtatttgggagaa	4491
ABCC8	14	intron 3 + 2359	tgaactgcaggggacagaaagg A/C aatgggtatttggagaaatgg	4492
ABCC8	15	intron 3 + 2370	gacagaaggaaatgggtatt G/A ggagaatggccagcccctcca	4493
ABCC8	16	intron 3 + 2382	tgggtatttgggagaatggcc A/G gccctccaaggggctgatgt	4494
ABCC8	17	intron 3 + 4910	ggggacagccttcagctgtg G/A aattcctccagtcctctagaga	4495
ABCC8	18	intron 3 + 4969	cattatccagtcctcaggcc A/G tgagagcagaagggccgatgc	4496
ABCC8	19	intron 3 + 5003	ccgatgcttctgcctcccat C/G ctaatgtcctcctgcaggga	4497
ABCC8	20	intron 3 + 5019	ccatcctaattgtcctcctgc A/C gggacccaaggtggatggca	4498
ABCC8	21	intron 4 + 14	ggtgagggtaagcaggccac C/T tgggccagggtggggtggga	4499
ABCC8	22	intron 4 + 187	agacactgcactctggcccac G/A tgtgtcttaccacagggtcc	4500
ABCC8	23	intron 4 + 204	caagtgtctctaccacagg G/C tcccagagggagaggggggt	4501
ABCC8	24	intron 4 + 254	gttcgctgaggttggcggat G/A actttccgtagaaaaggggaag	4502
ABCC8	25	intron 4 + 357	tgtattcatatcgtcacgct G/C gtaaatgaaatgagtaagtgt	4503
ABCC8	26	intron 5 + 92	ggcattaggtcaaaaatcctg G/A tgggacaaaaggggaaactg	4504
ABCC8	27	intron 6 + 4205	tctgtagaaagtacatgggg G/A catgaagatcatttggcttga	4505
ABCC8	28	intron 6 + 5519	gattccccagggaatgttaaa A/C aggaccgggtcttctcctaaac	4506
ABCC8	29	intron 6 + 5575	tctgaccagtagtaccagccag G/C ggggcaagtttccatcccc	4507
ABCC8	30	intron 6 + 6587	gttgccatctgagatcttgc C/T ggaagtacacaaagagaccct	4508
ABCC8	31	intron 6 + 6747	ttccactggcctttttctgct C/T agtaattgtctacattacagg	4509
ABCC8	32	intron 9 + 191	gaggaagctgcctcccggtg A/G ggacaggaagcgggcatggc	4510
ABCC8	33	intron 10 + 1963	ccaggagtcacaacctccct T/G tgtccagctagaccatgggtg	4511
ABCC8	34	intron 10 + 2724	cctgggacatgttttcttat A/G taaacagcatcaaaaagatgt	4512
ABCC8	35	intron 10 + 2938	gccccccaggactcctcac G/C tgtccaagtcacctagggag	4513
ABCC8	36	intron 10 + 3094	tccgaggatgtgtttttttt T/ Δ ccctccgttagtcagcagtg	4514
ABCC8	37	intron 10 + 3368	tcctgctcatatgcggccac A/G tcagacttcttgggcaggcaa	4515
ABCC8	38	intron 10 + 8897	ggtattgattaaaagcctca C/T gggcagagaaattcggccatc	4516
ABCC8	39	intron 11 + 308	tgtgtattgtagaagtgatg G/A gaaatccagaaacagaaagct	4517
ABCC8	40	intron 11 + 1171	gcccctctcatttcccttcca G/A tgcgtgagcgtttccagtggtg	4518
ABCC8	41	exon 12 + 7	gcctctgtccacagacttttc G/A tgggccacgtcagcttcttc	4519

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC8	42	intron 12 + 356	accaagaatgagccatccc G/T tccccacgtggctgccccat	4520
ABCC8	43	intron 12 + 934	tgggttcaaaagatggaatgg G/T gcataactcagcaaaattat	4521
ABCC8	44	intron 12 + 1370	gggaggaggctggacaggg C/G atgaaggcagagcctggtgg	4522
ABCC8	45	intron 15 + 412	ggaggtgggacccaggtgg C/T gttcttgggaccacaagga	4523
ABCC8	46	intron 15 + 688	actccccggccccactcac A/G ttgcccacttccccctctg	4524
ABCC8	47	intron 16 + 4464	actcattccaagtattgata G/A agaagagaggttaggtactgg	4525
ABCC8	48	intron 16 + 4574	ttgaagatcttaagtgtttt T/C tgggtcactcatcttcgcaaa	4526
ABCC8	49	intron 16 + 5011	agctaaaagcaaaaacagcct C/T tgacctggcaagcattccca	4527
ABCC8	50	intron 16 + 7608	tgtcctacttttcttttgac C/G cttataacttccctgactctg	4528
ABCC8	51	intron 16 + 7730	ccagctcctagtgggctgga G/A ggaaggacatgcggttgggg	4529
ABCC8	52	intron 16 + 8369	ttgcaaaactgagttaggccc T/C ggagagcttactgtgtgctg	4530
ABCC8	53	intron 16 + 9708	tgcacttgccgctacttat T/G ccagaccctaatgattgggtc	4531
ABCC8	54	intron 17 + 651	tatagattaatgaggctctg A/G gtccctcaaaaaccttccctc	4532
ABCC8	55	intron 17 + 692	cccttacctctccaaaaaac A/G cttgagatacccttagaggtg	4533
ABCC8	56	intron 17 + 1541	ctcaggatcttctctggagga C/T atggttcaactcccatgagag	4534
ABCC8	57	intron 18 + 580	actaagcagatttctaccaa C/T tgcacctccccatcccccttg	4535
ABCC8	58	intron 18 + 658	gaacaagccccctgagaatgc C/T ttccgcacccccctactcccg	4536
ABCC8	59	intron 18 + 660	acaagccccctgagaatgcct T/C ccgcacccccctactcccgcc	4537
ABCC8	60	intron 19 + 93	gcccttccatcgatcaccca T/C acccagccatctcactcccc	4538
ABCC8	61	intron 19 + 123	tctcactccccaggtgctta T/C ctgcactccagcctctccat	4539
ABCC8	62	intron 19 + 219	cataggggagaggggcaggaa C/T ggagggaaggagagagccc	4540
ABCC8	63	intron 19 + 845	tagtatattaacctgccc aaa C/T gctgtgtgaagtgtgtgacct	4541
ABCC8	64	intron 20 + 338	tccccctccacaagcttagac A/G aacaggattctcctgtgact	4542
ABCC8	65	exon 21 + 10	tttgggtgacaggggcataaac C/T tgtctgtgtgtgtcaacgccag	4543
ABCC8	66	intron 21 + 192	caaggatagcacaaaatgacc C/A attgcagacttcagatggag	4544
ABCC8	67	intron 23 + 17	gaaggtgggtatatatccagg A/G tggccaagcagccacccccctg	4545
ABCC8	68	intron 23 + 67	gttctgtgtagaacctgaact C/T ataaaggtcttctctgtcctt	4546
ABCC8	69	intron 26 + 268	gtgagcgtctgcacatccaa G/C taaagattgttttctcctcc	4547
ABCC8	70	intron 26 + 308	cgataagtgggtgtaatttg C/T ccatccccacccatgagttc	4548
ABCC8	71	intron 26 + 348	cagctccctgccccctccctc A/G ctctctctcctcagccagc	4549
ABCC8	72	intron 26 + 807	gacagctgctgagtcaggcc G/A agccggcagctgagaaaaggc	4550
ABCC8	73	intron 26 + 834	cagctgagaaaaggcggcagt G/C gtcagatgggcttgagaaaac	4551
ABCC8	74	intron 28 + (118-121)	cctccaaaaataaaaaaaa AAAA/ Δ cagaaatgaaggaaatagaa	4552
ABCC8	75	intron 28 + 1348	tggggtaagcgggaagacggg G/A ttgaacgctttgagtttgggt	4553
ABCC8	76	intron 29 + 1253	ctcttaggggattcttgtctaa G/T taaagaagagcagagcaaaag	4554
ABCC8	77	intron 29 + 1589	cagatccccagcttccctgtaa A/G cagcctcagatcaggccaaa	4555
ABCC8	78	intron 29 + 2322	gcgcctcacactcctataac G/A cgcacatgccctgatgcaca	4556
ABCC8	79	intron 29 + 2348	atgcccctgatgcacacacat T/C ttcaacacgcacttactcta	4557
ABCC8	80	intron 29 + 2418	agacacgtcacccctccaca C/T gtctccacccctgggggtgtg	4558
ABCC8	81	intron 29 + 2494	tcagtcctcctcagacacatg C/A cctctctccacgcagagaca	4559
ABCC8	82	intron 29 + 2735	gcggccaaaggagagtgatga C/T ggcagcccaggttgatcaga	4560
ABCC8	83	intron 30 + 386	gtcctctggggtccagcctt C/T gcagcccttgtgtgtgtctg	4561
ABCC8	84	intron 33 + 93	ggcttcgcagtcacctcgtg G/T cctccagggcccgaggcctc	4562

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC8	85	intron 33 + 358	aggacctggggcagacag C/T gaggccacccttgattgag	4563
ABCC8	86	intron 38 + 54	cccaggacaggactggcct G/C ttgtggccgtcatcagtgca	4564
ABCC8	87	intron 38 + 466	aggacattctggccacatgc C/Δ tcatcctcctcctccaagcc	4565
ABCC8	88	intron 38 + 529	tggcccccaccgcggtggt A/G ttcccaccatcctgaccgc	4566
ABCC9	1	intron 3 + 38	tggtgttctcctctaaagag C/A tattgtgttttccccccaaa	4567
ABCC9	2	intron 3 + 305	gctggccttctggcttgag T/A agttgtattttaagaatcag	4568
ABCC9	3	intron 3 + 320	tgcagaagtgtgtattttaag A/G atcagagctcttgtgaggag	4569
ABCC9	4	intron 3 + 631	ttctgtggaaaatcagaggct G/C tctaaaaatctcctaatttt	4570
ABCC9	5	intron 3 + 8644	tggacgcactcaacattttc A/G agttattactccttcaactc	4571
ABCC9	6	intron 4 + 757	aggatatcatgaacactga A/C tcttagtaaaaaactatcttt	4572
ABCC9	7	intron 4 + 1022	tactgtggaatttttcttgc A/C acagagatatgtatttttca	4573
ABCC9	8	intron 5 + 1217	cagtggtagatgtgttttct A/G ttgccatcatctacaaaatat	4574
ABCC9	9	intron 6 + (100-106)	tatgagttgttcaaataggc (T)8-9 cagagaattgaatgctttct	4575
ABCC9	10	intron 6 + 1347	tcagtcgtattcctactaaa A/Δ caaaattttgtaagttatgt	4576
ABCC9	11	intron 6 + 1618	ctttttatttgctgcttacc G/A ttttactaaggttggtatata	4577
ABCC9	12	intron 6 + 1835	cttttaataaatgcacactg C/T acacctggctctataaaaaaga	4578
ABCC9	13	intron 7 + 407	cctatagaatttttcttttc T/G tttttctcaaaaaaattaaa	4579
ABCC9	14	intron 7 + 423	tttcttttttctcaaaaaaa C/T taaatgtttgtttattttt	4580
ABCC9	15	intron 8 + 743	ttctgtagatgaagccttaag A/T gctagatctttatttgaaaaaa	4581
ABCC9	16	intron 8 + 850	tttttaacttattgttttggc T/G tttcatttttttaataagaaaa	4582
ABCC9	17	intron 9 + 585	cgaatttgctgcttttttagag A/T aatcttttgcaaaataaaaa	4583
ABCC9	18	intron 9 + 1394	atttttcttctgttaagtat G/C agttagagctgactgacag	4584
ABCC9	19	intron 12 + 1167	atttgaagactttttaaatt G/A agataattgtgctggtgtct	4585
ABCC9	20	intron 12 + 1195	tgtgctggtgtctatatctt A/G ctgagaaaaactagaatttat	4586
ABCC9	21	intron 12 + 2123	ataagtgtctctccagtggt G/A attggacttagagcattttc	4587
ABCC9	22	intron 12 + (2653-2656)	caaaacagaaataatgaaaag TAAC/Δ tattatctaaaaataaaaa	4588
ABCC9	23	intron 13 + (3043-3044)	aacatactctcctcctctct (CTCTTT) aagtcaaaaatattagtat	4589
ABCC9	23	intron 13 + (3043-3044)	aacatactctcctcctctct (CT) aagtcaaaaatattagtat	4590
ABCC9	23	intron 13 + (3043-3044)	aacatactctcctcctctct aagtcaaaaatattagtat	4591
ABCC9	24	intron 14 + 85	ttctgtgaaagtgtcccaaa T/A tgtgccttttaaatgttttt	4592
ABCC9	25	intron 14 + 275	agtgtcacatgtattttttc T/C ggtattcctatgtttatcaa	4593
ABCC9	26	intron 14 + 453	ctcatttcaaaacttggctat T/C tggactctccccaggcattg	4594
ABCC9	27	intron 14 + 3709	atccccctagtgtgtacact G/A agcttgctcctcctcttctct	4595
ABCC9	28	intron 14 + 3813	ctgattttatatattagctga C/T tttccaagttcagacatcta	4596
ABCC9	29	intron 14 + 4000	ttcttttacttcaatgtagc A/Δ ccaaatcagaaggtgacatt	4597
ABCC9	30	intron 16 + 1466	atccccctggattttaattac A/C ttgtgtagcttgtacaacca	4598
ABCC9	31	intron 16 + 5357	attttggaagagaaaattata T/G aaccttccacaactgaattt	4599
ABCC9	32	intron 17 + 1368	aatcctgggtgttttttttt T/Δ ctttttcattttttcagtagg	4600
ABCC9	33	intron 20 + 98	aagtaactcaaggaaaagatg G/A ttttaacttgtgaaaatcgtaa	4601
ABCC9	34	intron 22 + 28	ctcatagtccagaagagttc A/C gagcccaattcagaagagtt	4602
ABCC9	35	intron 22 + 194	tgaacctataaaatttctaat G/Δ ccattcttggatgaggtgca	4603
ABCC9	36	intron 22 + 1370	ccagggacaaaagaagatga C/T gtaaaacttaaggattgggac	4604
ABCC9	37	intron 22 + 1487	agcaagccagggaagaagtc C/G attaaagtgtatttagaaat	4605

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCC9	38	intron 23 + (455-462)	atagccatgaaggataagaa AATTAGAA/Δ tgccatttgttatgtttcag	4606
ABCC9	39	intron 24 + (460-465)	aactcttctcttcatctgc TTATAAA/TTTAA gcaagccttgaaggagagtg	4607
ABCC9	40	intron 24 + 595	gcatgcaaaataatgaagaa A/G acaatcttgtctgacattga	4608
ABCC9	41	intron 28 - 926	aaatatttcagaatttgggg G/A tgtagagcatttgcgcgtcat	4609
ABCC9	42	intron 29 + 2692	cttgaagtctctttttttt T/Δ aaagtaataaaaaatttctaa	4610
ABCC9	43	intron 29 + 5464	agacaacactgctttttttt G/A tgttcacaattcaacgacag	4611
ABCC9	44	intron 29 - 1830	aactggctgaaaggaaaaa A/T tcataattgtgtataaatatt	4612
ABCC9	45	intron 31 + 102	tgcttttgccttccacttca G/A taccagaaaaactctctcat	4613
ABCC9	46	intron 33 + 877	aacatggaactatagtaaat A/G tagtttttttggggttcaga	4614
ABCC9	47	intron 36 + 1281	aatttacactttttttttt T/Δ gcaggagaataattttgcaaa	4615
ABCC9	48	3' flanking + 197	aatggagctcatgcatgtgt T/G ttcaaatatatacatgcaaa	4616
ABCD1	1	(5' flanking region -1772)	agtccagggttagggcaca G/A gcaccctcctgcctaaactcg	4617
ABCD1	2	(5' untranslated region -59)	acaatccttccagccacctg C/T ctcaactgctgccccaggca	4618
ABCD1	3	(intron 1 906)	gggcacaaatggcatccatcc C/T ccgaaggcctgtgtgtgctc	4619
ABCD1	4	(intron 1 2924)	gagacctggccccacccaat C/T gtaacctctggctctcgccc	4620
ABCD1	5	(intron 1 3056)	aagcctctctgtgtgttca C/T cccccgcagggtggagctggc	4621
ABCD1	6	(intron 2 2972)	agaagtttcccttgcctttcc G/A tcaagcttggctctgtctga	4622
ABCD1	7	(intron 2 3258)	gcgagacagcacctgcagcc G/A ctctgctccatggctgcat	4623
ABCD1	8	(intron 2 4612)	ggtccttcacaggacattcc C/T accacttcagccacacccca	4624
ABCD1	9	(intron 5 2748)	aatggcctgcgtgctggcct C/T gggcatttgggagcctctcaa	4625
ABCD1	10	(intron 6 212)	atctgtgtgggtgtgtgtga C/T gggcggcgatgtgagcgtgt	4626
ABCD1	11	(intron 5 2835)	ggcgtcagcggcgtgtgtccc C/Δ tgcagggtggaggaggcag	4627
ABCD3	1	(5' flanking region -2834)	acatcccttcttgcctggc A/G gatttgaactcttttgagtca	4628
ABCD3	2	(5' flanking region -2118)	tacagaatcacctttgtcaa G/A ccttaagcctttattgaaag	4629
ABCD3	3	(5' untranslated region -40)	gtagccgcgcgcgcgcgcgc C/T gccgcgtccccctgcgcgct	4630
ABCD3	4	(intron 1 -6763)	atactttgccatttgagata T/C cagtttggagttgtagctg	4631
ABCD3	5	(intron 2 731)	ctttggacctatactagtgtt C/T cttaggcattgtgcttagaa	4632
ABCD3	6	(intron 2 3551)	accacagtgggtctttttttt A/G tatttaaaaaaattattggg	4633
ABCD3	7	(intron 2 5936)	cagaactcacttcccttattc A/G gtttttagataaacattgttt	4634
ABCD3	8	(intron 2 6083)	tggttctttaatttttatgat A/G tgtttgttatagctatctta	4635
ABCD3	9	(intron 3 614)	tctcttgttctgaagtatt A/T ttctatttttttttttatgtga	4636
ABCD3	10	(intron 3 651)	gtgaaatgctagggtactgc C/T atacagctaccctaaatgggt	4637
ABCD3	11	(intron 4 395)	aaagcatttcaaaagaatacac G/A ttgagcatgtttattagaag	4638
ABCD3	12	(exon 7 555)	gacaaacagaatagctaatcc A/G gaccagctgcttacacaaga	4639
ABCD3	13	(intron 7 124)	aaataatttaattgcttttata A/G gaaaatttagagttgttgttaa	4640
ABCD3	14	(intron 7 838)	ggtcacagttgaccttagata T/C acagtttttgagacaaaagaa	4641
ABCD3	15	(intron 8 1150)	aatcttgaatacttactagc A/C catatattgtgctagatagt	4642
ABCD3	16	(intron 9 1493)	tcattcttctccataggctt A/G ggtgtggagaggagatagaa	4643
ABCD3	17	(intron 13 1534)	tctgttgagttggggatcct A/G tggaaacctcttctctcatc	4644
ABCD3	18	(intron 16 4310)	gaaaagtgaatgctgagtag G/T ttagccaggccttgatttaga	4645
ABCD3	19	(intron 20 273)	ttctaaaaagttcagagaaaac T/A ctgtagctcattattctctgg	4646
ABCD3	20	(intron 20 1664)	ctcaaaaagaaaaa A/C aaaaaacacatgatccataa	4647
ABCD3	21	(intron 20 6693)	cttaaggttctgtgttttact C/T tgagcaatttagtatttccca	4648

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCD3	22	(intron 21 7171)	atcataaacagagagaaataat A/G tcttaaatgagctctgaaaa	4649
ABCD3	23	(intron 22 1220)	ctagaaatcaaggcattta A/G aatatagccaagcctttatg	4650
ABCD3	24	(intron 22 1358)	agtagcaaaataatcatcac G/A ccagtgcacatgtgaaggag	4651
ABCD3	25	(intron 4 4448~4461)	taactttcttctgtagttagcg (T)11-14 aactgttttacttttttaggg	4652
ABCD3	26	(intron 5 268)	gttttttggcattttttttt T/ Δ aaccttcagtcagggttttc	4653
ABCD3	27	(intron 5 891~902)	ttgggtgtaaaacctgtagtg (T)10-13 acaaatgcaaatatagtgt	4654
ABCD3	28	(intron 7 1226~1227)	gggaatggggggtgtatcta (T) tacaactttccatgtaattt	4655
ABCD3	28	(intron 7 1226~1227)	gggaatggggggtgtatcta tacaactttccatgtaattt	4656
ABCD3	29	(intron 8 1129)	cagatttactttttttttt T/ Δ aatcttgaatacttactagc	4657
ABCD3	30	(intron 13 1595~1596)	tgaacataataaaagcacac (TA) gttatcatttaatactttatg	4658
ABCD3	30	(intron 13 1595~1596)	tgaacataataaaagcacac gttatcatttaatactttatg	4659
ABCD3	31	(intron 16 7337~7351)	ttaattacttcacagactga (T)13-15 caggttcgatctggggctaa	4660
ABCD3	32	(intron 18 12)	gttcctcaggtaagacacctag C/ Δ ttgagttatctttgatctaa	4661
ABCD3	33	(intron 20 1652~1670)	gcaagactctgtctcaaaag (A)17-20 cacatgatccataatagagg	4662
ABCD3	34	(intron 20 2262~2273)	ttaatccattttgttaaatc (T)11-13 accttaaatgcaactatc	4663
ABCD3	35	(3' untranslated region 2072~2079)	taaaaataaagttgagcttag (T)8-9 aaaaaaaaaaacaagcaaca	4664
ABCD3	36	(3' untranslated region 2080~2091)	gttgagcttagttttttttt (A)10-11 caaagcaacaaataaactag	4665
ABCD3	37	(3' untranslated region 3349~3368)	acttattttctgttcagatt (A)16-19 ctcaatatctctatacaacc	4666
ABCD4	1	(intron 1 276)	tggcatcttttttttgaaaa G/A aagaacctcaggtgcacaaa	4667
ABCD4	2	(intron 1 329)	cttctcagttcttgacaccc T/C gtggcccaatgcaaggctcc	4668
ABCD4	3	(intron 3 171)	ttaagcacgttgatcttgct A/G ttggccacacgtgggactgat	4669
ABCD4	4	(intron 3 449)	cctaccctcatttcagtagg G/A gggctaccacacctgctcactc	4670
ABCD4	5	(intron 5 273)	gacaggggctacctgagagg G/T aacaggagtcagggtgagg	4671
ABCD4	6	(intron 7 240)	tagtcttagtggcctagcgt G/A gggcctgaaattgtcaaatg	4672
ABCD4	7	(intron 7 267)	gaaattgtcaaatgaatgaa T/C gcctcatcctctcttgctggtg	4673
ABCD4	8	(coding region 910 (Ala 304 Thr))	tctatggagacctgagtgccc G/A cagagcttagcacacctgggtc	4674
ABCD4	9	(coding region 981 (Leu 327 Leu))	atcagctgcttcacccagct C/A atcgacctgtccacgagct	4675
ABCD4	10	(coding region 1102 (Glu 367 Lys))	gcgagatcctgggcgagagc G/A agtggggcttggacacgtga	4676
ABCD4	11	(intron 13 191)	tggattggggcccaactactca T/C agcagctcctgaggcaggta	4677
ABCD4	12	(intron 13 262)	acgcgtatgtcaaacaccca A/G ggtcggattcttggggccct	4678
ABCD4	13	(intron 17 848)	cctctgctcctctggcccat C/G ctctctcctgagggcagggt	4679
ABCD4	14	(intron 17 946)	gtgggaggagaagcagcggc G/A gcagagggcagggtctttgat	4680
ABCD4	15	(intron 18 41)	ggcctgaggaggagaaaagaa C/T ccaaaggctcagcctggcca	4681
ABCD4	16	(3' untranslated region 2001)	gcccaggtctaggtttctgt G/A ggggacactgaatctcccag	4682
ABCG1	1	(5' flanking region -386)	gcaataatcattggcctagag G/A tattgtgatatgatgtcatt	4683
ABCG1	2	(intron 1 199)	cacaaaatattggtgagctg C/T ctggatttgggagatgcagt	4684
ABCG1	3	(intron 1 291)	acttgggtccgggtgtgagg A/C tcctgcactcgggtttctgtg	4685

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCG1	4	(intron 1 318)	actcgggtttctgtgatggtg T/A gtgcaggggagtcacaaagt	4686
ABCG1	5	(intron 1 468)	ggtcccaaggggtttcttaga T/C cctccagagaagcctttgg	4687
ABCG1	6	(intron 2 434)	ctgggtacaggtttttgttcc G/A gttggtctgctattgagtat	4688
ABCG1	7	(intron 3 1839)	ttaaaatgagttgttttttct C/G cttaaagcctttaggaggtg	4689
ABCG1	8	(intron 3 3076)	tttgtacttctctgtctc C/T ggctctacttccctgggggt	4690
ABCG1	9	(intron 3 3352)	gttcccttgaggaaacgtgg G/A gtacacagtgttcccagtta	4691
ABCG1	10	(intron 3 8030)	acagtgaagcacaaggcagc C/T gaagacacagcagggcaggtc	4692
ABCG1	11	(intron 3 8066)	aggtcaggtctgtgtgcaca T/C tggcaggtgc a/g tgcagacc	4693
ABCG1	12	(intron 3 8092)	ggctgc a/g tgcagaccagcct C/T ggcccaggtggagaagcaga	4694
ABCG1	13	(intron 3 8285)	ctggacatgtgactccctg C/T acccaccctcacaagcacca	4695
ABCG1	14	(intron 3 8860)	caggtgataggaggatccaa T/C tggacacaggttcagttgc	4696
ABCG1	15	(intron 4 2319)	gggggtgaacagagaggcaga G/A gcctgggcatcttcactcag	4697
ABCG1	16	(intron 4 2557)	gaagggaagaagcagcagca A/G gaaagaagccccctggccct	4698
ABCG1	17	(intron 5 139)	tgaccacagggcaccctagag T/A ggcgccggctccgacgtc	4699
ABCG1	18	(intron 5 177)	gctgccccctgccccctccgc A/C ggccacacctggagcctcggg	4700
ABCG1	19	(intron 6 13)	cagttactgttaagtgtgtt T/C ccaggggtgtgtca g/a gaatct	4701
ABCG1	20	(intron 6 27)	gctgtt t/c ccaggggtgtgtca G/A gaatctccctttctgtgttt	4702
ABCG1	21	(intron 6 1191)	gctaagcagagttaggcccc G/A gctagtccttgaatgagaga	4703
ABCG1	22	(intron 6 1449)	atgctggagccccctgagttc G/A gtgggcatacaagggtggc	4704
ABCG1	23	(intron 6 2282)	ctcgcatcacgcagttttca C/T gatcctatttaattgggtgag	4705
ABCG1	24	(intron 6 3853)	ccctgggttcagcaggggcc T/C cacacctgcaatgggtg c/t ct	4706
ABCG1	25	(intron 6 3871)	cc t/c cacacctgcaatgggtg C/T ctggggagaggggtgcagatg	4707
ABCG1	26	(intron 6 4175)	tccaaagcccagatttgggtg T/C ttttggggctcttttggaaat	4708
ABCG1	27	(intron 7 4)	ctggtggaggaaagaaagta G/A ggaggggcgtgctttgtgt	4709
ABCG1	28	(intron 7 576)	agctcaggaggtgtctggaa C/T gccacacagtcgagagattt	4710
ABCG1	29	(intron 7 1426)	aattctccttctcaacttaa A/G gaaatattttatagaaaaat	4711
ABCG1	30	(intron 7 2342)	agagcctgcaatggggccc G/A agggacctgccccatgactca	4712
ABCG1	31	(intron 7 2399)	gaggggttgacagacaggat A/G tgtctg c/g tgtgttccagctg	4713
ABCG1	32	(intron 7 2406)	tgacagacaggat a/g tgtctg C/G tgtgttccagctgctgttt	4714
ABCG1	33	(intron 7 2911)	ccctctctgtgccactgtt G/C tcccaacacacagcctgtct	4715
ABCG1	34	(intron 7 4363)	tataatagattccttagcaga A/G aacataattgtgagaggaaac	4716
ABCG1	35	(intron 7 4752)	gctttcagagccccattcaca C/T aagggtctcattttattagg	4717
ABCG1	36	(intron 7 5026)	ccaggtctgtgggatttcag G/A ccaaaaaggagcgtagcaag	4718
ABCG1	37	(intron 7 5532)	gggttaaatattccggggcag C/T gccaaagtcagattatctgta	4719
ABCG1	38	(intron 7 5681)	gctaaagtgcagtgaaggca T/C catgaataaaatcctttcagg	4720
ABCG1	39	(intron 7 9243)	gcctgagagcgctggcagta G/A gaagggtcgcagtggtggac	4721
ABCG1	40	(intron 7 11371)	gggtctcttggagccccctt T/G tctctccagccccctgcgtct	4722
ABCG1	41	(intron 7 12420)	gggatttcgaatctcaaac T/C ctgagctctgtgctttcccc	4723
ABCG1	42	(intron 7 12985)	ctattggcaggtcgtgaaca T/C tgttcttggttttgcaata	4724
ABCG1	43	(intron 7 20041)	acatggccggcttcccttct T/C cctc g/a gaatggcctggaatt	4725
ABCG1	44	(intron 7 20046)	gccggcttcccttct t/c cctc G/A gaatggcctggaattcgatc	4726
ABCG1	45	(intron 7 21058)	acaagacttagaatttgacc G/A tgattttaaaaactattctaa	4727
ABCG1	46	(intron 7 26189)	ttcttggtatgtggccatgca C/T gggggcagggttttgatgag	4728

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCG1	47	(intron 7 27453)	atcatgtggtttggggaaa G/C ctggacccccacttggtaca	4729
ABCG1	48	(intron 7 29810)	attgtttctcctgggtttgt T/C tgtgtgactttccctttaa	4730
ABCG1	49	(intron 10 2116)	aaacagggcttgagtcctcc G/A taaggacagagagaccttcc	4731
ABCG1	50	(intron 13 1196)	tgaaaaagaaaatggatgagt G/A gaa a/c ccaaaagagagaaaaat	4732
ABCG1	51	(intron 13 1200)	aagaaaatggatgagt g/a gaa A/C ccaaaagagagaaaaatgtgg	4733
ABCG1	52	(intron 13 2041)	aagcagaggttttccacc G/A gagactcaagaagctgctcc	4734
ABCG1	53	(intron 13 2490)	gtggtgaagtagagctgagc A/T cacgggggagccctccatcc	4735
ABCG1	54	(intron 13 2822)	cagcaggtctcgtgctgaag T/C cacagcaagccaggcccttg	4736
ABCG1	55	(intron 13 2850)	agccaggcccttggccctgcc G/A gagctggaagacccagaaca	4737
ABCG1	56	(intron 13 2919)	gcctcccaggagtagctaca C/T gggacccgaaggcagatggc	4738
ABCG1	57	(intron 13 3506)	ggcagcctgggctgccgaga T/C cctccttgagcgcccgccg	4739
ABCG1	58	(intron 13 3538)	cgcccgccgggaagccccag G/A ggggctggagctaca a/g gtgg	4740
ABCG1	59	(intron 13 3554)	ccag g/a ggggctggagctaca A/G gtggccttgagggttttttg	4741
ABCG1	60	(intron 13 3721)	ccagctcatgggcagggggtg C/T ggagggaagggcaccacag	4742
ABCG1	61	(intron 13 3921)	gaagaccagcagtcgatgcc A/G gctgggaagagggtctgtcc	4743
ABCG1	62	(intron 13 3979)	accacaccagccttttccaga C/T agccttccagaagctgttct	4744
ABCG1	63	(intron 13 4291)	gagcgcctggagtaggggtcc G/A cttgctatggctccagggg	4745
ABCG1	64	(intron 13 4968)	tattgactggacaccttctc C/T gtatggggcactgggctagg	4746
ABCG1	65	(intron 16 672)	atcagtaacgggtcactaac G/A gatgctgctgagtggggcag	4747
ABCG1	66	(intron 16 891)	tggccactgttgagggtgt G/A ggtgaccagaggggccttga	4748
ABCG1	67	(intron 18 1616)	ctggaggagaagacaggata A/C agtctaagacgtg c/t tgtcac	4749
ABCG1	68	(intron 18 1630)	aggata a/c agtctaagacgtg C/T tgtcacagagttcagggtcc	4750
ABCG1	69	(intron 18 1674)	gcttccaaaggccgcacatccg G/T gttgttctcttgagc c/t gagga	4751
ABCG1	70	(intron 18 1689)	atccg g/t gttgttctcttgagc C/T gaggacggcttgcgaacgc	4752
ABCG1	71	(intron 19 446)	tggctgacagtgaacacagc G/A gctgcttctccagaacttta	4753
ABCG1	72	(intron 22 243)	acccggagagccatggcagg A/C ccaagtgttctggacgttgc	4754
ABCG1	73	(3' flanking region 1257)	atggggccacacagccctgcc T/C cagaagcagcttttgggtctcg	4755
ABCG1	74	(3' flanking region 1438)	gggggaagagcttgggaacc A/G tgagggtgttaggctgcaa	4756
ABCG1	75	(3' flanking region 1518)	tgaagggtgaactggagtag G/C tgaggattctgcagttgacg	4757
ABCG1	76	(intron 3 3754~3755)	ctccacccctgcacctccctg (G) cctccttgatttccctcatc	4758
ABCG1	76	(intron 3 3754~3755)	ctccacccctgcacctccctg cctccttgatttccctcatc	4759
ABCG1	77	(intron 3 7848~7854)	cagtttccagaatttggggg (A) 6-7 tcccataagctgtcatactt	4760
ABCG1	78	(intron 4 190~191)	tgtcgagagctcccttggc (C) tggttgatacctcagggttct	4761
ABCG1	78	(intron 4 190~191)	tgtcgagagctcccttggc tggttgatacctcagggttct	4762
ABCG1	79	(intron 4 198~206)	agctcccttgcctgggtga TCCTCAGGG/Δ tctacttagaatgcctcga	4763
ABCG1	80	(5' untranslated region (-713)~(-741))	cgcagctcaagcctcgtccc (CGC) 8-10 cccggggcagtgccctgtct	4764
ABCG1	81	(intron 6 376~387)	tcttgcccttgagctcaagag (A) 10-12 tagccaggtttctgcgcag	4765
ABCG1	82	(intron 7 19944~19945)	ctgatgaggaggggagggggg (CACCAGGCAGCAGACTCTGATGAGGAGGGGAGGGGG)	4766
ABCG1	82	(intron 7 19944~19945)	caccaggcagcagactctga	
ABCG1	82	(intron 7 19944~19945)	ctgatgaggaggggagggggg	4767
ABCG1	83	(intron 7 25136~25137)	catgaacttgcctgaccata (G) ccctgtgaggagctagggt	4768
ABCG1	83	(intron 7 25136~25137)	catgaacttgcctgaccata ccctgtgaggagctagggt	4769

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCG2	1	(intron 1 152)	tcatttgaaagtgggtatgc G/A gtttaaaactgacagtcca	4770
ABCG2	2	(intron 1 614)	agctagtataataaataac G/A ccagagtagtaaggaagaga	4771
ABCG2	3	(intron 1 10002)	cctcatgaatggtatatacatg T/A cccaacatatctctttcgat	4772
ABCG2	4	(intron 1 10123)	acagtgtccctttgggtgc G/A tatacccaaaatccctgcata	4773
ABCG2	5	(intron 1 10768)	ataggaataattgagaacag G/A gtctgaagaactctgcagga	4774
ABCG2	6	(intron 1 10791)	ctgaagaactctgcaggaaa T/C g/a aaaatagttccctgctttt	4775
ABCG2	7	(intron 1 10792)	tgaagaactctgcaggaaa t/c G/A aaaatagttccctgctttta	4776
ABCG2	8	(intron 1 14183)	tcacttaaggcttgcagggg T/G gtctaggacacagaaagaga	4777
ABCG2	9	(intron 1 14934)	aaagtgtctttaaaatttcc A/G tcttgagtcagtgagctatt	4778
ABCG2	10	(intron 1 14955)	tcttgagtcagtgagctatt G/T aaattcaagcaataaagtatt	4779
ABCG2	11	(intron 1 17251)	ctgtttgggaacagcaactc A/C atcataggcagagagaaagt	4780
ABCG2	12	(intron 1 17347)	atttcaaacctgttttcacaa G/A ttgttaagctcatctttaagg	4781
ABCG2	13	(intron 1 17626)	gaaggtgcataaacaacttcc T/G acataaagctctggagctata	4782
ABCG2	14	(intron 1 18369)	ctattgcttttctgtctgca G/T aaagataaaaaactctccaga	4783
ABCG2	15	(coding region 34 (Val 12 Met))	atgtcgaagttttttatocca G/A tgtcacaaaggaaacacacaat	4784
ABCG2	16	(intron 2 36)	tgtaaaaagacagcttttta A/G tttacctacagtgaaacctca	4785
ABCG2	17	(intron 2 4230)	caaccctaaattggagggcc C/T gggcgtggtgattgagaaag	4786
ABCG2	18	(intron 2 4518)	gttgacagacttttatagtg A/C gggacactgacctgcatgca	4787
ABCG2	19	(intron 2 6278)	atgtatgtaccacgtcttca T/C attcttaaaaggatgacctta	4788
ABCG2	20	(intron 3 10)	ggcaaatctctcgtgagtata A/G gagagtataagtaagcgttt	4789
ABCG2	21	(coding region 421 (Gln 141 Lys))	tgacggtgagagaaaaactta C/A agttctcagcagctcttcgg	4790
ABCG2	22	(intron 6 3203)	tcctattctgtttttaataaaa A/G gcattgaatttaggtttgct	4791
ABCG2	23	(intron 6 3287)	gtcaggctgaactagagacaa A/G caatctaaaggcaagaatag	4792
ABCG2	24	(intron 9 5974)	tatactaataaaatgggtgtg A/T taagtttttatctctctaattg	4793
ABCG2	25	(intron 10 1908)	gacgcttatgtgcagcctat G/T ttgatgtcttggaaggctga	4794
ABCG2	26	(intron 10 2094)	ccctgagggtgaggtatct G/A gattatttccagacttgcta	4795
ABCG2	27	(intron 11 20)	tgtgagtaggtctttgttct A/G ggaacggggctgtccagcag	4796
ABCG2	28	(intron 11 1447)	tgttcttcaaggaaagcccc C/T gtcaaaagaggaaagaaagc	4797
ABCG2	29	(intron 12 49)	atgtcttttagtcttgcttat G/T ggtgaagtcagttgcacctt	4798
ABCG2	30	(intron 12 1566)	tatgcagttacatggacaga C/T acaacattggagaccgaggg	4799
ABCG2	31	(intron 13 40)	gctctgataagggaattgttt C/T tttccttcatcttcttctgc	4800
ABCG2	32	(intron 13 1823)	ttactcaagcaggcctgact C/T ttagtatttgccttttttag	4801
ABCG2	33	(intron 14 497)	ctaataaaaaaacaacaagaa T/C gaaagattgtcactgtataat	4802
ABCG2	34	(intron 14 815)	taactctttggaaacttctt A/G aaatttaaaactgtttacct	4803
ABCG2	35	(intron 15 110)	ccaggggcactgaattttt C/T gagcctacgttttctcatcc	4804
ABCG2	36	(intron 15 566)	gccgcatagtcattgttgt T/A gtttttaaaattaaacttgaa	4805
ABCG2	37	(intron 15 639)	aacaagaaacacttgaataa G/A ttgagaaaaaaccccgcttt	4806
ABCG2	38	(intron 15 1197)	tgagtagctgggattacagg C/T gccaccaccacacacctggct	4807
ABCG2	39	(5' flanking region (-998) ~ (-995))	gttgggatggctacactcac TCAC/△ aaagcctgatggcccgcttc	4808
ABCG2	40	(intron 13 405)	ctgctagttttatttttttt T/△ aacatttttaatttatgttt	4809

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCG2	41	(intron 13 692~702)	tcaatatgtttctgtctatc (T)9-11 aatggttacttaactccta	4810
ABCG2	42	(intron 15 645~650)	aaacacttgaataaG/Attgag (A)7-8 cccggtttcacataatgtt	4811
ABCG4	1	(intron 1 84)	ggcctgggtgtcccatgttc G/A gaaagtctgcaccagtg	4812
ABCG4	2	(intron 2 77)	gaacacagaaggtattctga A/G aggcattgacccccatcct	4813
ABCG4	3	(coding region 679 (Leu 227 Leu))	tggtgtccctcatgaagtcc C/T tggcacaggggggcccgtacc	4814
ABCG4	4	(intron 7 95)	ggcctccttaggggttagagat C/T tcaccgtgcgcctgccttccc	4815
ABCG4	5	(intron 7 158)	cttgcccttgggaagtgaat G/A tgaatctaaactgagctctc	4816
ABCG4	6	(intron 8 106)	ccccagagccattgcaacca A/G tgggtgcttaggaagaacct	4817
ABCG4	7	(intron 11 1120)	acgagataagtga t/c ggtcat A/G tggccaggagggaaggac	4818
ABCG4	8	(intron 11 1173)	ggggacagcttgaacaaga A/G tgtggaggcaggatggacac	4819
ABCG4	9	(3' untranslated region 2758)	gagtgacaggcacatacatg A/C gaacaggccatctcagccct	4820
ABCG5	1	(intron 3 40)	ccctggccccccggccgcc C/A cgggggcttaggctacactg	4821
ABCG5	2	(intron 4 841)	gcttggaggcatcttgaatg C/T gcctcatcccaactggactg	4822
ABCG5	3	(intron 4 1145)	gagcaaatccagccccacagc G/A tgtaaaat c/a ctgataagtaa	4823
ABCG5	4	(intron 4 1154)	cagccccagc g/a tgtaaaat C/A ctgataagtaattcagtg	4824
ABCG5	5	(intron 4 1690)	acagagatgagaaggaggct T/C gggaatctaccctggctgg	4825
ABCG5	6	(intron 4 1806)	tcttttgttccagaataatat T/C tatatctagttttattatgc	4826
ABCG5	7	(intron 4 1878)	atttcagatatgtccattct C/T tgggtgggtcctcaagctacat	4827
ABCG5	8	(intron 4 2052)	gggtgtctggaacacaaaact C/T attaccataatgagtatcttc	4828
ABCG5	9	(intron 4 2108)	tccccctgggttttctgcag A/T tagaggttaatcagtagcagg	4829
ABCG5	10	(intron 4 2230)	agcttcttgattagaaattc G/A gtaagaatttttttttagtc	4830
ABCG5	11	(intron 4 2318)	ggagttacaggtctttaaagta G/C agcgaagagaattggaagaa	4831
ABCG5	12	(intron 4 2367)	ttaaatgtggtgggggtta C/T aaattgggtccccattaaag	4832
ABCG5	13	(intron 4 2464)	gattatatgtcttttgatgtg A/G actcacactgagattgtacc	4833
ABCG5	14	(intron 4 2586)	aaagcatttatgataataaa G/A tttcaaaaaccccaaacattta	4834
ABCG5	15	(intron 6 1318)	cagagacattcaaaagtgcac C/T gctacccttgtgatcacaca	4835
ABCG5	16	(intron 9 164)	caactattgagttaccaaca T/C gtttaatatgaatgagctcac	4836
ABCG5	17	(intron 9 365)	gtaccgttagcttctctcttg A/G agctgatttttaggacagcca	4837
ABCG5	18	(intron 10 64)	tcatggagctagtgaggactc G/A tgcaggagagagctccaggg	4838
ABCG5	19	(intron 10 2406)	tcaacaagcctgcttactgc G/A gttagttgtgaccttgtct	4839
ABCG5	20	(intron 10 2442)	tgtctaagtaatttaattgtt T/G tcctatgagagctgaaggag	4840
ABCG5	21	(intron 11 4150)	aaggccctgaaaatggctgtt G/T ctggctattgttccgagctc	4841
ABCG5	22	(intron 11 4623)	caaacagaaaagaattttata C/T cttttgattgacagaaaaata	4842
ABCG5	23	(intron 11 4737)	attttcacaaatgaatgttgg T/G tgggtctctctctctctctt	4843
ABCG5	24	(intron 11 4791)	ggttagttctaaactttctac G/A ttggtaccttcaactttctg	4844
ABCG5	25	(3' untranslated region 2578)	tgaggattaaaaataaaaaac C/T gtaggaatgggctcaacagt	4845
ABCG5	26	(3' flanking region 1560)	catagcactcagcaagaac G/C tgtgctaaagactgaggttc	4846
ABCG5	27	(intron 4 1078~1080)	gggcacagctccctgggagc AGG/Δ agaactcccagatagcagagt	4847
ABCG5	28	(intron 10 2321~2327)	agcgggttgggtgagccctt TAACAT/Δ aggtaggtgtgtgtggct	4848
ABCG5	29	(intron 11 422~433)	ggaattaagactagtcagac (A)10-12 gcctgcaggataaaagactg	4849
ABCG5	30	(intron 11 3988~4004)	ctttttttagtctgtgtcc (T)15-17 cttttcctgttcttactctg	4850

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ABCG5	31	(3' untranslated region 2719~2731)	taccctaaaaacttaaagtat (A)11-13 cctaccgaaaaa	4851
ABCG8	1	(5' untranslated region -19)	aagagagctgcagccagg G/T cacagacctgtggcccat	4852
ABCG8	2	(intron 1 898)	ccttgactgaattcgggat A/G tggcaggatttgaagcagga	4853
ABCG8	3	(intron 1 1548)	cctcacaacctgaaaggcca G/T gtgtaaattgagaaattcta	4854
ABCG8	4	(intron 1 1611)	tggtaaggggagccacttc C/T agcccagccacaaacctgtc	4855
ABCG8	5	(intron 1 3245)	tgggacaatgaagcaatgtg T/C acagtgcagcggagagggc	4856
ABCG8	6	(intron 1 3430)	gggttgaggtgggaatggaa A/C tctggagttctactcactgg	4857
ABCG8	7	(intron 1 3509)	tacacaaatcagcttaaga T/A ctctcatgtacacaccacca	4858
ABCG8	8	(intron 1 3980)	gaaataaaacctggtcaga C/T gcttgaggtcagcctccctc	4859
ABCG8	9	(intron 1 4123)	aagggtgttctgggtccccc G/A taagtgttctggtgcat	4860
ABCG8	10	(intron 1 5354)	cagcttctaaaggagccct A/C atctctcctgtct t/c ccacag	4861
ABCG8	11	(intron 1 5368)	gcccc a/c atctctcctgtct T/C ccacagggcctccaggatag	4862
ABCG8	12	(coding region 161 (Cys 54 Tyr))	ggaggtcagagacctcaact G/A ccaggtagaggcaagcctgg	4863
ABCG8	13	(intron 2 86)	gaaataaaagggtgggcca C/A cttgcaggccctctgccc c/g c	4864
ABCG8	14	(intron 2 105)	a c/a cttgcaggccctctgccc C/G caaggacagagtcagtcga	4865
ABCG8	15	(intron 4 43)	gacccaggtccaaagaagc C/T acagtgtccatgccccgctc	4866
ABCG8	16	(intron 6 1035)	caggaggacaggccgcccct C/T gccctctgtactcacattct	4867
ABCG8	17	(intron 6 1085)	cacagaaaggtcacctccct C/A cctgtgctcaggtggcagcc	4868
ABCG8	18	(intron 6 1184)	gcacctgccgacctggccat C/T ggggaataatttaagtaac	4869
ABCG8	19	(coding region 1199 (Thr 400 Lys))	tggggcgtgcagcagttta C/A gacgctgatccggtaattat	4870
ABCG8	20	(intron 8 137)	gaaaaaacagcatccagca G/A gccgttggtggttatgcct	4871
ABCG8	21	(intron 9 412)	ttctcttttctcttccctta T/C tttttaggttactcagagag	4872
ABCG8	22	(intron 10 343)	aggaagcagaggttcagaga G/A gctacgtggctctccaaaggc	4873
ABCG8	23	(intron 10 614)	cttttaaactgtttataataa T/C ggcagtgaagtgctggctt	4874
ABCG8	24	(coding region 1695 (Ala 565 Ala))	gcctccttcttcagcaatgc C/T ctctacaactccttctacct	4875
ABCG8	25	(intron 11 82)	tgccttctcatctggagatgga C/T acttataccttagatccaac	4876
ABCG8	26	(intron 1 2882~2893)	ttctcttagaaatggataaga (T)11-13 gacagagttctcacgctgtgg	4877
ABCG8	27	(intron 1 3654)	tttatcttctcccatcttttt T/ Δ ctgtataattttgggtcttt	4878
ABCG8	28	(intron 1 5045)	tcagagcacagaggttttttt T/ Δ atagaactctctccggtcca	4879
ABCG8	29	(intron 9 292~302)	tggcttactgtgcctattt (A)10-12 tgagagacttgggcaatatg	4880
ABCG8	30	(intron 9 417~418)	tttcccttccctta t/c ttttt (T) aggttactcagagagggcaa	4881
ABCG8	30	(intron 9 417~418)	tttcccttccctta t/c ttttt aggttactcagagagggcaa	4882
ABCG8	31	(intron 10 28~34)	ggcagggttgagagcaagtg (C)7-9 acccaccaggtgggggtaa	4883
ABCG8	32	(3' untranslated region 2118)	tcctggggacagtgaggaca A/ Δ tgaccctacagatgctcagc	4884
ABCE1	1	(5' flanking region -158)	aactcagatttctcggcacct C/T cagcagctggcttcgccaac	4885
ABCE1	2	(intron 9 237)	ctgaaattatatgcacaaatc C/T gtagctttatagggaagcaga	4886
ABCE1	3	(intron 9 4203)	ttgtgttaggaagctgataca T/G taatttgacatatagatgt	4887
ABCE1	4	(intron 10 1811)	ccaagaaacttcagctttct C/T ttcacttaaatataggaaac	4888
ABCE1	5	(intron 17 2301)	atatccagaacacagatggta T/C gtgcagaacaggttgttag	4889

GENE	number	position	SEQ.	SEQ ID NO.
ABCE1	6	(3' untranslated region 1810)	tggatgattagactgactct G/C agaataattgataagccattt	4890
ABCE1	7	(intron 1 5349~5363)	ttgtctgggttggttggg (T)13-16 gagactgggtctgactctca	4891
ABCE1	8	(intron 1 5845~5854)	tacatttgtcaaaatttata (T)9-10 gcagataatcatttcattc	4892
ABCE1	9	(intron 5 836~851)	taaatcacatgattctgta (T)14-16 aggatcctcctgactggcag	4893
ABCE1	10	(intron 8 1153~1169)	tcttcaaaacttatatttgc (T)13-17 catagtctcatgtttgatga	4894
ABCE1	11	(intron 9 1023~1024)	ttgctctgttttcaaatctct (T) attcatgggcccagcagctcg	4895
ABCE1	11	(intron 9 1023~1024)	ttgctctgttttcaaatctct attcatgggcccagcagctcg	4896
ABCE1	12	(intron 9 2338~2346)	agtgtagatggacctgggg (A)8-9 ctagttaaggaaaaagtaata	4897
ABCE1	13	(intron 9 3213~3221)	ttccaattttccattgttac (T)8-9 cttgccagattactcctgaa	4898
ABCE1	14	(intron 10 284~299)	tctctgcattttgggtctct GCAGTATTACTGTAGT/Δ atttgtcattttcaaaattaa	4899
ABCE1	15	(intron 10 840~853)	tttttgggtttctttcttttc (T)13-14 aatcttggaggaaatttttt	4900
ABCE1	16	(intron 16 1163~1172)	gattagaaatccagggttaaa (T)9-10 gttttgcacaaaaatattac	4901
ABCE1	17	(intron 16 1372~1382)	taaaatttaatacaaaattga (T)10-11 ctcttagtcttcaaacctt	4902
ABCF1	1	(5' untranslated region -60)	gccagccccatcggggttcc C/T cgccgccggaagcggaata	4903
ABCF1	2	(intron 1 101)	gcacgagactgacggggccc C/G tgcgggagttactgcgcag	4904
ABCF1	3	(intron 20 69)	tgactttaaccgaccacctc C/T ctctcttctcgggcagaaaa	4905
ABCF1	4	(intron 23 35)	agtgtccctcatccctgct C/A catggggaccaagctgtagt	4906
ABCF1	5	(intron 7 342~354)	acagagcgagactccgtctc (A)10-14 gaaaaaaacacattt	4907
ABCF1	6	(intron 7 356~369)	cgtctcaaaaaaaacaaag (A)13-15 catttcatcagacctgtctt	4908
ABCF1	7	(3' untranslated region 2425)	tcagcggccccgagagtga A/Δ gctttccttcccagaagtct	4909
ABCF1	8	(3' flanking region 1067~1068)	attaatttgatcaattgtct (T) aatatgtcgtactctagatt	4910
ABCF1	8	(3' flanking region 1067~1068)	attaatttgatcaattgtct aatatgtcgtactctagatt	4911
OAT1	1	(5' untranslated region -127)	gcagctcggactcagctccc G/A gagcaaccagctgcggagg	4912
OAT1	2	(5' untranslated region -20)	gaaggcctcagccccagcc A/G ctgggctggcctggcccaa	4913
OAT1	3	(intron 3 150)	caatagaacaaacctttctc G/A ggctcatgccgacctgaccc	4914
OAT1	4	(intron 4 211)	ttctctggcttccccactc A/C gttctccagcctgcctgctc	4915
OAT1	5	(intron 5 33)	gagacttcccatgataacct C/T ccagggttccacccccaaac	4916
OAT1	6	(intron 6 168)	gaaccagatgccccagcct C/T gactcagttcccagttctccac	4917
OAT1	7	(intron 1 58~71)	ggaagatggggcctttgtt (A)13-15 gtacatggagaaattaactg	4918
OAT1	8	(intron 3 1306~1319)	aataggttgaggaggagcag (A)12-15 tcaagagtgtggaggggca	4919
OAT2	1	(intron 4 842)	ttgacctccaaaagtgtttg G/A attacaggcatgggcccattg	4920
OAT2	2	(intron 5 183)	ccacatccatcatctcgagac A/C a/c actcgtctcagctgccatg	4921
OAT2	3	(intron 5 184)	cacatccatcatctcgagac a/c A/C actcgtctcagctgccatga	4922
OAT2	4	(coding region 1269 (Ser423Ser))	actagactgctagtgtctctc C/T ggtgagccccagttcccatagg	4923
OAT2	5	(3' untranslated region 1792)	ataaatgtgtacatgagtgt A/G tgaacacaaaatacataaggt	4924
OAT2	6	(3' flanking region 1386)	tgtagcagccccacatcgcca G/A tgttcacacctgagagagag	4925
OAT3	1	(5' flanking region -463)	ttcctgagagggcaaatcccc T/C tccccactactcgggaggtgcc	4926
OAT3	2	(5' untranslated region -16)	cctgcccacagctctggctc G/A tcttggccccagtgccatgac	4927
OAT3	3	(coding region 153 (Pro51Pro))	cctgtccaccactgtcggcc G/A ccccaaatgcctccacagg	4928

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OAT3	4	(intron 2 177)	gcaccaagacccttggtctc T/C tccactcagagtcaccaagca	4929
OAT3	5	(intron 2 6201)	gctcatcctctctggtcctt T/G tgccccagcacaggttcctc	4930
OAT3	6	(intron 3 79)	tctgtccaccctgcaccc G/C caaagaggcaaaagagctggg	4931
OAT3	7	(coding region 723 (Thr241Thr))	tggcgttggtgcagttaac T/A gtgtccattcccttcttcgt	4932
OAT3	8	(intron 5 524)	tcgaagtacaaaaggaaagt T/C aaagagaagcctgagcctgg	4933
OAT3	9	(intron 7 386)	gaccaatgggtttcagactc G/A aagacaaaaattatgtttat	4934
OAT3	10	(intron 9 81)	attgtcctgtcctctaccca G/A gggagccatccttttatgaac	4935
OAT3	11	(5' flanking region (-661)~(-660))	tacatttgggtcccccagggg (G) aagcggctgatcaggagaga	4936
OAT3	11	(5' flanking region (-661)~(-660))	tacatttgggtcccccagggg aagcggctgatcaggagaga	4937
OAT3	12	(intron 8 211~212)	tctgacttggactgggcaaa AA/ Δ gtatgggtgtatctggatag	4938
OATP1	1	(5' flanking region -916)	acagagtagatgttcaataa G/A tttttgtgtatctgtgaga	4939
OATP1	2	(5' flanking region -843)	tagtcagcagactatgcctt G/A atgtgtgtgtgttttgggatt	4940
OATP1	3	(5' flanking region -526)	aaatgtgtgcctgtatgtta T/C acatctgtacatatatttcc	4941
OATP1	4	(5' flanking region -172)	acaaacacaaactcaaat G/A tgtgttattaaaagtagcta	4942
OATP1	5	(intron 1 206)	ttgattcaggcgaagttagtc C/G taaatggcctttgagagactt	4943
OATP1	6	(intron 1 454)	caacataacaaataatttcc G/A taagaaaaatggccattttg	4944
OATP1	7	(intron 1 999)	gttagcaaggtagatatt A/G atgtggatgttaagacaaaa	4945
OATP1	8	(intron 1 1223)	ttgtagaagcgtagtaggac C/T agctttataaaatcacagagat	4946
OATP1	9	(intron 1 1326)	aactagtagggcaaccatg T/C gtttaggg G/A aaaagcaatg	4947
OATP1	10	(intron 1 1336)	gcaaccatg t/c gtttaggg G/A aaaagcaatgaggtcatgat	4948
OATP1	11	(intron 1 1498)	atagtttgcctttaagaata C/T actctgagaagggtttatagt	4949
OATP1	12	(intron 1 5041)	ttatgctcccgaggaggttag C/T tctctaaatgcataaggaga	4950
OATP1	13	(intron 1 9532)	aaagactgggagcacttccc A/G atgacaaaatactagactaga	4951
OATP1	14	(intron 2 961)	aaaaagttatatagaaaaat A/G agtgtcactccttctctagt	4952
OATP1	15	(intron 2 1110)	gtctactagtgttcaactcc T/C ttagatctttagcctgtatca	4953
OATP1	16	(intron 2 1419)	aaagcctaagaaggatgcag T/C gcaatagcctatgtgagaag	4954
OATP1	17	(intron 2 3339)	tatggtttgcacaaaaactta T/C tcgtatatattgttttttcca	4955
OATP1	18	(intron 3 66)	caggaaaatgaagttgcactt T/C cctctctaggagcaaatgctt	4956
OATP1	19	(intron 3 205)	tcagttttgtcaatttacac A/G atggggattttgggacctttt	4957
OATP1	20	(intron 3 6377)	aatgaatagacttttgagttta C/T tggatttttttagtggataaat	4958
OATP1	21	(intron 3 7238)	tgaatgtcacatttttttaa G/A tttgtgttcccttatctcata	4959
OATP1	22	(intron 4 1016)	ttttattcttgatttcattgtt T/C gtggaattgcagtagtcca	4960
OATP1	23	(intron 5 110)	tccacaatgatgagtagagt A/G tcttggcacagttggccttc	4961
OATP1	24	(intron 6 496)	agtgtctgaattataagcca A/G ttttatagttggttgggacc	4962
OATP1	25	(intron 7 1934)	aaagtgaaggaaaattaaaa G/C tgagaacttgagcctgaatg	4963
OATP1	26	(intron 7 2140)	tagaatgtaccacaaatgaatc A/G gcatctctgaggatgggacc	4964
OATP1	27	(intron 7 2365)	tgaactcttcttttatcaact C/T gattttcctccagactttac	4965
OATP1	28	(intron 8 88)	gaaactcctaagttgaagt G/C ttttaggatatatttttgact	4966
OATP1	29	(intron 9 534)	tcataattgtatttttaaag G/A ttatctgggttttactgaaa	4967
OATP1	30	(intron 9 1286)	tattcttctgagataaaatca T/C tgaaggagtggtctatgtgt	4968

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OATP1	31	(intron 11 215)	ttcactcctattcctcgcga C/T ttttcttcttattttcttag	4969
OATP1	32	(intron 11 663)	ttcttcttcttcttggagctc T/A aaagtagagttcagtttaac	4970
OATP1	33	(intron 11 999)	atcatcactgcagtagagtt A/G gaattatctaaactttgtgat	4971
OATP1	34	(intron 11 16727)	ttctttttattttacaaaactt A/G tttacttttccaggtgtatga	4972
OATP1	35	(intron 12 48)	ctatcagaacaattattatta T/G tattattttttattacactt	4973
OATP1	36	(intron 12 686)	tatgttttgataaaactttgc C/A gtacaaaataaagaaaattga	4974
OATP1	37	(intron 12 708)	tacaaaataaagaaaattgaa A/G tatttccaaaataaatcaagt	4975
OATP1	38	(intron 13 418)	tctctggtctccaaaatcat A/G tatttctccctcttta c/a at	4976
OATP1	39	(intron 13 436)	at a/g tatttctccctcttta C/A atttgcgtgaaaacaatcttc	4977
OATP1	40	(3' untranslated region 2130)	gtctttaagaacacctaaaaa C/A ctcttaactcaaaaataaa	4978
OATP1	41	(3' flanking region 57)	agtgaactaaagtttttctta C/A aaacaagtgtctgaatcaaa	4979
OATP1	42	(3' flanking region 572)	aatacactatggtttatttat G/A tgtactataaatggagtgag	4980
OATP1	43	(3' flanking region 788)	atttccctaaatgatcagatg C/T atcatatgaaaaaagaaagc	4981
OATP1	44	(3' flanking region 1356)	aggtgactgacataaaatggg G/A gcagaggacataaatgaggtt	4982
OATP1	45	(5' untranslated region (-189)~(-188))	attttcttaactctgtattaaa (A) gcgtccagggtatttttgta	4983
OATP1	45	(5' untranslated region (-189)~(-188))	attttcttaactctgtattaaa gcgtccagggtatttttgta	4984
OATP1	46	(intron 4 725~726)	tgatcttttaataagcgggaa AA/ Δ caggcaagtagcctatagtt	4985
OATP1	47	(intron 4 1082~1083)	attgagtcaggaaaaccacaaa CA/ Δ gttcaaaaaatttgaaaaat	4986
OATP1	48	(intron 4 2301)	aatgtcatgtcttttttttt T/ Δ aatgcagaggtgtacaaaagga	4987
OATP1	49	(intron 9 241~46)	attgtatgtgcatgtggtg TGTGTG/ Δ catgattgtctttgtgatat	4988
OATP2	1	(5' flanking region -2574)	ggataaggcaacccctatgt A/G tcaactgtcaggagagggga	4989
OATP2	2	(5' flanking region -1723)	tctttcagacttcaaaagcc A/G tgatatattcatcagagctgt	4990
OATP2	3	(5' flanking region -1180)	tgcttatttaacaggcataa T/G ctttgggtctcctgagccaga	4991
OATP2	4	(5' flanking region -811)	tatgtgcataatgtgtataca G/A gtaaaagtgtgtatatatgt	4992
OATP2	5	(intron 1 7188)	aatcatttgaaaatttaagaa A/G aaaatatgttccagagaaaaa	4993
OATP2	6	(intron 1 7331)	gtgaaatgagggaacaaaagt T/C ccaccttttttctcctgaata	4994
OATP2	7	(intron 1 7391)	agagagatgtgaaatagtat T/G tttctgggggaagttaggggaa	4995
OATP2	8	(intron 1 7886)	tgttagtagaaaagaaaaatc G/A aagcctaaaaactaaaaggaag	4996
OATP2	9	(intron 1 7958)	ttgctattatataaatttttt T/A a/t aaaaaagatttcttaatat	4997
OATP2	10	(intron 1 7959)	tgctattatataaatttttt t/a A/T aaaaaagatttcttaatat	4998
OATP2	11	(intron 1 8036)	ggaaaaaatggggtgaaatt A/T atcaaaagggcagcttattac	4999
OATP2	12	(intron 1 9164)	acattatattctatatataaaa G/T agtcagttgaagtataaaagt	5000
OATP2	13	(intron 2 193)	tgattaagtatttctttggc G/A aaatttttgatgctttaatag	5001
OATP2	14	(intron 2 1020)	ttgagtaaacattttaggccc G/A tggcagtcataaagggaagaaag	5002
OATP2	15	(intron 2 14865)	agaggaattaatcataaagag G/T ttattttggctaaagtgaca	5003
OATP2	16	(intron 2 14931)	gttagttaataaacagaaaaa A/T tatcagaaaatttttaaaaaat	5004
OATP2	17	(intron 2 15417)	ttctaaaaataagtaagctaa A/T tattctatattataactacta	5005
OATP2	18	(intron 2 20823)	ttgtataagagatacaaaaac A/C aattcctactaggggaaata	5006
OATP2	19	(intron 2 20852)	ctaggggaaaataaagcttca G/C taaggaggtggcatttaagct	5007
OATP2	20	(intron 2 21360)	ttcaaaagctgtatttctca T/C tagtgcttttttgtgaataaa	5008
OATP2	21	(intron 2 21467)	tatatacacaataacctgtcc A/G gaagatgtggtataagccaa	5009

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OATP2	22	(intron 2 21621)	tatcaatacttatgaagaga A/G ctaactatttctaactaggga	5010
OATP2	23	(intron 2 22760)	ttccccacctcctgttggtt C/G tctctttaaacttctccttg	5011
OATP2	24	(intron 2 23199)	cctatctgcacataaacatta C/T aaacttatggcaattata a/g a	5012
OATP2	25	(intron 2 23218)	a c/t aaacttatggcaattata A/G aactcaatacatattatact	5013
OATP2	26	(intron 2 23330)	gccttgttctcctgttctct G/A tacctgcctcaactacatag	5014
OATP2	27	(intron 2 23673)	ctggagacggtagctcaaac T/C gaggatgaaaaatagacattt	5015
OATP2	28	(intron 3 89)	ggttatcaactggggtaaat T/G tatctctcacaggcaatttg	5016
OATP2	29	(intron 3 224)	tgctaaatattctataatgc A/G caaagaatgatgtaactgaa	5017
OATP2	30	(intron 4 97)	ccctttaaataaggcagttac C/A ttttgagaagatacccacta	5018
OATP2	31	(intron 4 568)	ttcatgatccaaaattgtggc A/G acgtatttccaggccaacaag	5019
OATP2	32	(intron 4 599)	aggcaacaagatagaagaag A/G aaagaataagaagcaacaaa	5020
OATP2	33	(intron 4 753)	aaaatagacattattccaag T/A taccaagtcccggttaaaa	5021
OATP2	34	(intron 4 781)	ttcccggttaaaaaatcccaa G/C tataattactgtggaaggaa	5022
OATP2	35	(intron 4 1196)	aaggaccacaatctagatca G/T cattgctctaaatatgccaat	5023
OATP2	36	(intron 4 1229)	tatgccataatatgtgacac T/C ttgcaacctgggtatttctac	5024
OATP2	37	(intron 4 1623)	catctagtgaatggatta G/C attttatttttactacattt	5025
OATP2	38	(coding region 388 (Asn130Asp))	attctaaagaaaactaatatc A/G attcatcagaaaaattcaaca	5026
OATP2	39	(coding region 452 (Asn151Ser))	taatcaaaattttatcactca A/G tagagcatcacctgagatag	5027
OATP2	40	(intron 5 165)	ttaatatatacacagttcgccc A/T ttaacaaacacaggtttaaac	5028
OATP2	41	(intron 5 189)	acaacacaggtttaaaactac G/A c g/a ttttcacttctatgcaaa	5029
OATP2	42	(intron 5 191)	aacacaggtttaaaactac g/a c G/A ttttcacttctatgcaaat	5030
OATP2	43	(intron 5 507)	atataaacttgccttctcattg C/T aaaaggcaaat a/g ttatatc	5031
OATP2	44	(intron 5 520)	ttcattg c/t aaaaggcaaat A/G ttatatcattttaaagacttt	5032
OATP2	45	(intron 5 856)	agtcataataaaacctaatag A/G ataaaaacaaaaaaagaaa	5033
OATP2	46	(intron 5 1157)	acagataaatttttacttggt T/C gtgcttttctctgtatgatg	5034
OATP2	47	(intron 5 1226)	ccttgattgtaataaatctcc A/C c a/c tgccaagagtggggccag	5035
OATP2	48	(intron 5 1228)	ttgattgtaataaatctcc a/c c A/C tgccaagagtggggccaggt	5036
OATP2	49	(intron 5 1304)	actgttctcgtggtaaatgaa G/T aagttctcaaatgtctgatg	5037
OATP2	50	(intron 5 1348)	ttataaatgagagtctccct G/A caaaagctctcttgccctgcc	5038
OATP2	51	(intron 5 1407)	ttgctctctccttcatcttcc G/A ccatgattgtgaggcccccc	5039
OATP2	52	(coding region 521 (Val174Ala))	gtcatacatgtggatatatg T/C gttcatgggtaaatatgcttc	5040
OATP2	53	(coding region 571 (Leu191Leu))	gggagactcccatagtagtcca T/C tggggcttttcttacttgat	5041
OATP2	54	(coding region 597 (Phe199Phe))	ctttcttactatgatgattt C/T gctaaagaaggacattcttc	5042
OATP2	55	(intron 7 33)	agaacaagggtaccatgataa C/T gtcttttctaagcacacatgc	5043
OATP2	56	(intron 7 267)	caaaataaccacaaatgtaaaa T/A gtctccctcccaaaactgact	5044
OATP2	57	(intron 7 1260)	gtaatctcacatttctctgc A/G tttaacacttggtaaaaacttt	5045
OATP2	58	(intron 7 2273)	ttctcacgtcctatctagcg C/T gattatgaccttagttact	5046
OATP2	59	(intron 8 207)	gtggaagagaattagggttg T/C acttttttagcaggaggaaac	5047

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OATP2	60	(intron 8 546)	tgggagaagtcttcccta T/C gtaattagagtaaatattt a/c t	5048
OATP2	61	(intron 8 565)	a t/c gtaattagagtaaatattt A/C ttttggaattatctatcta	5049
OATP2	62	(intron 8 668)	taagtaattgaaattaggat G/T catcagcatttgacagtgc	5050
OATP2	63	(intron 8 739)	tggagaaccattgagagtca A/G taaacaaagagaatgacttg	5051
OATP2	64	(intron 9 112)	atttagtaatacacaggataa G/C tataattttcttctgtattctt	5052
OATP2	65	(intron 9 266)	ttagaggtagtatctgtata A/G ttggatcttataaatttagtg	5053
OATP2	66	(intron 9 305)	tgctaagatctgagacaaac C/G cttttgtaattataatcatt	5054
OATP2	67	(intron 11 10224)	tacactgttccataaaaaa T/C tctctatattattctctagt	5055
OATP2	68	(intron 11 10359)	attaatagattcaacgtgag G/C ttcccttaaaacttttagccta	5056
OATP2	69	(intron 11 10916)	cttatatagaaagaaatcca C/G aaaactattttaccttttat	5057
OATP2	70	(intron 11 10997)	aataatttagtttgaacaag T/C gagacttcactaaatataat	5058
OATP2	71	(intron 11 11018)	gagacttcactaaatataat G/A caatgtatttgcagcactgt	5059
OATP2	72	(intron 12 442)	aacattccaaaaacttttaac C/T ga c/t t c/a acagcatgactttta	5060
OATP2	73	(intron 12 445)	attccaaaacttttaac c/t ga C/T t c/a acagcatgacttttataa	5061
OATP2	74	(intron 12 447)	tccaaaacttttaac c/t ga c/t t C/A acagcatgacttttataata	5062
OATP2	75	(intron 12 907)	aatgaaaaagaagctggcaga T/C tgaacataactgaatgagag	5063
OATP2	76	(intron 13 65)	tatatatatatatatatata C/T acacacacatacatatatatta	5064
OATP2	77	(intron 13 870)	aattctgagtatctctatttc G/A atgtatccaatctgtggcac	5065
OATP2	78	(intron 13 1935)	taaaaaaataaaagctctgc T/C ttacagcaattgagccaag	5066
OATP2	79	(intron 13 2261)	aacgaatcctccaaaattttt G/C aacttttatttaatacaaaat	5067
OATP2	80	(intron 14 248)	tcaaggataataaaccaactt G/A tcaaaaatcagagataaatag	5068
OATP2	81	(intron 14 2463)	atttgtttactaataatggaa C/G ctcttccaagacatatatttt	5069
OATP2	82	(intron 14 2857)	tcatcatgtatttccaggac A/T cctggcaagatgctcctcag	5070
OATP2	83	(intron 14 11458)	atctccagaggtcctgctgt C/T tcccaaaagtccactgaccc	5071
OATP2	84	(3' untranslated region 2243)	ataataaaaacaaactgtagg T/C agaaaaatgagagtactca	5072
OATP2	85	(3' untranslated region 2404)	tcttaataaaaacaaatgagt A/G tcatacaggtagaggttaaa	5073
OATP2	86	(3' untranslated region 2515)	cagagtttgaactataatac T/G aaggcctgaagtctagcttg	5074
OATP2	87	(3' untranslated region 2539)	gcctgaagtctagcttggtat A/G tatgtacaataataatctgt	5075
OATP2	88	(intron 1 457~458)	taattggcaaacacataaaaaa (A) caggtgtctcaaaagtcacat	5076
OATP2	88	(intron 1 457~458)	taattggcaaacacataaaaaa caggtgtctcaaaagtcacat	5077
OATP2	89	(intron 1 753 ~7538)	gacagcattacaaccaaga (G) atggagaatgacattcagga	5078
OATP2	89	(intron 1 753 ~7538)	gacagcattacaaccaaga atggagaatgacattcagga	5079
OATP2	90	(intron 1 10032~10035)	tgtgtgattcttatattactt ACTT/Δ gtttcaaatcttctctccaca	5080
OATP2	91	(intron 1 10058~10061)	ttcaaatcttctctccacaaa TTTA/Δ ttttctatttaaatgtaat	5081
OATP2	92	(intron 2 413~423)	acttatttaaaaaattctttt (A)11-13 caaaaaacaggatttaaaaa	5082
OATP2	93	(intron 3 1595~1603)	ttgccaagtaattcaagtgc (T)8-10 gattttaaacaacttttca	5083
OATP2	94	(intron 4 10~23)	ttcatgggtagtaagtgtt (A)12-14 cctctgtgccactatcagta	5084
OATP2	95	(intron 5 1567~1572)	gtgaatataaattacttgta CTGTA/Δ aattaaaaaaaataagtag	5085
OATP2	96	(intron 5 1577~1585)	attacttgtagtctgtaaat (A)9-10 taagtagaataataagagt	5086
OATP2	97	(intron 8 1939~1941)	ttctctaactccttctactc CTT/Δ atttcaagcagatgcaactg	5087
OATP2	98	(intron 10 3077~3078)	aaattctttatctacttttt (CTT) ttccctcttctctgctttc	5088
OATP2	98	(intron 10 3077~3078)	aaattctttatctacttttt ttccctcttctctgctttc	5089
OATP2	99	(intron 11 11011)	aacaag t/c gagacttcactaa A/Δ tataat g/a caatgtatttgca	5090

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OATP2	100	(intron 12 1160~1169)	agcatgacatggtagagatg (A)9-11 gcatttttaacatttgttaa	5091
OATP2	101	(intron 12 1310~1312)	tccatcttaataataaaatgt TGT/△ ctactcaaaaggagaagtct	5092
OATP2	102	(intron 13 9~34)	tacgagcactaggtatgatg (A)24-27 tatatatatatatatata	5093
OATP2	103	(intron 13 35~64)	aaaaaaaaaaaaaaaaaaaa (TA)10-21 c/t acacacacatacatatatt	5094
OATP2	104	(intron 13 1379~1387)	aaaattattcaccacaatac (A)8-10 caaagtaaagttatgaacac	5095
OATP2	105	(intron 13 1916~1928)	aattctcttaaaaaaatggtt (A)11-13 gctgc t/c ttacagcaattg	5096
OATP2	106	(intron 14 588~596)	caattatactttacctctttt (A)8-10 ctaatttcaaatctcatat	5097
OATP8	1	(5' flanking region -1413)	aataggggcttaataaactct G/C aaacttatgatttctcatat	5098
OATP8	2	(intron 1 38962)	atgaaattagtttaaaaaa G/A caaccttaactataactcctc	5099
OATP8	3	(intron 2 253)	acagacttaccaacaaagaa T/G tatccttccccaaaaatgtcta	5100
OATP8	4	(intron 2 329)	actcatggtttgcaaaataa C/G ttttttaggaaaaactttatctc	5101
OATP8	5	(intron 2 2568)	ccattctggtgctttctttc G/A tgaactatatttccatcagt	5102
OATP8	6	(intron 2 2679)	ctcttattgctcttcttcca T/C gtttaactctaaataattta	5103
OATP8	7	(intron 2 2753)	caggaacttccacaaagcc C/A ctaatttaatttaagctccct	5104
OATP8	8	(intron 2 3132)	tggtttaagttaggagagtt T/C acctcaccagtttaaaattaca	5105
OATP8	9	(intron 2 3193)	aatgctttgggcatatttgc A/G ttcatttggggca t/c tcagtt	5106
OATP8	10	(intron 2 3207)	atttgc a/g ttcatttggggca T/C tcagttctactagatacaaa	5107
OATP8	11	(coding region 334 (Ser112Ala))	gaactggaagtattttgaca T/G ctttaccacatttcttctcatg	5108
OATP8	12	(intron 3 76)	agaattttattttttatactt G/A taagtgggcagttacctttt	5109
OATP8	13	(intron 3 2443)	tcaatttctatggttgccttta C/T agttataggtatttctaaaga	5110
OATP8	14	(intron 4 67)	taatcacgtctataaaagttt C/G tgataattctttaaacaataat	5111
OATP8	15	(intron 4 91)	tattctttaacaaaaattgat T/A taagaacaaaataggagaac	5112
OATP8	16	(intron 4 197)	ggttgaactgcacctgttc G/A cttatatgcagcttttctcc	5113
OATP8	17	(intron 4 813)	tttaacagaaataaaaaaaa T/A attttgttaacgacacaaaaagaa	5114
OATP8	18	(intron 4 974)	atagcaccttaaaaaataac C/G tggattttttaaataatgtaat	5115
OATP8	19	(intron 4 1003)	taaatatgtaattgtacataa G/T gaatatattgcataattttgt	5116
OATP8	20	(intron 6 155)	cattaataatcagaataaaa A/G agaaatttagctcctatttta	5117
OATP8	21	(intron 6 750)	atccaaactgggttttagatt T/G cctcttttctgcctctctctcc	5118
OATP8	22	(intron 6 780)	gcctctccctccatctgcacc C/T tctcttttctcctcagcaaaa	5119
OATP8	23	(intron 6 1248)	ctatgccctgtaattctcaca C/T ttcccttttattttaaattgg	5120
OATP8	24	(intron 6 1500)	tcgtgtctgtgttagcatat A/G ataactcatcagggtttgtg	5121
OATP8	25	(intron 6 2008)	ataacataaatgagtaaaga A/G tatcaagggcaggaaaattag	5122
OATP8	26	(intron 6 2087)	actactctccccatacacac T/C aaaactcatgtgctccccag	5123
OATP8	27	(intron 6 12305)	tcacttatggaggactgcaa T/C cattatcattatttccccaga	5124
OATP8	28	(intron 7 363)	taacaaatgataccagccat C/G atactattctcttggttaatag	5125
OATP8	29	(intron 7 411)	cctttatttttgagaacct G/A gtggatgatattaaga c/a gta	5126
OATP8	30	(intron 7 428)	cct g/a gtggatgatattaaga C/A gtatatagatcactgtaata	5127
OATP8	31	(intron 7 634)	aaaattatatatacatat A/G taactttacctaagtattca	5128
OATP8	32	(intron 7 1791)	tgttttttttaagggtagtga T/C gtgaatagtaaagcgaattt	5129
OATP8	33	(intron 7 2000)	agttgagcaaatgtctctca G/A tagcataaatgtcacttgaa	5130
OATP8	34	(intron 7 2043)	gtttattgatccatttttta A/G tggatcaacattgttagtgag	5131
OATP8	35	(intron 7 2171)	atttattttgagcaaaaggtc G/A c g/a actct c/t cttagaaagcct	5132

Table 1

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GENE	number	position	SEQ.	SEQ ID NO.
OATP8	36	(intron 7 2173)	ttattttgagcaaggctc g/a c G/A actct c/t ttagaaagcctcac	5133
OATP8	37	(intron 7 2179)	tgagcaaggctc g/a c g/a actct C/T ttagaaagcctcacaaatca	5134
OATP8	38	(intron 7 2219)	atttgtaactttaagtctta T/G ataacttatattacaaaat	5135
OATP8	39	(intron 7 2261)	cagataattaataatatttt A/T ttattgaaatatgttatttt	5136
OATP8	40	(intron 8 150)	acaaaatttctccatcttgt A/G ata t/a catcgttgttctgcat	5137
OATP8	41	(intron 8 154)	aatttctccatcttgt a/g ata T/A catcgttgttctgcatctga	5138
OATP8	42	(intron 8 1303)	tttttttgagatggagctc C/T gctctgttgcccaggctggg	5139
OATP8	43	(intron 8 1372)	aagctccgctccagggttc T/G ccacccttctcttaagaaa	5140
OATP8	44	(coding region 1272 (Leu424Leu))	tccttctgtttcaacttct A/G tatttccctctaaatctgcga	5141
OATP8	45	(intron 10 63)	tcacagatttgatttaataa A/T tacttatcaaatcttctctat	5142
OATP8	46	(intron 10 911)	cttgcccaataatccctaccaa C/T gtattattaaacggcatgga	5143
OATP8	47	(intron 10 972)	tcctagtttcccttgaagata G/A gctacaaacttttagtaaaactt	5144
OATP8	48	(intron 10 1101)	tccttggtcctgtgtgtgtcc A/T g t/c agtgaagacctgaaagag	5145
OATP8	49	(intron 10 1103)	ccctggtcctgtgtgtgtcc a/t g T/C agtgaagacctgaaagagag	5146
OATP8	50	(intron 10 2027)	ccatttctcatgagtggtgcta A/G g/a ttttgtcccggtttcaaaact	5147
OATP8	51	(intron 10 2028)	ccatttctcatgagtggtgcta/g G/A ttttgtcccggtttcaaaact	5148
OATP8	52	(intron 10 2372)	tgtattttggcaaatgtattt G/T ttaatatattcaaaaactatt	5149
OATP8	53	(intron 11 10538)	caacagaggatcaaatgtaaa T/G gaaatctcttaaaattaaaca	5150
OATP8	54	(intron 12 55)	ataaatattaaatgttaata C/T taaagactgaatgcaatttaa	5151
OATP8	55	(intron 12 1802)	taaaatgaatcggtgtaaaaca T/G tcatgtataaaatcactgtca	5152
OATP8	56	(intron 12 2612)	ataggcatataataactcttt C/A ttccctctgtatataggagg	5153
OATP8	57	(coding region 1833 (Gly611Gly))	aacagctgtggagcacaagg G/A gcttgtaggatatataatttc	5154
OATP8	58	(5' flanking region (-1590)~(-1587))	tacataacatatataacctatat CTAT/Δ gttatgtgtctgttatata	5155
OATP8	59	(5' untranslated region (-28)~(-11))	agcatcagcaacaattaaaa ATATTCACTTGGTATCTG/Δ tagtttaataatggaccaac	5156
OATP8	60	(5' untranslated region (-7)~(-4))	tattcacttgggtatctgttag TTTA/Δ ataattggaccaaatcaaca	5157
OATP8	61	(intron 4 213~214)	ttc g/a cttatatgcagctttt (T) gtccaaccaaacagaggag	5158
OATP8	61	(intron 4 213~214)	ttc g/a cttatatgcagctttt gtccaaccaaacagaggag	5159
OATP8	62	(intron 4 505)	tataactttctctttataaa G/Δ atgcaaaaattgttatagcatt	5160
OATP8	63	(intron 4 616)	aatgaagtggaggagaaaaaaa A/Δ tgatttcaagttttctgtct	5161
OATP8	64	(intron 4 804~812)	acatccatgtttaacagaat (A)9-11 t/a attttgtaacgacaaaaga	5162
OATP8	65	(intron 4 855)	agattgtttaaccacaaattag G/Δ aaactattattcaacacact	5163
OATP8	66	(intron 7 619~628)	ttttatatatgaattaaaa (AT)4-5 catat a/g taatcttacctaag	5164
OATP8	67	(intron 7 1773~1779)	atcttctatatattgaactg (T)7-8 aagggtagtga t/c gtgaatag	5165
OATP8	68	(intron 8 1270~1290)	tagtgtgccacccttctctc (T)19-23 gagatggagtct c/t gctctgt	5166
OATP8	69	(intron 10 665)	aactcaaggcctttttttt T/Δ ccattgtgacacatatccctgt	5167
OATP8	70	(intron 11 247~250)	aaaaatcttaaggcacacac TGAT/Δ tgacagttgccttgattgta	5168
OATP8	71	(intron 12 1622~1630)	aaataaattgttggcatcta (T)8-10 attttctaagggtcgtgt	5169

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OATP8	72	(3' untranslated region 2464~2465)	cctgatgccttttaaaaaaa A/ Δ tgaacacactttggatgtatt	5170
TAP1	1	5'flanking - 673	agctaaagagtaaaagcacc G/C ctttttccaccagcctcgcg	5171
TAP1	2	5'flanking - 646	ccaccagcctcgctgcctg T/G tcccttcacggacactctag	5172
TAP1	3	5'flanking - 563	ttgcaagcgtggtgctgtac A/C ggcgacctcctcgctccc	5173
TAP1	4	5'flanking - 236	gcttgccgcgcgcgctaac G/T tgtgtaggcagatctgccc	5174
TAP1	5	intron 3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaaactgcaca	5175
TAP1	6	exon 4 + 153	ccctcaccatggtcaccctg A/G tcacccctgcctctgcttttc	5176
TAP1	7	intron 4 + 289	gtattctttagcatccaag G/T ggcatagctgtgtctcttttc	5177
TAP1	8	intron 4 + 291	atttcttttagcatccaagg C/G catagctgtgtctcttttc	5178
TAP1	9	intron 5 + 1139	ttccttcagggttaagtactg C/T ggttctttgtgtcccccca	5179
TAP1	10	intron 7 + 375	gtctctgcccttgcctttgc C/T gcttctctatctctactcc	5180
TAP1	11	3'flanking + 71	agcgcacttttcagctgcgg G/A tgtctctctcttttatactcc	5181
TAP1	12	3'flanking + 129	aactgcatacacttttccct T/C aagctttttaaattccctatga	5182
TAP1	13	3'flanking + 459	cattcaggaggccccaggtc G/A tgtgacgtcgacagttgctg	5183
TAP2	1	intron 3 + 8	tctcctttggcaggtaggtg G/A tggcagctgggtccatttg	5184
TAP2	2	intron 4 + 104	cttcacccgtatgccaggac C/T tggggatgcttttctcttgt	5185
TAP2	3	intron 10 + 219	gcagcagtggtgctccctcc A/G tgggcagccccctcaggtcc	5186
TAP2	4	intron11 + (317-319)	atggtgccaggtggatgtg GTG/ Δ tccatctcattcctgtcttt	5187
TAP2	5	exon 12 + 19	agctgcaggactgggaattcc T/C gtgggagtcgcacagtgtg	5188
TAP2	6	exon 12 + (356-357)	aggtggggtgggtgggtgggtg GG/TGGTGGGGTGGGA ggctgtctgtgtccaggaaa	5189
OCTN1	1	intron1+6602	agcgagccaggttatgtgg C/T gaaggataaggcctctctccc	5190
OCTN1	2	intron1+6790	gacaaaaggggaaaaaccttc C/T gtgataggcaggttttgtgga	5191
OCTN1	3	intron1+14019	cactgtctccactggggccc G/A ccatgtcactgtttaaccaca	5192
OCTN1	4	intron1+14136	ccggtttcctaagaaaaagcc T/C tttctaaaggacccctctta	5193
OCTN1	5	intron1+14266	agctttccaaaaaagacactt G/T cggcaccataaactccccaaa	5194
OCTN1	6	intron1+14412	cttggggcaaacggccactg C/T gtgtgcatggctctctcctgt	5195
OCTN1	7	intron1+15776	acataggagacacttctttc G/A gatctcagttattcagaacaa	5196
OCTN1	8	intron1+15817	ctgtgcttctgcgaataagc A/G gactacttcggatactgtaa	5197
OCTN1	9	intron1+15889	agagccagttttggagcccc G/A tctggcaagcaggcagggccc	5198
OCTN1	10	intron1+16063	acctgtgtctgtgcagaat A/G aggtgtgatataataatgtg	5199
OCTN1	11	intron2+1105	atatttccacaaggctccttg C/A gtacactgtctccatgctttt	5200
OCTN1	12	intron3+1022	cttctgtcaagtggccaggga T/C ggaataattccaaactctact	5201
OCTN1	13	intron3+1217	tccccctctgcaggggggaa G/A gagcgggggcaagattttctt	5202
OCTN1	14	intron3+1596	aagccagagaagctctctcc G/A tgggaatgggaacaagggtgg	5203
OCTN1	15	intron3+1720	ggagcctccaagcctccct G/A tgtgagcgggtgagggcaggg	5204
OCTN1	16	intron3+2104	tatgagactcgttgtgtgtgg G/A ttctcaggtctgaaagtta	5205
OCTN1	17	intron3+8323	cctttcccttttcttaagt G/C tgatagtttgaactctaact	5206
OCTN1	18	intron4+926	tttttggaaactcacaattta G/T actagacctcatggttgcct	5207
OCTN1	19	intron4+1055	cacctgtctgacgagatagc G/A caggtcaggtgggctcactc	5208
OCTN1	20	intron5+ (1197-1202)	caacaacaacaacaacaaca ACAACA/ Δ ttgggaggtgtctaacttc	5209
OCTN1	21	intron5+ (2071-2083)	gtctgtctcattgtctcatgc (T)11-13 caaaaaaagaaactaaggca	5210
OCTN1	22	intron5+2781	tgatcattcctagaaaaaaag G/A acactcacatttggagagga	5211

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
OCTN1	23	intron6+ (882-917)	tcctactctatgatggcagc (AC)15-18 gatgatcgctcagaactggta	5212
OCTN1	24	intron6+924	acacacacacacacgatgat A/C gtcagaactggtagatttag	5213
OCTN1	25	intron7+511	attattgataagtaataagaa T/C acataatttcttaataaag	5214
OCTN1	26	exon8+124	ggtcaggaacatggcggtgg G/A ggtcacatccacggcctcca	5215
OCTN1	27	intron8+3514	acacacacacacacacat G/A tatgaattctcaggaaaggt	5216
OCTN1	28	intron8+3902	aagcaagatgaggatctgtt T/C ttctcctgtgtgagtaaagc	5217
OCTN1	29	intron8+ (4064-4089)	gtgaacataataacttagttg (T)18-26 gagtctcatagccctgtgga	5218
OCTN1	30	3'flanking+115	aacaaatgattatatgcag T/A attcctatccagaaacctt	5219
OCTN2	1	5'flanking - 225	cggcgtagaggagcgagtt C/T ggactcggaccccaaggcct	5220
OCTN2	2	5'flanking - 124	gctggcagagggcgggcctc G/T ccaggtccccaggacaggcc	5221
OCTN2	3	5'flanking - 13	ggcgccgtctgcctgccag C/G gggcgcgcccttgcggccca	5222
OCTN2	4	intron 1 + 232	gggtgtcagtcctggcctccc G/A tctgatggccactttgaag	5223
OCTN2	5	intron 1 + 314	atggccctgtgtgtccagga C/T ttactctagttggggttggg	5224
OCTN2	6	intron 1 + 5055	catgtggtacactagcagcat G/A tctgactgttgatacgggtca	5225
OCTN2	7	intron 1 + 6437	gaagcttggcctcacacaca G/C agccggcaccctgtcatca	5226
OCTN2	8	intron 2 + (173-174)	tagtaagaagagcccaacaaa TC/A atctgactccgtaattcttg	5227
OCTN2	9	intron 2 + 608	agcaggttatttgtataatt C/A taaagcttttaactcaagga	5228
OCTN2	10	intron 2 + 4370	taatttattgatataccaagt G/A cctctataatagatgctca	5229
OCTN2	11	intron 5 + 969	caccagaaaggggtcctgtg C/T gcaaaggtcaggcaggagtg	5230
OCTN2	12	exon 10 + (1028-1044)	ttagcctcctggtttgtgtc (T)16-18 aaacagaaatcactctggca	5231
OCT1	1	intron 1 + 7715	tagtctcctgactcacacatgg G/T tctgtgctttctcctcct	5232
OCT1	2	intron 2 + 97	ggtaggaacatgaccagtt G/A gaattaactgcagaagctgc	5233
OCT1	3	intron 2 + 797	gtggagttgtgtgaacaact C/G tttaaaagagtgtggggagg	5234
OCT1	4	intron 2 + 1768	cgtgaactggagagggtctg T/C gggcactgcccggctgagct	5235
OCT1	5	intron 3 + 1244	gcagatggttaaaggagcaga C/T gcggaagcgacgggtcagg	5236
OCT1	6	intron 4 + 865	agcgtccagtggtaggaaag G/T ctccacaggtggcaatccca	5237
OCT1	7	intron 4 + 1028	gtcatctctgctctcttccc A/G cttcttcatttttatagtac	5238
OCT1	8	intron 4 + 1040	cttctccacttcttctattt T/G tatagtactatttggtattat	5239
OCT1	9	intron 4 + 1485	agcctgcccttccccctgcct C/T gtccttgtgaaacagggac	5240
OCT1	10	intron 4 + 1997	tgagggattacagcccccaac G/A tggggaggggcaggctgcact	5241
OCT1	11	exon 5 + 9	tgggttctgcagggtgtgtgc C/T ggagtccccctcgggtggctgt	5242
OCT1	12	exon 5 + 20	gggtgtgtccggaggtccccct C/G ggtggctgttatcacaaaa	5243
OCT1	13	intron 6 + 379	gaggaagttccattccctcat A/G tctaaacacccctagagaccc	5244
OCT1	14	intron 6 + 2125	tattgaccacaaatctgttct C/A acaatgtaaatatgactgta	5245
OCT1	15	intron 6 + (2935-2953)	tttctccatctgcgaggggc (T)18-20 cttcagttctctgactcatgc	5246
OCT1	16	intron 7 + (6-7)	ttttatctcacctggtaagt (TGGTAAGT) tggtaagttgtctgctttca	5247
OCT1	16	intron 7 + (6-7)	ttttatctcacctggtaagt tggtaagttgtctgctttca	5248
OCT1	17	intron 7 + (1780-1781)	gttttcttttccctttttttt (T) catggagaaagaacagagaa	5249
OCT1	17	intron 7 + (1780-1781)	gttttcttttccctttttttt catggagaaagaacagagaa	5250
OCT1	18	intron 8 + 3247	ccaggccaaaacaattccatt G/T tcatggccactgggccaagg	5251
OCT1	19	intron 8 + 10521	cccttaaccaatgaacgcca G/A tggcagatccctcattctga	5252
OCT1	20	intron 10 + 393	tcagattcttttagtaacttt G/C ttcacaaaaatctttttgaca	5253
OCT1	21	3'flanking + 1755	tgaatgatgttttttcaaatg T/C gtataaaaatgtcctctct	5254

GENE	number	position	SEQ.	SEQ ID NO.
OCT1	22	3'flanking + 1799	ctttcttagaatacctcttgg G/Δcaaaacttctgaggaaggcc	5255
OCT2	1	intron 2 + 1329	tggcagcagaaggggaagg G/Δ ataaaagtggaggaacagggc	5256
OCT2	2	intron 2 + 1867	cctctgtcaaggtaagtact C/Δ attattcttccccaaagggc	5257
OCT2	3	intron 9 + (340-343)	cagcaggccccctaactctct CTCT/Δ gctgatttccacccttcctg	5258
OCT2	4	intron 9 - 396	atacataattcattactttt A/G ttgctagaaaatgatccaag	5259
OCT2	5	intron 9 - 386	cattacttttatttgctaga A/C atgacccaagtttctgactt	5260
OCT2	6	intron 9 - 86	atagaaaaatgctaaaaaaa A/Δ gtttaaacaaaaataaaggg	5261
OCT2	7	intron 10 + 1725	tggaagagggccttttgaatcc G/A agcggaggtcacacactcgc	5262
OCT2	8	intron 10 - 195	caagataatttttaggaataa C/T tctgtcgacatgagttatca	5263
OCT2	9	exon 11 + 328	gttttctggaggggttttttt T/Δ ccatctttgtatttttttaa	5264
OCT2	10	exon 11 + 427	aggcaaaaaaatagaaaaa A/T gtgtgaaaaaacagtaaaagt	5265
OCT2	11	exon 11 + 455	aaacagtaaaagtgggagag G/A agcatctatttttctttaaaga	5266
OCT2	12	3'flanking + 34	agaaatgtatgtcaagaattt T/A agataggccttttcagtaaca	5267
NTCP	1	exon 1 + 307	tatggcatcatgccccctcac G/A gcctttgtgctgggcaaggt	5268
NTCP	2	intron 1 + 607	cccagcaccactccagata G/C gccagccccatctcagccac	5269
NTCP	3	intron 1 + 702	gcagaaatcagcaagggtc G/A ctctggagacgcagcacac	5270
NTCP	4	intron 1 + (3950-3966)	cacatcacctaacagcttgc (T)14-17 gagaaataggcatgtaaaga	5271
NTCP	5	intron 1 + 9597	aaggacataattattcaggct C/G tgagtgtcataattttttt	5272
NTCP	6	intron 2 + 4808	cctatggagaagcaactacc C/T ggggccacttgtctcagcag	5273
NTCP	7	intron 2 + 5032	acacctggagactagcagag G/C cagctttccaccaggatca	5274
NTCP	8	intron 2 + 5046	gcagaggcagctttcccacc A/T ggatcatatcaaatattgtg	5275
NTCP	9	intron 3 + (8-21)	gcctcaatggacggtaggta (T)12-15 aagaaagggtctcactctgt	5276
NTCP	10	intron 4 + (484-495)	taataataacccagaaataaag (A)10-13 gattcctcaactctagtac	5277
NTCP	11	intron 4 + (728-754)	tgcactttaacacccaatttt (A)25-27 caggacattcaaacccactt	5278
NTCP	12	intron 4 + 747	taaaaaiaaaaaaaaaaaaa A/C aaaaaaacaggacattcaaaa	5279
NTCP	13	intron 4 + 1339	cccagtggaacacactaaaat C/A aaagcaacgtattttcttgg	5280
NTCP	14	intron 4 + 1545	accacggacaagaagaggta G/C atcaattgggggttgagggg	5281
NTCP	15	3'flanking + 559	caagacaatatagttttctgg G/A tatcagtttggcacaatgtgc	5282
PEPT1	1	exon 1 + 25	ctgccaggagcacgtccccg C/T ggcaggtcgcaggagccctg	5283
PEPT1	2	intron 1 + 88	cgagggccgggagggcgcgaa G/A ggtacggcgggcggggaagc	5284
PEPT1	3	intron 1 + 106	aagggtaacgcgggcggggga A/T gcggggagcaccgaaagggccc	5285
PEPT1	4	intron 1 + 248	cgaggttgcgacacctggccc G/A ccgcccgtggggcactgta	5286
PEPT1	5	intron 1 + 326	tggagcgggacgggacccag C/A gggtagcggcgaggggcgcca	5287
PEPT1	6	intron 1 + 1238	tttagcatttccagcagatc C/T aatcccagagagctgttagag	5288
PEPT1	7	intron 1 + 3001	tcttatatgctgggaagaag C/T gtcagtaagaaaaagcagcc	5289
PEPT1	8	intron 1 + 5673	ttgggaagtgtccacagccac G/C gggcacaggggacaggggtctt	5290
PEPT1	9	intron 1 + 5679	agtgccacagccacgggggca C/G agggacaggggtcttccacag	5291
PEPT1	10	intron 1 + 5917	aaattcacaaaaatgtacttc C/T ataagaaggctcgttataaag	5292
PEPT1	11	intron 1 + 5966	ctaggcattttagaacttcta C/T aatctgcccttagtgacaag	5293
PEPT1	12	intron 1 + 9255	tggtcatttcaggcctcttc A/G gcctatgatttttagatagtt	5294
PEPT1	13	intron 1 + 10278	catgacccatgtaggcggga A/G aagcagccctgttagcagcag	5295
PEPT1	14	intron 1 + 20251	aagaagagccctgtgtttatt C/T agtgattgcaatgtgttggg	5296
PEPT1	15	intron 1 + 20509	aaacaccacttctgcatttg C/A gctttctaagatagcaatcc	5297

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
PEPT1	16	intron 1 + 20532	tttttaagatagcaatctctg T/C tgacacaggtacattaagat	5298
PEPT1	17	intron 3 + 55	agagcgggagtgccataac C/A agtcttaactttgtttccccc	5299
PEPT1	18	intron 5 + 1720	atcctctcttttactggaaa C/A aataaagctacaaaaaagacc	5300
PEPT1	19	intron 5 + 1790	gctactgtttttatgttttcc G/A gatggtaaattattagatgg	5301
PEPT1	20	intron 5 + 1860	agtttgcatttgactatcac G/A ctgcattcctgtgagctggc	5302
PEPT1	21	intron 5 + 1943	agggccactgagggaactg G/A ggaagagagagggcctttctac	5303
PEPT1	22	intron 8 + 1478	tgttttcagatcttagtagt A/G catggaataggaccgttttc	5304
PEPT1	23	intron 8 + 1898	ttaaatattagtggtgtaaaag A/G aaacatagactcaatctctt	5305
PEPT1	24	intron 10 + 388	ttaaatagtttagacatttt C/T gatttttctaaagaaaactgc	5306
PEPT1	25	intron 11 + 985	atccataaggtactcagtg C/T tggcctgtatgaagaactca	5307
PEPT1	26	intron 11 + (1022-1045)	ctcaaacaggggtagatttc (T) 20-24 gagtcaagagtcactctg	5308
PEPT1	27	intron 11 + 1320	tgtgagccactgcacctggc C/T aatttcctgactttctatga	5309
PEPT1	28	exon 16 + 107	tggagagatggtgacacttg G/C cccaatgtctcaagtaagta	5310
PEPT1	29	intron 18 + 6048	tttgttgtgggtttttttt T/A gttgttgtttgtttgttttg	5311
PEPT1	30	intron 18 + (6141-6142)	tcactgcagcctccgcccc (T) gggttcaagcaattatctctg	5312
PEPT1	30	intron 18 + (6141-6142)	tcactgcagcctccgcccc gggttcaagcaattatctctg	5313
PEPT1	31	intron 18 + (6241-6242)	tatttttagtagagacgggg (G) ttccaccatattggccaggc	5314
PEPT1	31	intron 18 + (6241-6242)	tatttttagtagagacgggg ttccaccatattggccaggc	5315
PEPT1	32	intron 18 + 12102	gtgggaattctagctaaagg C/T cgtgtggatctgtctcaggt	5316
PEPT1	33	intron 18 + 12203	gacctgagtttaattcatag C/A cttttctccagcacctaa	5317
PEPT1	34	intron 18 + 12307	gaaaggttaaattattcttt A/G cactgctgaggtgtacacta	5318
PEPT1	35	intron 20 + 79	tcacaacacacttaggacata A/G tatgatttaactagagtgtat	5319
PEPT1	36	exon 23 + (348-370)	tctttttctttttttttttt (T) 18-23 gagacagagttttgtctcttg	5320
PEPT1	37	exon 23 + 790	ccacattgggtcatcttccct A/G tcacacaaatgatgttattt	5321
PEPT1	38	3'flanking + 2	aaataaaatttctgttcttaa G/A cctaaggtttcatgtatctc	5322
EPHX1	1	intron 1 + 110	tgcataaattgtgtcttactag C/T ttctagtgcataaaaaatttg	5323
EPHX1	2	intron 1 + 143	aaatattgggtggagctcttc G/A ctgtgctgggcccagtcacca	5324
EPHX1	3	intron 1 + 1097	aatccagagagggagataga T/G tggaagttcaaggggtggaca	5325
EPHX1	4	intron 1 + 1717	ttccaagacagagcaggggg T/C gctgtggggcgtggttttgc	5326
EPHX1	5	intron 1 + 1772	aactcgatgctttctctcc G/T tctgggtcttaactgcagtg	5327
EPHX1	6	intron 1 + 2054	gaaatgtaacagggcaacact A/G tggacacagaaagtagatta	5328
EPHX1	7	intron 2 + 1414	atttccaaaaatctgttttggg G/T gtaactgaaacacttgggaa	5329
EPHX1	8	exon 3 + 174	tacctcacttcaagactaa G/A attgaagggtatgtttgcaaa	5330
EPHX1	9	intron 3 + 6583	ctgtcaataaccatgaagggg G/C ggcgggggcaactaagggttg	5331
EPHX1	10	intron 4 + 34	agaggttccataaactgcccc G/A tcctcgcccaagggtggccc	5332
EPHX1	11	intron 4 + 63	aaggggtggcccggtgttcc C/T accaggtctctctccggcg	5333
EPHX1	12	intron 5 + 154	gcagtgctgagggcagcttg G/A ctggatcctcctctgtctgta	5334
EPHX1	13	intron 5 + 276	tgtggaccaagctctggga T/C agccctgagcagaactcccc	5335
EPHX1	14	exon 6 + 130	gatgtggagctgctgtaccc C/T gtcaaggagaaggtattcta	5336
EPHX1	15	intron 8 + 206	ggtgcctggctcccgggcg C/A cctcagtagcgtccccagt	5337
EPHX1	16	intron 8 + 353	tggccctccagaaaaagaga A/G ggcctcagtgaggggagag	5338
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagaggtgagagag	5339
EPHX2	1	5'flanking - (523-522)	aaagtcactggatatgcccc (C) tccccgcccccccaacagg	5340

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
EPHX2	1	5'flanking - (523-522)	aaagtcactggatatgcccc	5341
EPHX2	2	5'flanking - 522	aaagtcactggatatgcccc T/C cccccgcccccaaacagg	5342
EPHX2	3	5'flanking - 521	aagtcactggatatgcccc C/T cccccgcccccaaacagg	5343
EPHX2	4	5'flanking - 516	actggatatgcccccccc G/C ccccccaaacaggctcttatg	5344
EPHX2	5	5'flanking - 515	ctggatatgcccccccc C/G ccccccaaacaggctcttatg	5345
EPHX2	6	intron 1 - 74	tggctgcttctcaatgaata T/C gaacagtgtctgtttccatg	5346
EPHX2	7	intron 3 + 72	gagcattaggtcagaatcca T/C tgaagtgaagctttgagatca	5347
EPHX2	8	intron 4 + 473	gtgtgtctctactttaattct A/G caaaagggtgattgaatggag	5348
EPHX2	9	intron 5 + 276	caagagtgaggatgttcaagg C/T catcctgacctcacttttga	5349
EPHX2	10	intron 8 + 8	tctgctctctcccggtgggtg T/C gctgtcttgcagctgtctta	5350
EPHX2	11	intron 9 + 1573	atgtcgtgaagactgatgaa C/T gatggacggctgcactgctc	5351
EPHX2	12	intron 10 + 207	gaacaggatggagatgagct T/C gtttattgtcttttaataga	5352
EPHX2	13	intron 12 + 911	tgaagagacctcgacatgtc G/T catcccacatactacagggga	5353
EPHX2	14	intron 12 + 2425	atcttctcagctgagcaaac C/T gaggctcagagggcttaacc	5354
EPHX2	15	intron 12 + 2460	ttaaccccaactggccccaa G/A ccagggtacatgattgggtca	5355
EPHX2	16	intron 12 - 281	aagtcctttcaagagattat T/C ataagtagtaccttctcatt	5356
EPHX2	17	intron 12 - 268	agattattataagtagtacc T/G tctcattatagggaattatga	5357
EPHX2	18	exon 13 + 50	cctgagtcggacttttcaaaa G/T cctcttcagagcaagcgatg	5358
EPHX2	19	intron 13 + 1739	ttgtcgtaaacagggttttca G/T atgagcatatttctcttga	5359
EPHX2	20	exon 14 + 33	atgcataaagtctgtgaagc G/A ggtaagagacatgcttggga	5360
EPHX2	21	intron 14 + 314	ggattgagagcttacctcta T/C ggggtcacctcgtgtatgc	5361
EPHX2	22	intron 14 + 878	attcccttattccttccacac C/T gtctgtcactcattcattca	5362
EPHX2	23	intron 14 + 948	gcacaggctgggtatgaagc T/C ggggctgcatgctcagctac	5363
EPHX2	24	intron 15 + 259	agagggttttcaactactttt C/T agtcatggctcctcagagaa	5364
EPHX2	25	intron 16 + 459	tcctcatttgtcaagcagaa G/C atgagtttccaaatctctggg	5365
EPHX2	26	intron 16 + 645	gtaagtgaacacacactgtac G/A tgcagacttctcctgccagac	5366
EPHX2	27	intron 16 + 985	gtcattatcatcatatgacc G/A atgaaaaatgaccaaactgca	5367
EPHX2	28	3'flanking + 12	aggtggccttacacacatct T/C gcattggatggcagcattgtt	5368
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atggggatgaaccccttccc	5369
EPHX2	30	3'flanking + 544	tagccacctgcctttctccc G/A gcttccctagcagagtttgc	5370
COMT	1	5'flanking - 1287	cgtatgatattccccattct G/A agtccagaataacctagaaat	5371
COMT	2	5'flanking - 1217	tgtgagtatgggaaggga G/A cttttctgtctgttgcctccc	5372
COMT	3	5'flanking - 503	caggggctccagaggagcga G/A tgtgtatcctccattgctc	5373
COMT	4	5'flanking - 425	gagaagttgggaagtctggc C/T agtggggccggtgcctgggtg	5374
COMT	5	5'flanking - 277	cccagccccagtttccccac C/T tgggaagggggctacttctg	5375
COMT	6	intron 1 + 12058	ctggcccatggaaggagggg G/A agggggcccccgacggggcca	5376
COMT	7	intron 1 + 12070	agggaggggagggggcccc G/A cggggccacagtaaaaggagt	5377
COMT	8	intron 1 + 18831	tgtgtatgttcttgggtaaac C/T agcccttgggtcttacacatc	5378
COMT	9	intron 2 + 832	cctctccttggccaccct G/C actaccccccaactccgggccc	5379
COMT	10	intron 3 + 90	ggagaagctgttatccccc A/G ttccaggggggctgggaacc	5380
COMT	11	intron 3 + 425	ccccagggtggcggttcgg T/G gattcagagagggcgactct	5381
COMT	12	intron 3 + 671	ggctcctgctcttggggaga G/A gtggggggccgtgcctggggg	5382
COMT	13	intron 3 + 676	ctgctcttgggagaggtgg G/T gggccgtgctggggatcca	5383

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
COMT	14	intron 5 + 75	tcagcctcagcctctccaaa G/C agccaggcattccagtagag	5384
COMT	15	intron 5 + 310	accagacaccaggggcagaaa C/T ggcacaggaccaaggagatg	5385
COMT	16	intron 5 + 346	agatggggtgggaaggcc G/A ctctggggccagcctgctct	5386
COMT	17	intron 5 + 3023	aaggcagcgccctgctcaa G/A gctagggccattgtcctcct	5387
GAMT	1	intron 1 + 429	ctcgaaaagctgagctcagg G/A agacagctgtccccgggtg	5388
GAMT	2	intron 5 + 1411	ggtgacctggtgccatcccc G/A accaggagacgcaggtgccc	5389
GAMT	3	3'flanking + 626	cactgacctccttgccctga G/A agaaggccggctcctgtgct	5390
PNMT	1	5'flanking - 367	aagagtgaaatggctgcggg G/A ggctggagaagagagatggg	5391
PNMT	2	intron 1 + 35	ctgaggcacgagggaacaaga G/T gtcgtcggggagtgaaagca	5392
HNMT	1	5'flanking - 211	cagaggcagatgacagtctt C/T cgtaaagatttcactgctg	5393
HNMT	2	intron 1 + 5409	aataaactgatataattgg A/G acatttcattgttggcctagt	5394
HNMT	3	intron 2 + 2561	cacttgcttggaacaaga A/G agaaggcctacaagaaaaag	5395
HNMT	4	intron 2 + 2895	caatcagaaaatgtaagaaaa A/C ctccaagaaaaatttaagtt	5396
HNMT	5	intron 2 + 3977	acaaaacttggaagtgtaaa G/A ttatgcatgtatgttcatgt	5397
HNMT	6	intron 2 + 5296	ttaacatagtgtgttggag T/C ccaggattttattttcctt	5398
HNMT	7	intron 2 + 13317	caacctcatgaattcttag C/T tgggatgggtccctataaca	5399
HNMT	8	intron 2 + 14682	gtagatgagcaaatgagttc A/ Δ ggagagattttaatacccta	5400
HNMT	9	intron 2 + 15406	gtctatgcattcatgcatcc G/A tctaaccagctgtctaccta	5401
HNMT	10	intron 2 + 28943	atgtgacttaaaacttcaggt A/G tatcaatatcccttgaatgt	5402
HNMT	11	intron 4 + 49	cagaaaagaagacttttcaga A/G tatatatataatgaatatct	5403
HNMT	12	intron 4 + (1942-1943)	tttgagaaaaatttaaggta (A) tcttctatggcccacttcca	5404
HNMT	12	intron 4 + (1942-1943)	tttgagaaaaatttaaggta tcttctatggcccacttcca	5405
HNMT	13	intron 4 + 2405	ccctgtgaccaagcagataa C/A ctcatgctttatttagtcca	5406
HNMT	14	intron 5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatatatttgtcttcaattat	5407
HNMT	14	intron 5 + (80-81)	cctgtgtttgaaagaagctt atatatatttgtcttcaattat	5408
HNMT	15	intron 5 + 235	ctttcttttggaaaaatatg T/C ctttgtcttctatatatgaa	5409
HNMT	16	intron 5 + (702-703)	tacttacaggttgatttttag (AT) acacagcagactctgtcttc	5410
HNMT	16	intron 5 + (702-703)	tacttacaggttgatttttag acacagcagactctgtcttc	5411
HNMT	17	intron 5 + 749	ttacaccagacccccatactt T/G aacaccatatgtcacaaaat	5412
HNMT	18	intron 5 + 1101	gtaggcagcctattcttgat T/G atattcatcaatcatcacaga	5413
HNMT	19	intron 5 + 1137	acagaaaaagtattgttagac G/A gaaataacaattcattgaga	5414
HNMT	20	intron 5 + 1348	aaggagcatgaatagtcca C/G aagtaactgagaactgatta	5415
HNMT	21	intron 5 + 1673	caaaaagaaaggagtaaaaga C/G tcaacaatcagttagctttt	5416
HNMT	22	intron 5 + 2022	atthtatttggggctttcta C/T gtctctctctcctaagccta	5417
HNMT	23	intron 5 + 2285	tgctcacttaactctttaa G/C atccagagtaaatgatggag	5418
HNMT	24	intron 5 + 4159	taccagttgacccagcaacc C/T tcttatagatgtgtttaa	5419
HNMT	25	intron 5 + 4501	aatgatcccaaaaattacta C/G tcaattgttttcttccaatga	5420
HNMT	26	intron 5 + 5251	cacacacacacacacacaca C/G caaatgggaagcagccagaca	5421
HNMT	27	intron 5 + 5802	gaaaaagaaaaatctggctta C/T atcatgttgaaaaacaaagt	5422
HNMT	28	intron 5 + 6189	tccaatccaccttctccta G/C agcatatcctgcagttacct	5423
HNMT	29	intron 5 + 6297	gtcttggttcatctctttgag T/A taaattagatctgggaactt	5424
HNMT	30	3'flanking + 458	tatgtcactctcaagaactc C/T tataagaccaagagtcactt	5425
HNMT	31	3'flanking + 993	ctgaaaatgaacactgaacc G/A ttaatcatactgatattgtac	5426

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
HNMT	32	3'flanking + 1793	gtggagcacagcatatttagg G/A cttagatatttggcttattata	5427
NNMT	1	5'flanking - 228	ataattttcttgacgagctc A/T agtgcctcctctggtcttaca	5428
NNMT	2	intron 1 + 44	ccccactaatgtgagtcata T/C agatggaggtctcagggcacg	5429
NNMT	3	intron 1 + 149	ggataaaaacgaatattggt A/G tagcgattccacagtttaca	5430
NNMT	4	intron 2 + 158	agataggcccatgtgtgtgc G/A tgtagtaaaatttgtgtatg	5431
NNMT	5	intron 2 + 433	gctgtagccatccaagccta T/C agaacttggctgtgagtgtg	5432
NNMT	6	intron 2 + 10826	atcatctgactggtaagtcc C/T agttctgtggttaactcaagt	5433
NNMT	7	intron 2 + 13630	atttcattggagggaagtcca T/C ggtagaagcagggtgctagg	5434
NNMT	8	3'flanking + 71	ggctcagtggttggggccca A/G tggttcatcttaggacgggac	5435
PEMT	1	intron 1 + (297-299)	attgtgtgagactcagaggt TGT/ Δ ccgtgttagtctttgggatt	5436
PEMT	2	intron 1 + 817	tcataagccctgtaaggcac A/G tctctgccccaaagcagcttc	5437
PEMT	3	intron 1 + 830	aaggcacatctctgccccaa G/A cagcttctaataccagttctt	5438
PEMT	4	intron 1 + 1035	gagttctctgaaggagctaa T/C accagttagtgttttgaaga	5439
PEMT	5	intron 1 + 1573	agtgggcaggggagactaac C/T ggggtgtgtgaggggtgggct	5440
PEMT	6	intron 1 + 1759	gattttctttaaagaagaa A/G gaaagaacatacaacatac	5441
PEMT	7	intron 1 + 2768	gcattctgtgtccacaggg C/A ggggcacctccaggattcag	5442
PEMT	8	intron 1 + 2785	ggccggggcacctccaggat T/C cagaagatgactccagtagg	5443
PEMT	9	exon 2 + 162	agctcagcagacctcctggc C/T gtgggtgggtagctcctttcc	5444
PEMT	10	intron 2 + 4598	ccgtgggttttttttttttt t/ Δ ctctatttcttttgggtgtg	5445
PEMT	11	intron 4 + 39	actgtccagacgggagtagtc C/T cactgcttgggtgagccccac	5446
PEMT	12	intron 4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggcctctg	5447
PEMT	13	intron 4 + 1355	ctggagccaggctgcagccg A/C agtgcctggccatccctggcg	5448
PEMT	14	intron 4 + 5925	gtccaggcactgtggcccta C/T gtgggagttctccagttcca	5449
PEMT	15	intron 4 + 6028	ggcagtggtccaaaggaccag G/C atggactcctctctctccacc	5450
PEMT	16	intron 4 + 6078	atctgtacctctcgaggactc C/T acctggctctgtgcccacac	5451
PEMT	17	intron 4 + 6089	cgggactctacctgggttc A/G tgccatcacccccgccagat	5452
PEMT	18	intron 4 + 6379	tcagggtgtccccctccctcat G/A cctcctcaccctgccccctc	5453
PEMT	19	intron 4 + 7339	tgtaaggaaatcctgccaaga C/T ggcagatgcacacggggtca	5454
PEMT	20	intron 4 + 7619	ctcctgcacatgtgtctccag A/G gaggaaggcatttgacagg	5455
PEMT	21	intron 4 + 8858	ggcatgtgtgtgtgtgtgta T/G gtgtgtgagttgtgtgcatgt	5456
PEMT	22	intron 4 + 9029	tttctggaccagaaaagcgtc G/A tctctgccaggggcctcttg	5457
PEMT	23	intron 4 + 9056	gccaggccctctctgcaacttg C/T gggaaagctgagctgagctg	5458
PEMT	24	intron 4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgtgtgtgtgcaact	5459
PEMT	25	intron 4 + 9523	agcagcattactctgtgtgtgc T/C gctggcactggcctgggtggg	5460
PEMT	26	intron 4 + 9622	gacaaagtgtacaacaagggt G/A tctcgaactgggtcagctca	5461
PEMT	27	intron 4 + 10776	ccattcctgggtcttcttcttg G/A aggtgaatgaaattcccatg	5462
PEMT	28	intron 4 + 10912	tctgccccactttgtctcaga G/C gtgcaacaaggccttcagga	5463
PEMT	29	intron 4 + 11590	ggacactggcctgatgcaga G/C gtgtgtgtctctctcctgcag	5464
PEMT	30	intron 4 + 12090	ggccagggcacccctaccag G/C ctgagtcaccacctgtccagc	5465
PEMT	31	intron 4 + 12263	taccgccttcccagatgga G/A cgggctgtctcatgggaactta	5466
PEMT	32	intron 4 + 12448	tctgggtccctctctctgctt G/A tagtttctctgggctaaaatc	5467
PEMT	33	intron 4 + 12730	tgggaccagtgccgccacca C/T ggcccaaggacctggtgttc	5468
PEMT	34	intron 4 + 13240	gggctccagggcacacagcgg T/C ccagtagacacctgtcgcttt	5469

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
PEMT	35	intron 4 + 13494	tccgtggaactcagagatgg T/C acctccctcgaggtggggc	5470
PEMT	36	intron 4 + 13817	aacttccctcgtgtgtgag A/G cagatcttgagcctcgcc	5471
PEMT	37	intron 4 + 14773	ccgcccgtgtctcatgcc C/T ctatgcctctcactgcctgg	5472
PEMT	38	intron 4 + 14951	gtccctgagggccctccacc G/A gagcctgggtgcccctcaca	5473
PEMT	39	intron 4 + 16896	gctgtgactgtcttggagac T/C gggctcttgccggcctggtg	5474
PEMT	40	intron 4 + 19439	ccaggagcctctgagggcagc G/A ggggcttctcaaccacacac	5475
PEMT	41	intron 4 + 19557	attttgtcagcatgtcacgt C/T cctttcataatgaagcaagg	5476
PEMT	42	intron 4 + 20051	acagcactgcgggagccacg A/G catctgcagacgcatttgat	5477
PEMT	43	intron 4 + 20816	tggactctctggcgctccatc C/T agccacttcagtgcgacgtg	5478
PEMT	44	intron 4 + 21196	ggctggctgggcccctgggat C/G atcgtgacagggcttttagtgg	5479
PEMT	45	intron 4 + 21528	acaggtgggagccgagggctc G/T ggaggtgggcccggctgagc	5480
PEMT	46	intron 4 + 21596	ccgcttcccctgctctctggc C/T gtagcagaaaagtgtcccact	5481
PEMT	47	intron 4 + 22672	agcctcccactgccttctgtg C/T tgaggggagggggcccgggtc	5482
PEMT	48	intron 4 + 22713	tctaacgctgtcttcttctgt A/T ctgaaaaacaaaacaccttct	5483
PEMT	49	intron 4 + 23010	tgccggggcagcggggaggga G/A ggcgagtgggtcccccagt	5484
PEMT	50	intron 4 + 23588	gtgcaggcgcctgcctcc C/T gcagccaagttctggggcga	5485
PEMT	51	intron 4 + 23627	gacactgccctgagccaggga C/T ggtgaggtgggacgccttcc	5486
PEMT	52	intron 4 + 23941	tgaggggttgaggactctaca G/A aggagagtggactcacgggg	5487
PEMT	53	intron 4 + 24091	gacaccttctcactgtctcagc G/T ctgagacacgcccctgcccct	5488
PEMT	54	intron 4 + 25348	caggccagtgtggaatccctac G/A tagagtgaagcatctcagc	5489
PEMT	55	intron 4 + 25603	taagcagttaacactgatgc G/A tgatgaaaaattccaaacagca	5490
PEMT	56	intron 4 + 31540	cctccaggtggcaggaaacac T/C gtgaggagcatgcaacgtgc	5491
PEMT	57	intron 4 + 31637	gtgggctggagcggccaggac G/A gtgaggggcttcaaggtgtg	5492
PEMT	58	intron 4 + 31642	ctgggacgccaggacgggtga G/A gggcttcaaggtgtgtttgt	5493
PEMT	59	intron 4 + 35593	ggaggagctgaaagagctgg G/A gctcgggatcaggtggttca	5494
PEMT	60	intron 4 + 35647	actttgaggcaccaccgcac C/A gtccctgcgtgagggagac	5495
PEMT	61	intron 4 + 35862	tcccagtggtggctctgtcc C/T cgtctcagccgagcactcag	5496
PEMT	62	intron 4 + 35882	ccgtctcagccgagcactca T/G cggccagggtggctggactc	5497
PEMT	63	intron 4 + 37141	ccacaggccggatgccttga T/C acttctcagctgcagggtg	5498
PEMT	64	intron 4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgccatgg	5499
PEMT	65	intron 4 + 38872	acctcagacagcaaggacgg G/T catgccatgggtcccggcag	5500
PEMT	66	intron 4 + 39140	atgtctcaaatctccctccc C/T gggaaaatctaggcacaggtc	5501
PEMT	67	intron 4 + 39635	caggcccaggagcagggtggg G/T cctcctcacaggagcagggc	5502
PEMT	68	intron 4 + 39713	actctgagcatgctggctcc C/T tccctcttccaggggcagca	5503
PEMT	69	intron 4 + 40436	cctgggtgtgcttcggacc C/G gaggcagacagaggaggcct	5504
PEMT	70	intron 4 + 47485	acaaatgactgttgagccct C/T gaggcagctgtgtcacgtgg	5505
PEMT	71	intron 4 + 48131	actgggggatacctgaatccc G/A cctcctgatgccagtggagc	5506
PEMT	72	intron 4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttggccggag	5507
PEMT	73	intron 4 + 48702	gagatggggggcgttctggga G/A gcaaaagcaggaaggcagaa	5508
PEMT	74	intron 4 + 50302	gcatgtgcatgggagagggc T/C gtcccatctgagtgaggacc	5509
PEMT	75	intron 4 + 54102	ggccgcgtgctccctgcagcc A/T tgggctcctctggcagttct	5510
PEMT	76	intron 4 + 54220	ccagggacagatcttctcc G/A ccagacgtctcttctgctc	5511
PEMT	77	intron 4 + 54371	gcagataatgtgcagctggg G/A tgcagtgtgtgtgtgtctccc	5512

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
PEMT	78	exon 5 + 79	tggcctgctactctcttaagc G/C tcaccatcctgctcctgaac	5513
PEMT	79	intron 5 - 6796	ggaggaagtcagcttcttac A/C gatggtggctcccagcttcc	5514
PEMT	80	intron 5 - 6636	ttttctctctcaccttttg T/C gttcagaggcagaggtgtgc	5515
PEMT	81	intron 5 - 6448	gtgggcccaggctctgacag G/A accctcgggaccagctcctg	5516
PEMT	82	intron 5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	5517
PEMT	83	intron 5 - 4824	ggacaggccgggggttgagc G/A gctgcatgaaggaggagggg	5518
PEMT	84	intron 5 - 4249	tcaccagagtgatttctctcg C/A ggcaggtgcctggggtagcc	5519
PEMT	85	intron 5 - 4230	gaggcaggtgcctggggttag C/T cactgggctgggtcccatgag	5520
PEMT	86	intron 5 - 4182	ggagagtaagggtggggggg G/A cacttaggacaggggaagctg	5521
PEMT	87	intron 5 - 3369	ccaggtggggccgtgtgcct G/C tggcctgggtgtgtggcccag	5522
PEMT	88	intron 5 - 2625	cagggaaagctggcccctgaa C/T gagctgggcttttggggccac	5523
PEMT	89	intron 5 - 1200	attattgtgagcatgggaag A/T gcacatttgggtcacacatgt	5524
PEMT	90	intron 6 + 606	gcctggctagacgcccacca A/G tgaccctgatgatggcagca	5525
PEMT	91	intron 6 + 1229	tttggctccaggaagggggac G/A gcagccaggagcgctctggat	5526
PEMT	92	intron 7 + 716	atggagatgtgtctcccccg C/G gggctcagaggacctgctggtc	5527
PEMT	93	intron 7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	5528
PEMT	94	intron 7 + 1718	gggcttccagggtgtctgagc T/C cccccggcatgtaggacccca	5529
PEMT	95	intron 7 + 2695	ggctttgggggacccctggac C/T catttctagaaaaacagcctt	5530
PEMT	96	intron 8 + 140	ccagggtctccagggtcagag C/T ggccatggtagcttacaatg	5531
PEMT	97	3'flanking + 179	tacttaggaggcgtcagggg C/T tcacctggccatggccatgg	5532
PEMT	98	3'flanking + 394	gatgacactgtcattctctaa A/G tgaatggccttgtgtgctgacc	5533
ALDH1A1	1	intron 1 + 564	cattatttcttcagccaagt T/C tgttgccattggagcagatg	5534
ALDH1A1	2	intron 1 + 710	gttctgagagtaactctgaa C/T tttgctgttttcacactgct	5535
ALDH1A1	3	intron 1 - 3868	ccctttttatatccagaata C/G agcctaaaacttcttctctg	5536
ALDH1A1	4	intron 2 + 2933	taagtatgctatactataatt T/C gatagataatactatactata	5537
ALDH1A1	5	intron 2 - 1646	caatgtgatttaactgaatgc C/T gcaaatatgcactgtatag	5538
ALDH1A1	6	exon 3 + 54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	5539
ALDH1A1	7	intron 3 + 157	tagggcccttaacattggaac T/G attctcaaatagtaaatctgc	5540
ALDH1A1	8	intron 3 + 339	tgagtctcctagaatgatat G/A ttaggtttattcaagcattt	5541
ALDH1A1	9	intron 3 + 655	agcagttagatgagtcagag C/A ataataatagttggggaggg	5542
ALDH1A1	10	intron 3 + 735	gaagccaatttaacataaac C/A aataccaagatcagggtttca	5543
ALDH1A1	11	intron 3 + 863	gcaagtatggttaatacaag G/A accatttattactcaaatat	5544
ALDH1A1	12	intron 3 + 1757	agatgacaagaatttcttcta T/A ttcaaaaaattccctagcaca	5545
ALDH1A1	13	intron 5 + 90	ttctctaaaaacagatggatg C/A ttatgtatttgttaaatgtg	5546
ALDH1A1	14	intron 6 + 213	caggaagcccaaacacaaaagg T/C ttgggtgtcaaacagtcact	5547
ALDH1A1	15	intron 6 + 1323	ttttgaattaaattcttata C/T tgtaactttttaaaacttttta	5548
ALDH1A1	16	intron 7 + 638	gcaaaaagaaagtgggtggaag C/A atactgtaccatgcaaaaaa	5549
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattcttatgtttttt (T) gttgtgattatttattctatc	5550
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattcttatgtttttt gttgtgattatttattctatc	5551
ALDH1A1	18	intron 9 + 1757	tgatctagaatttagttttct A/G taaatgaatagaatccagt	5552
ALDH1A1	19	intron 12 - 1383	aatcccaacttattactctcc T/G gagagcttcaagtgcctata	5553
ALDH1A1	20	3'flanking + 40	ttttaagtacaagtttttgggt T/C acagtgatttcttcttctgca	5554
ALDH1A2	1	5'flanking - 716	cagggatcctcattctgagc C/G cgaggcaggggggactcgca	5555

Table 1

GENE	number	position	SEQ.	SEQ ID NO.
ALDH1A2	2	intron 1 + 314	cggtccgactgcccgggg G/ Δ aaggcgtcggaaccgcttag	5556
ALDH1A2	3	intron 1 + (664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaacgttgacatctt	5557
ALDH1A2	4	intron 1 + 1370	gcatgcagcttagaagtttt A/G tttatgagggtctctaaacc	5558
ALDH1A2	5	intron 1 + 1557	ggtacgtttttcagaattta A/ Δ ttgggaagctcttccagttc	5559
ALDH1A2	6	intron 1 + 1934	tcagctcttttagtgagactt C/G taaatttttctaagacaagca	5560
ALDH1A2	7	intron 1 + (1971-1980)	agcatagtggaacaagcagta (T)9-11 aaacgtgaagagcagaagct	5561
ALDH1A2	8	intron 1 + 2295	tactgtaagacaatatgtta T/C tgttttttctgtctgtctaaac	5562
ALDH1A2	9	intron 1 + 2387	ttgggaccacacatagagtca C/T tacttaaaataaatgaccag	5563
ALDH1A2	10	intron 1 + 2841	aggaatgtgcttttttaaaac T/ Δ agatggtgttagtcaaggag	5564
ALDH1A2	11	intron 1 + 3035	gacttttataaattttgtata A/G ctgatattataggaatacac	5565
ALDH1A2	12	intron 1 + 3319	aaagagtattgtttttttttt T/ Δ ctgcatctgatattatatgg	5566
ALDH1A2	13	intron 1 + 3474	ttgtcttttattatttcat T/C taaacttctgttttctgtggg	5567
ALDH1A2	14	intron 1 + 4186	ccttccaaacctttacttaa G/C attgtctgttttctgtcataa	5568
ALDH1A2	15	intron 1 + 4222	cataaattgtcagtcacaaact A/G catgttaatatagaggacttca	5569
ALDH1A2	16	intron 1 + 4254	aggacttcagggtttttttttt T/ Δ aaatacttttttcataaactat	5570
ALDH1A2	17	intron 1 + 4397	ccttccactacatagggcct A/G tgttaccatgtgggaattatc	5571
ALDH1A2	18	intron 1 + 5935	aactccagggttgcataataga T/C gttctgtgtatttttaagtag	5572
ALDH1A2	19	intron 1 + 6206	ttttgaaagccctccttagca T/G ttctttaattttcttttattga	5573
ALDH1A2	20	intron 1 + 9559	agataaattgatgaattatt C/T actctgtgtgtgtgtgatagat	5574
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaaa (AAGA) ccttttttttgaataaactct	5575
ALDH1A2	22	intron 1 + (9631-9632)	taaaaagaatttctaaaaa ccttttttttgaataaactct	5576
ALDH1A2	23	intron 1 + 12731	ctgaaatagaaacccctttcag T/A gtacctgtcagagcagtgaa	5577
ALDH1A2	24	intron 1 + 13442	cagtgctataaagatccagc G/A gaaatcaaaatgttttcatat	5578
ALDH1A2	25	intron 1 + (14173-14176)	tctaaaaataataataaata AAAA/ Δ gagaaaaataagtttaagat	5579
ALDH1A2	26	intron 1 + 14586	actcattttattggtttcaaag C/G cttcttcaaccttaggatat	5580
ALDH1A2	27	intron 1 + 14595	ttggttcaaaagccttcttca A/G ccttaggatatgcattgagg	5581
ALDH1A2	28	intron 1 + 14711	gtttgagacattaaacttcta A/G ttcaactgaagatgctagtt	5582
ALDH1A2	29	intron 1 + (15327-15337)	gaagagcacagttagaaagac (T)9-11 aacctagcaatactattga	5583
ALDH1A2	30	intron 1 + 17258	atcagtacaatgtgttgggc A/G tacaacacttaatttaaaat	5584
ALDH1A2	31	intron 1 + 18277	taatacaaatcatttgaagc A/G ttactattaaaaaaacaaa	5585
ALDH1A2	32	intron 1 + 18734	ccttgagcacctactgcatt T/A taagtgtgttaagatgtgg	5586
ALDH1A2	33	intron 1 + 19081	ttaatcacctcaatctttaa C/T gaatttcttgatttttcttt	5587
ALDH1A2	34	intron 1 + 21514	aatcaggatatgggggttc G/A ttctttattctgtccacaaaat	5588
ALDH1A2	35	intron 1 + 21732	cattttaaataagtgcttta A/G taggacttggctgtttaaagt	5589
ALDH1A2	36	intron 1 + 21865	tggcataggttttaaaaaatgt C/T tgtttaggactcttttcca	5590
ALDH1A2	37	intron 1 + 26282	taaagaaggagaaaaaa A/ Δ ctaactgtgagacttttgcagg	5591
ALDH1A2	38	intron 1 + 27805	ggatgatgctacccaaggaa T/C tgcacacttccagacgtac	5592
ALDH1A2	39	intron 1 + 28204	tcactccattttttaaactgt C/G cttcctaaatgtgtggttaa	5593
ALDH1A2	40	intron 1 + 28521	tccttgttacacttctttaa T/C cggggtatcagataaatcttc	5594
ALDH1A2	41	intron 1 + 49478	gaataaaaggataggacat G/T ggtaagaccactttttccct	5595
ALDH1A2	42	intron 1 + 49834	gcctctcaattttctcatgt G/T taatagagagaaaaaccctgc	5596
ALDH1A2	43	intron 1 + 50351	gactgactggttcataagtt C/G agaaatttccactgtgtgtgt	5597
ALDH1A2	43	intron 1 + 51181	tgttattaccatagtagttc C/T gtaacacttggcgttgact	5598

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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JUMBO APPLICATIONS/PATENTS

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NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS

- 5 1. A method of identifying individuals having a polymorphism, comprising;
 a. providing nucleic acid from a subject; and
 b. detecting the presence of at least one polymorphism in said nucleic
 acid, said at least one polymorphism selected from the group
 consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-
10 7669.
2. The method of Claim 1, further comprising step c) providing a prognosis
to said subject based on the presence or absence of said at least one polymorphism.
- 15 3. The method of Claim 2, wherein said prognosis comprises a genotype
relative risk.
4. The method of Claim 2, wherein said prognosis comprises a population
attributable risk.
- 20 5. The method of Claim 1, wherein said detecting step comprises use of a
hybridization assay.
6. The method of Claim 1, wherein said detecting step comprises use of a
25 TAQMAN assay.
7. The method of Claim 1, wherein said detecting step comprises use of an
invasive cleavage assay.
- 30 8. The method of Claim 1, wherein said detecting step comprises use of mass
spectroscopy.

9. The method of Claim 1, wherein said detecting step comprises use of a microarray.

5 10. The method of Claim 1, wherein said detecting step comprises use of a polymerase chain reaction.

11. The method of Claim 1, wherein said detecting step comprises use of a rolling circle extension assay.

10

12. The method of Claim 1, wherein said detecting step comprises use of a sequencing assay.

13. The method of Claim 1, wherein said detecting step comprises use of a hybridization assay employing a probe complementary to a polymorphism.

15

14. The method of Claim 1, wherein said detecting step comprises use of a bead array assay.

20 15. The method of Claim 1, wherein said detecting step comprises use of a primer extension assay.

16. The method of Claim 1, wherein said detecting step comprises use of an enzyme mismatch cleavage assay.

25

17. The method of Claim 1, wherein said detecting step comprises use of a branched hybridization assay.

18. The method of Claim 1, wherein said detecting step comprises use of a NASBA assay.

30

19. The method of Claim 1, wherein said detecting step comprises use of a molecular beacon assay.

20. The method of Claim 1, wherein said detecting step comprises use of a
5 cycling probe assay.

21. The method of Claim 1, wherein said detecting step comprises use of a ligase chain reaction assay.

10 22. The method of Claim 1, wherein said detection step comprises use of a sandwich hybridization assay.

23. A composition comprising a nucleic acid, said nucleic acid comprising a sequence selected from the group consisting of SEQ ID NO:1-3360 and 3361-7669 or
15 complements thereof.

24. The composition of Claim 23, wherein said nucleic acid is 200 or less nucleotides in length.

20 25. The composition of Claim 23, wherein said nucleic acid molecule comprises a label.

26. The composition of Claim 23, wherein said nucleic acid comprises a gene sequence.

25

27. The composition of Claim 23, wherein said nucleic acid is attached to a solid support.

28. The vector comprising the nucleic acid of Claim 23.

30

29. A host cell comprising the vector of Claim 28.

30. A polypeptide encoded by the nucleic acid of Claim 23.

31. A kit for detecting a polymorphism, comprising at least one reagent that specifically detects a polymorphism in a sequence selected from the group consisting of
5 SEQ ID Nos:3360 and 3361-.

32. The kit of Claim 31, further comprising instructions for determining whether the subject is at increased risk of having a drug metabolism disorder.

10 33. The kit of Claim 31, wherein said at least one reagent comprises a nucleic acid probe.

34. The kit of Claim 31, wherein said kit comprises an in vitro diagnostic detection assay.

15

35. The kit of Claim 31, wherein said kit comprises an analyte specific reagent detection assay.

20 36. The kit of Claim 31, wherein said kit comprises a research-use-only detection assay.

37. A method for screening subjects for genetic markers associated with drug metabolizing enzyme(s), comprising:

- 25
- a) providing a biological sample comprising a nucleic acid from a subject;
 - b) testing said nucleic acid for a polymorphism in a genetic marker associated with a drug metabolizing enzyme, said genetic marker comprising one or more nucleotide polymorphisms designated by n, said n selected from a base substitution, an insertion, or a deletion
30 found in a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

38. The method of Claim 37, wherein said biological sample is selected from the group consisting of blood, saliva, amniotic fluid, and tissue.

5 39. The method of Claim 37, wherein said subject is a human.

40. The method of Claim 37, wherein said nucleic acid comprises DNA.

41. The method of Claim 37, wherein said nucleic acid comprises RNA.

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42. A composition comprising an array of detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of detecting one or more nucleotide polymorphisms designated by n in SEQ ID Nos:1-3360 and 3361-7669, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.

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43. The composition of Claim 42, wherein said detection assay is selected from the group consisting of a sequencing assay, a polymerase chain reaction assay, a hybridization assay, a hybridization assay employing a probe complementary to a polymorphism, a microarray assay, a bead array assay, a primer extension assay, an enzyme mismatch cleavage assay, a branched hybridization assay, a rolling circle replication assay, a NASBA assay, a molecular beacon assay, a cycling probe assay, a ligase chain reaction assay, and a sandwich hybridization assay.

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44. A composition comprising a detection probe for determining the presense or absence a single nucleotide polymorphism in a gene encoding a drug metabolizing enzyme, said gene comprising a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

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45. A kit comprising the detection probe of Claim 44, and at least one

PCR primer for amplifying at least a portion of said gene.

- 5 46. A method of determining the effectiveness of or side-effect of a drug or treatment protocol, comprising;
- a. administering a drug or treatment protocol to one or more subjects;
 - b. obtaining nucleic acid from said one or more subjects;
 - c. using a detection assay to detect the presence of at least one
10 polymorphism in said nucleic acid from said one or more of subjects,
said at least one polymorphism selected from the group consisting of
polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669; and,
 - d. assigning an effectiveness rating, side-effect rating, or score for said
drug or treatment protocol based upon a result of one or more said
detection assays.

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47. The method of Claim 46, wherein said detection assay comprises a hybridization assay.

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48. The method of Claim 46, wherein said detection assay comprises a TAQMAN assay.

49. The method of Claim 46, wherein said detection assay comprises an invasive cleavage assay.

25

50. The method of Claim 46, wherein said detection assay comprises mass spectroscopy.

51. The method of Claim 46, wherein said detection assay comprises a microarray.

30

52. The method of Claim 46, wherein said detection assay comprises a polymerase chain reaction.

53. The method of Claim 46, wherein said detection assay comprises a rolling
5 circle extension assay.

54. The method of Claim 46, wherein said detection assay comprises a sequencing assay.

10 55. The method of Claim 46, wherein said detection assay comprises a hybridization assay employing a probe complementary to a polymorphism.

56. The method of Claim 46, wherein said detection assay comprises a bead
array assay.

15

57. The method of Claim 46, wherein said detection assay comprises a primer extension assay.

58. The method of Claim 46, wherein said detection assay comprises an
20 enzyme mismatch cleavage assay.

59. The method of Claim 46, wherein said detection assay comprises a branched hybridization assay.

25 60. The method of Claim 46, wherein said detection assay comprises a NASBA assay.

61. The method of Claim 46, wherein said detection assay comprises a molecular beacon assay.

30

62. The method of Claim 46, wherein said detection assay comprises a cycling probe assay.

63. The method of Claim 46, wherein said detection assay comprises a ligase
5 chain reaction assay.

64. The method of Claim 46, wherein said detection step comprises a sandwich hybridization assay.

10 65. The method of Claim 46, in which said detection assay comprises a kit for detecting a polymorphism, said kit comprising at least one reagent that specifically detects a polymorphism in a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

15 66. The method of Claim 65, further comprising instructions for determining whether the subject is at increased risk of having a drug metabolism disorder.

67. The method of Claim 65, wherein said at least one reagent comprises a nucleic acid probe.

20

68. The method of Claim 65, wherein said kit comprises an analyte specific reagent detection assay.

25 69. The method of Claim 65, wherein said kit comprises a research-use-only detection assay.

70. The method of Claim 46, wherein said nucleic acid is obtained from a biological sample, said sample being selected from the group consisting of blood, saliva, amniotic fluid, and tissue.

30

71. The method of Claim 70, wherein said subject is a mammal.

72. The method of Claim 70, wherein said nucleic acid comprises DNA.

73. The method of Claim 70, wherein said nucleic acid comprises RNA.

74. The method of Claim 65, wherein said kit comprises PCR primers.

75. The method of Claim 74, in which said kit comprises an array of detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of detecting one or more nucleotide polymorphisms designated by n in SEQ ID Nos:1-3360 and 3361-7669, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.

76. A method of prescribing a drug to or treatment protocol for a subject, comprising;

- a. providing nucleic acid from said subject;
- b. using a detection assay to detect the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669; and,
- c. prescribing said drug or treatment protocol based upon the result of said detection assay.

77. The method of Claim 76, further comprising step d) providing a prognosis to said subject based on the presence or absence of said at least one polymorphism.

78. The method of Claim 77, wherein said prognosis comprises a genotype relative risk.

79. The method of Claim 77, wherein said prognosis comprises a population attributable risk.

5 80. The method of Claim 76, wherein said detection assay comprises a hybridization assay.

81. The method of Claim 76, wherein said detection assay comprises a TAQMAN assay.

10 82. The method of Claim 76, wherein said detection assay comprises an invasive cleavage assay.

83. The method of Claim 76, wherein said detection assay comprises mass spectroscopy.

15 84. The method of Claim 76, wherein said detection assay comprises a microarray.

20 85. The method of Claim 76, wherein said detection assay comprises a polymerase chain reaction.

86. The method of Claim 76, wherein said detection assay comprises a rolling circle extension assay.

25 87. The method of Claim 76, wherein said detection assay comprises a sequencing assay.

88. The method of Claim 76, wherein said detection assay comprises a hybridization assay employing a probe complementary to a polymorphism.

30

89. The method of Claim 76, wherein said detection assay comprises a bead array assay.

90. The method of Claim 76, wherein said detection assay comprises a primer
5 extension assay.

91. The method of Claim 76, wherein said detection assay comprises an enzyme mismatch cleavage assay.

10 92. The method of Claim 76, wherein said detection assay comprises a branched hybridization assay.

93. The method of Claim 76, wherein said detection assay comprises a NASBA assay.

15

94. The method of Claim 76, wherein said detection assay comprises a molecular beacon assay.

95. The method of Claim 76, wherein said detection assay comprises a cycling
20 probe assay.

96. The method of Claim 76, wherein said detection assay comprises a ligase chain reaction assay.

25 97. The method of Claim 76, wherein said detection step comprises a sandwich hybridization assay.

98. The method of Claim 76, in which said detection assay comprises a kit for detecting a polymorphism, said kit comprising at least one reagent that specifically
30 detects a polymorphism in a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

99. The method of Claim 98, further comprising instructions for determining whether the subject is at increased risk of having a drug metabolism disorder.

5 100. The method of Claim 99, wherein said at least one reagent comprises a nucleic acid probe.

101. The method of Claim 98, wherein said kit comprises an in vitro diagnostic detection assay.

10 102. The method of Claim 98, wherein said kit comprises an analyte specific reagent detection assay.

15 103. The method of Claim 98, wherein said kit comprises a research-use-only detection assay.

104. The method of Claim 76, wherein said nucleic acid is obtained from a biological sample, said sample being selected from the group consisting of blood, saliva, amniotic fluid, and tissue.

20 105. The method of Claim 104, wherein said subject is a human.

106. The method of Claim 104, wherein said nucleic acid comprises DNA.

25 107. The method of Claim 104, wherein said nucleic acid comprises RNA.

108. The method of Claim 104, wherein said kit comprises PCR primers.

30 109. The method of claim 98, in which said kit comprises an array of detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of

detecting one or more nucleotide polymorphisms designated by n in SEQ ID Nos:1-3360 and 3361-7669, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.

5 110. The method of Claim 109, wherein said detection assay is selected from the group consisting of a sequencing assay, a polymerase chain reaction assay, a hybridization assay, a hybridization assay employing a probe complementary to a polymorphism, a microarray assay, a bead array assay, a primer extension assay, an enzyme mismatch cleavage assay, a branched hybridization assay, a rolling circle
10 replication assay, a NASBA assay, a molecular beacon assay, a cycling probe assay, a ligase chain reaction assay, and a sandwich hybridization assay.

 111. A method for generating assay data comprising:
 a. obtaining a sample from a subject containing nucleic acid;
15 b. transferring said sample to a laboratory; and
 c. receiving data from said laboratory, wherein said data corresponds to the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669.

20

 112. A data set generated by the method of Claim 111.

 113. A composition comprising a nucleic acid, said nucleic acid comprising a gene sequence, said gene sequence having at least one polymorphism, said at least one
25 polymorphism selected from the group consisting of polymorphisms found in SEQ ID NOs:1-3360 and 3361-7669.

 114. The composition of Claim 113, wherein said at least one polymorphism is located in a non-coding portion of said gene.

30

115. The composition of Claim 113, wherein said at least one polymorphism is located in an intron.

116. The composition of Claim 113, wherein said at least one polymorphism is located in an exon.

117. The composition of Claim 113, wherein said at least one polymorphism is located in a 5' untranslated portion of said gene.

118. The composition of Claim 113, wherein said at least one polymorphism is located in a 3' untranslated portion of said gene.

119. The composition of Claim 113, wherein said at least one polymorphism is located in an untranslated regulatory portion of said gene.

120. The composition of Claim 113, wherein said at least one polymorphism is located in a region of said gene affecting splicing.

121. The composition of Claim 113, wherein said at least one polymorphism is located in a region of said gene affecting level of transcription of said gene.

122. The composition of Claim 113, wherein two or more of said polymorphisms are located in a gene sequence, said gene sequence comprising an intron, an exon, a 5' untranslated portion of said gene, a 3' untranslated portion of said gene, a regulatory portion of said gene, a portion of said gene affecting splicing, and a portion of said gene affecting level or transcription of said gene.

123. A composition comprising an oligonucleotide, said oligonucleotide comprising at least one polymorphism, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669, and

said oligonucleotide comprising at least five bases upstream or five bases downstream of said polymorphism.

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FIGURE 1

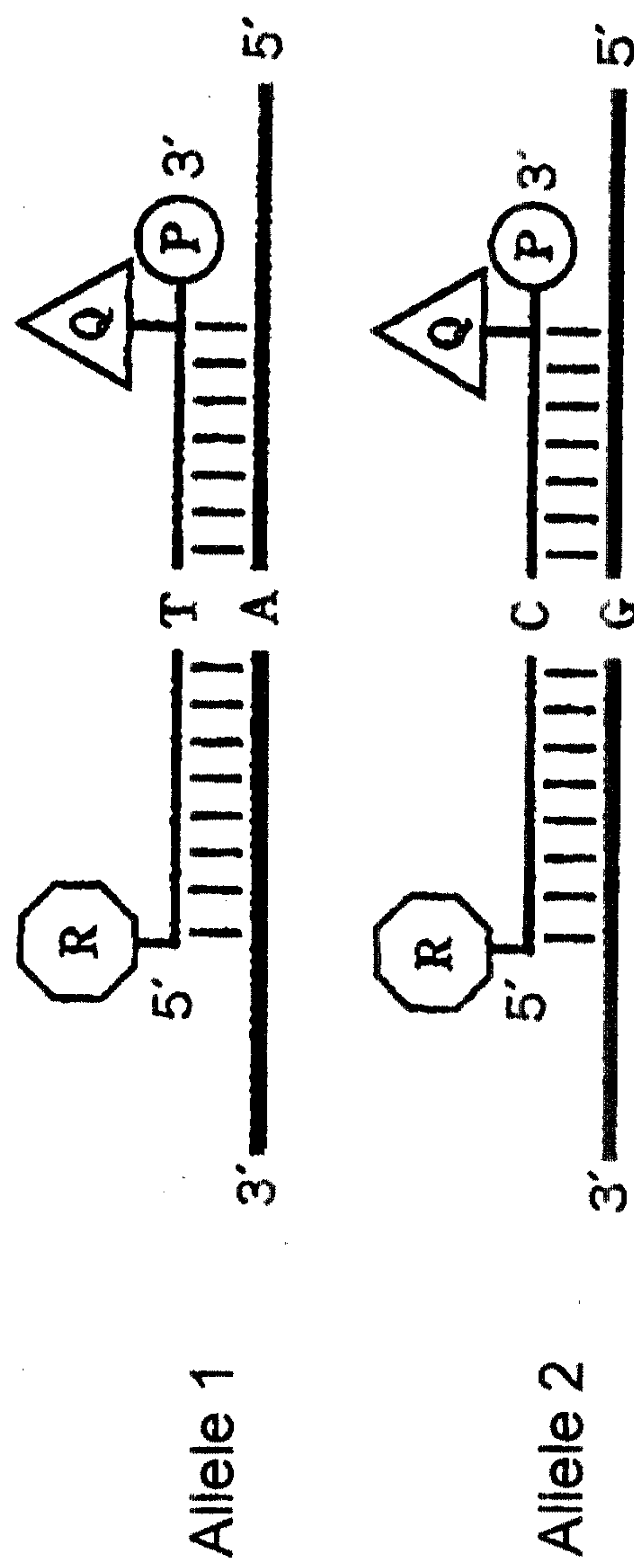


FIGURE 2

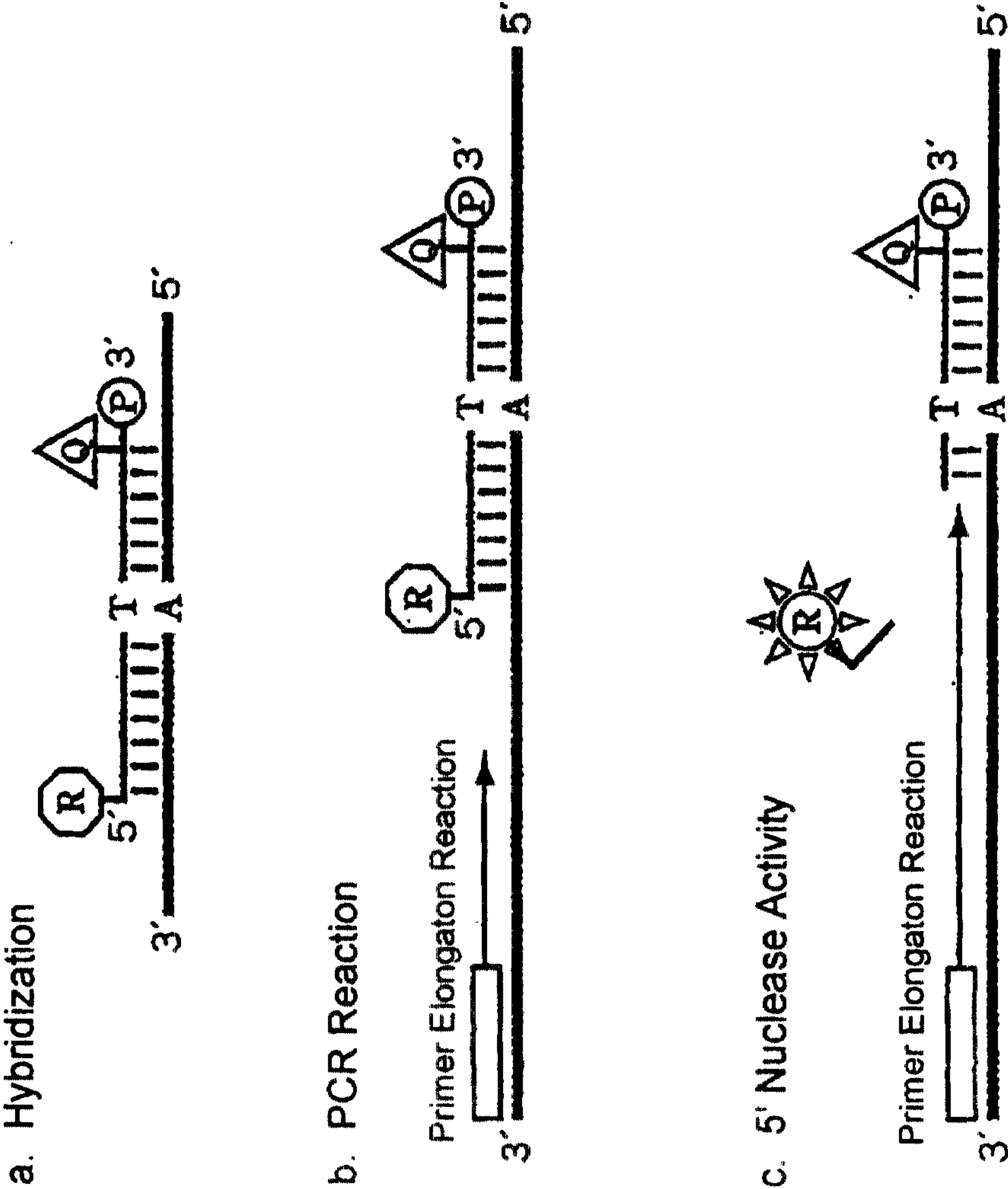


FIGURE 3

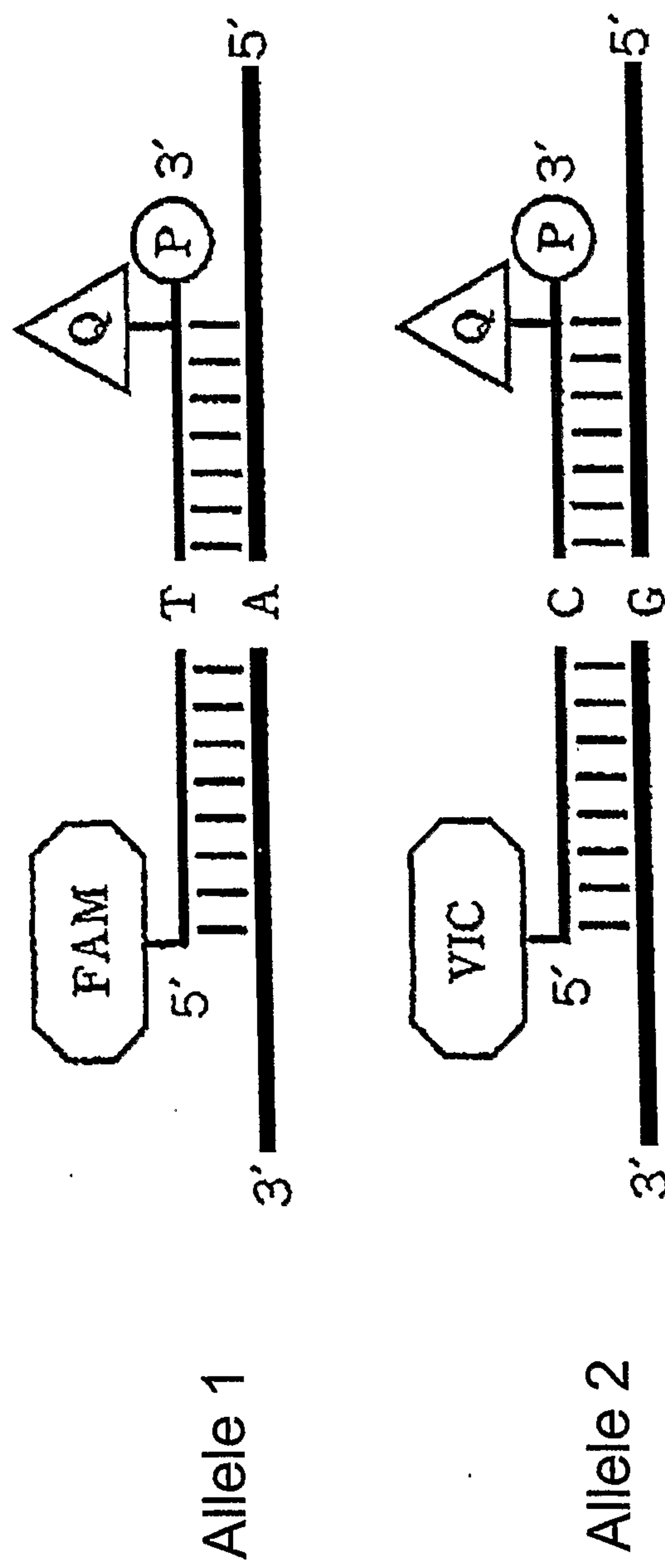


FIGURE 4

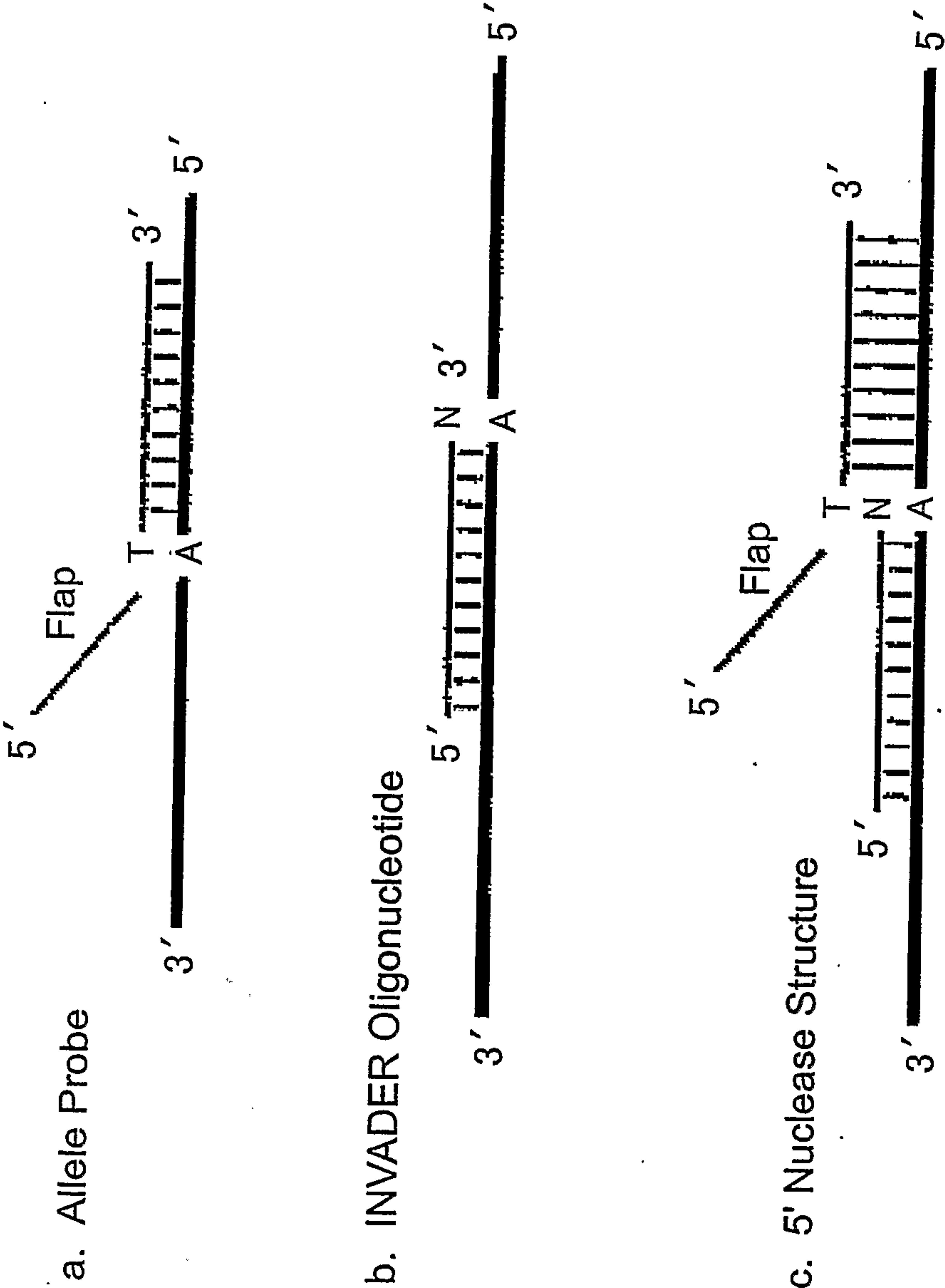


FIGURE 5

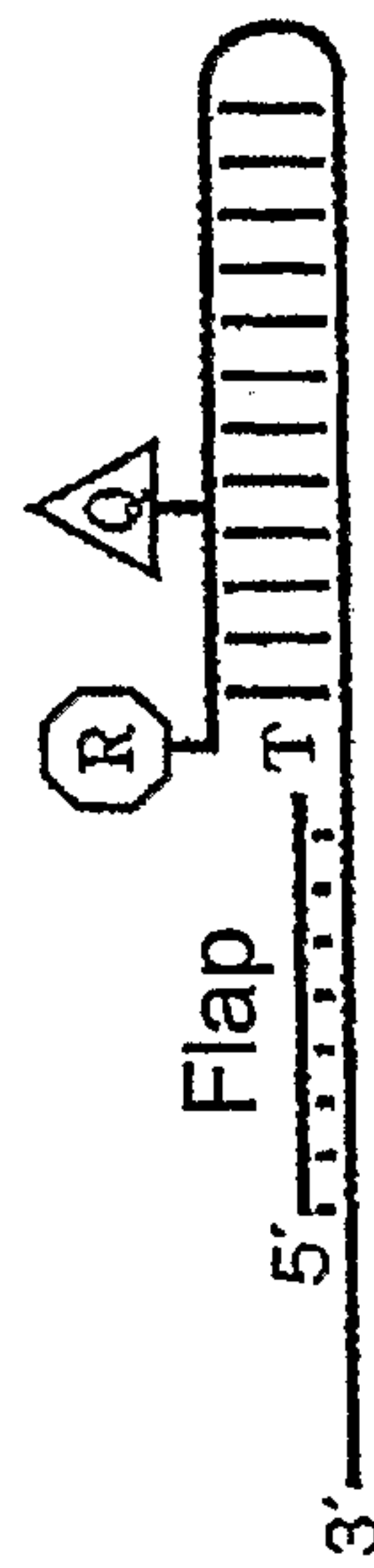


FIGURE 6

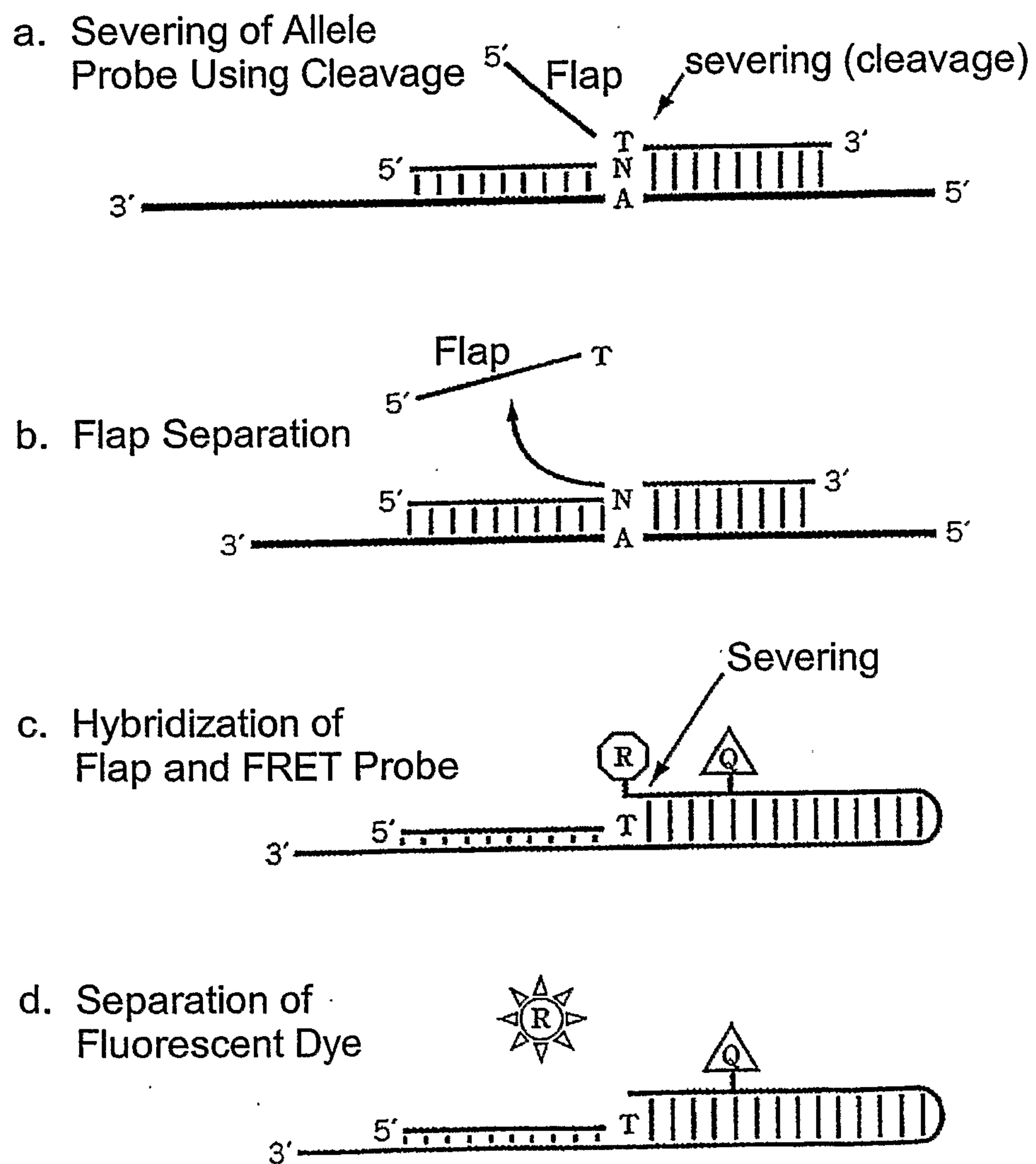


FIGURE 7

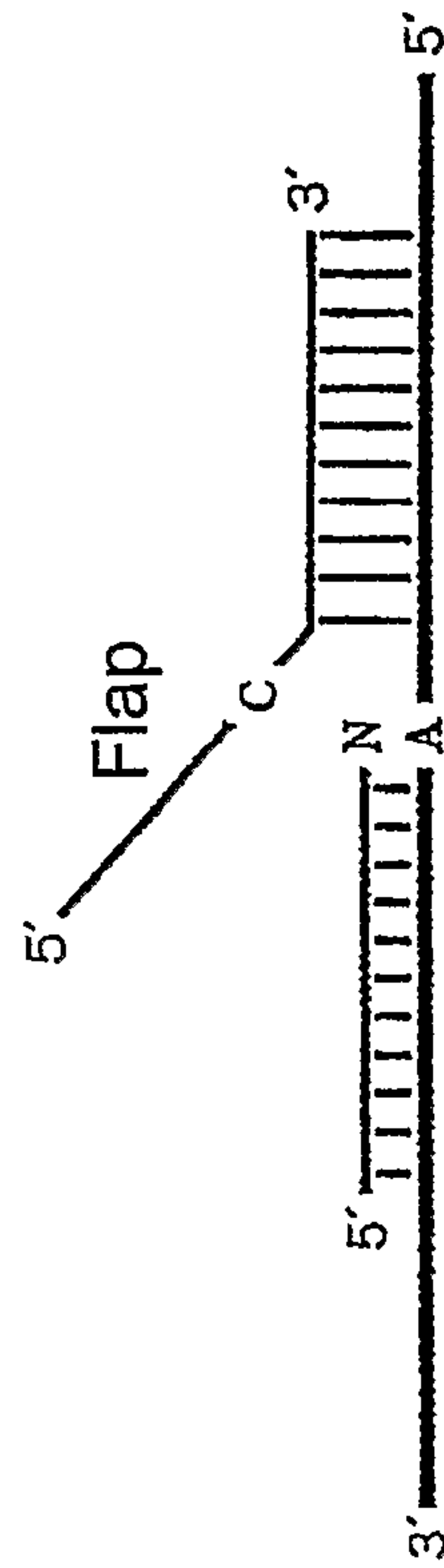


FIGURE 8

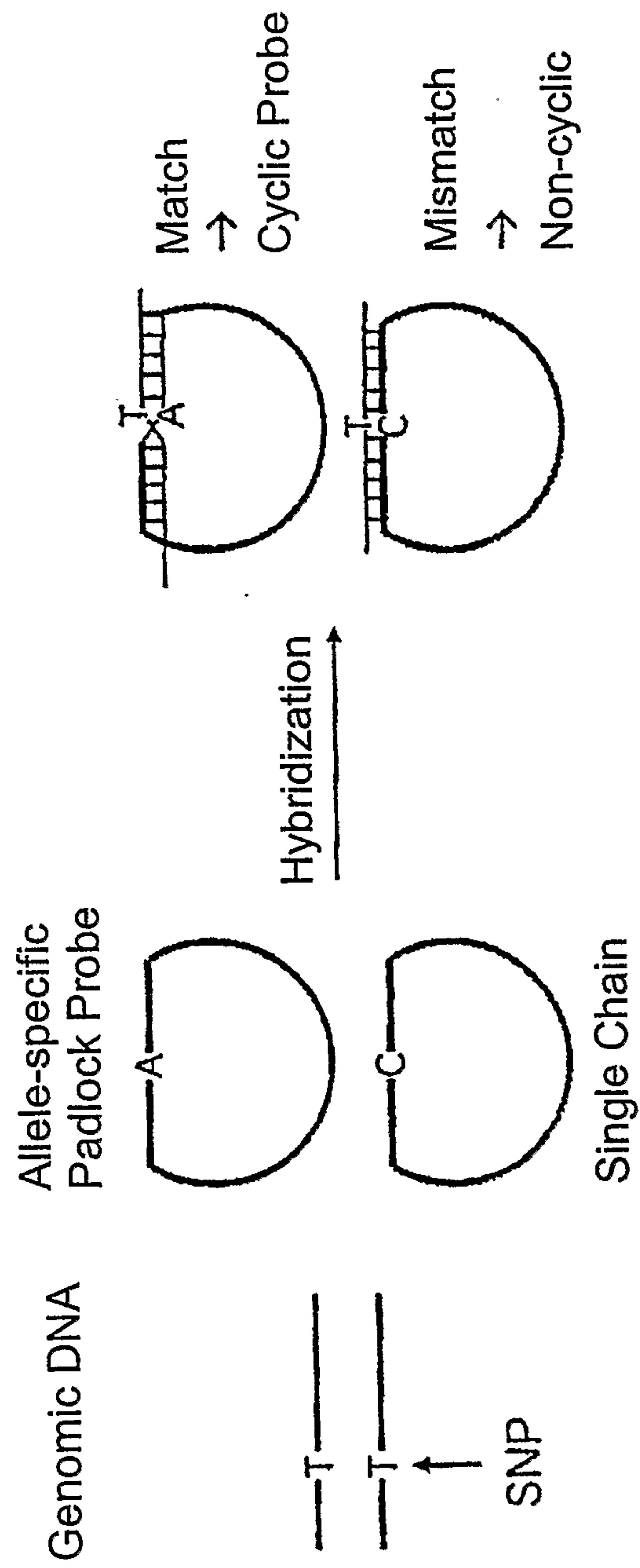


FIGURE 9

ATP binding cassette, sub-family B, member 2 (ABCB2)

ACCESSION X66401



ATP binding cassette, sub-family B, member 2 (ABCB2)

ACCESSION X66401

FIGURE 9

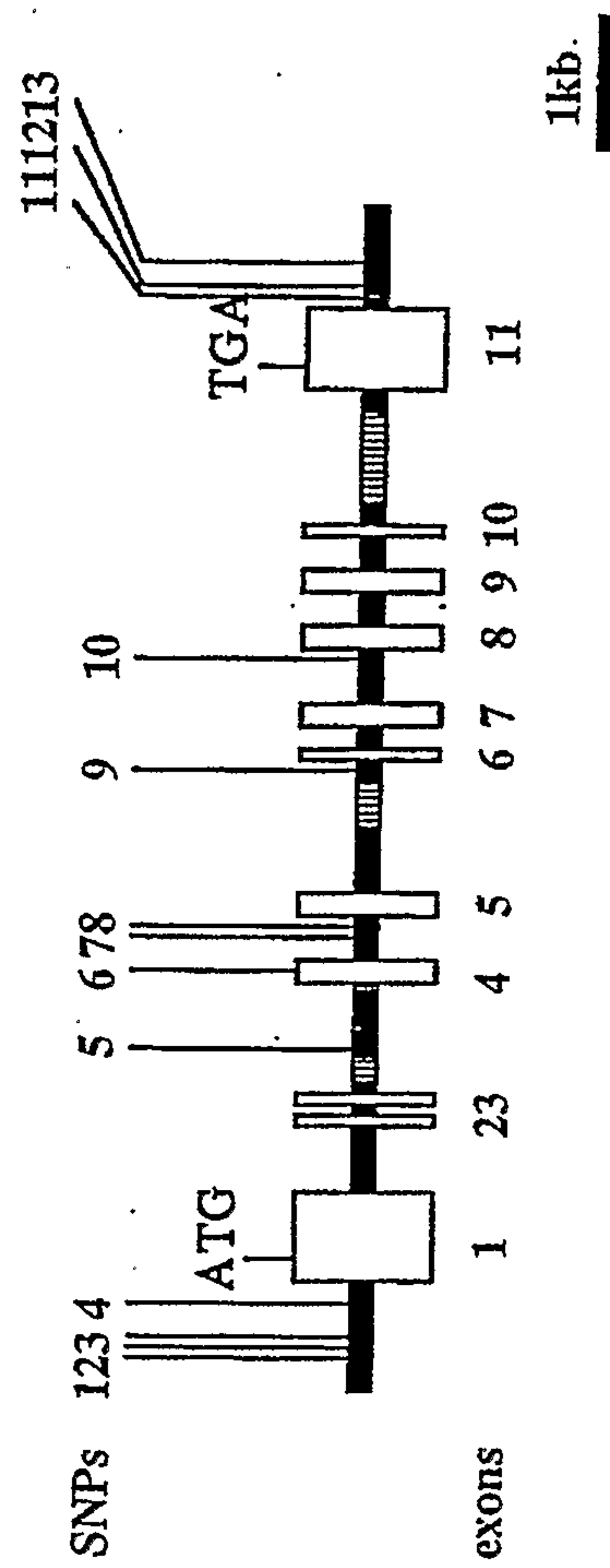


FIGURE 10
ATP-binding cassette, sub-family B, member 4 (ABCB4)
ACCESSION AC079591
AC079303
AC005045

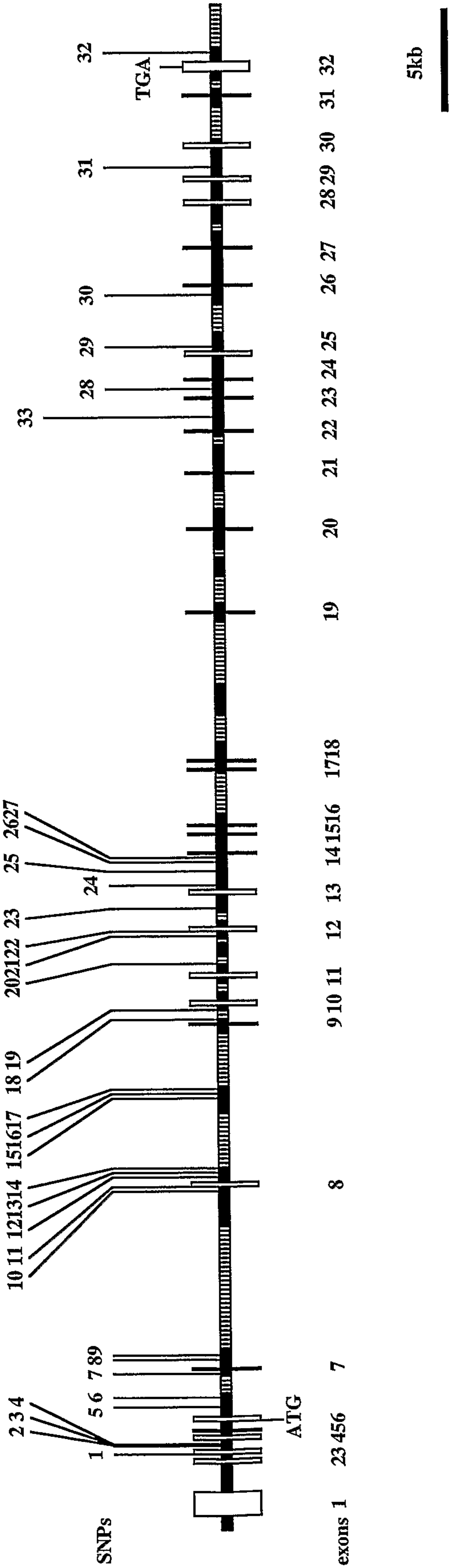


FIGURE 11

Epoxide hydrolase 1, microsomal (EPHX1)

ACCESSION AC058782

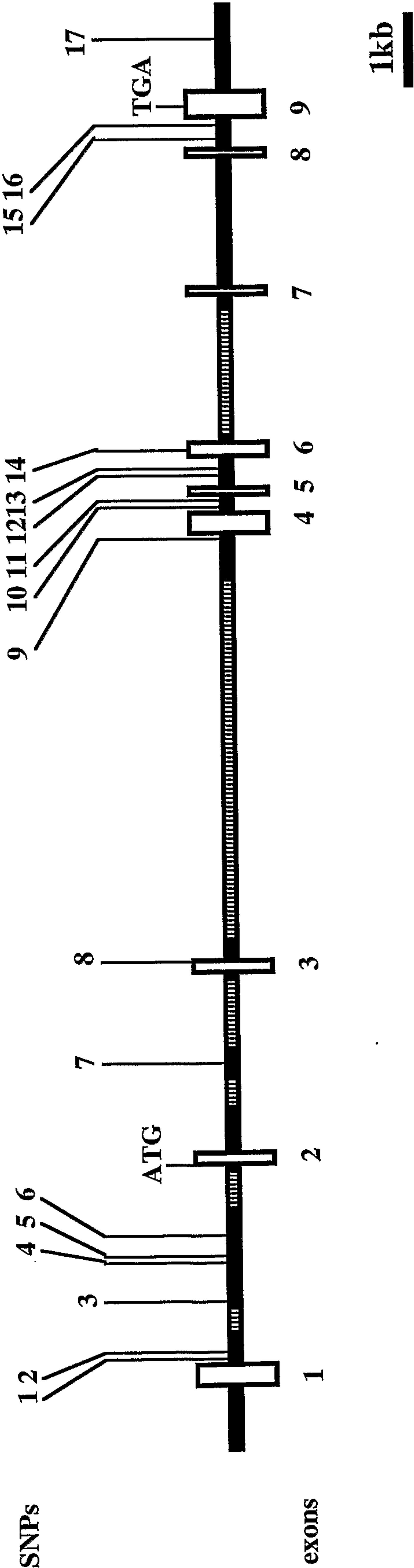
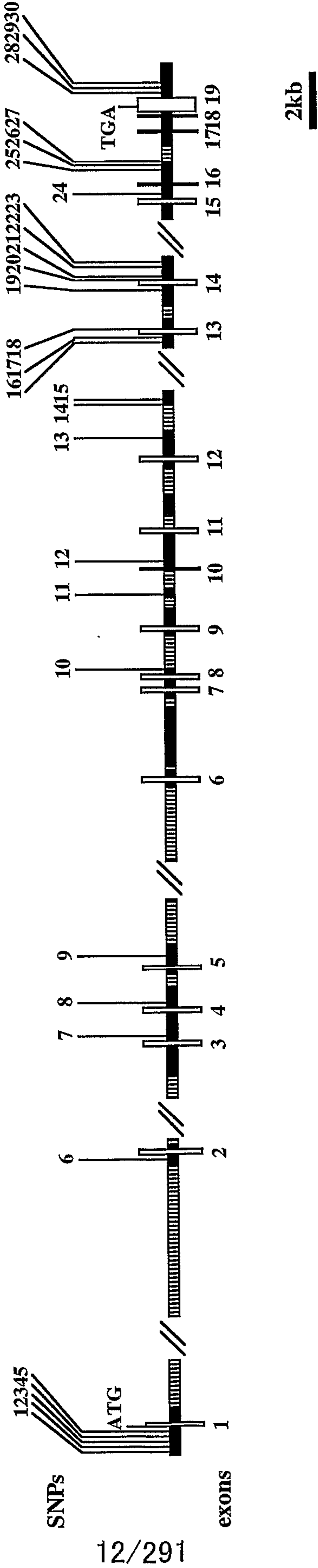


FIGURE 12

Epoxide hydrolase, cytoplasmic (EPHX2)

ACCESSION AC010856



Guanidinoacetate N-methyltransferase (GAMT)

ACCESSION NT_000879

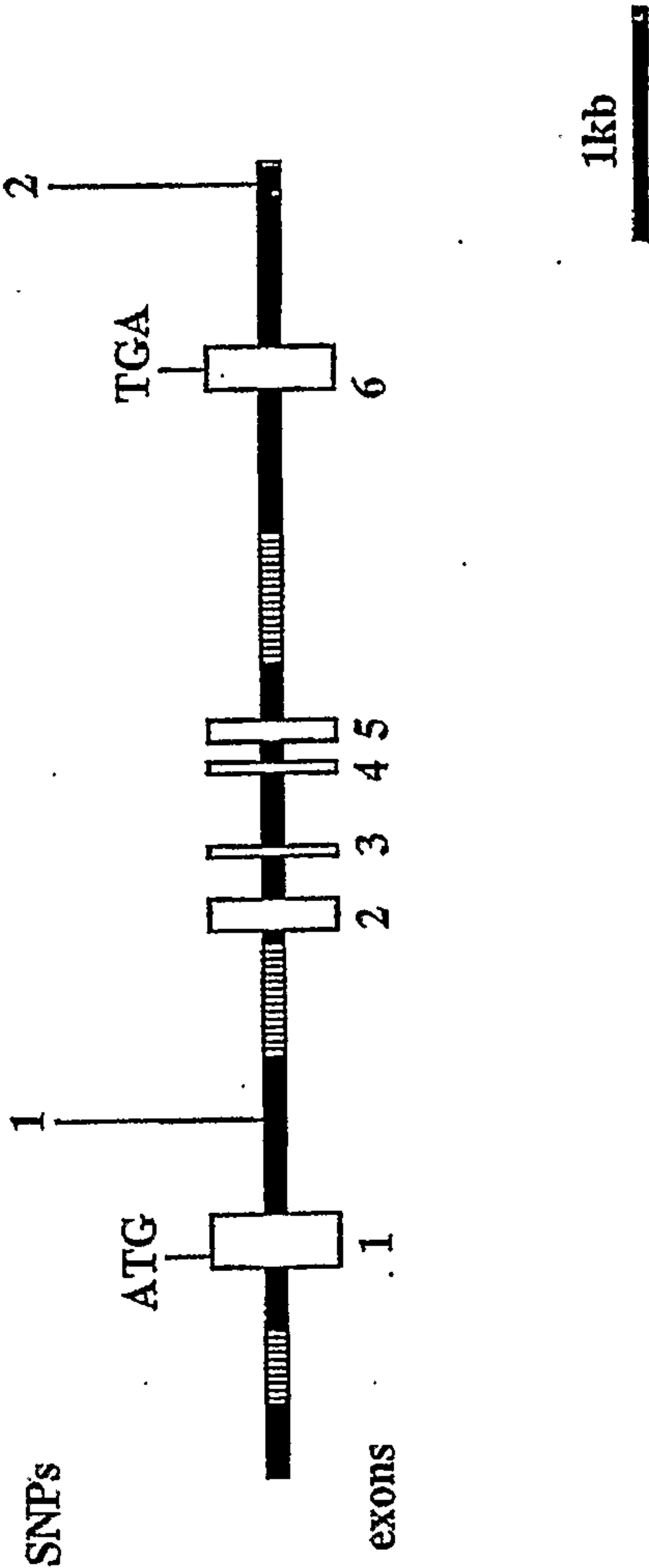


FIGURE 13

FIGURE 14

Nicotinamide N-methyltransferase (NNMT)

ACCESSION AC019290

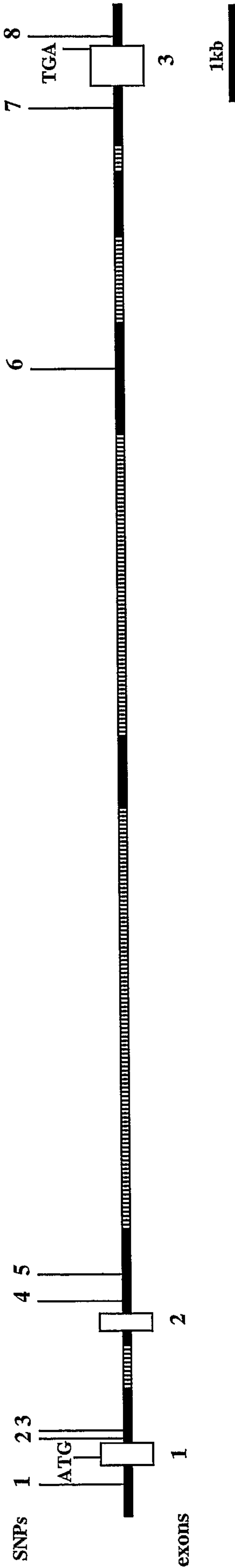


FIGURE 15

Phenylethanolamine N-methyltransferase (PNMT)

ACCESSION AC040933

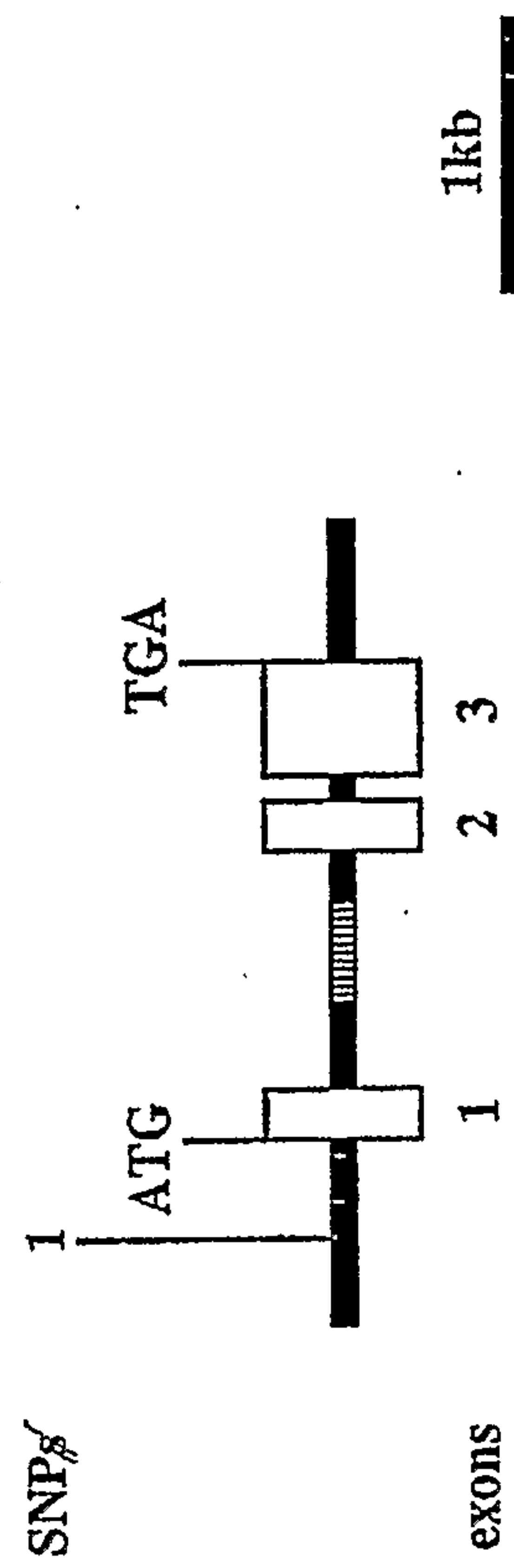


FIGURE 16

Phosphatidylethanolamine N-methyltransferase (PEMT)

ACCESSION AC020558

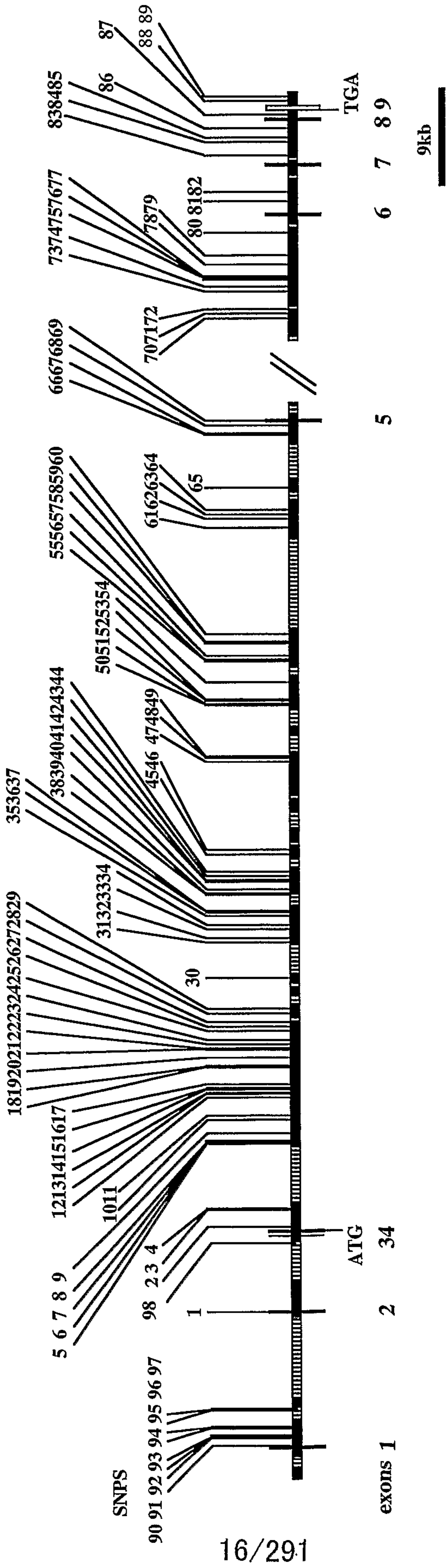


FIGURE 17

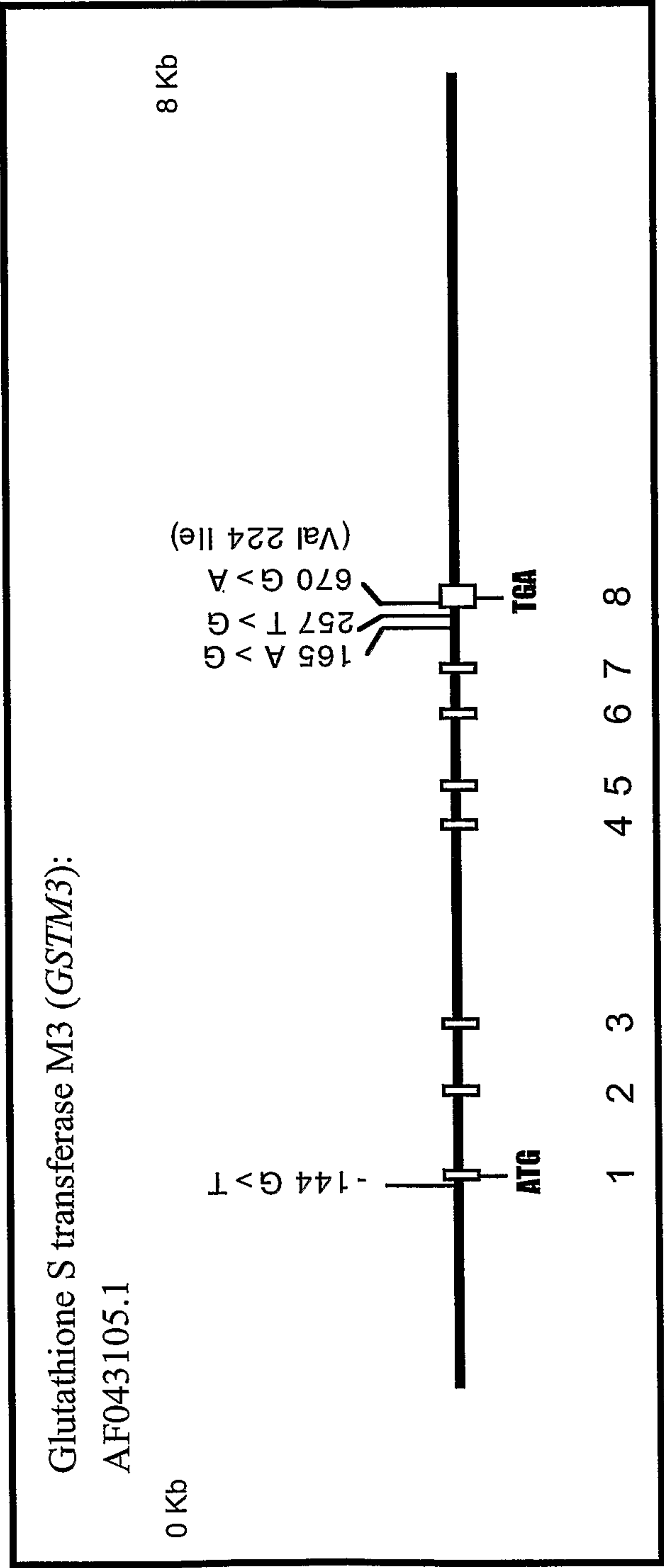


FIGURE 18

Aldehyde dehydrogenase 5 (ALDH5)

ACCESSION AL135785

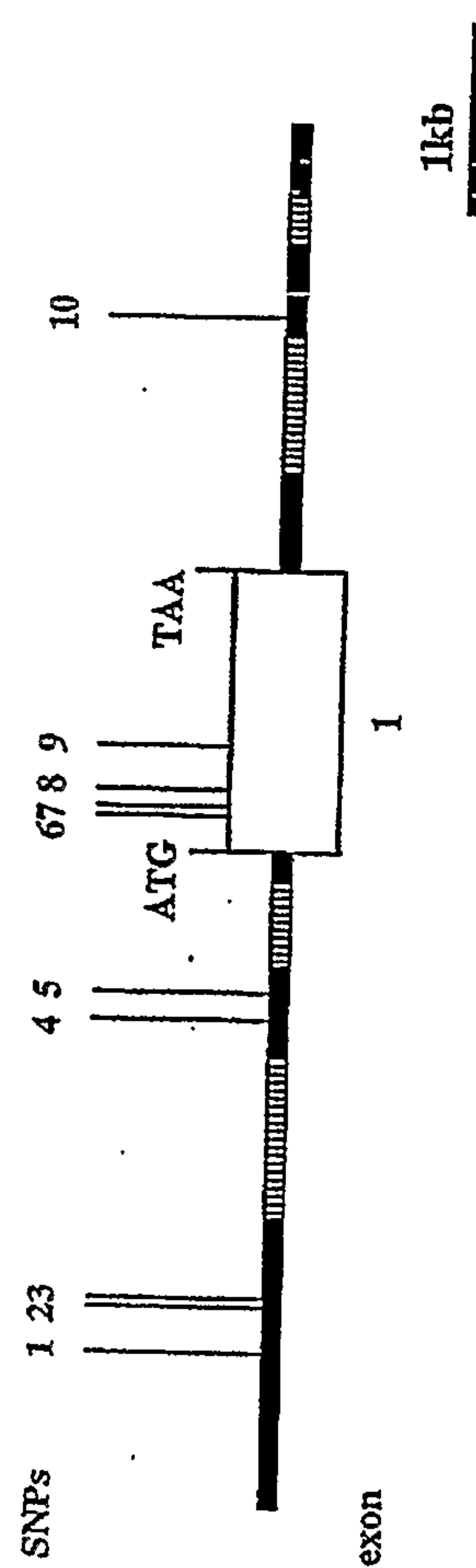
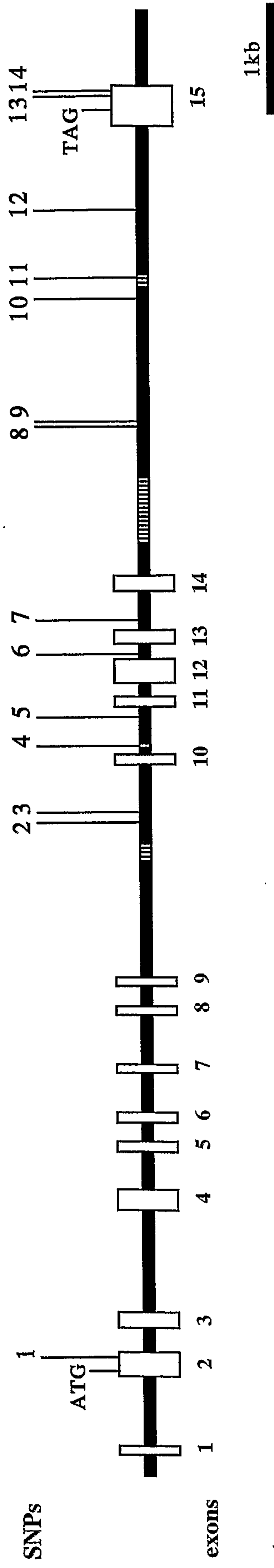


FIGURE 19

Transglutaminase 1 (TGM1)

ACCESSION M98447



Gamma- glutamyltransferase 1 (GGT1)

ACCESSION D87002

FIGURE 20

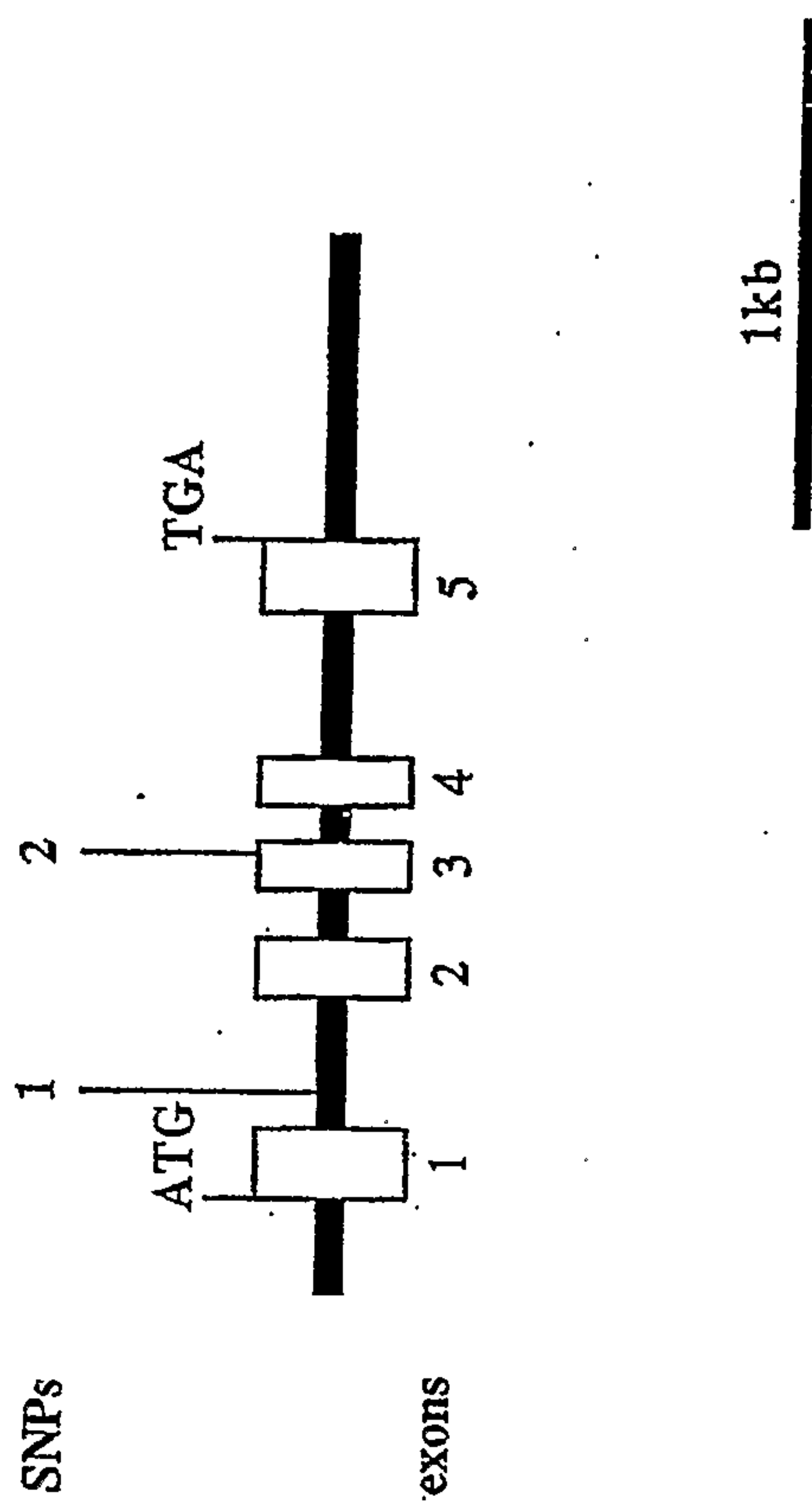


FIGURE 21

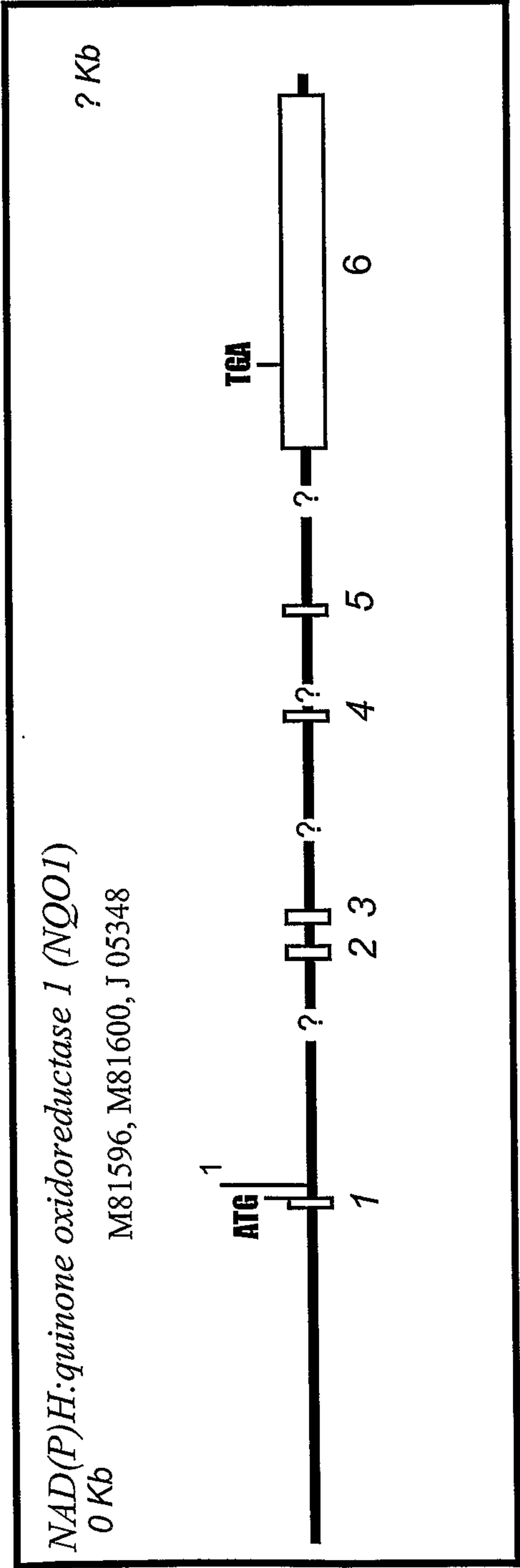


FIGURE 22

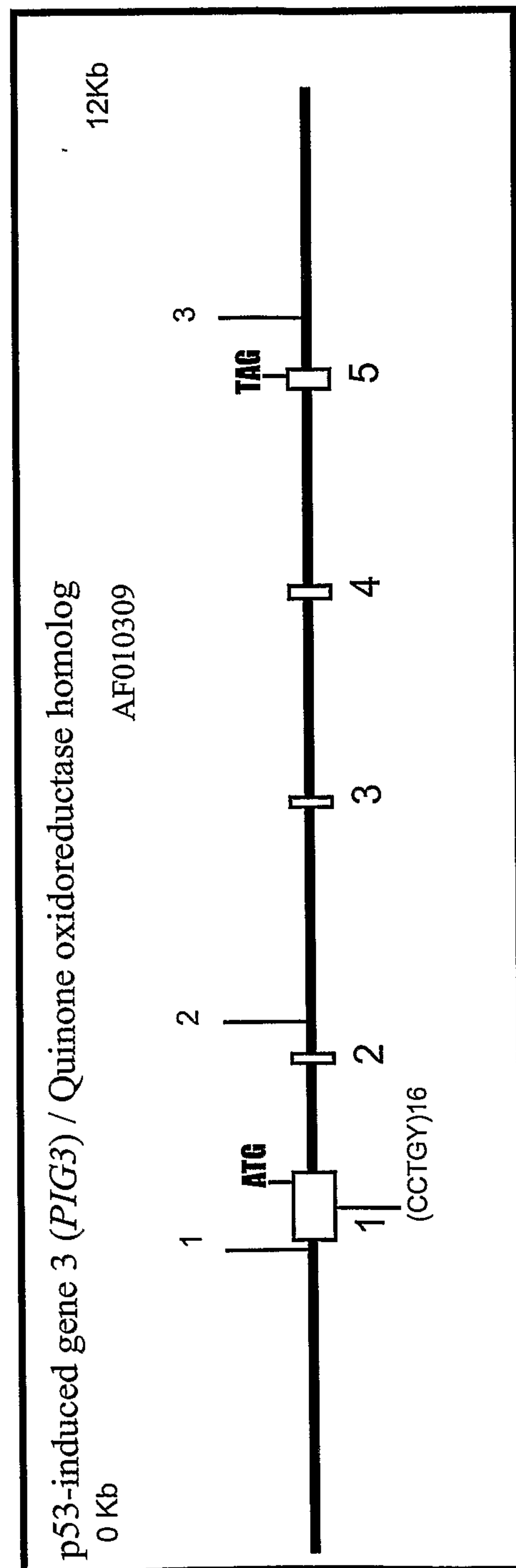


FIGURE 23

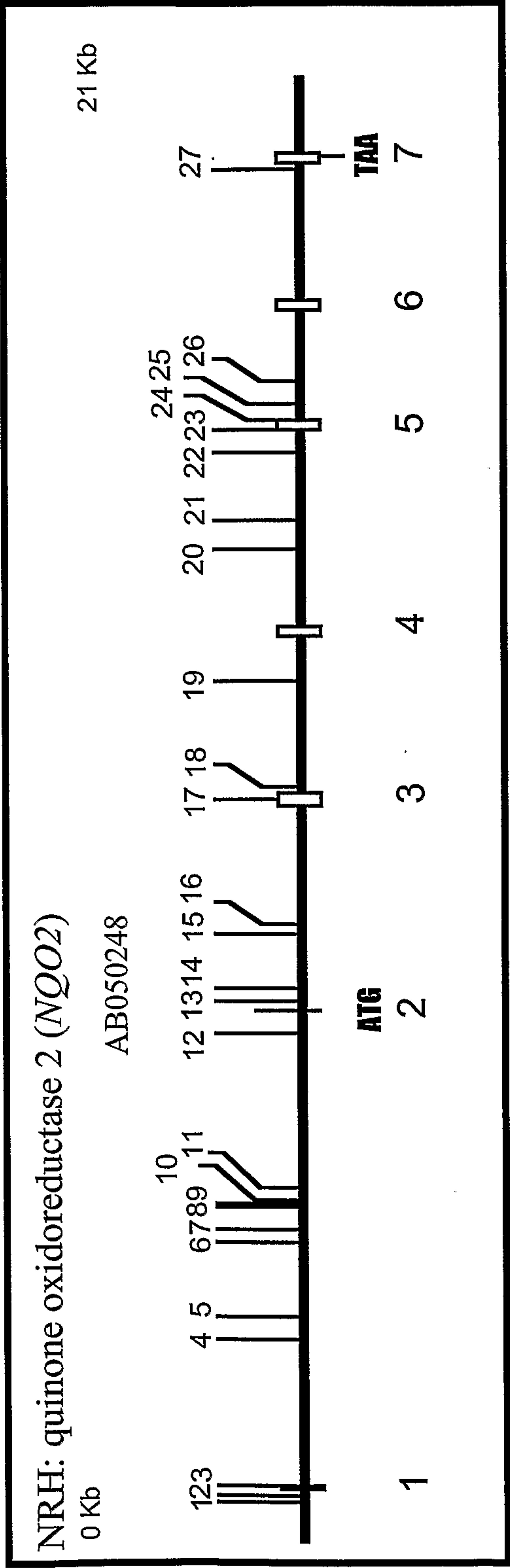


FIGURE 24

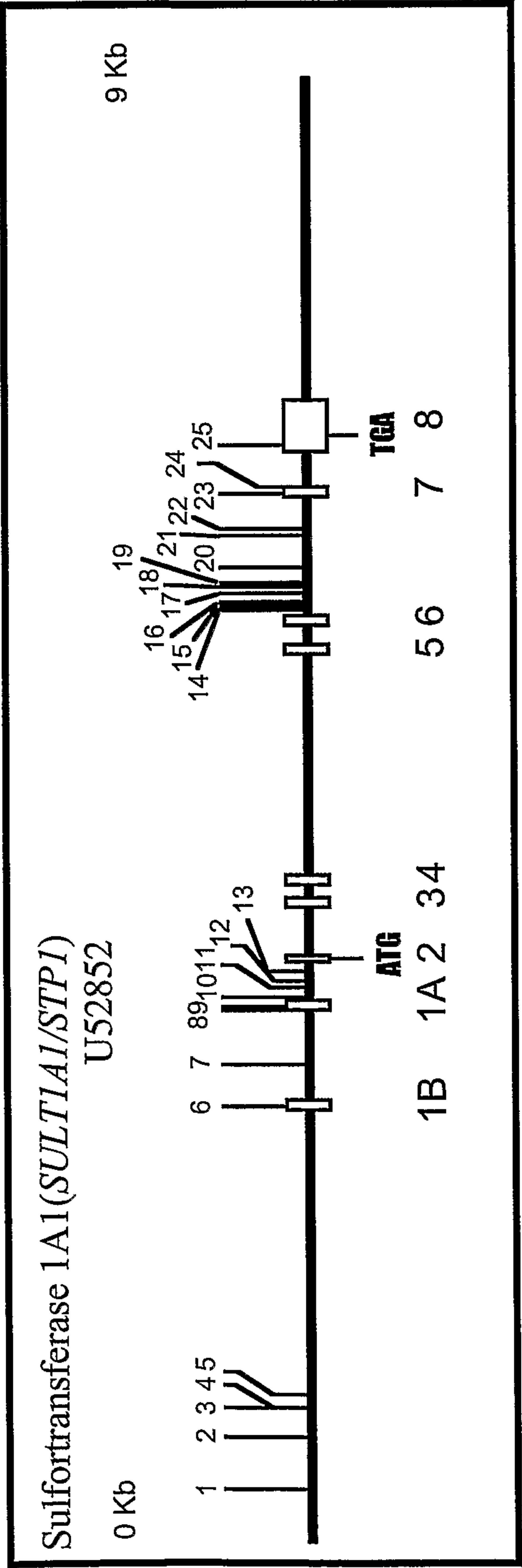


FIGURE 25

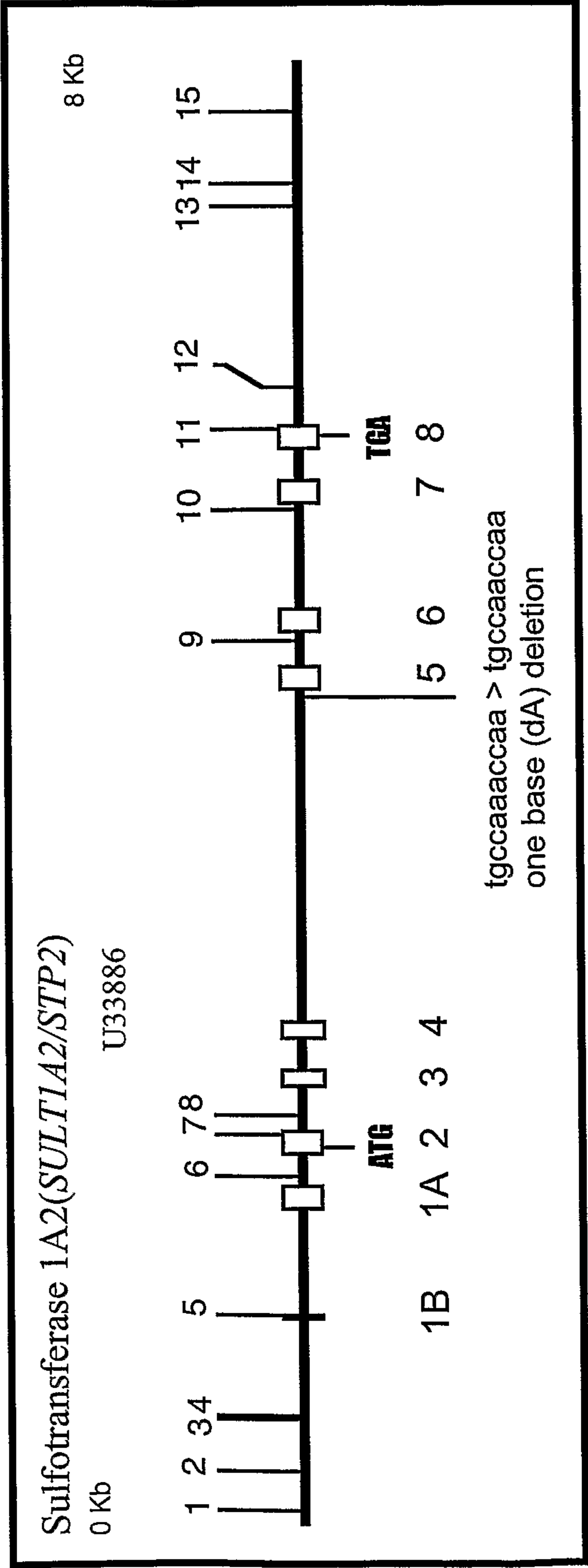


FIGURE 26

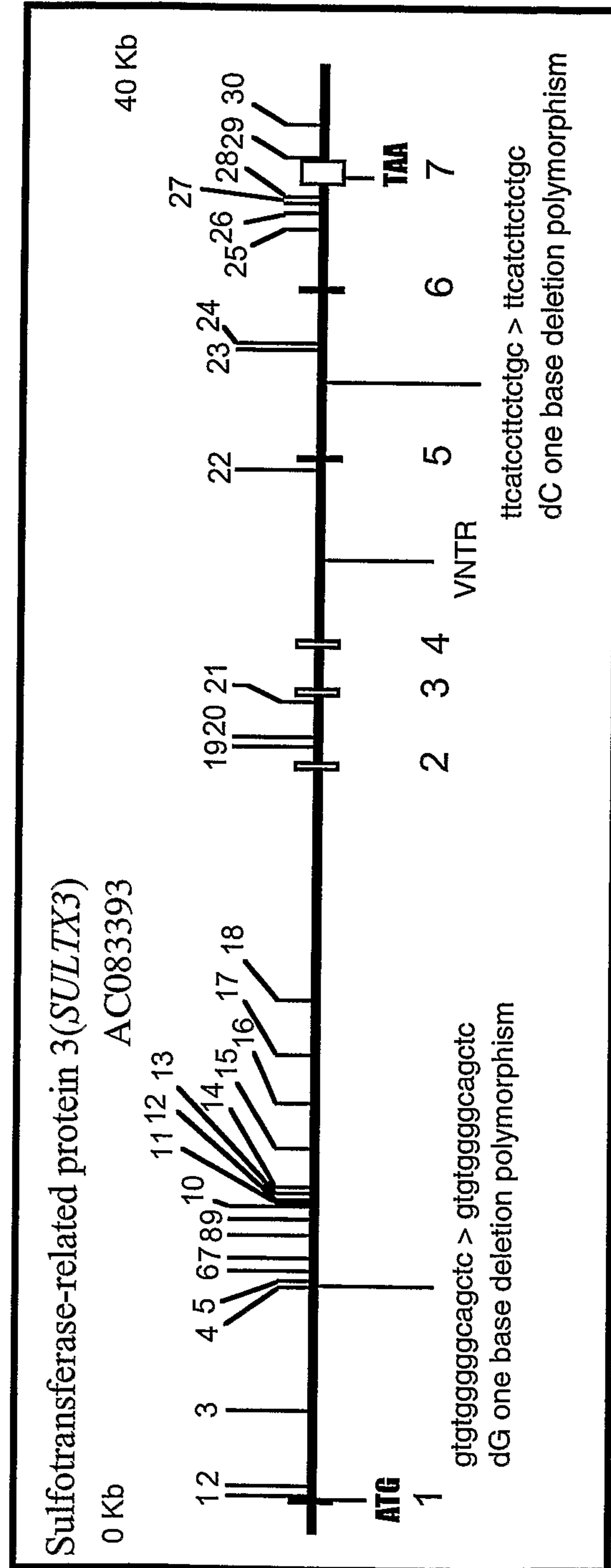


FIGURE 27

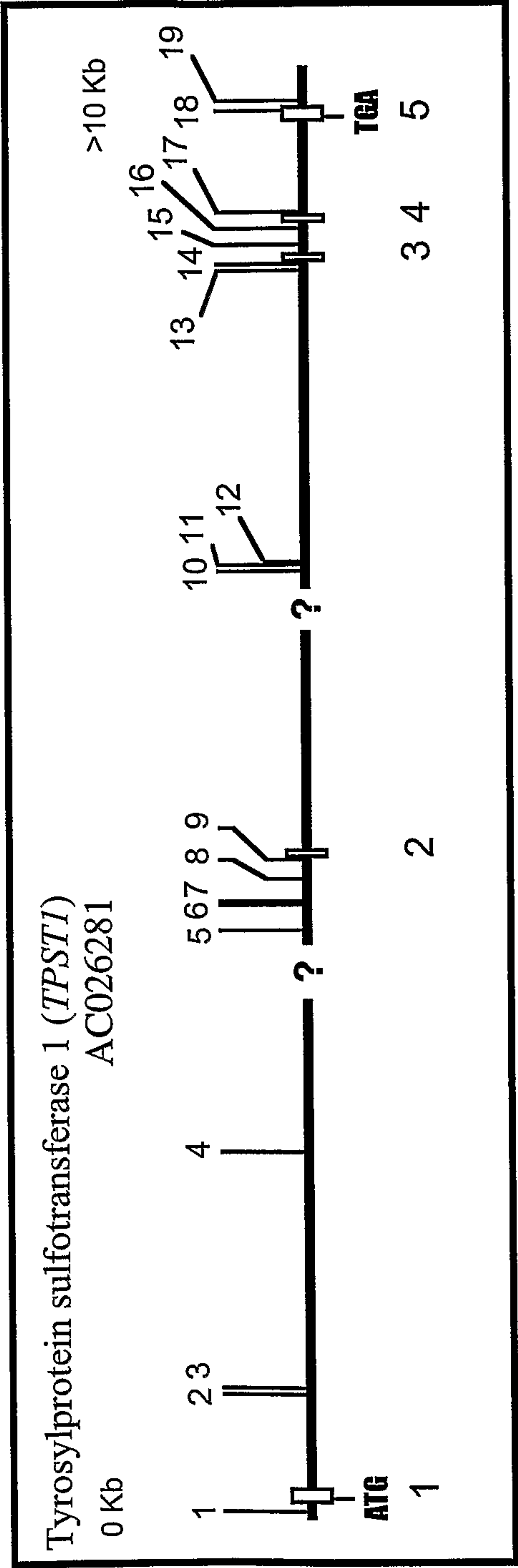


FIGURE 28

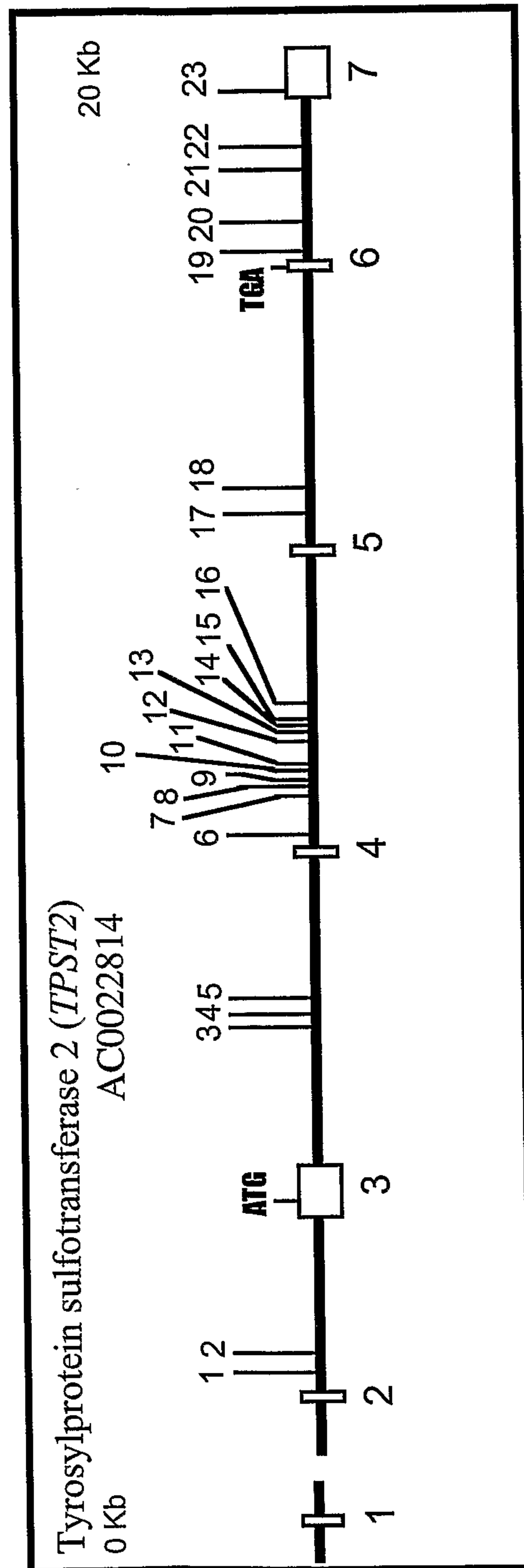


FIGURE 29

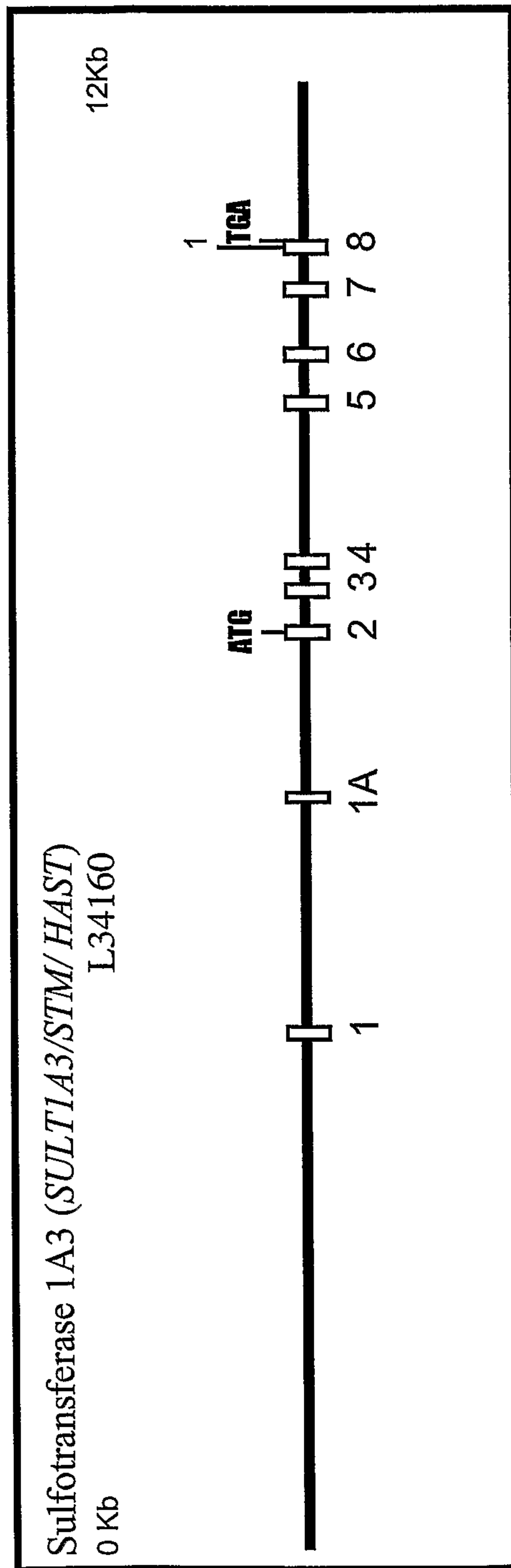


FIGURE 30

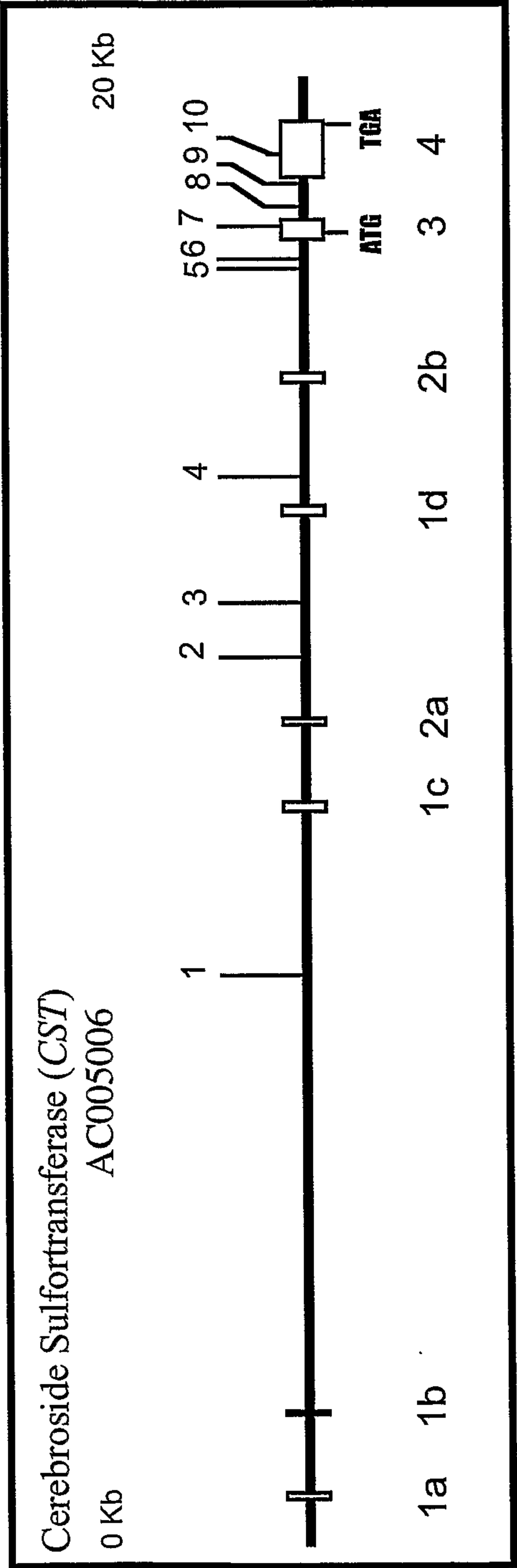


FIGURE 31

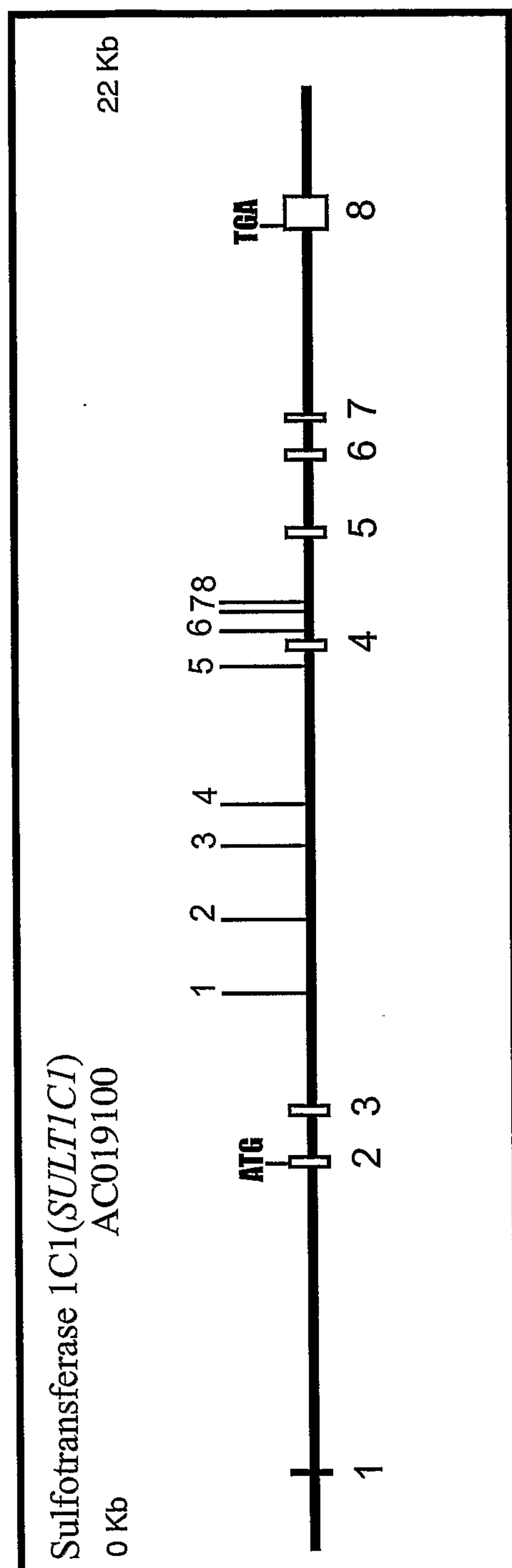


FIGURE 32

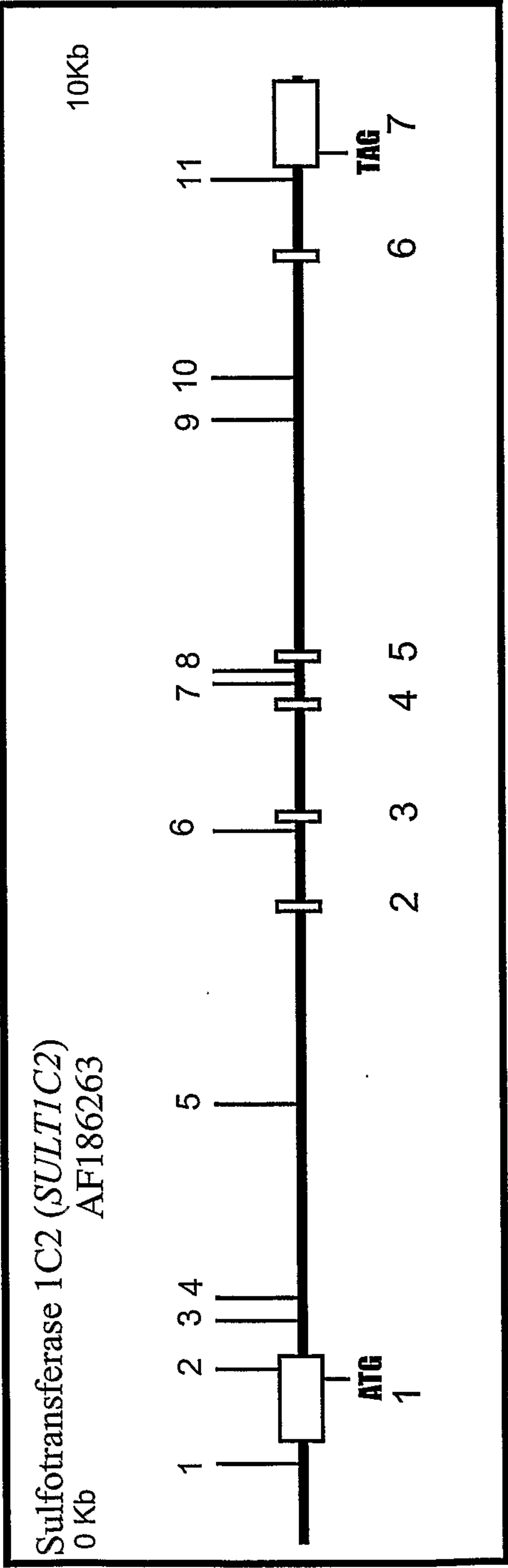


FIGURE 33

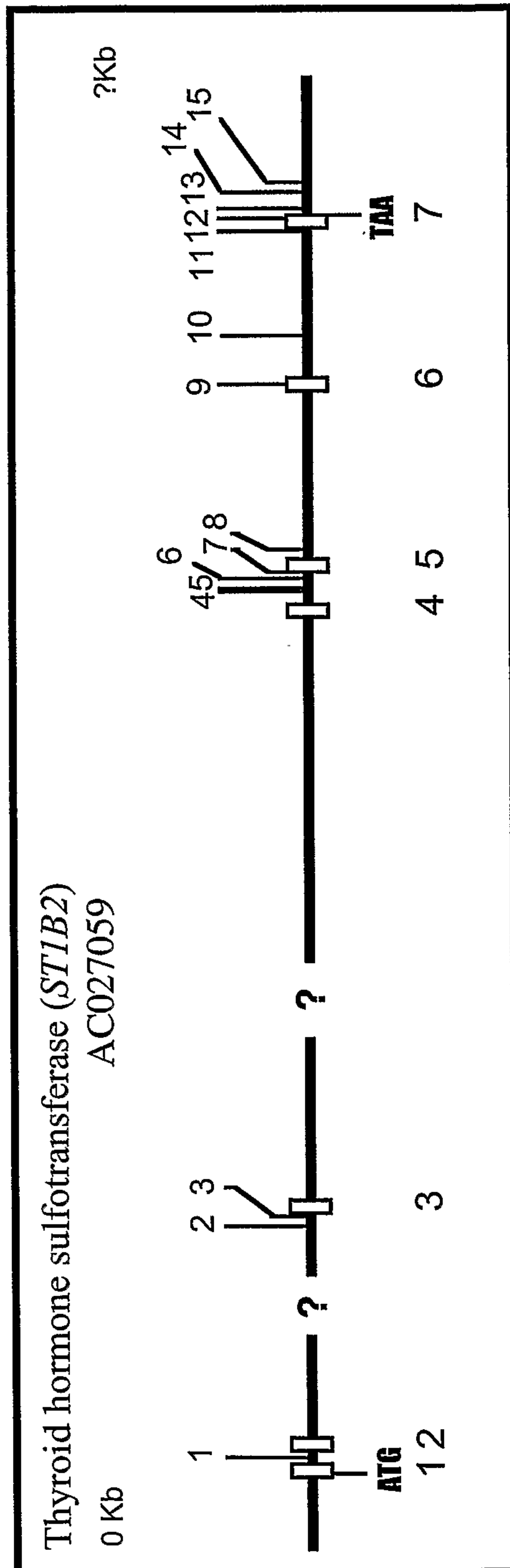


FIGURE 34

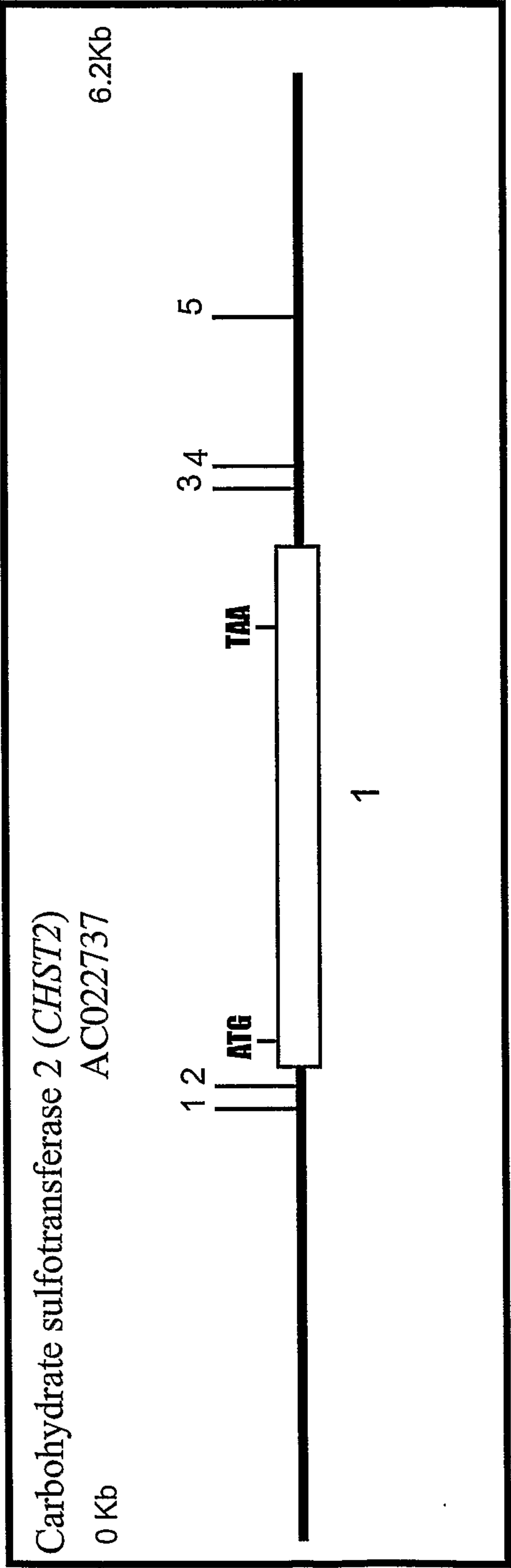


FIGURE 35

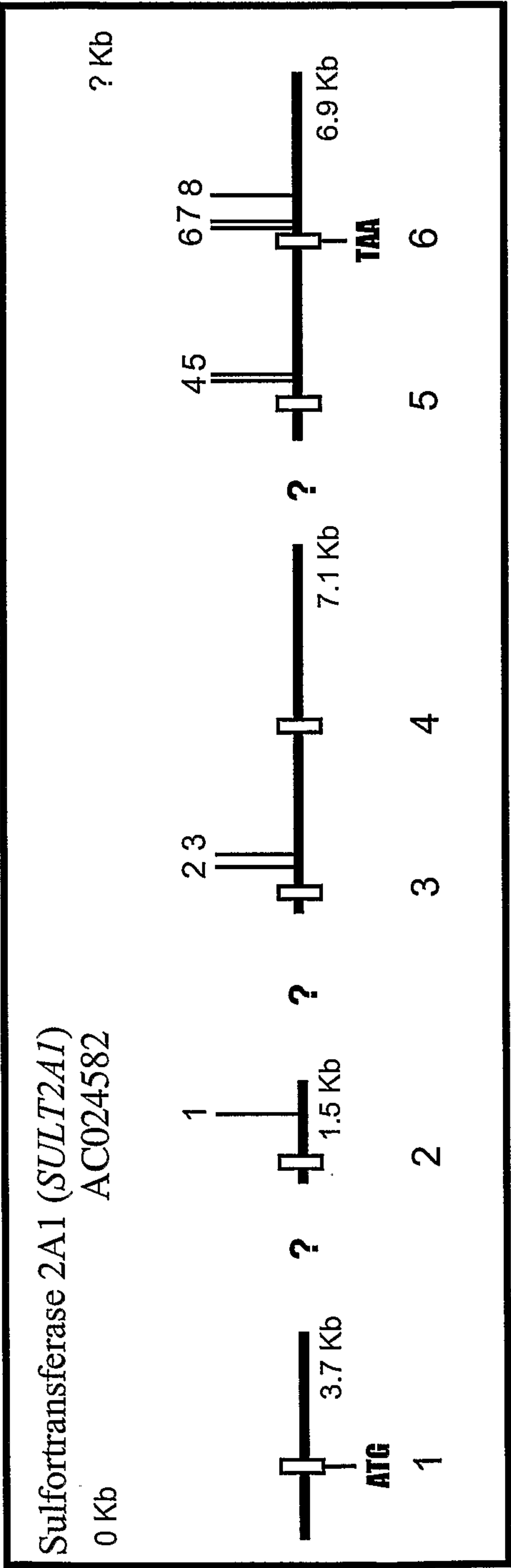


FIGURE 36

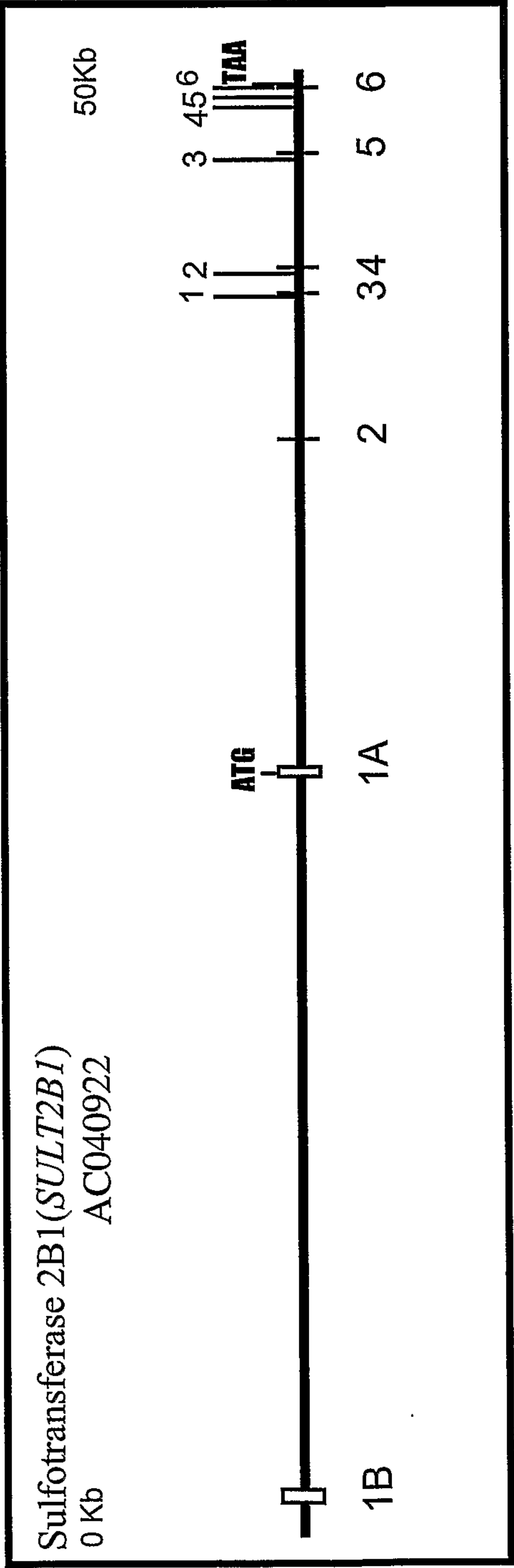


FIGURE 37

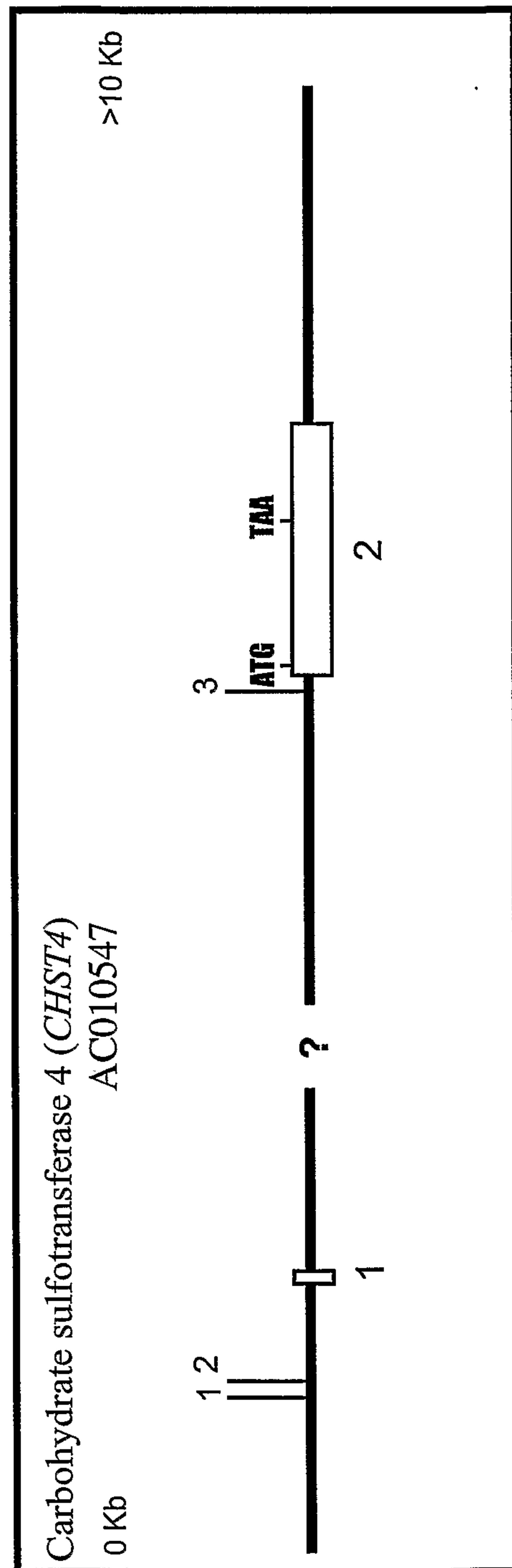


FIGURE 38

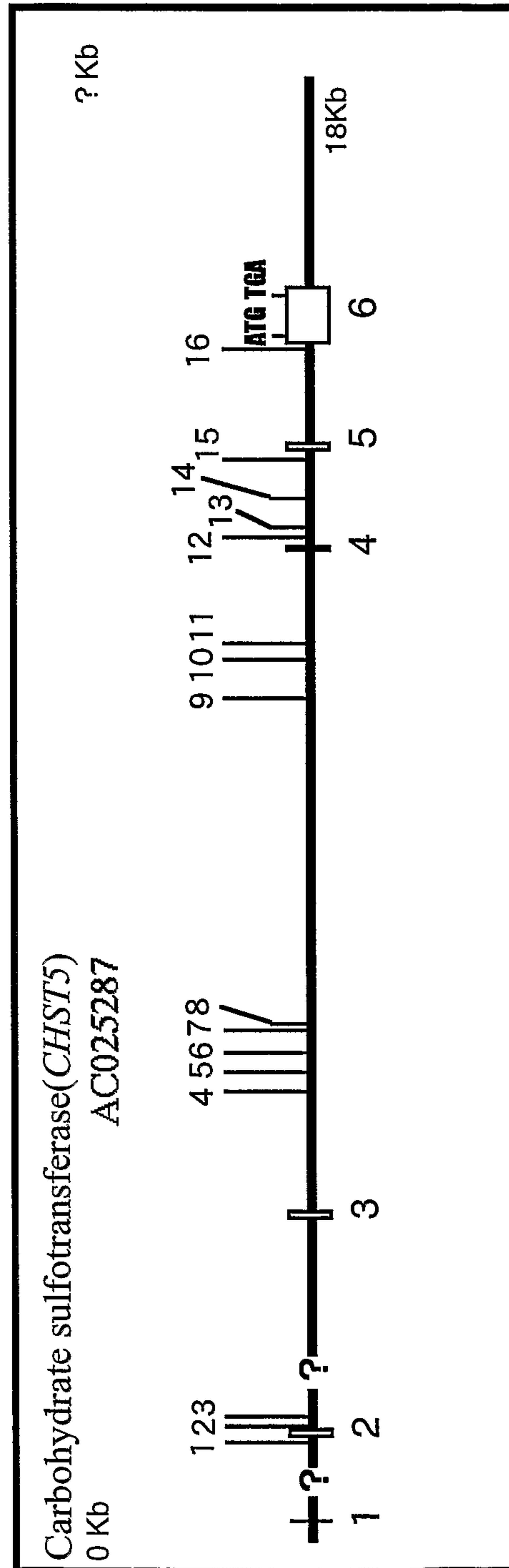


FIGURE 39

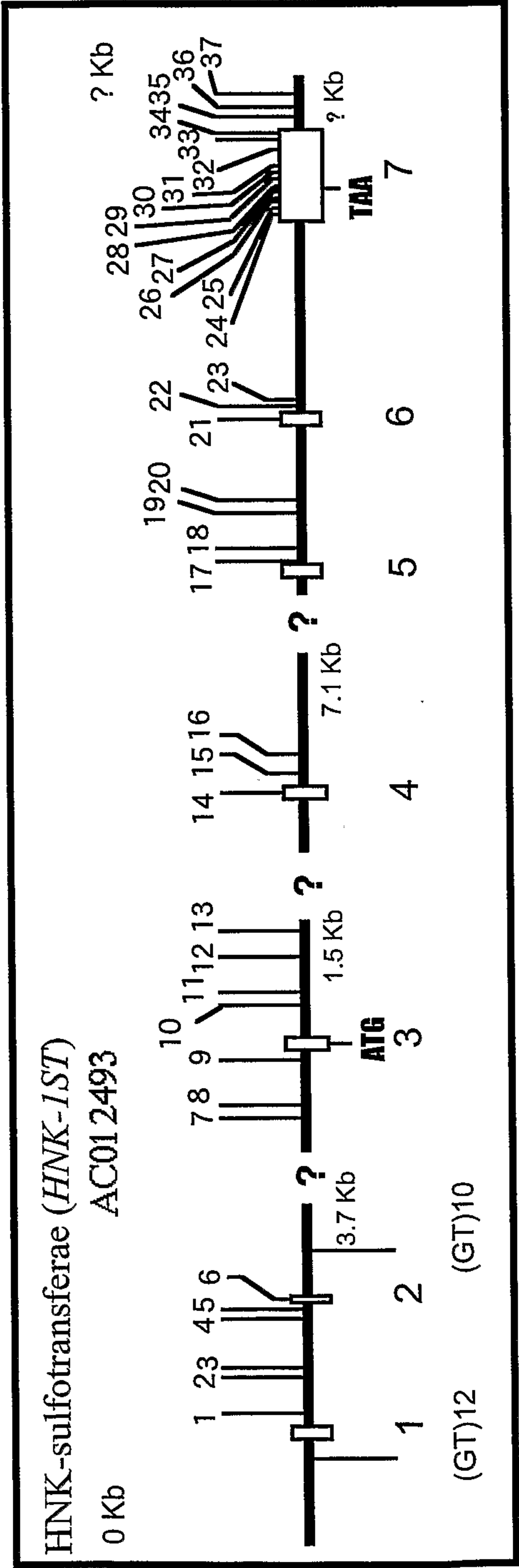


FIGURE 40

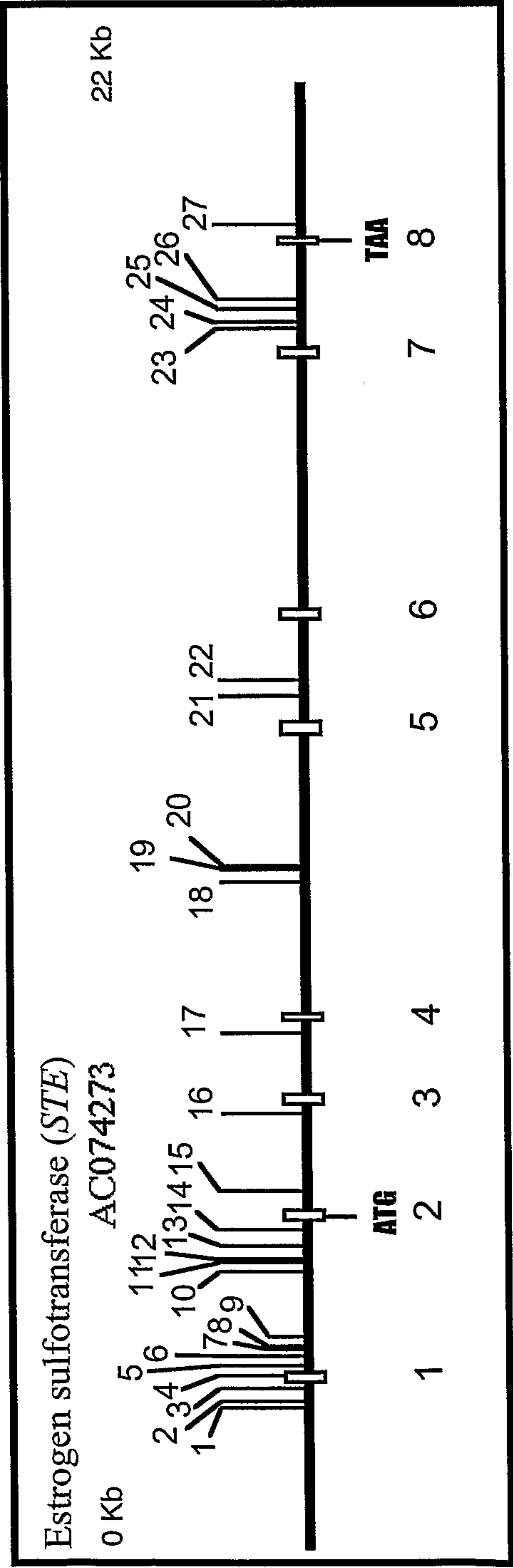


FIGURE 41

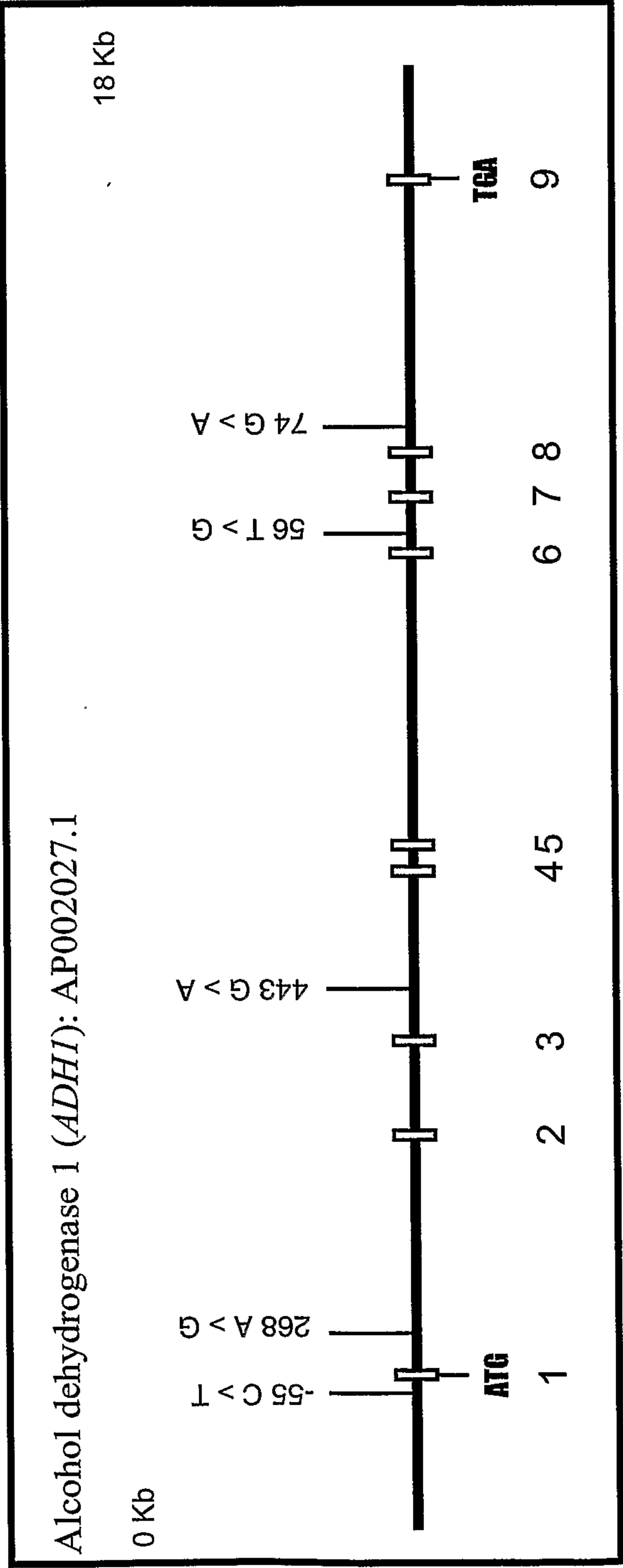




FIGURE 42

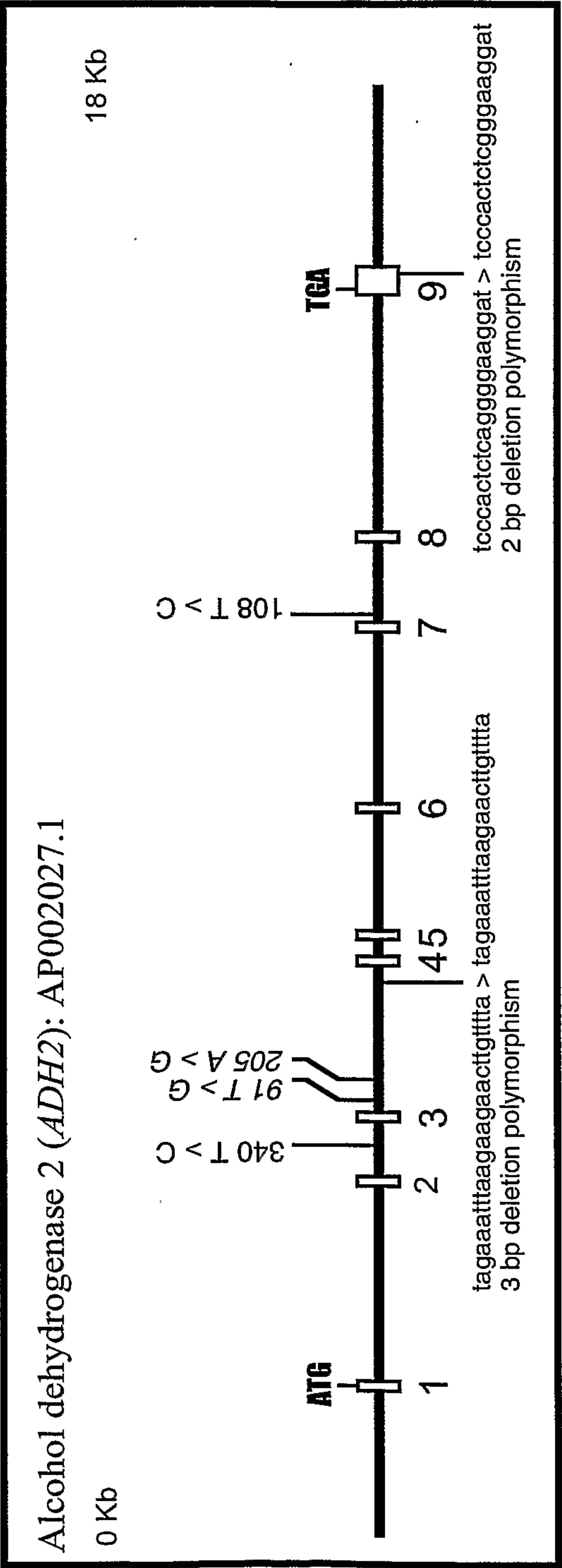


FIGURE 43

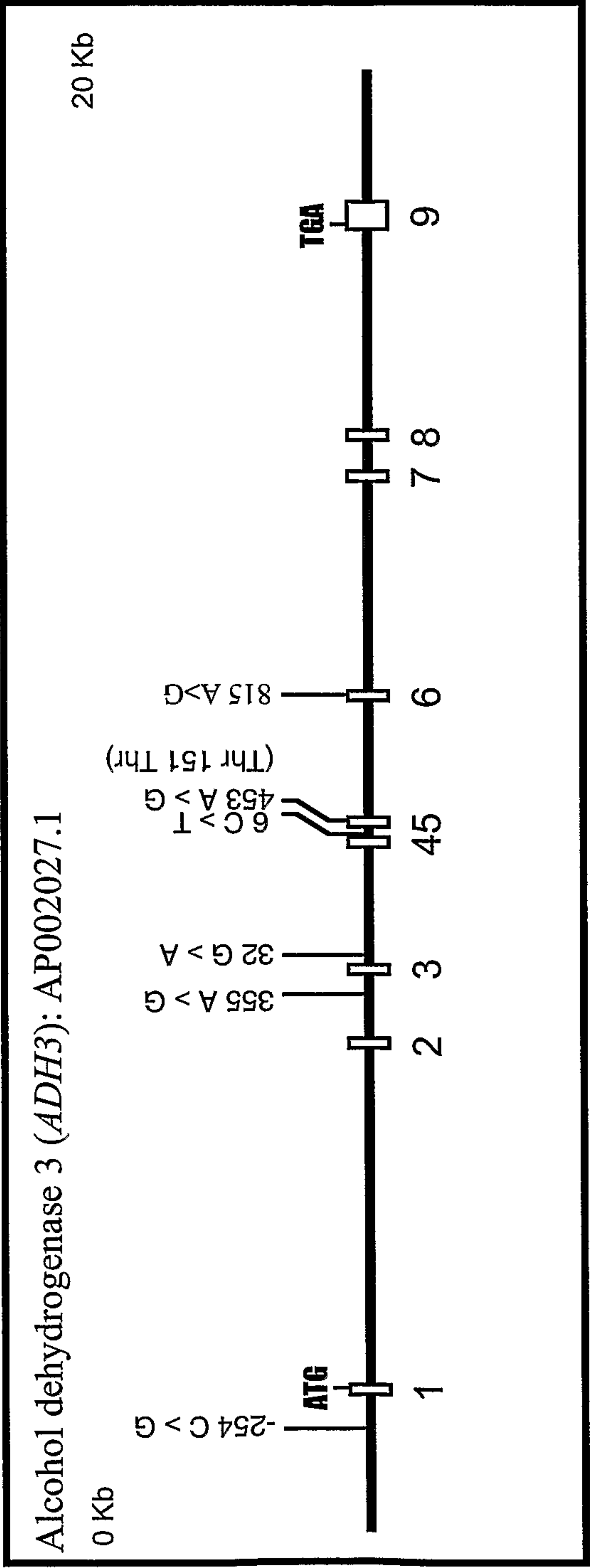


FIGURE 44

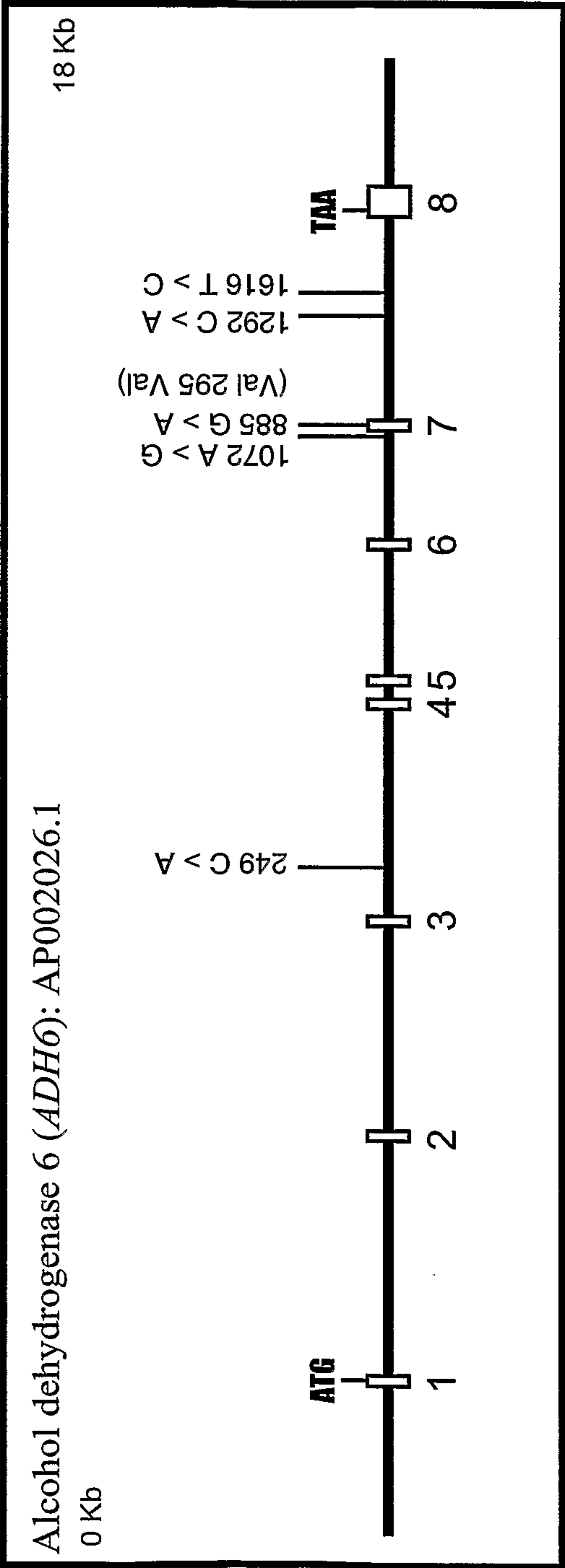


FIGURE 45

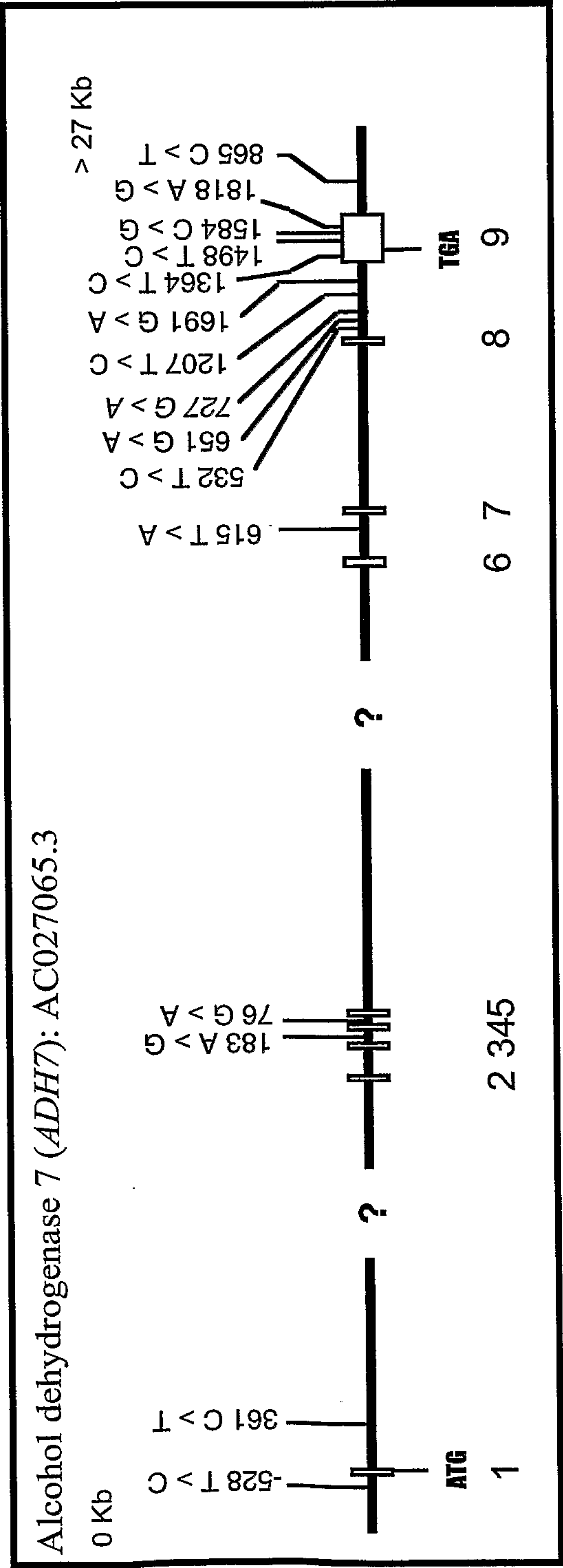


FIGURE 46

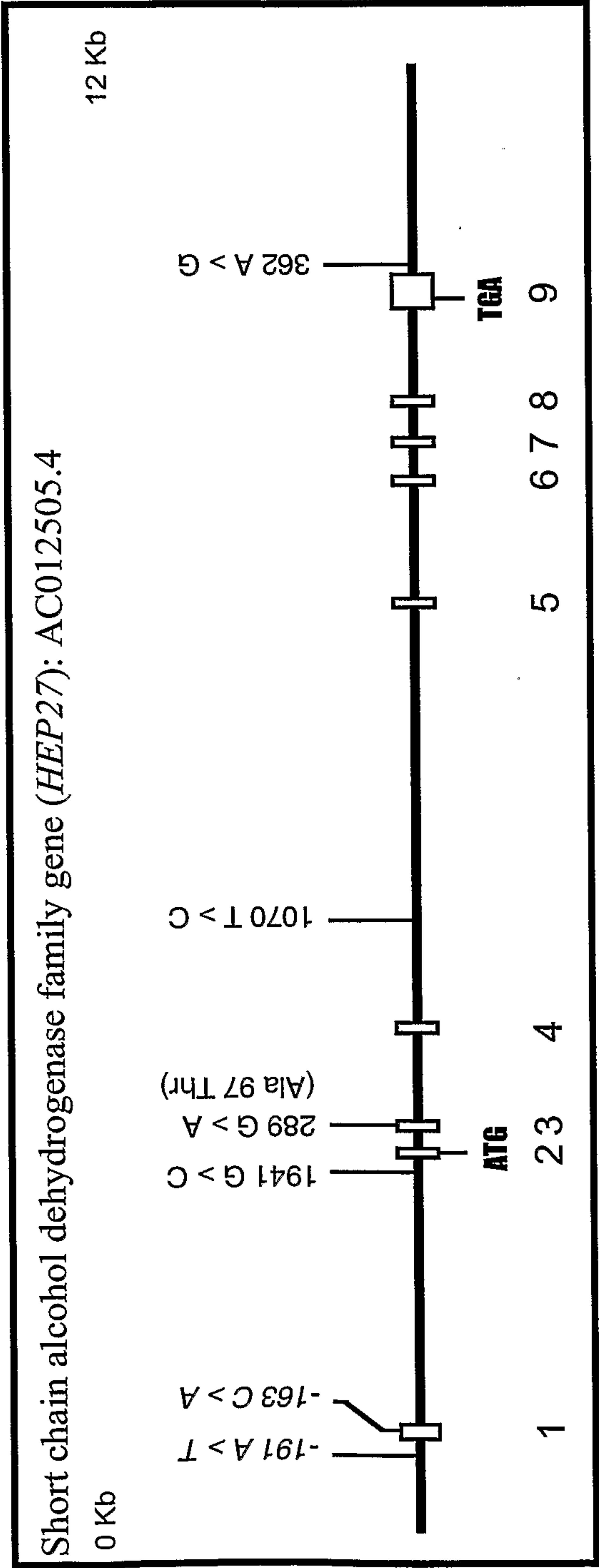


FIGURE 47

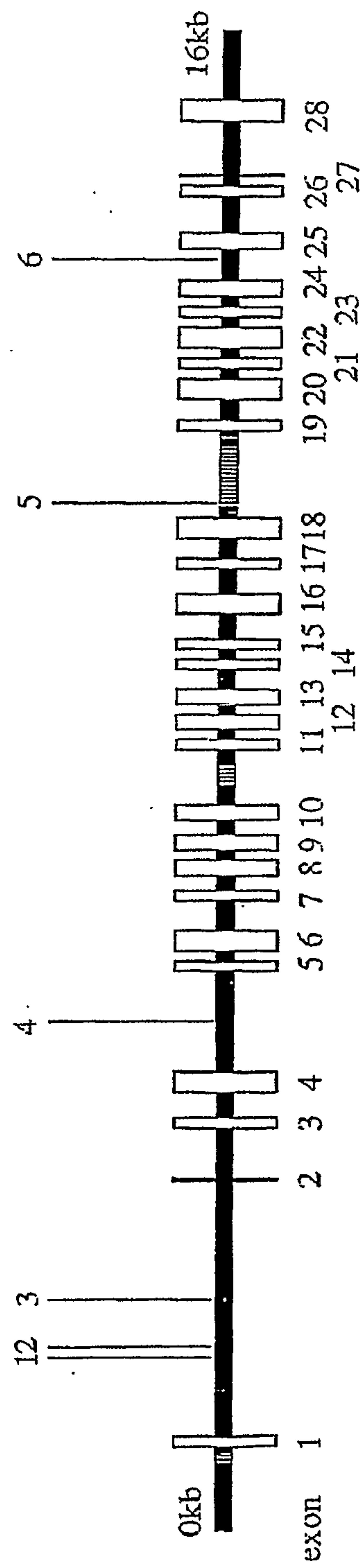
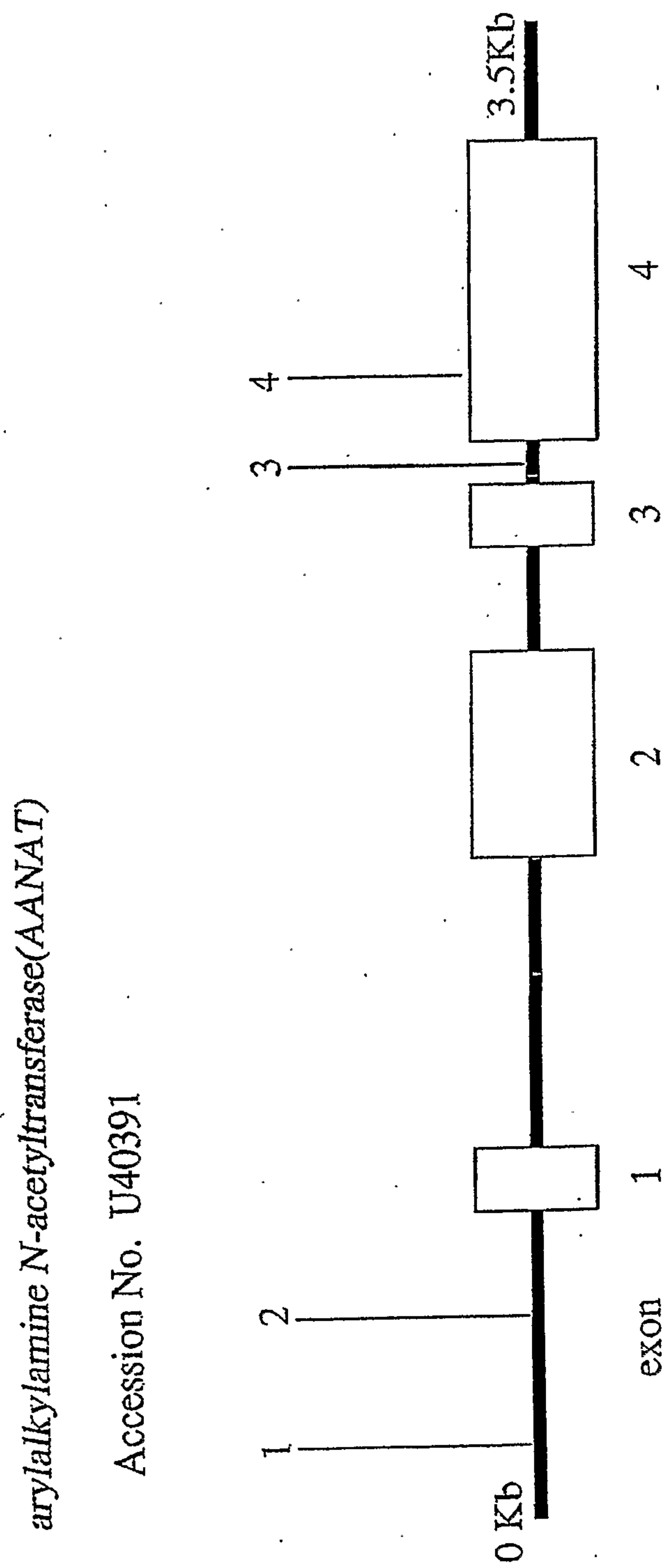


FIGURE 48



arylalkylamine N-acetyltransferase (AANAT)

Accession No. U40391

FIGURE 49

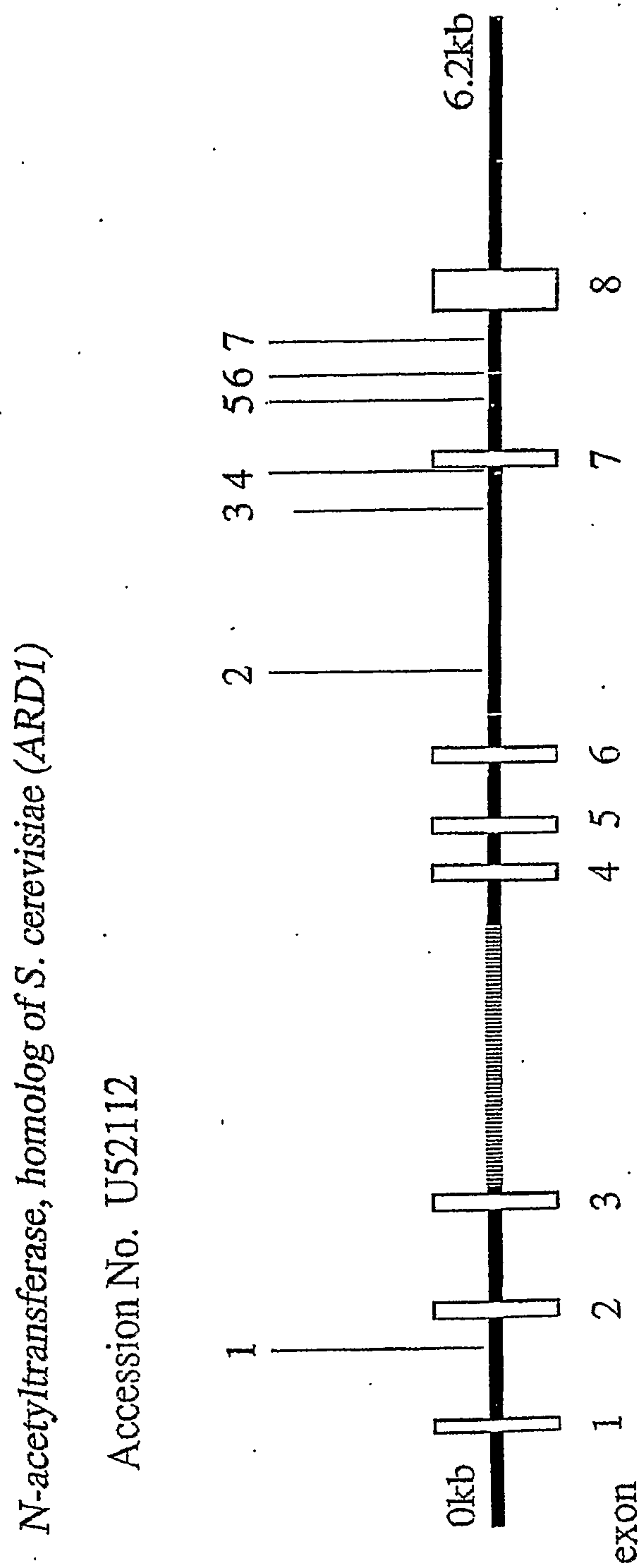


FIGURE 50

N-acetyltransferase (NAT1)

Accession No. X17059

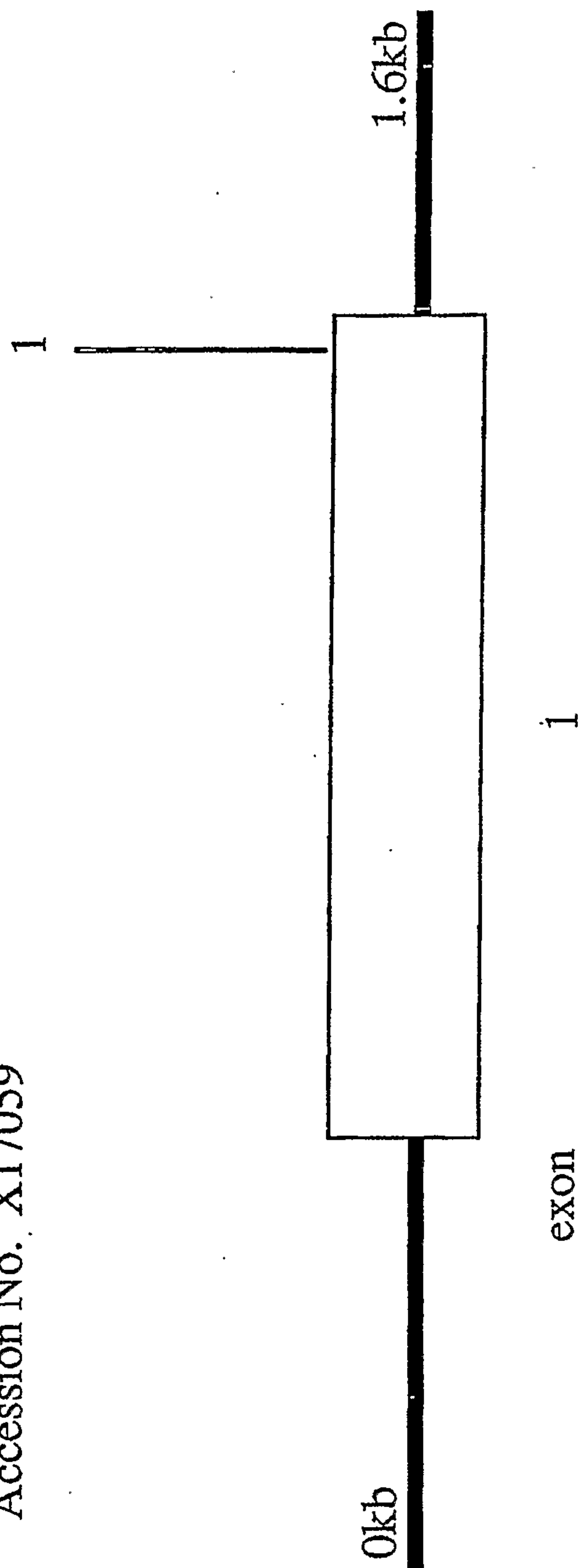


FIGURE 51

arylamine N-acetyltransferase (NAT2) Accession No.: I22255, AC025062, AC025648, D10870

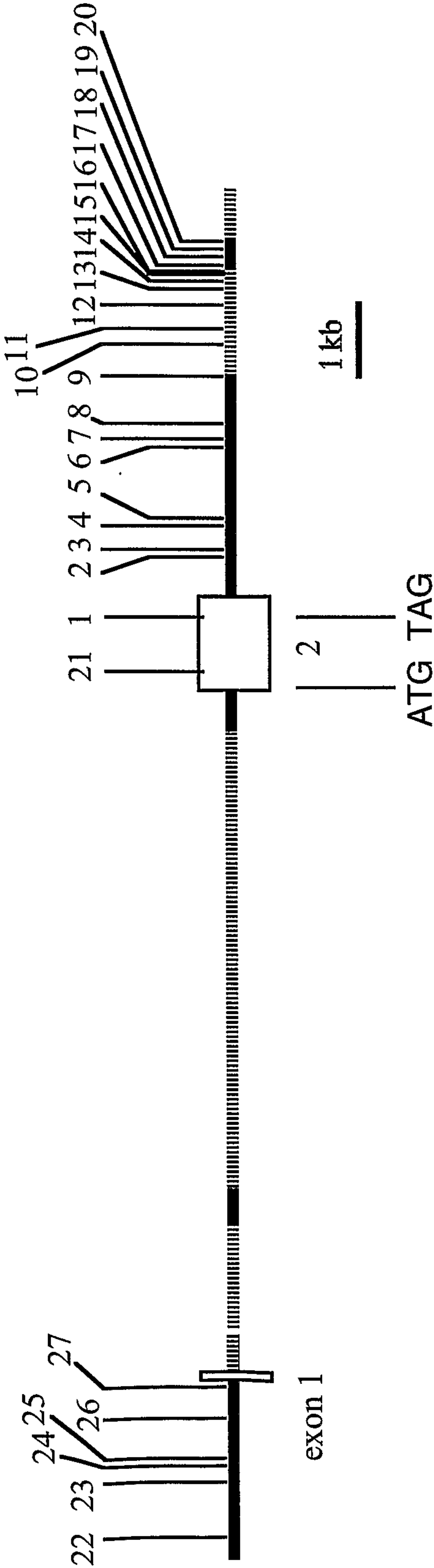
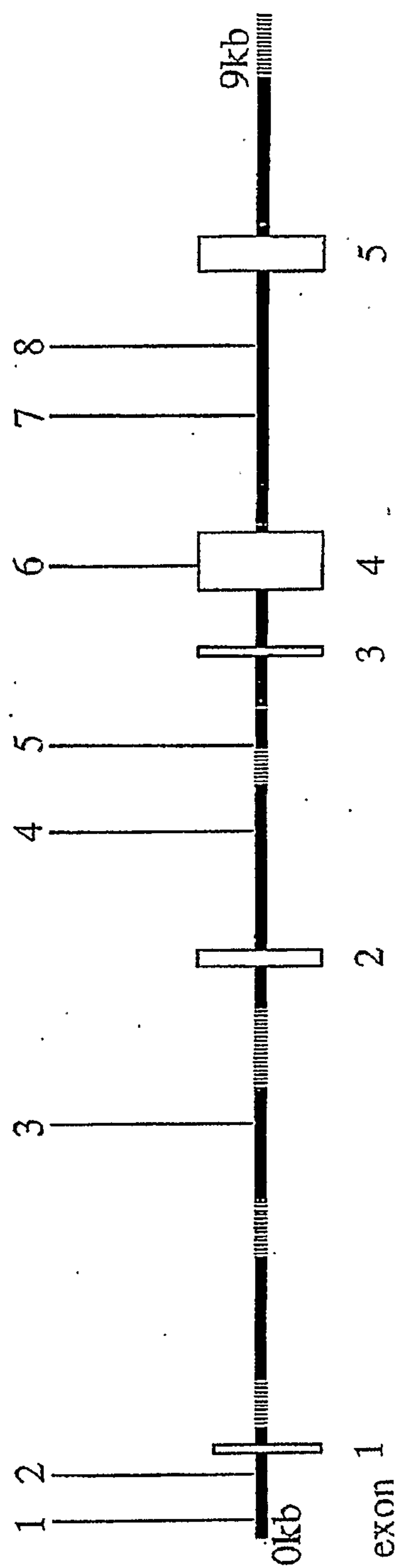


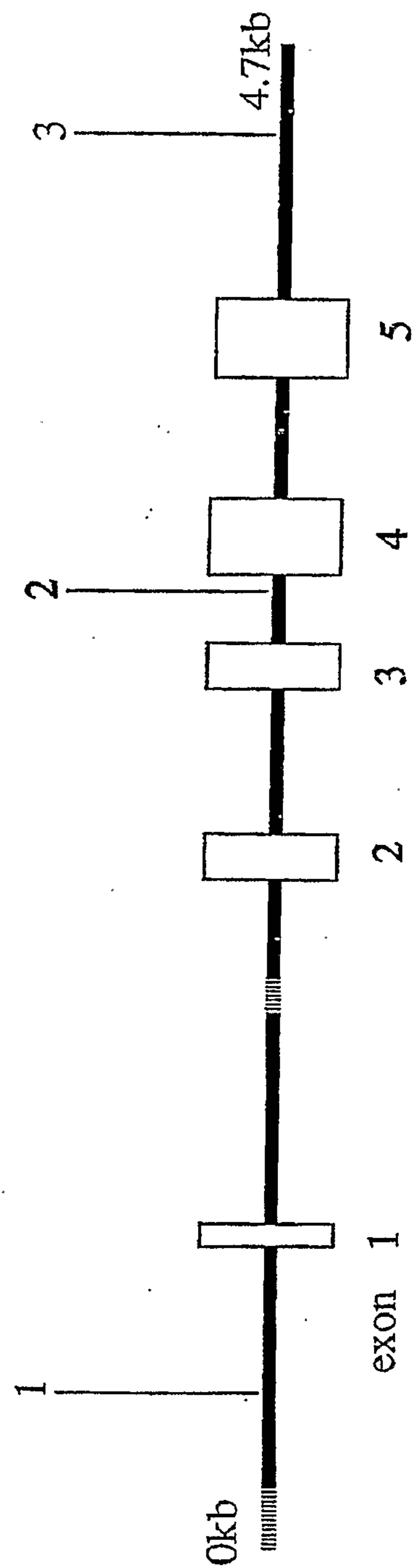
FIGURE 52



Granzyme A(GZMA)

Accession No. AC025790

FIGURE 53



Granzyme B (GZMB)

Accession No. M72150

dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

Accession No. D89060

FIGURE 55

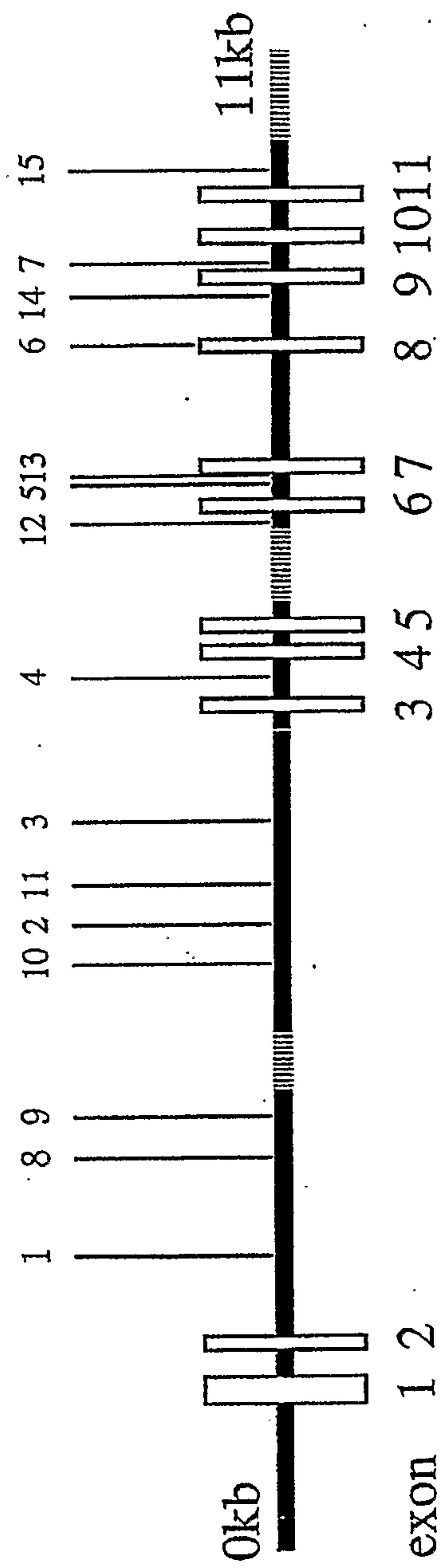


FIGURE 56

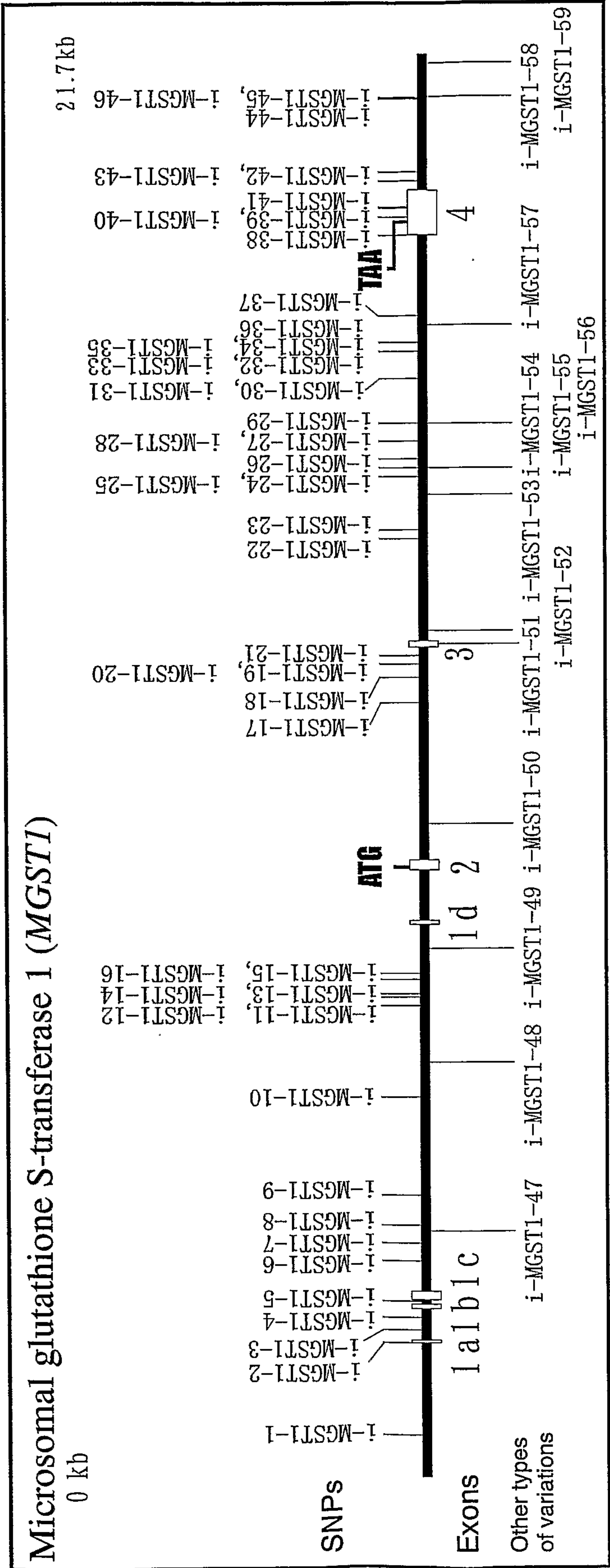


FIGURE 57

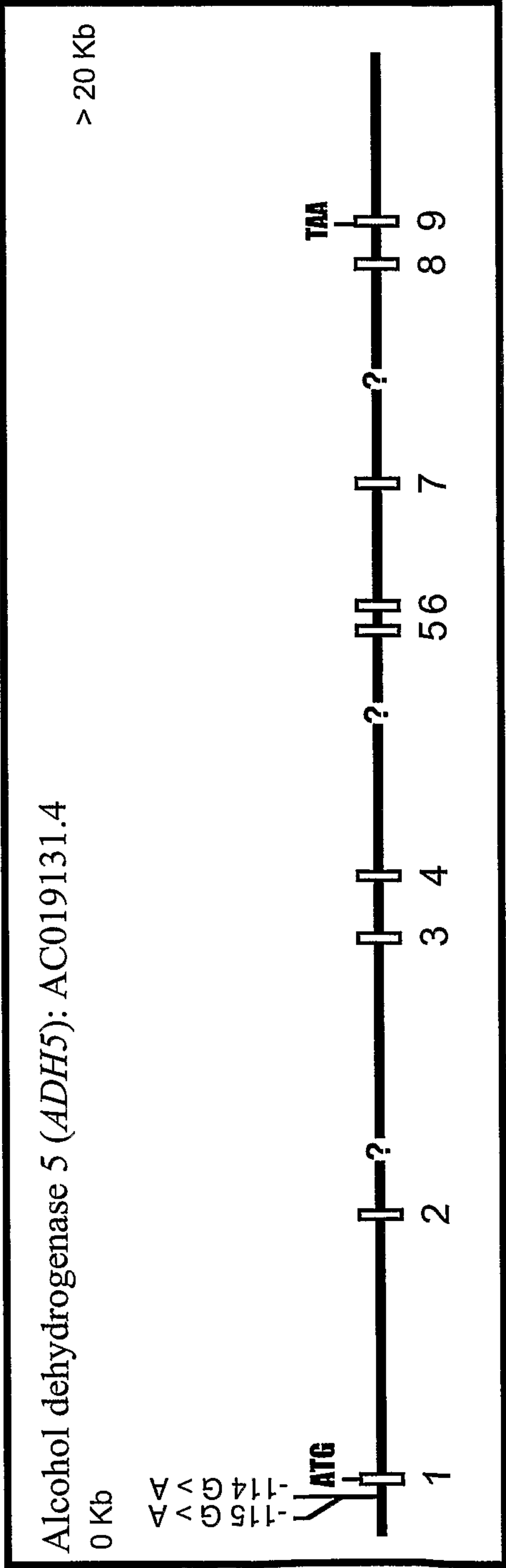


FIGURE 58

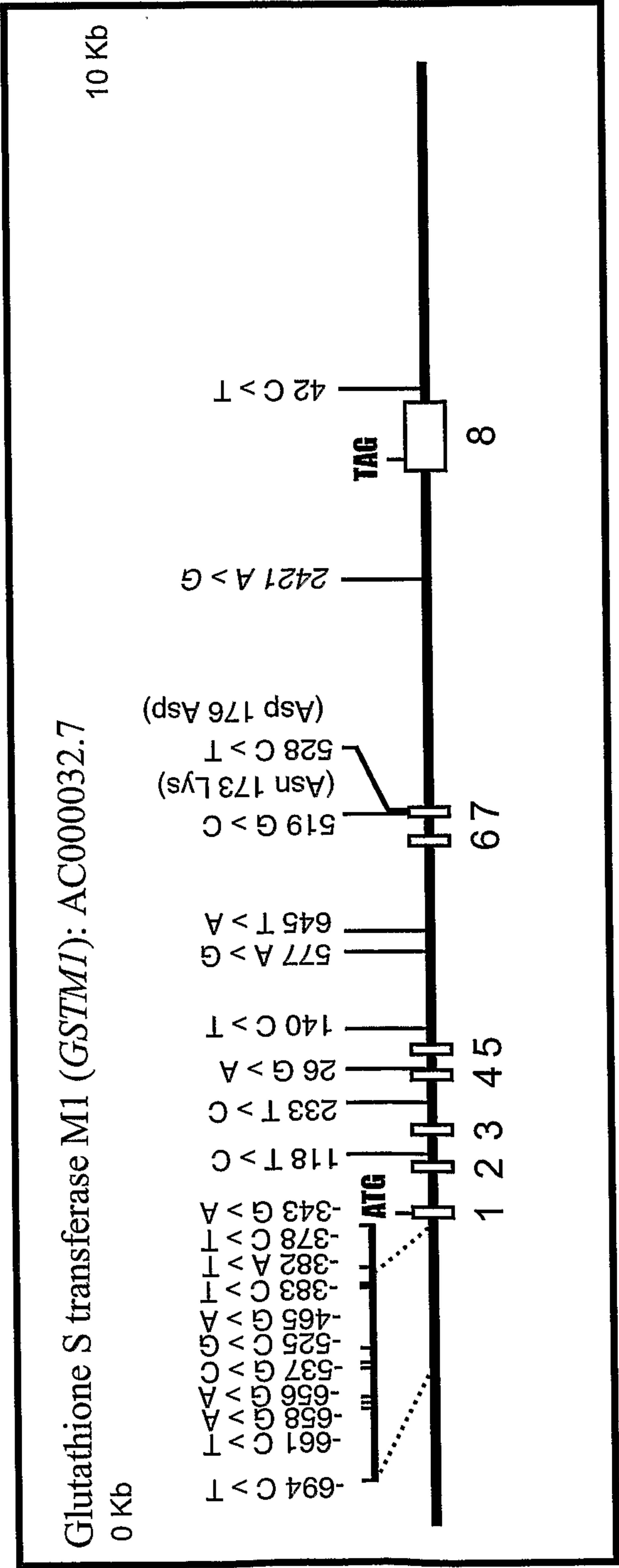


FIGURE 59

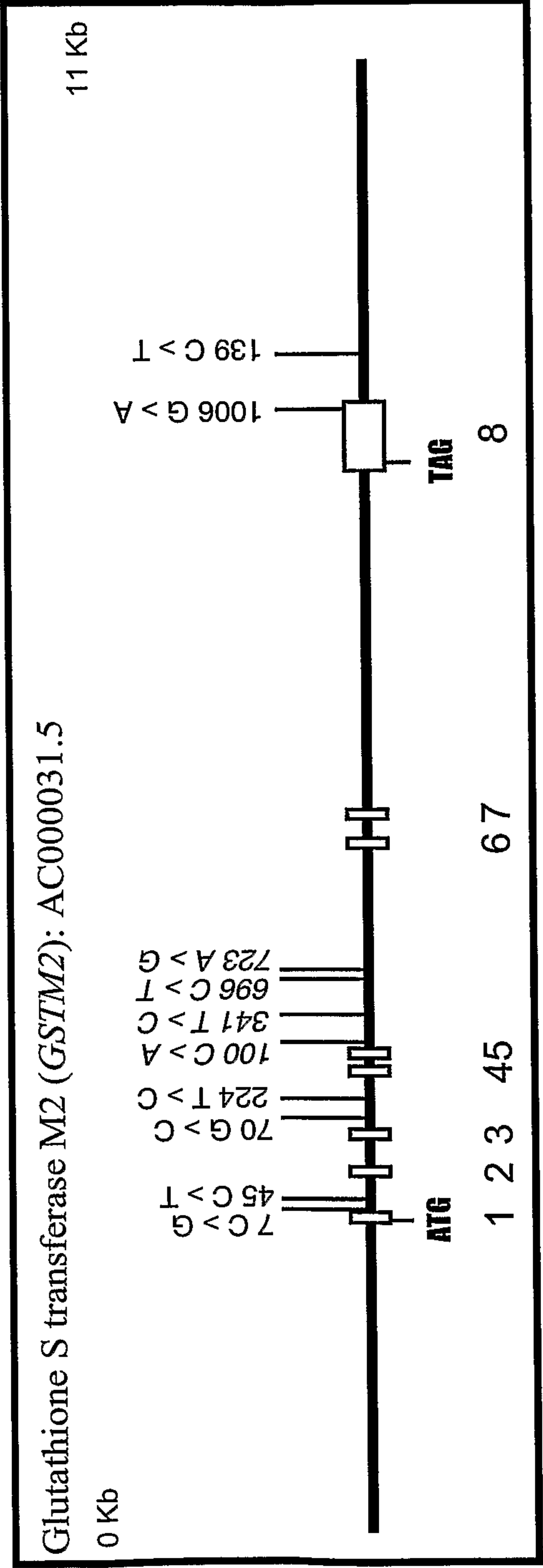


FIGURE 60

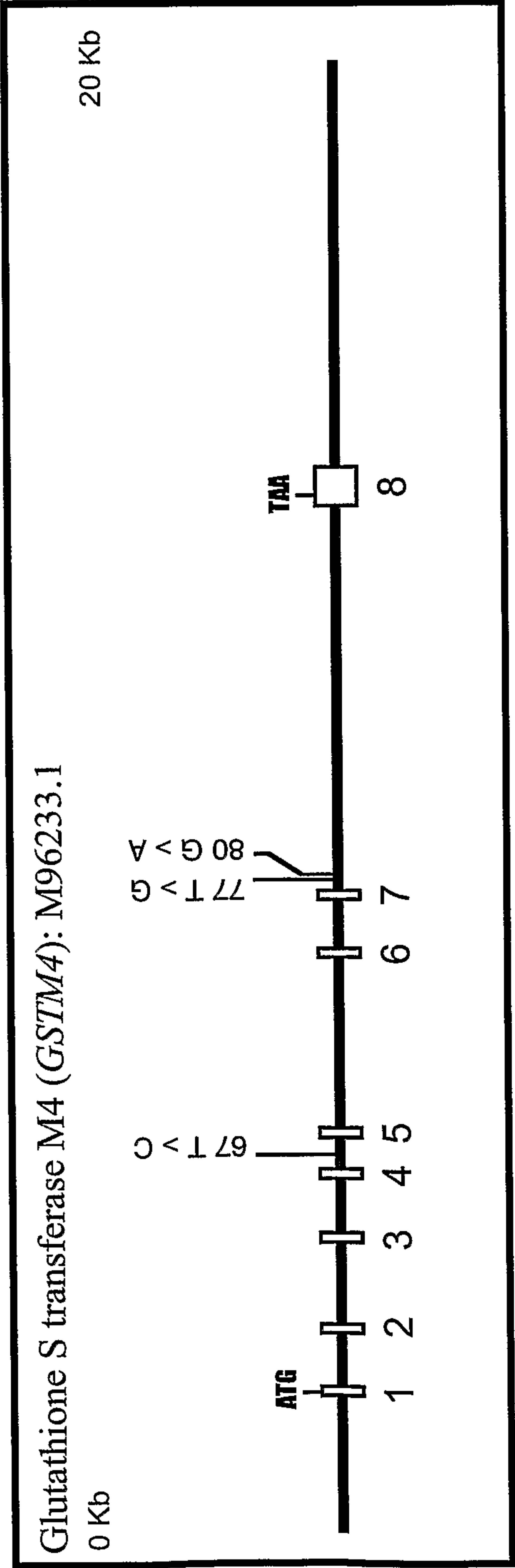


FIGURE 61

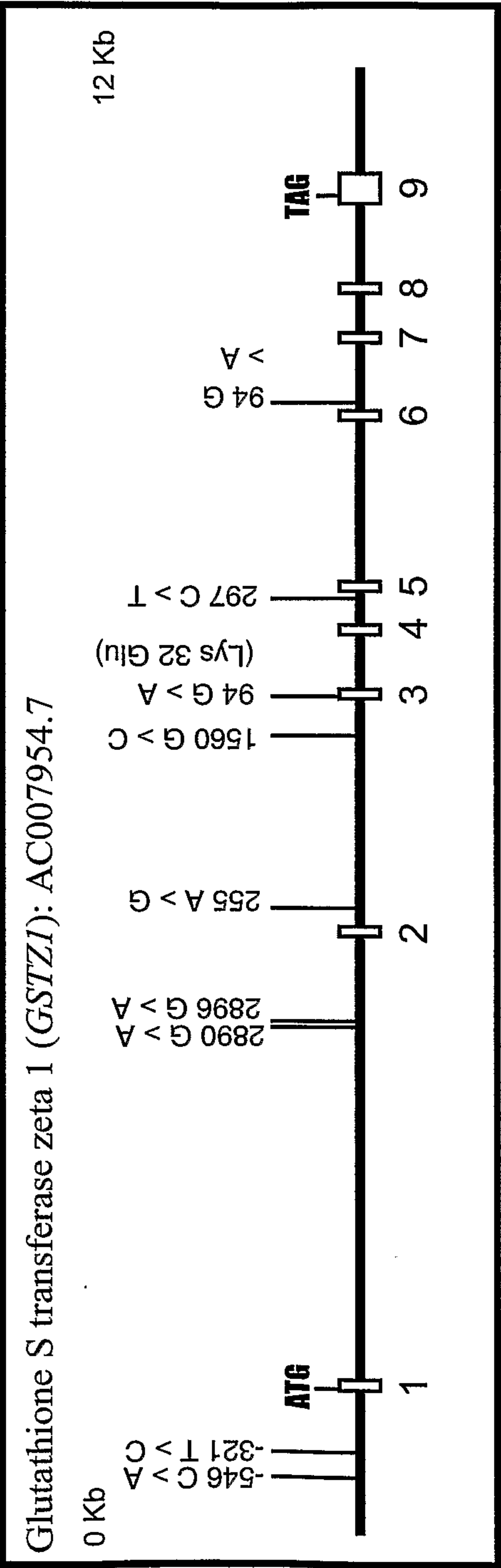


FIGURE 62

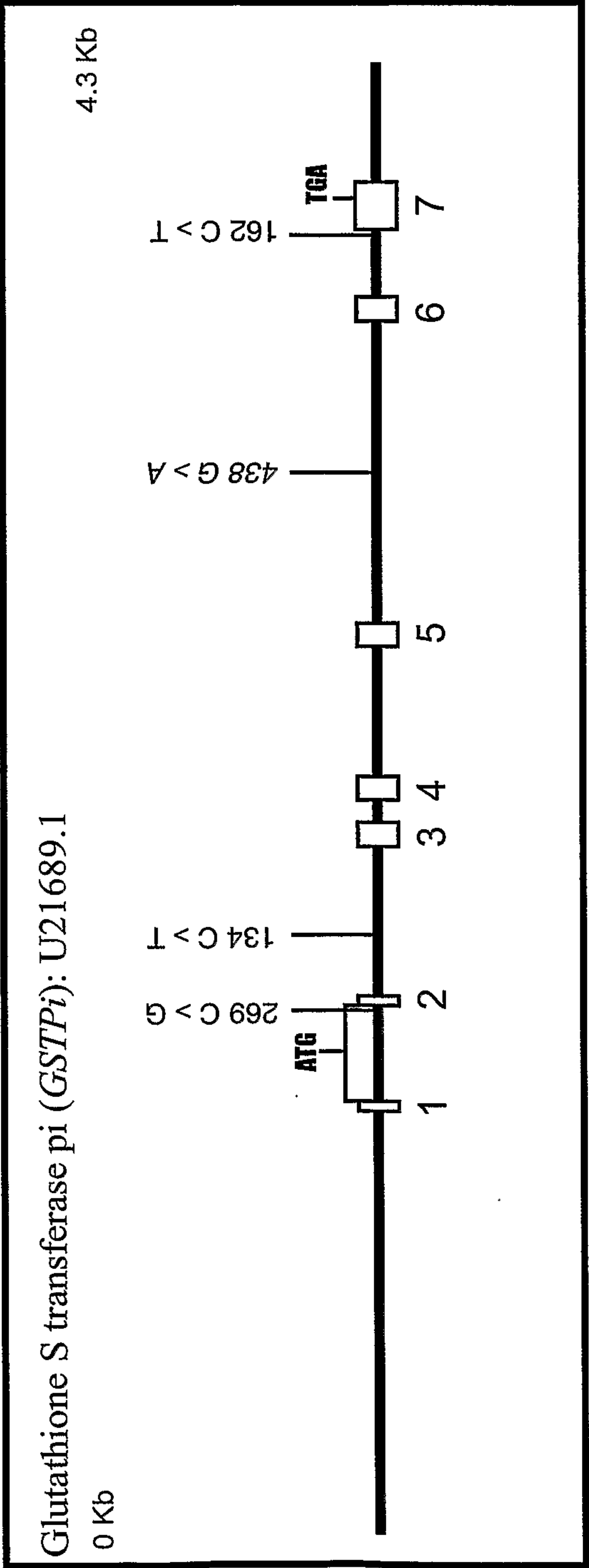


FIGURE 63

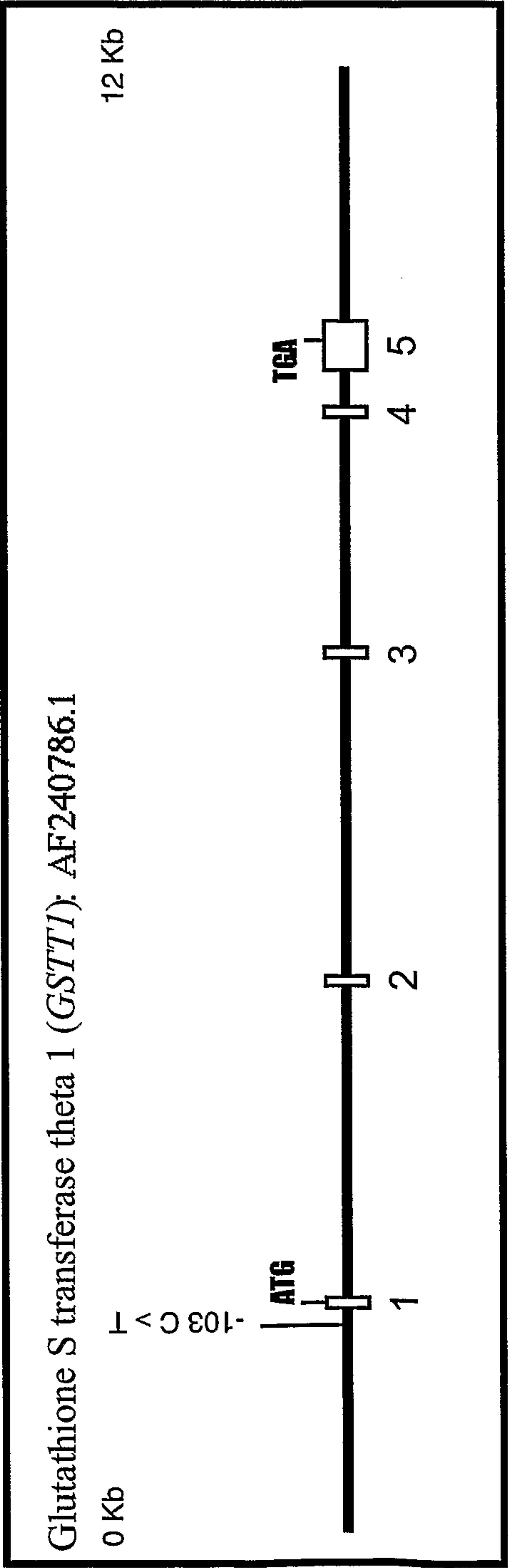


FIGURE 64

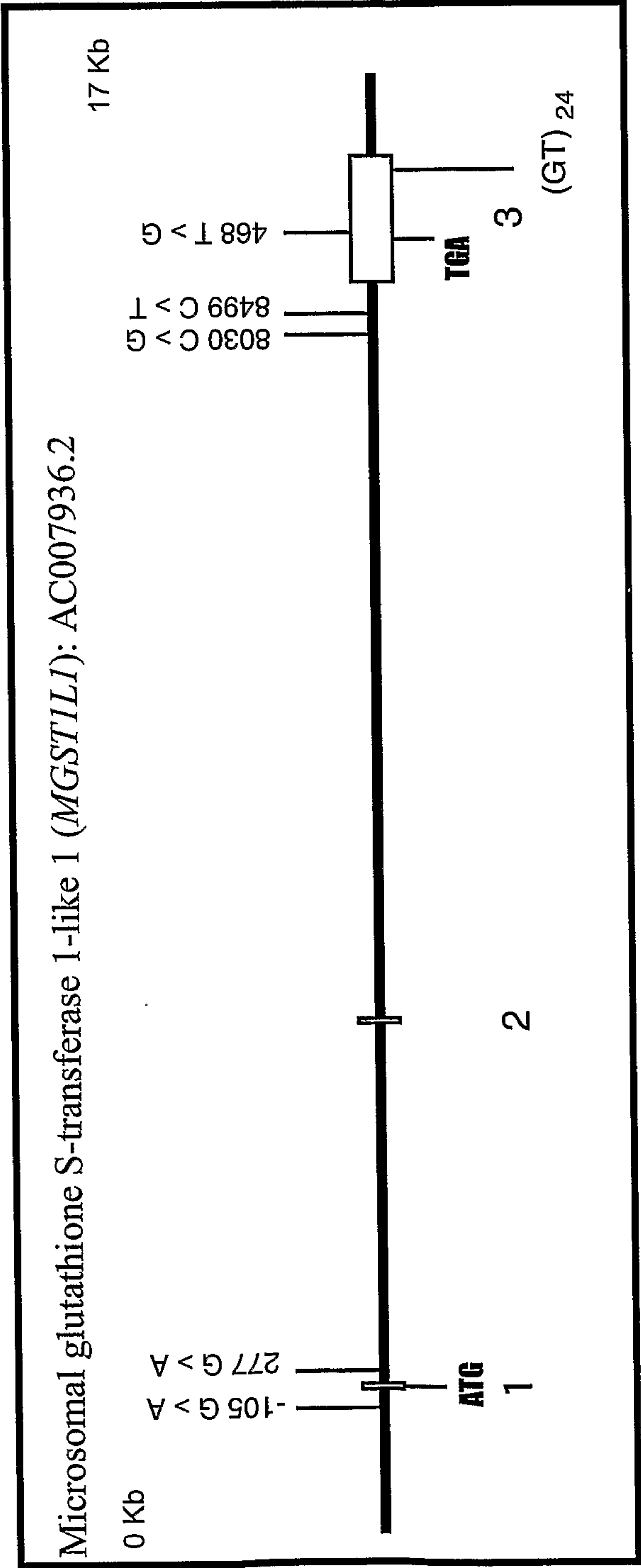


FIGURE 65

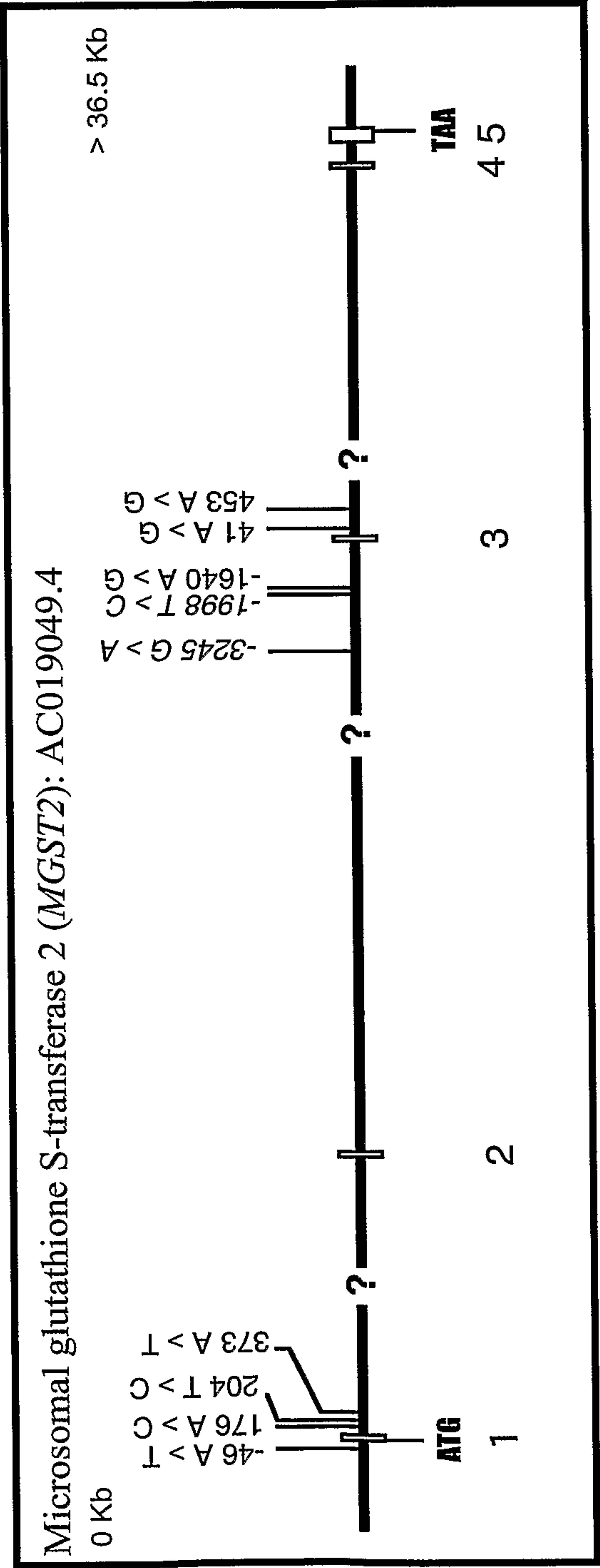


FIGURE 66

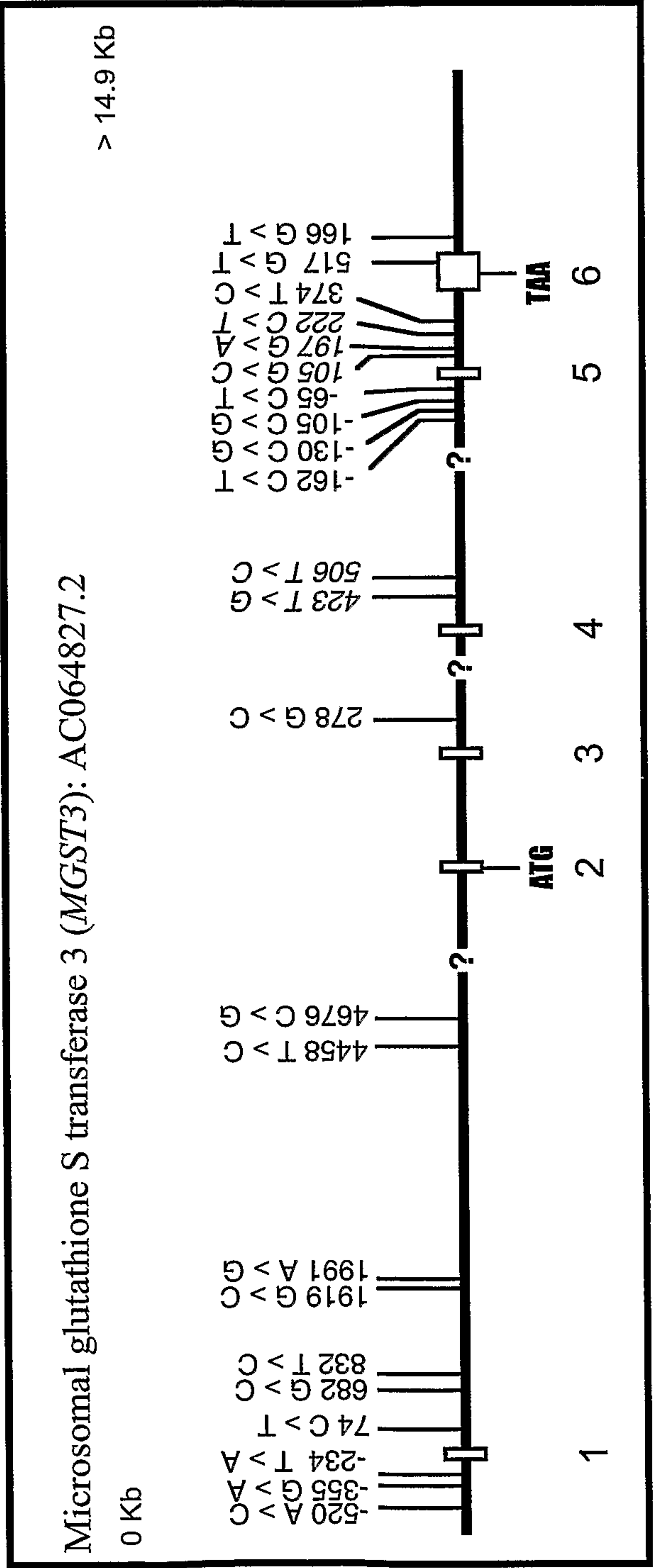


FIGURE 67

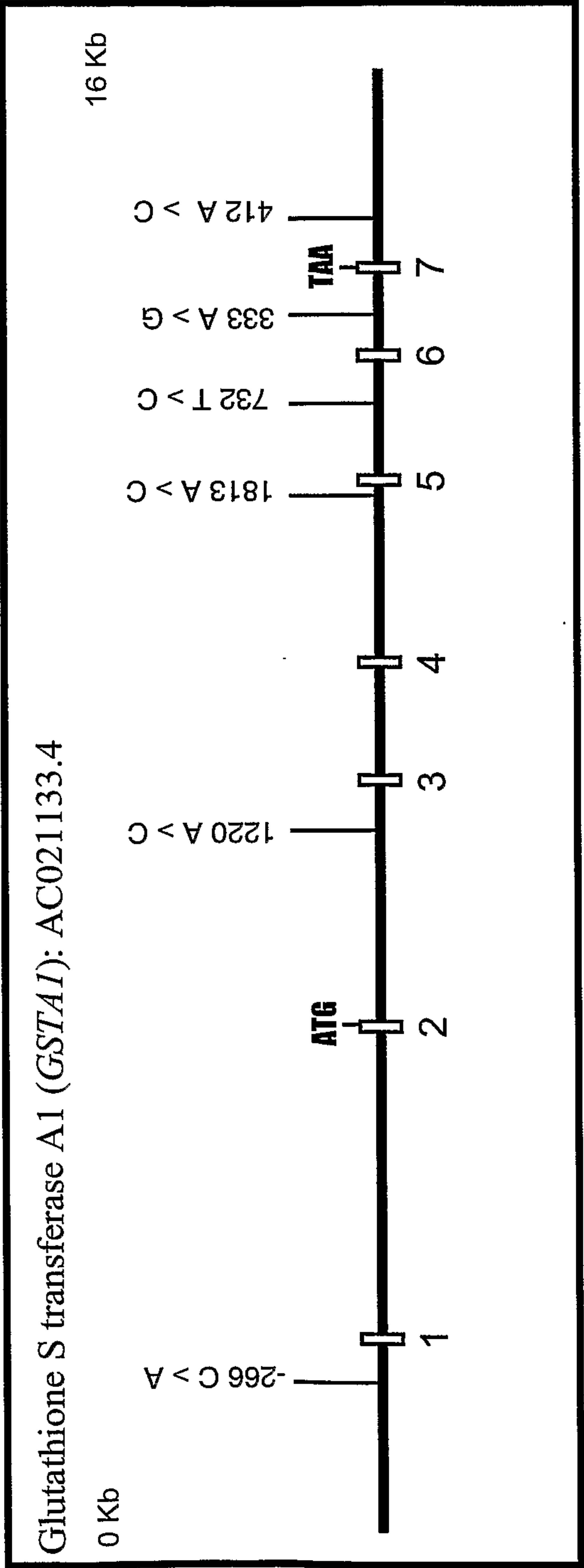


FIGURE 68

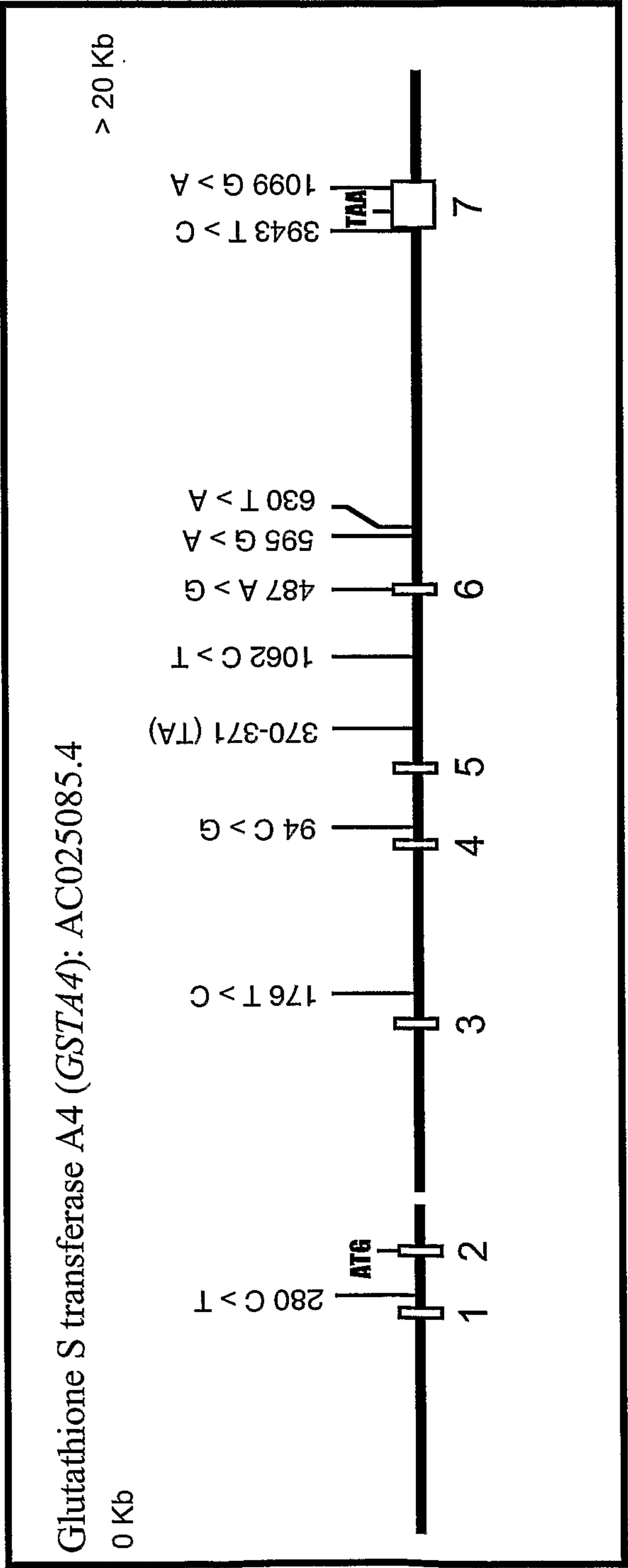


FIGURE 69

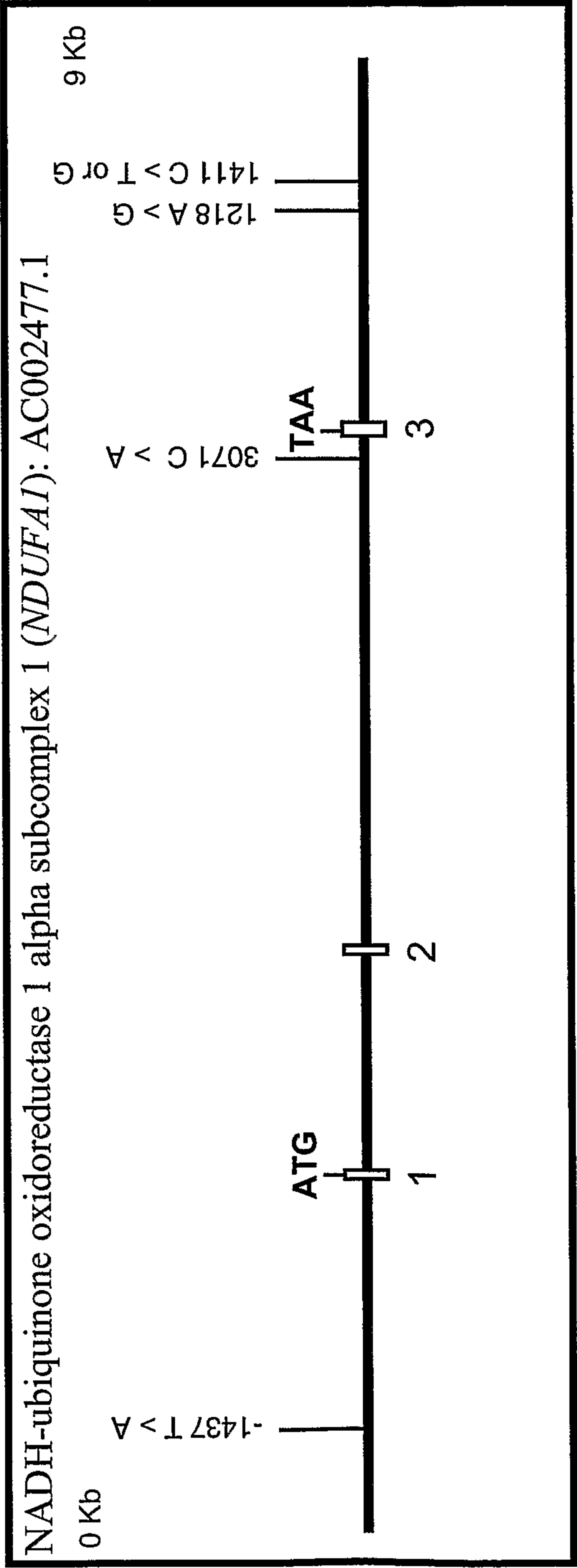


FIGURE 70

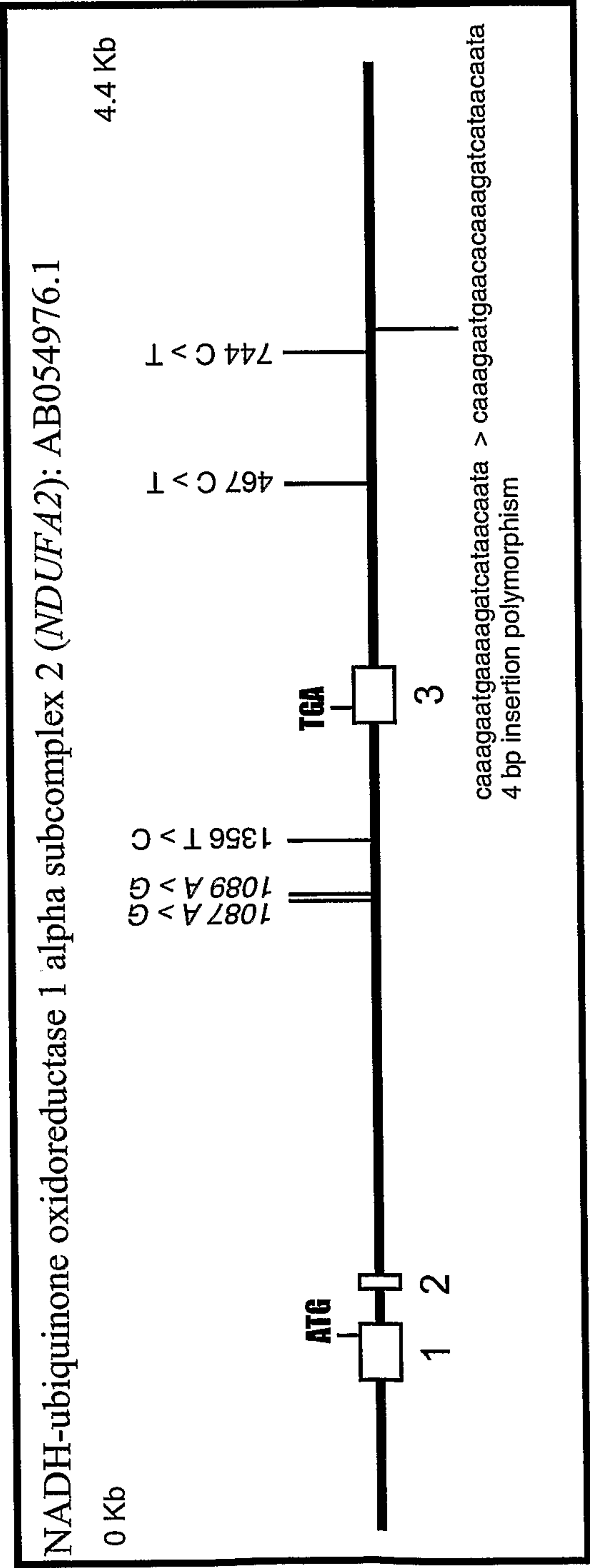


FIGURE 71

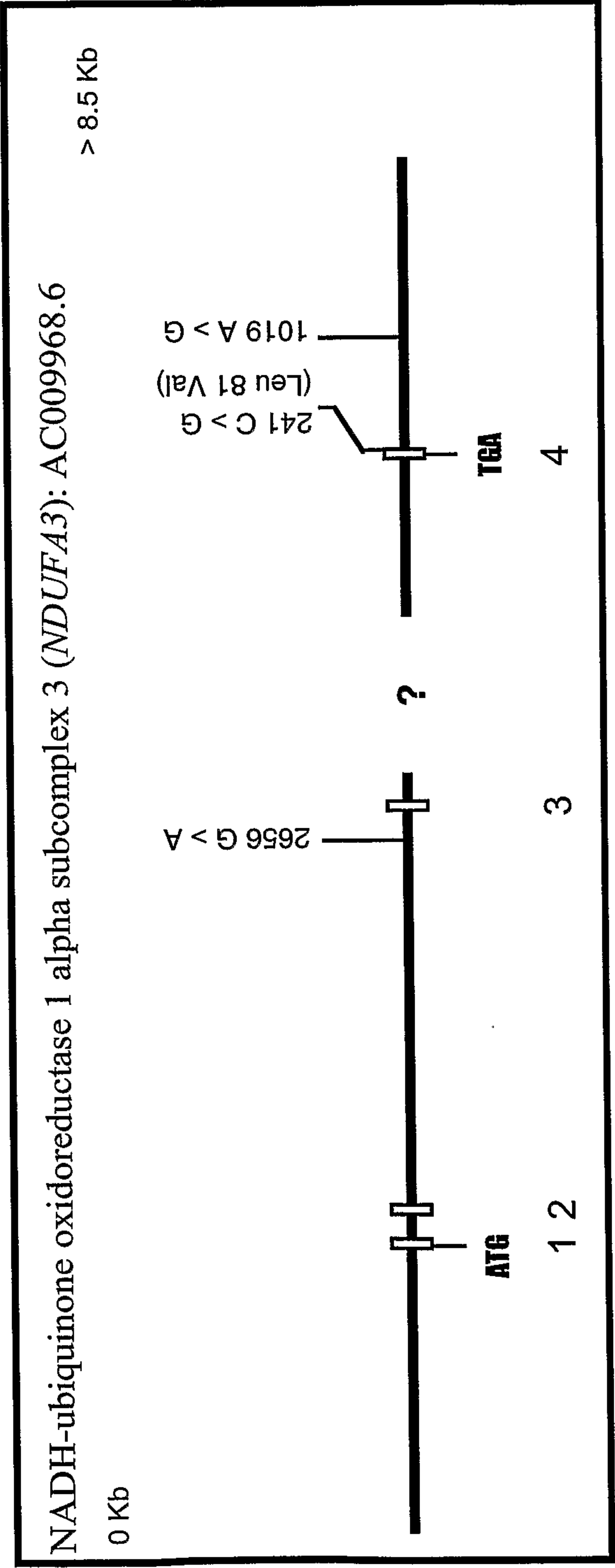


FIGURE 72

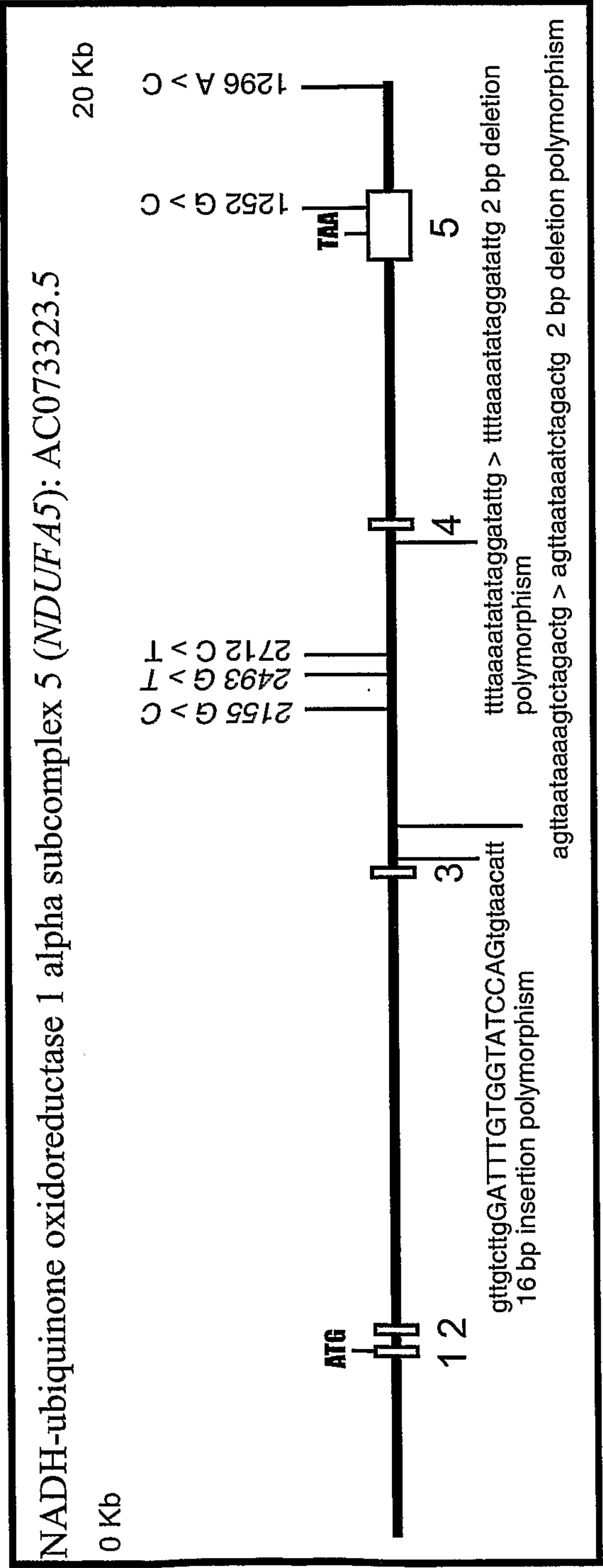


FIGURE 73

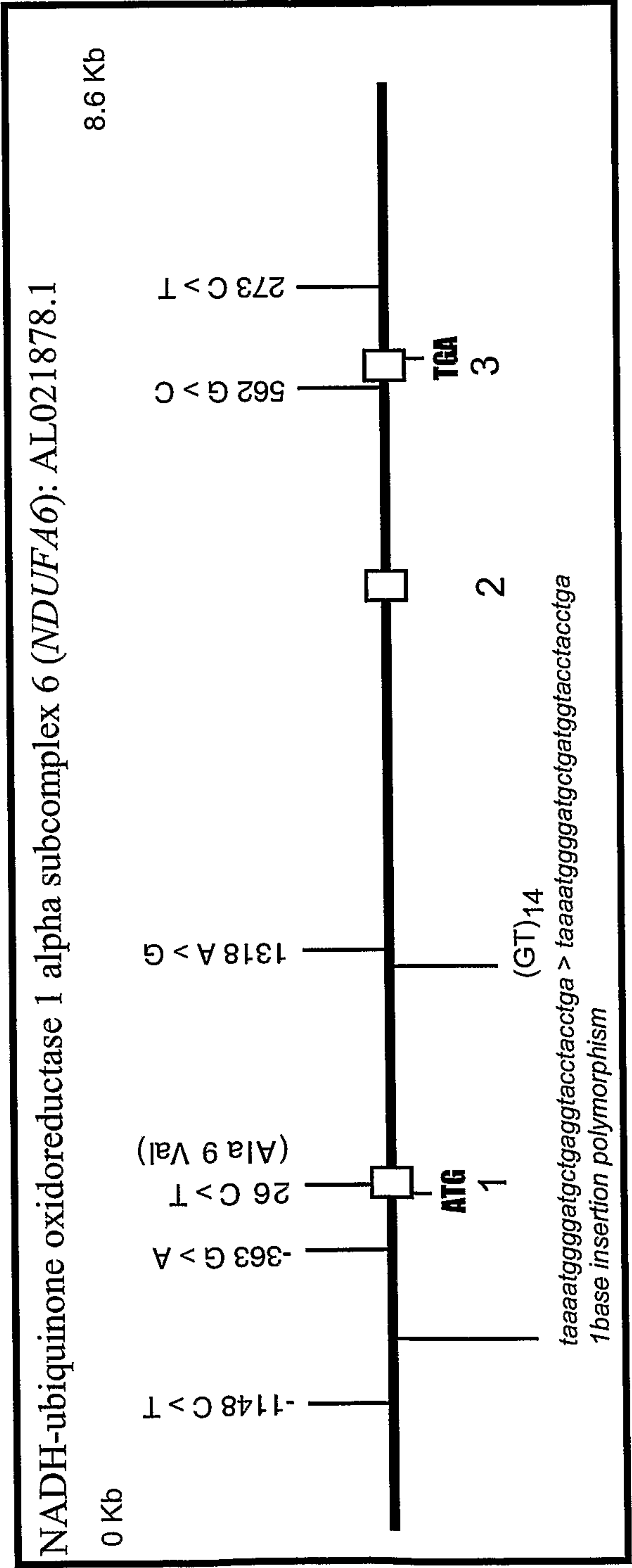


FIGURE 74

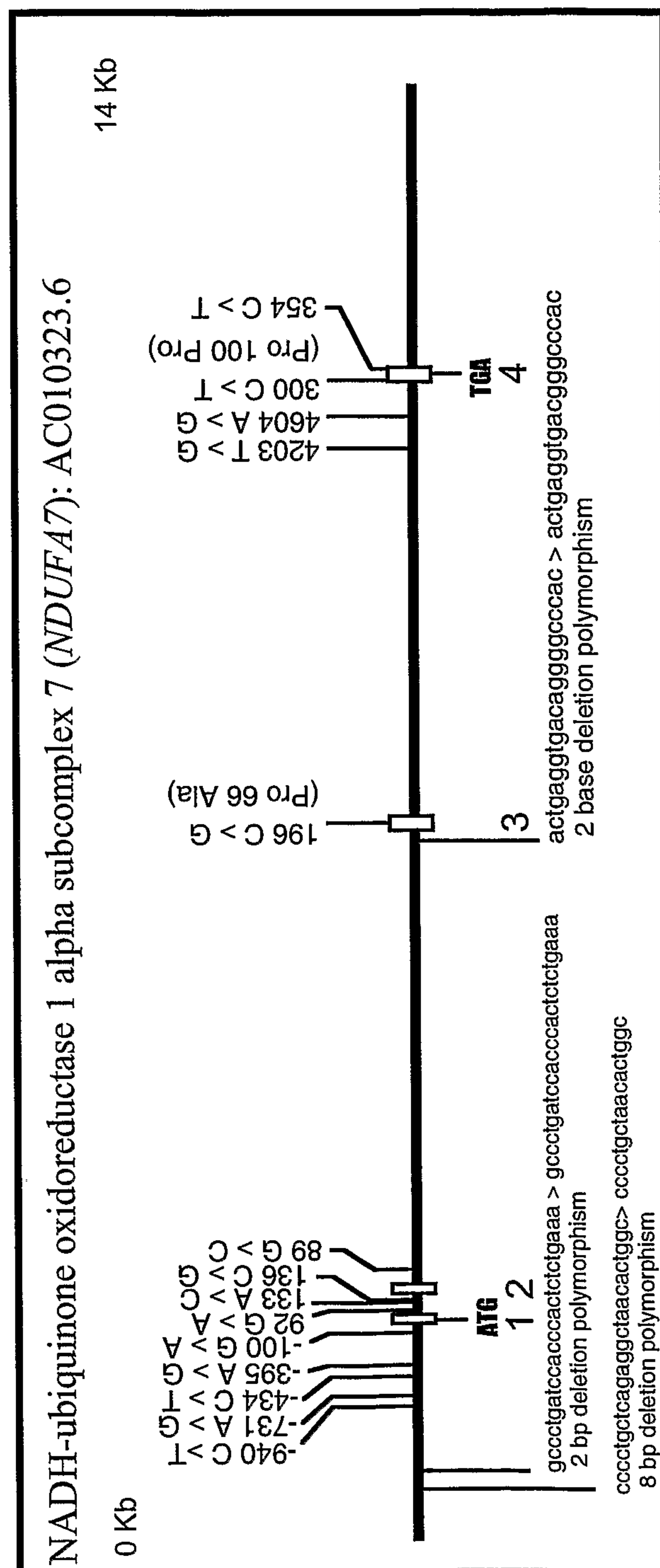


FIGURE 75

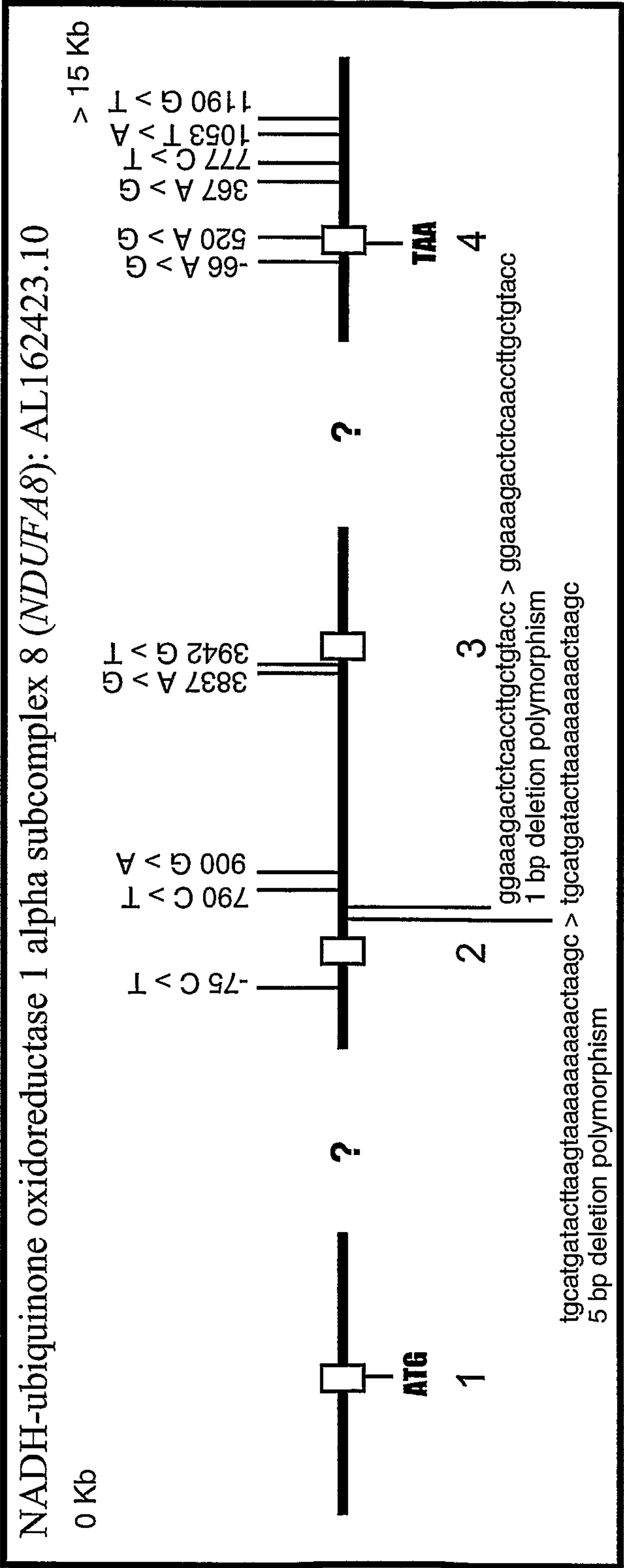


FIGURE 76

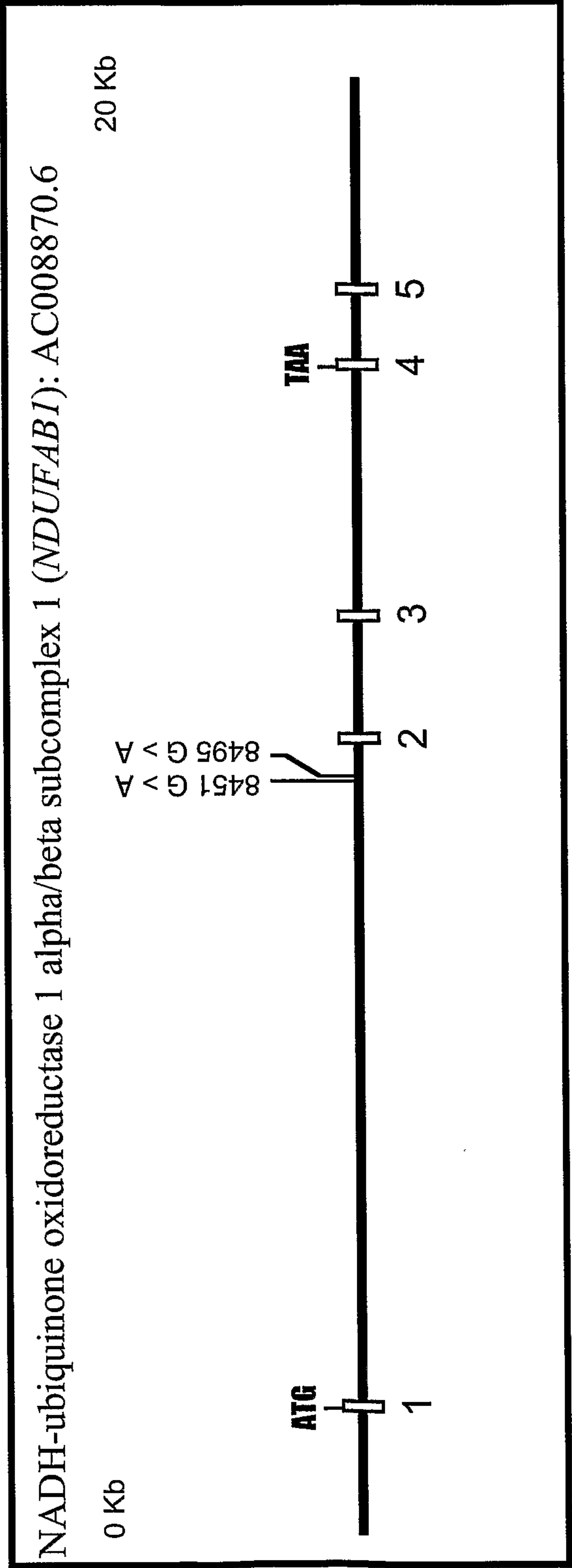


FIGURE 77

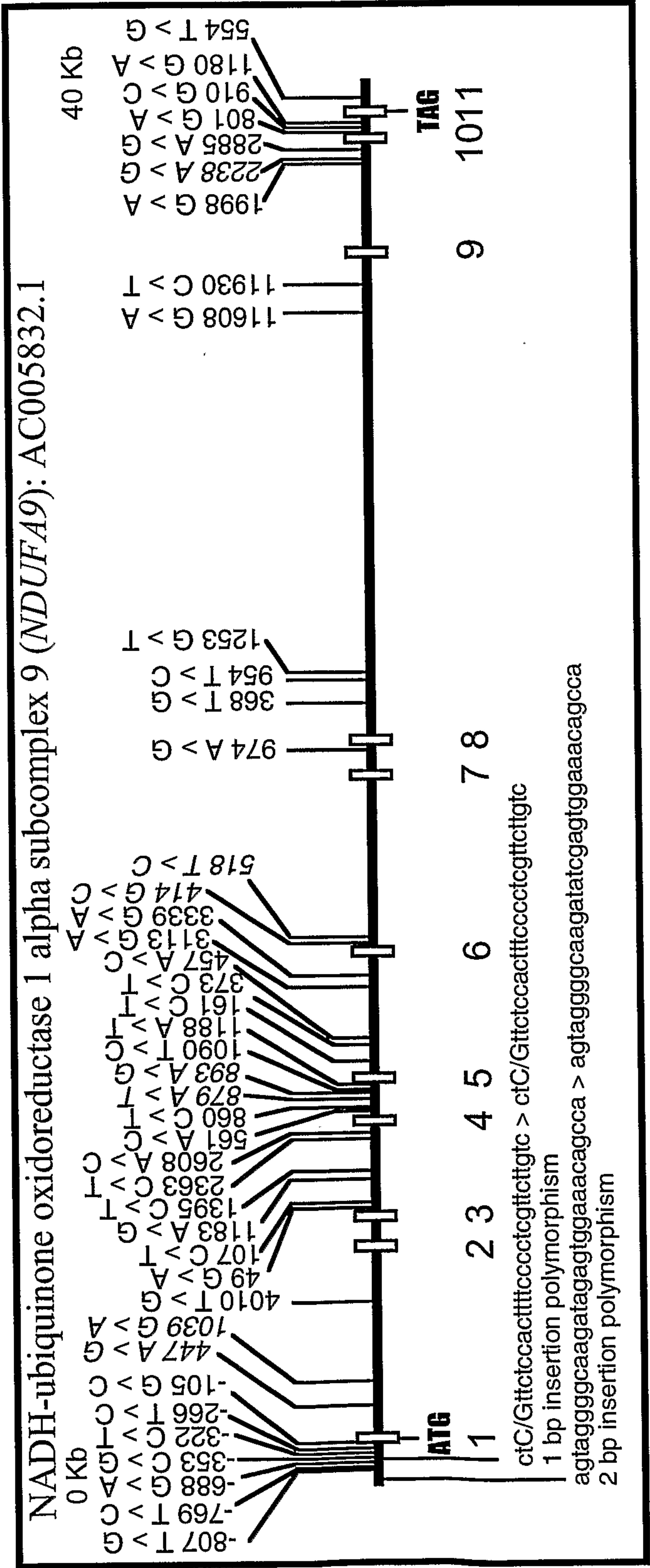


FIGURE 78

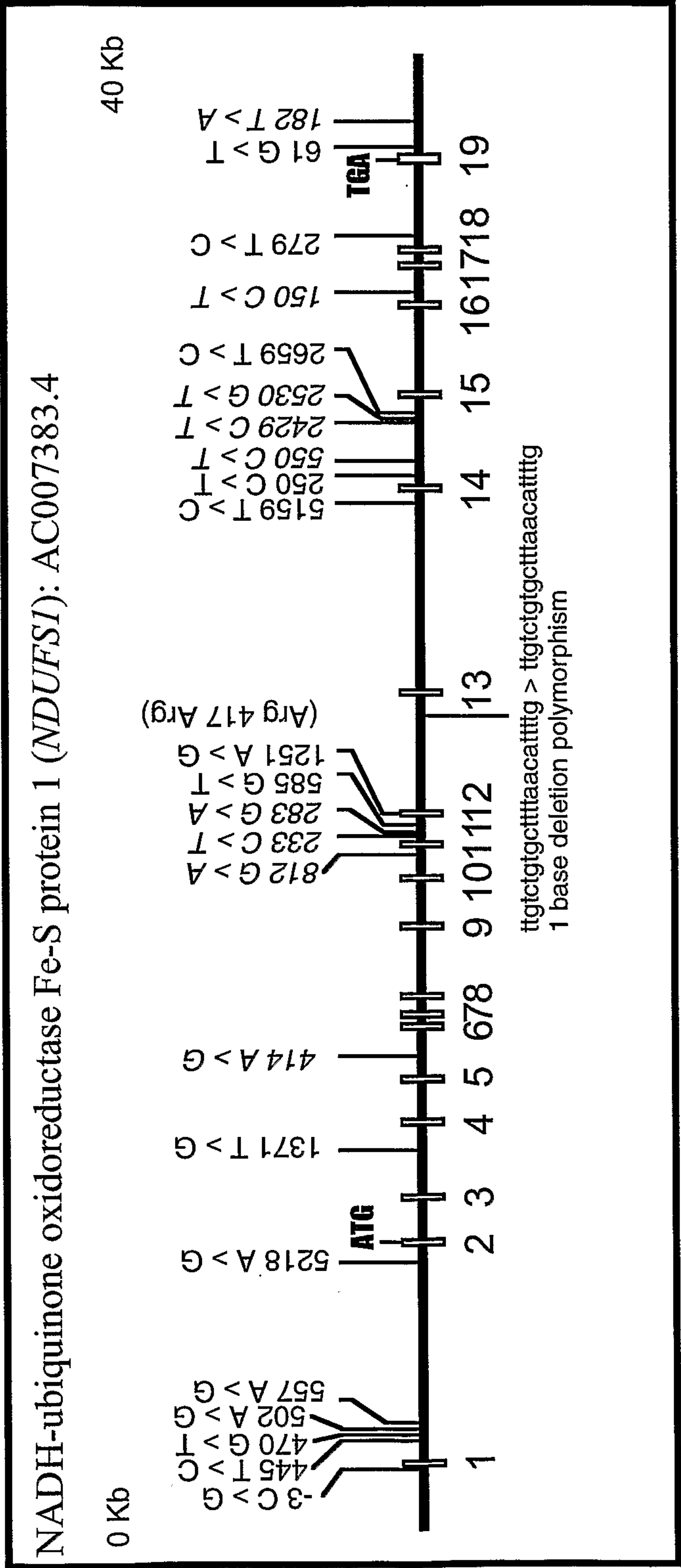


FIGURE 79

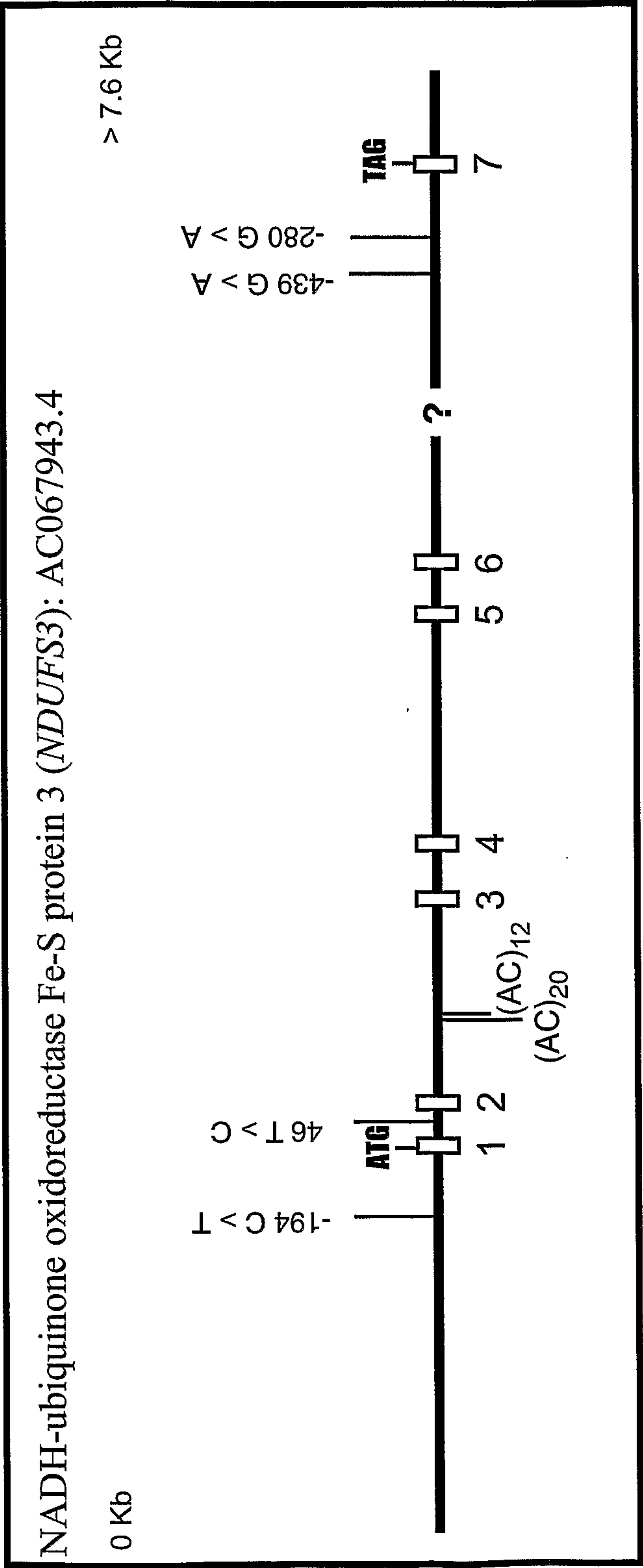


FIGURE 80

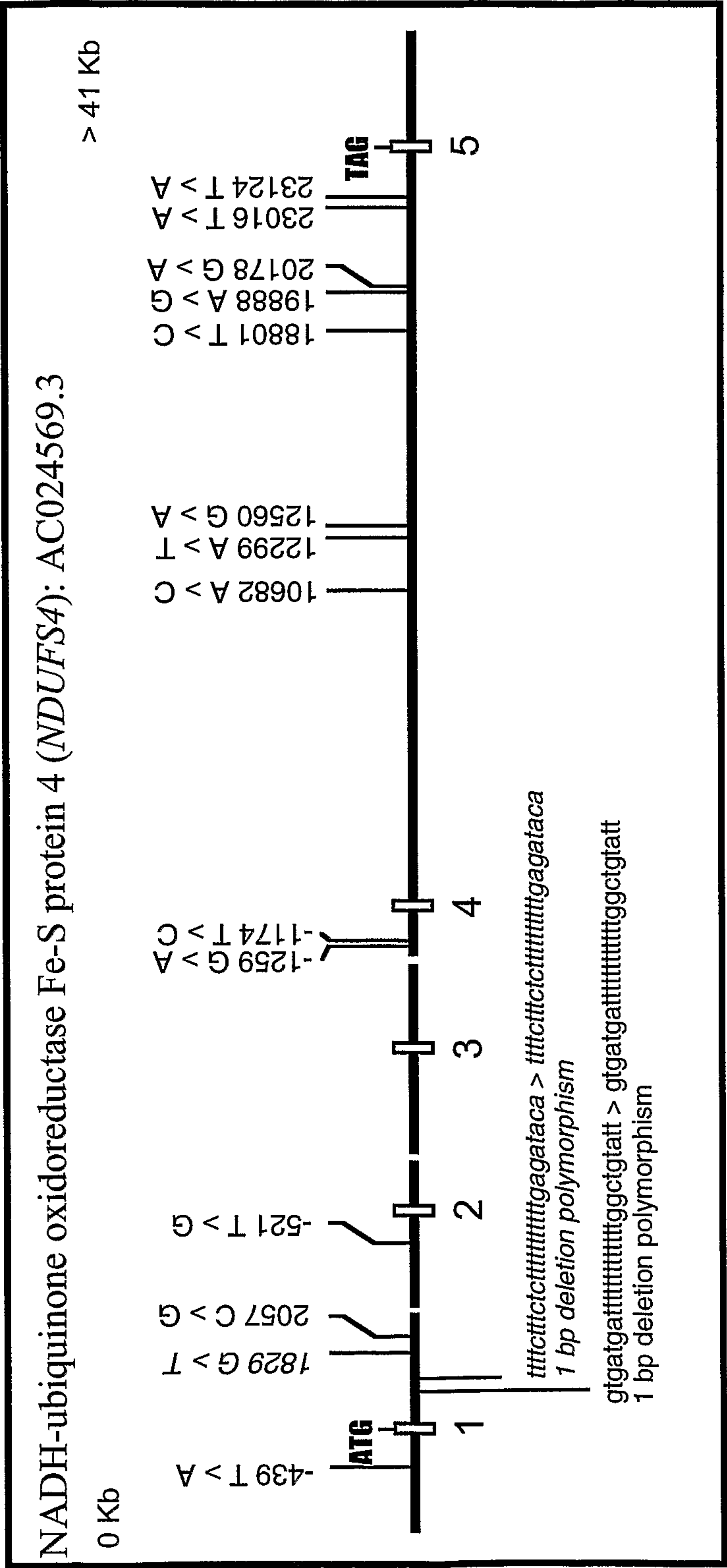


FIGURE 81

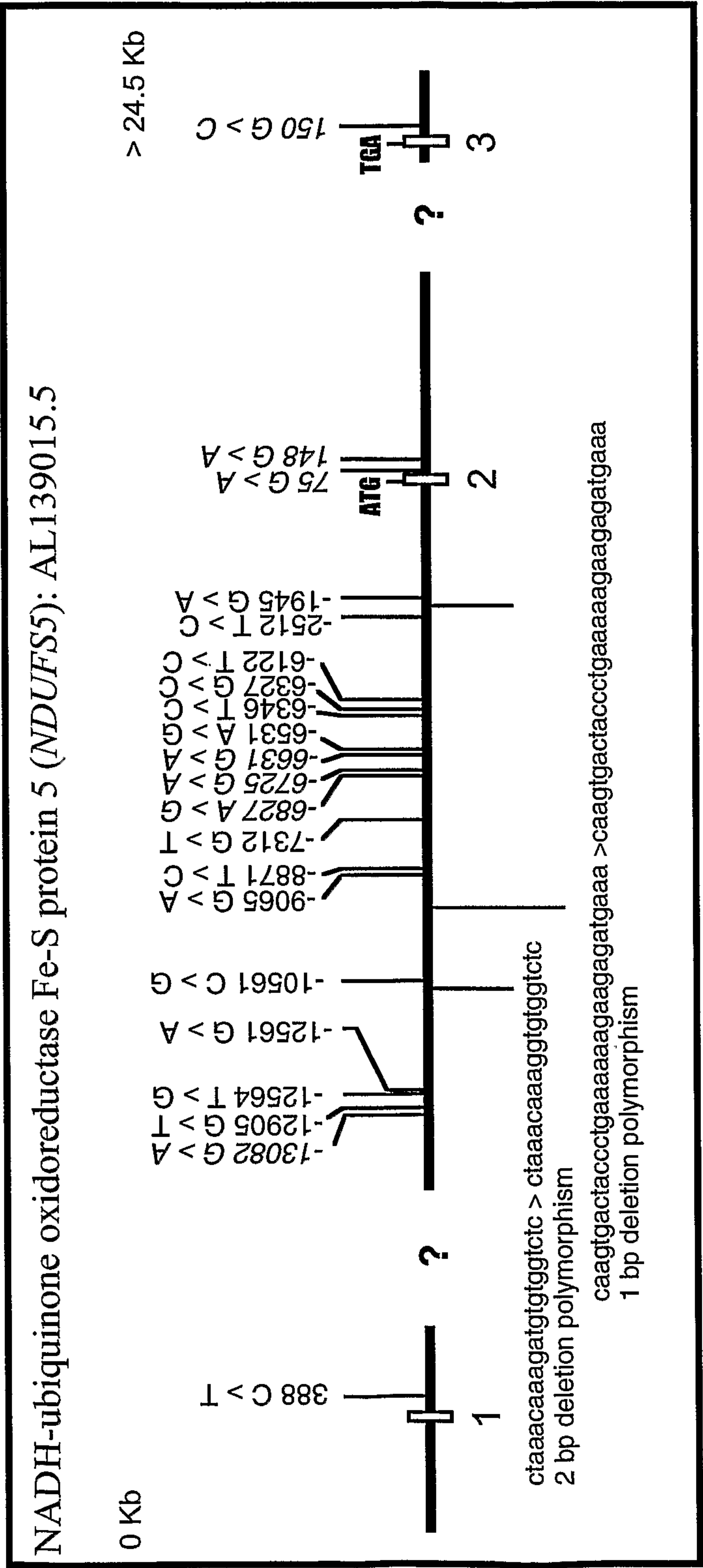


FIGURE 82

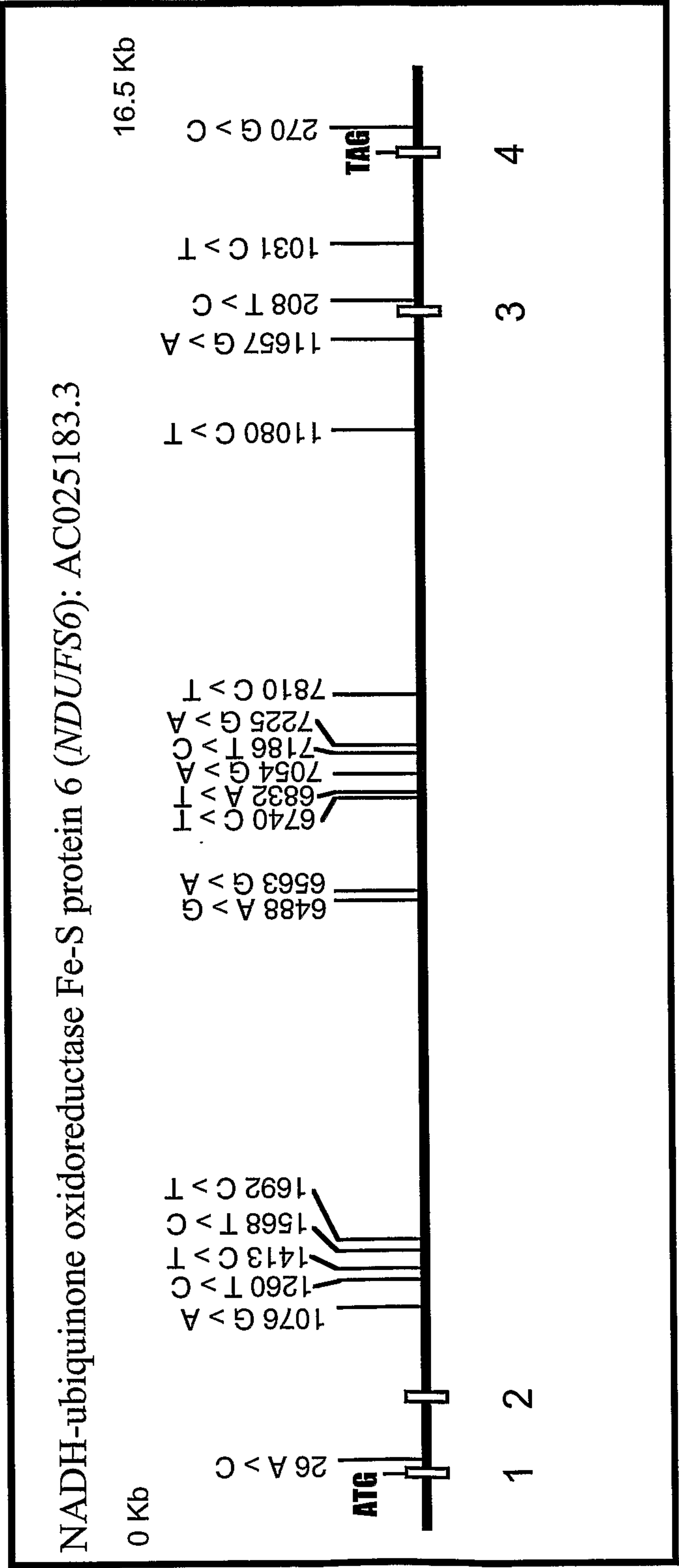


FIGURE 83

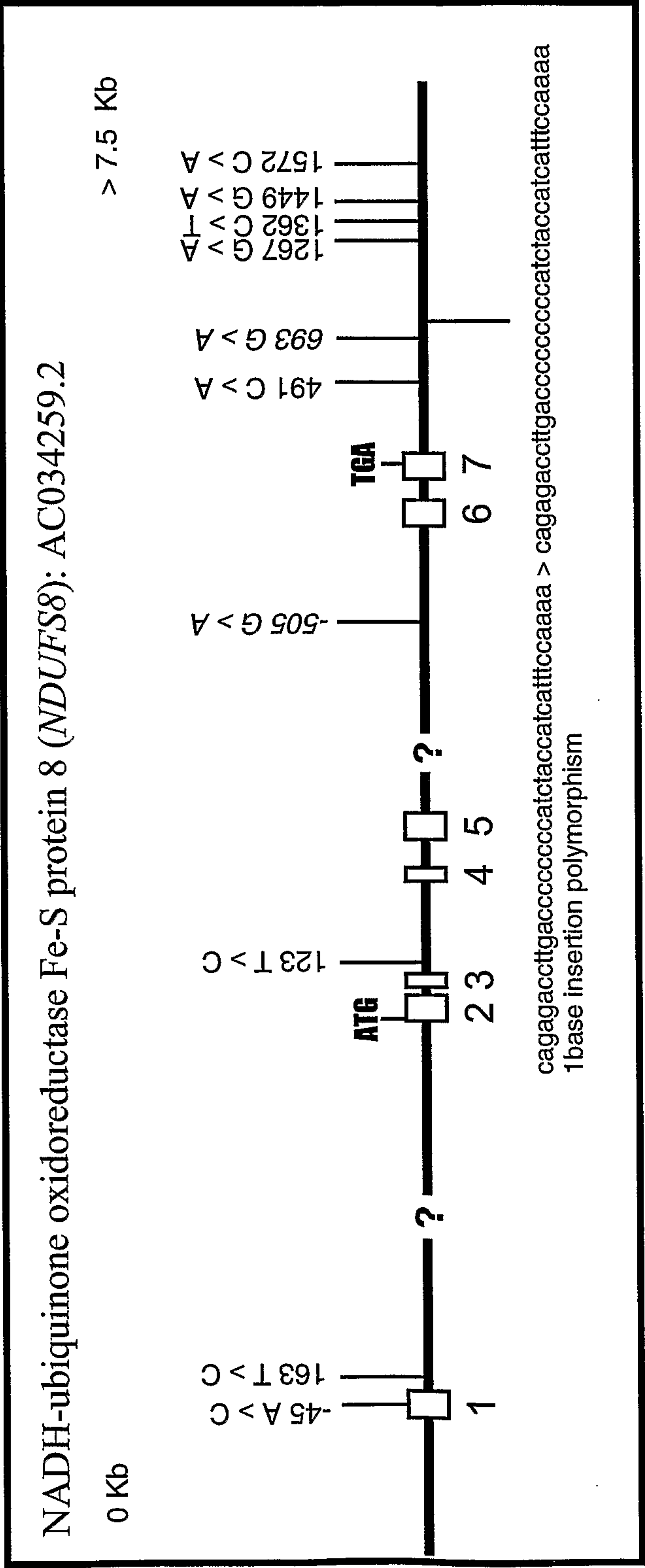


FIGURE 84

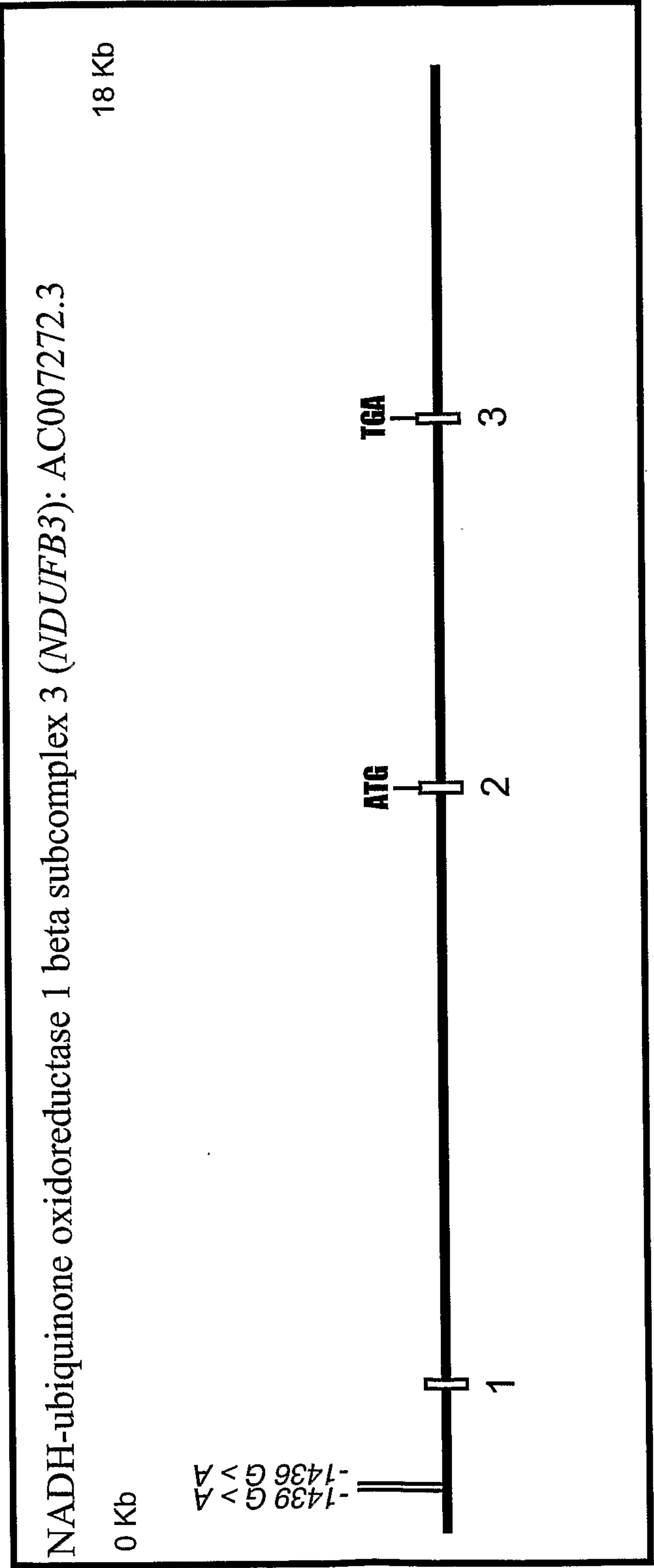


FIGURE 85

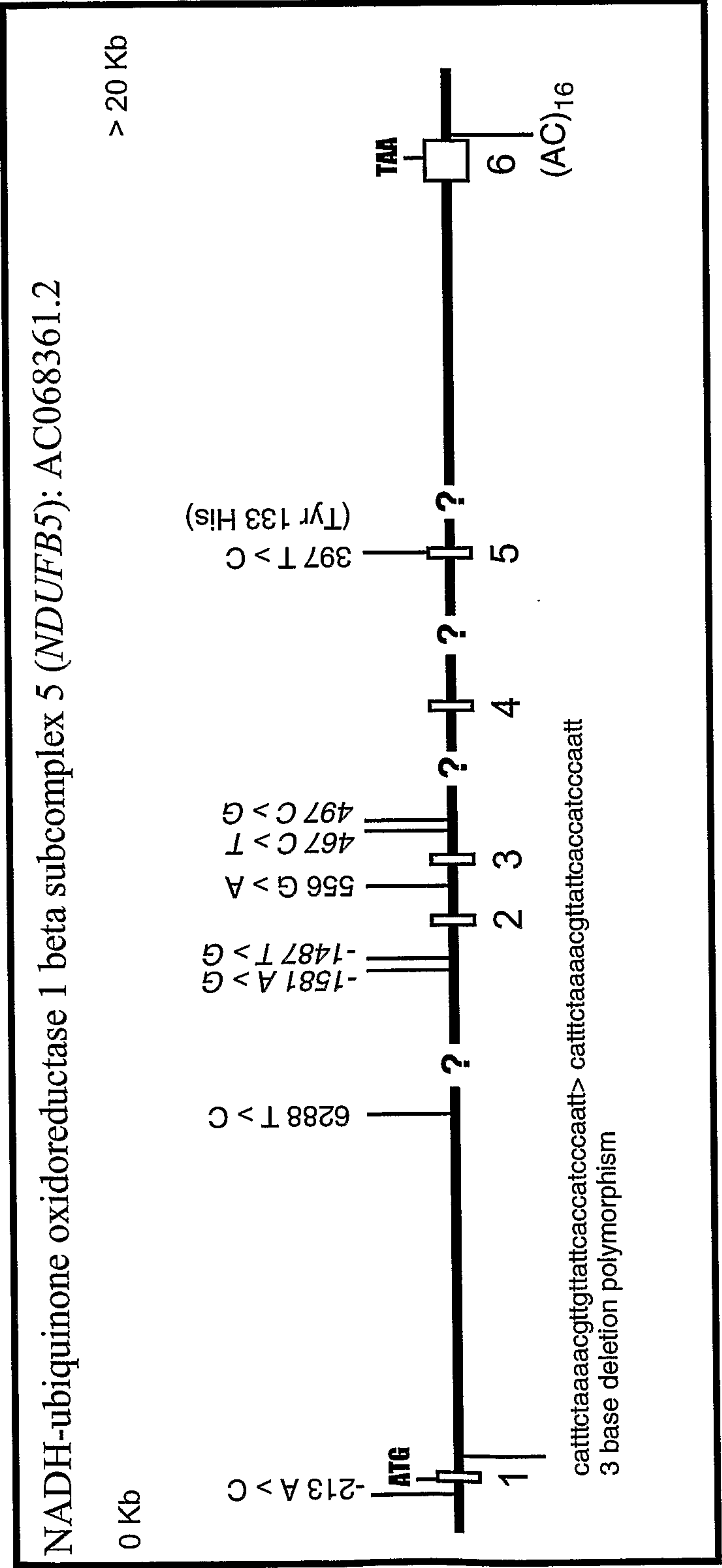
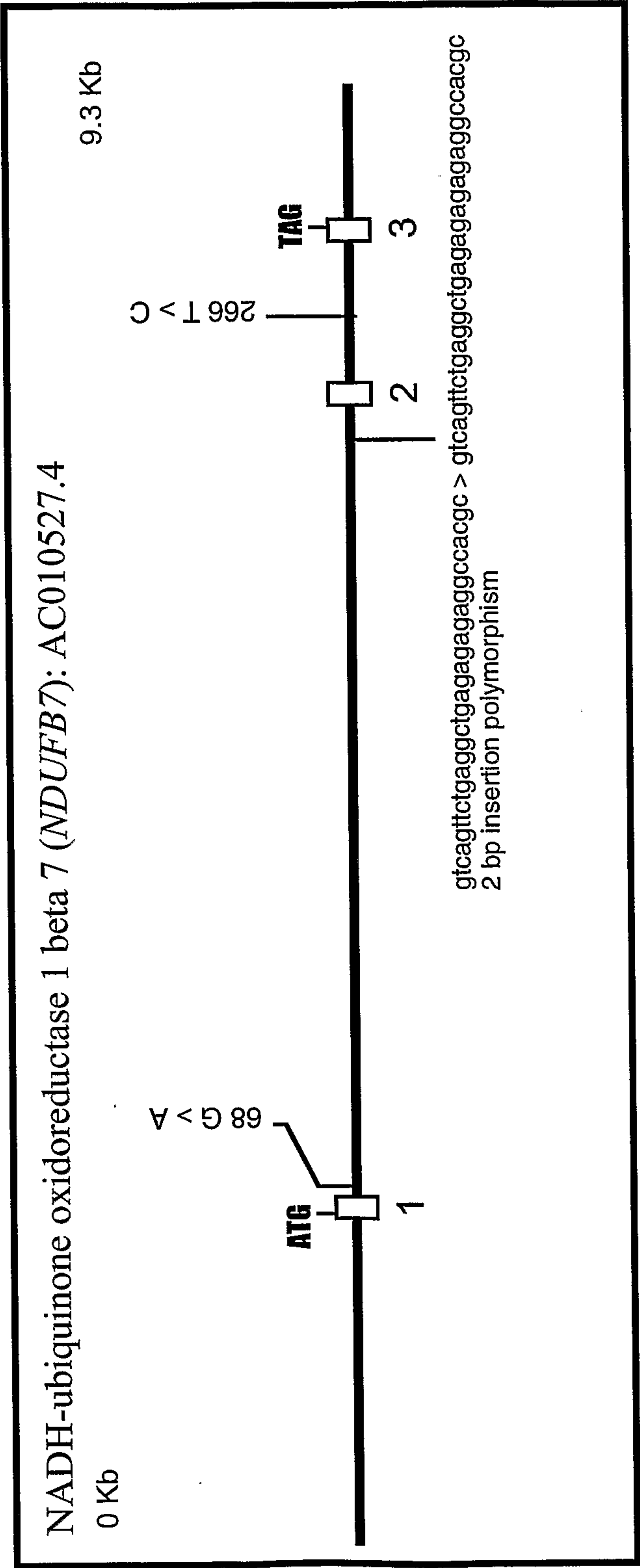


FIGURE 86



ABCA1 ACCESSION AF275948.1

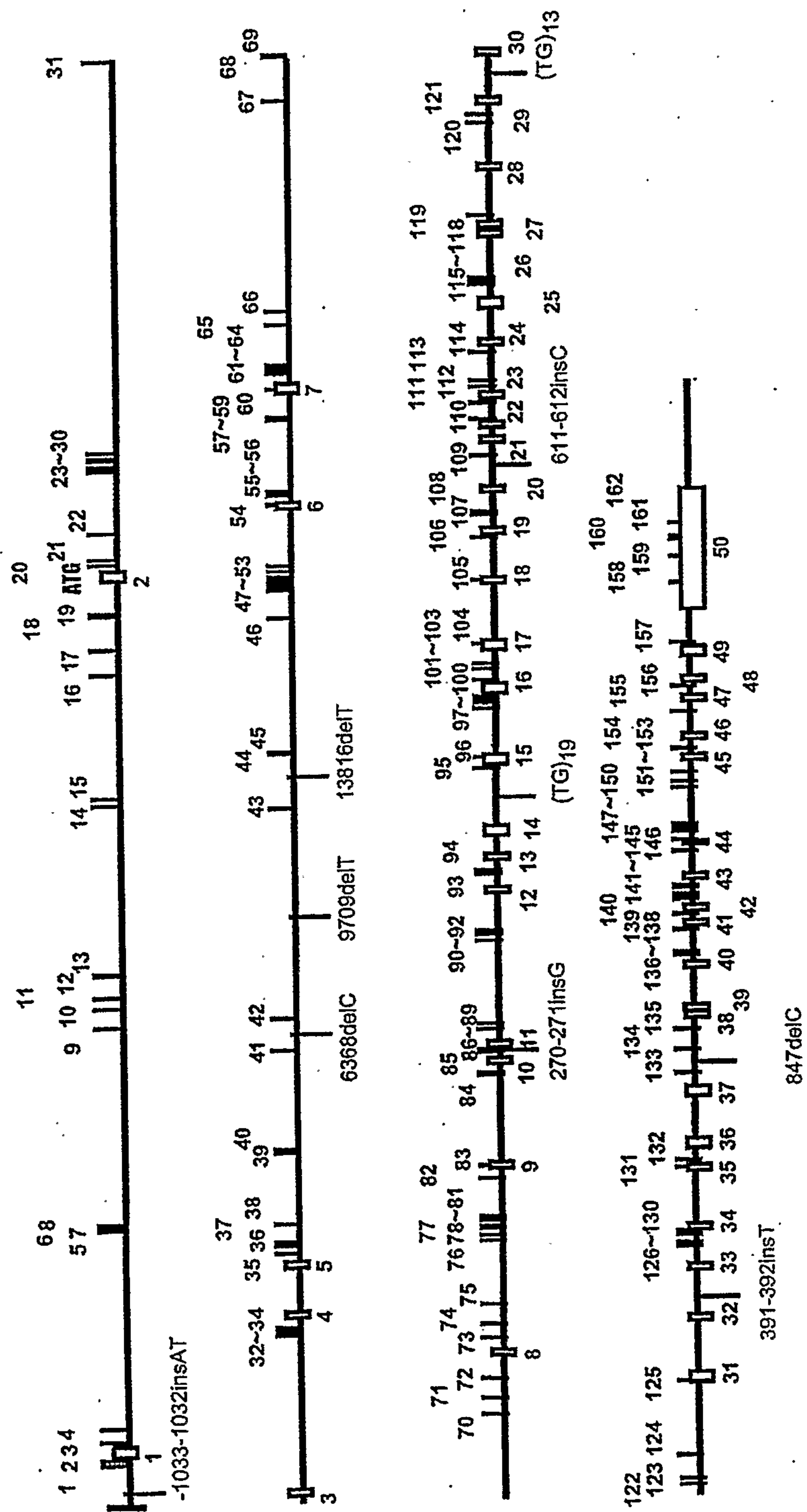


FIGURE 88

Catechol-O-methyltransferase (COMT)

ACCESSION AC0000080

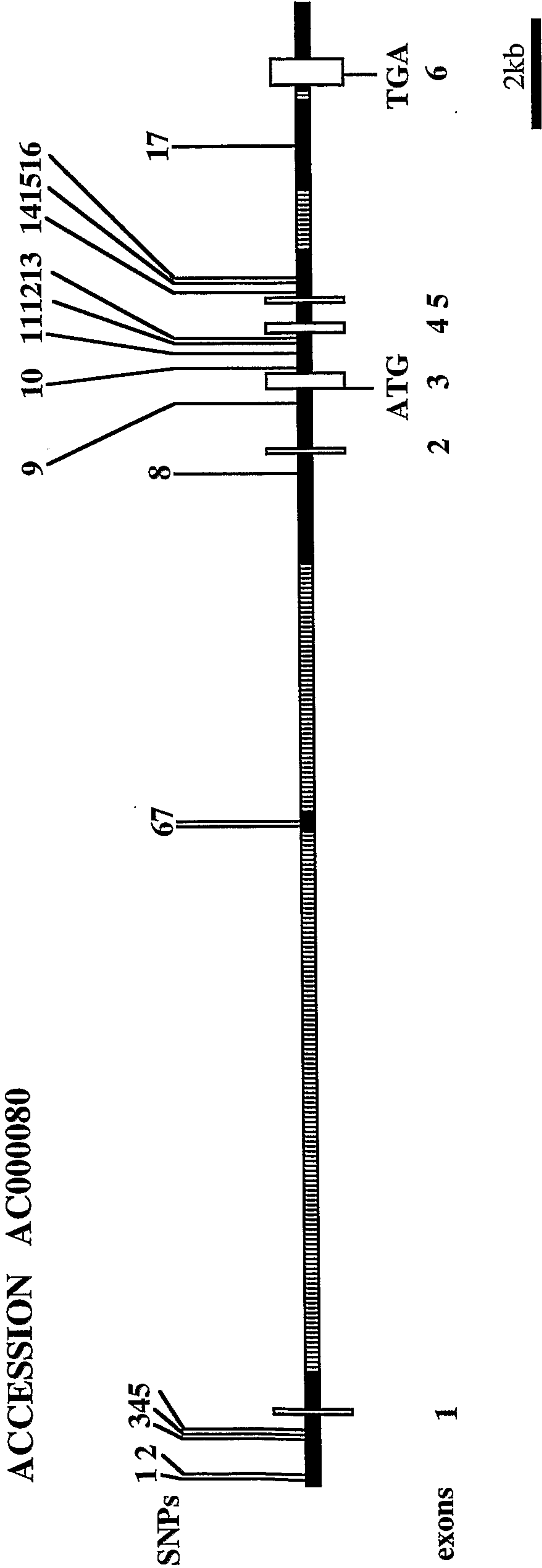


FIGURE 89

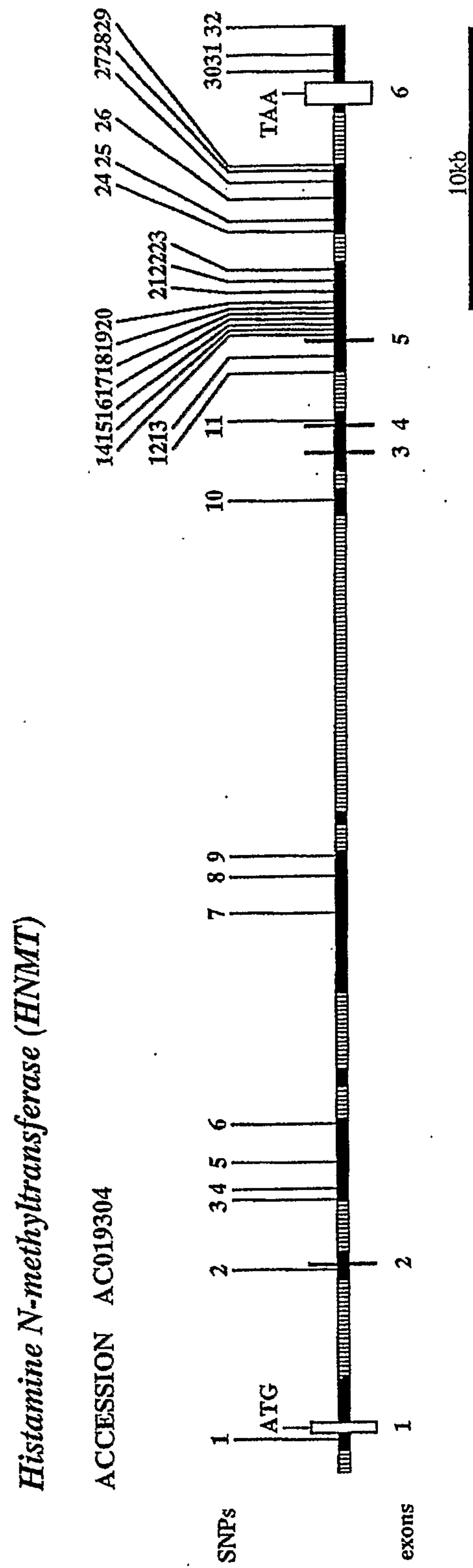


FIGURE 90
Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)

ACCESSION X04300

47/291

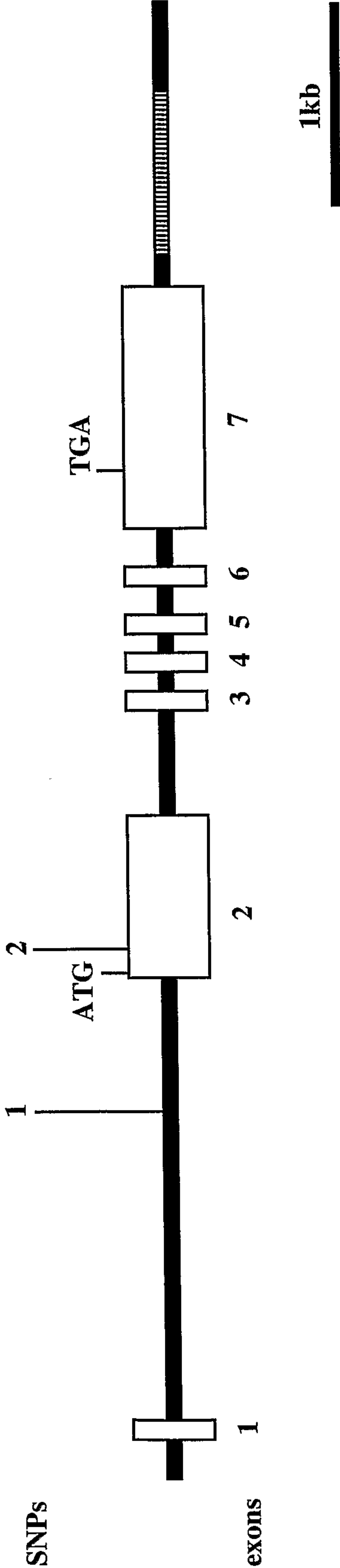
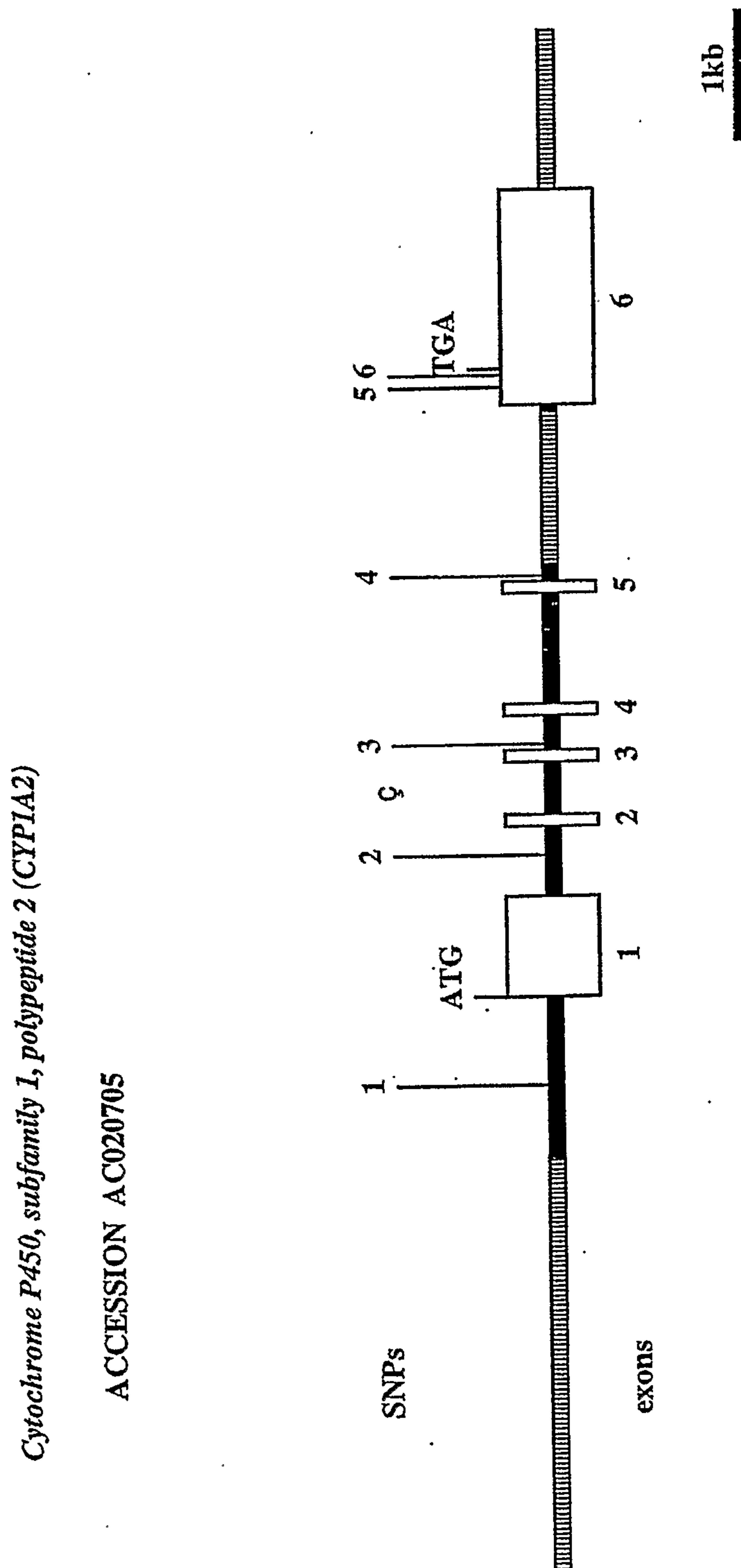


FIGURE 91



Cytochrome P450, subfamily I, polypeptide 1 (CYP1B1)

ACCESSION AC009229

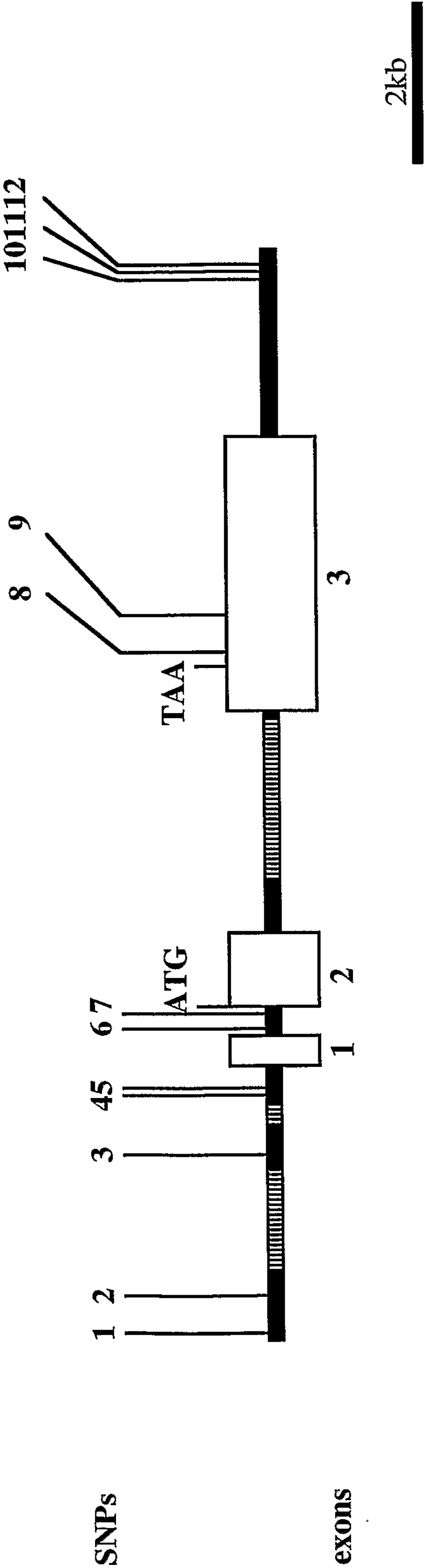


FIGURE 93

Arylacetamide deacetylase (AADAC)

ACCESSION AC068647

50/291

SUBSTITUTE SHEET(RULE26)

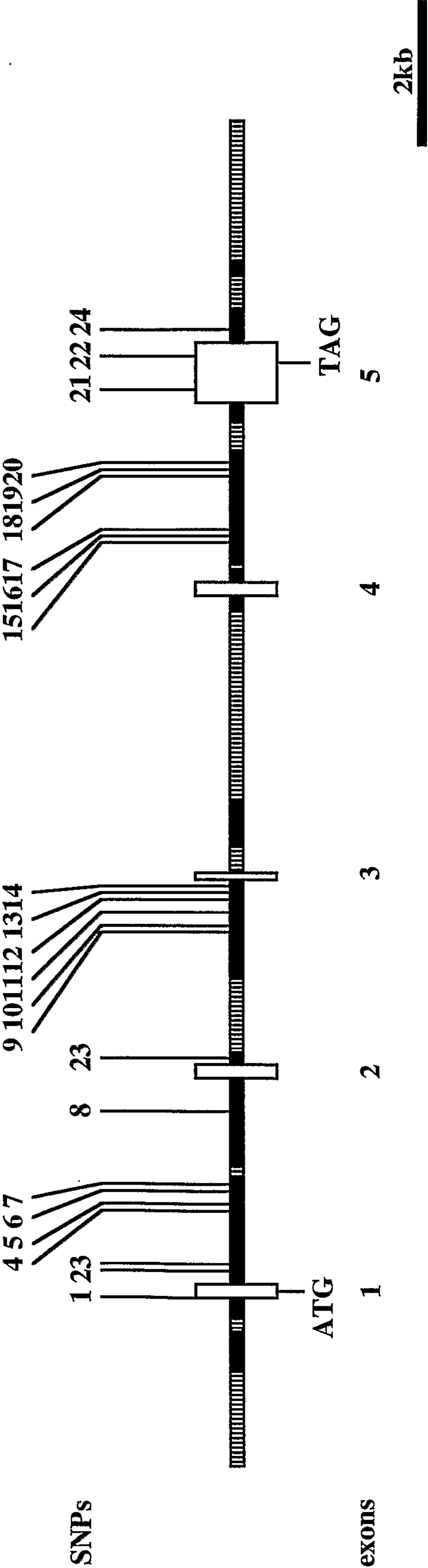


FIGURE 94

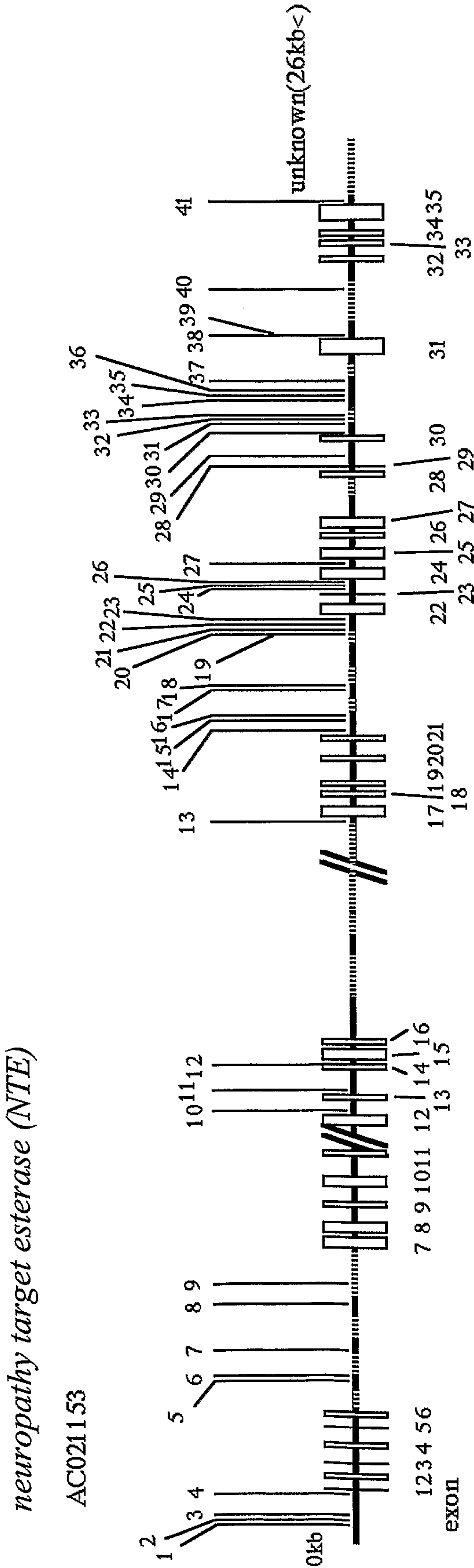


FIGURE 95

ATP-binding cassette, sub-family C (CFTR/MRP), member2 (MRP2)

ACCESSION AL392107

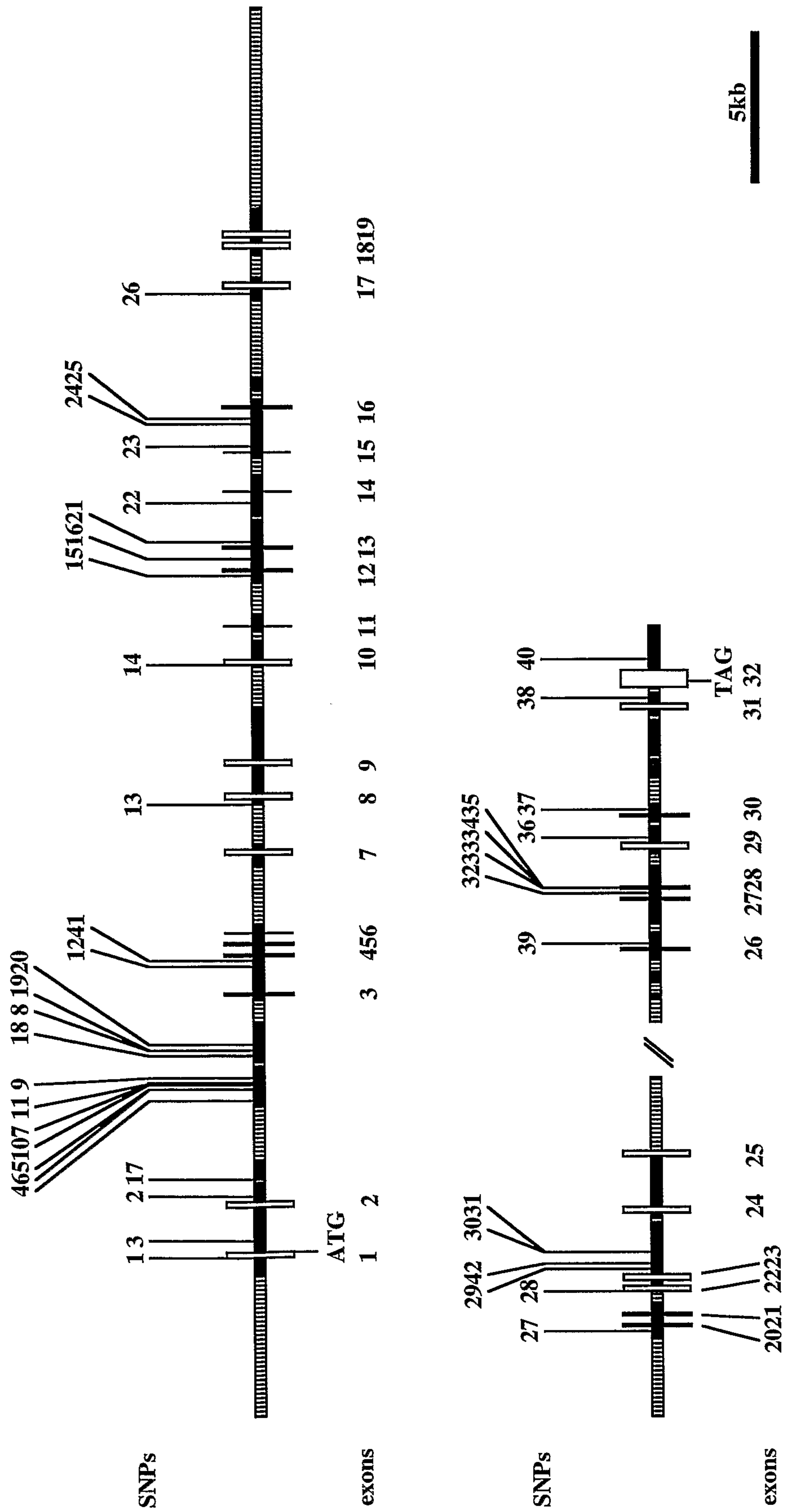


FIGURE 96-1
ATP-binding cassette, sub-family B, member 1 (ABCB1)

ACCESSION AC002457
AC005068

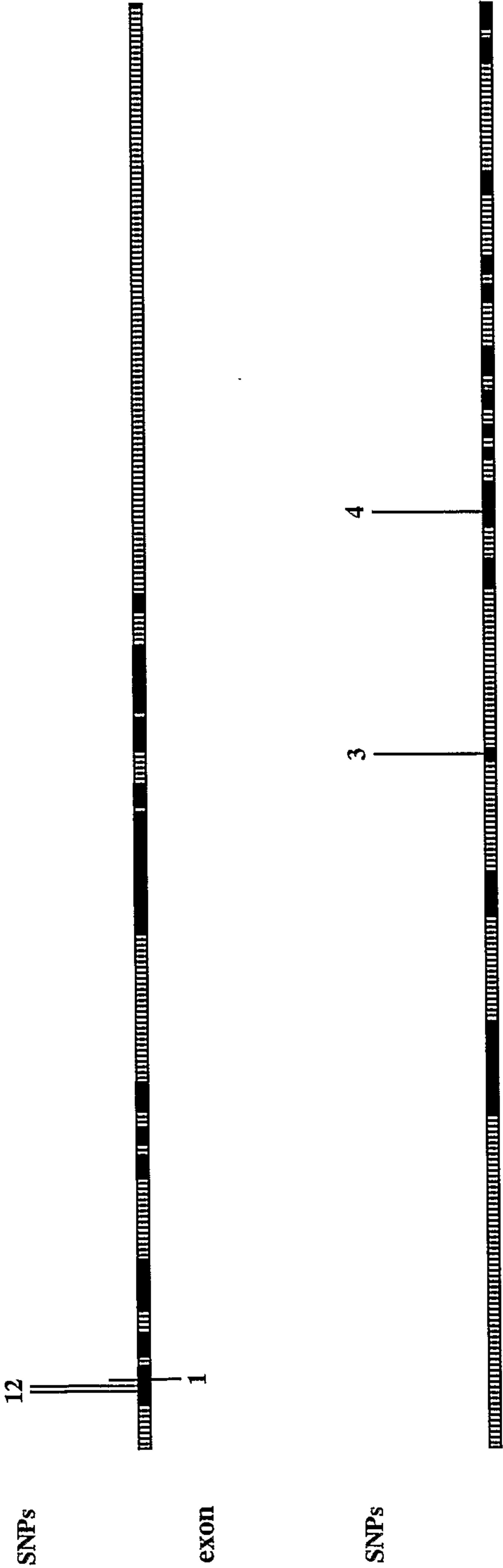


FIGURE 96-2
ATP-binding cassette, sub-family B, member1 (ABCB1)

ACCESSION AC002457
AC005068

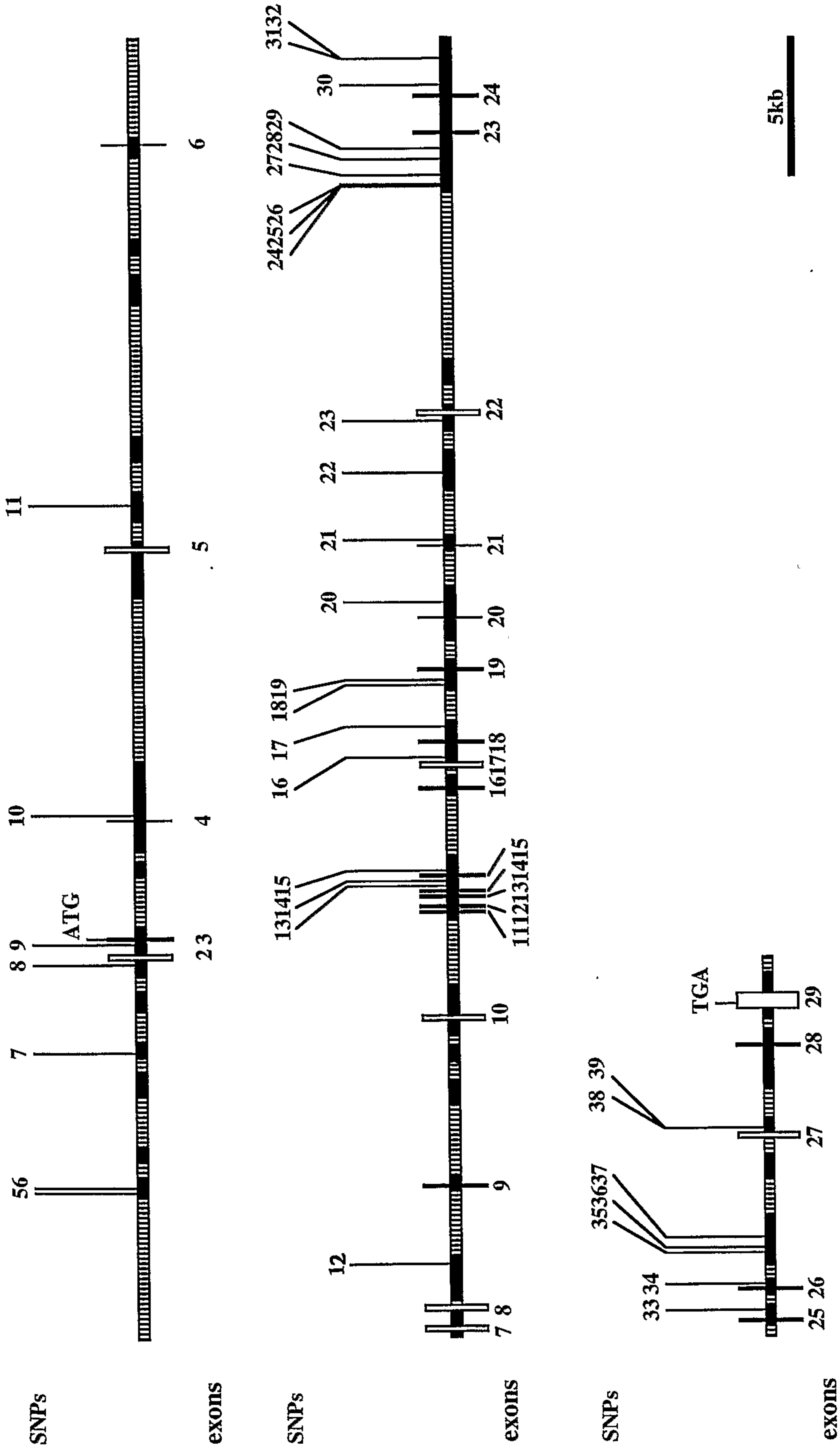


FIGURE 97

ATP-binding cassette, sub-family B, member 3 (ABCB3)
ACCESSION X66401

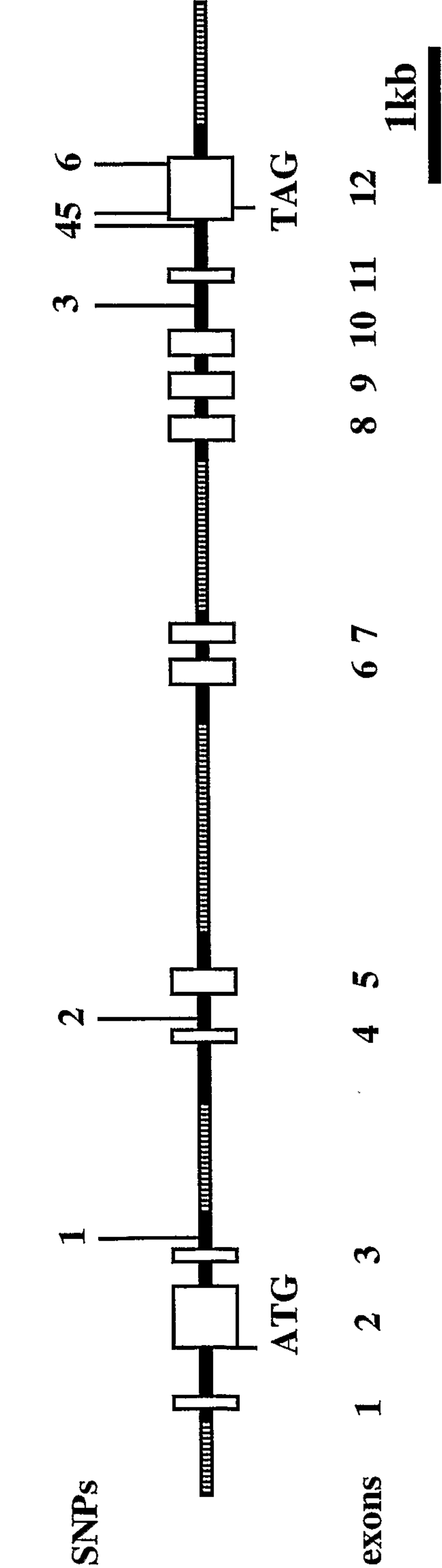


FIGURE 98

ATP-binding cassette, sub-family B, member 7 (ABCB7)

ACCESSION
AL360179

AC002417

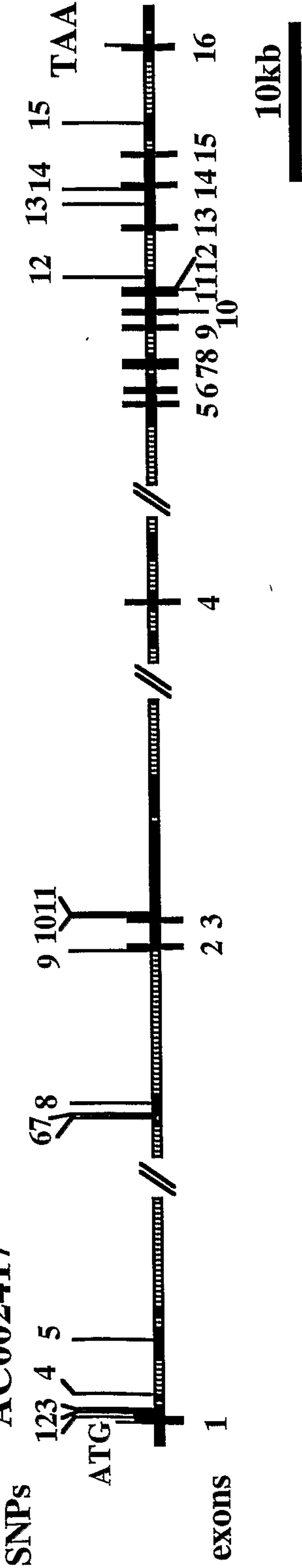
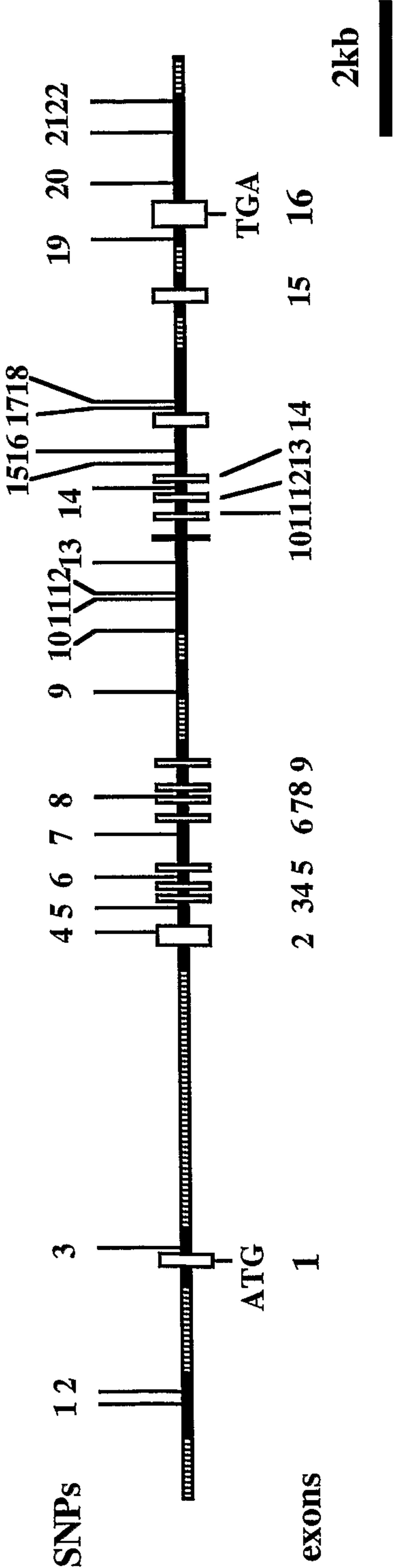
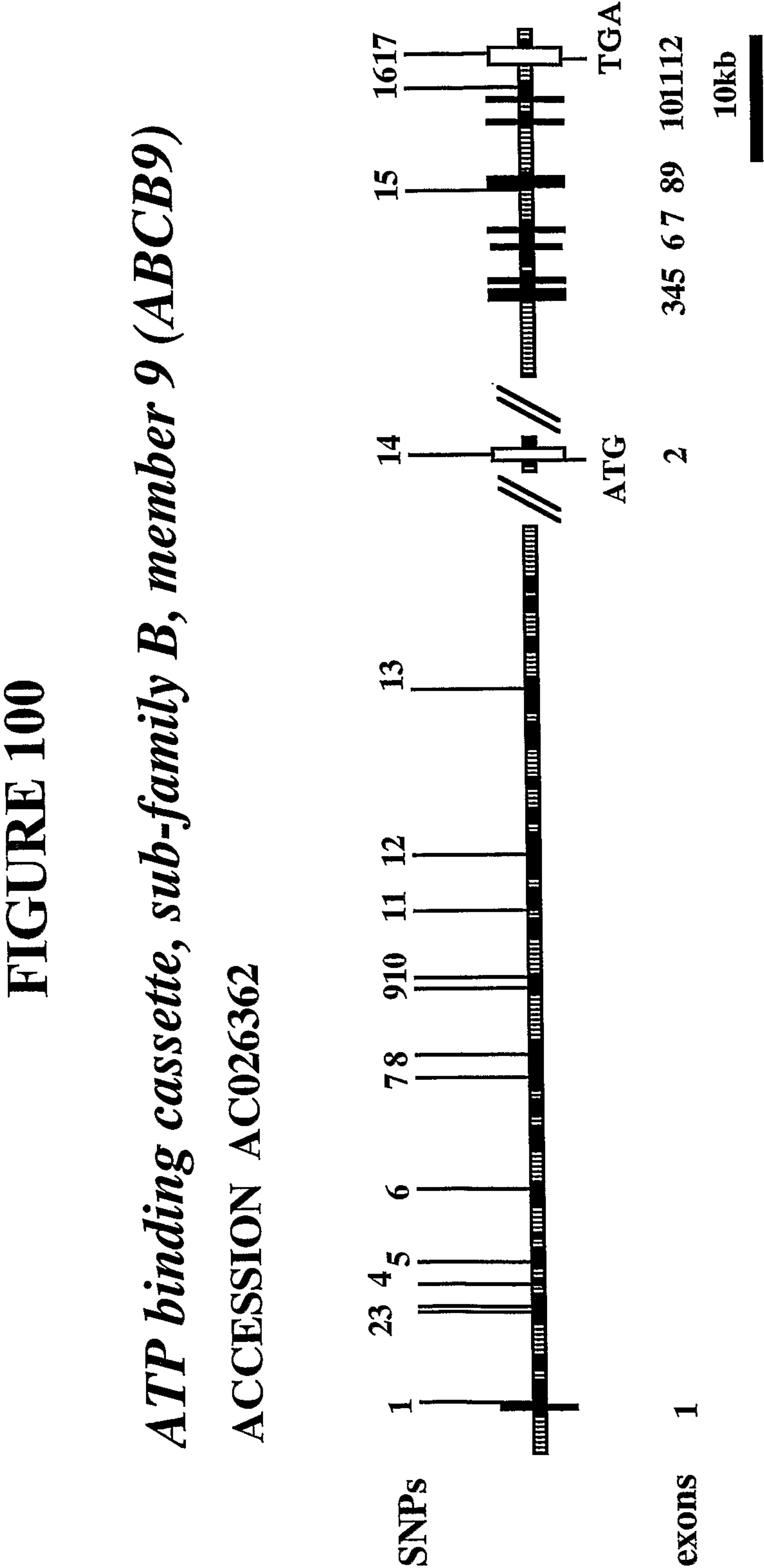


FIGURE 99

ATP-binding cassette, sub-family B, member 8 (ABCB8)
ACCESSION AC010973





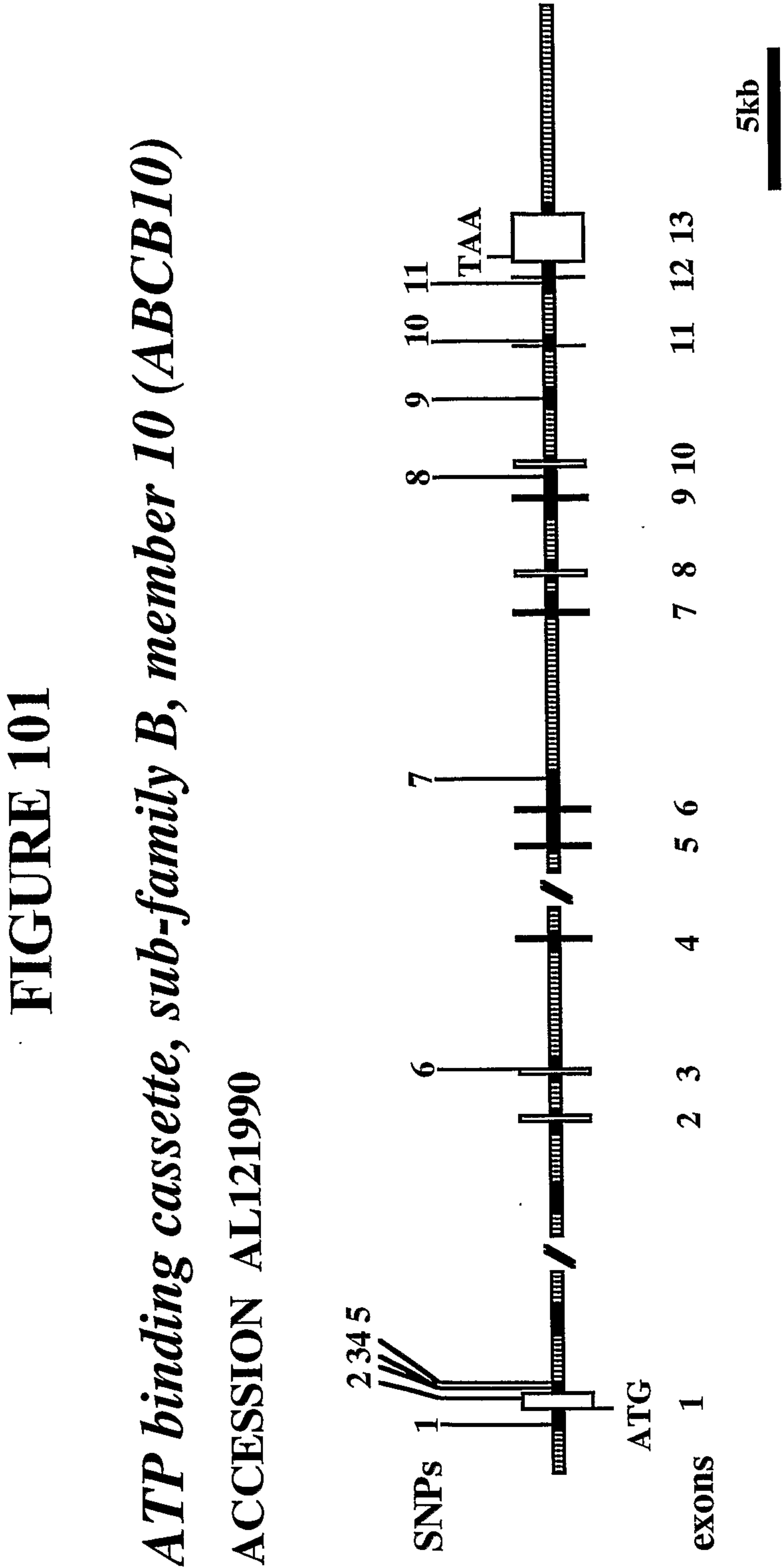


FIGURE 102-1

ATP-binding cassette, sub-family B, member 11 (ABCB11)

ACCESSION AC008177
AC069137

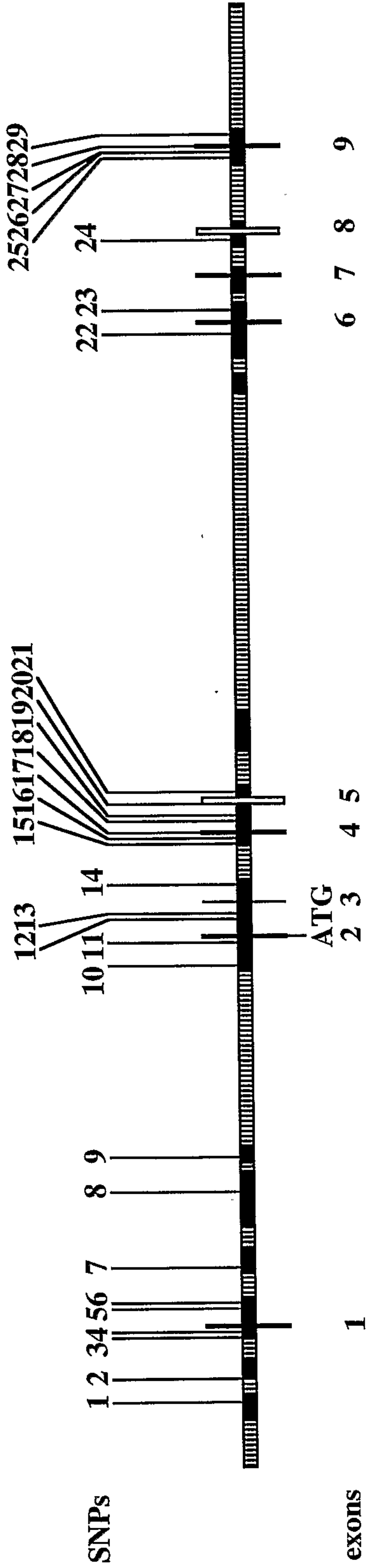


FIGURE 102-2

ATP-binding cassette, sub-family B, member 11 (ABCB11)

ACCESSION AC008177

AC069137

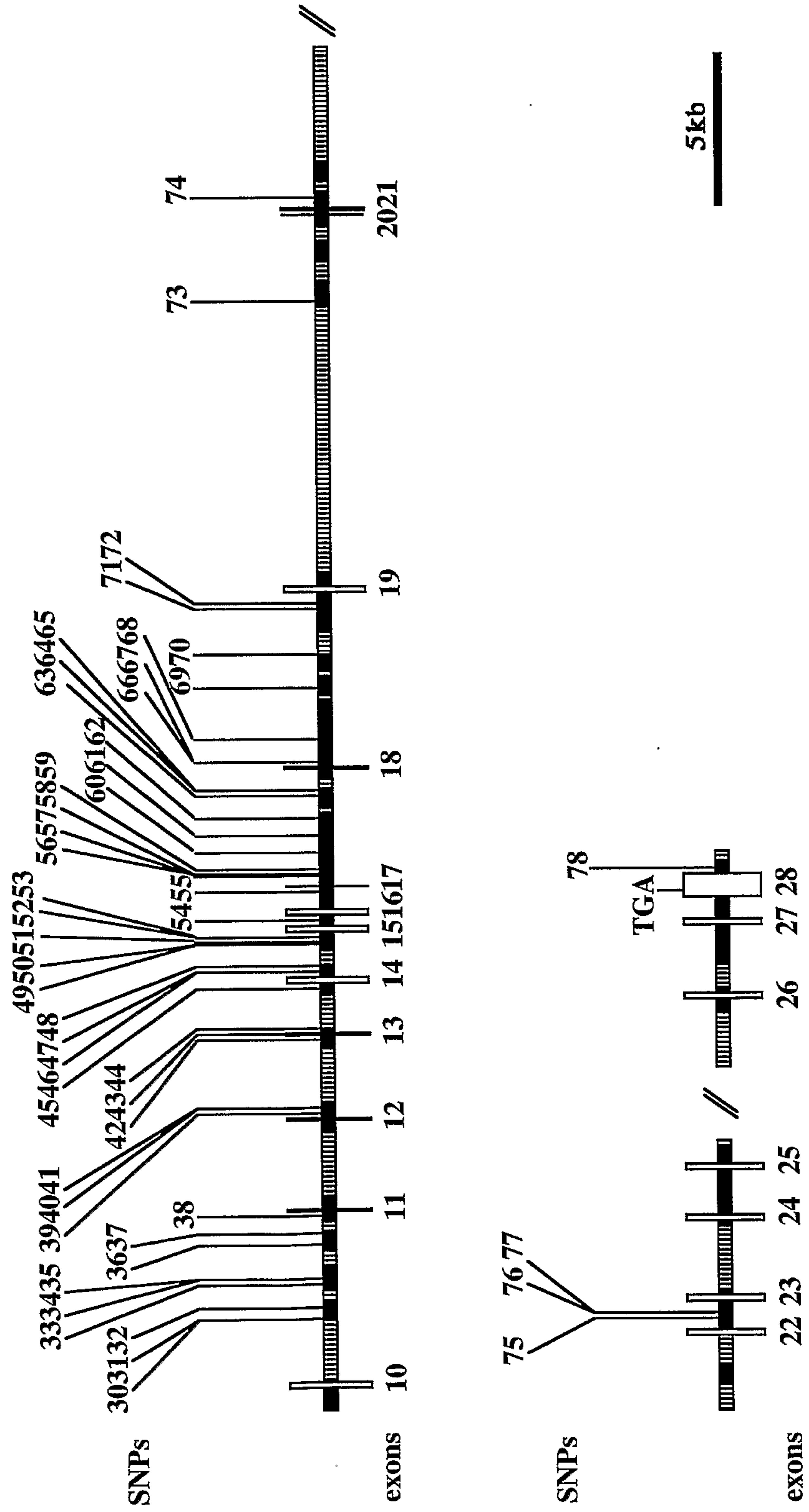


FIGURE 103

Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)

ACCESSION AL356793

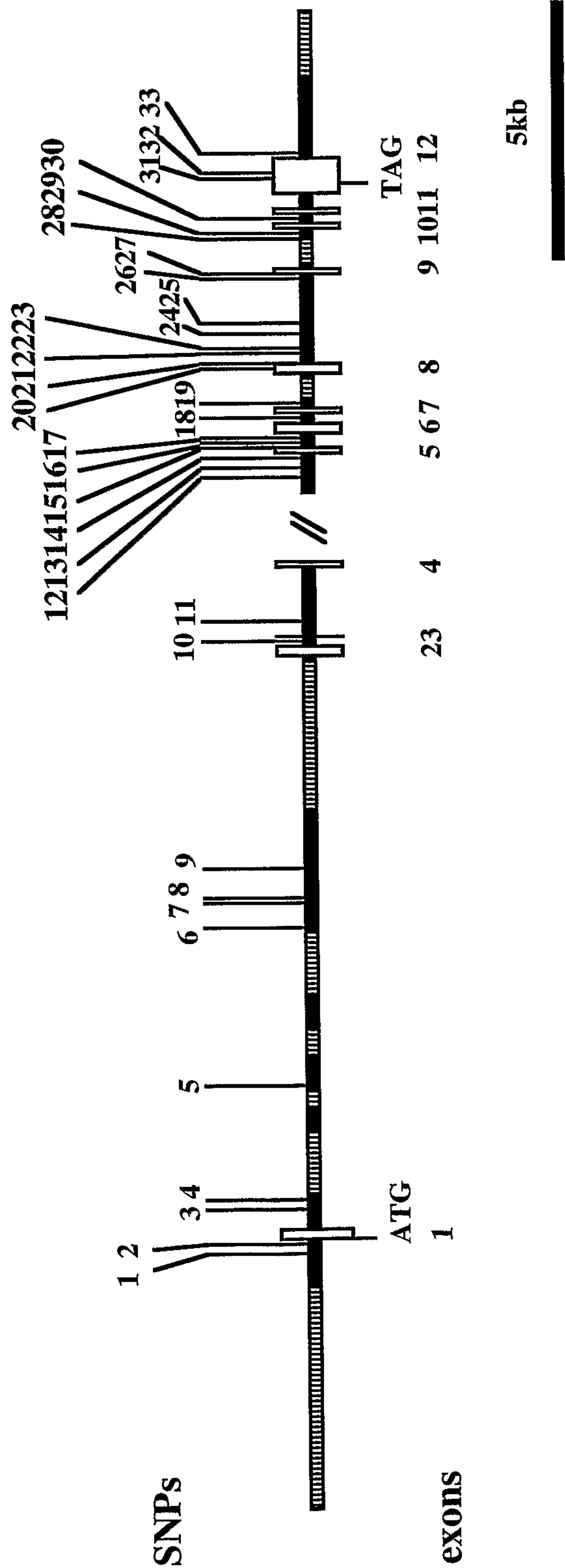


FIGURE 104

Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)

ACCESSION AC009974

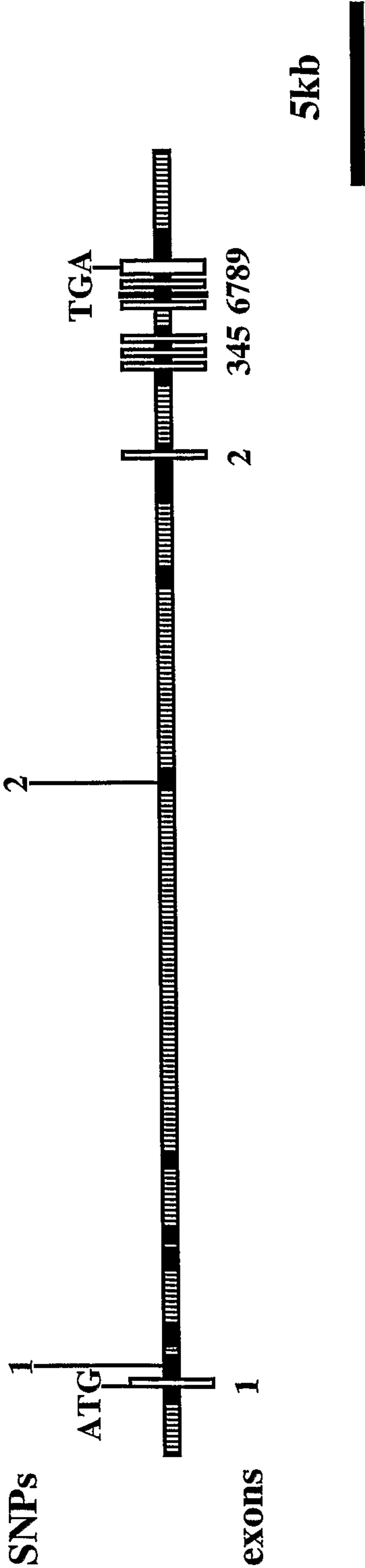


FIGURE 105

Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2)

ACCESSION AC005336

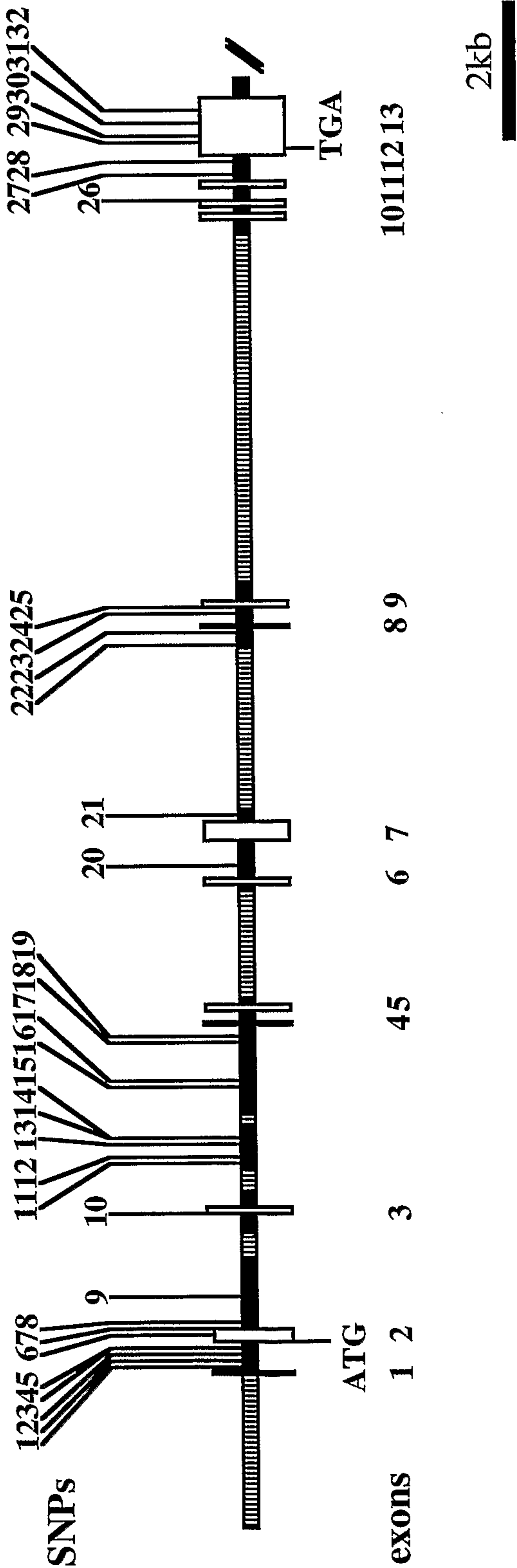
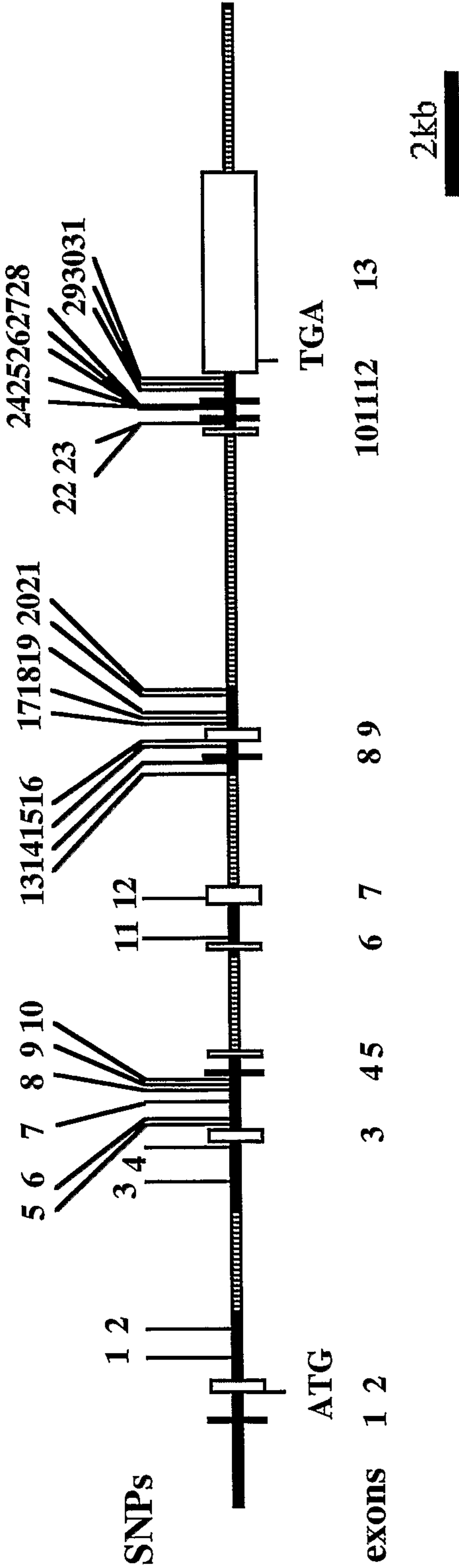


FIGURE 106

Cytochrome P450, subfamily 4F, polypeptide 3 (CYP4F3)

ACCESSION AD000685



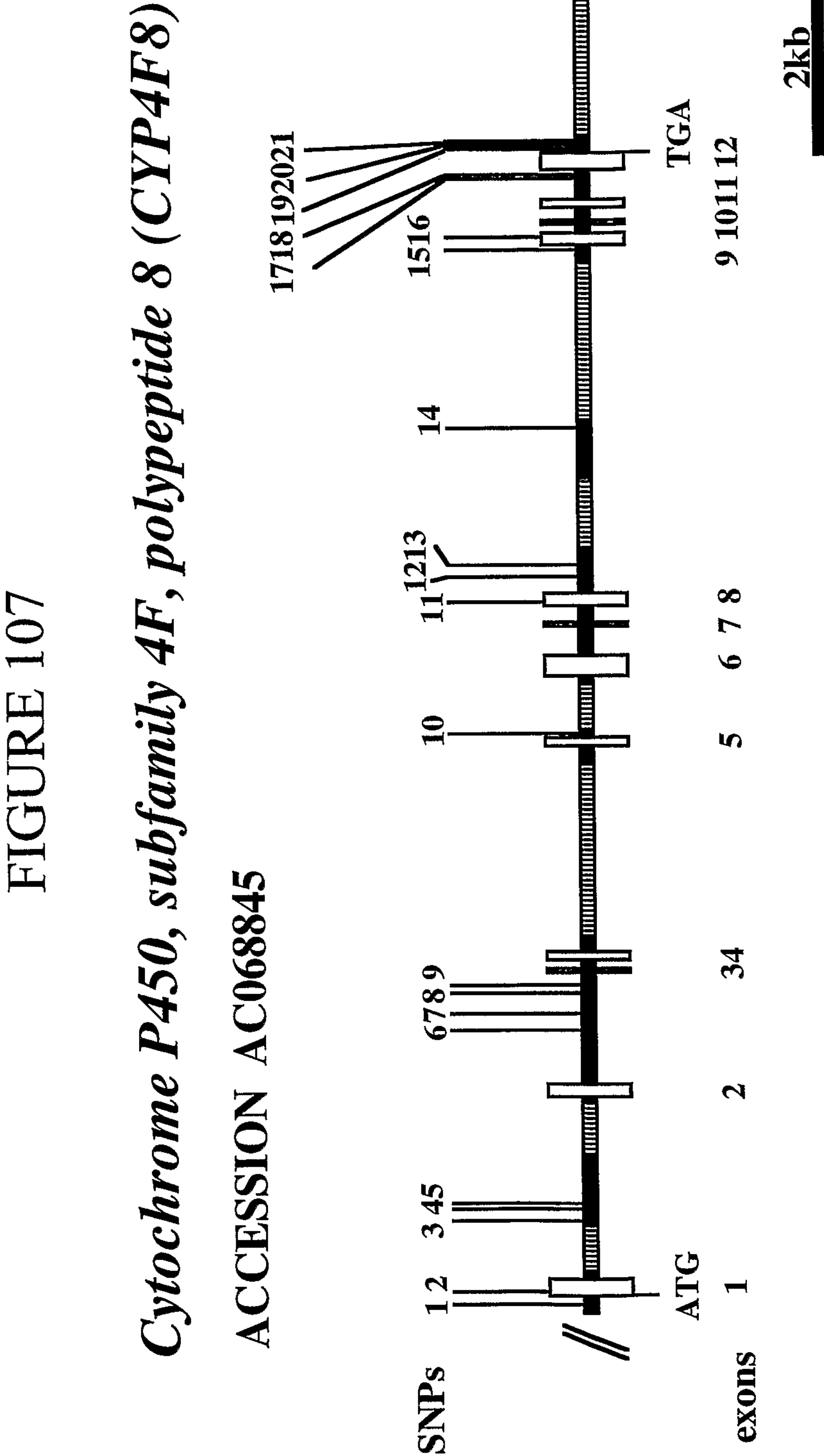


FIGURE 108

Aldehyde dehydrogenase 1 (ALDH1)

ACCESSION
AC0009284

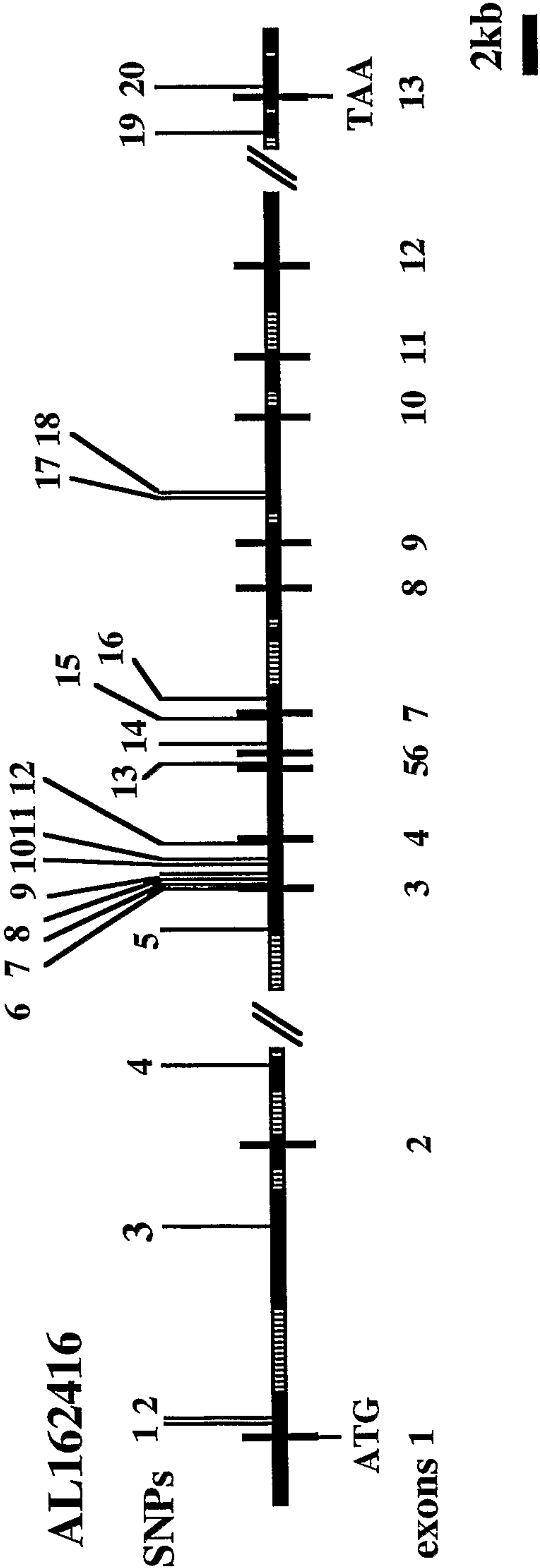


FIGURE 109

Aldehyde dehydrogenase 2 (ALDH2)

ACCESSION AC002996
AC003029

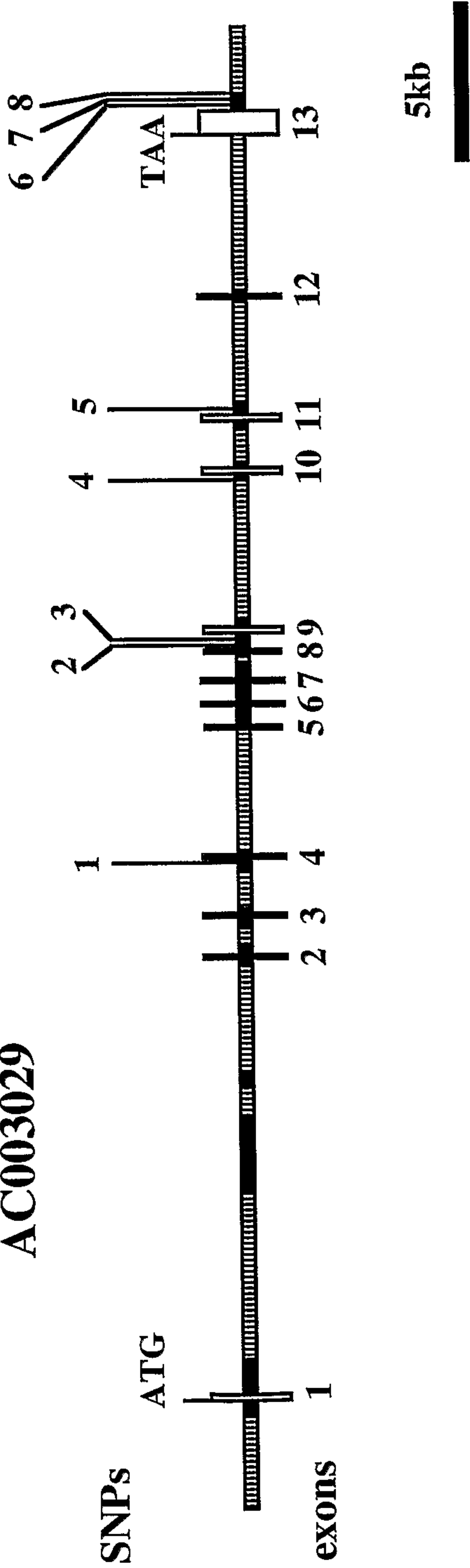


FIGURE 110

Aldehyde dehydrogenase 7 (ALDH7)

ACCESSION AC004923

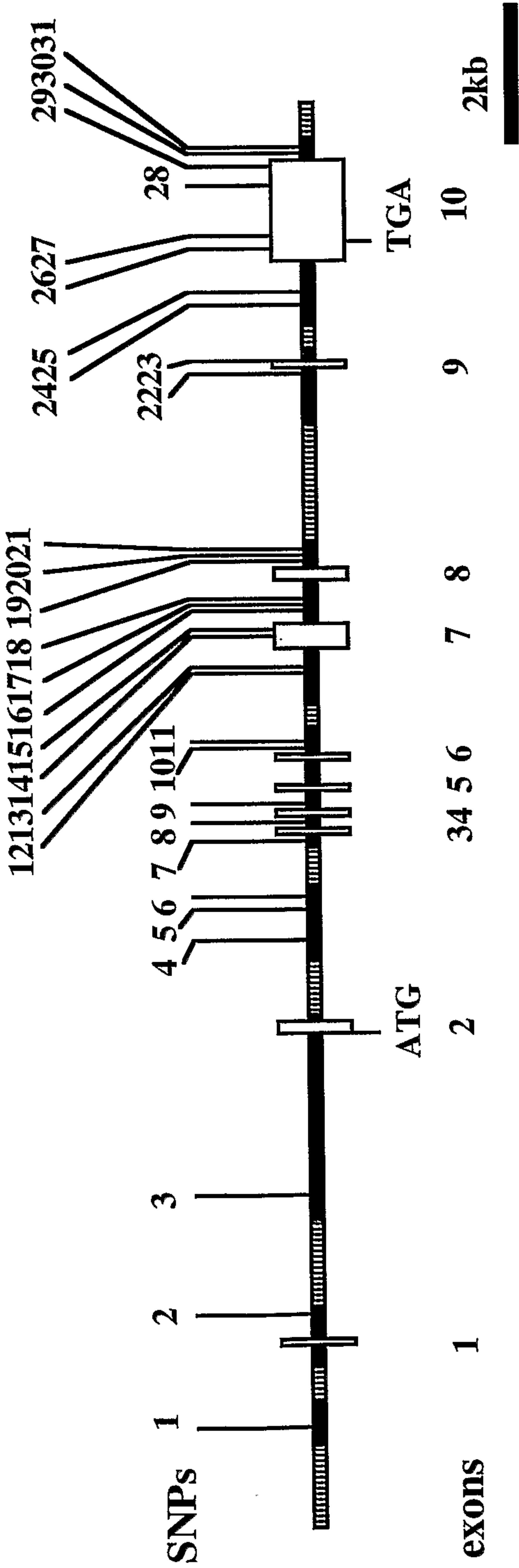


FIGURE 111

Aldehyde dehydrogenase 8 (ALDH8)

ACCESSION AC021987

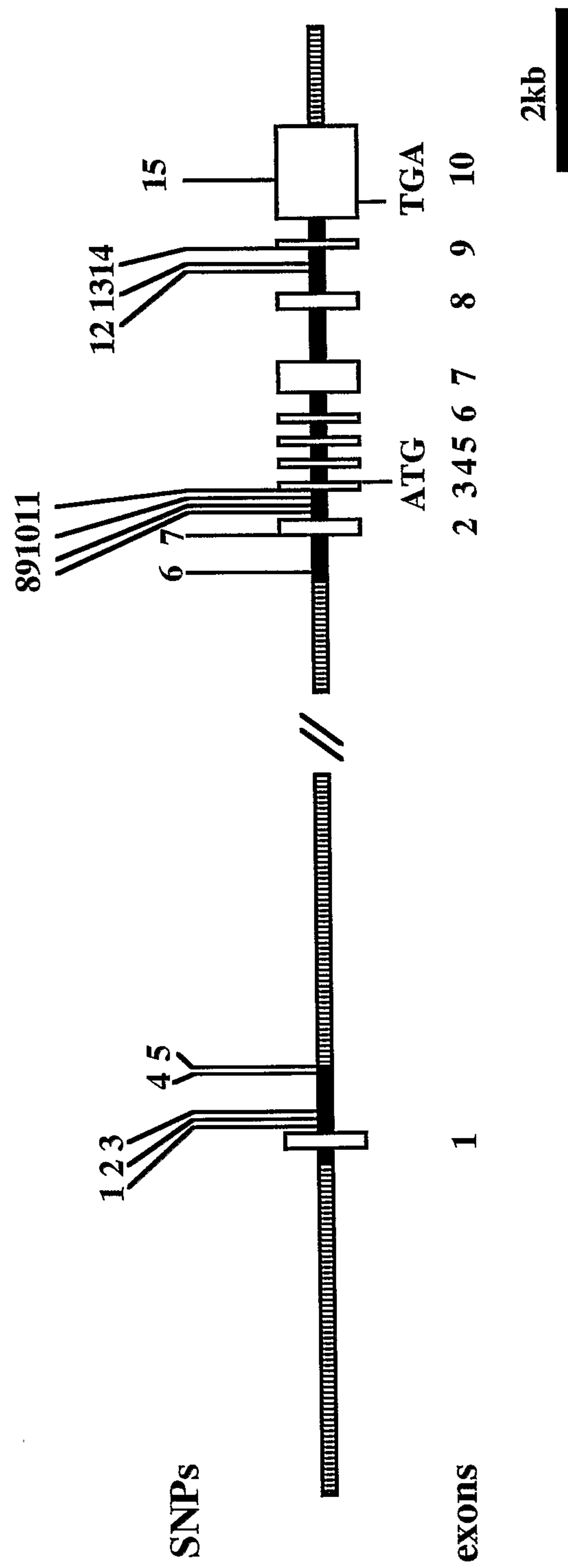


FIGURE 112

Aldehyde dehydrogenase 9 (ALDH9)

ACCESSION AL451074

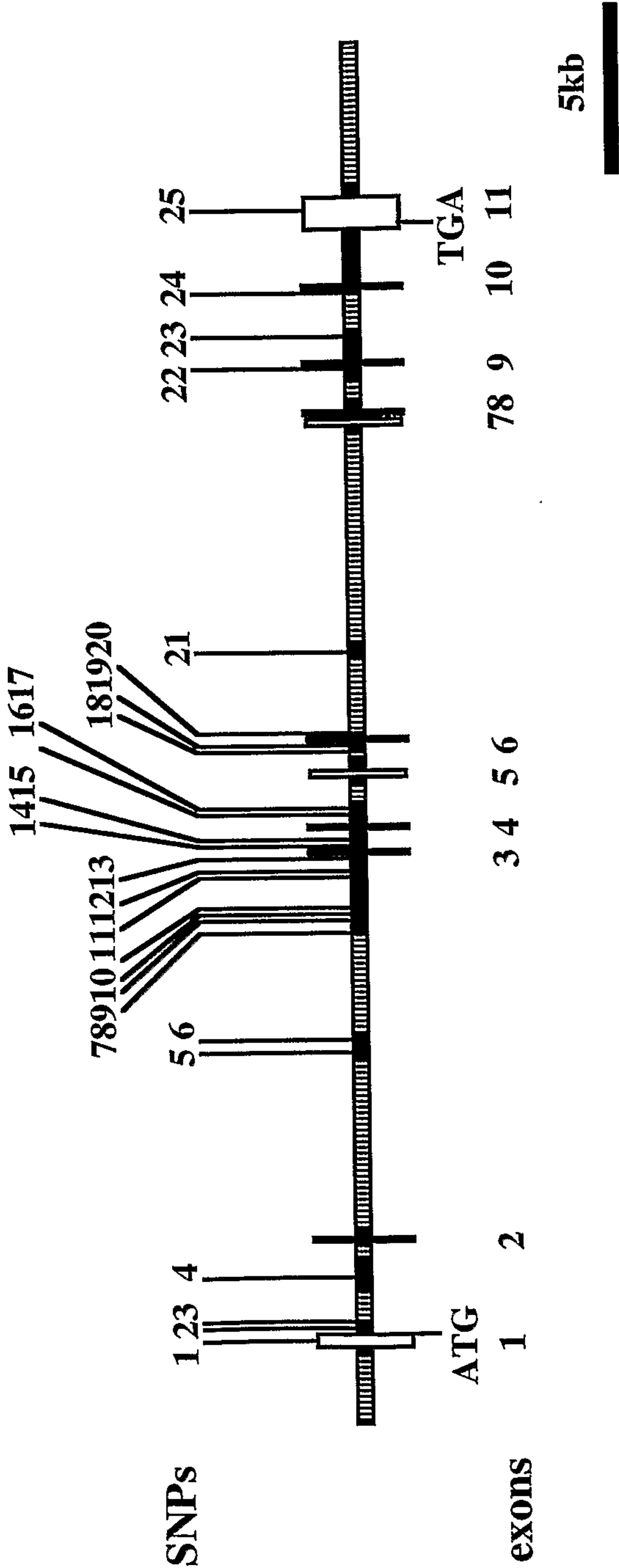


FIGURE 114-1

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061

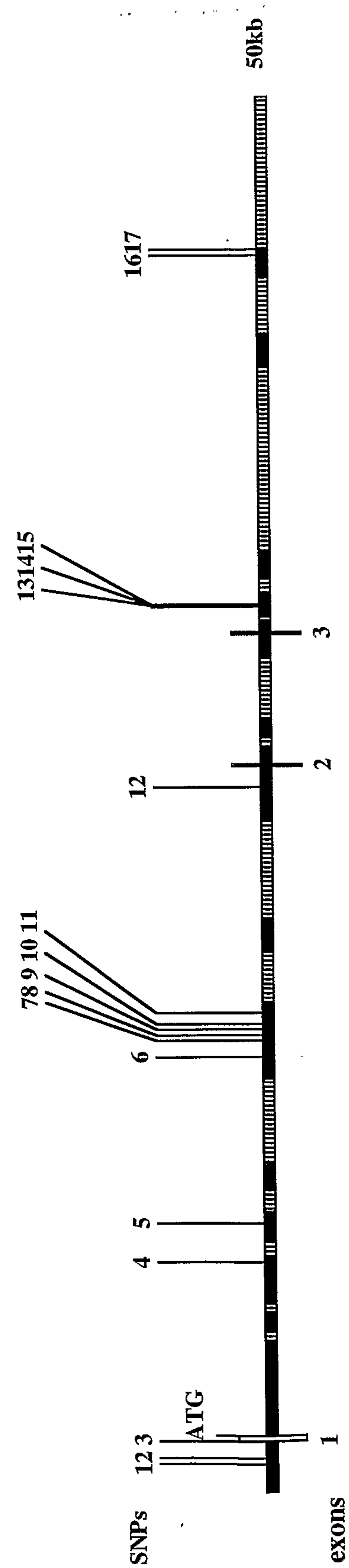


FIGURE 114-2

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061

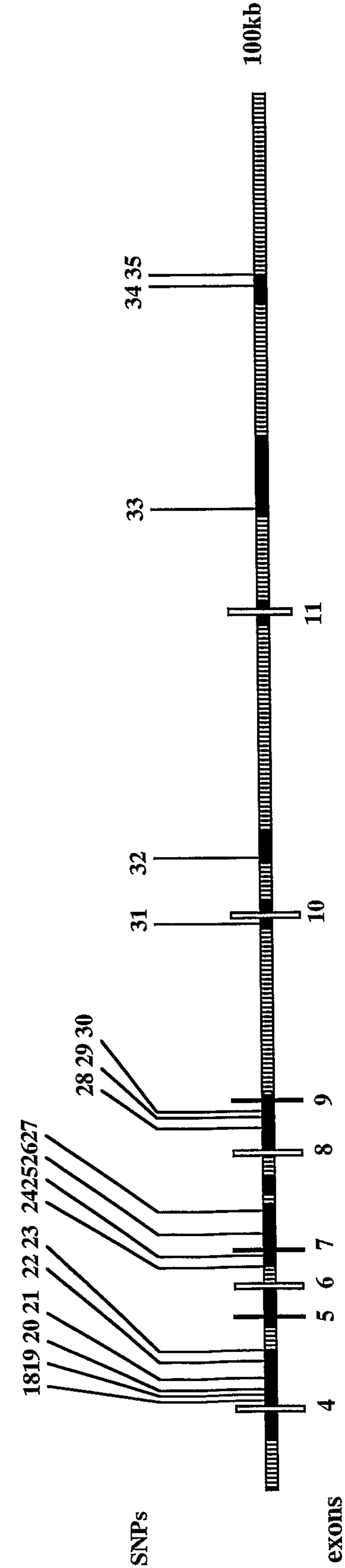


FIGURE 114-3

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061

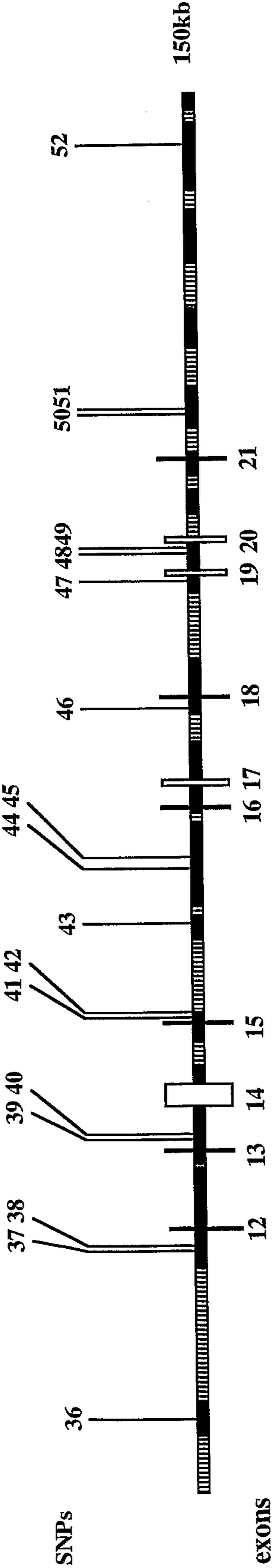


FIGURE 114-4

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061

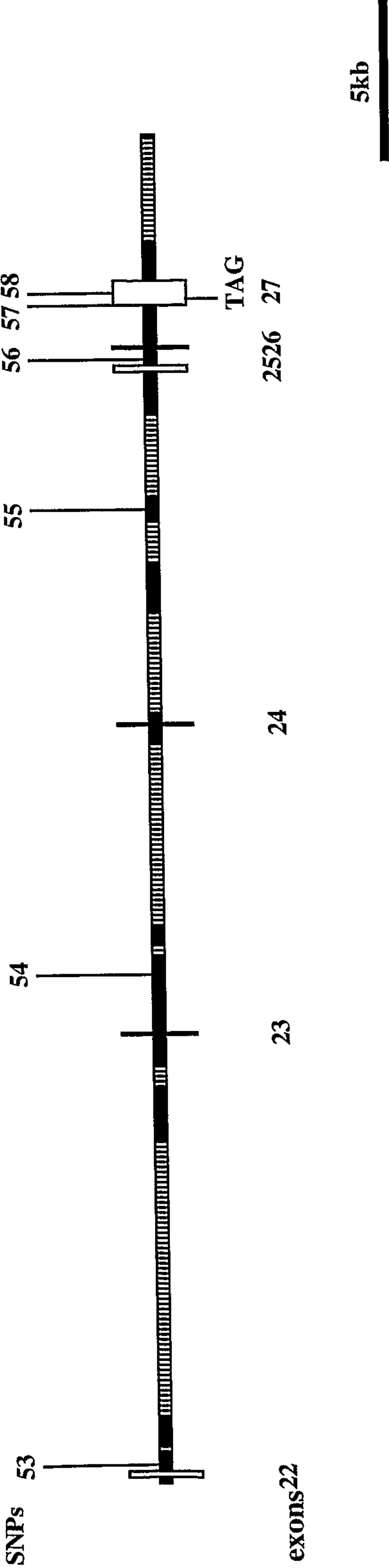


FIGURE 115

ATP binding cassette, sub-family C, member 8 (ABCC8)

ACCESSION AC000406

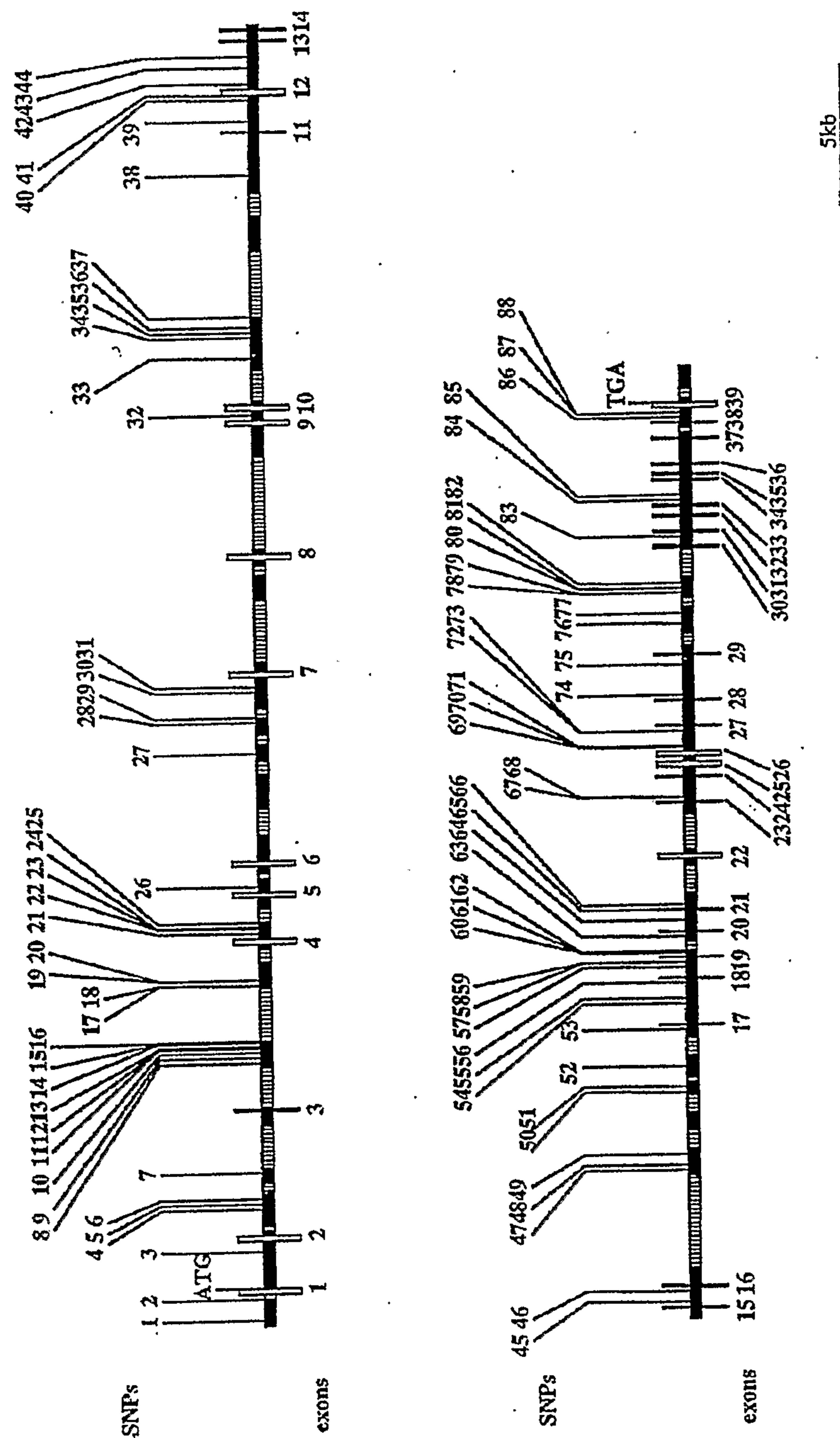


FIGURE 116-1

ATP binding cassette, sub-family C, member 9 (ABCC9)

ACCESSION AC084806
AC008250

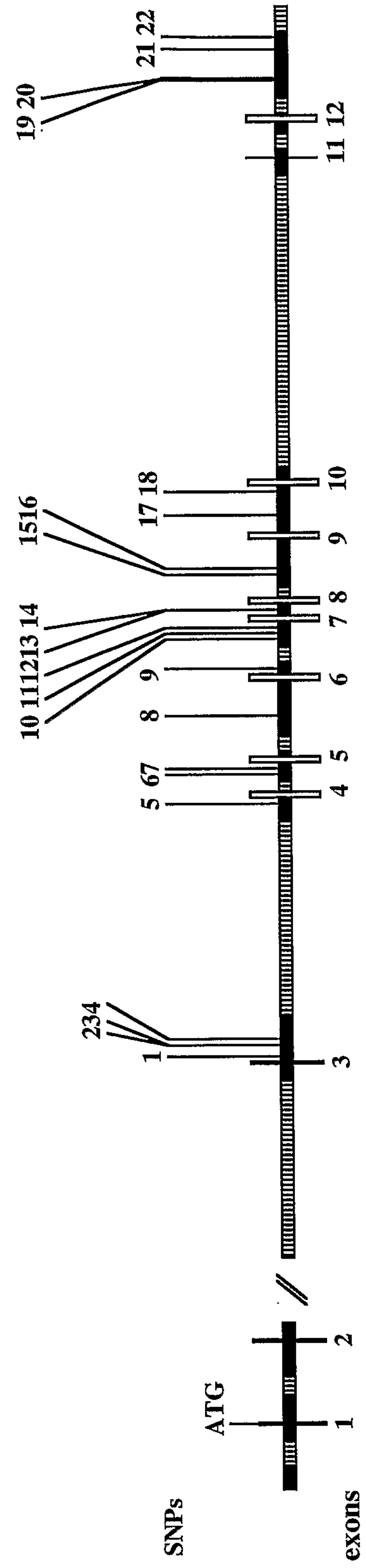


FIGURE 116-2

ATP binding cassette, sub-family C, member 9 (ABCC9)

ACCESSION AC084806
AC008250

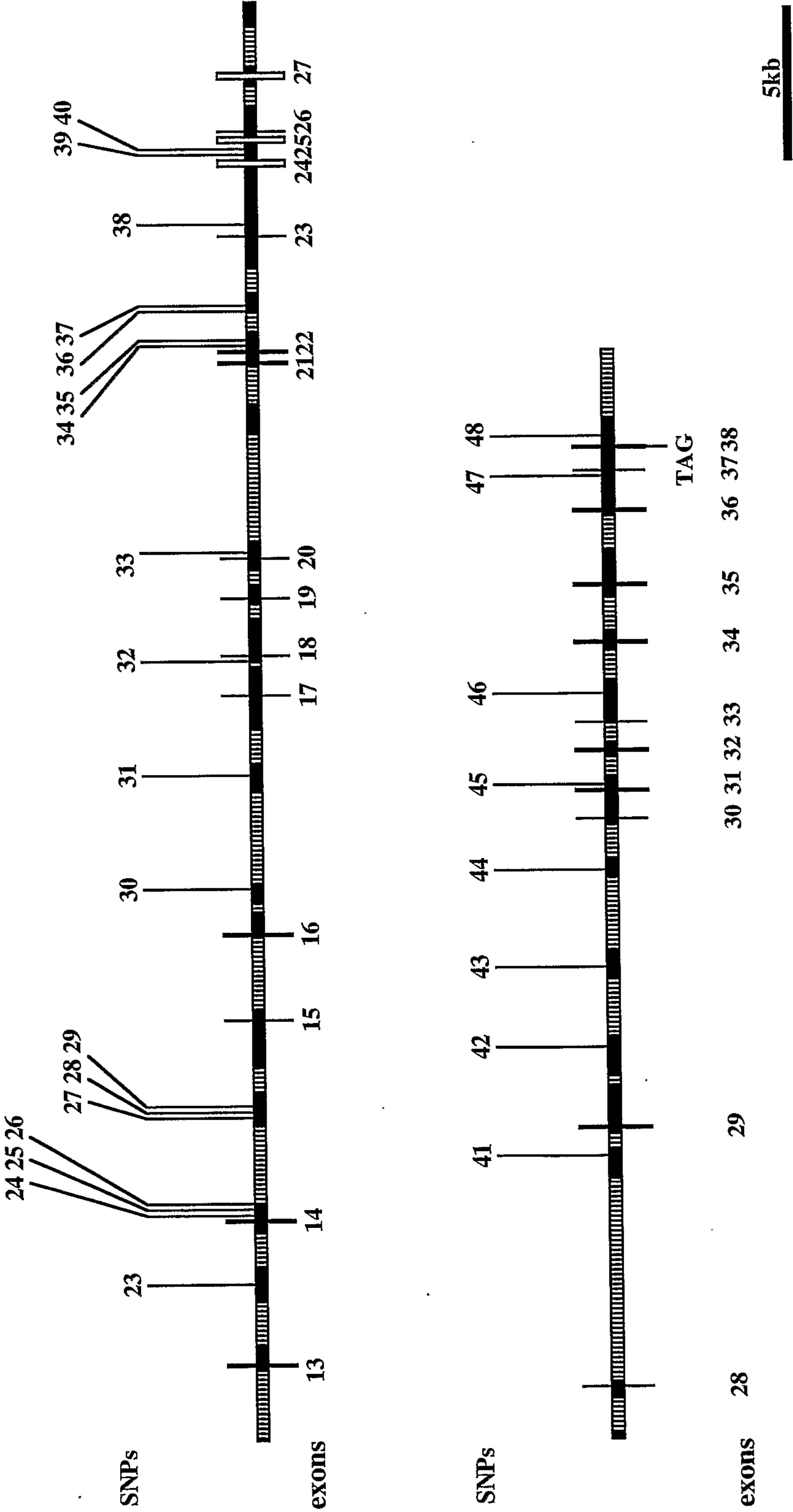


FIGURE 117

Carboxylesterase 1 (CES1)

ACCESSION AC007602

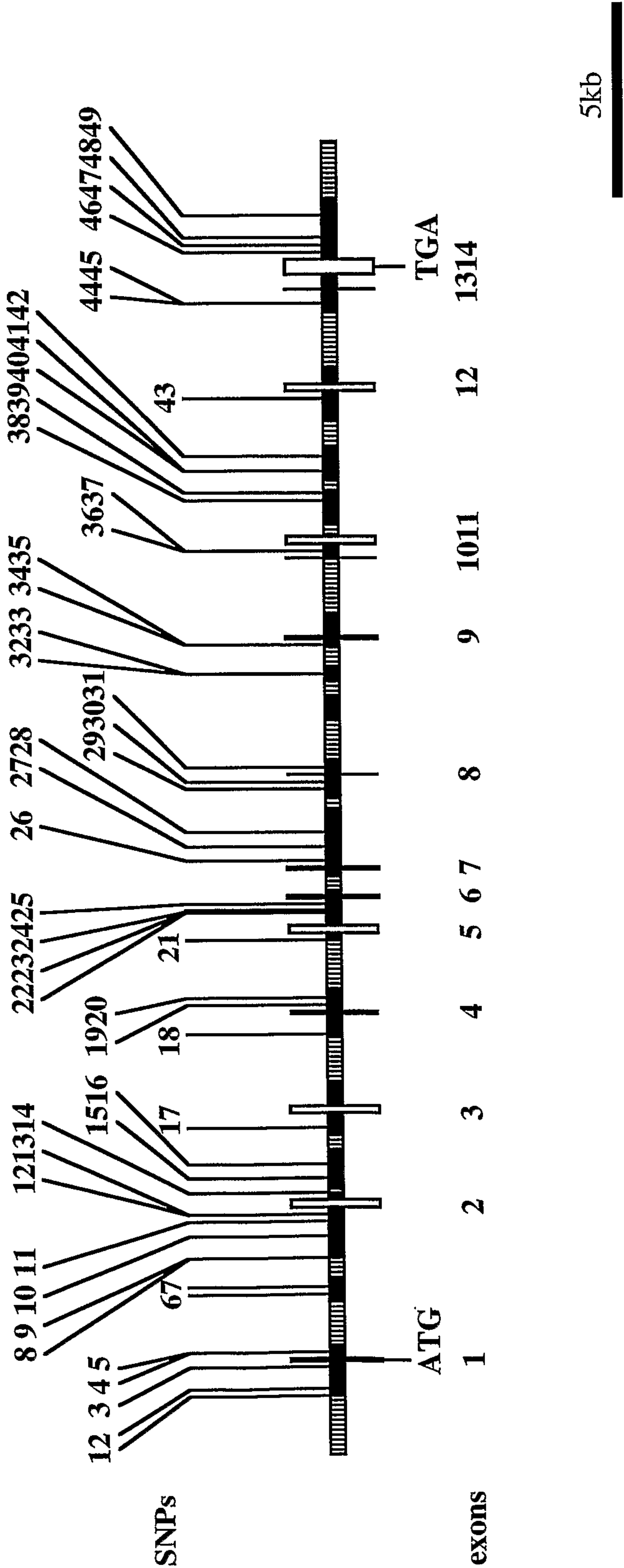


FIGURE 118-1

ATP binding cassette, subfamily A, member 4 (ABCA4)

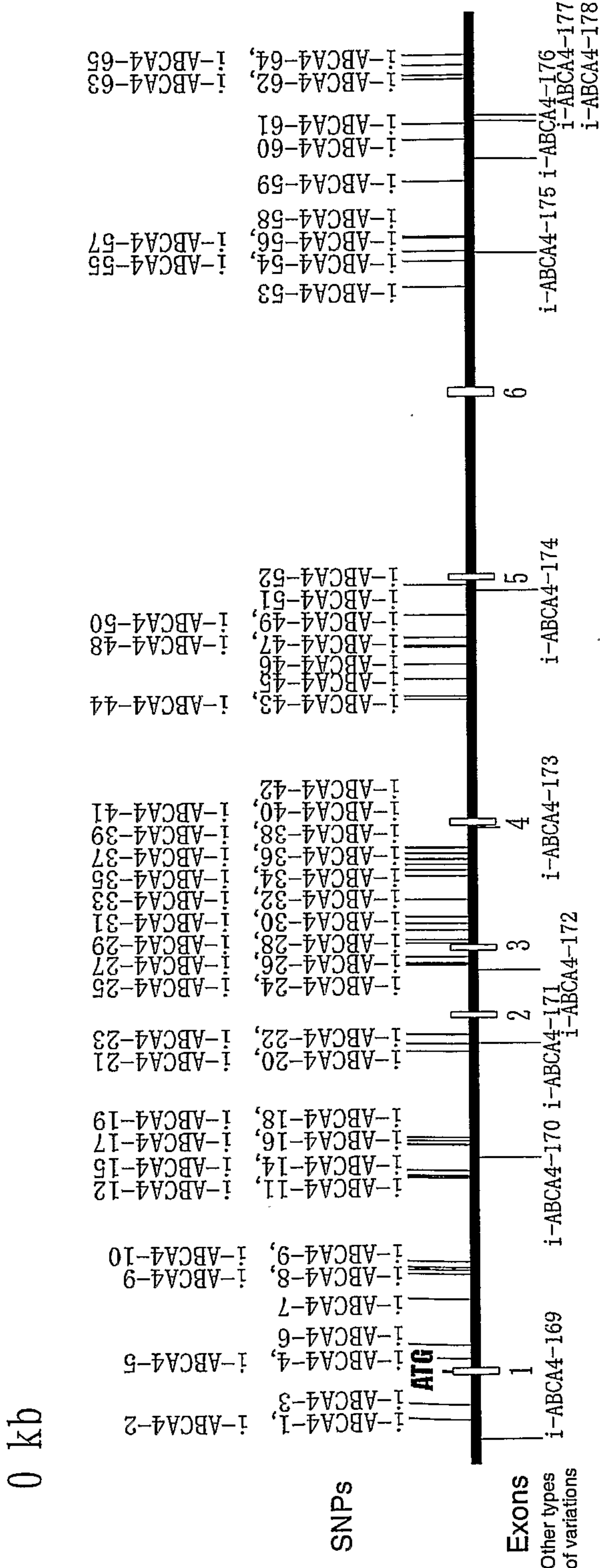


FIGURE 118-3

ATP binding cassette, subfamily A, member 4 (ABCA4)





FIGURE 118-4

ATP binding cassette, subfamily A, member 4 (*ABCA4*)

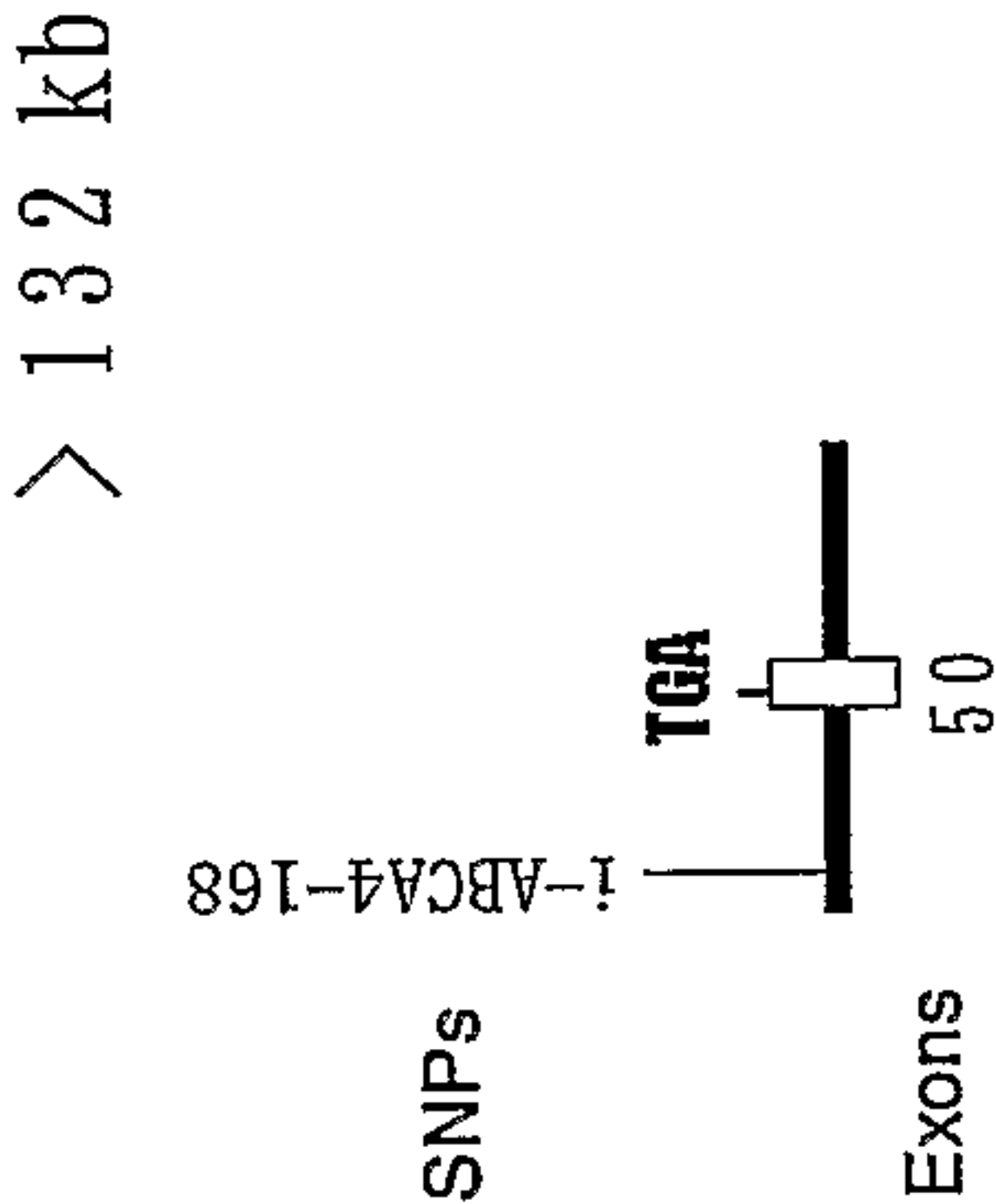


FIGURE 119

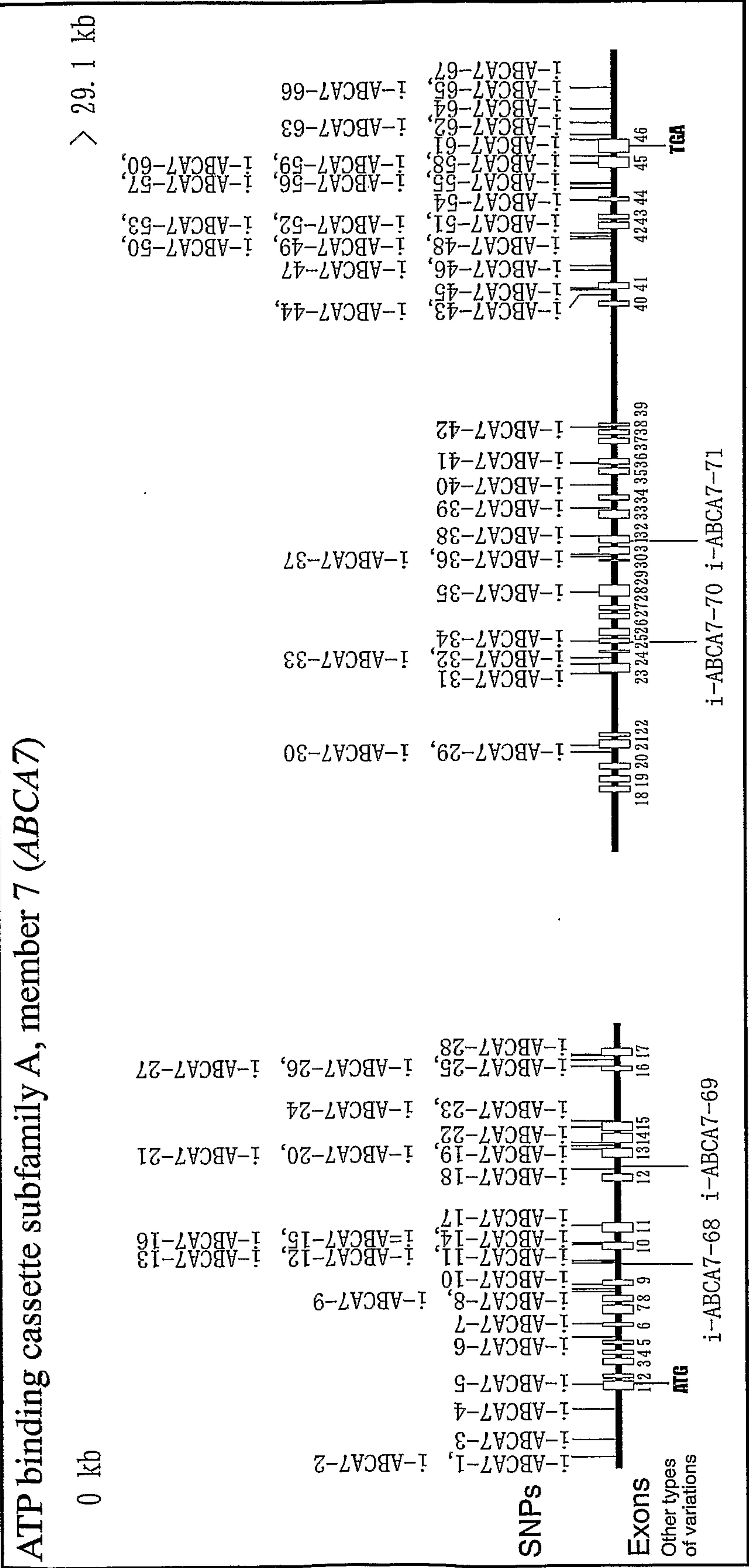


FIGURE 120-1

ATP binding cassette subfamily G, member 1 (*ABCG1*)

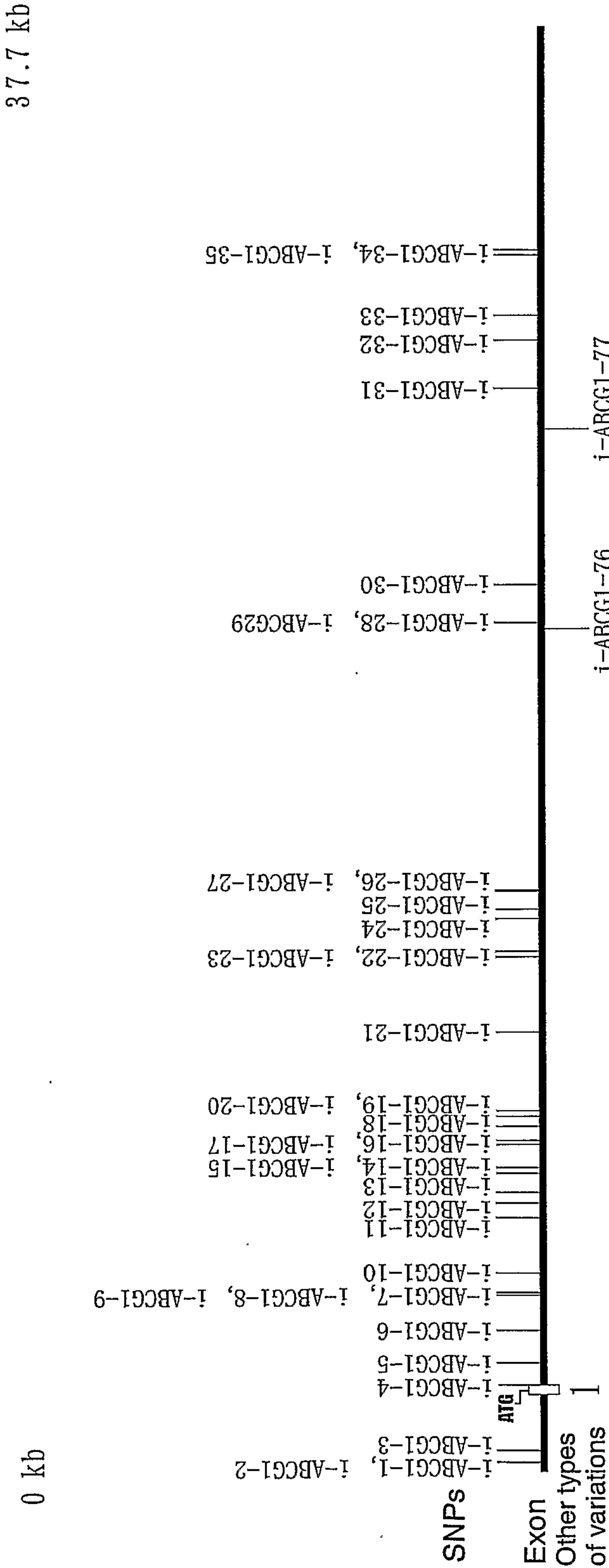


FIGURE 120-2

ATP binding cassette subfamily G, member 1 (*ABCG1*)

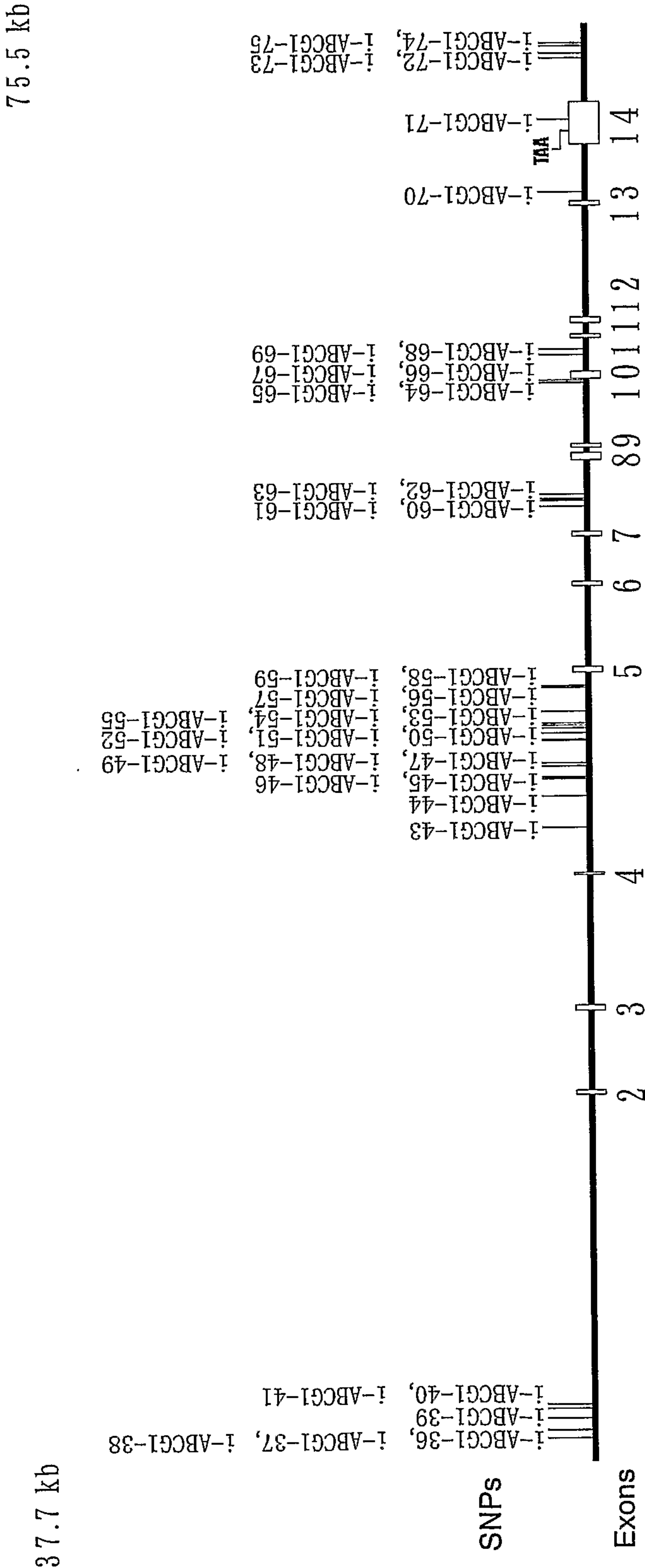


FIGURE 121-1

ATP binding cassette subfamily G, member 2 (ABCG2)

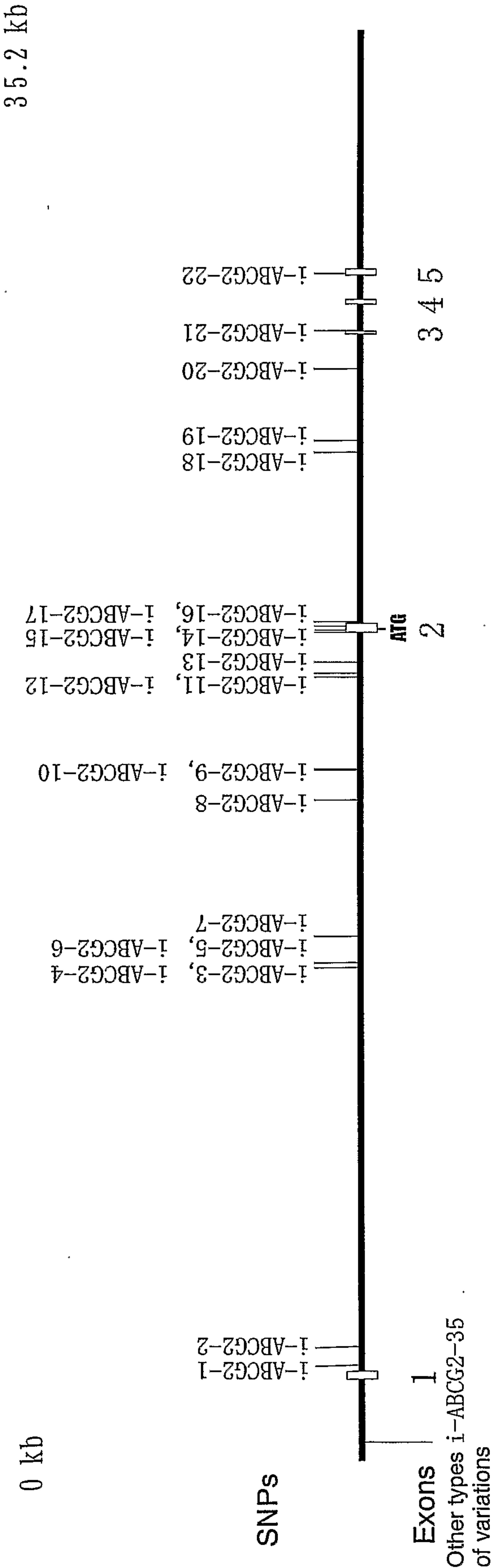


FIGURE 121-2

ATP binding cassette subfamily G, member 2 (*ABCG2*)
35.2 kb

70.5 kb

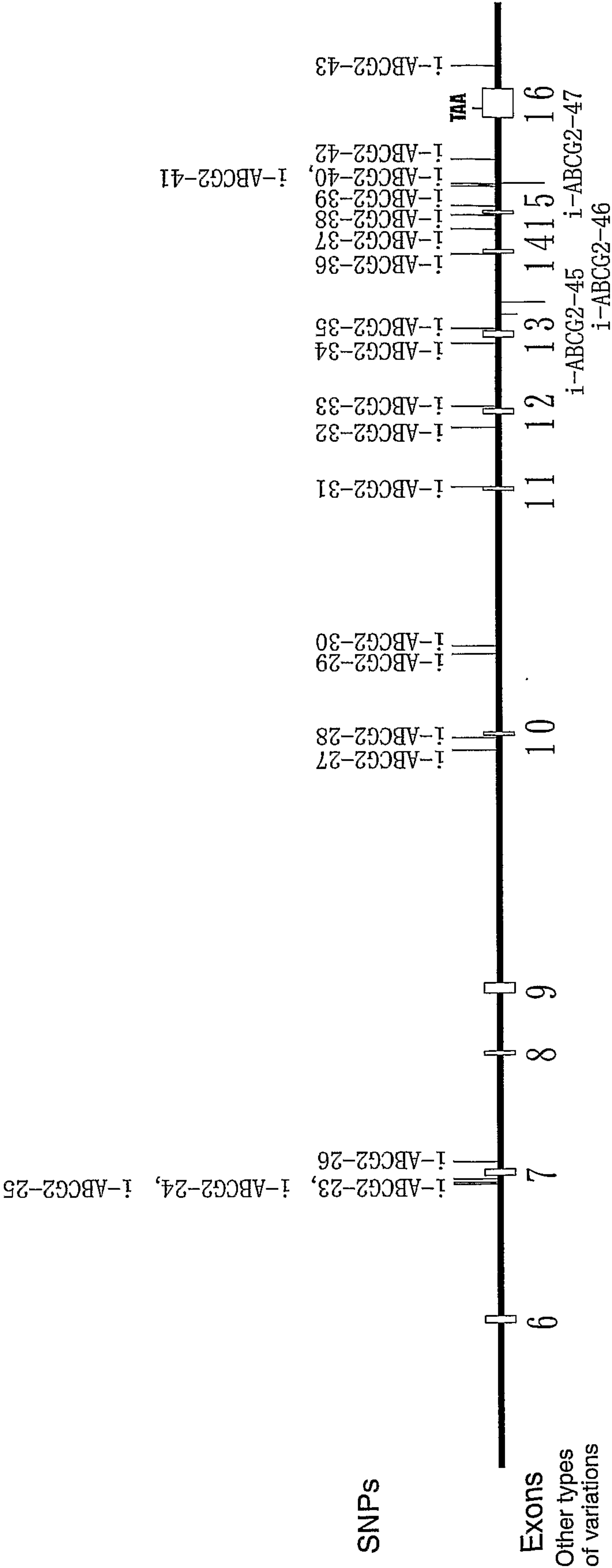


FIGURE 122

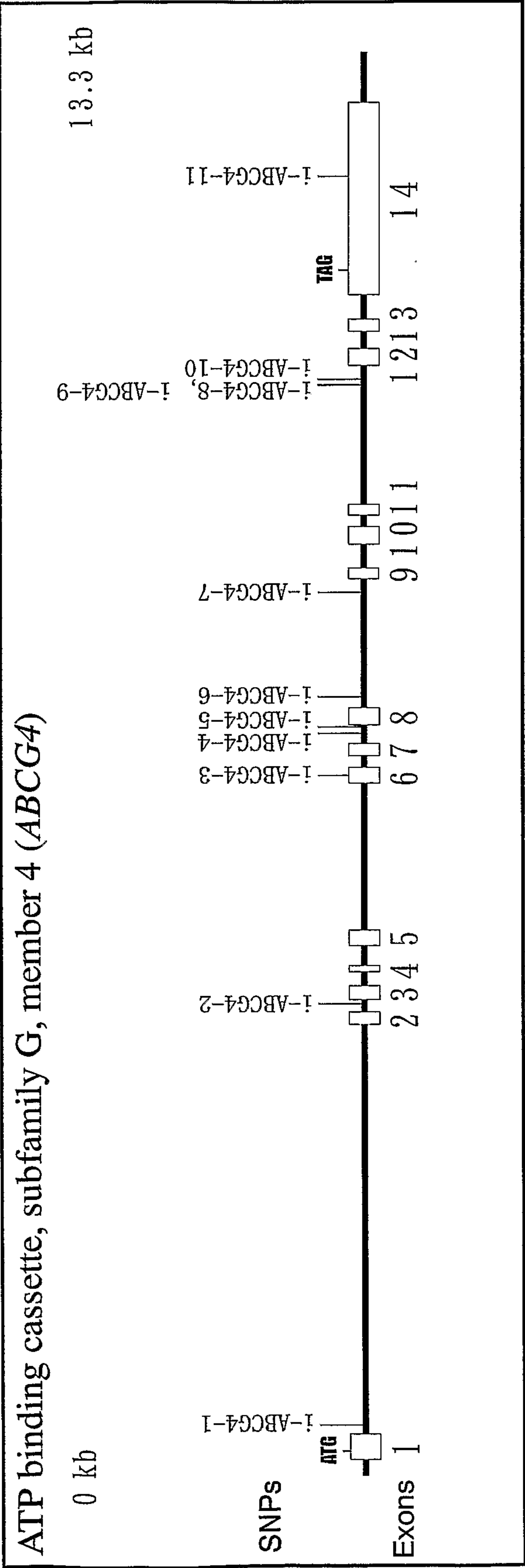


FIGURE 123

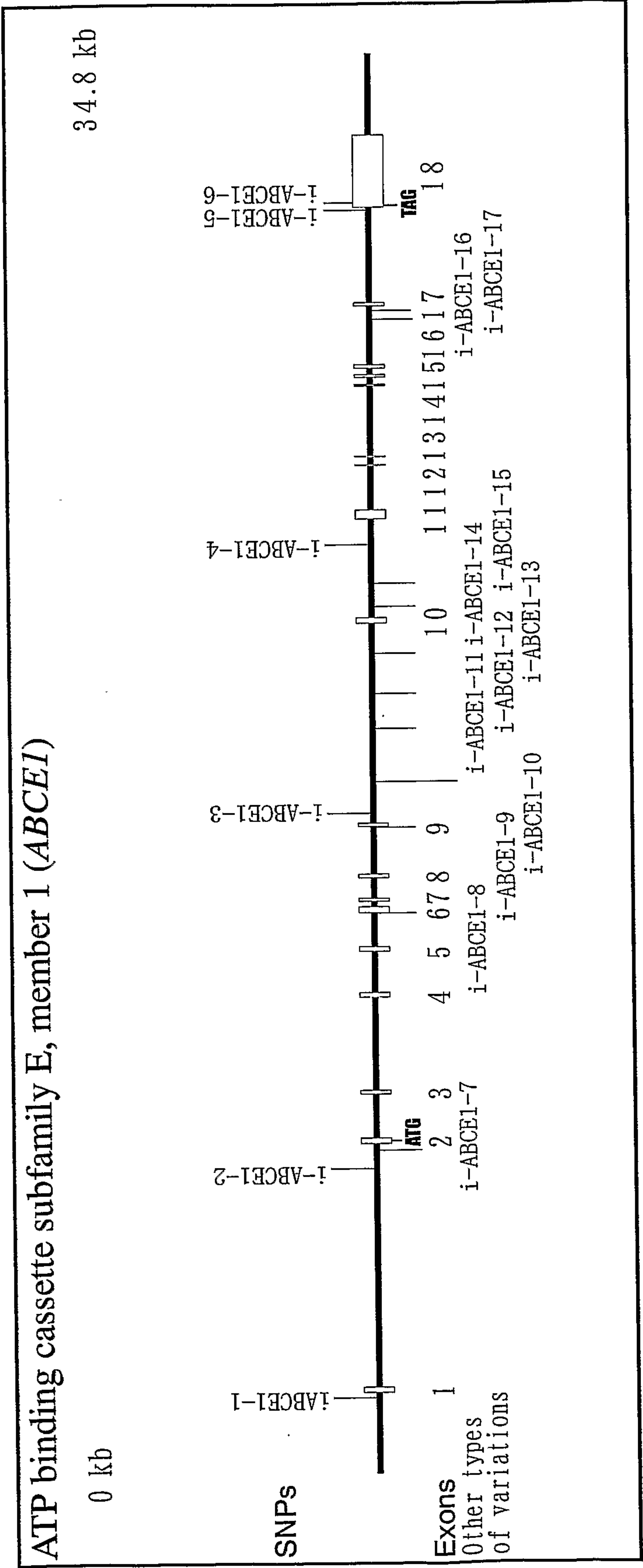


FIGURE 124

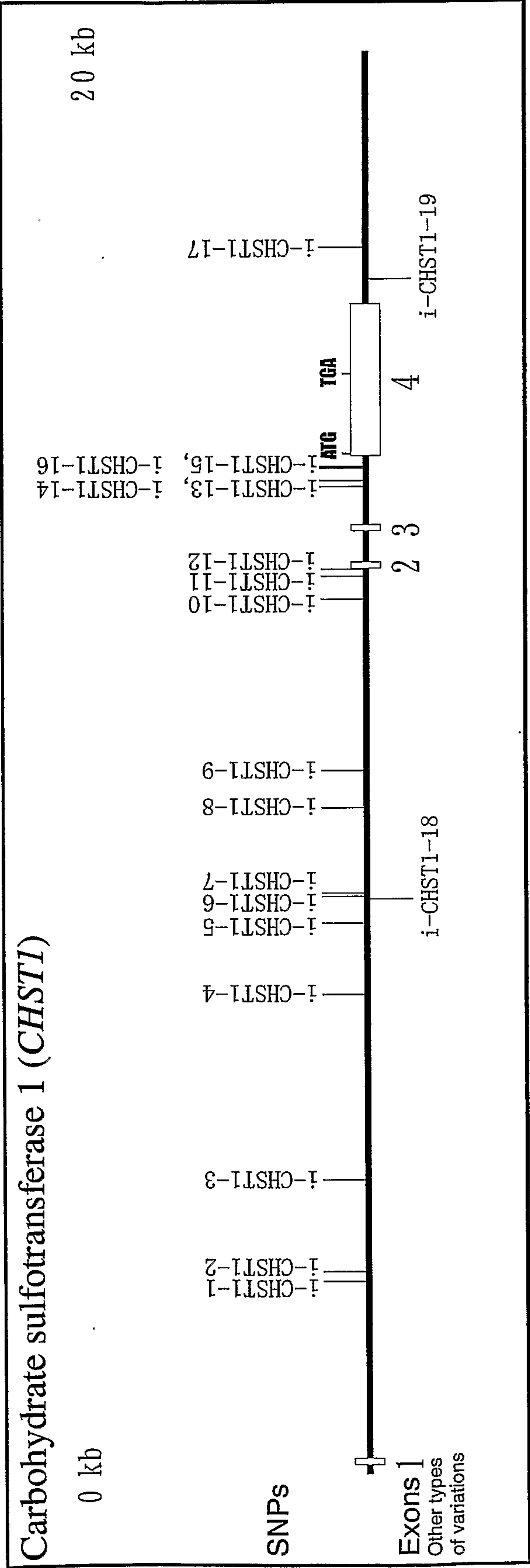


FIGURE 125

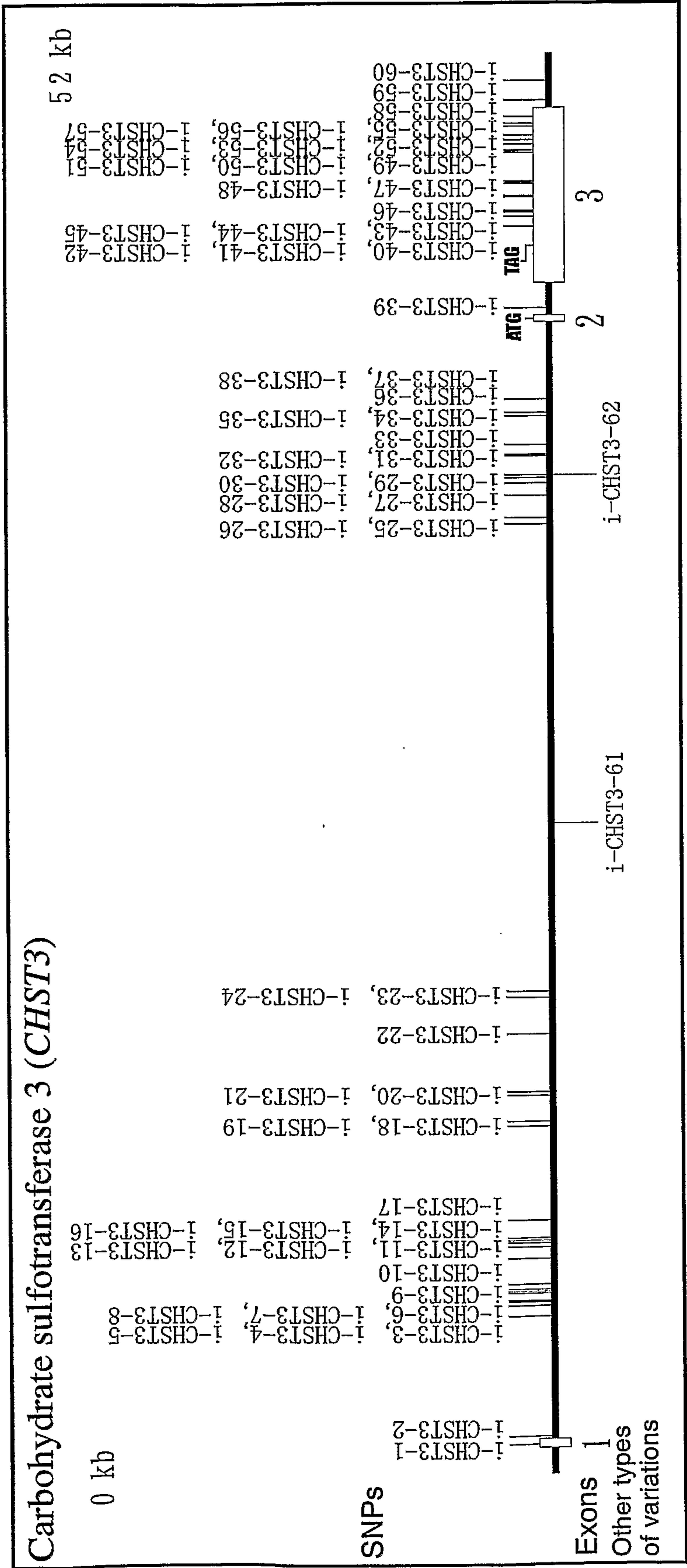


FIGURE 126

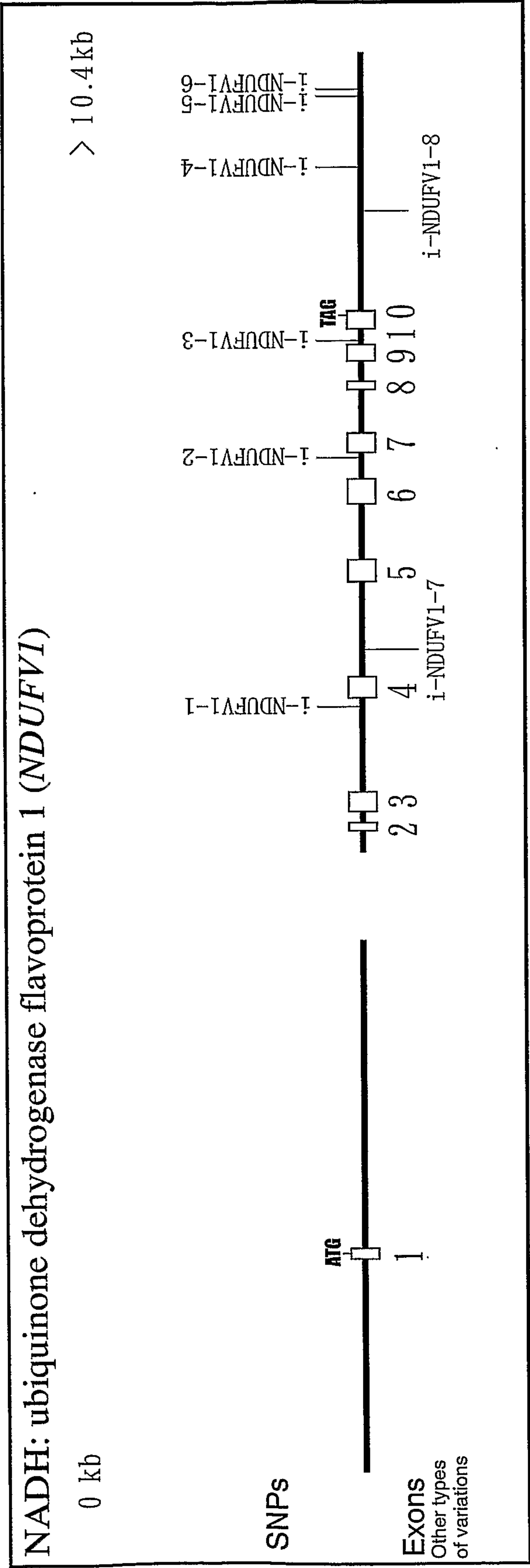


FIGURE 127

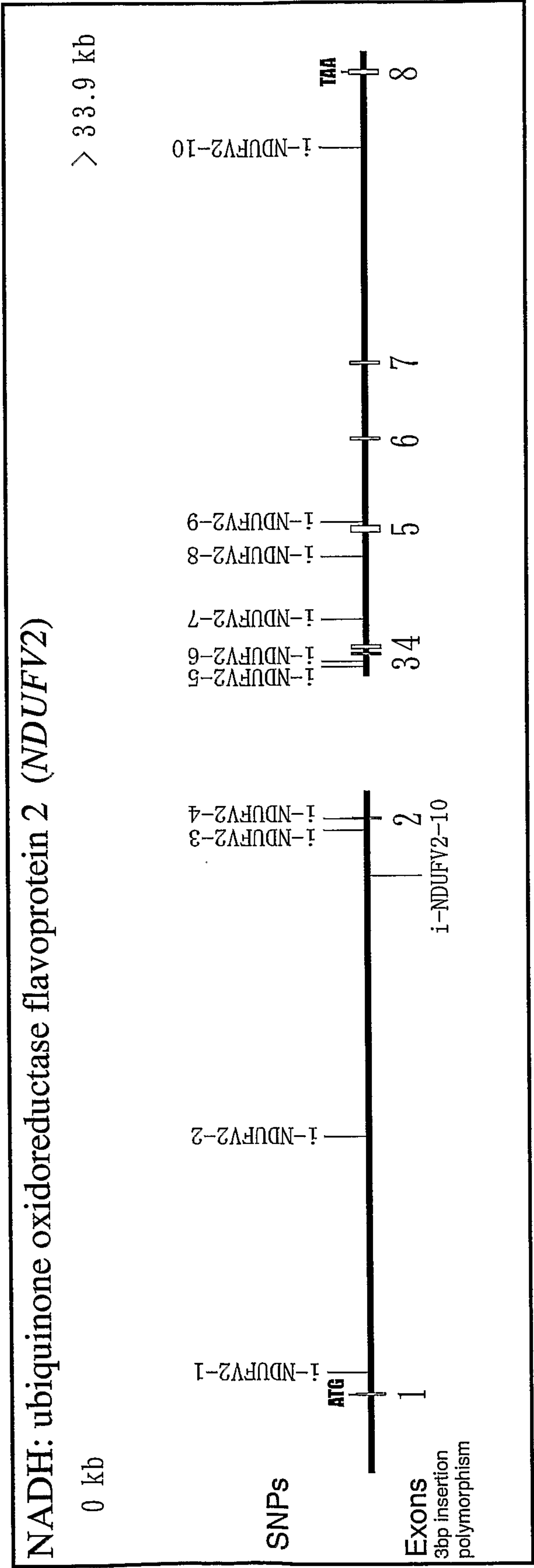


FIGURE 128

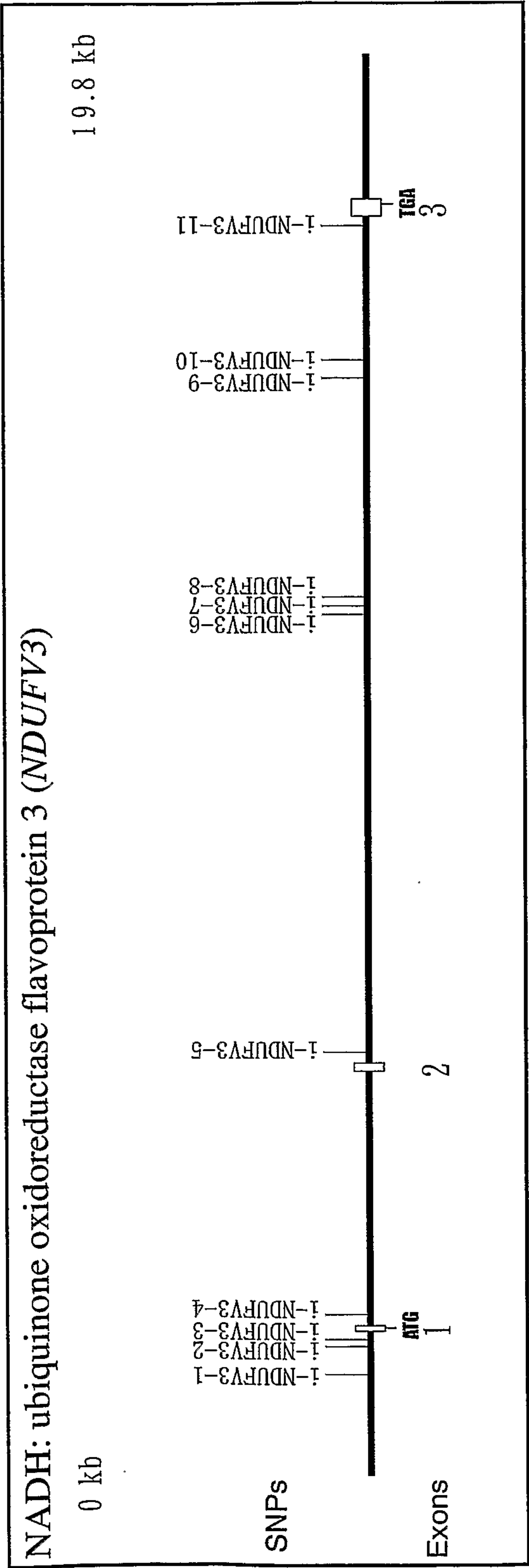


FIGURE 129

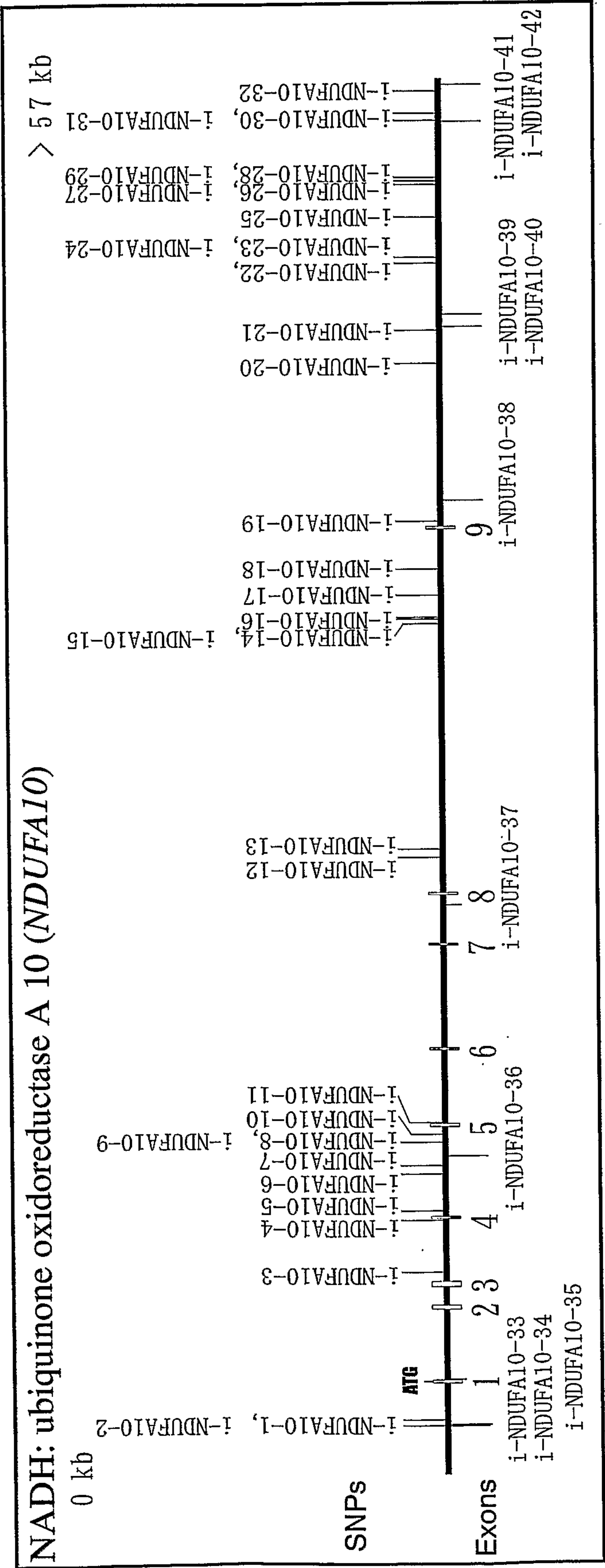
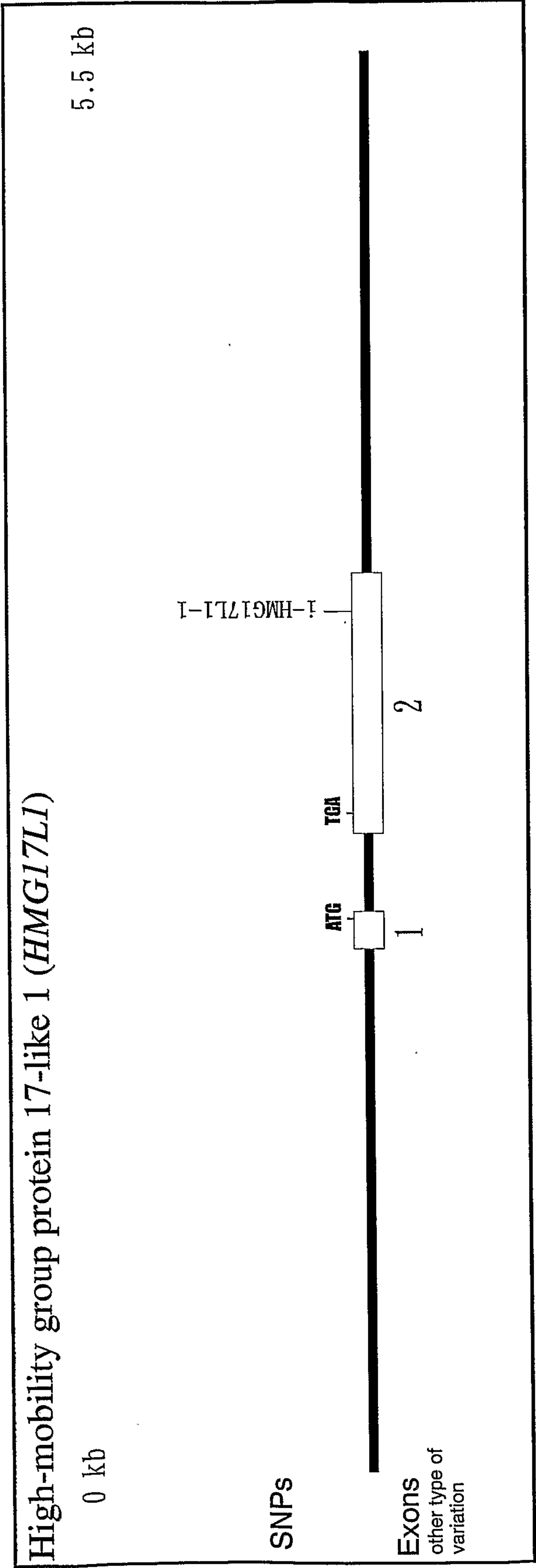


FIGURE 130



UDP glycosyltransferase 2 family, polypeptide A1 (*UGT2A1*)

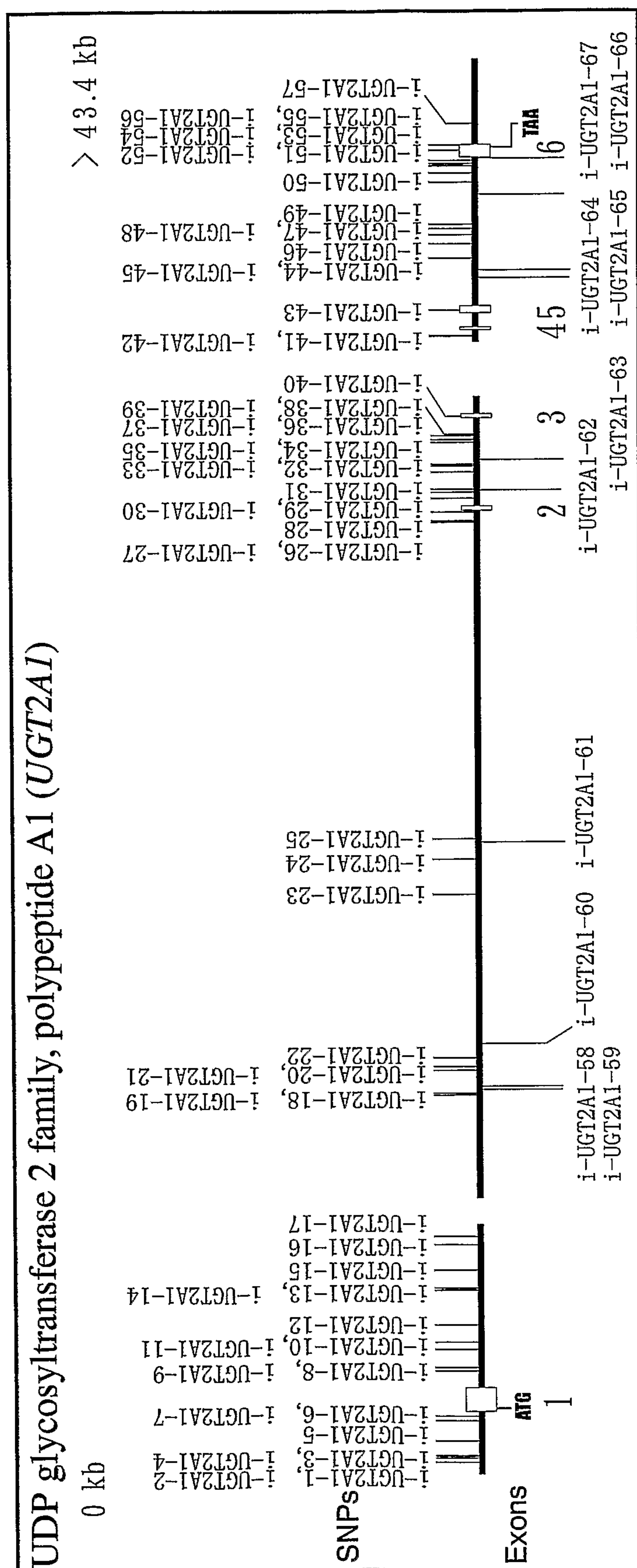


FIGURE 132-1
Human organic anion transporting polypeptide 1 (*hOATP1*)

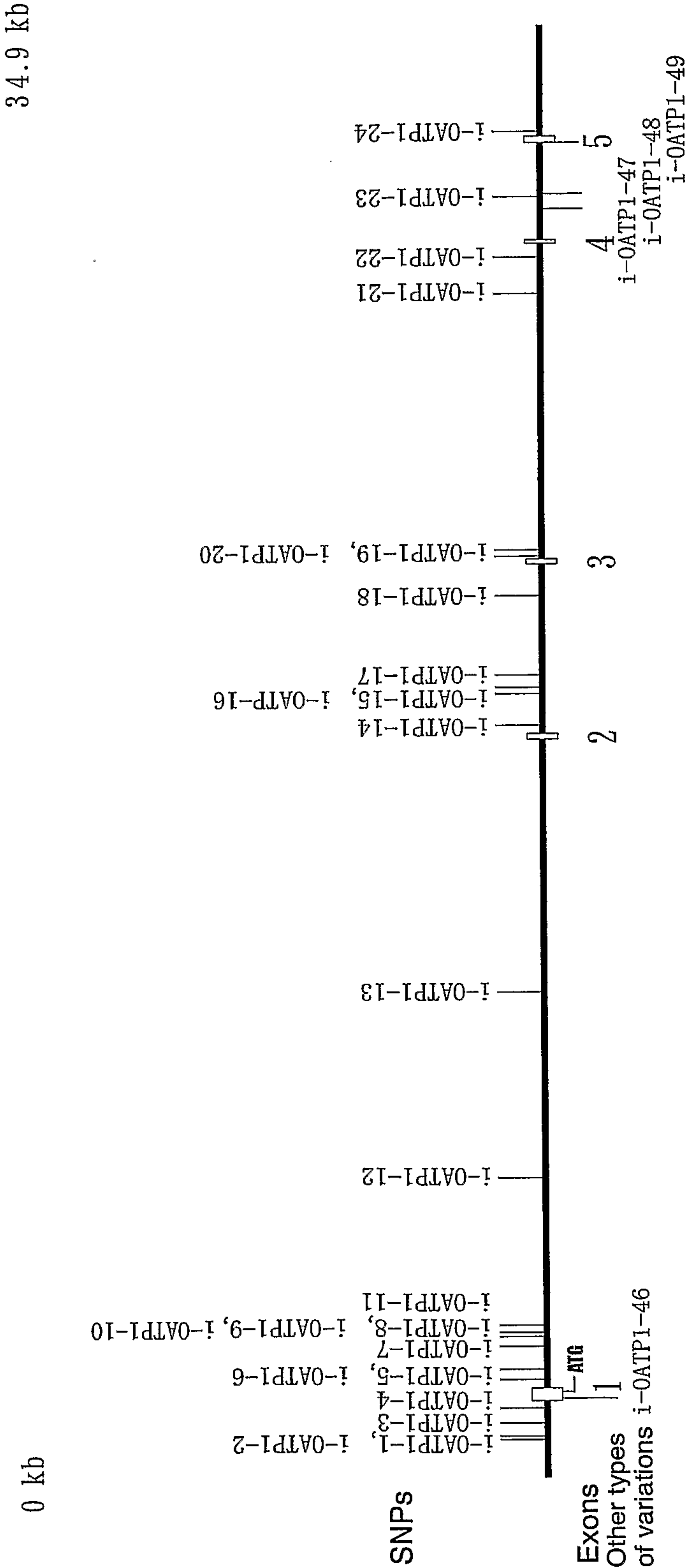


FIGURE 132-2

Human organic anion transporting polypeptide 1 (*hOATP1*)

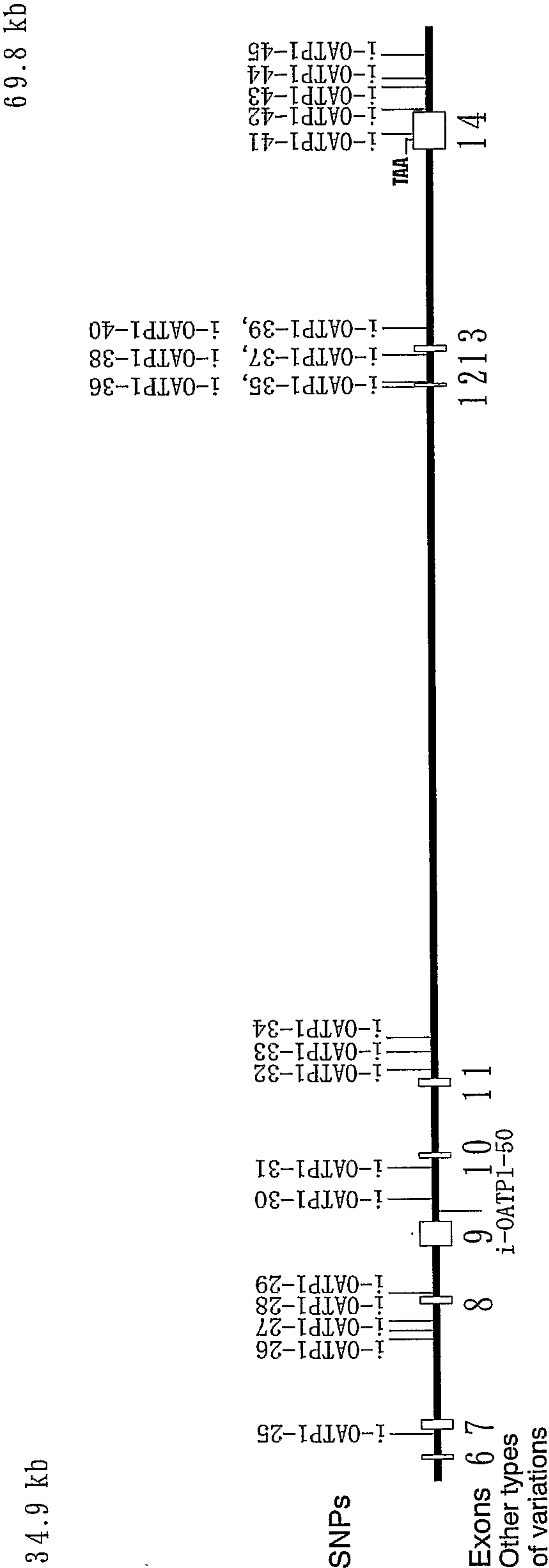


FIGURE 133-1
 Human organic anion transporting polypeptide 2 (*hOATP2*)

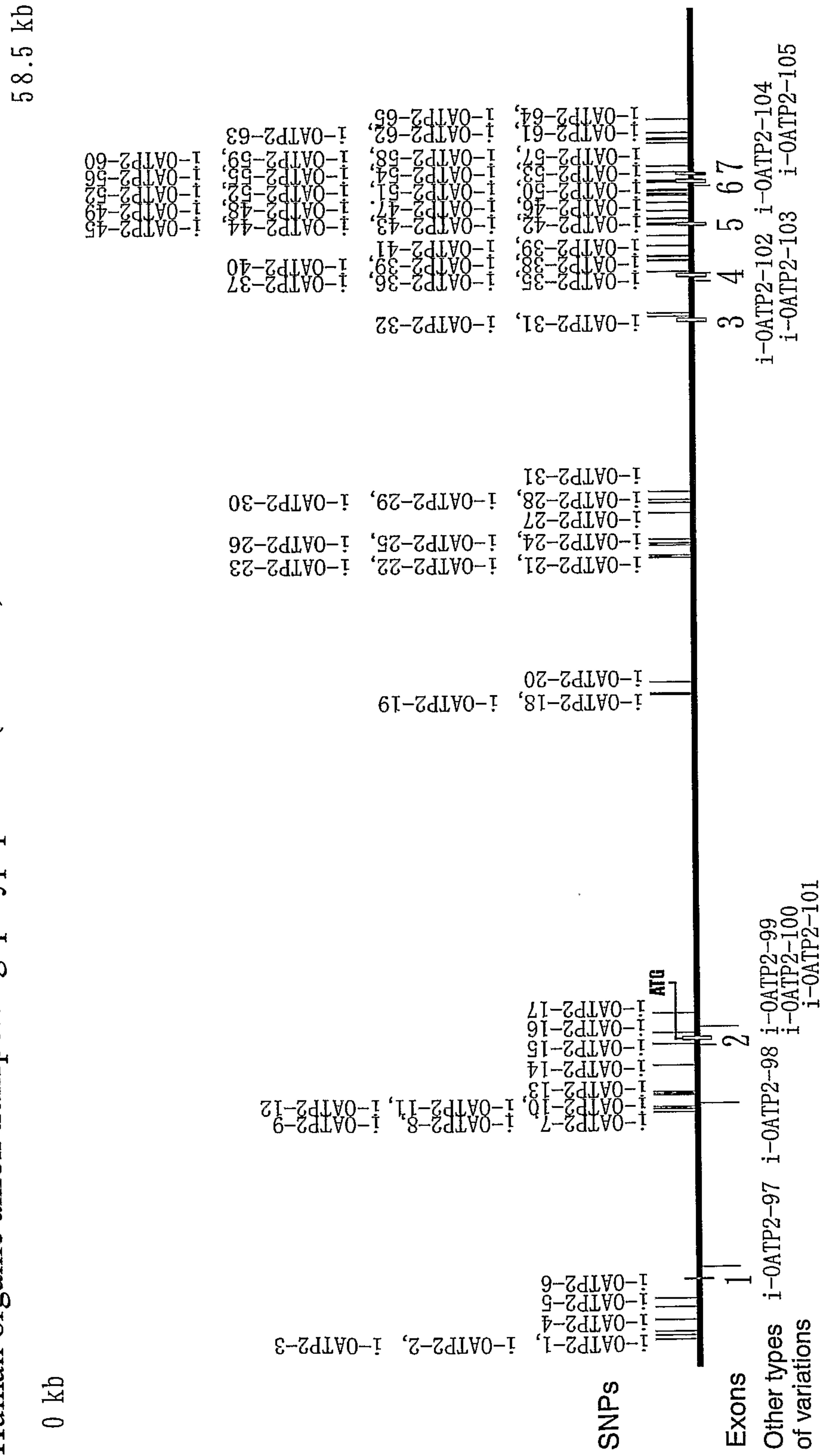


FIGURE 133-2

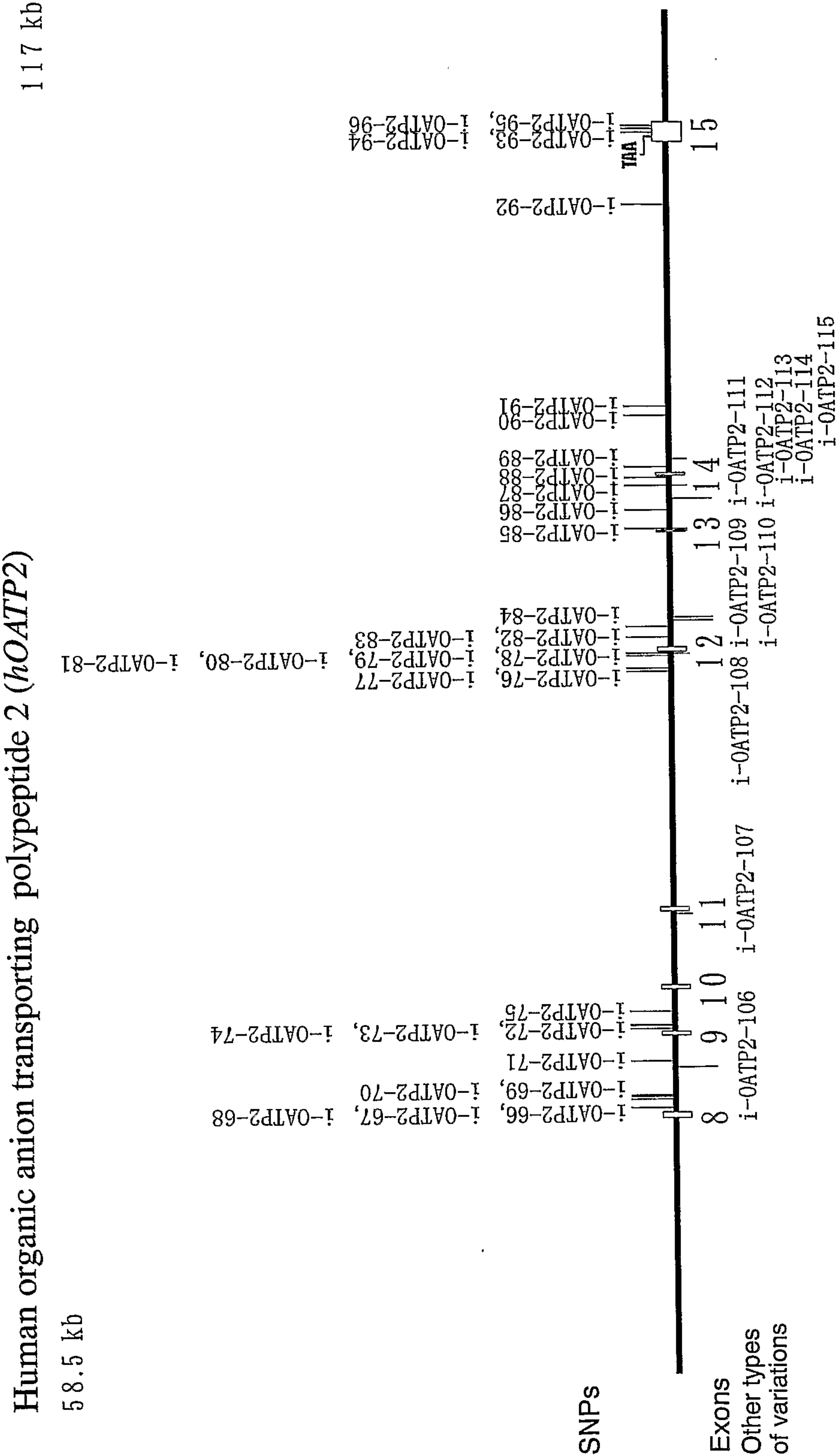


FIGURE 134-1

Human organic anion transporting polypeptide 8 (*hOATP8*)

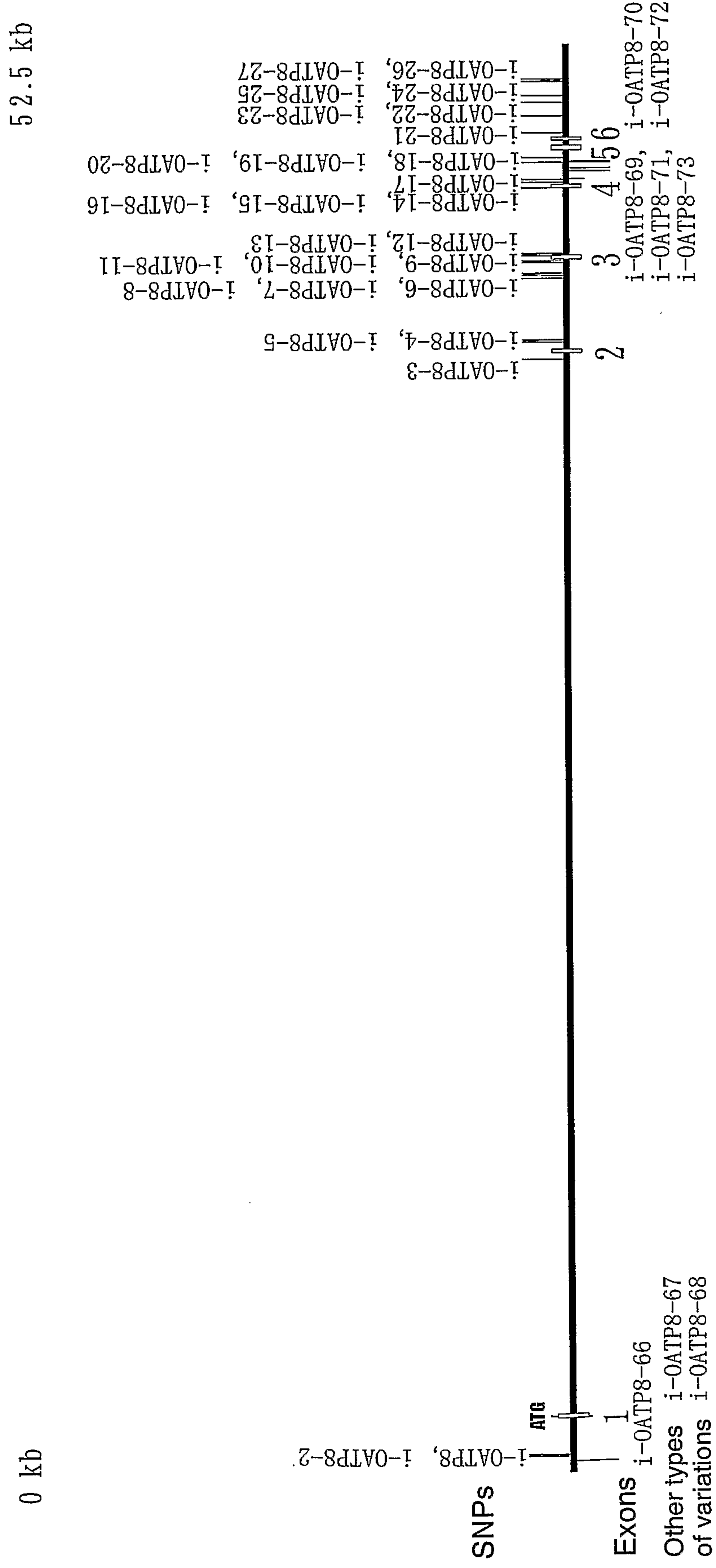


FIGURE 134-2

Human organic anion transporting polypeptide 8 (*hOATP8*)

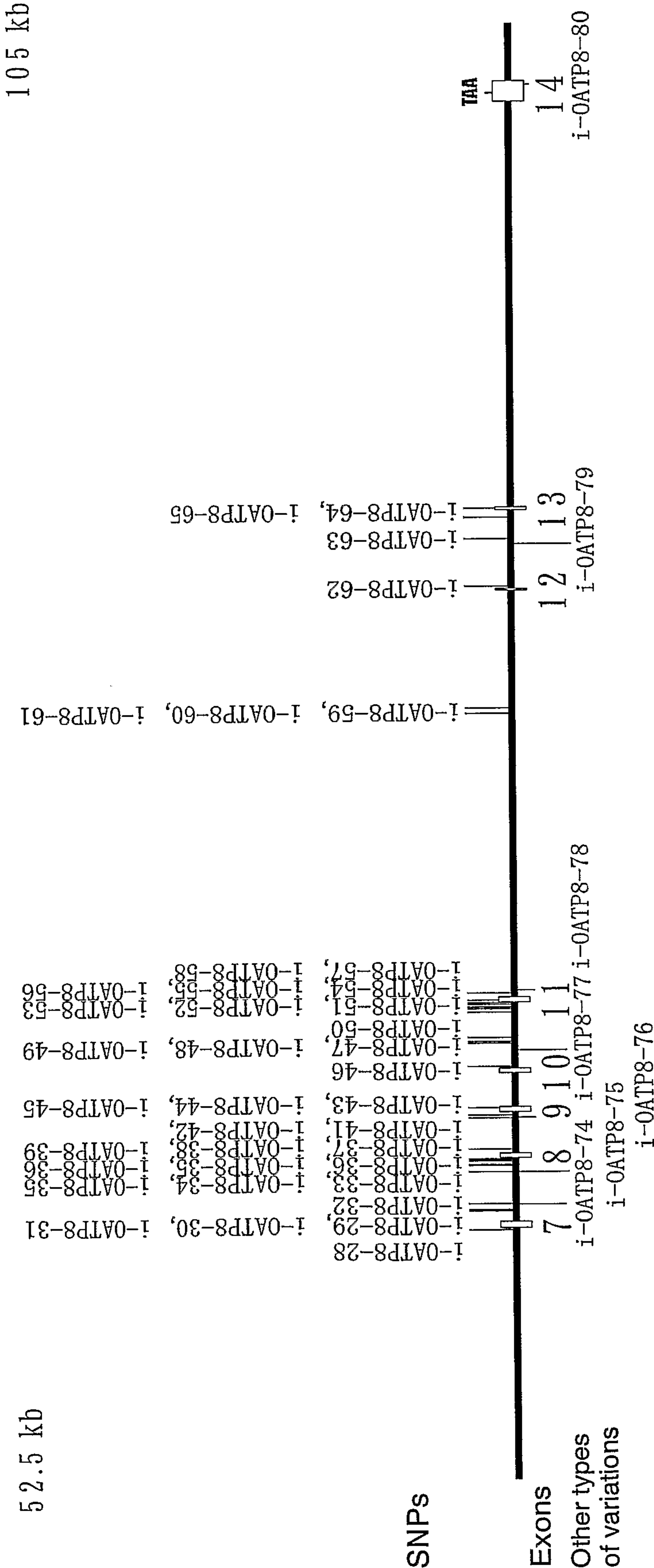
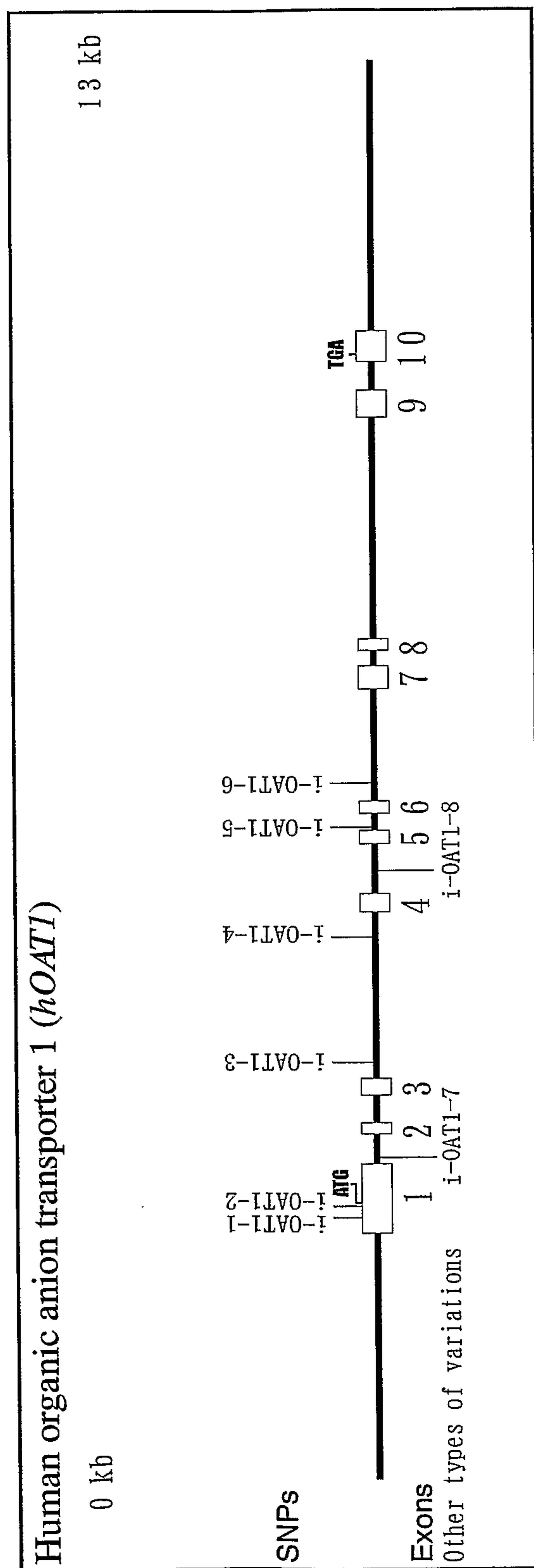


FIGURE 135



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FIGURE 136

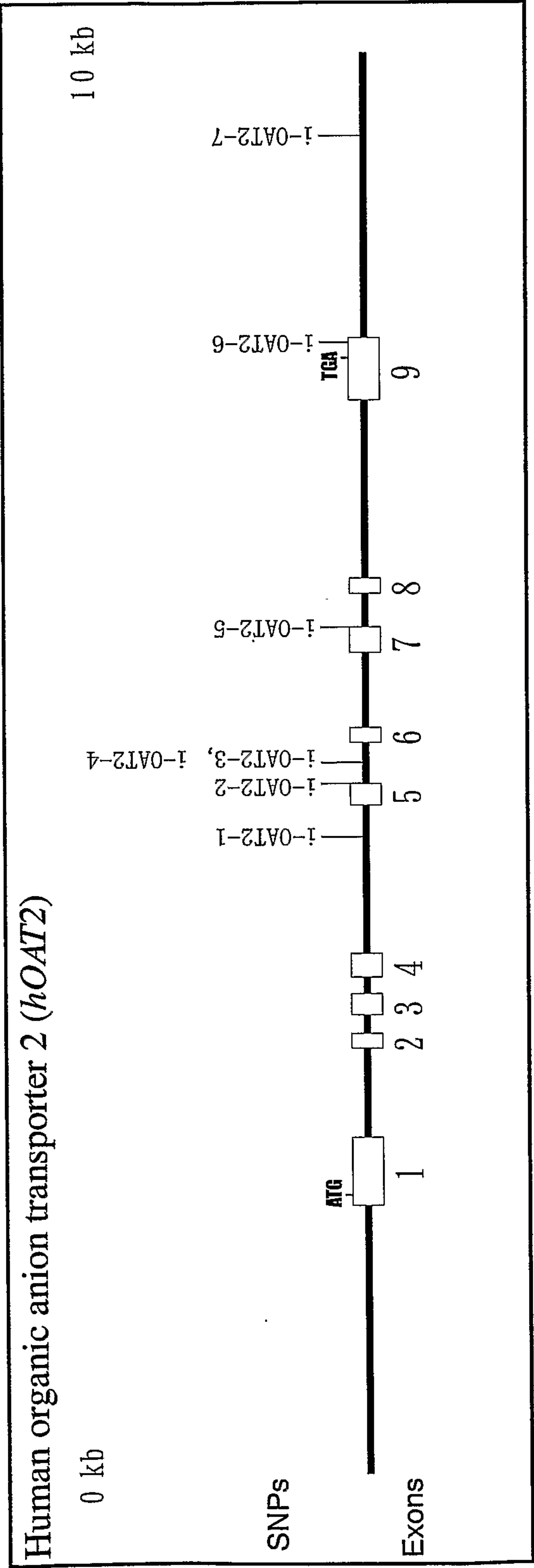
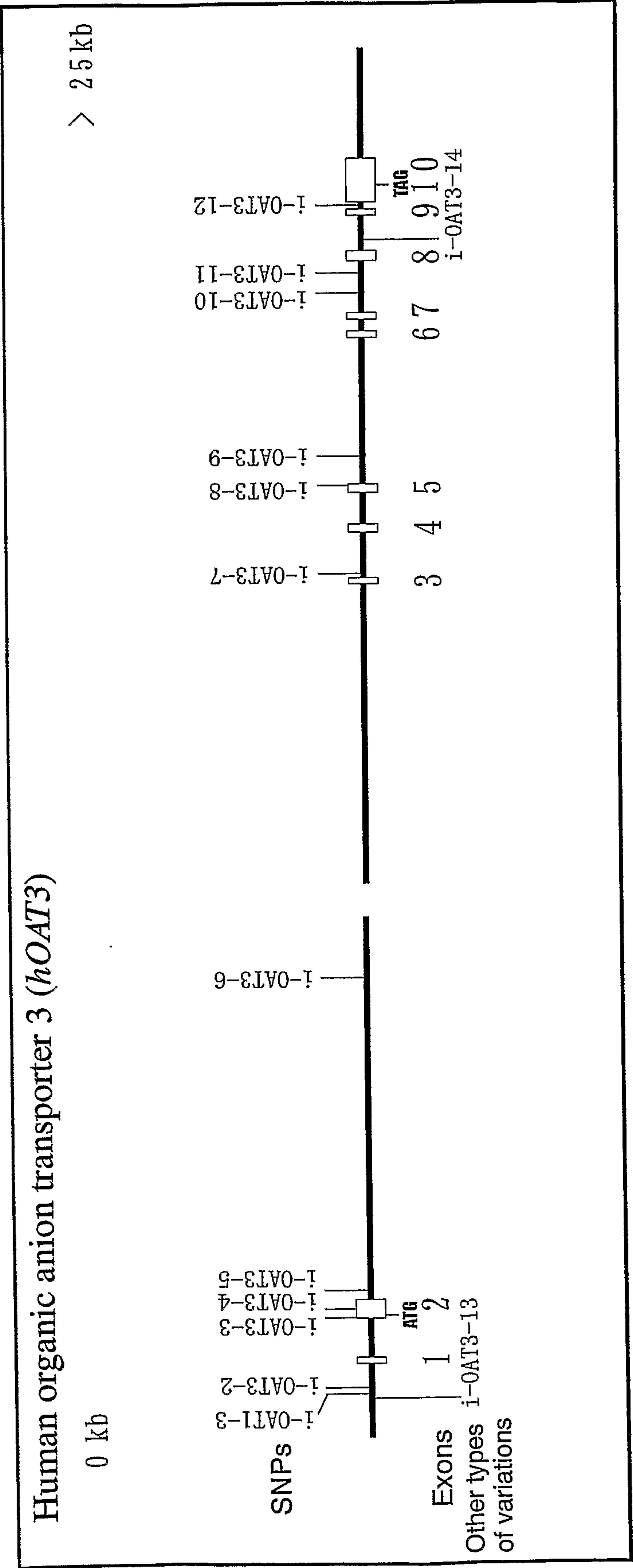


FIGURE 137



ACCESSION AC025431
AC012653

FIGURE 138 *Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)*

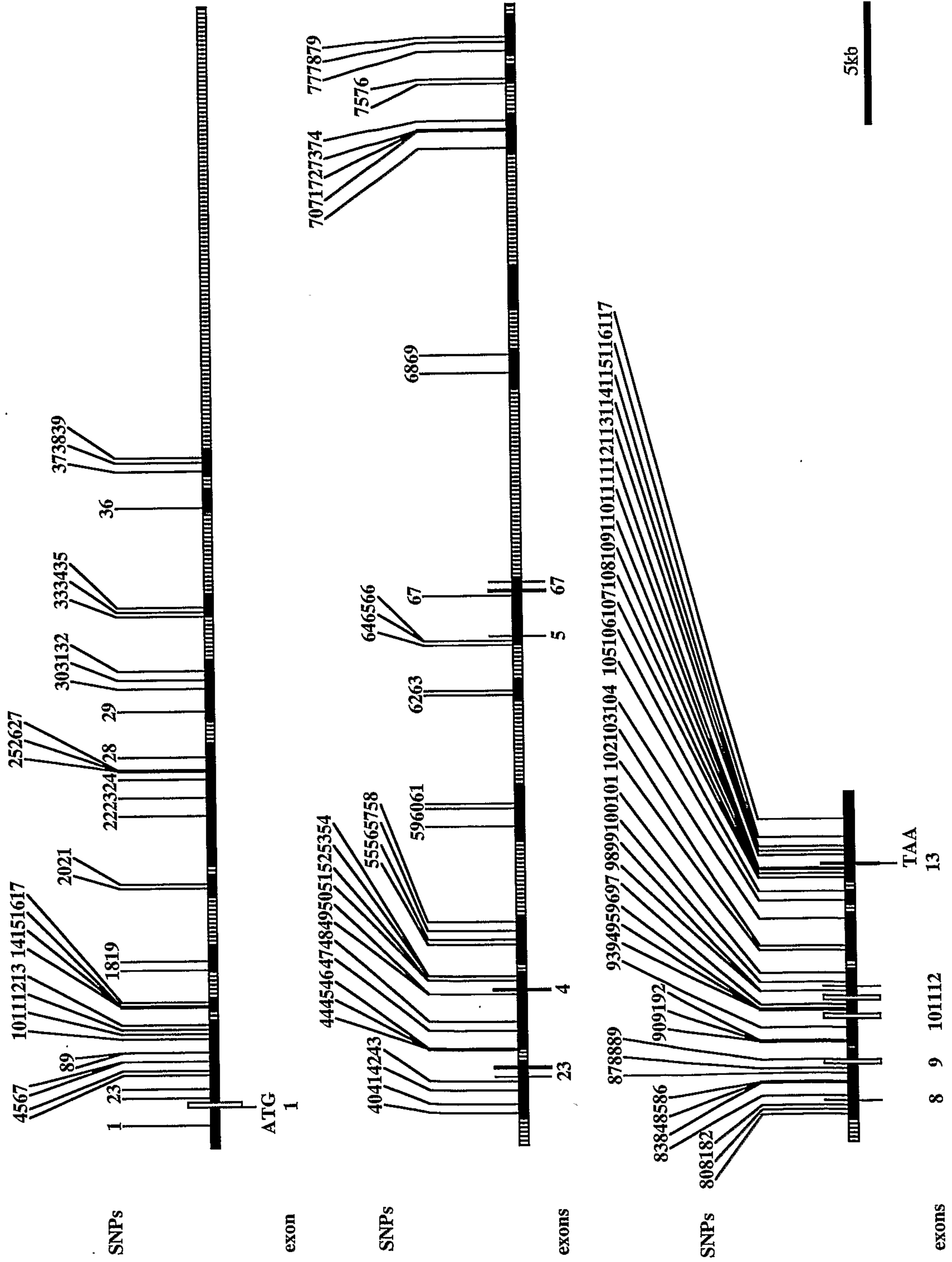


FIGURE 139

Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)

ACCESSION AC015712

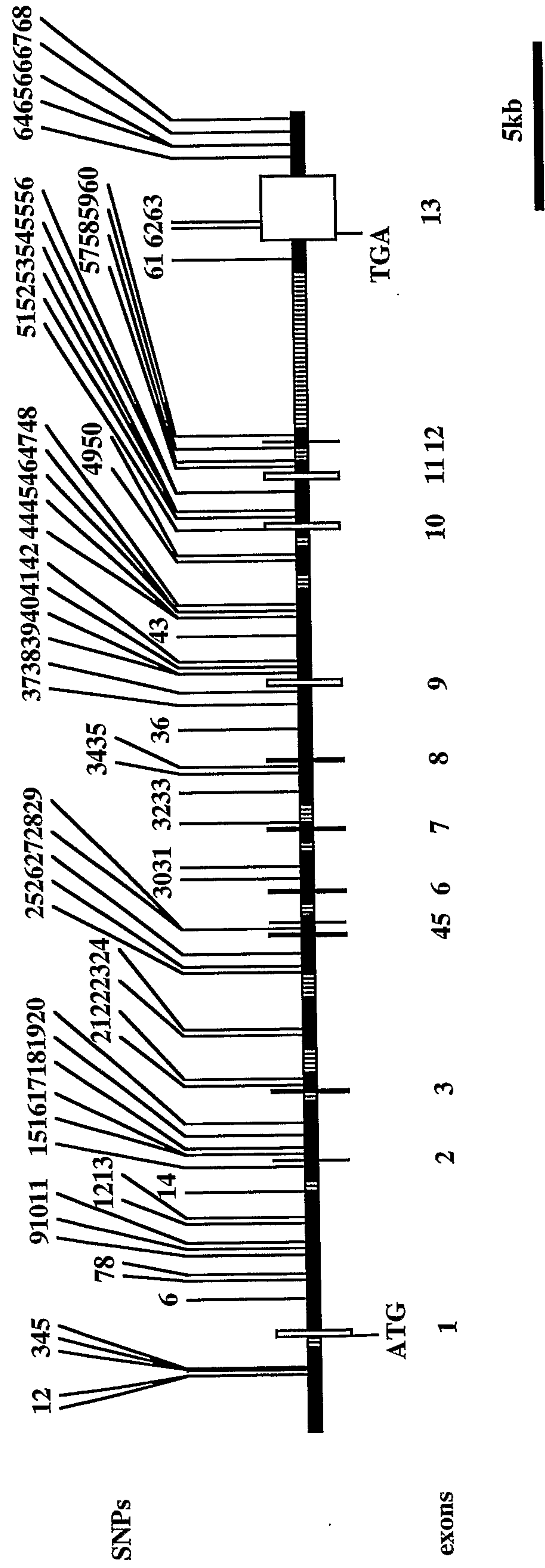


FIGURE 140

Formyltetrahydrofolate dehydrogenase (FTHFD /ALDH1L1)

ACCESSION AC079848

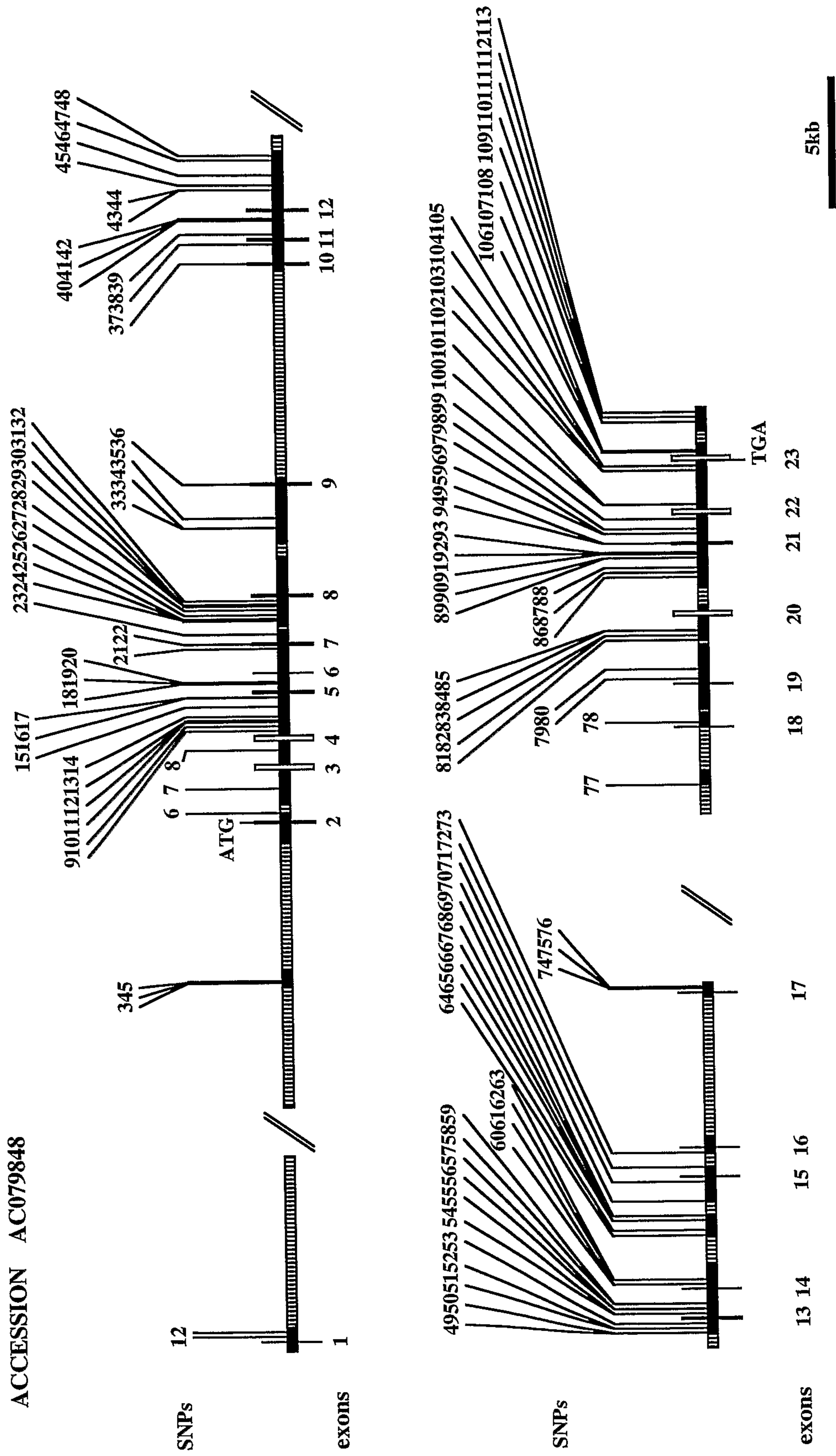
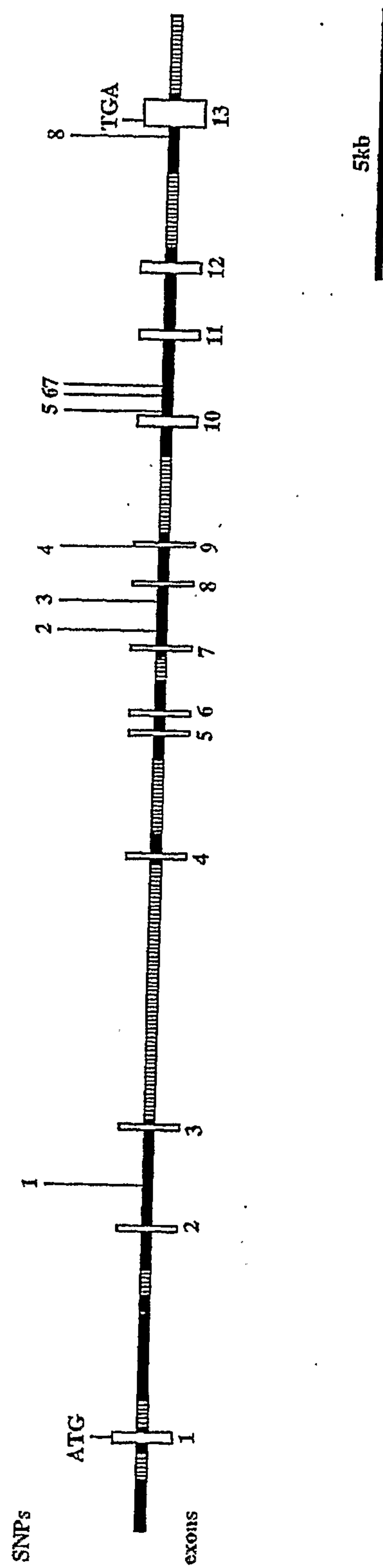


FIGURE 141



Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)

ACCESSION AF280107

FIGURE 142

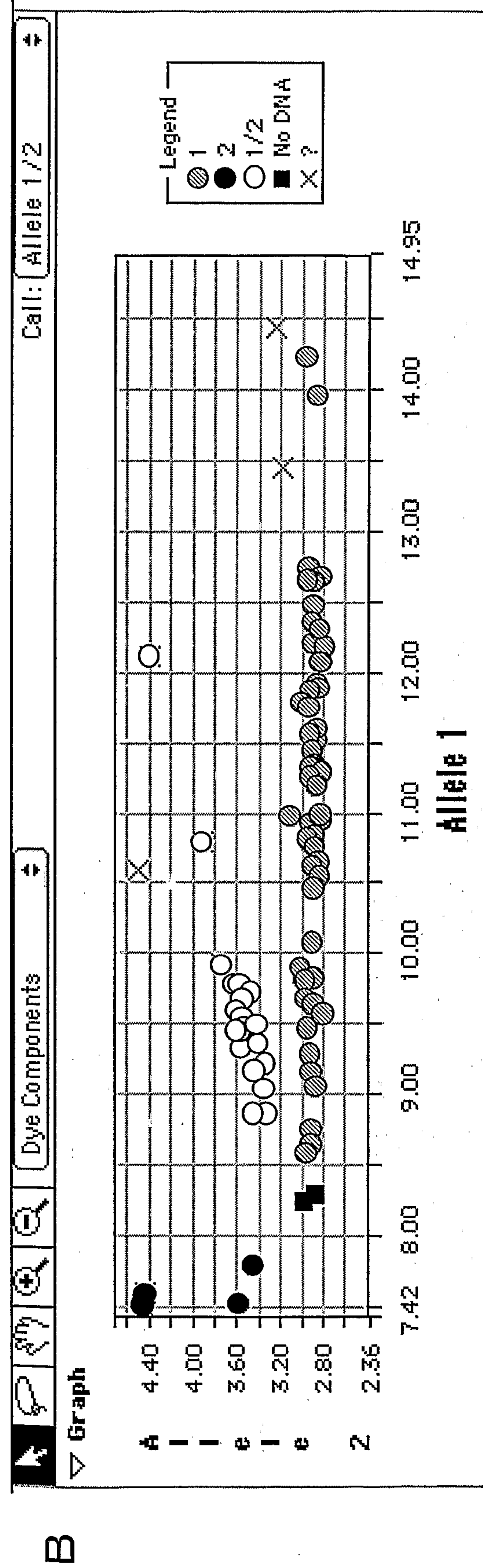
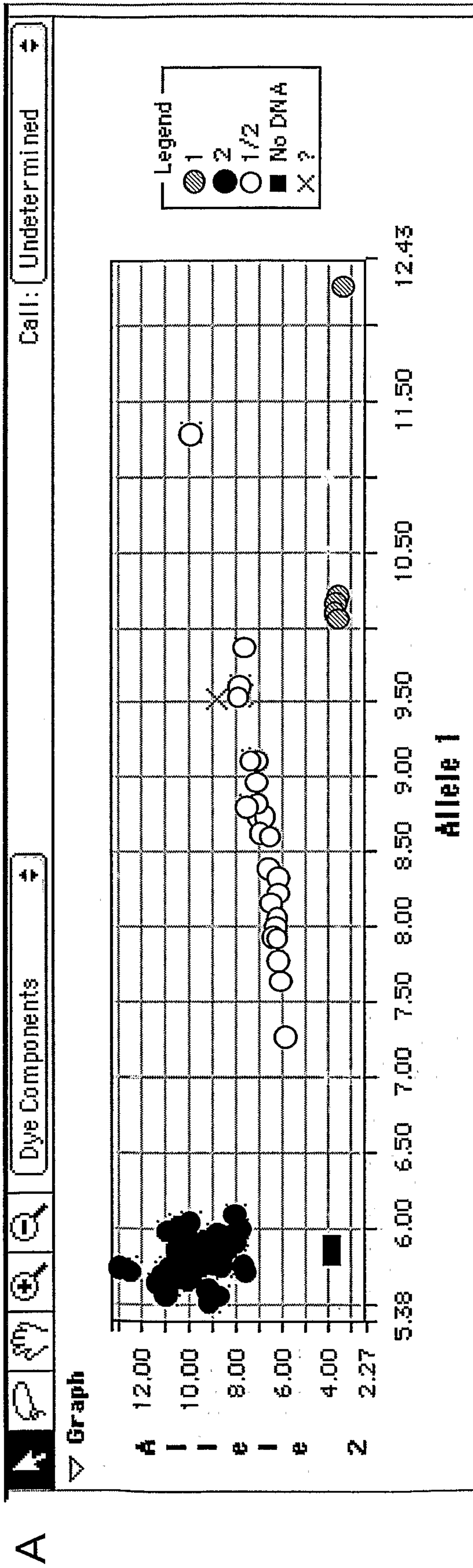


FIGURE 143

NO	GENE	LONG_GENE_NAME	CHROM.	REF. MRNA	L-LINK	OMIM_ID	EXONS	NO GENE
1	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	1
2	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	2
3	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	3
4	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	4
5	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	5
6	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	6
7	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	7
8	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	8
9	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	9
10	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	10
11	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	11
12	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	12
13	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	13
14	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	1
15	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	2
16	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	3
17	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	4
18	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	5
19	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	6
20	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	7
21	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	8
22	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	9
23	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	10
24	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	11
25	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	12
26	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	13
27	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	14
28	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	15
29	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	16
30	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	17
31	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	18
32	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	19
33	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	20
34	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	21
35	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	22
36	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	23

37	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	24
38	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	25
39	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	26
40	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	27
41	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	28
42	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	29
43	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	30
44	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	31
45	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	32
47	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	1
48	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	2
49	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	3
50	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	4
51	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	5
52	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	6
53	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	7
54	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	8
55	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	9
56	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	10
57	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	11
58	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	12
59	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	13
60	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	14
61	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	15
62	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	16
63	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	17
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67	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	3
68	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	4
69	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	5
70	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	6
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74	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	10
75	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	11
76	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	12

77 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	13
78 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	14
79 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	15
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82 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	18
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84 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	20
85 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	21
86 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	22
87 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	23
88 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	24
89 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	25
90 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	26
91 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	27
92 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	28
93 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	29
94 EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	30
95 GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	1
96 GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	2
97 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	1
98 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	2
99 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	3
100 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	4
101 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	5
102 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	6
103 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	7
104 NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	8
105 PNMT	phenylethanolamine N-methyltransferase	chr17	NM_002686	5409	171190	3	1
106 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	1
107 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	2
108 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	3
109 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	4
110 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	5
111 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	6
112 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	7
113 PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	8

114	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	9
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117	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	12
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120	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	15
121	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	16
122	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	17
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125	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	20
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146	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	41
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149	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	44
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153	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	48
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155	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	50
156	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	51
157	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	52
158	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	53
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161	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	56
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163	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	58
164	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	59
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166	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	61
167	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	62
168	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	63
169	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	64
170	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	65
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190	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	85
191	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	8
192	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	6
193	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	87
194	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	88
195	GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	1
196	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	1
197	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	2
198	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	3
199	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	4
200	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	5
201	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	6
202	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	7
203	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	8
204	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	9
205	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	10
206	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	1
218	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	13
219	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	14
221	GGT1	gamma-glutamyltransferase 1	chr22	NM_005265	2678	231950	15	
222	DIA4	NAD(P)H menadione oxidoreductase 1,	chr16	NM_000903	1728	125860	6	1
223	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	1
224	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	2
225	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	3
226	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	1
227	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	2
228	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	3
229	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	4
230	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	5
231	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	6
232	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	7
233	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	8
234	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	9
235	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	10
236	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	11

237	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	12
238	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	13
239	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	14
240	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	15
241	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	16
242	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	17
243	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	18
244	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	19
245	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	20
246	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	21
247	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	22
248	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	23
249	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	24
250	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	25
251	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	26
252	NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	27
253	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	1
254	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	2
255	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	3
256	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	4
257	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	5
258	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	6
259	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	7
260	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	8
261	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	9
262	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	10
263	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	11
264	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	12
265	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	13
266	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	14
267	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	15
268	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	16
269	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	17
270	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	18
271	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	19
272	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	20
273	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	21

274	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	22
275	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	23
276	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	24
277	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	25
278	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	1
279	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	2
280	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	3
281	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	4
282	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	5
283	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	6
284	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	7
285	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	8
286	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	9
287	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	10
288	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	11
289	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	12
290	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	13
291	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	14
292	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	15
293	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	1
294	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	2
295	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	3
296	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	4
297	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	5
298	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	6
299	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	7
300	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	8
301	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	9
302	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	10
303	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	11
304	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	12
305	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	13
306	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	14
307	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	15
308	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	16
309	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	17
310	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	18

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311	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	19
312	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	20
313	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	21
314	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	22
315	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	23
316	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	24
317	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	25
318	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	26
319	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	27
320	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	28
321	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	29
322	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	30
323	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	1
324	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	2
325	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	3
326	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	4
327	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	5
328	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	6
329	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	7
330	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	8
331	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	9
332	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	10
333	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	11
334	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	12
335	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	13
336	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	14
337	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	15
338	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	16
339	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	17
340	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	18
341	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	19
342	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	1
343	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	2
344	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	3
345	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	4
346	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	5
347	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	6

348	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	7
349	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	8
350	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	9
351	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	10
352	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	11
353	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	12
354	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	13
355	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	14
356	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	15
357	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	16
358	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	17
359	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	18
360	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	19
361	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	20
362	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	21
363	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	22
364	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	23
365	SULT1A3	sulfotransferase family, cytosolic, 1A,	chr16	NM_003166	6818	600641	9	1
366	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	1
367	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	2
368	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	3
369	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	4
370	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	5
371	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	6
372	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	7
373	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	8
374	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	9
375	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	10
376	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	1
377	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	2
378	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	3
379	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	4
380	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	5
381	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	6
382	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	7
383	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	8
384	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	1

385	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	2
386	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	3
387	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	4
388	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	5
389	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	6
390	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	7
391	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	8
392	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	9
393	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	10
394	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	11
395	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	1
396	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	2
397	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	3
398	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	4
399	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	5
400	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	6
401	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	7
402	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	8
403	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	9
404	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	10
405	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	11
406	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	12
407	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	13
408	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	14
409	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	15
410	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	1
411	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	2
412	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	3
413	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	4
414	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	5
415	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	1
416	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	2
417	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	3
418	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	4
419	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	5
420	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	6
421	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	7

422	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	8
423	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	1
424	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	2
425	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	3
426	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	4
427	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	5
428	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	6
429	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	1
430	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	2
431	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	3
432	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	1
433	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	2
434	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	3
435	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	4
436	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	5
437	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	6
438	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	7
439	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	8
440	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	9
441	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	10
442	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	11
443	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	12
444	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	13
445	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	14
446	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	15
447	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	16
448	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	1
449	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	2
450	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	3
451	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	4
452	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	5
453	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	6
454	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	7
455	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	8
456	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	9
457	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	10
458	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	11

459	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	12
460	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	13
461	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	14
462	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	15
463	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	16
464	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	17
465	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	18
466	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	19
467	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	20
468	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	21
469	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	22
470	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	23
471	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	24
472	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	25
473	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	26
474	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	27
475	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	28
476	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	29
477	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	30
478	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	31
479	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	32
480	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	33
481	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	34
482	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	35
483	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	36
484	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	37
485	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	1
486	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	2
487	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	3
488	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	4
489	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	5
490	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	6
491	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	7
492	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	8
493	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	9
494	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	10
495	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	11

496 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	12
497 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	13
498 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	14
499 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	15
500 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	16
501 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	17
502 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	18
503 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	19
504 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	20
505 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	21
506 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	22
507 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	23
508 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	24
509 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	25
510 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	26
511 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	27
512 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	1
513 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	2
514 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	3
515 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	4
516 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	5
517 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	1
518 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	2
519 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	3
520 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	4
521 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	1
522 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	2
523 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	3
524 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	4
525 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	5
526 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	6
527 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	1
528 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	2
529 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	3
530 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	4
531 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	5
532 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	1

533 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	2
534 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	3
535 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	4
536 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	5
537 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	6
538 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	7
539 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	8
540 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	9
541 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	10
542 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	11
543 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	12
544 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	13
545 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	14
546 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	15
547 HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	1
548 HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	2
549 HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	3
550 HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	4
551 HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	5
552 HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	6
553 L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	1
554 L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	2
555 L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	3
556 L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	4
557 L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	5
558 L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	6
559 AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	1
560 AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	2
561 AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	3
562 AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	4
563 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	1
564 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	2
565 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	3
566 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	4
567 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	5
568 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	6
569 ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	7

570	NAT1	N-acetyltransferase 1	chr8	NM_000662	9	108345	1	1
571	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	1
572	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	2
573	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	3
574	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	4
575	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	5
576	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	6
577	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	7
578	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	8
579	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	9
580	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	10
581	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	11
582	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	12
583	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	13
584	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	14
585	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	15
586	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	16
587	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	17
588	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	18
589	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	19
590	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	20
591	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	1
592	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	2
593	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	3
594	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	4
595	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	5
596	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	6
597	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	7
598	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	8
599	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	1
600	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	2
601	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	3
602	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				1
603	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				2
604	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				3
605	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				4
606	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				5

607	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			6
608	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			7
609	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			8
610	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			9
611	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			10
612	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			11
613	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			12
614	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			13
615	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			14
616	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			15
617	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			16
618	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			17
619	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			18
620	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			19
621	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			20
622	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			21
623	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			22
624	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			23
625	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			24
626	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			25
627	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158			26
628	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
629	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
630	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
631	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
632	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
633	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
634	DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11
635	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
636	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
637	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
638	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
639	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
640	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
641	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
642	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4
643	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4

644	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	10
645	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	11
646	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	12
647	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	13
648	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	14
649	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	15
650	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	16
651	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	17
652	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	18
653	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	19
654	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	20
655	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	21
656	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	22
657	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	23
658	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	24
659	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	25
660	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	26
661	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	27
662	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	28
663	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	29
664	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	30
665	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	31
666	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	32
667	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	33
668	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	34
669	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	35
670	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	36
671	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	1
672	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	1
672	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	2
673	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	1
674	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	4
675	ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	5
676	ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	6
677	ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	1
678	ADH5	class III alcohol dehydrogenase 5 chi subunit	chr4	NM_000671	128	103710	9	2
679	ADH5	class III alcohol dehydrogenase 5 chi subunit	chr4	NM_000671	128	103710	9	

680 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	16
681 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	1
682 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	2
683 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	3
684 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	4
685 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	5
686 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	6
687 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	7
688 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	8
689 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	9
690 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	10
691 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	11
692 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	12
693 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	13
694 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	14
695 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	15
696 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	16
697 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	17
698 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	18
699 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	19
700 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	20
701 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	21
702 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	1
703 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	2
704 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	3
705 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	4
706 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	5
707 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	6
708 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	7
709 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	8
710 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	9
711 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	10
712 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	2
713 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	3
714 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	4
715 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	5
716 GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	1

717	GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	2
718	GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	3
719	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	1
720	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	2
721	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	3
722	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	4
723	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	5
724	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	6
725	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	7
726	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	8
727	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	9
728	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	1
729	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	2
730	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	3
731	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	4
732	GSTT1	glutathione S-transferase theta 1	chr22	NM_000853	2952	600436	5	1
733	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	1
734	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	2
735	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	3
736	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	4
737	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	5
738	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	1
739	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	2
740	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	3
741	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	4
742	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	5
743	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	6
744	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	7
745	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	8
746	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	9
747	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	1
748	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	2
749	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	3
750	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	4
751	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	5
752	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	6
753	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	7

754	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	8
755	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	9
756	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	10
757	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	11
758	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	12
759	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	13
760	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	14
761	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	15
762	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	16
763	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	17
764	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	18
765	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	19
766	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	20
767	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	21
768	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	22
769	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	23
770	GSTA1	glutathione S-transferase A1	chr6	None	2938	138359	1	1
771	GSTA1	glutathione S-transferase A1	chr6	None	2938	138359	1	2
772	GSTA1	glutathione S-transferase A1	chr6	None	2938	138359	1	3
773	GSTA1	glutathione S-transferase A1	chr6	None	2938	138359	1	4
774	GSTA1	glutathione S-transferase A1	chr6	None	2938	138359	1	5
775	GSTA1	glutathione S-transferase A1	chr6	None	2938	138359	1	6
776	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	1
777	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	2
778	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	3
779	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	4
780	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	5
781	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	6
782	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	7
783	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	8
784	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	9
785	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	10
786	GSTA4	glutathione S-transferase A4	chr6	NM_001512	2941	605450	7	10
787	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha	chrX	NM_004541	4694	300078	3	1
788	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha	chrX	NM_004541	4694	300078	3	2
789	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha	chrX	NM_004541	4694	300078	3	3
790	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha	chrX	NM_004541	4694	300078	3	4

791	NDUFA1	NADH dehydrogenase (ubiquinone)	1	alpha	chrX	NM_004541	4694	300078	3	5
792	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	1
793	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	2
794	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	3
795	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	4
796	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	5
797	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	6
798	NDUFA2	NADH dehydrogenase (ubiquinone)	1	alpha	chr5	NM_002488	4695	602137	3	6
799	NDUFA3	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_004542	4696	603832	4	1
800	NDUFA3	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_004542	4696	603832	4	2
801	NDUFA3	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_004542	4696	603832	4	3
802	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	1
803	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	2
804	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	3
805	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	4
806	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	5
807	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	5
808	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	6
809	NDUFA5	NADH dehydrogenase (ubiquinone)	1	alpha	chr7	NM_005000	4698	601677	5	7
810	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	1
811	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	2
812	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	3
813	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	4
814	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	5
815	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	6
816	NDUFA6	NADH dehydrogenase (ubiquinone)	1	alpha	chr22	NM_002490	4700	602138	3	6
817	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	1
818	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	2
819	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	3
820	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	4
821	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	5
822	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	6
823	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	7
824	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	8
825	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	9
826	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	10
827	NDUFA7	NADH dehydrogenase (ubiquinone)	1	alpha	chr19	NM_005001	4701	602139	4	11

828	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	12
829	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	12
830	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	13
831	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	14
832	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	1
833	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	2
834	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	3
835	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	4
836	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	5
837	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	6
838	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	7
839	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	8
840	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	9
841	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	10
842	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	11
843	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	12
844	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	12
845	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	13
846	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	13
847	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta	chr16	NM_005003	4706	603836	5	1
848	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta	chr16	NM_005003	4706	603836	5	2
849	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	1
850	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	2
851	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	3
852	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	4
853	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	5
854	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	6
855	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	7
856	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	8
857	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	9
858	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	10
859	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	11
860	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	12
861	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	13
862	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	14
863	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	15
864	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	16

865	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	17
866	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	18
867	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	19
868	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	20
869	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	21
870	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	22
871	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	23
872	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	24
873	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	25
874	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	26
875	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	27
876	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	28
877	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	29
878	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	30
879	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	31
880	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	32
881	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	33
882	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	34
883	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	35
884	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	36
885	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	37
886	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	38
887	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	39
888	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	40
889	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	40
890	NDUFA9	NADH dehydrogenase (ubiquinone)	1	alpha	chr12	NM_005002	4704	603834	11	41
891	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	1
892	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	2
893	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	3
894	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	4
895	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	5
896	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	6
897	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	7
898	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	8
899	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	9
900	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	10
901	NDUFS1	NADH dehydrogenase (ubiquinone)	Fe-S	protein 1	chr2	NM_005006	4719	157655	19	11

902	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	12
903	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	13
904	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	14
905	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	15
906	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	16
907	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	17
908	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	18
909	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	19
910	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	20
911	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	21
912	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	22
913	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	23
914	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	chr11	NM_004551	4722	603846	7	1
915	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	chr11	NM_004551	4722	603846	7	2
916	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	chr11	NM_004551	4722	603846	7	3
917	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	chr11	NM_004551	4722	603846	7	4
918	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	1
919	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	2
920	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	3
921	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	4
922	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	5
923	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	6
924	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	7
925	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	8
926	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	9
927	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	10
928	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	11
929	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	12
930	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	13
931	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	14
932	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	15
933	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	chr5	NM_002495	4724	602694	5	16
934	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	1
935	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	2
936	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	3
937	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	4
938	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	5

939	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	6
940	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	7
941	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	8
942	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	9
943	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	10
944	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	11
945	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	12
946	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	13
947	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	14
948	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	15
949	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	16
950	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	17
951	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	18
952	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	19
953	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	20
954	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	21
956	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	22
957	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	24
958	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	1
959	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	2
960	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	3
961	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	4
962	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	5
963	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	6
964	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	7
965	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	8
966	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	9
967	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	10
968	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	11
969	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	12
970	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	13
971	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	14
972	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	15
973	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	16
974	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	17
975	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	18
976	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	19

977	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	1
978	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	2
979	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	3
980	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	4
981	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	5
982	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	6
983	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	7
984	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	8
985	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	9
986	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	10
987	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	11
988	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	chr11	NM_002496	4728	602141	7	11
989	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta	chr2	NM_002491	4709	603839	3	1
990	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta	chr2	NM_002491	4709	603839	3	2
991	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	1
992	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	2
993	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	3
994	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	4
995	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	5
996	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	6
997	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	7
998	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	8
999	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta	chr3	NM_002492	4711	603841	6	9
1000	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta	chr19	NM_004146	4713	603842	3	1
1001	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta	chr19	NM_004146	4713	603842	3	2
1002	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	1
1003	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	2
1004	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	3
1005	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	4
1006	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	5
1007	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	6
1008	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	7
1009	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	8
1010	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	9
1011	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	10
1012	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	11
1013	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	12

1014	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	13
1015	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	14
1016	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	15
1017	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	16
1018	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	17
1019	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	18
1020	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	19
1021	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	20
1022	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	21
1023	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	22
1024	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	23
1025	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	24
1026	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	25
1027	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	26
1028	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	27
1029	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	28
1030	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	29
1031	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	30
1032	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	31
1033	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	32
1034	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	33
1035	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	34
1036	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	35
1037	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	36
1038	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	37
1039	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	38
1040	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	39
1041	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	40
1042	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	41
1043	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	42
1044	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	43
1045	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	44
1046	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	45
1047	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	46
1048	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	47
1049	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	48
1050	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	49

1051 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	50
1052 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	51
1053 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	52
1054 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	53
1055 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	54
1056 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	55
1057 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	56
1058 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	57
1059 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	58
1060 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	59
1061 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	60
1062 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	61
1063 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	62
1064 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	63
1065 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	64
1066 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	65
1067 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	66
1068 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	67
1069 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	68
1070 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	69
1071 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	70
1072 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	71
1073 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	72
1074 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	73
1075 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	74
1076 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	75
1077 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	76
1078 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	77
1079 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	78
1080 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	79
1081 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	80
1082 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	81
1083 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	82
1084 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	83
1085 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	84
1086 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	85
1087 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	86

1088 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	87
1089 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	88
1090 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	89
1091 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	90
1092 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	91
1093 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	92
1094 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	93
1095 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	94
1096 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	95
1097 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	96
1098 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	97
1099 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	98
1100 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	99
1101 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	100
1102 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	101
1103 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	102
1104 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	103
1105 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	104
1106 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	105
1107 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	106
1108 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	107
1109 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	108
1110 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	109
1111 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	110
1112 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	111
1113 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	112
1114 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	113
1115 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	114
1116 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	115
1117 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	116
1118 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	117
1119 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	118
1120 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	119
1121 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	120
1122 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	121
1123 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	122
1124 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	123

1125 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	124
1126 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	125
1127 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	126
1128 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	127
1129 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	128
1130 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	129
1131 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	130
1132 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	131
1133 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	132
1134 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	133
1135 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	134
1136 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	135
1137 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	136
1138 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	137
1139 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	138
1140 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	139
1141 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	140
1142 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	141
1143 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	142
1144 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	143
1145 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	144
1146 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	145
1147 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	146
1148 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	147
1149 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	148
1150 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	149
1151 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	150
1152 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	151
1153 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	152
1154 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	153
1155 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	154
1156 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	155
1157 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	156
1158 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	157
1159 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	158
1160 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	159
1161 ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	160

1162	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	161
1163	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	162
1164	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	163
1165	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	163
1166	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	164
1167	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	165
1168	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	166
1169	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	167
1170	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	167
1171	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	168
1172	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	168
1173	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	169
1174	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	169
1175	ABCA1	ATP-binding cassette, sub-family A member 1	chr9	NM_005502	19	600046	48	170
1176	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	1
1177	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	2
1178	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	3
1179	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	4
1180	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	5
1181	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	6
1182	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	7
1183	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	8
1184	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	9
1185	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	10
1186	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	11
1187	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	12
1188	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	13
1189	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	14
1190	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	15
1191	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	16
1192	COMT	catechol-O-methyltransferase isoform MB-COMT	chr22	NM_000754	1312	116790	6	17
1193	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	1
1194	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	2
1195	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	3
1196	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	4
1197	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	5
1198	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	6

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1199 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	7
1200 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	8
1201 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	9
1202 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	10
1203 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	11
1204 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	12
1205 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	12
1206 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	13
1207 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	14
1207 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	14
1209 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	15
1210 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	16
1211 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	16
1212 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	17
1213 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	18
1214 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	19
1215 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	20
1216 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	21
1217 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	22
1218 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	23
1219 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	24
1220 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	25
1221 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	26
1222 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	27
1223 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	28
1224 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	29
1225 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	30
1226 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	31
1227 HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	32
1228 GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	3
1229 PNMT	phenylethanolamine N-methyltransferase	chr17	NM_002686	5409	171190	3	2
1230 CYP1A1	cytochrome P450, subfamily I (aromatic	chr15	NM_000499	1543	108330	7	1
1231 CYP1A1	cytochrome P450, subfamily I (aromatic	chr15	NM_000499	1543	108330	7	2
1232 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	1
1233 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	2
1234 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	3
1235 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	4

1236 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	5
1237 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	6
1238 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	1
1239 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	2
1240 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	3
1241 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	4
1242 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	5
1243 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	6
1244 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	7
1245 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	8
1246 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	8
1247 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	9
1248 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	10
1249 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	11
1250 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	11
1251 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	12
1252 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	90
1253 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	91
1254 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	92
1255 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	93
1256 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	94
1257 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	95
1258 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	96
1259 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	97
1260 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	98
1261 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	21
1262 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	22
1263 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	23
1264 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	24
1265 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	25
1266 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	26
1267 NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	27
1268 AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	1
1269 AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	2
1270 AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	3
1271 AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	4
1272 AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	5

1273 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	6
1274 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	7
1275 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	8
1276 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	9
1277 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	10
1278 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	11
1279 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	12
1280 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	13
1281 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	14
1282 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	15
1283 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	16
1284 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	17
1285 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	18
1286 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	19
1287 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	20
1288 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	21
1289 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	22
1290 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	1
1291 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	2
1292 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	3
1293 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	4
1294 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	5
1295 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	6
1296 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	7
1297 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	8
1298 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	9
1299 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	10
1300 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	11
1301 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	12
1302 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	13
1303 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	14
1304 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	15
1305 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	16
1306 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	17
1307 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	18
1308 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	19
1309 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	20

1310 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	21
1311 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	22
1312 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	23
1313 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	24
1314 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	25
1315 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	26
1316 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	27
1317 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	28
1318 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	29
1319 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	30
1320 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	31
1321 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	32
1322 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	33
1323 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	34
1324 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	35
1325 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	36
1326 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	37
1327 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	38
1328 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	39
1329 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	40
1330 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	41
1331 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	8
1332 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	9
1333 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	10
1334 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	11
1335 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	12
1336 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	13
1337 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	14
1338 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	15
1339 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	1
1340 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	2
1341 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	3
1342 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	4
1343 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	5
1344 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	6
1345 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	7
1346 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	8

1347 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	9
1348 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	10
1349 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	11
1350 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	12
1351 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	13
1352 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	14
1353 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	15
1354 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	16
1355 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	17
1356 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	18
1357 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	19
1358 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	20
1359 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	21
1360 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	22
1361 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	23
1362 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	24
1363 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	25
1364 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	26
1365 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	27
1366 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	28
1367 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	29
1368 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	30
1369 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	31
1370 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	32
1371 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	33
1372 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	34
1373 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	35
1374 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	36
1375 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	37
1376 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	38
1377 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	39
1378 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	40
1379 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	41
1380 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	42
1381 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	1
1382 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	2
1383 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	3

1384	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	4
1385	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	5
1386	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	6
1387	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	7
1388	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	8
1389	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	9
1390	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	10
1391	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	11
1392	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	12
1393	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	13
1394	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	14
1395	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	15
1396	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	16
1397	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	17
1398	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	18
1399	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	19
1400	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	20
1401	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	21
1402	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	22
1403	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	23
1404	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	24
1405	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	25
1406	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	26
1407	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	27
1408	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	28
1409	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	29
1410	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	30
1411	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	31
1412	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	32
1413	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	33
1414	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	34
1415	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	35
1416	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	36
1417	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	37
1418	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	37
1419	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	38
1421	TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	1

1422	TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	2
1423	TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	3
1424	TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	4
1425	TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	5
1426	TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	6
1427	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	1
1428	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	2
1429	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	3
1430	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	4
1431	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	5
1432	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	6
1433	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	7
1434	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	8
1435	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	9
1436	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	10
1437	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	10
1438	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	11
1439	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	12
1440	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	13
1441	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	14
1442	ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	15
1443	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	1
1444	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	2
1445	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	3
1446	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	4
1447	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	5
1448	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	6
1449	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	7
1450	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	8
1451	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	9
1452	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	10
1453	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	11
1454	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	12
1455	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	13
1456	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	14
1457	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	14
1458	ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	15

1459 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	16
1460 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	17
1461 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	18
1462 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	19
1463 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	20
1464 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	21
1465 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	22
1466 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	1
1467 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	2
1468 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	3
1469 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	4
1470 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	5
1471 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	6
1472 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	7
1473 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	8
1474 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	9
1475 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	10
1476 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	11
1477 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	12
1478 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	13
1479 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	14
1480 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	15
1481 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	16
1482 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	17
1483 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	1
1484 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	2
1485 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	3
1486 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	4
1487 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	5
1488 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	6
1489 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	7
1490 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	8
1491 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	9
1492 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	10
1493 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	11
1494 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	1
1495 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	1

1496 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	2
1497 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	3
1498 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	4
1499 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	5
1500 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	6
1501 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	7
1502 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	8
1503 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	9
1504 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	10
1505 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	11
1506 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	12
1507 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	13
1508 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	13
1509 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	14
1510 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	15
1511 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	16
1512 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	17
1513 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	18
1514 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	19
1515 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	20
1516 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	21
1517 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	22
1518 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	23
1519 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	24
1520 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	25
1521 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	26
1522 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	27
1523 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	28
1524 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	29
1525 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	30
1526 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	31
1527 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	32
1528 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	33
1529 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	34
1530 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	35
1531 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	36
1532 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	37

1533 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	38
1534 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	39
1535 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	40
1536 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	41
1537 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	42
1538 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	43
1539 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	44
1540 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	45
1541 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	45
1543 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	47
1544 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	48
1545 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	49
1546 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	49
1547 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	50
1548 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	51
1549 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	52
1550 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	53
1551 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	54
1552 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	55
1553 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	56
1554 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	57
1555 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	58
1556 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	58
1557 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	59
1558 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	59
1559 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	59
1560 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	60
1561 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	61
1562 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	62
1563 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	63
1564 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	64
1565 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	65
1566 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	66
1567 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	67
1568 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	68
1569 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	69
1570 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	70

1571 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	71
1572 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	72
1573 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	72
1574 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	73
1575 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	74
1576 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	75
1577 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	76
1578 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	77
1579 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	78
1580 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	1
1581 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	2
1582 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	3
1583 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	4
1584 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	5
1585 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	6
1586 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	7
1587 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	8
1588 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	9
1589 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	10
1590 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	11
1591 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	12
1592 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	13
1593 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	14
1594 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	15
1595 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	16
1596 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	17
1597 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	18
1598 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	19
1600 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	20
1601 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	21
1602 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	22
1603 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	23
1604 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	24
1605 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	25
1606 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	26
1607 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	27
1608 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	28

1609 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	29
1610 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	30
1611 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	31
1612 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	32
1613 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	33
1614 CYP27A1	cytochrome P450, subfamily XXVIA, polypeptide 1	chr2	NM_000784	1593	213700	9	1
1615 CYP27A1	cytochrome P450, subfamily XXVIA, polypeptide 1	chr2	NM_000784	1593	213700	9	2
1616 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	1
1617 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	2
1618 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	3
1619 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	4
1620 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	5
1621 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	6
1622 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	7
1623 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	8
1624 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	9
1625 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	10
1626 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	11
1627 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	12
1628 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	13
1629 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	14
1630 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	15
1631 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	16
1632 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	17
1633 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	18
1634 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	19
1635 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	20
1636 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	21
1637 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	22
1638 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	23
1639 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	23
1640 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	24
1641 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	25
1642 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	26
1643 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	27
1644 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	28
1645 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	29

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1646 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	30
1647 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	31
1648 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	32
1649 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	1
1650 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	2
1651 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	3
1652 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	4
1653 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	5
1654 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	6
1655 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	7
1656 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	8
1657 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	9
1658 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	10
1659 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	11
1660 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	12
1661 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	13
1662 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	14
1663 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	15
1664 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	16
1665 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	17
1666 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	18
1667 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	19
1668 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	20
1669 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	21
1670 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	22
1671 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	23
1672 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	24
1673 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	25
1674 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	26
1675 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	27
1676 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	28
1677 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	29
1678 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	30
1679 CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	chr19	NM_000896	4051	601270	14	31
1680 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	1
1681 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	2
1682 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	3

1683 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	4
1684 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	5
1685 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	6
1686 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	7
1687 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	8
1688 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	9
1689 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	10
1690 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	11
1691 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	11
1692 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	12
1693 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	13
1694 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	14
1695 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	15
1696 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	16
1697 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	17
1698 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	18
1699 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	19
1700 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	20
1701 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	21
1702 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	1
1703 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	2
1704 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	3
1705 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	4
1706 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	5
1707 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	6
1708 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	7
1709 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	8
1710 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	9
1711 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	10
1712 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	11
1713 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	12
1714 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	13
1715 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	14
1716 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	15
1717 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	16
1718 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	17
1719 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	17

1720	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	18
1721	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	19
1722	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	20
1723	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	1
1724	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	2
1725	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	3
1726	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	4
1727	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	5
1728	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	6
1729	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	7
1730	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	8
1731	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	1
1732	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	2
1733	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	3
1734	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	4
1735	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	5
1736	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	6
1737	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	7
1738	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	8
1739	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	9
1740	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	10
1741	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	11
1742	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	12
1743	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	13
1744	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	14
1745	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	15
1746	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	16
1747	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	17
1748	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	18
1749	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	19
1750	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	20
1751	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	21
1752	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	22
1753	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	23
1754	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	24
1755	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	25
1756	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	26

1757 ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	27
1758 ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	28
1759 ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	29
1760 ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	30
1761 ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	31
1762 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	1
1763 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	2
1764 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	3
1765 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	4
1766 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	5
1767 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	6
1768 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	7
1769 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	8
1770 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	9
1771 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	10
1772 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	10
1773 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	11
1774 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	12
1775 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	13
1776 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	14
1777 ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	15
1778 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	1
1779 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	2
1780 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	3
1781 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	4
1782 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	5
1783 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	6
1784 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	7
1785 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	8
1786 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	9
1787 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	10
1788 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	11
1789 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	12
1790 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	13
1791 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	14
1792 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	15
1793 ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	16

1794	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	17
1795	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	18
1796	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	19
1797	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	20
1798	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	21
1799	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	22
1800	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	23
1801	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	24
1802	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	25
1803	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	1
1804	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	2
1805	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	3
1806	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	4
1807	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	5
1808	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	6
1809	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	7
1810	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	8
1811	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	9
1812	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	10
1813	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	11
1814	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	12
1815	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	13
1816	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	14
1817	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	15
1818	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	16
1819	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	17
1820	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	18
1821	ALDH3A2	aldehyde dehydrogenase 3A2	chr17	NM_000382	224	270200	10	19
1823	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	1
1824	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	2
1825	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	3
1826	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	4
1827	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	5
1828	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	6
1829	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	7
1830	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	8
1831	CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	9

1832 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	10
1833 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	11
1834 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	12
1835 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	13
1836 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	14
1837 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	15
1838 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	16
1839 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	17
1840 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	18
1841 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	19
1842 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	20
1843 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	21
1844 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	22
1845 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	23
1846 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	24
1847 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	25
1848 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	26
1849 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	26
1850 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	27
1851 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	28
1852 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	29
1853 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	30
1854 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	31
1855 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	31
1856 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	32
1857 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	33
1858 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	34
1859 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	35
1860 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	36
1861 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	37
1862 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	38
1863 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	39
1864 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	40
1865 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	41
1866 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	42
1867 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	43
1868 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	44

1869 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	45
1870 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	46
1871 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	47
1872 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	48
1873 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	49
1874 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	50
1875 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	51
1876 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	52
1877 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	53
1878 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	54
1879 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	55
1880 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	56
1881 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	57
1882 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	58
1883 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	1
1884 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	2
1885 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	3
1886 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	4
1887 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	5
1888 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	6
1889 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	7
1890 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	8
1891 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	9
1892 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	9
1893 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	10
1894 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	11
1895 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	12
1896 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	13
1897 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	14
1898 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	15
1899 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	16
1900 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	17
1901 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	18
1902 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	19
1903 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	20
1904 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	21
1905 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	22

1906 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	23
1907 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	24
1908 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	25
1909 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	26
1910 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	27
1911 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	28
1912 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	29
1913 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	30
1914 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	31
1915 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	32
1916 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	33
1917 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	34
1918 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	35
1919 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	36
1920 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	37
1921 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	38
1922 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	39
1923 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	40
1924 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	41
1925 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	42
1926 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	43
1927 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	44
1928 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	45
1929 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	46
1930 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	47
1931 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	48
1932 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	49
1933 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	50
1934 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	51
1935 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	52
1936 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	53
1937 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	54
1938 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	55
1939 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	56
1940 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	57
1941 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	58
1942 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	59

1943 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	60
1944 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	61
1945 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	62
1946 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	63
1947 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	64
1948 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	65
1949 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	66
1950 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	67
1951 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	68
1952 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	69
1953 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	70
1954 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	71
1955 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	72
1956 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	73
1957 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	74
1958 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	75
1959 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	76
1960 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	77
1961 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	78
1962 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	79
1963 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	80
1964 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	81
1965 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	82
1966 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	83
1967 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	84
1968 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	85
1969 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	86
1970 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	87
1971 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	88
1972 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	1
1973 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	2
1974 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	3
1975 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	4
1976 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	5
1977 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	6
1978 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	7
1979 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	8

1980 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	9
1981 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	10
1982 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	11
1983 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	12
1984 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	13
1985 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	14
1986 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	15
1987 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	16
1988 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	17
1989 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	18
1990 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	19
1991 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	20
1992 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	21
1993 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	22
1994 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	23
1995 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	23
1996 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	23
1997 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	24
1998 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	25
1999 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	26
2000 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	27
2001 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	28
2002 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	29
2003 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	30
2004 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	31
2005 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	32
2006 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	33
2007 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	34
2008 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	35
2009 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	36
2010 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	37
2011 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	38
2012 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	39
2013 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	40
2014 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	41
2015 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	42
2016 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	43

2017 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	44
2018 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	45
2019 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	46
2020 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	47
2021 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	48
2022 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	1
2023 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	2
2024 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	3
2025 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	4
2026 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	5
2027 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	6
2028 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	7
2029 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	8
2030 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	9
2031 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	10
2032 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	11
2033 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	12
2034 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	13
2035 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	14
2036 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	15
2037 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	16
2038 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	17
2039 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	18
2040 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	19
2041 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	20
2042 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	21
2043 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	21
2044 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	22
2045 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	23
2046 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	24
2047 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	25
2048 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	26
2049 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	27
2050 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	28
2051 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	29
2052 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	30
2053 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	31

2054	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	32
2055	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	33
2056	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	34
2057	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	35
2058	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	36
2059	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	37
2060	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	38
2061	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	39
2062	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	40
2063	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	41
2064	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	42
2065	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	43
2066	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	44
2067	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	45
2068	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	46
2069	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	47
2070	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	48
2071	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	49
2072	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	33
2073	AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	23
2074	AADAC	arylamide deacetylase	chr3	NM_001086	13	600338	6	24
2075	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	1
2076	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	2
2077	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	3
2078	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	4
2079	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	5
2080	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	6
2081	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	7
2082	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	8
2083	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	9
2084	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	10
2085	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	11
2086	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	12
2087	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	13
2088	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	14
2089	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	15
2090	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	16

2091 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	17
2092 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	18
2093 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	19
2094 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	20
2095 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	21
2096 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	22
2097 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	23
2098 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	24
2099 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	25
2100 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	26
2101 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	27
2102 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	28
2103 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	29
2104 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	30
2105 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	31
2106 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	32
2107 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	33
2108 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	34
2109 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	35
2110 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	36
2111 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	37
2112 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	38
2113 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	39
2114 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	40
2115 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	41
2116 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	42
2117 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	43
2118 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	44
2119 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	45
2120 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	46
2121 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	47
2122 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	48
2123 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	49
2124 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	50
2125 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	51
2126 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	52
2127 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	53

2128	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	54
2129	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	55
2130	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	56
2131	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	57
2132	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	58
2133	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	59
2134	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	60
2135	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	61
2136	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	62
2137	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	63
2138	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	64
2139	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	65
2140	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	66
2141	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	67
2142	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	68
2143	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	69
2144	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	70
2145	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	71
2146	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	72
2147	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	73
2148	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	74
2149	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	75
2150	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	76
2151	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	77
2152	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	78
2153	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	79
2154	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	80
2155	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	81
2156	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	82
2157	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	83
2158	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	84
2159	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	85
2160	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	86
2161	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	87
2162	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	88
2163	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	89
2164	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	90

2165 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	91
2166 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	92
2167 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	93
2168 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	94
2169 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	95
2170 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	96
2171 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	97
2172 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	98
2173 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	99
2174 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	100
2175 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	101
2176 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	102
2177 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	103
2178 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	104
2179 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	105
2180 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	106
2181 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	107
2182 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	108
2183 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	109
2184 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	110
2185 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	111
2186 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	112
2187 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	113
2188 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	114
2189 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	115
2190 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	116
2191 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	117
2192 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	118
2193 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	119
2194 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	120
2195 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	121
2196 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	122
2197 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	123
2198 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	124
2199 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	125
2200 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	126
2201 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	127

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2202 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	128
2203 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	129
2204 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	130
2205 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	131
2206 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	132
2207 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	133
2208 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	134
2209 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	135
2210 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	136
2211 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	137
2212 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	138
2213 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	139
2214 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	140
2215 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	141
2216 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	142
2217 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	143
2218 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	144
2219 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	145
2220 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	146
2221 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	147
2222 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	148
2223 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	149
2224 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	150
2225 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	151
2226 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	152
2227 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	153
2228 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	154
2229 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	155
2230 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	156
2231 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	157
2232 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	158
2233 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	159
2234 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	160
2235 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	161
2236 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	162
2237 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	163
2238 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	164

2239	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	165
2240	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	166
2241	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	167
2242	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	168
2243	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	169
2244	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	170
2245	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	171
2246	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	172
2247	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	173
2248	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	174
2249	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	175
2250	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	176
2251	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	176
2252	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	177
2253	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	178
2254	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	179
2255	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	180
2257	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	181
2258	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	182
2259	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	183
2260	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	184
2261	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	185
2262	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	186
2263	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	187
2264	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	187
2265	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	188
2266	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	189
2267	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	190
2268	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	191
2269	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	192
2270	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	193
2271	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	194
2272	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	194
2273	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	195
2274	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	196
2275	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	197
2276	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	198

2277 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	199
2278 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	200
2279 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	201
2280 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	202
2281 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	1
2282 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	2
2283 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	3
2284 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	4
2285 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	5
2286 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	6
2287 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	7
2288 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	8
2289 BCCA7							9
2290 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	10
2291 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	11
2292 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	12
2293 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	13
2294 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	14
2295 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	15
2296 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	16
2297 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	17
2298 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	18
2299 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	19
2300 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	20
2301 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	21
2302 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	22
2303 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	23
2304 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	24
2305 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	25
2306 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	26
2307 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	27
2308 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	28
2309 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	29
2310 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	30
2311 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	31
2312 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	32
2313 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	33

2314 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	34
2315 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	35
2316 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	36
2317 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	37
2318 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	38
2319 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	39
2320 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	40
2321 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	41
2322 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	42
2323 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	43
2324 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	44
2325 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	45
2326 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	46
2327 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	47
2328 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	48
2329 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	49
2330 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	50
2331 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	51
2332 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	52
2333 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	53
2334 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	54
2335 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	55
2336 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	56
2337 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	57
2338 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	58
2339 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	59
2340 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	60
2341 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	61
2342 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	62
2343 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	63
2344 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	64
2345 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	65
2346 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	66
2347 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	67
2348 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	68
2349 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	69
2350 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	70

2351 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	71
2352 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	1
2353 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	2
2354 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	3
2355 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	4
2356 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	5
2357 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	6
2358 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	7
2359 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	8
2360 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	9
2361 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	10
2362 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	11
2363 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	12
2364 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	13
2365 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	14
2366 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	15
2367 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	16
2368 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	17
2369 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	18
2370 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	19
2371 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	20
2372 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	21
2373 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	22
2374 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	23
2375 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	24
2376 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	25
2377 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	26
2378 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	27
2379 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	28
2380 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	29
2381 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	30
2382 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	31
2383 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	32
2384 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	33
2385 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	34
2386 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	35
2387 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	36

2388	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	37
2389	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	38
2390	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	39
2391	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	40
2392	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	41
2393	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	42
2394	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	43
2395	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	44
2396	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	45
2397	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	46
2398	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	47
2399	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	48
2400	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	49
2401	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	50
2402	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	51
2403	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	52
2404	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	53
2405	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	54
2406	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	55
2407	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	56
2408	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	57
2409	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	58
2410	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	59
2411	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	60
2412	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	61
2413	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	62
2414	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	63
2415	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	64
2416	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	65
2417	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	66
2418	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	67
2419	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	68
2420	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	69
2421	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	70
2422	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	71
2423	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	72
2424	ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	73

2425 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	74
2426 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	75
2427 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	76
2428 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	77
2429 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	78
2430 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	79
2431 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	1
2432 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	2
2433 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	3
2434 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	4
2435 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	5
2436 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	6
2437 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	7
2438 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	8
2439 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	9
2440 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	10
2441 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	11
2442 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	12
2443 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	13
2444 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	14
2445 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	15
2446 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	16
2447 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	17
2448 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	18
2449 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	19
2450 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	20
2451 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	21
2452 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	22
2453 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	23
2454 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	24
2455 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	25
2456 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	26
2457 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	27
2458 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	28
2459 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	29
2460 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	30
2461 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	31

2462	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	32
2463	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	33
2464	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	34
2465	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	35
2466	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	36
2467	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	37
2468	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	38
2469	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	39
2470	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	40
2471	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	41
2472	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	42
2473	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	43
2474	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	44
2475	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	45
2476	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	46
2477	ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	47
2478	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	1
2479	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	2
2480	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	3
2481	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	4
2482	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	5
2483	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	6
2484	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	7
2485	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	8
2486	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	9
2487	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	10
2488	ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	11
2489	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	1
2490	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	2
2491	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	3
2492	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	4
2493	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	5
2494	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	6
2495	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	7
2496	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	8
2497	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	9
2498	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	10

2499	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	11
2500	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	11
2501	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	12
2502	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	13
2503	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	14
2504	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	15
2505	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	16
2506	ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	17
2507	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	1
2508	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	2
2509	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	3
2510	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	4
2511	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	5
2512	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	6
2513	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	7
2514	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	8
2515	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	9
2516	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	10
2517	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	11
2518	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	12
2519	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	13
2520	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	14
2521	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	15
2522	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	16
2523	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	17
2524	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	18
2525	CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	19
2526	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	1
2527	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	2
2528	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	3
2529	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	4
2530	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	5
2531	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	6
2532	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	7
2533	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	8
2534	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	9
2535	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	10

2536	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	11
2537	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	12
2538	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	13
2539	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	14
2540	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	15
2541	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	16
2542	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	17
2543	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	18
2544	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	19
2545	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	20
2546	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	21
2547	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	22
2548	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	23
2549	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	24
2550	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	25
2551	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	26
2552	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	27
2553	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	28
2554	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	29
2555	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	30
2556	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	31
2557	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	32
2558	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	33
2559	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	34
2560	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	35
2561	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	36
2562	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	37
2563	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	38
2564	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	39
2565	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	40
2566	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	41
2567	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	42
2568	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	43
2569	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	44
2570	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	45
2571	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	46
2572	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	47

2573	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	48
2574	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	49
2575	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	50
2576	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	51
2577	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	52
2578	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	53
2579	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	54
2580	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	55
2581	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	56
2582	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	57
2583	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	58
2584	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	59
2585	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	60
2586	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	61
2587	CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	62
2588	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	1
2589	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	2
2590	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	3
2591	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	4
2592	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	5
2593	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	6
2594	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	7
2595	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	chr11	NM_007103	4723	161015	10	8
2596	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	1
2597	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	2
2598	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	3
2599	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	4
2600	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	5
2601	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	6
2602	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	7
2603	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	8
2604	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	9
2605	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	10
2606	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	11
2607	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	chr18	NM_021074	4729	600532	8	11
2608	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	1
2609	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	2

2610	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	3
2611	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	4
2612	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	5
2613	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	6
2614	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	7
2615	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	8
2616	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	9
2617	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	10
2618	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	11
2619	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	1
2620	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	2
2621	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	3
2622	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	4
2623	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	5
2624	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	6
2625	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	7
2626	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	8
2627	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	9
2628	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	10
2629	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	11
2630	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	12
2631	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	13
2632	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	14
2633	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	15
2634	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	16
2635	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	17
2636	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	18
2637	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	19
2638	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	20
2639	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	21
2640	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	22
2641	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	23
2642	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	24
2643	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	25
2644	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	26
2645	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	27
2646	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	28

2647	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	29
2648	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	30
2649	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	31
2650	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	32
2651	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	33
2652	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	34
2653	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	35
2654	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	36
2655	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	37
2656	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	37
2657	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	38
2658	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	39
2659	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	40
2660	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	40
2661	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	41
2662	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	42
2663	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	37
2664	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	38
2665	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	39
2666	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	40
2667	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	41
2668	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	42
2669	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	43
2670	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	44
2671	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	45
2672	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	46
2673	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	47
2674	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	48
2675	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	49
2676	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	50
2677	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	51
2678	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	52
2680	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	54
2681	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	55
2682	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	56
2683	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	57
2684	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	58

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2685	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	59
2686	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	60
2687	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	61
2688	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	62
2689	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	63
2690	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	64
2691	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	65
2692	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	66
2693	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	67
2694	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	68
2695	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	69
2696	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	70
2697	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	71
2698	HMG17L1	high-mobility group (nonhistone chromosomal)	chr22	NM_021024	23605	0	2	1
2699	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	1
2700	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	2
2701	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	3
2702	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	4
2703	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	5
2704	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	6
2705	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	7
2706	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	8
2707	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	9
2708	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	10
2709	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	11
2710	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	12
2711	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	13
2712	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	14
2713	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	15
2714	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	16
2715	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	17
2716	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	18
2717	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	19
2718	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	20
2719	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	21
2720	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	22
2721	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	23

2722	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	24
2723	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	25
2724	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	26
2725	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	27
2726	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	28
2727	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	29
2728	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	30
2729	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	31
2730	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	32
2731	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	33
2732	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	34
2733	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	35
2734	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	36
2735	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	37
2736	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	38
2737	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	39
2738	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	40
2739	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	41
2740	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	42
2741	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	43
2742	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	44
2743	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	45
2744	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	46
2745	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	47
2746	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	48
2747	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	49
2748	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	50
2749	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	51
2750	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	52
2751	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	53
2752	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	54
2753	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	55
2754	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	56
2755	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	57
2756	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	58
2757	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	59
2758	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	60

2759	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	61
2760	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	62
2761	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	63
2762	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	64
2763	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	65
2764	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	66
2765	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	1
2766	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	2
2767	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	3
2768	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	4
2769	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	5
2770	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	6
2771	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	7
2772	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	8
2773	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	9
2774	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	10
2775	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	11
2776	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	12
2777	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	13
2778	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	14
2779	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	15
2780	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	16
2781	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	17
2782	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	18
2783	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	19
2784	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	20
2785	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	21
2786	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	22
2787	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	23
2788	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	24
2789	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	25
2790	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	26
2791	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	27
2792	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	28
2793	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	29
2794	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	30
2795	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	31

2796	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	32
2797	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	33
2798	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	34
2799	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	35
2800	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	36
2801	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	37
2802	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	38
2803	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	39
2804	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	40
2805	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	41
2806	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	42
2807	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	43
2808	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	44
2809	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	45
2810	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	46
2811	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	47
2812	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	48
2813	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	49
2814	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	50
2815	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	51
2816	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	1
2817	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	2
2818	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	3
2819	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	4
2820	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	5
2821	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	6
2822	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	7
2823	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	8
2824	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	9
2825	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	10
2826	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	11
2828	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	12
2829	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	14
2830	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	15
2831	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	16
2832	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	17
2833	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	18

2834	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	19
2835	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	20
2836	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	21
2837	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	22
2838	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	23
2839	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	24
2840	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	25
2841	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	26
2842	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	27
2843	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	28
2844	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	29
2845	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	30
2846	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	31
2847	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	32
2848	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	33
2849	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	34
2850	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	35
2851	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	36
2852	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	37
2853	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	38
2854	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	39
2855	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	40
2856	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	41
2857	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	42
2858	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	43
2859	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	44
2860	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	45
2861	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	46
2862	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	47
2863	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	48
2864	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	49
2865	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	50
2866	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	51
2867	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	52
2868	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	53
2869	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	54
2870	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	55

2871	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	56
2872	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	57
2873	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	58
2874	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	59
2875	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	60
2876	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	61
2877	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	62
2878	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	63
2879	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	64
2880	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	65
2881	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	66
2882	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	67
2883	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	68
2884	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	69
2885	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	70
2886	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	71
2887	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	72
2888	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	73
2889	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	74
2890	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	75
2891	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	76
2892	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	77
2893	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	78
2894	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	79
2895	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	80
2896	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	81
2897	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	82
2898	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	83
2899	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	84
2900	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	85
2901	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	86
2902	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	87
2903	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	88
2904	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	89
2905	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	90
2906	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	91
2907	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	92

2908	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	93
2909	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	94
2910	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	95
2911	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	96
2912	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	97
2913	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	98
2914	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	99
2915	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	100
2916	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	101
2917	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	102
2918	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	103
2919	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	104
2920	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	105
2921	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	106
2922	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	107
2923	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	108
2924	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	109
2925	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	110
2926	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	111
2927	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	112
2928	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	113
2929	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	114
2930	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	115
2931	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	116
2932	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	117
2933	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	118
2934	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	1
2935	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	2
2936	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	3
2937	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	4
2938	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	5
2939	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	6
2940	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	7
2941	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	8
2942	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	9
2943	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	10
2944	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	11

2945 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	12
2946 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	13
2947 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	14
2948 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	15
2949 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	16
2950 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	17
2951 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	18
2952 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	19
2953 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	20
2954 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	21
2955 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	22
2956 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	23
2957 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	24
2958 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	25
2959 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	26
2960 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	27
2961 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	28
2962 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	29
2963 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	30
2964 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	31
2965 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	32
2966 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	33
2967 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	34
2968 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	35
2969 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	36
2970 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	37
2971 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	38
2972 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	39
2973 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	40
2974 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	41
2975 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	42
2976 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	43
2977 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	44
2978 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	45
2979 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	46
2980 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	47
2981 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	48

2982 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	49
2983 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	50
2984 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	51
2985 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	52
2986 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	53
2987 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	54
2988 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	55
2989 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	56
2990 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	57
2991 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	58
2992 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	59
2993 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	60
2994 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	61
2995 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	62
2996 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	63
2997 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	64
2998 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	65
2999 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	66
3000 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	67
3001 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	68
3002 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	69
3004 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	71
3005 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	72
3006 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	73
3007 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	74
3008 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	75
3009 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	76
3010 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	78
3011 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	79
3012 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	80
3013 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	81
3014 SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	82
3015 SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	1
3016 SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	2
3017 SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	3
3018 SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	4
3019 SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	5

3020	SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	6
3021	NAT1	N-acetyltransferase 1	chr8	NM_000662	9	108345	1	7
3022	SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	8
3023	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	1
3024	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	2
3025	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	3
3026	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	4
3027	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	5
3028	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	6
3029	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	7
3030	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	1
3031	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	2
3032	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	3
3033	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	4
3034	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	5
3035	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	6
3036	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	7
3037	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	8
3038	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	9
3039	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	10
3040	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	11
3041	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	12
3042	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	13
3043	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	14
3044	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	15
3045	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	1
3046	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	2
3047	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	3
3048	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	4
3049	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	5
3050	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	6
3051	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	7
3052	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	8
3053	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	9
3054	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	10
3055	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	11
3056	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	12

3057	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	13
3058	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	14
3059	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	15
3060	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	16
3061	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	17
3062	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	18
3063	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	19
3064	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	20
3065	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	21
3066	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	21
3067	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	22
3068	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	23
3069	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	24
3070	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	25
3071	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	26
3072	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	27
3073	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	28
3074	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	29
3075	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	30
3076	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	31
3077	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	32
3078	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	33
3079	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	34
3080	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	35
3081	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	36
3082	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	37
3083	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	38
3084	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	39
3085	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	40
3086	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	41
3087	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	42
3088	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	43
3089	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	44
3090	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	45
3091	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	46
3092	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	47
3093	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	48

3094	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	49
3095	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	51
3096	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	50
3097	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	52
3098	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	53
3099	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	54
3100	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	55
3101	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	56
3102	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	57
3103	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	58
3104	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	59
3105	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	60
3106	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	61
3107	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	62
3108	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	63
3109	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	64
3110	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	65
3111	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	66
3112	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	67
3113	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	68
3114	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	69
3115	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	70
3116	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	71
3117	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	72
3118	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	73
3119	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	74
3120	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	74
3121	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	75
3122	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	76
3123	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	77
3124	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	78
3125	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	79
3126	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	80
3127	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	81
3128	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	82
3129	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	83
3130	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	84

3131	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	85
3132	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	86
3133	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	87
3134	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	88
3135	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	89
3136	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	90
3137	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	91
3138	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	92
3139	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	93
3140	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	94
3141	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	95
3142	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	96
3143	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	97
3144	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	98
3145	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	99
3146	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	100
3147	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	101
3148	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	102
3149	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	103
3150	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	104
3151	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	105
3152	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	106
3153	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	107
3154	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	108
3155	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	108
3156	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	109
3157	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	109
3158	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	110
3159	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	111
3160	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	112
3161	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	113
3162	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	114
3163	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	115
3164	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	116
3165	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	117
3166	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	13	1
3167	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	13	2

3168	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	3
3169	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	4
3170	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	4
3171	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	5
3172	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	6
3173	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	7
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3175	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	9
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3179	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	13
3180	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	14
3181	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	15
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3183	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	17
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3187	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	21
3188	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	22
3189	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	23
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3191	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	25
3192	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	26
3193	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	27
3194	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	28
3195	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	29
3196	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	30
3198	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	31
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3200	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	33
3201	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	34
3202	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	35
3203	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	36
3204	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	37
3205	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	38

3206	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	39
3207	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	40
3208	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	41
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3210	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	43
3211	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	44
3212	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	45
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3214	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	47
3215	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	48
3216	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	49
3217	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	50
3218	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	51
3219	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	52
3220	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	53
3221	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	54
3222	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	55
3223	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	56
3224	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	57
3225	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	58
3226	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	59
3227	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	60
3228	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	61
3229	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	62
3230	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	63
3231	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	64
3232	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	65
3233	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	66
3234	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	67
3235	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	68
3236	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	1
3237	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	2
3238	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	3
3239	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	4
3240	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	5
3241	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	6
3242	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	7

3243	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	8
3244	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	9
3245	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	10
3246	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	11
3247	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	12
3248	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	13
3249	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	14
3250	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	15
3251	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	16
3252	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	17
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3254	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	19
3255	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	20
3256	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	21
3257	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	22
3258	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	23
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3260	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	25
3261	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	26
3262	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	27
3263	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	28
3264	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	29
3265	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	30
3266	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	31
3267	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	32
3268	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	33
3269	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	34
3270	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	35
3271	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	36
3272	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	37
3273	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	38
3274	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	38
3275	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	39
3276	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	40
3277	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	41
3278	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	42
3279	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	43

3280	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	44
3281	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	45
3282	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	46
3283	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	47
3284	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	48
3285	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	49
3286	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	50
3287	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	51
3288	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	52
3289	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	53
3290	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	54
3291	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	55
3292	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	56
3293	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	57
3294	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	58
3295	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	59
3296	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	60
3297	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	61
3298	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	62
3299	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	63
3300	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	64
3301	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	65
3302	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	66
3303	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	67
3303	SLC21A8	solute carrier family 21 (organic anion	chr12	NM_019844	28234	605495	14	70
3304	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	68
3305	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	69
3306	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	70
3307	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	70
3308	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	71
3309	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	72
3310	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	73
3311	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	73
3312	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	74
3313	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	75
3314	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	76
3315	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	77

3316 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	78
3317 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	79
3318 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	80
3319 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	81
3320 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	82
3321 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	83
3322 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	84
3323 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	85
3324 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	86
3325 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	87
3326 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	88
3327 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	89
3328 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	90
3329 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	91
3330 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	92
3331 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	93
3332 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	94
3333 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	95
3334 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	96
3335 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	97
3336 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	98
3337 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	99
3338 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	100
3339 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	101
3340 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	102
3341 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	103
3342 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	104
3343 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	105
3344 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	106
3345 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	107
3346 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	108
3347 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	109
3348 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	110
3349 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	111
3350 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	112
3351 FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	113
3352 CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	1

3353	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	2
3354	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	3
3355	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	4
3356	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	4
3357	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	5
3358	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	6
3359	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	7
3360	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	8

Fig.144A **ATP binding cassette, subfamily A, member 1**
(*ABCA1*)

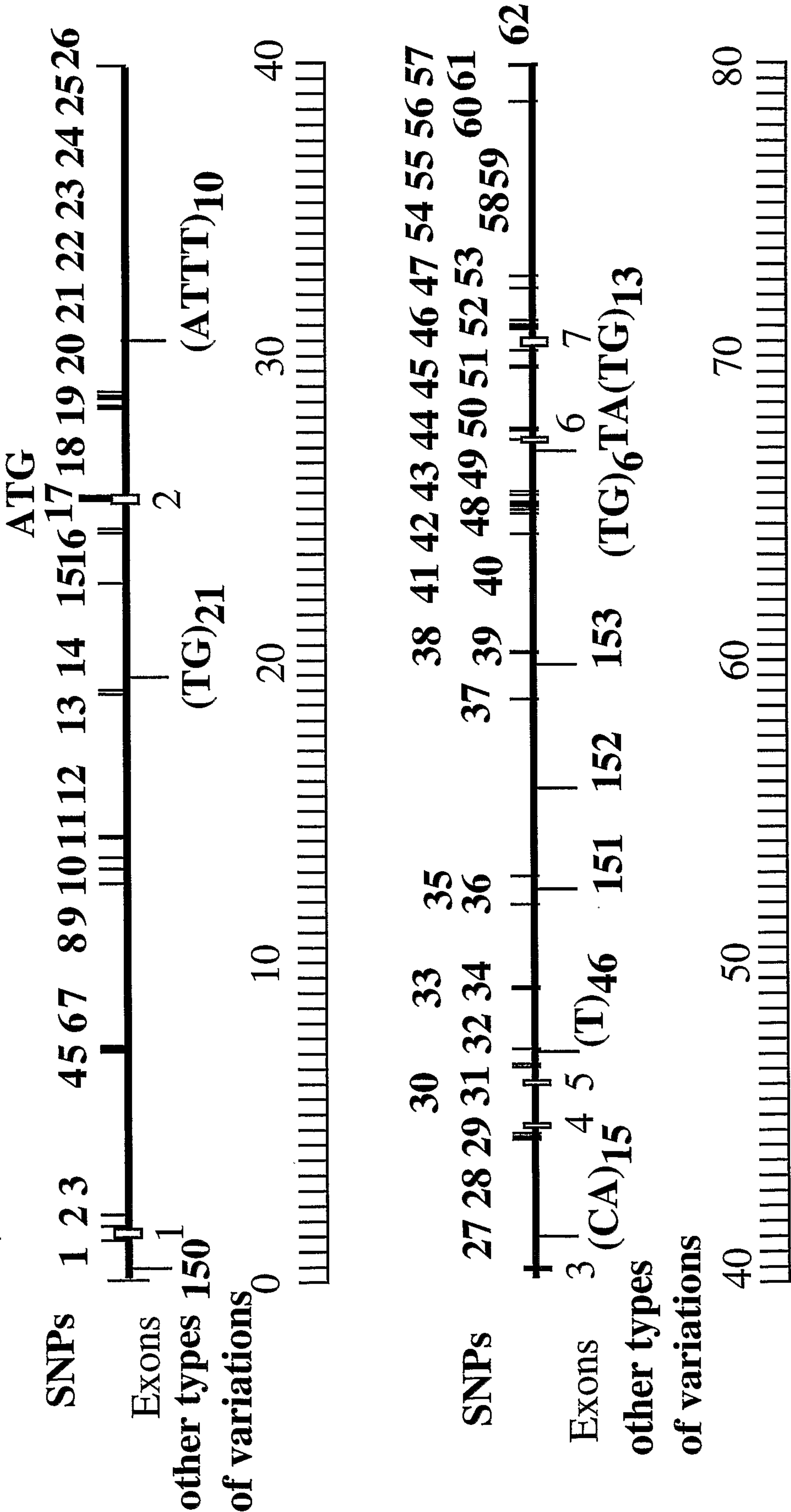


Fig.144B

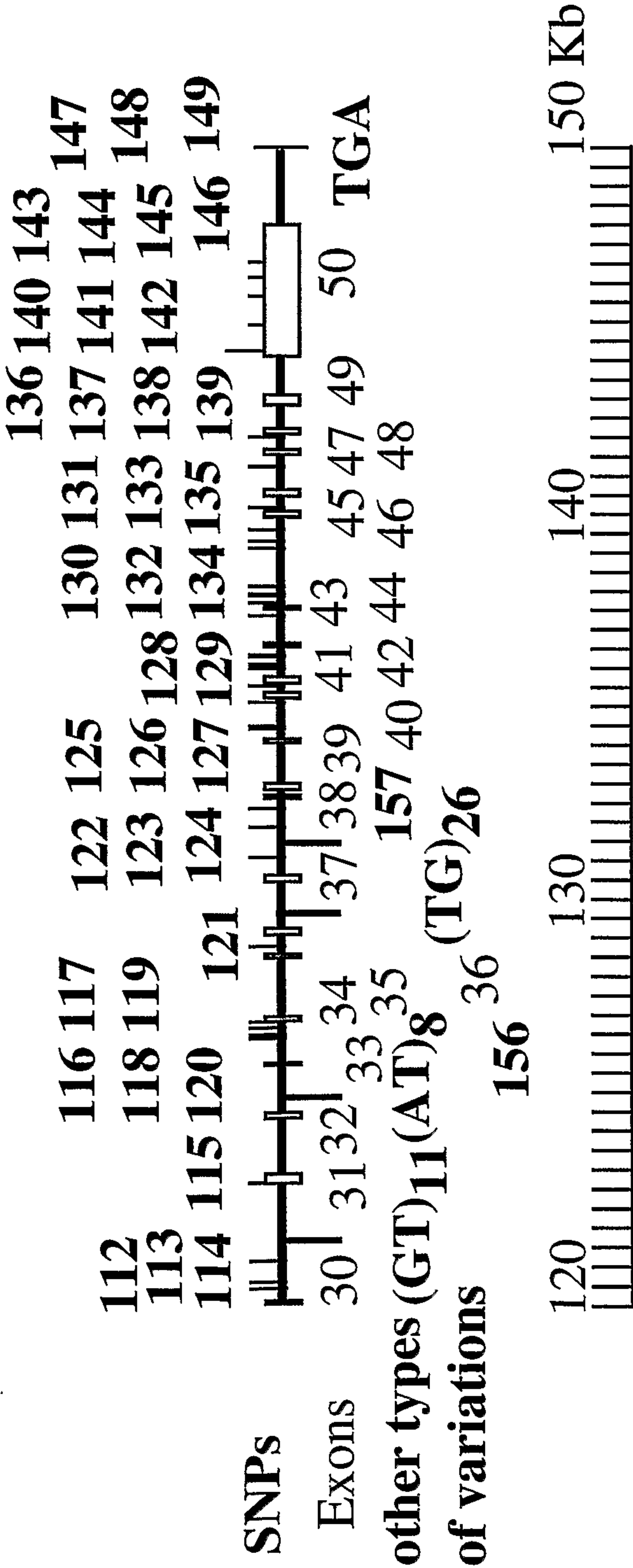
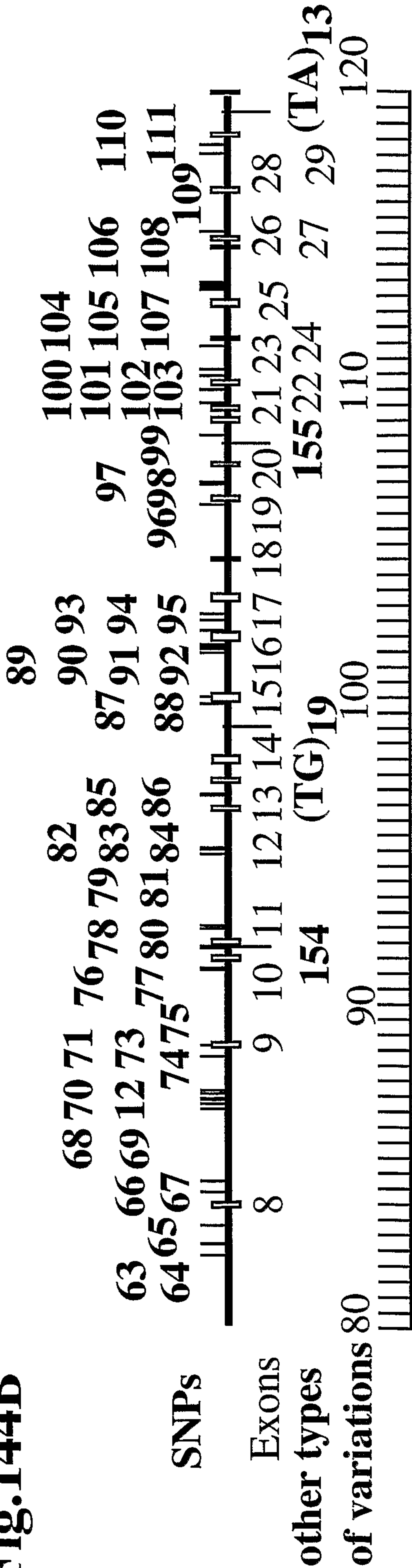


Fig. 145 ATP binding cassette, subfamily A, member 4 (ABCA4)

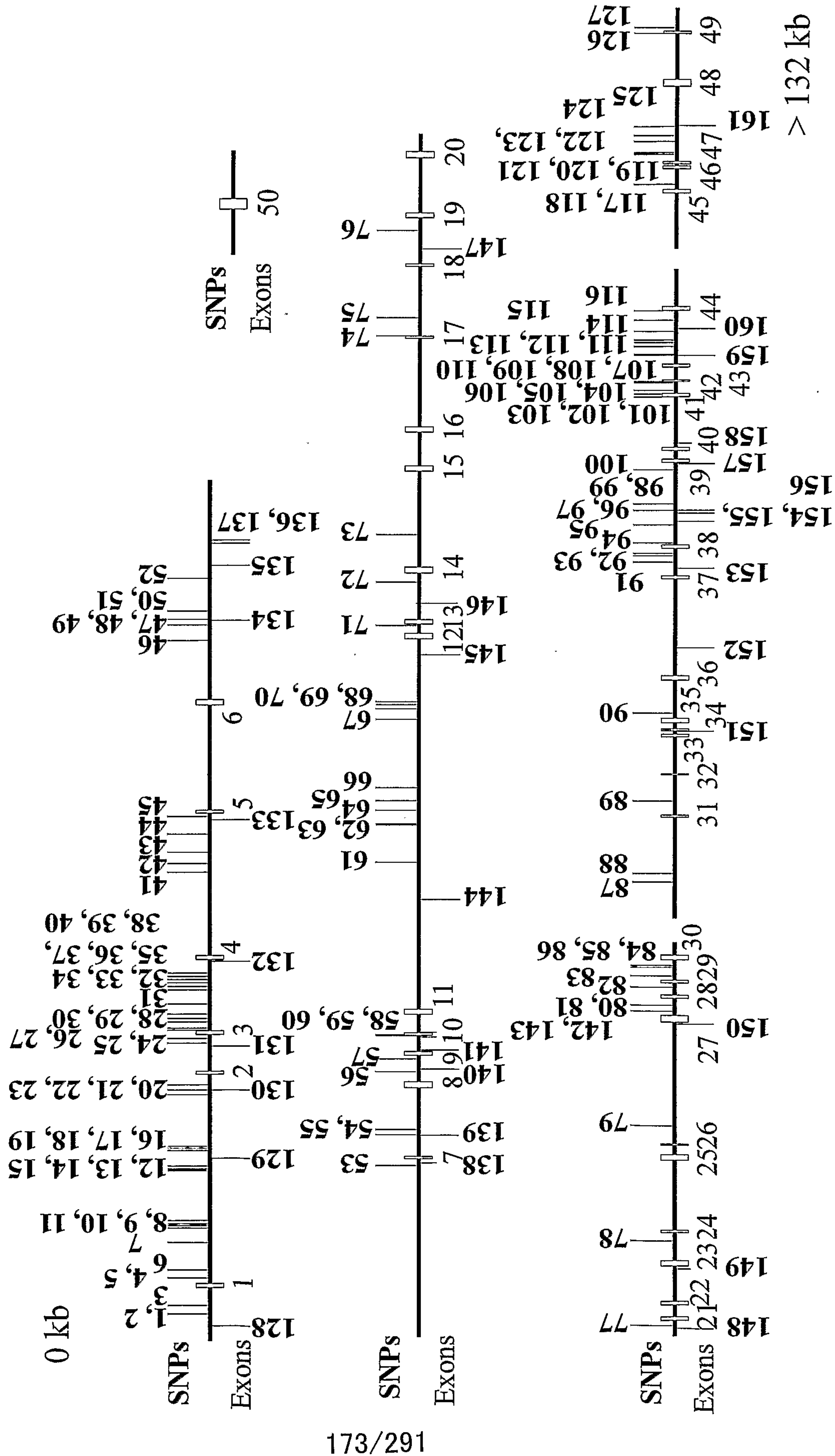


Fig. 146

ATP binding cassette subfamily A, member 7 (ABCA7)

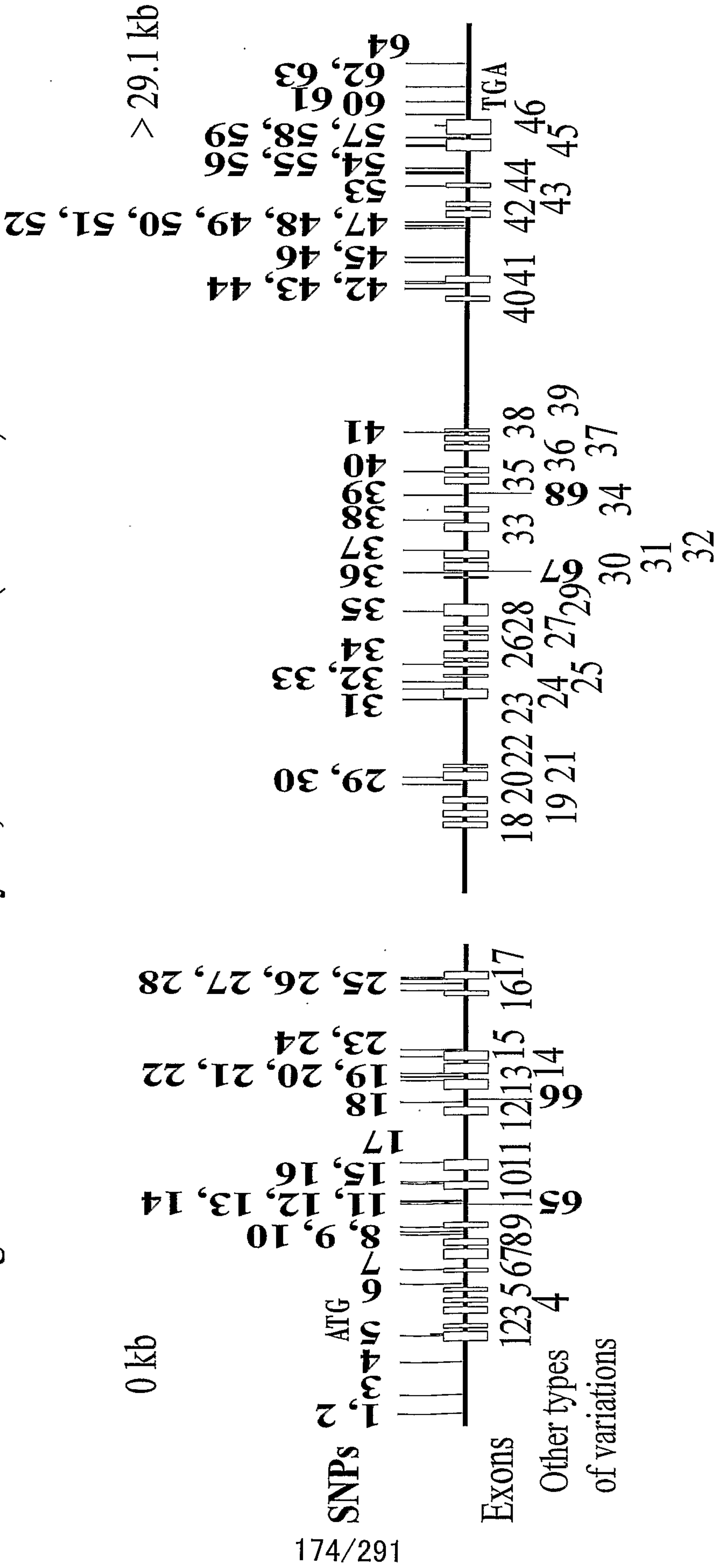
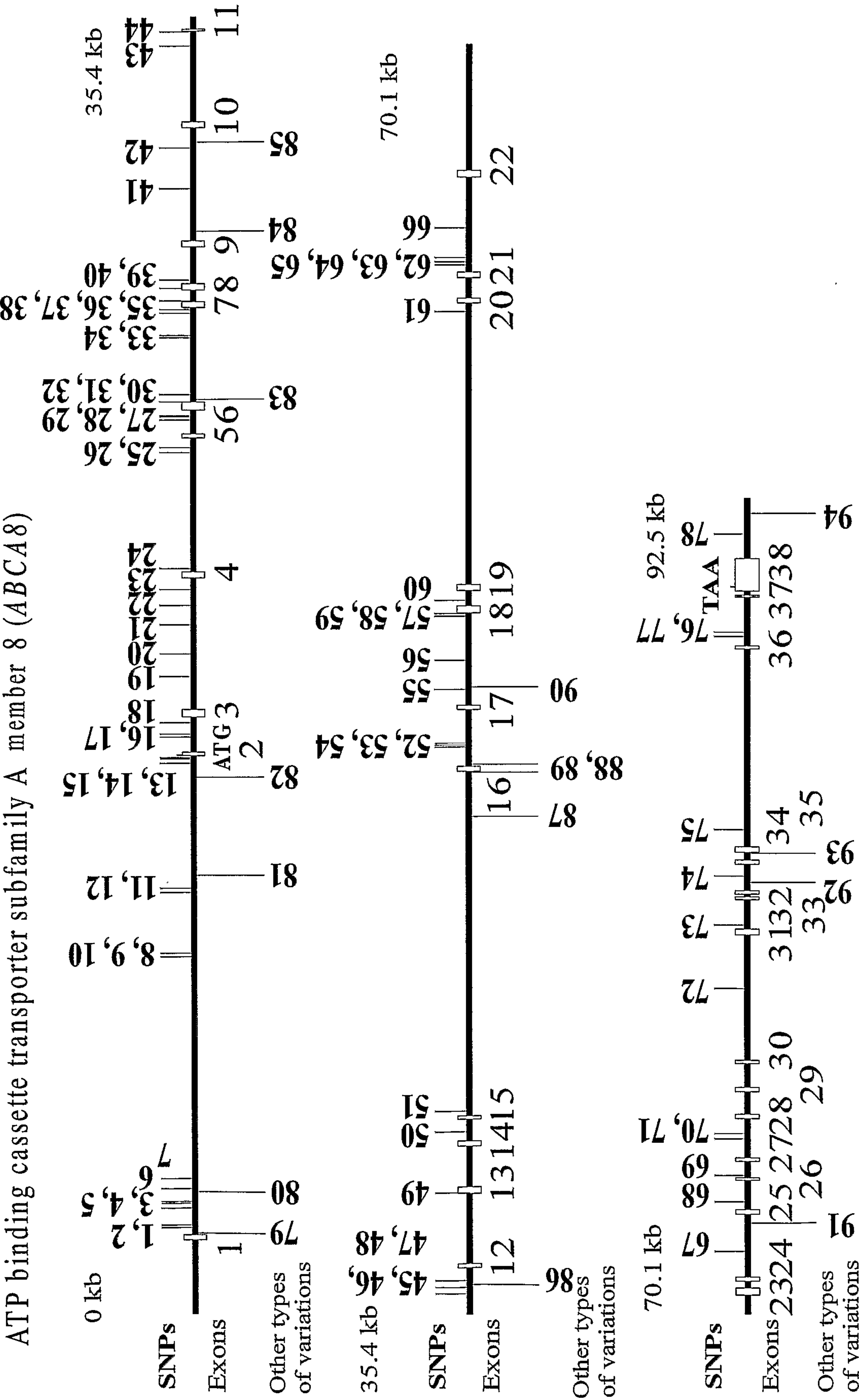


Fig. 147

ATP binding cassette transporter subfamily A member 8 (ABCA8)



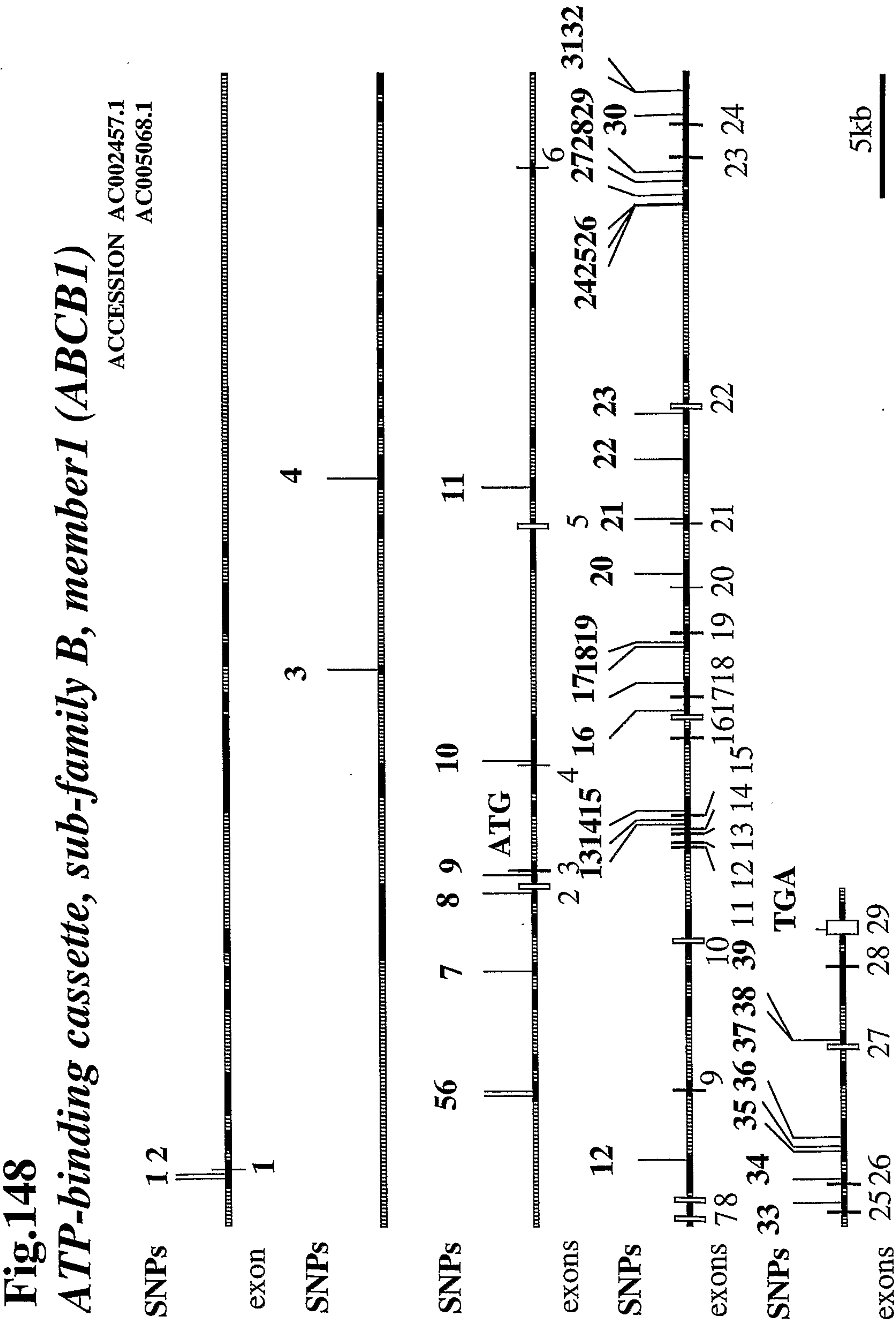


Fig.149 *ATP-binding cassette, sub-family B, member 4 (ABCB4)*

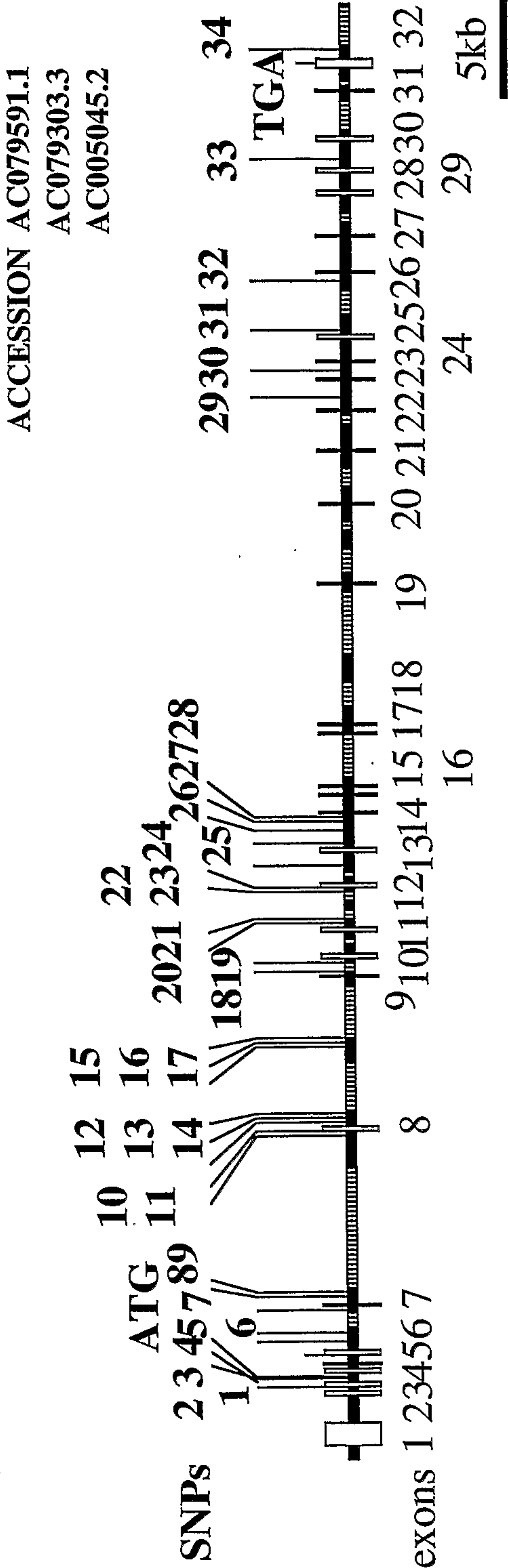


Fig.150 *ATP-binding cassette, sub-family B, member 7 (ABCB7)*

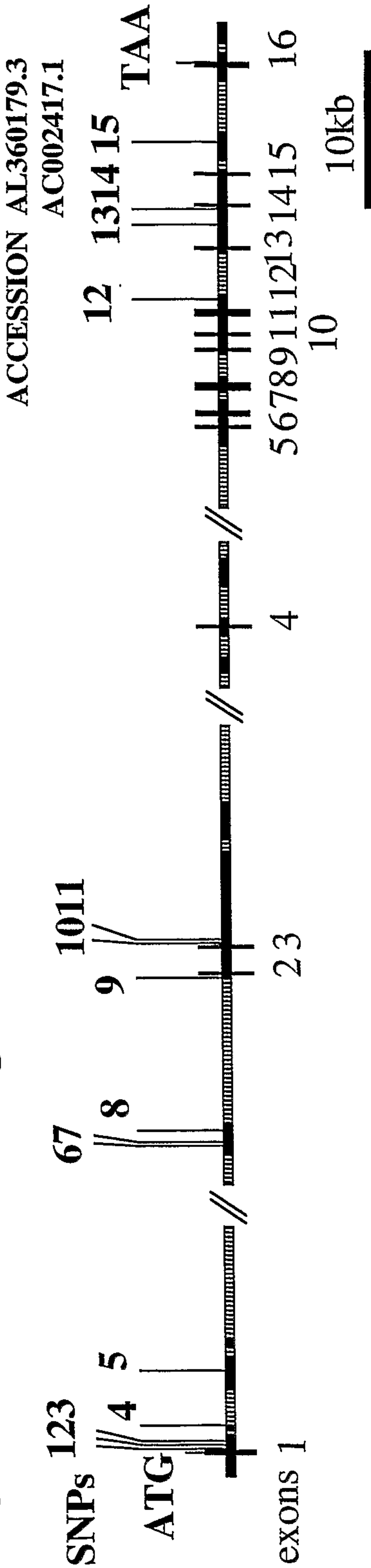


Fig.151
ATP-binding cassette, sub-family B, member 8 (ABCB8)
ACCESSION AC010973.4

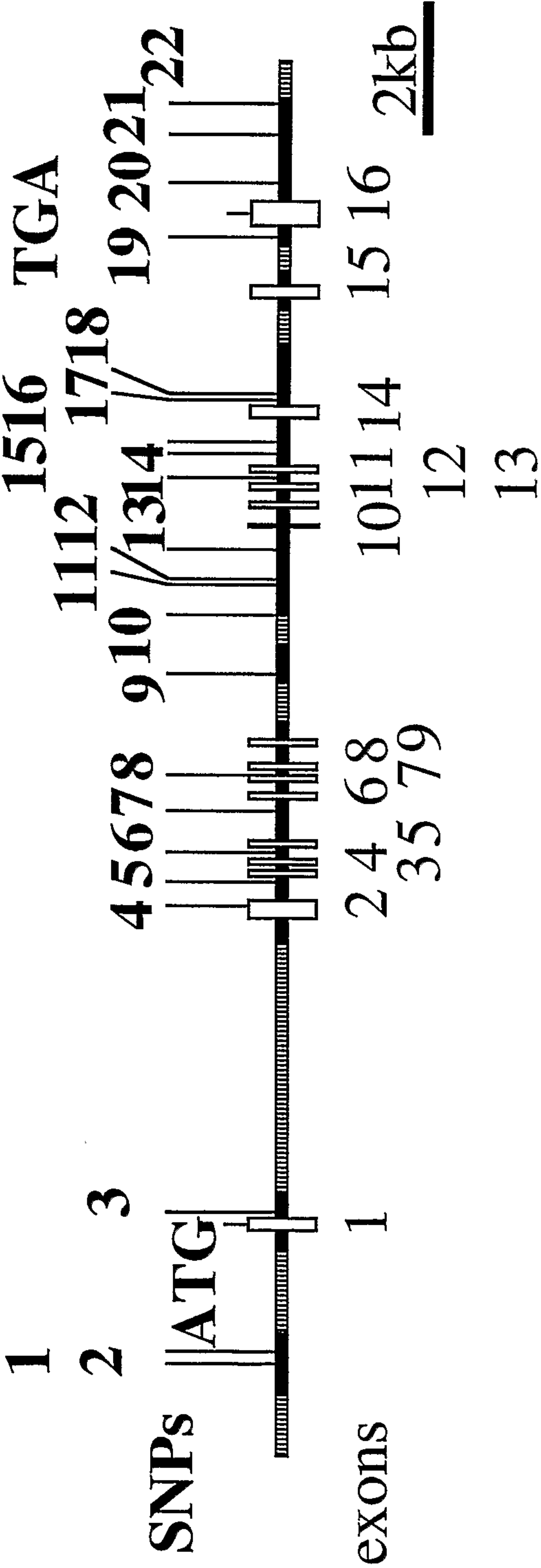


Fig.152

ATP binding cassette, sub-family B, member 9
(*ABCB9*)

ACCESSION AC026362.9
AC073857.10

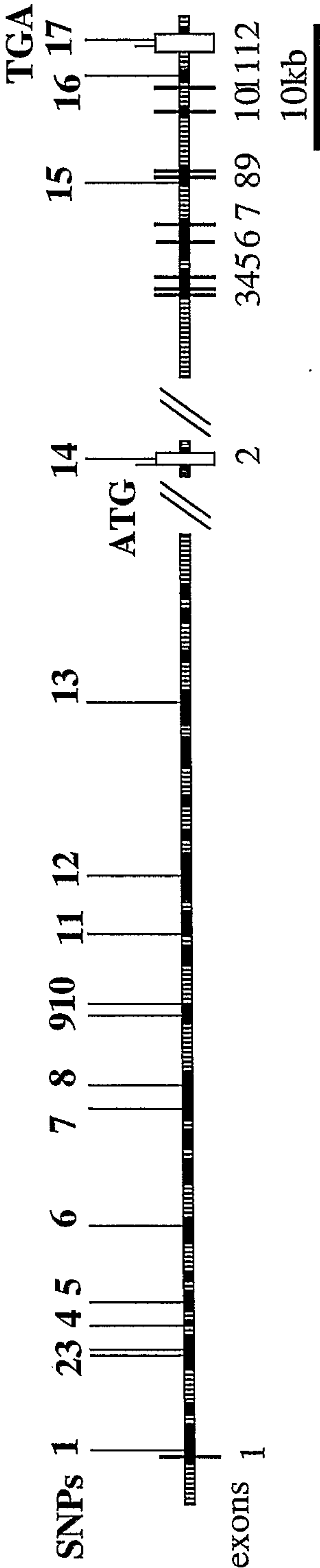
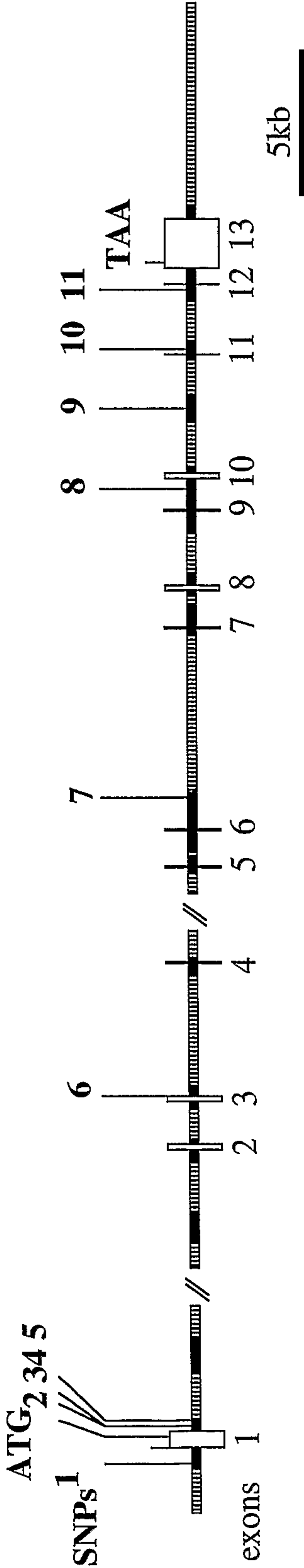


Fig.153

ATP binding cassette, sub-family B, member 10
(*ABCB10*)

ACCESSION AL121990.9



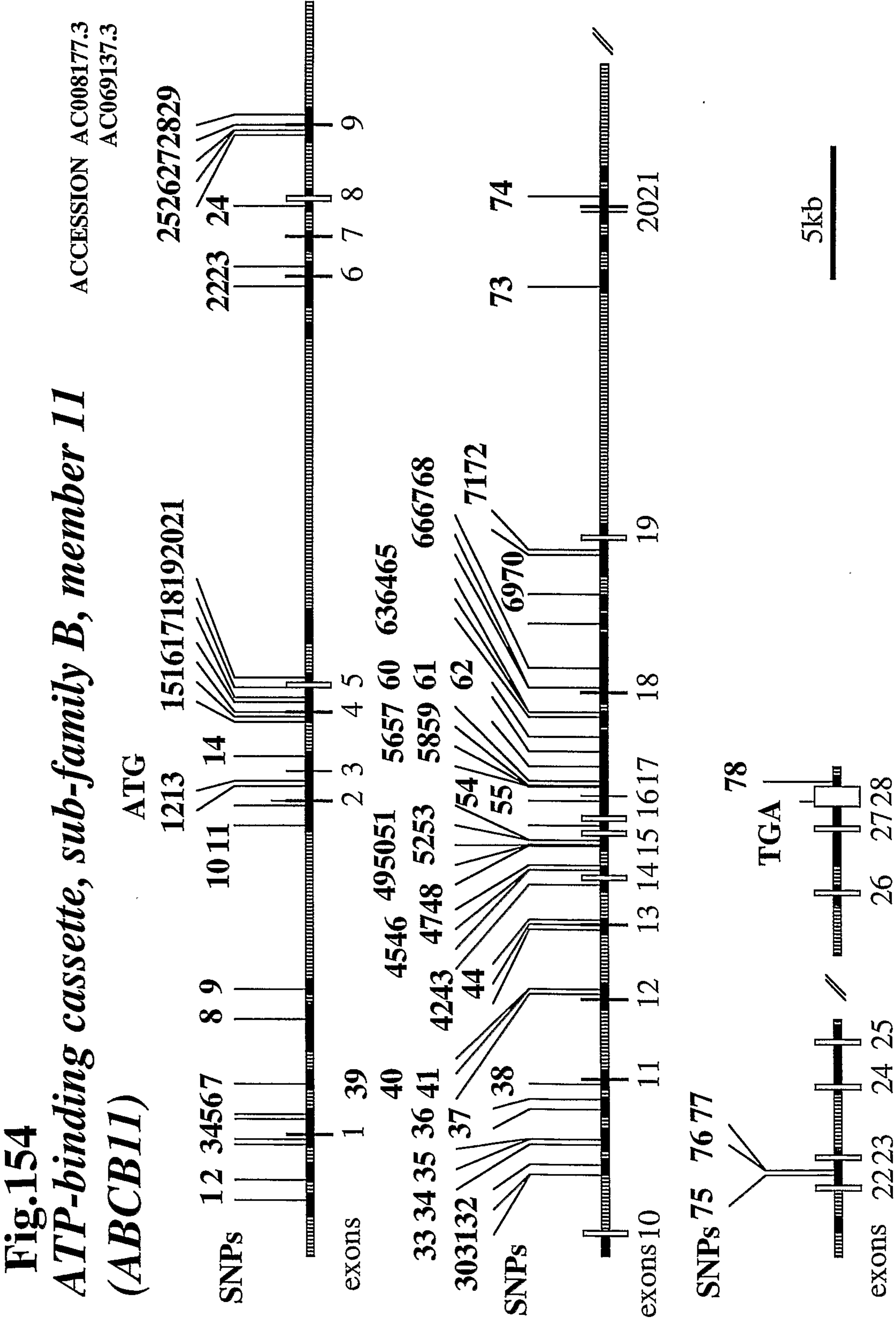


Fig.155
ATP-binding cassette, sub-family C (CFTR/MRP), member 1

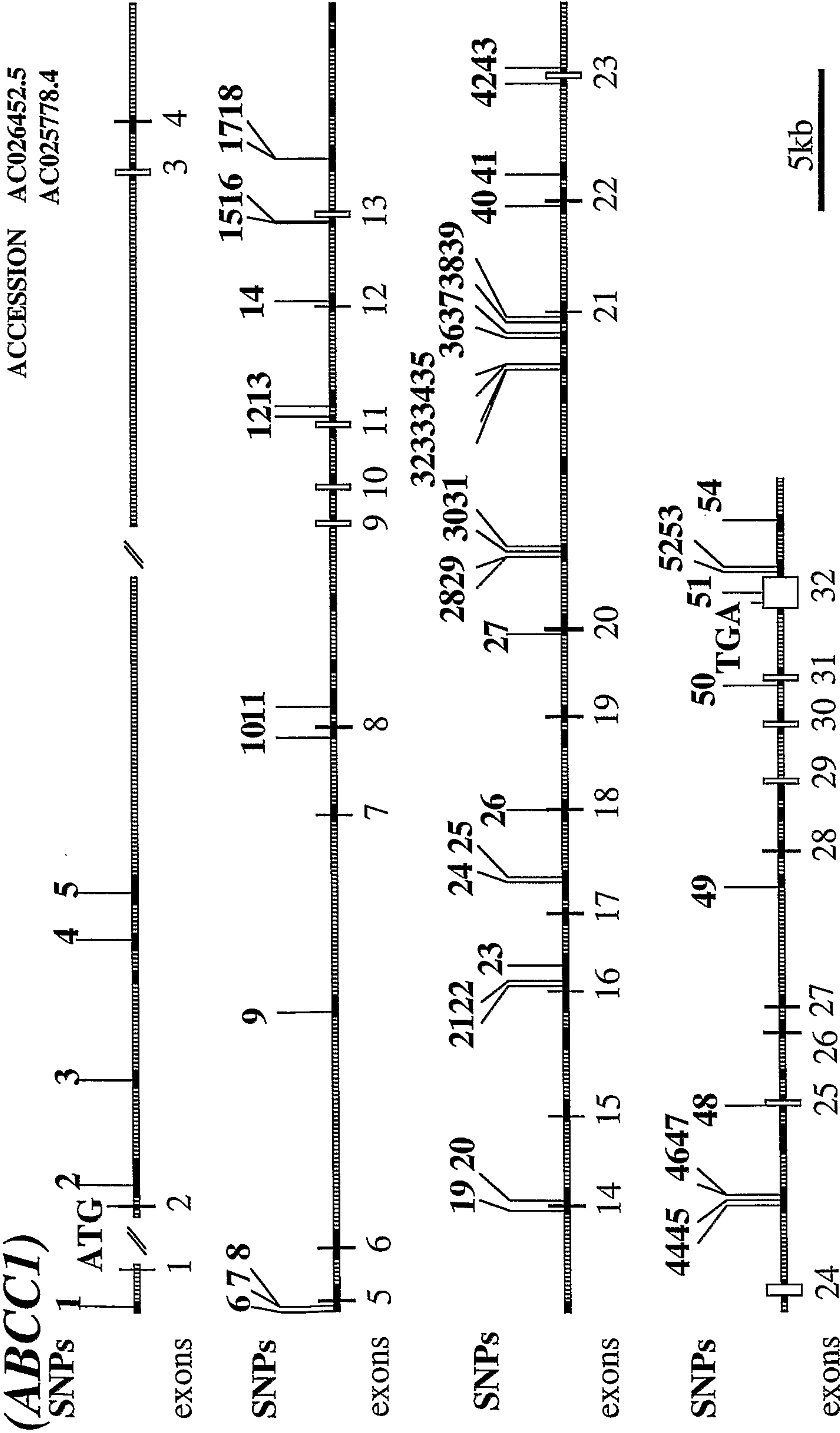


Fig.156
ATP-binding cassette, sub-family C, member2 (ABCC2)

ACCESSION AL392107.4

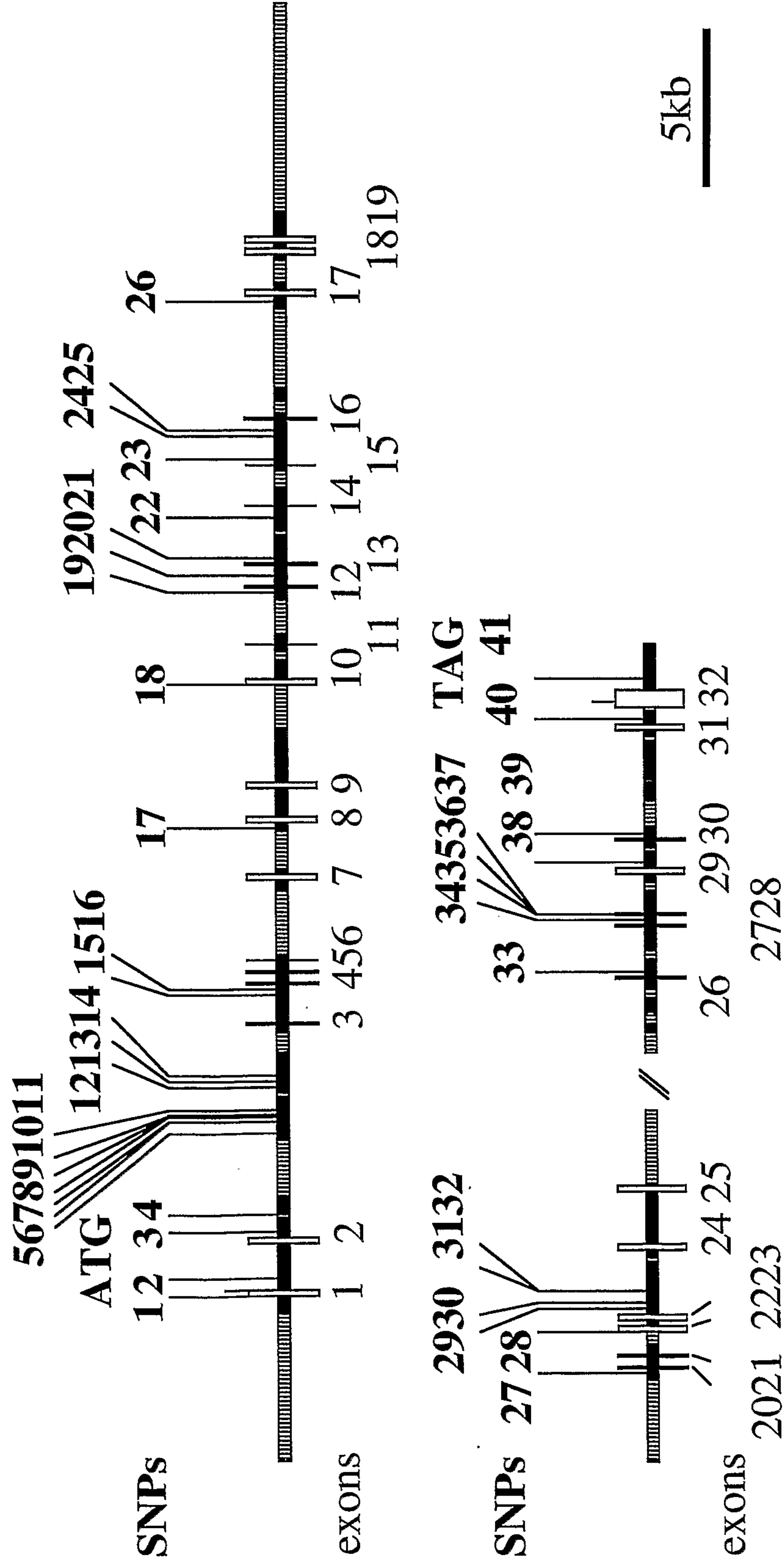


Fig.158A *ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4)*

ACCESSION AL356257.11 AL157818.12 AL139381.12

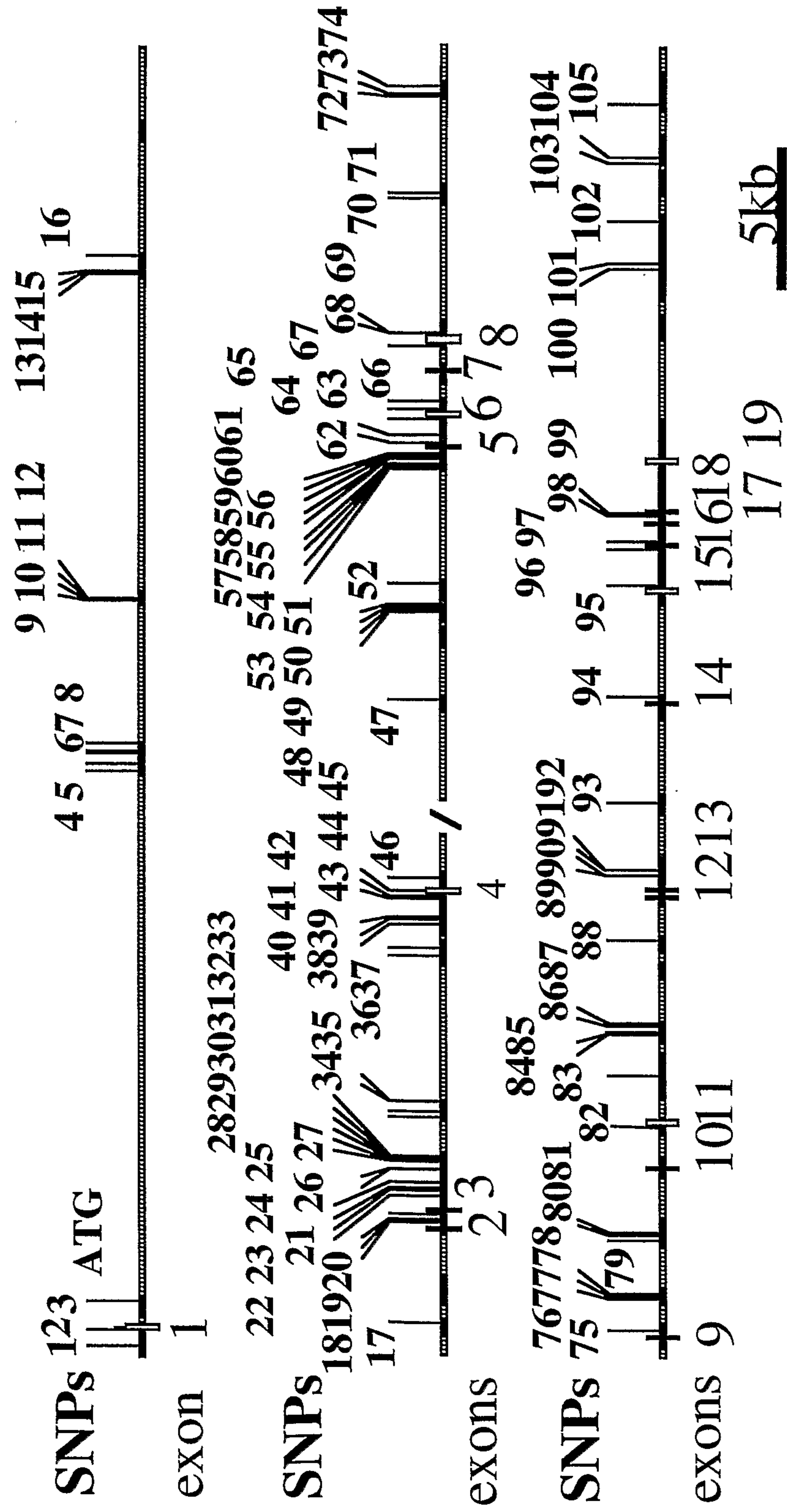


Fig.158B

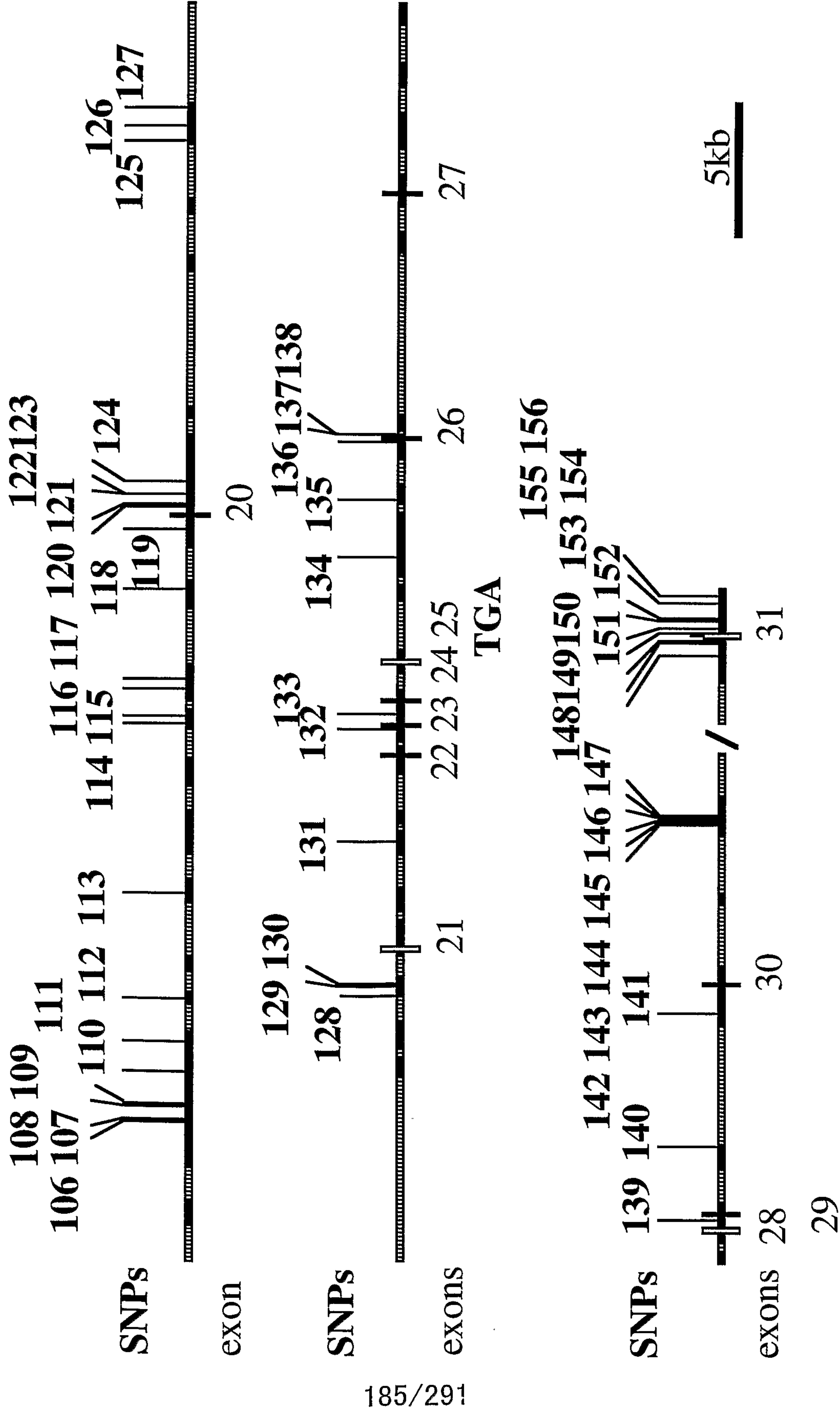


Fig.159 *ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)*

Fig.160 *ATP binding cassette, sub-family C (CFTR/MRP), member 7 (ABCC7)*

ACCESSION AC000111.1 AC000061.1

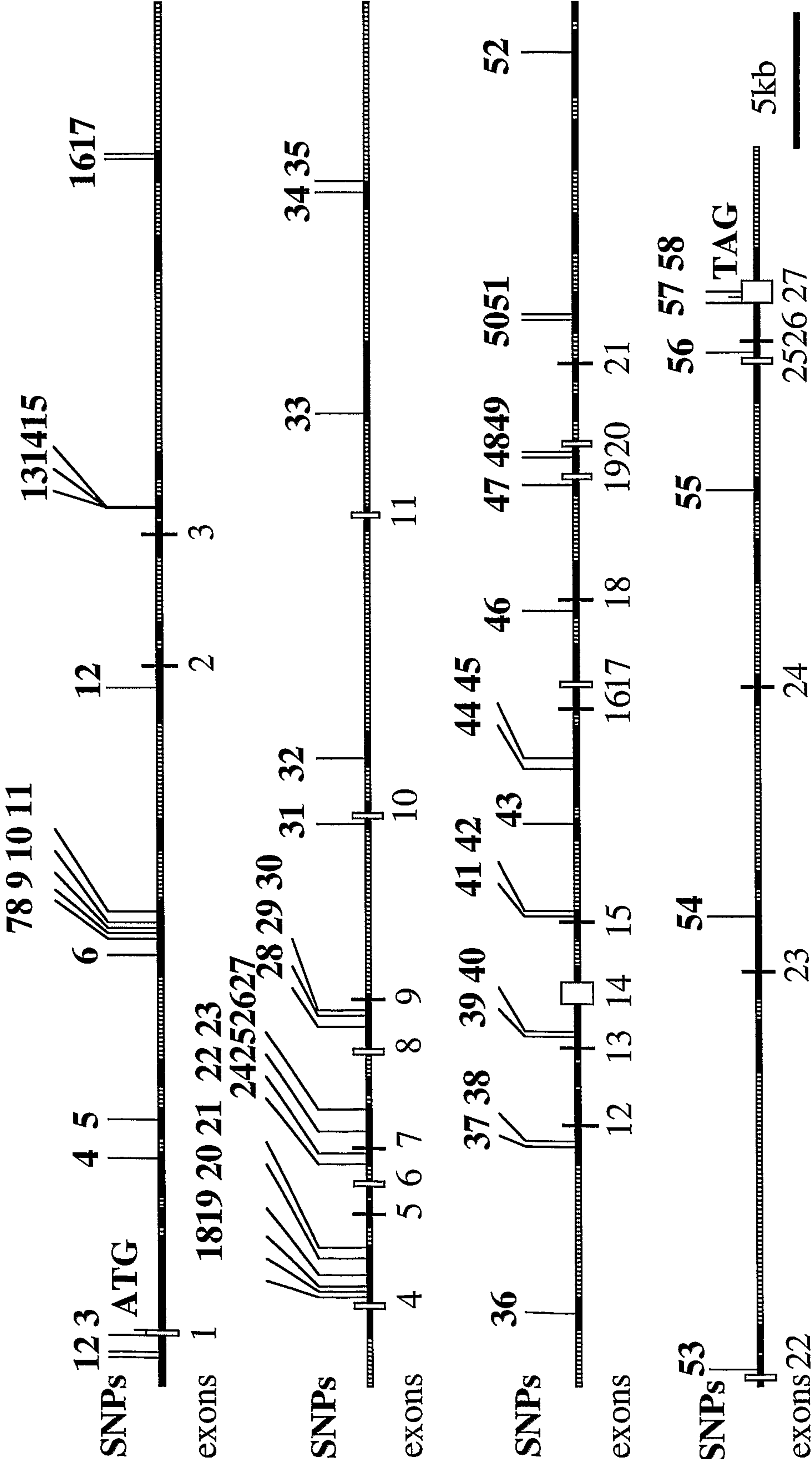


Fig.161 *ATP binding cassette, sub-family C (CFTR/MRP), member 8 (ABCC8)*

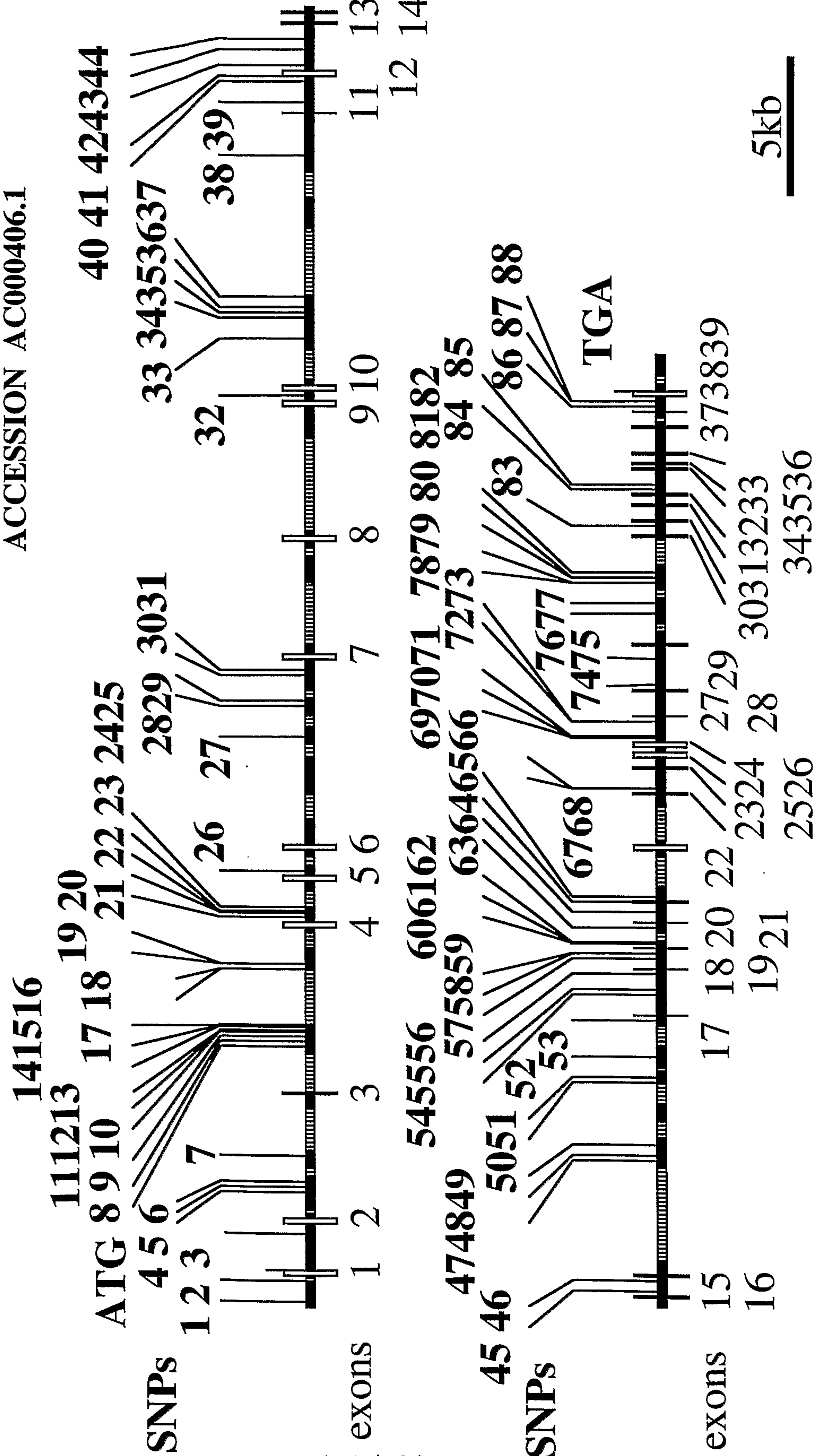


Fig.162 *ATP binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9)*

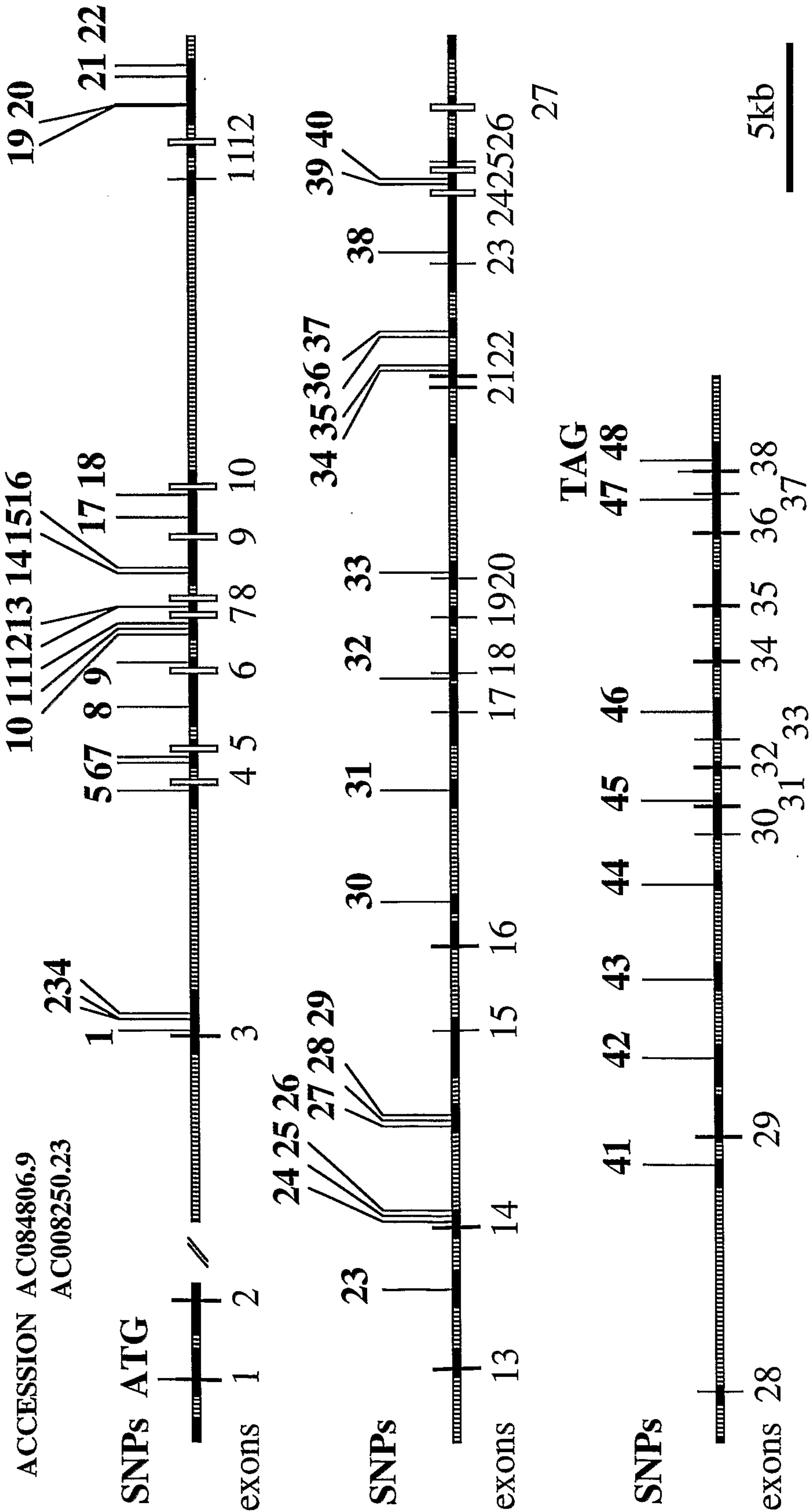


Fig. 163
ATP binding cassette subfamily D, member 1 (*ABCD1*)

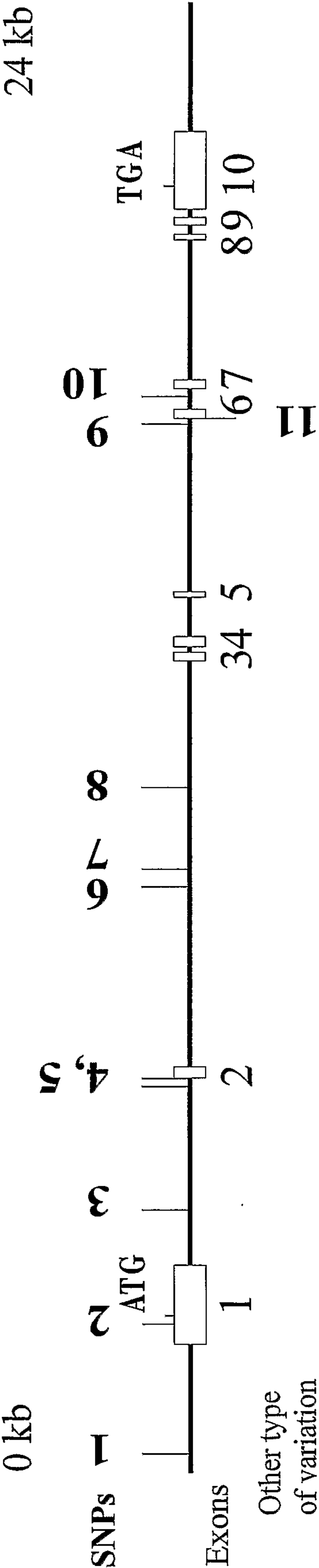


Fig. 164
ATP binding cassette subfamily D, member 3 (*ABCD3*)

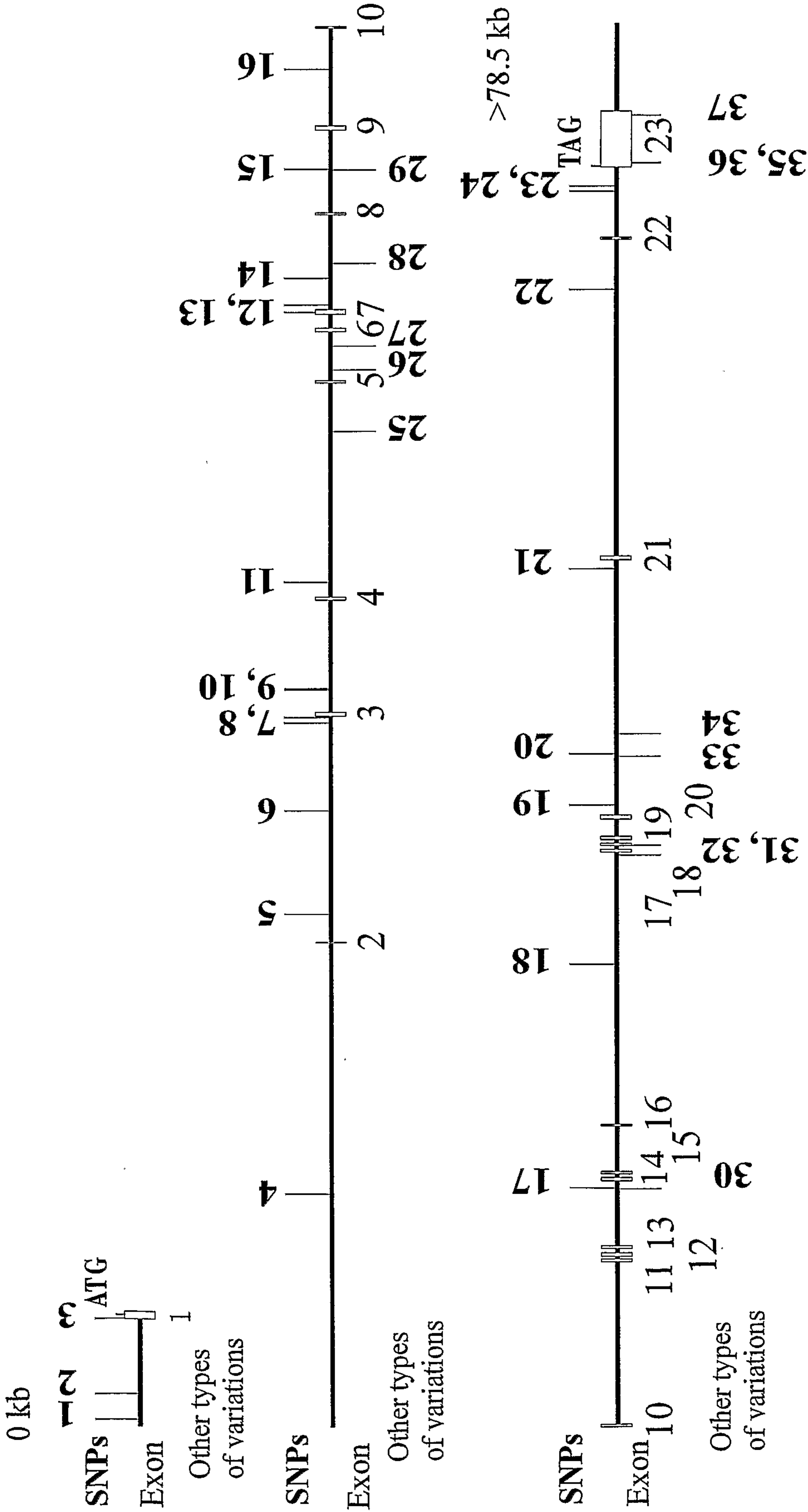


Fig. 165
ATP binding cassette subfamily D, member 4 (*ABCD4*)

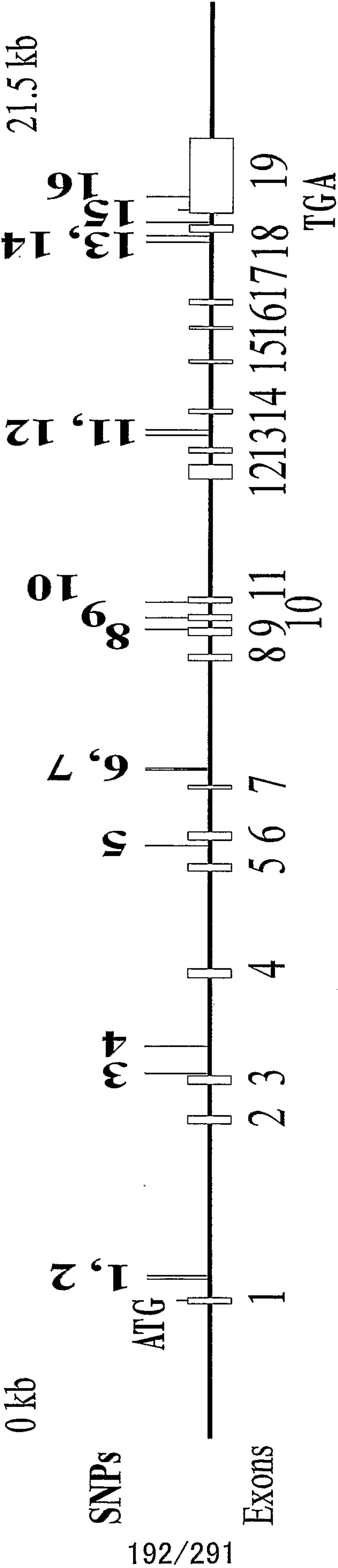


Fig. 166
ATP binding cassette subfamily G, member 1 (*ABCG1*)

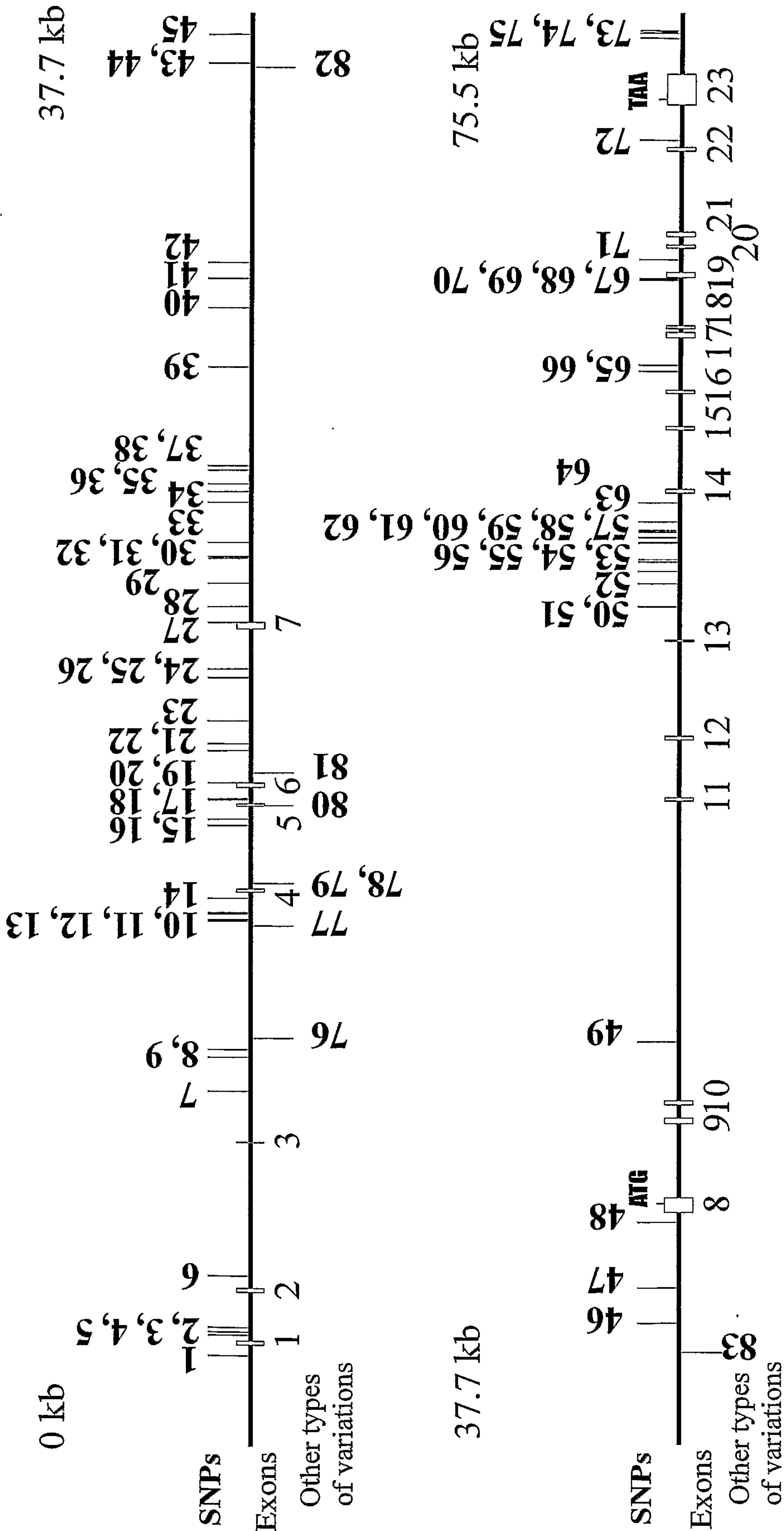


Fig. 167
ATP binding cassette subfamily G, member 2 (ABCG2)

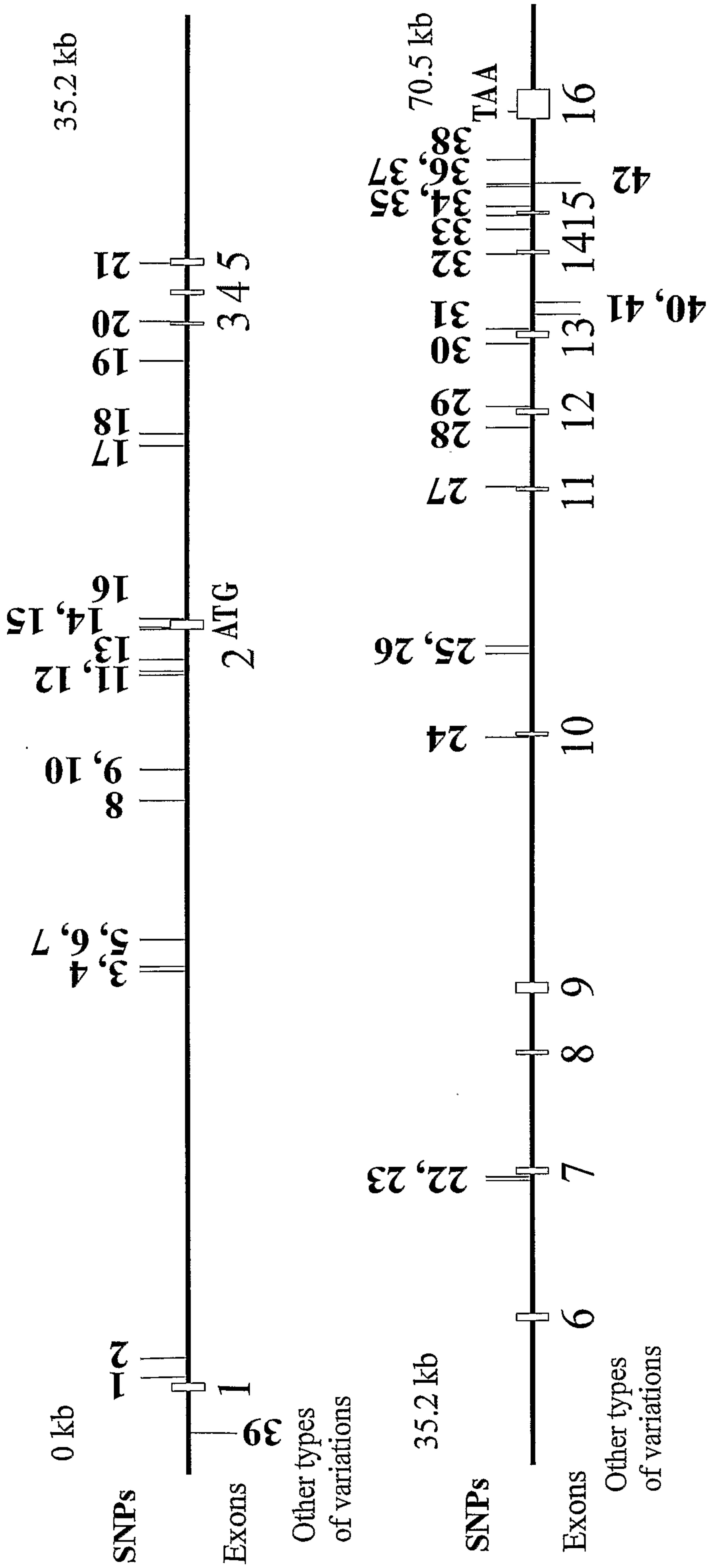


Fig. 168

ATP binding cassette, subfamily G, member 4 (*ABCG4*)

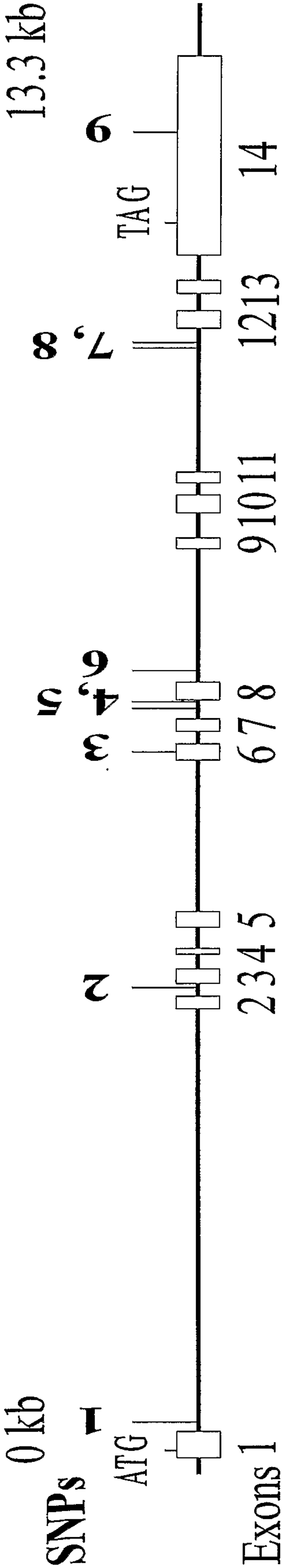


Fig. 169
ATP binding cassette transporter subfamily G number 5 (*ABCG5*)

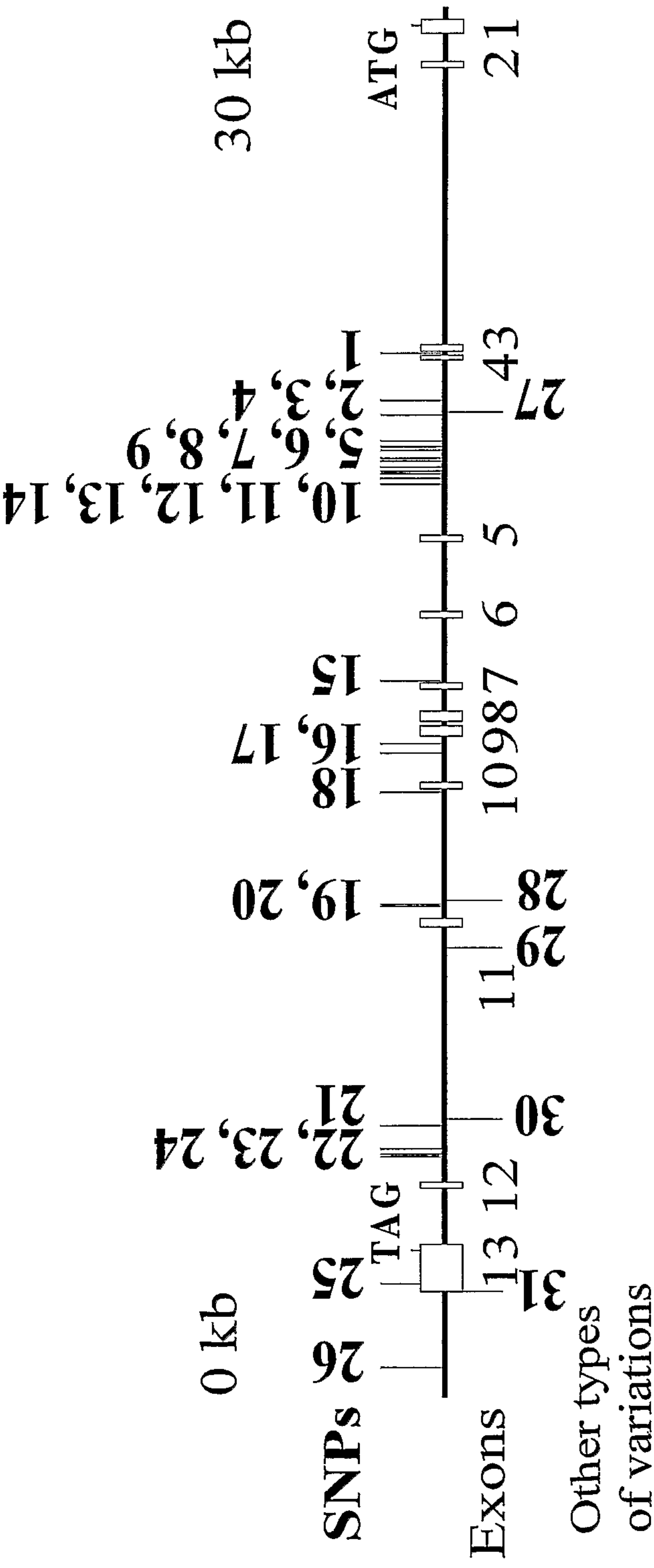


Fig. 170

ATP binding cassette transporter subfamily G number 8 (*ABCG8*)

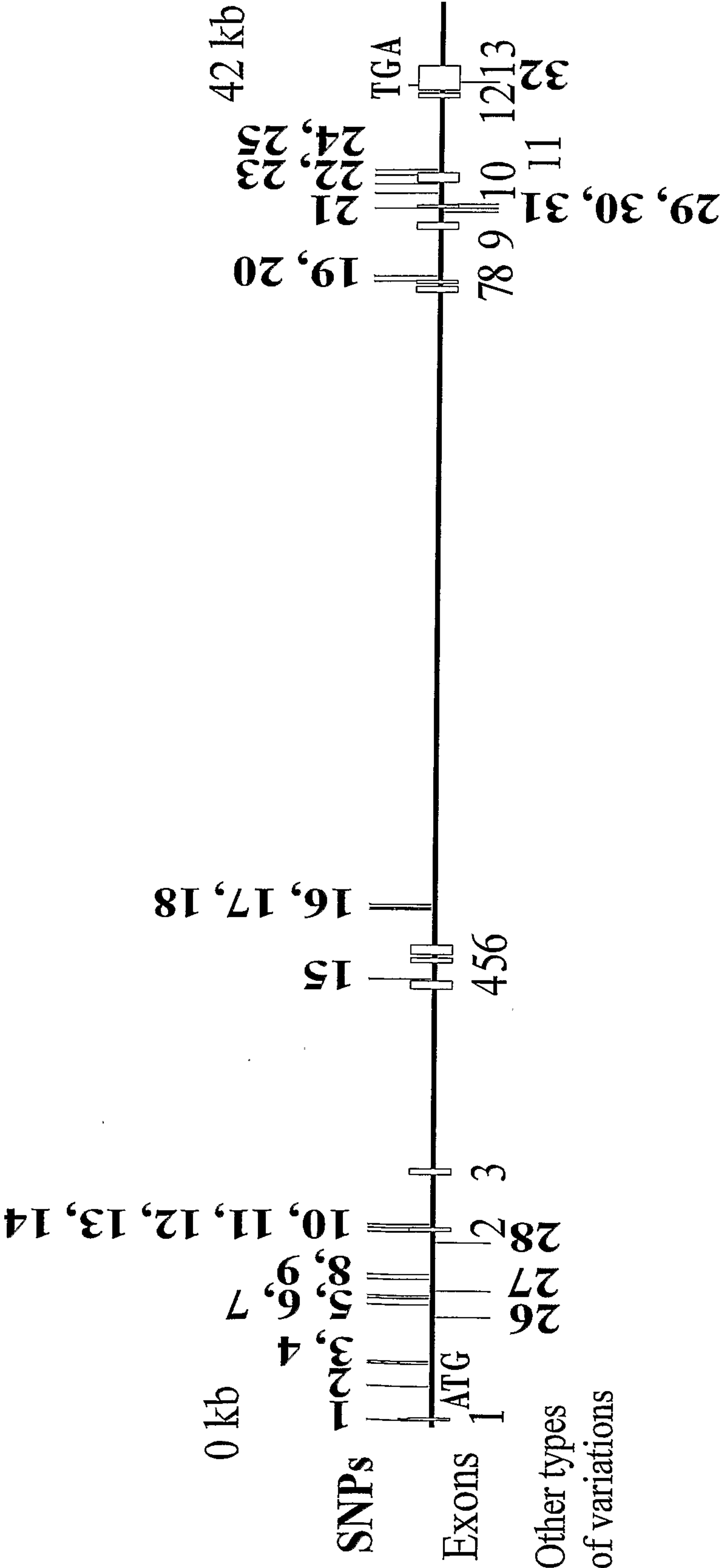


Fig. 171
ATP binding cassette subfamily E, member 1 (*ABCE1*)

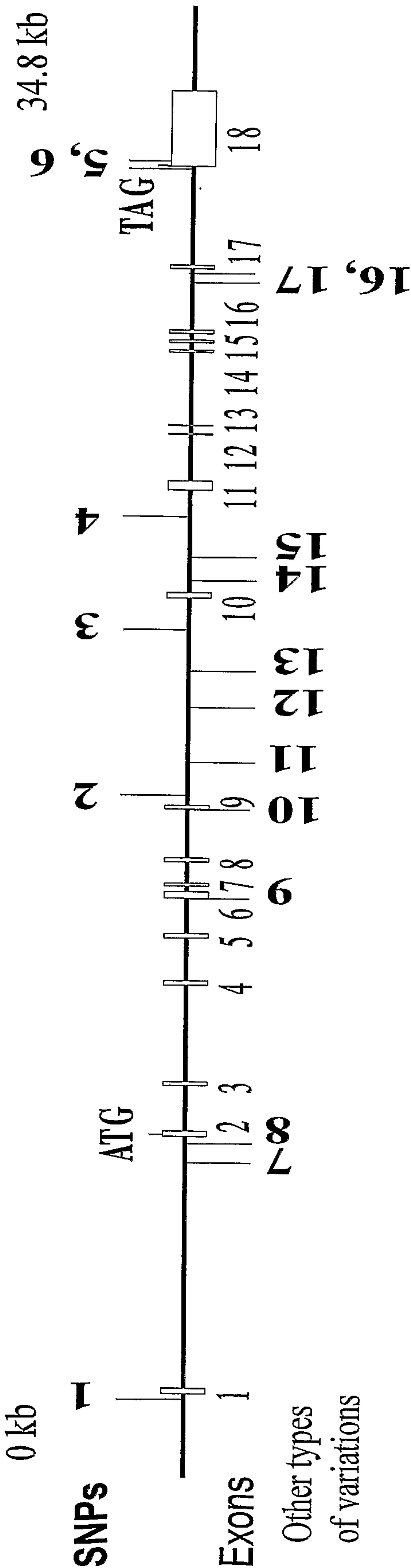


Fig. 172
ATP binding cassette superfamily F number 1 (*ABCF1*)

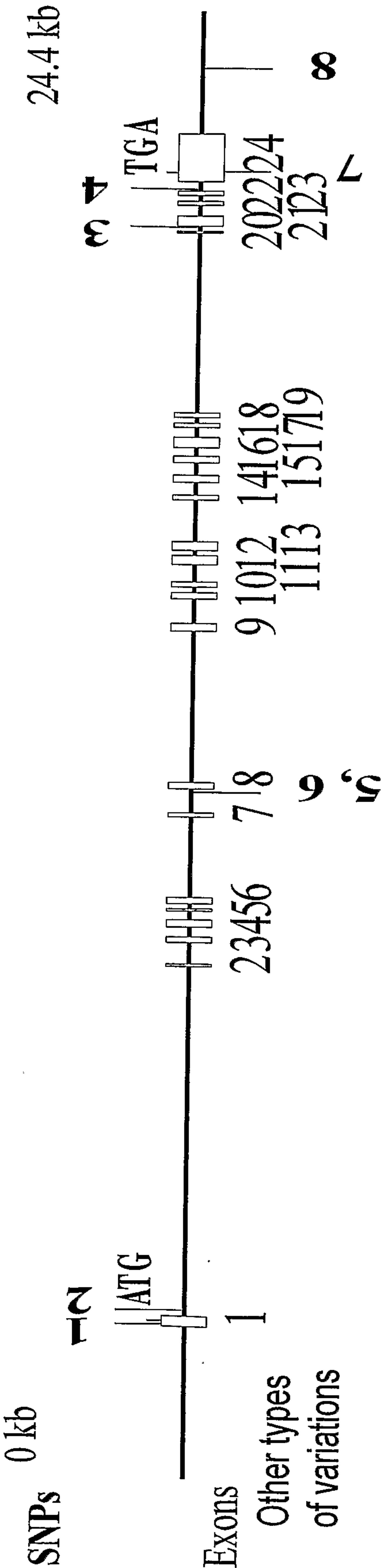


Fig. 173

Human organic anion transporter 1 (*hOAT1*)

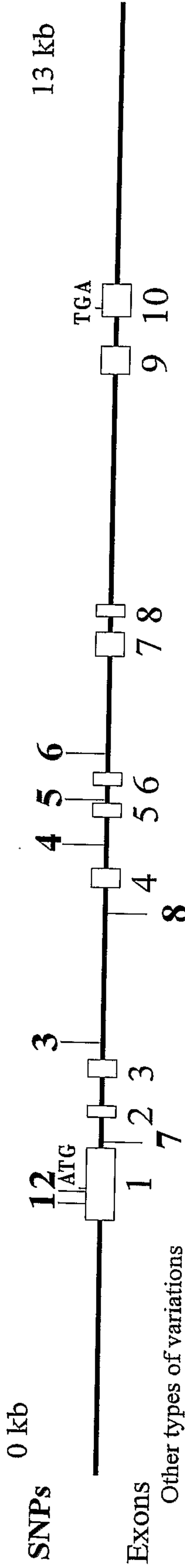


Fig.174

Human organic anion transporter 2 (*hOAT2*)

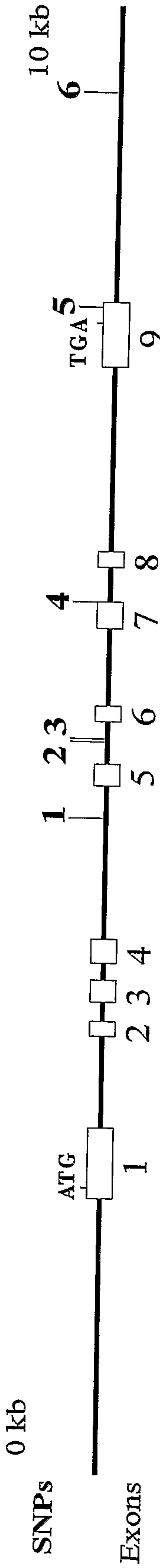


Fig. 175

Human organic anion transporter 3 (*hOAT3*)

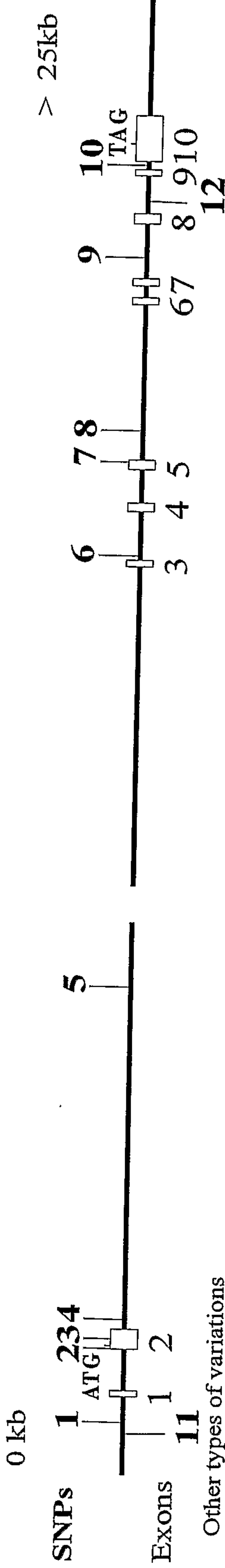
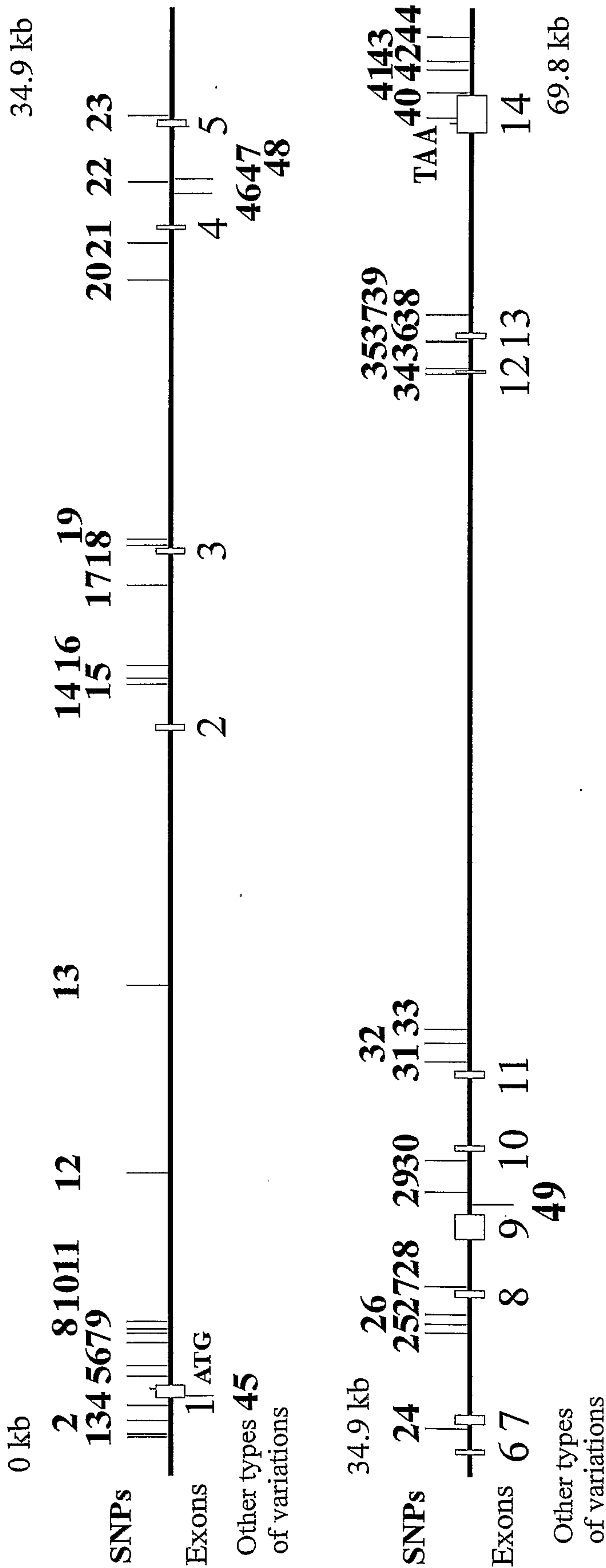


Fig. 176
Human organic anion transporting polypeptide 1 (*hOATP1*)



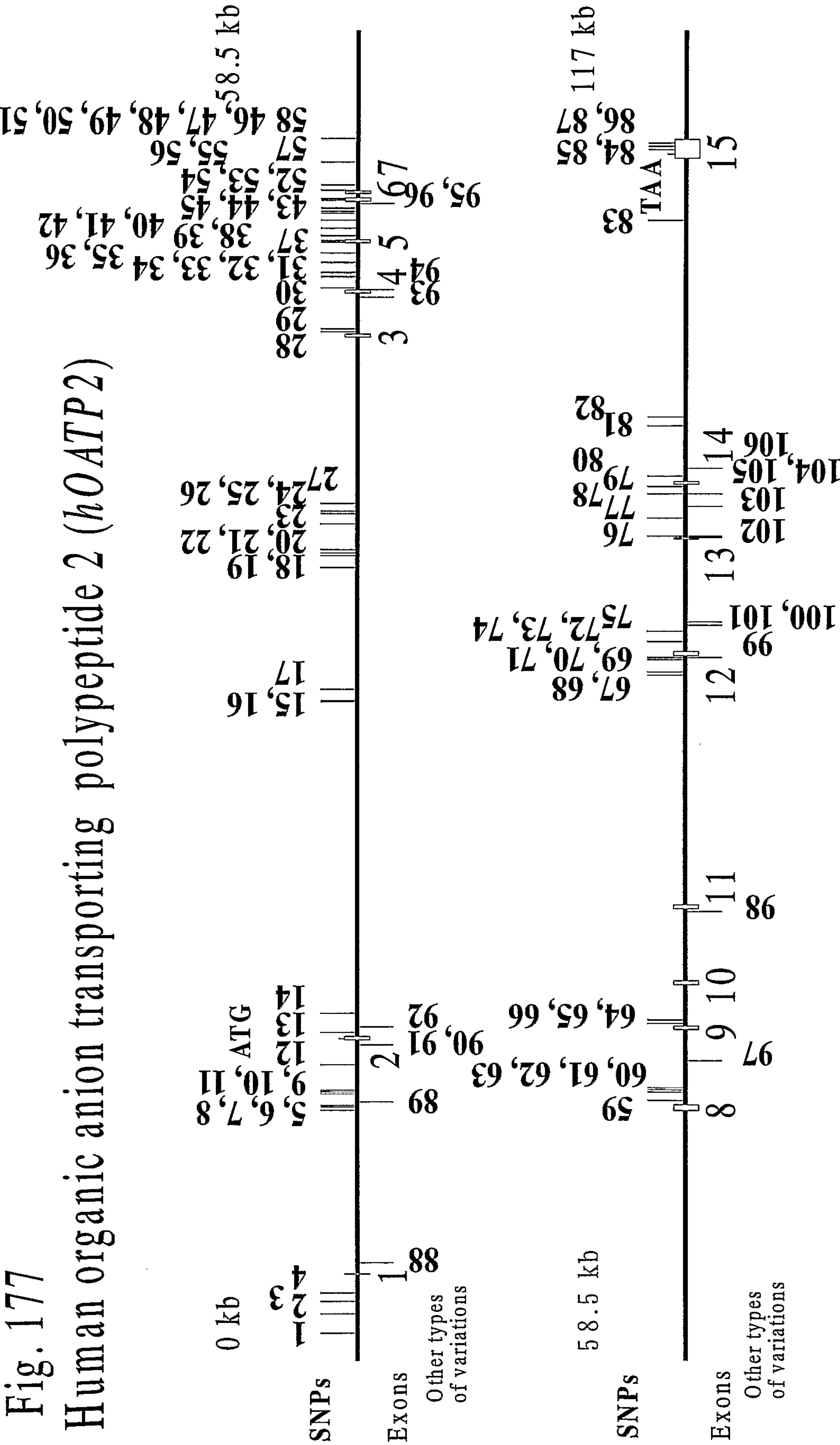


Fig. 178

Human organic anion transporting polypeptide 8 (*hOATP8*)

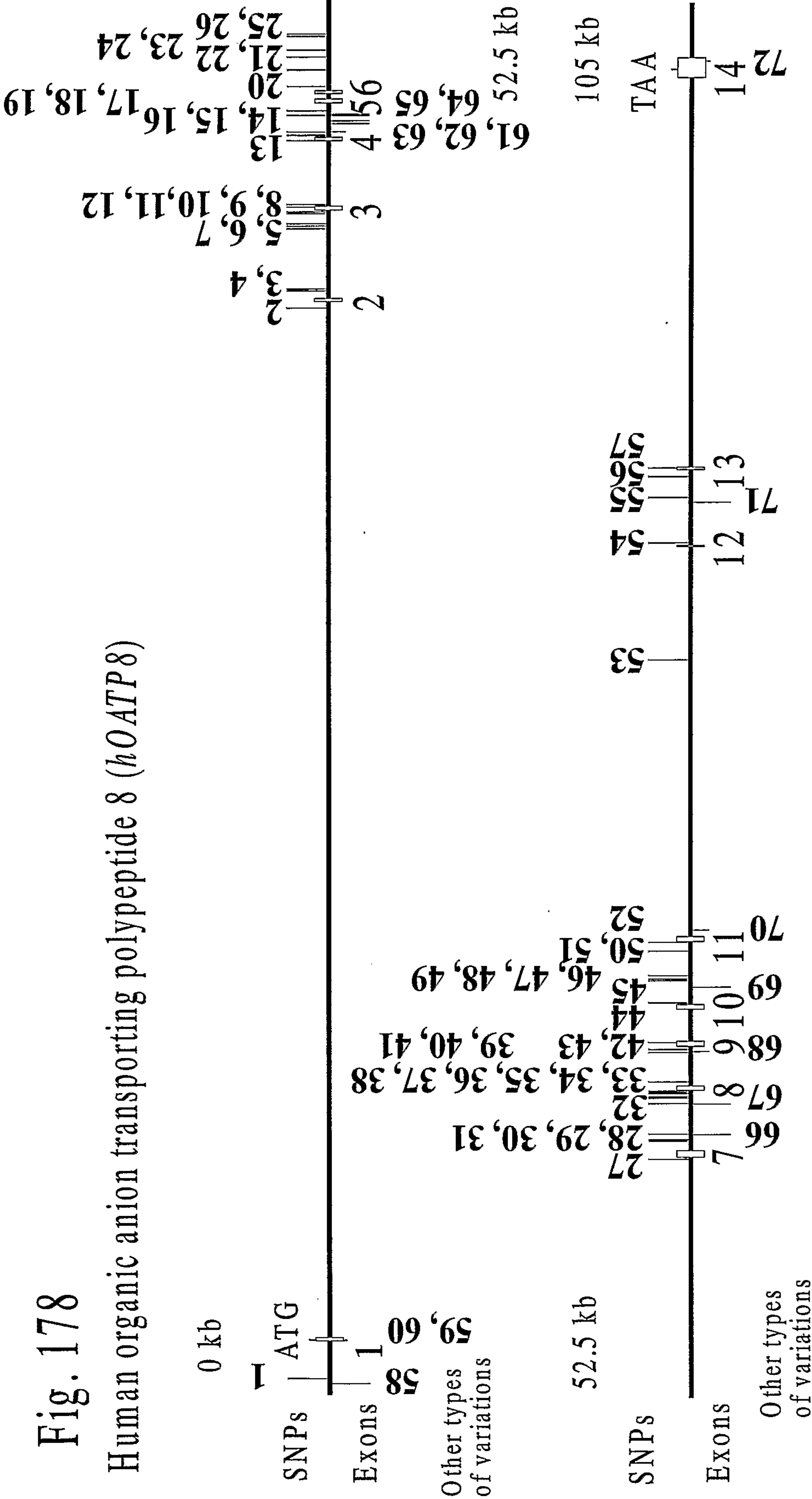


Fig.179 *Transporter associated with antigen processing 1 (TAP1)*
ACCESSION X66401.1

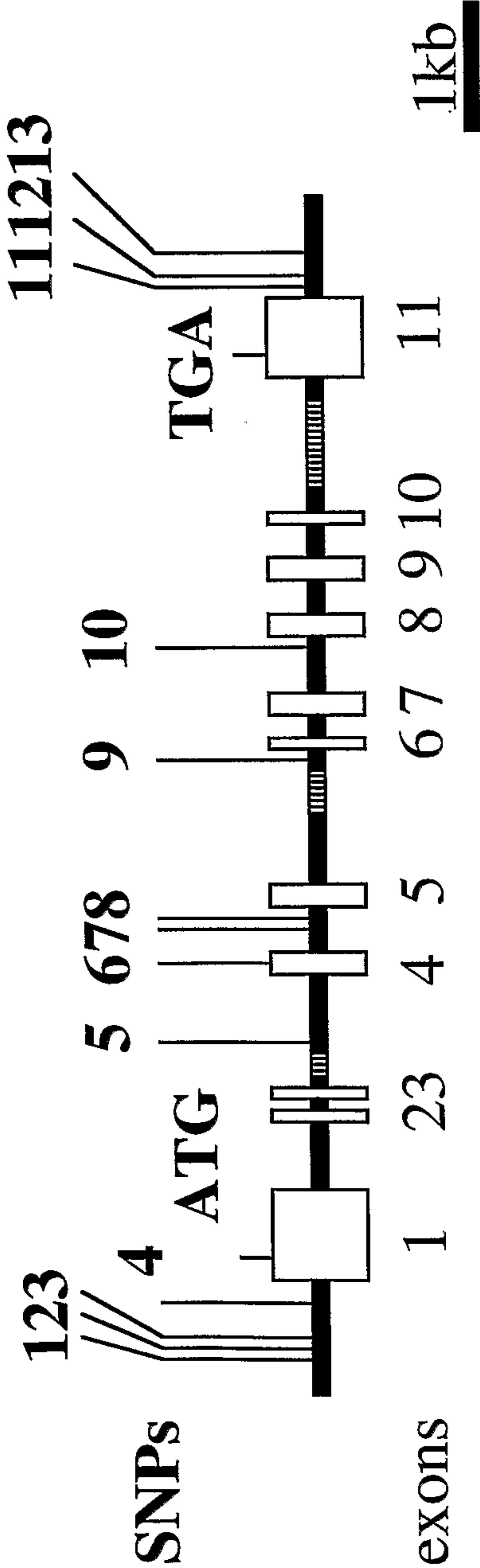


Fig.180 *Transporter associated with antigen processing 2 (TAP2)*
ACCESSION X66401.1

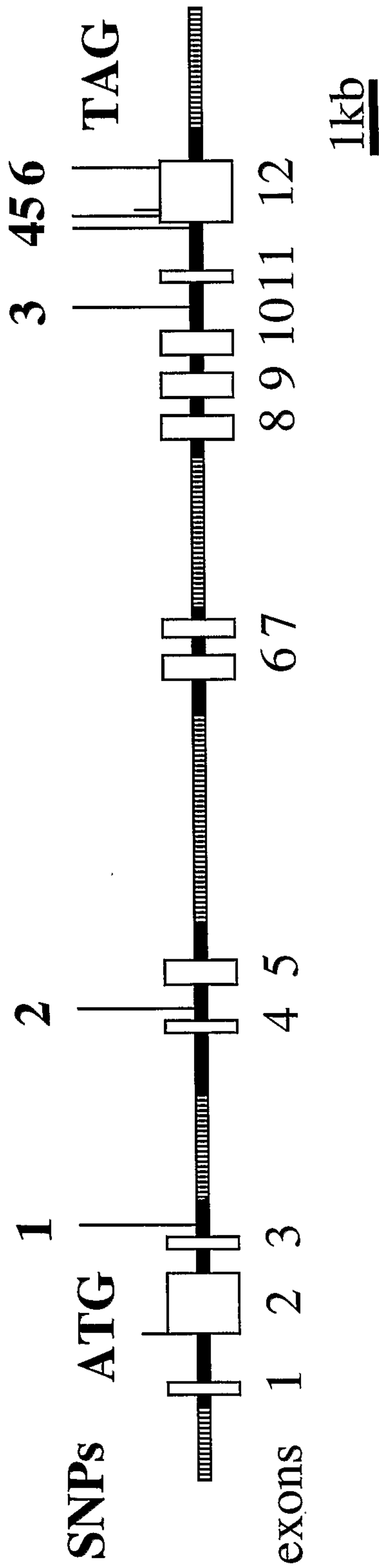


Fig.181
Solute carrier family 22, member 4 (SLC22A4)
Organic cation transporter, member 4 (OCTN1)

ACCESSION AC008599.6

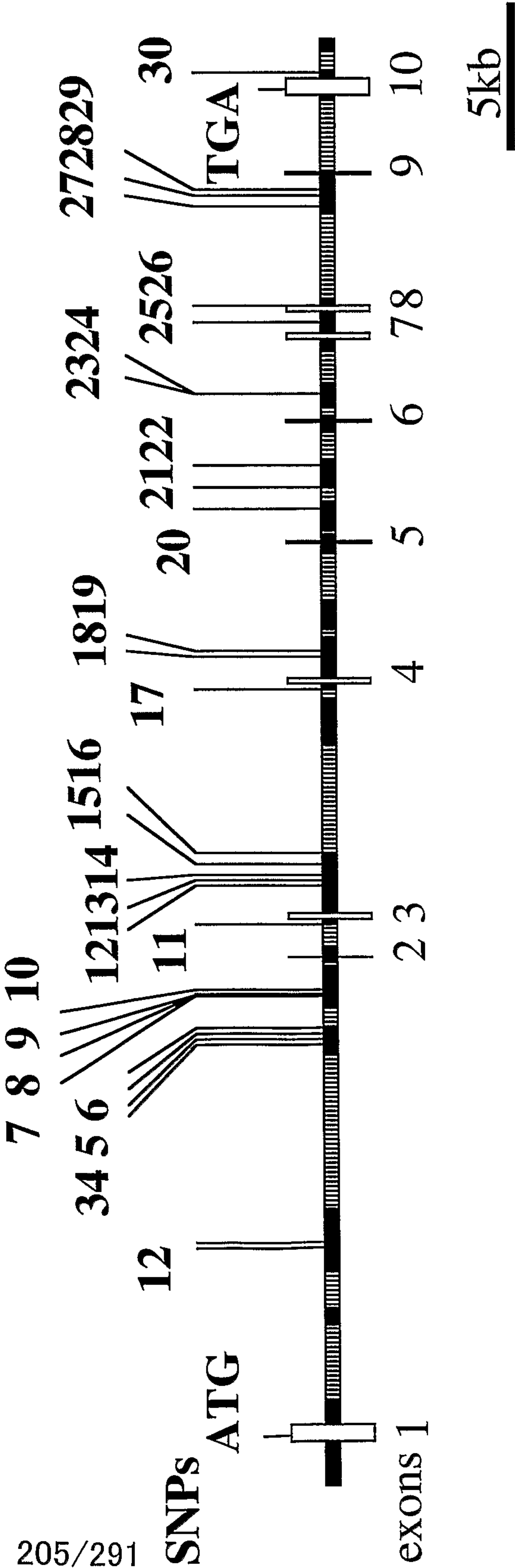


Fig.182
Solute carrier family 22, member 5 (SLC22A5)
Organic cation transporter, member 5 (OCTN2)

ACCESSION AC023861.3

ATG

123 45

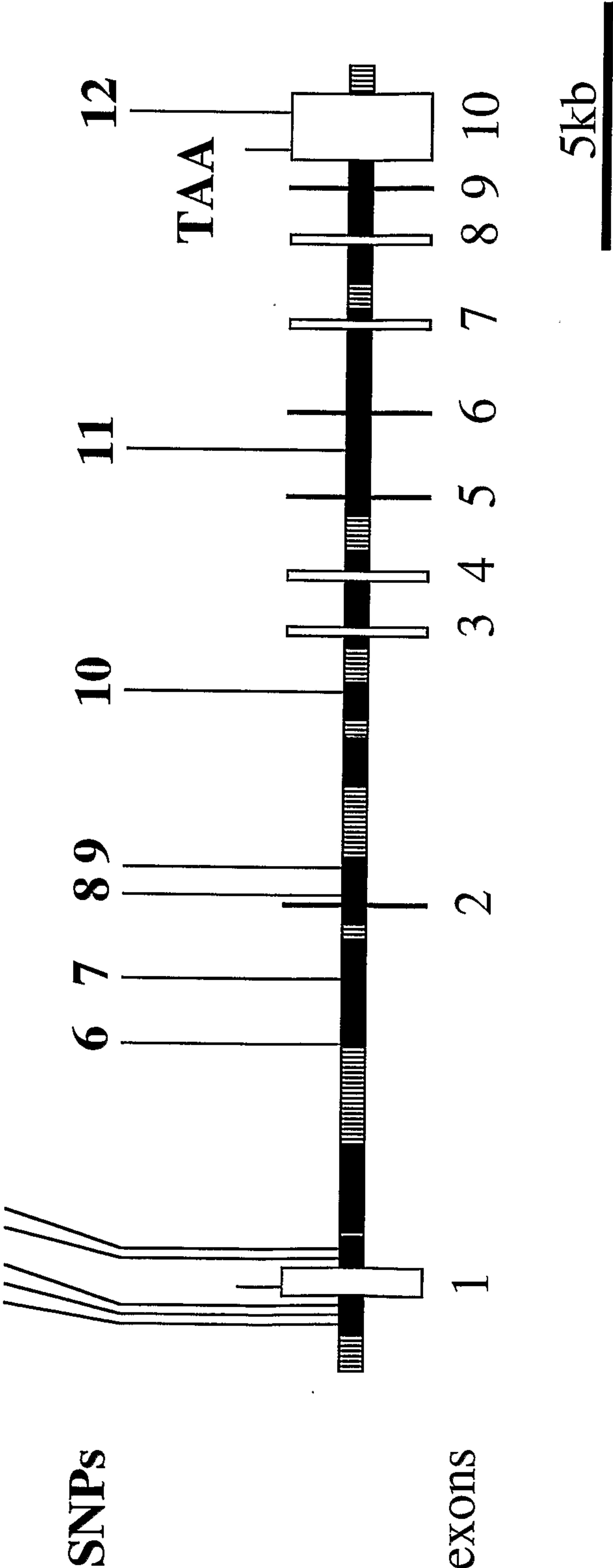


Fig.183 *Solute carrier family 22 (organic cation transporter), member 1*
(*SLC22A1, OCT1*)

ACCESSION AL35625.5

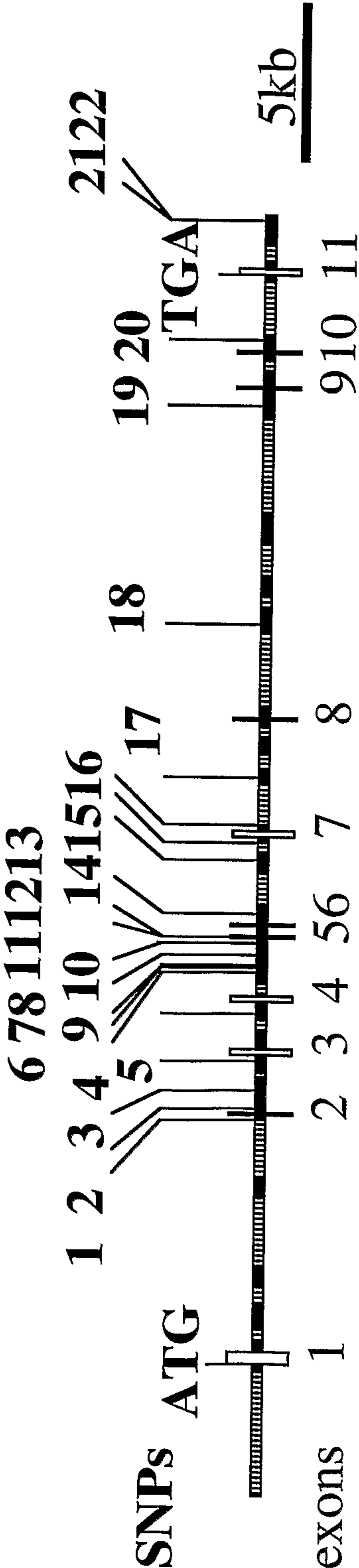


Fig.184 *Solute carrier family 22 (organic cation transporter), member 2*
(*SLC22A2, OCT2*)

ACCESSION AL162582.18

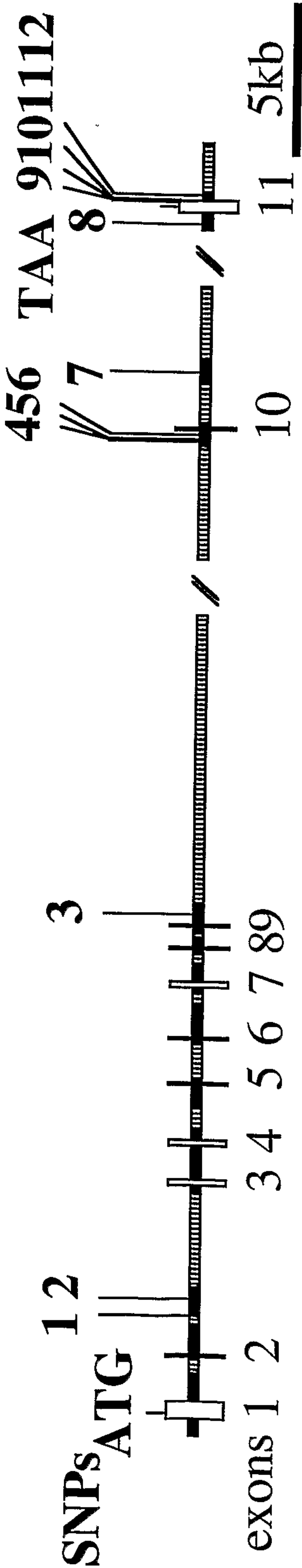


Fig.185

Solute carrier family 10, member 2 (SLC10A2)
Na/taurocholate cotransporting polypeptide (NTCP)

ACCESSION AL157789.6

TAG

23 678 1011121314

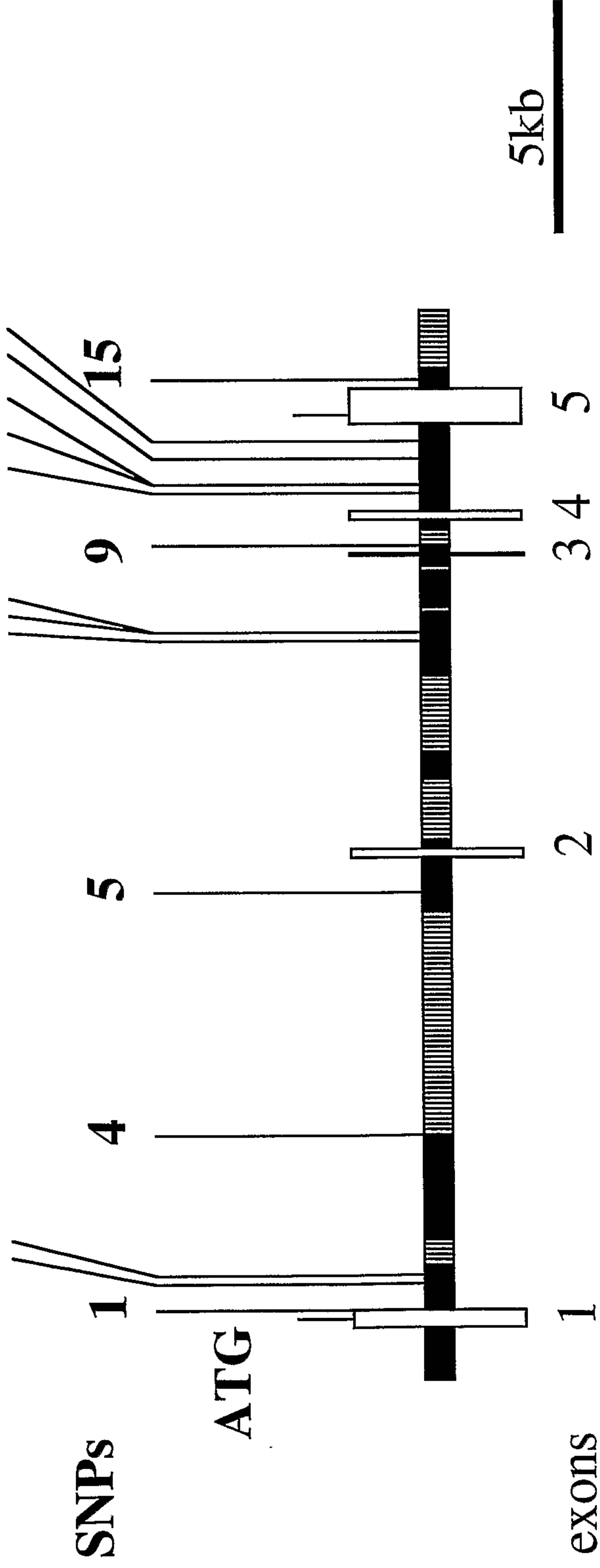


Fig.186
Solute carrier family 15, member 1 (SLC15A1)
Oligopeptide transporter, member 1 (PEPT1)

ACCESSION AL353574.8 AL391670.6

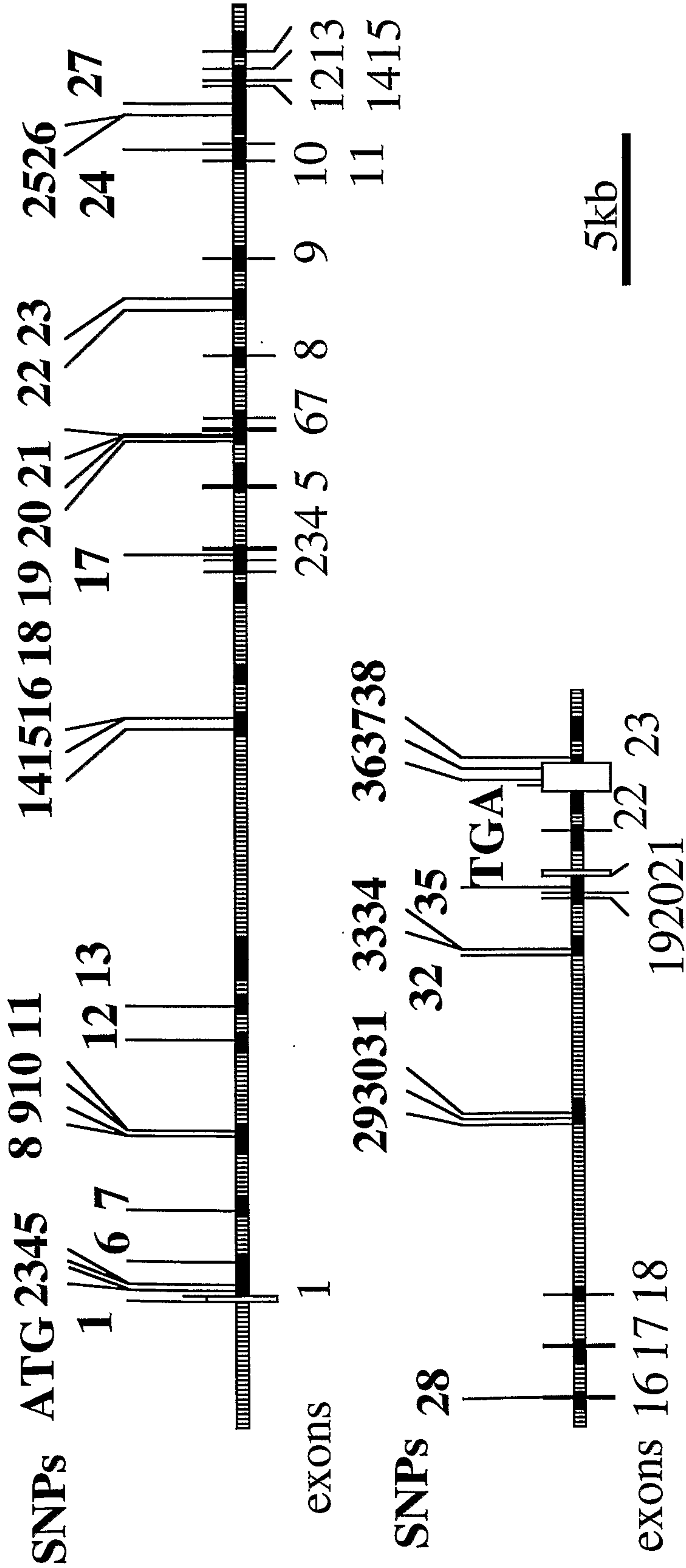


Fig.187

Epoxide hydrolase 1, microsomal (EPHX1)

ACCESSION AC058782.8

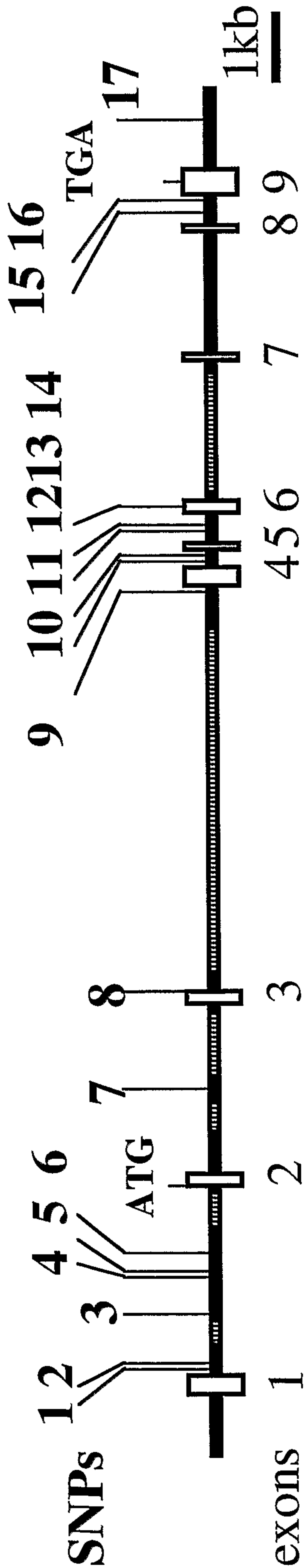
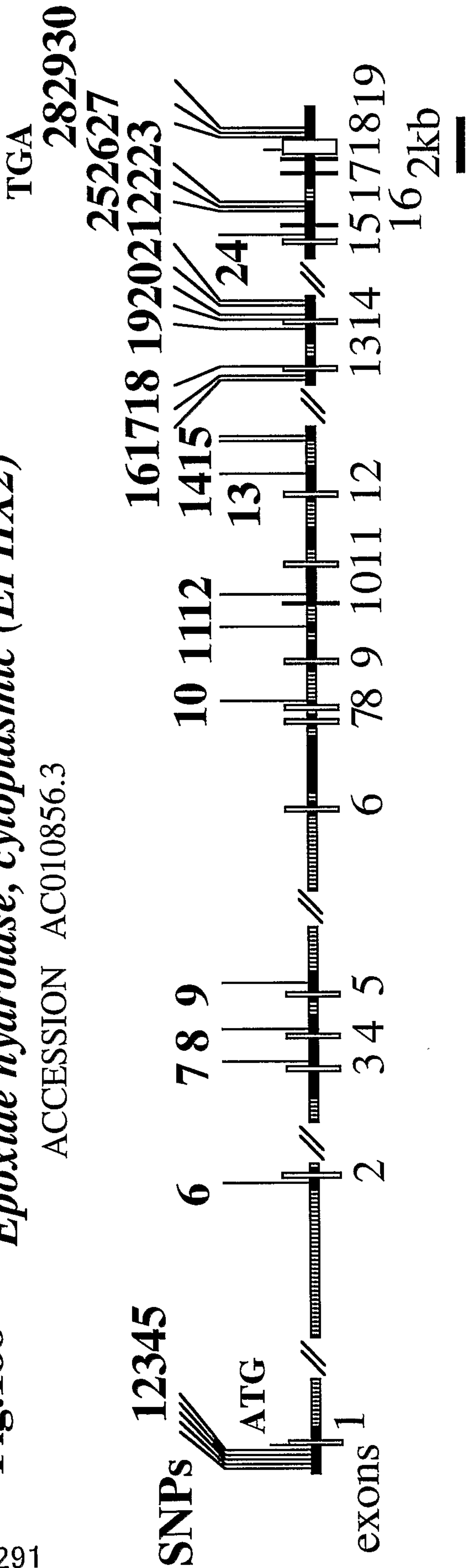


Fig.188

Epoxide hydrolase, cytoplasmic (EPHX2)

ACCESSION AC010856.3



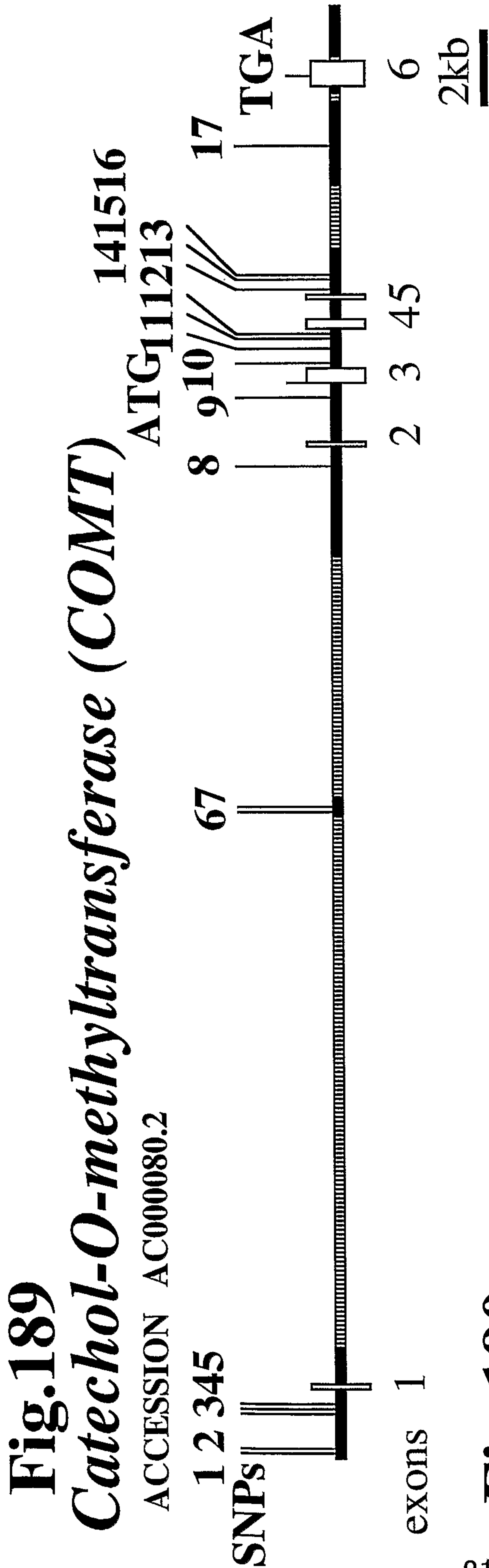


Fig.190
Guanidinoacetate N-methyltransferase (GAMT)
ACCESSION NT_000879.1

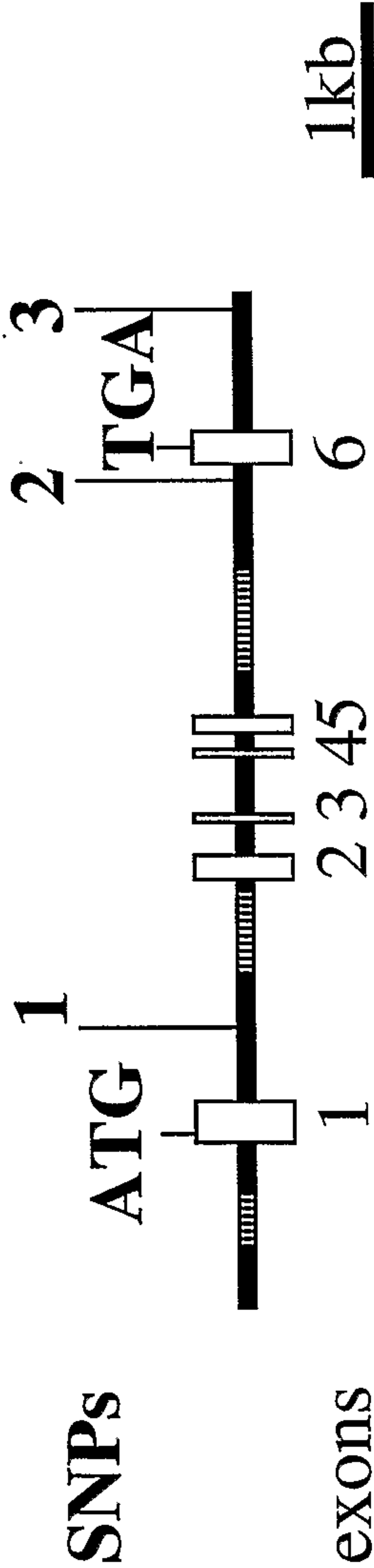


Fig.191 *Phenylethanolamine N-methyltransferase*

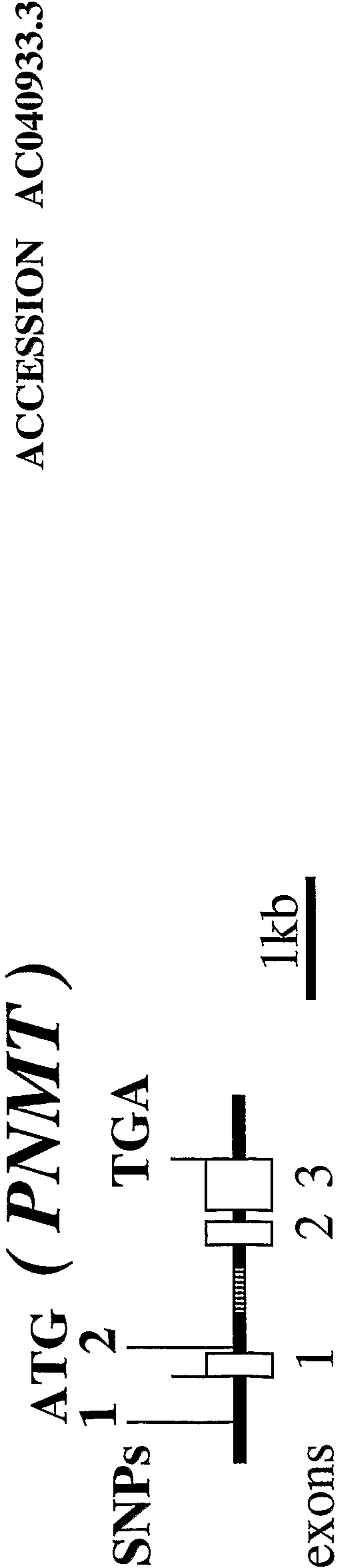


Fig.192 *Histamine N-methyltransferase (HNMT)*

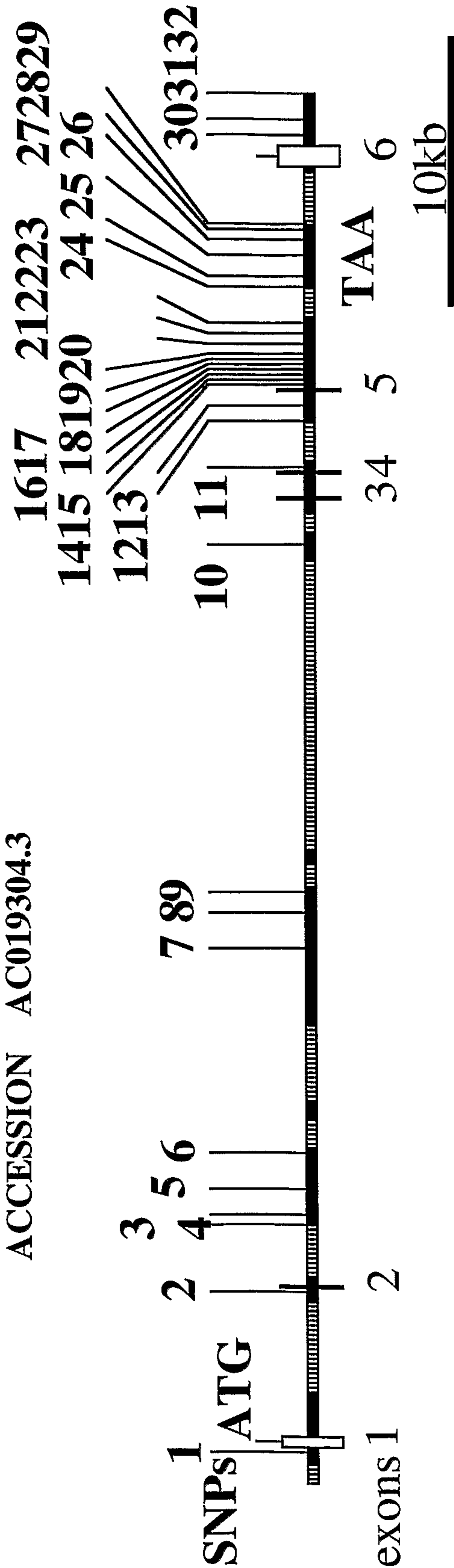


Fig.193 *Nicotinamide N-methyltransferase (NNMT)*

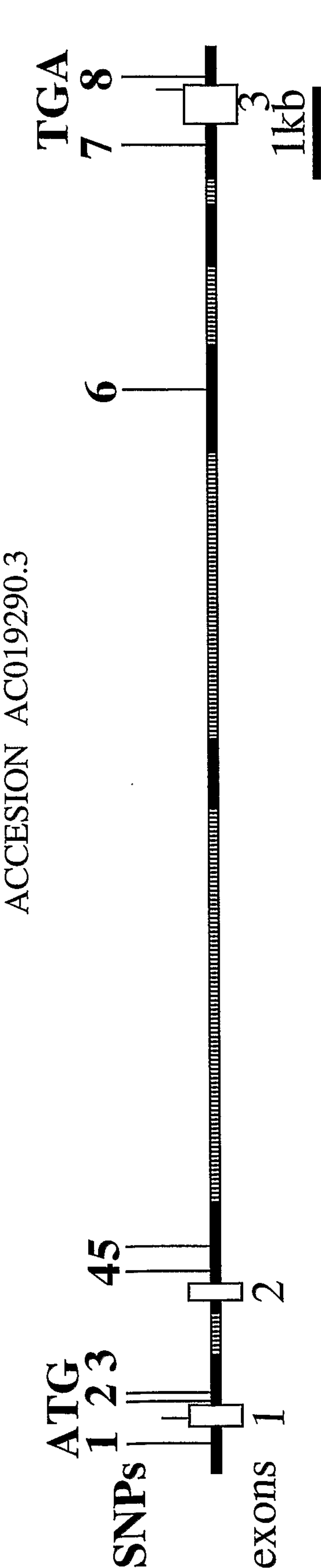
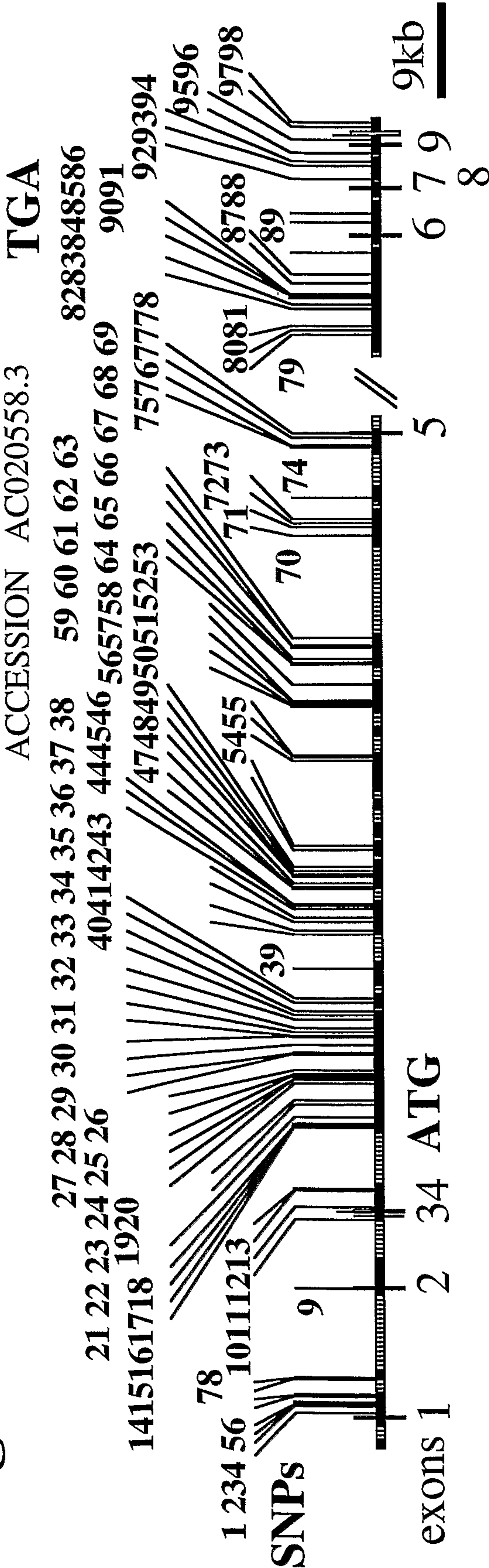


Fig.194 *Phosphatidylethanolamine N-methyltransferase (PEMT)*



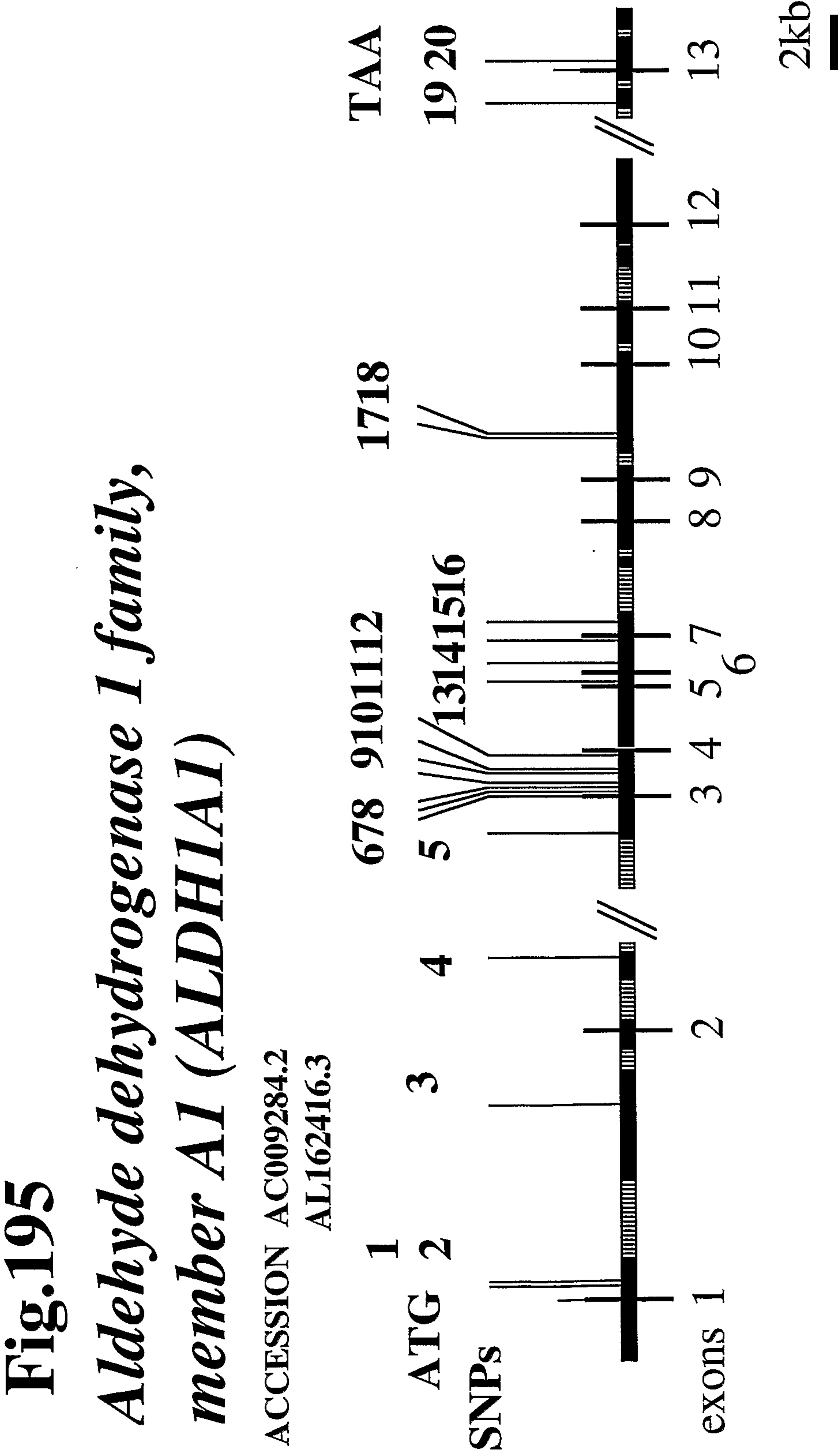


Fig.196
Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)

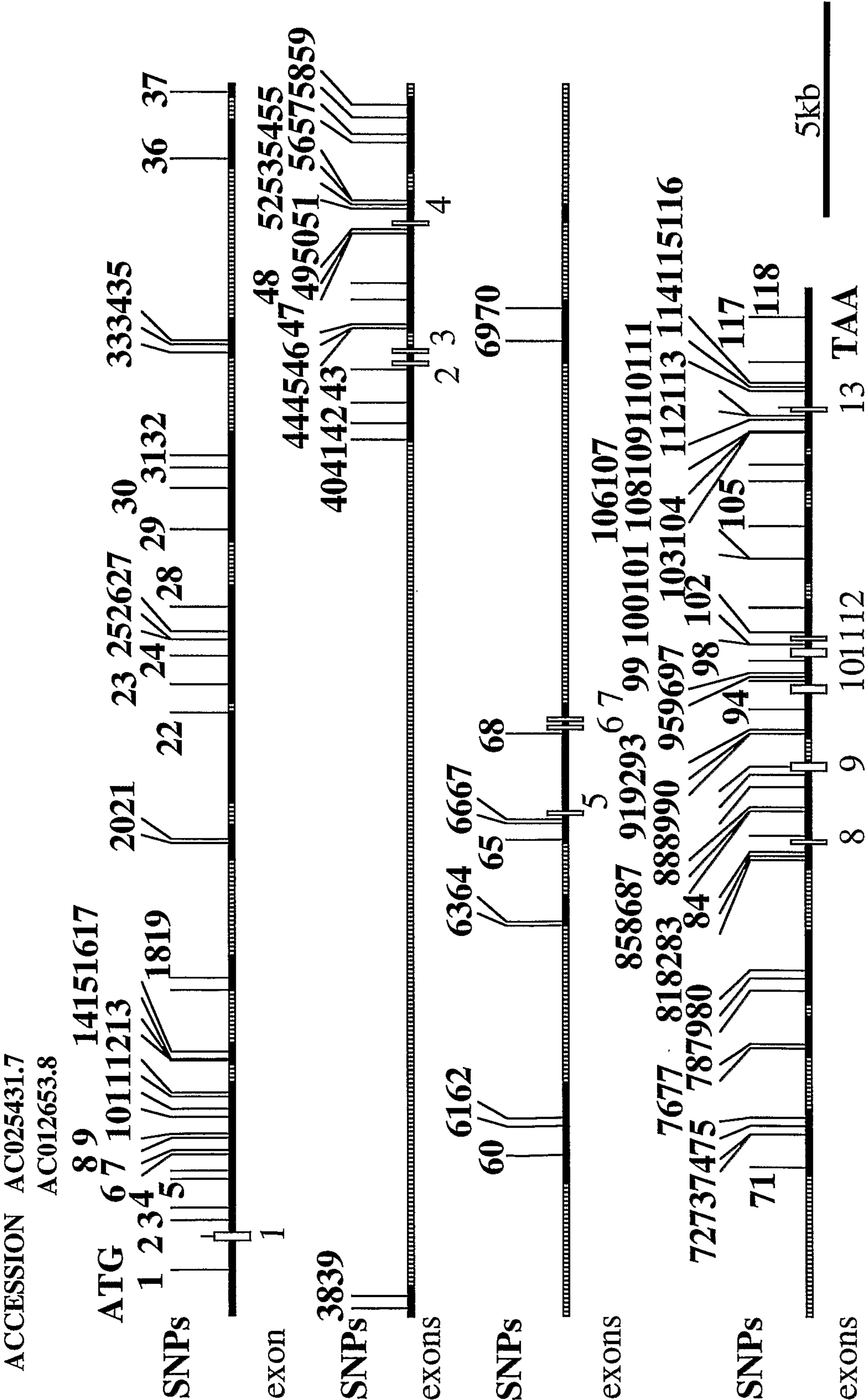


Fig.197 *Aldehyde dehydrogenase 1 family,*
 member A3 (ALDH1A3)

ACCESSION AC015712.7

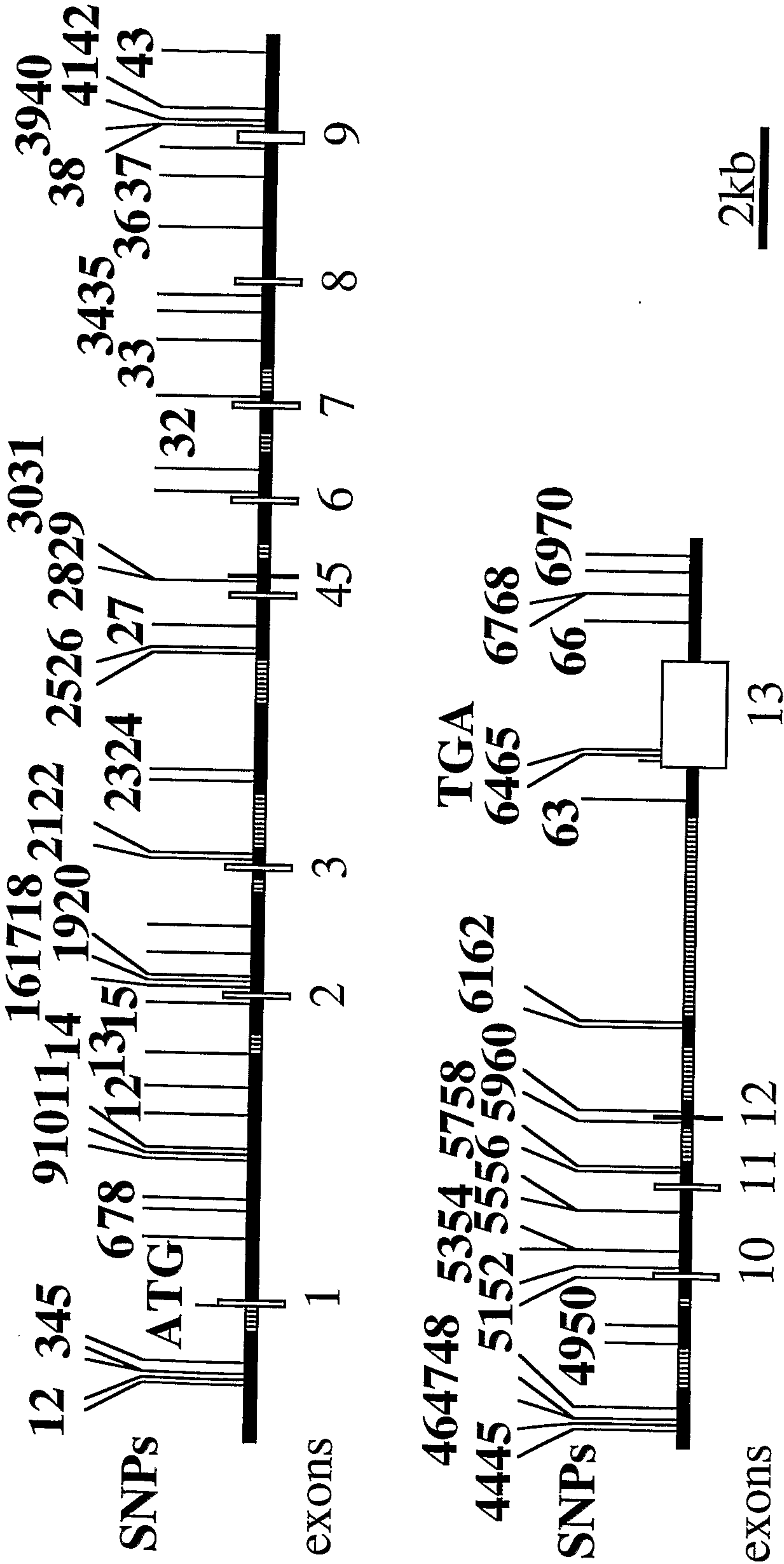


Fig.198
Aldehyde dehydrogenase 1 family, member B1 (ALDH1B1)

ACCESSION AL135785.9

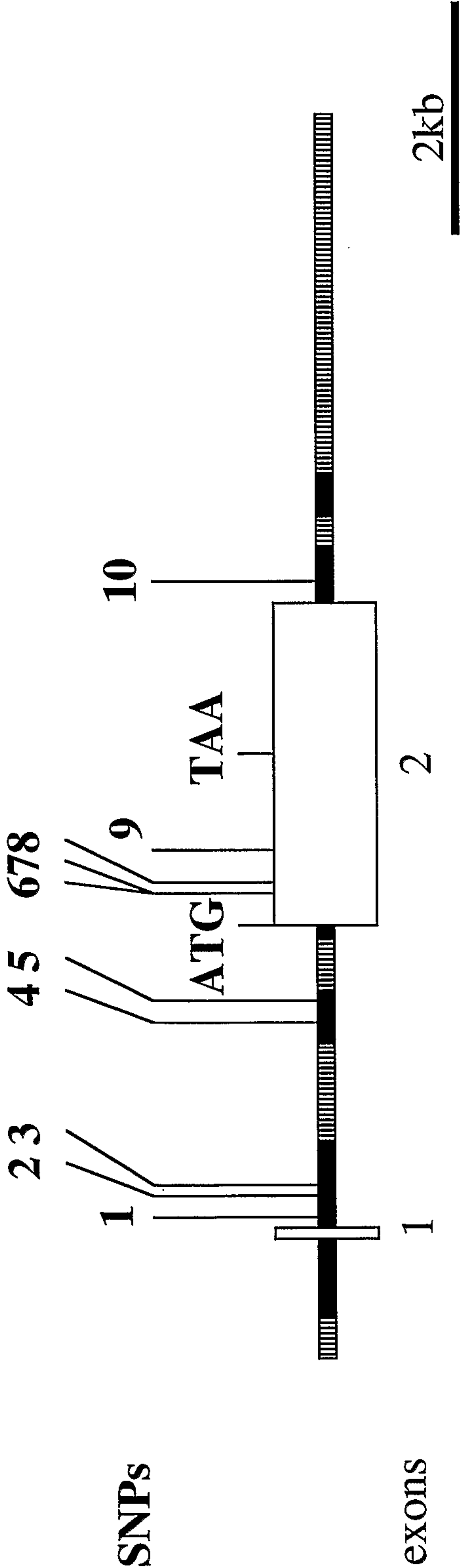


Fig.199A *Formyltetrahydrofolate dehydrogenase (FTHFD)*
Aldehyde dehydrogenase 1 family, member L1 (ALDH1L1)

ACCESSION AC079848.6

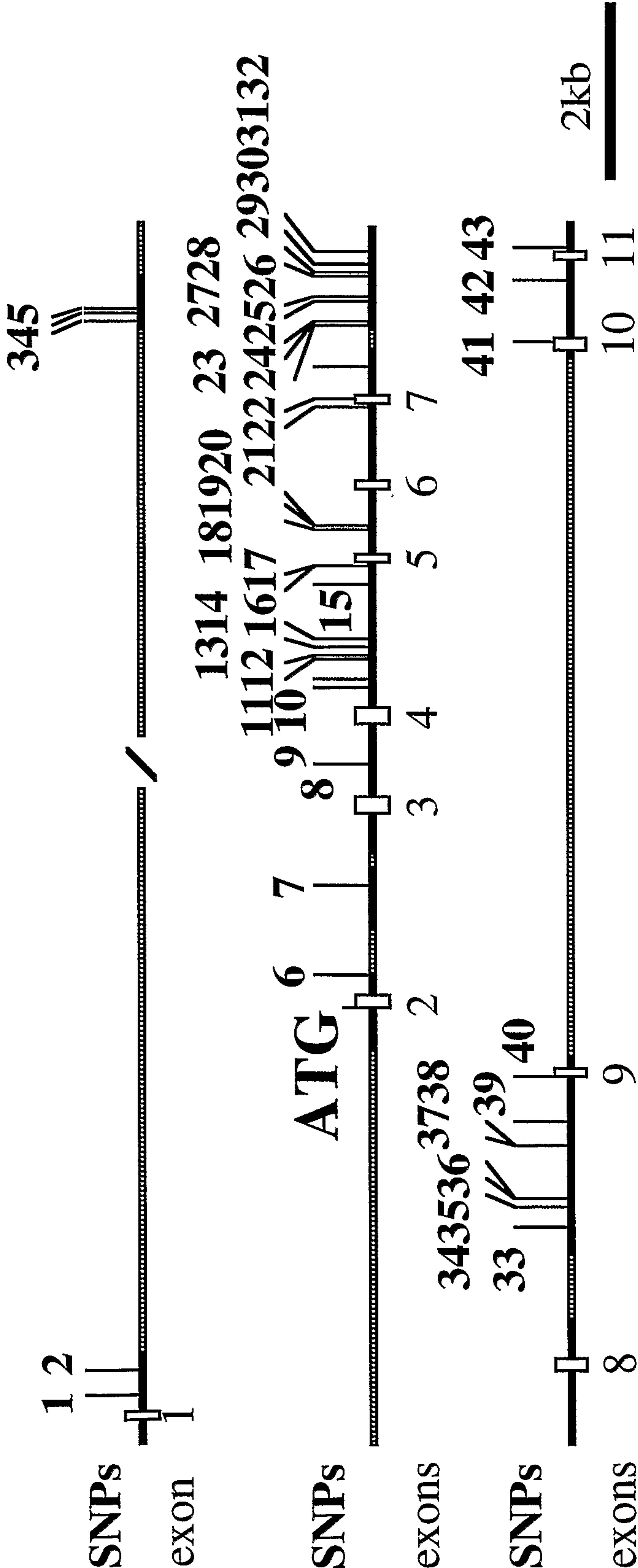


Fig.199B

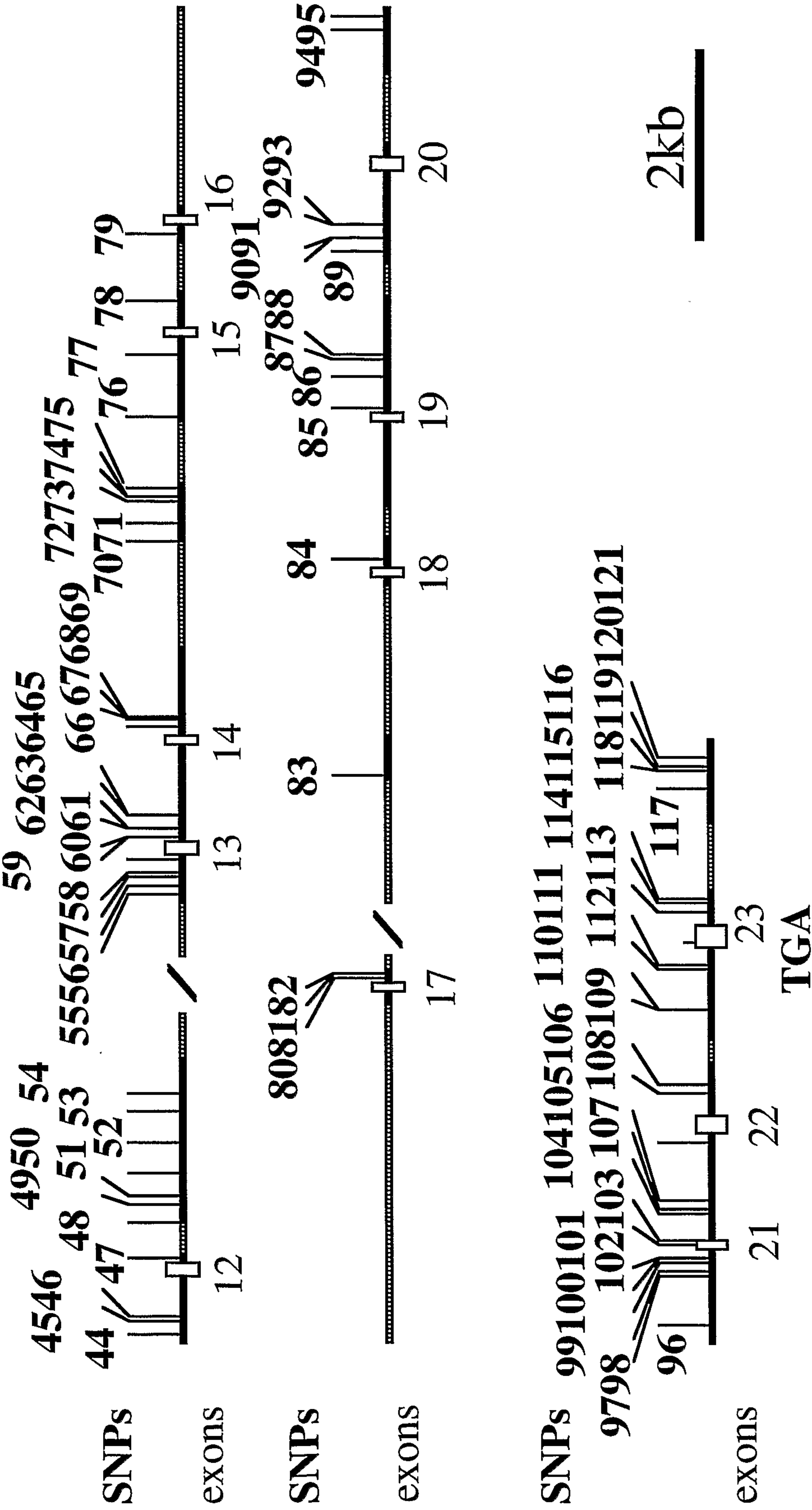


Fig.200 *Aldehyde dehydrogenase 2 (ALDH2)*

ACCESSION AC002996.1
AC003029.2

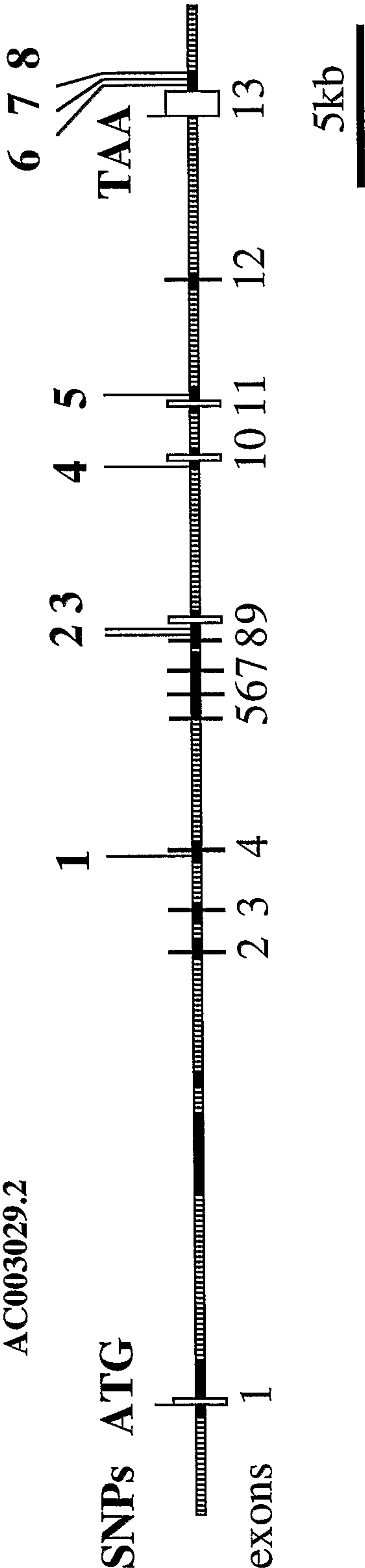


Fig.201 *Aldehyde dehydrogenase 3 family, member A1 (ALDH3A1)*

ACCESSION AC005722.1

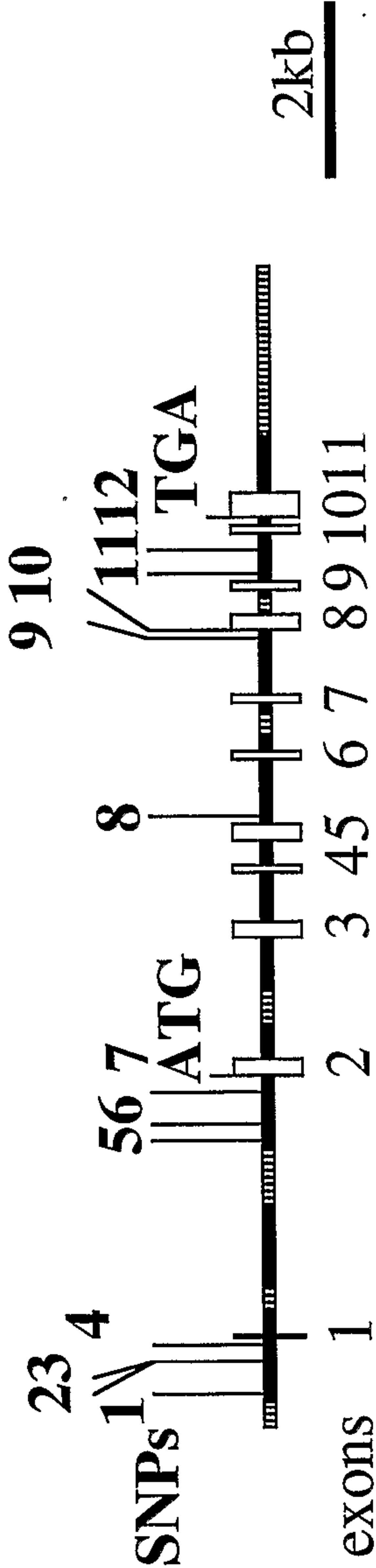


Fig.202 *Aldehyde dehydrogenase 3 family, member A2*
(*ALDH3A2*)
ACCESSION AC005722.1

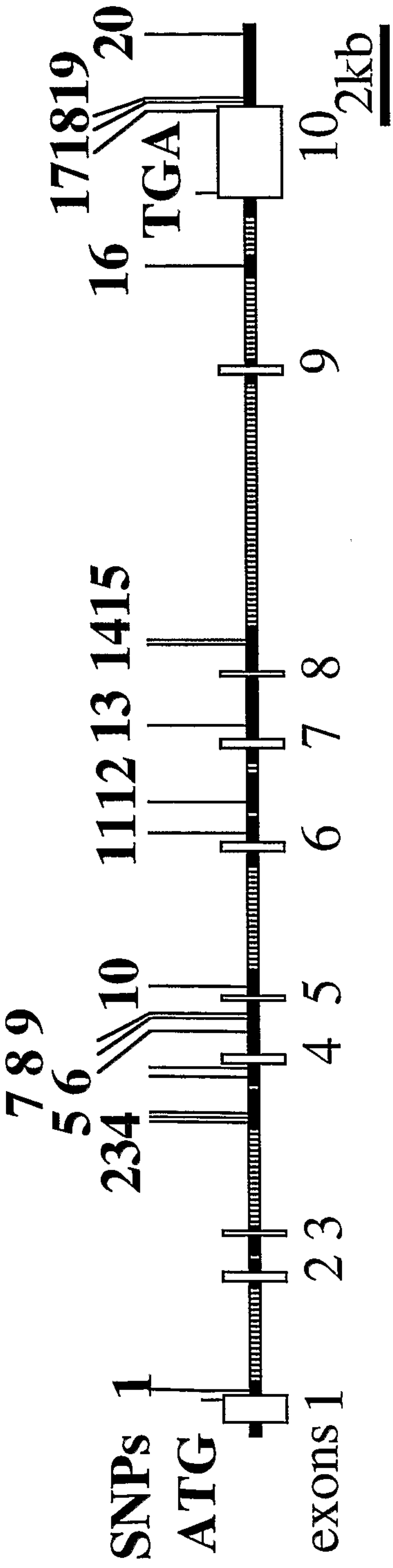


Fig.203 *Aldehyde dehydrogenase 3 family, member B1 (ALDH3B1)*
ACCESSION AC004923.2

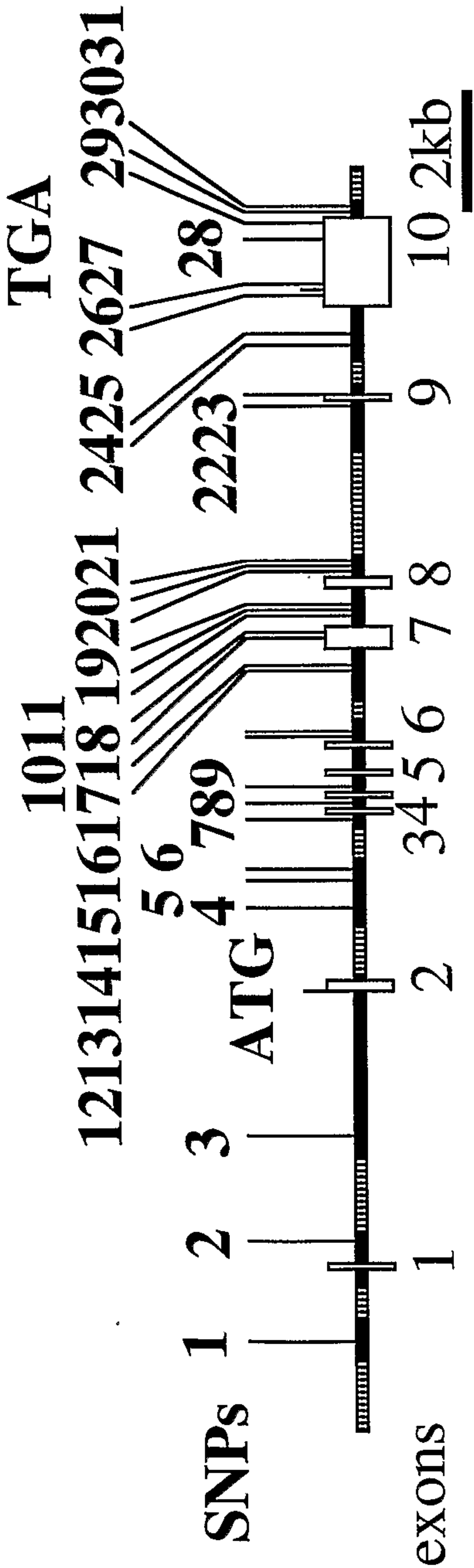


Fig.204 *Aldehyde dehydrogenase 3 family, member B2 (ALDH3B2)*

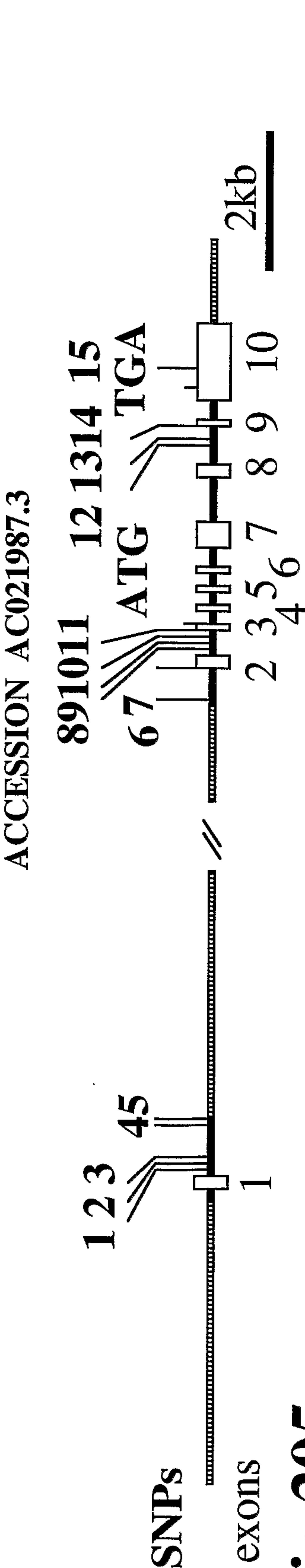


Fig.205 *Aldehyde dehydrogenase 5 family, member A1 (ALDH5A1)*

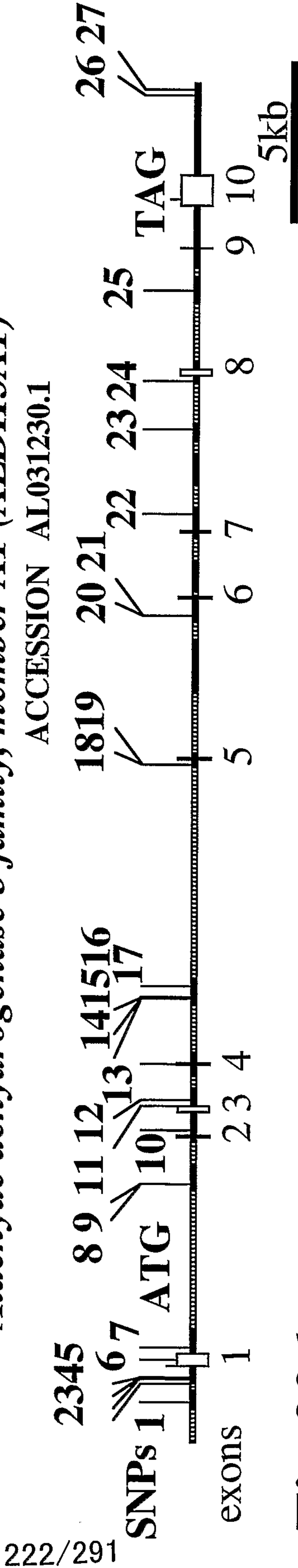


Fig.206 *Aldehyde dehydrogenase 6 family, member A1 (ALDH6A1)*

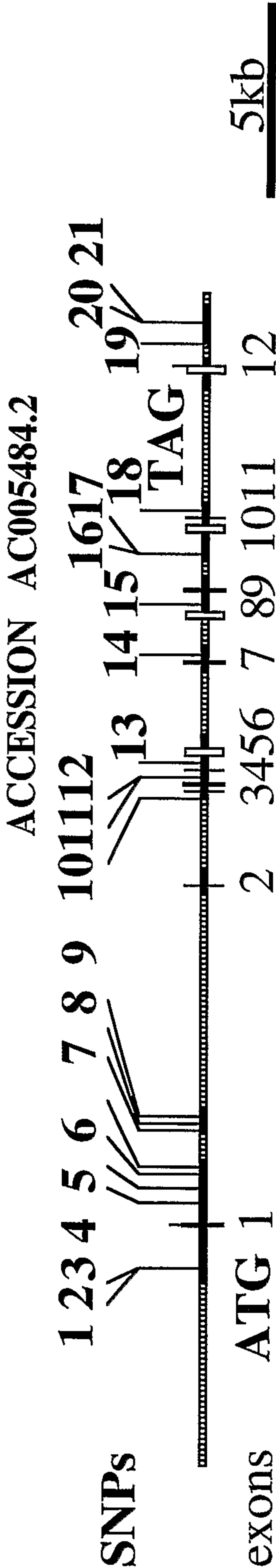


Fig.207 *Aldehyde dehydrogenase 8 family, member A1 (ALDH8A1)*

ACCESSION AL445190.9
AL021939.1

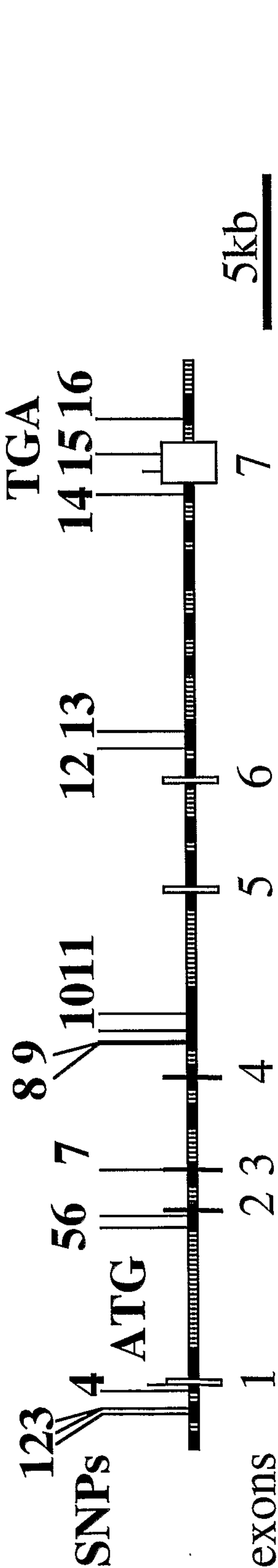


Fig.208 *Aldehyde dehydrogenase 9 family, member A1 (ALDH9A1)*

ACCESSION AL451074.4

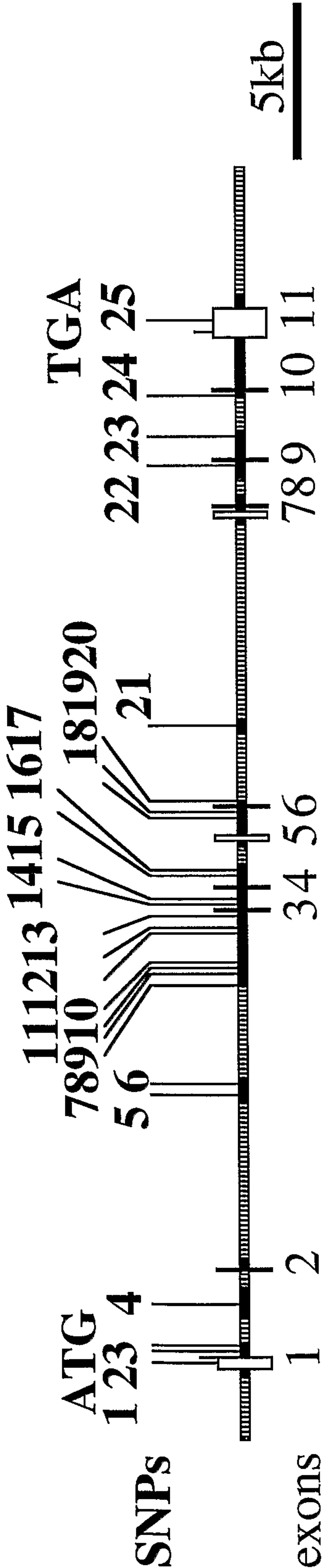


Fig.209Alcohol dehydrogenase 1 (*ADH1*)

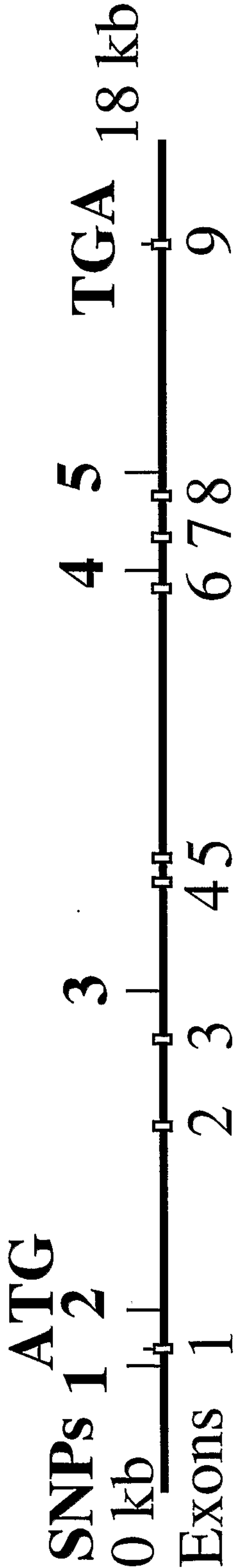


Fig.210 Alcohol dehydrogenase 2 (*ADH2*)

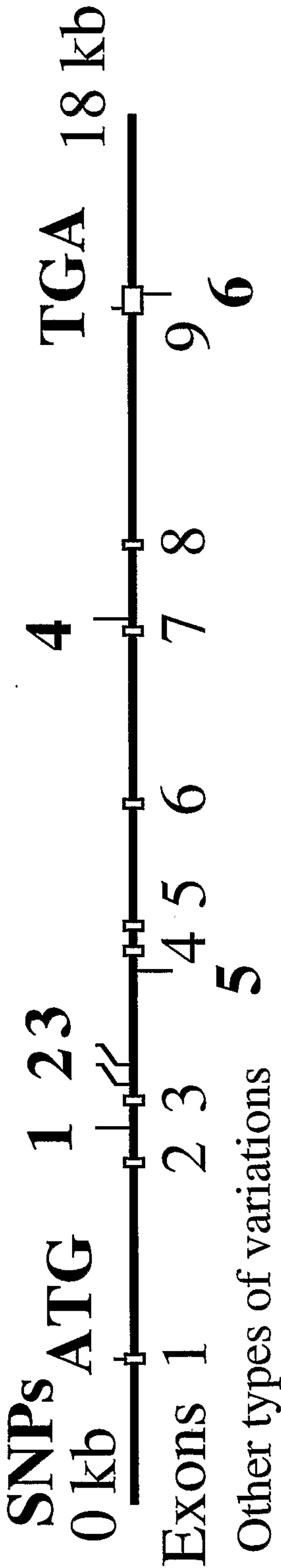


Fig.211 Alcohol dehydrogenase 3 (*ADH3*)

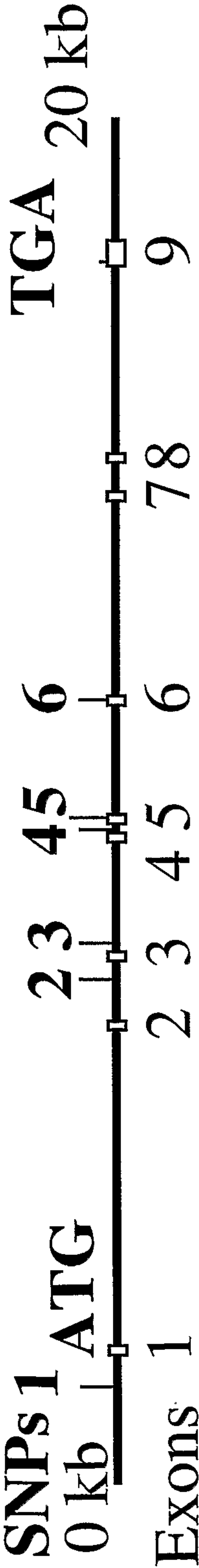


Fig. 212

Alcohol dehydrogenase 4 (ADH4)

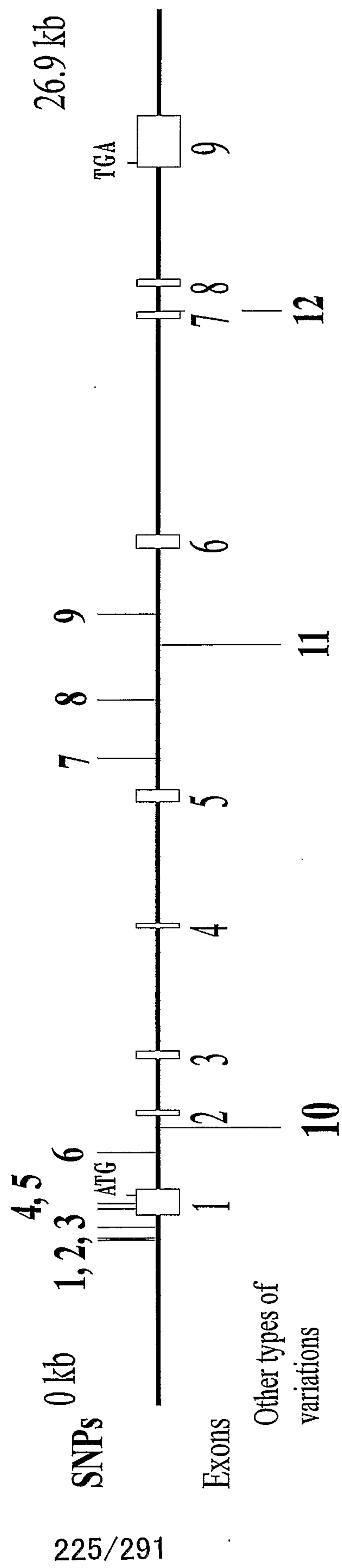


Fig.213 Alcohol dehydrogenase 5 (*ADH5*)

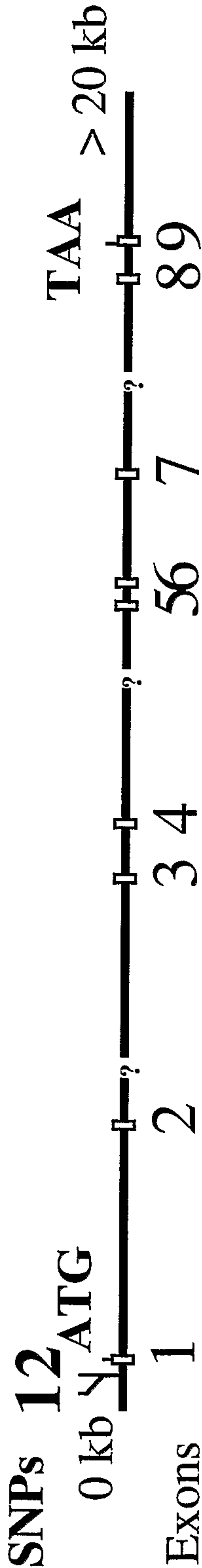


Fig.214 Alcohol dehydrogenase 6 (*ADH6*)

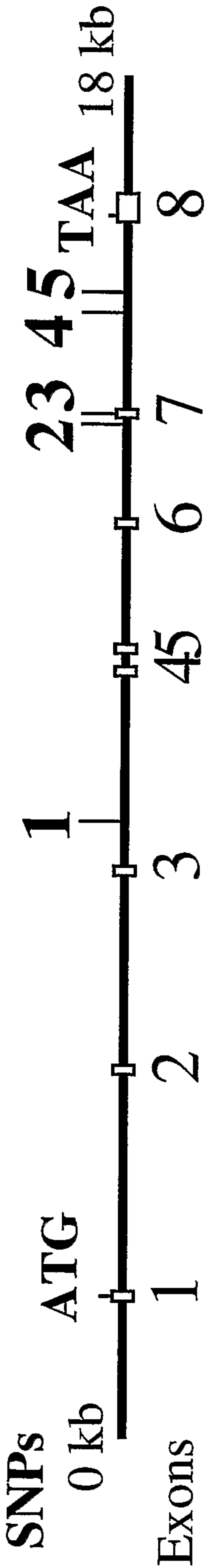


Fig.215 Alcohol dehydrogenase 7 (*ADH7*)

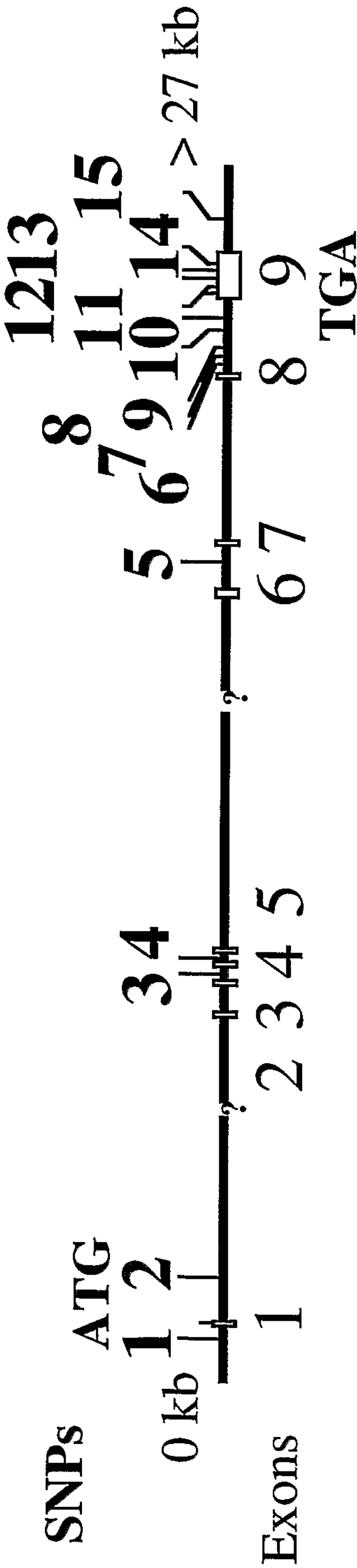


Fig.216 Short-chain alcohol dehydrogenase family gene
(*HEP27*)

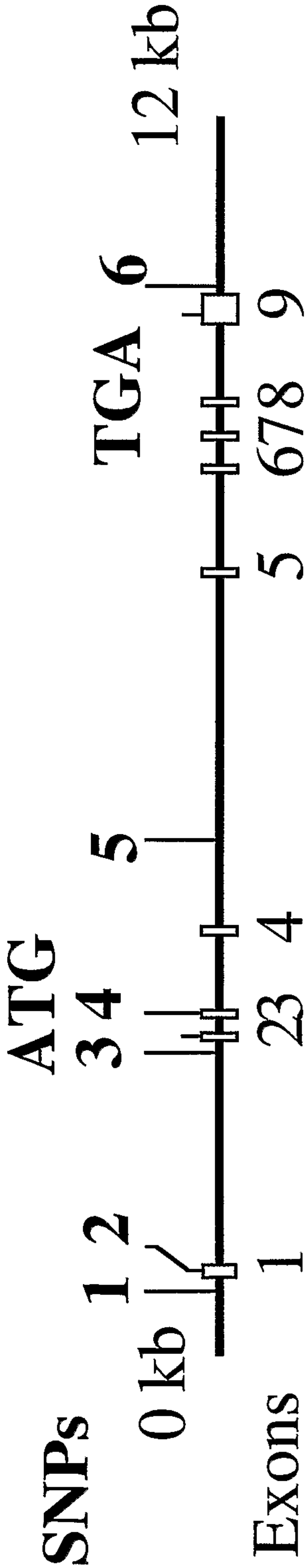


Fig.217
UDP glycosyltransferase 1 family, peptide A1
(*UGT1A1*)

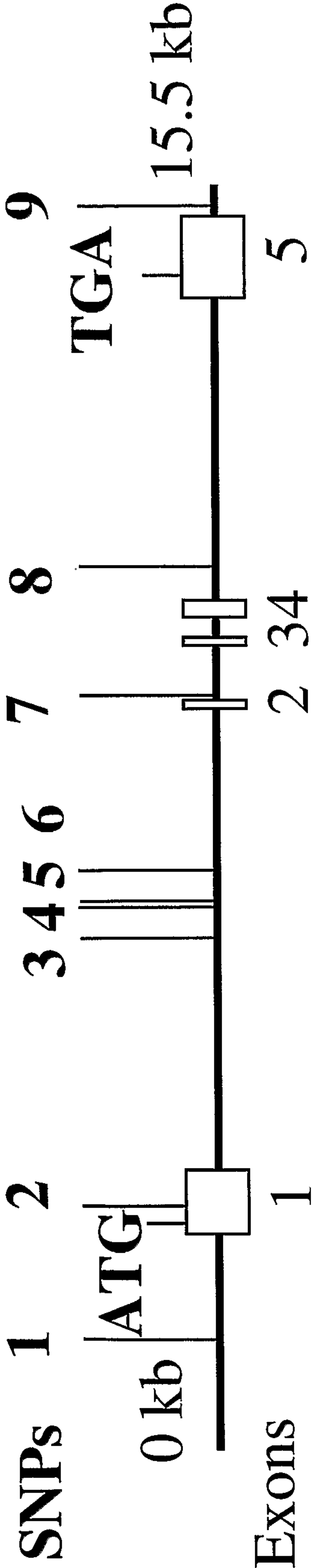


Fig. 218
UDP glycosyltransferase 2 family, polypeptide A1 (*UGT2A1*)

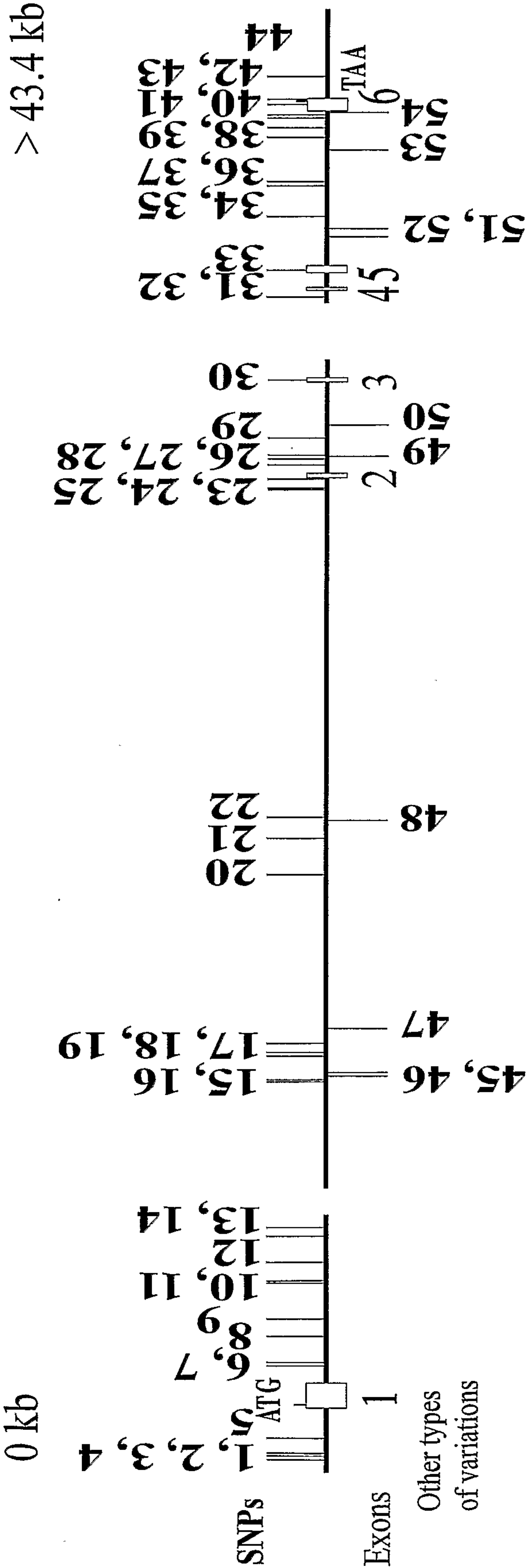


Fig. 219
UDP-glycosyltransferase 2 family, polypeptide B15(*UGT2B15*)

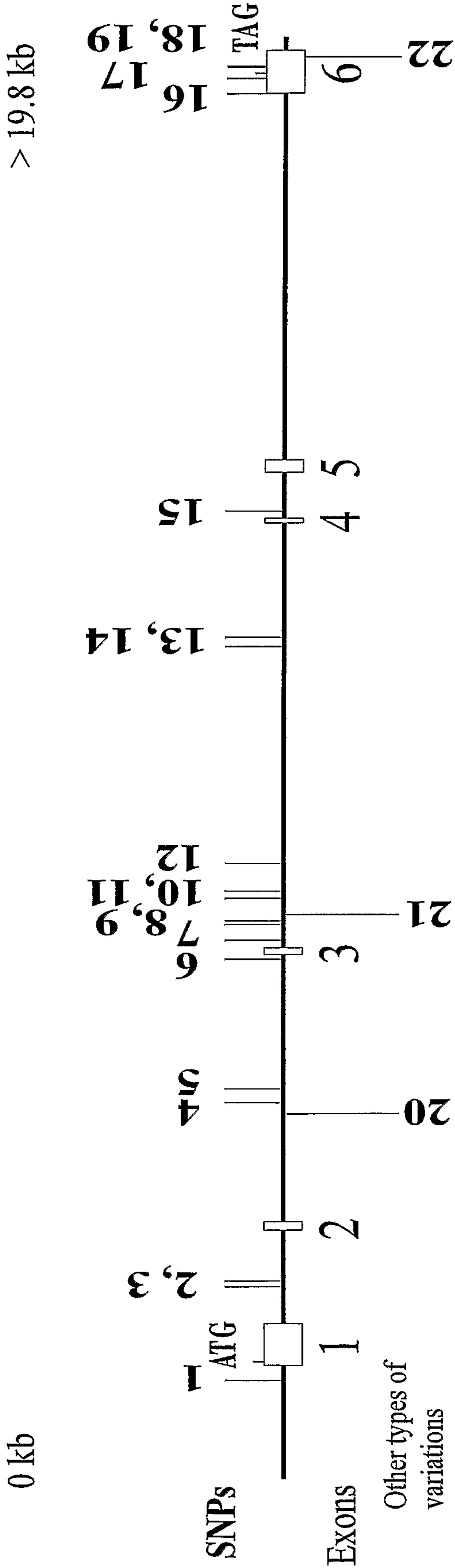
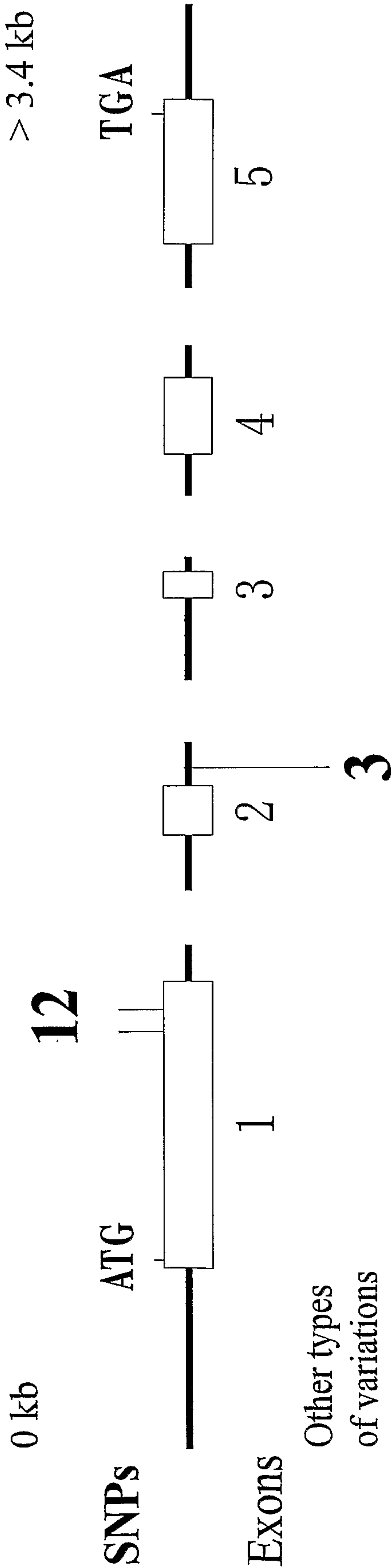


Fig. 220
UDP glycosyltransferase 8 (*UGT8*)



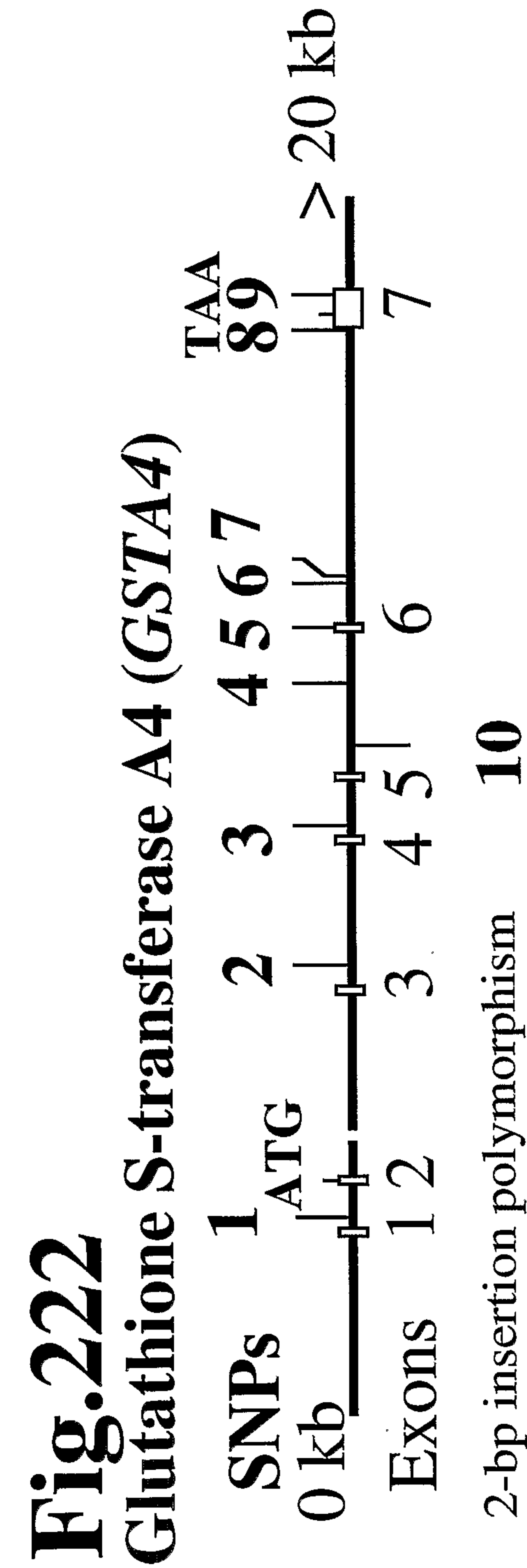


Fig.223

Glutathione S-transferase M1 (*GSTM1*)

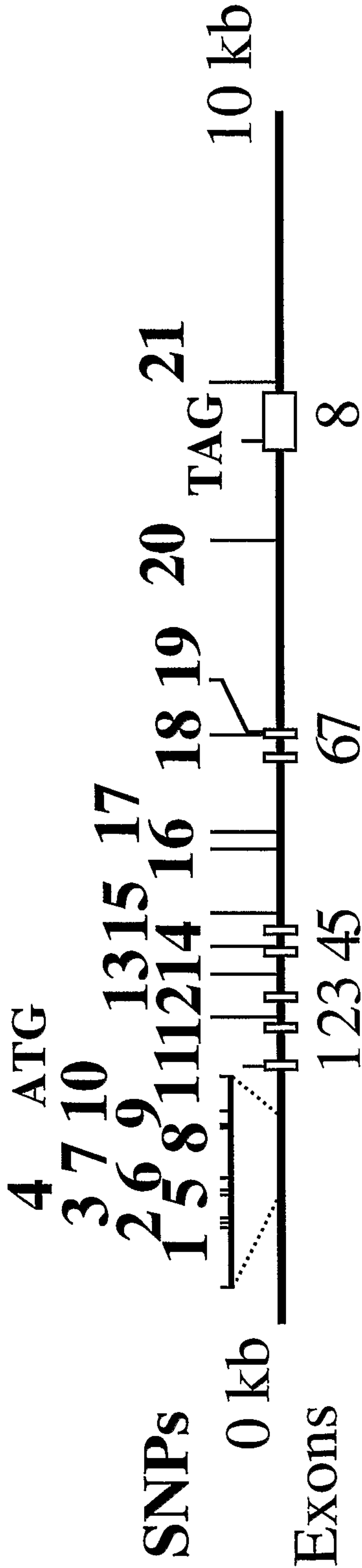
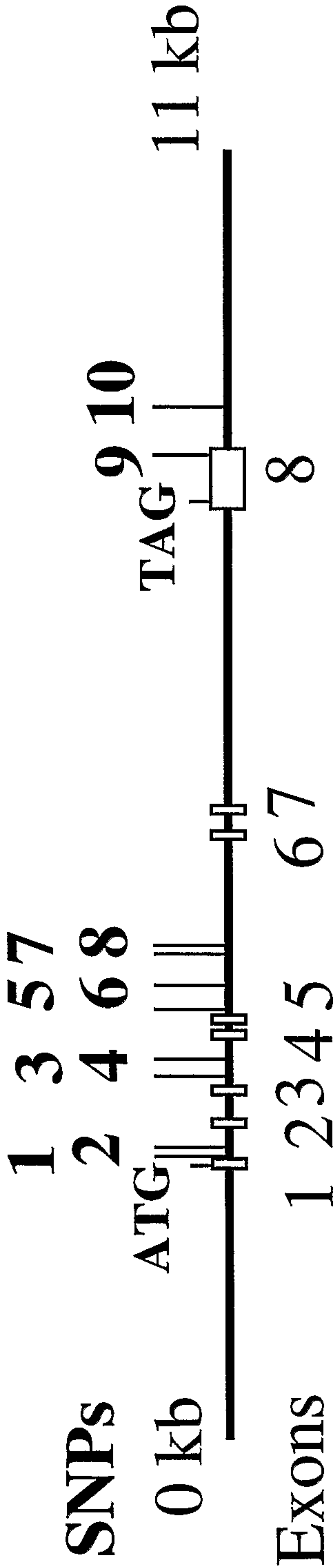


Fig.224

Glutathione S-transferase M2 (*GSTM2*)



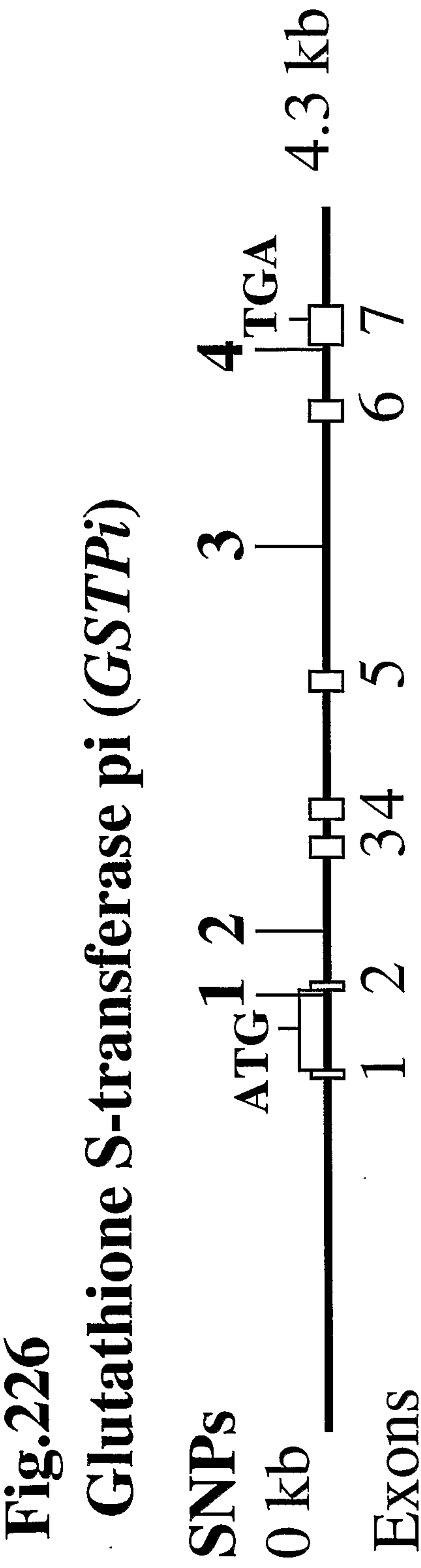


Fig.227
Glutathione S-transferase theta 1 (*GSTT1*)

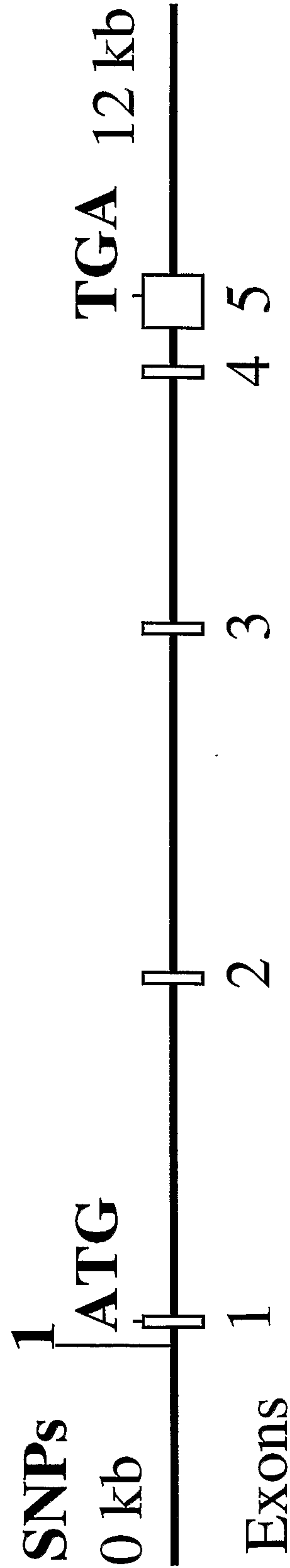


Fig. 228
Microsomal glutathione S-transferase 1 (*MGST1*)

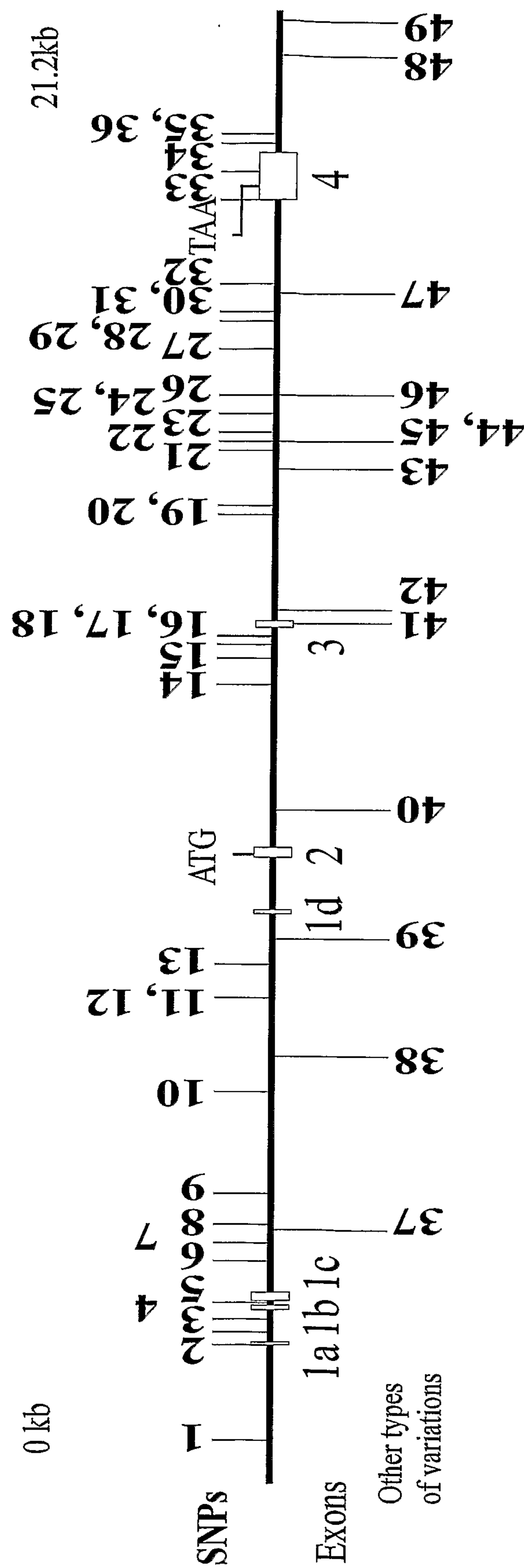


Fig.229
Microsomal glutathione S-transferase 1-like 1 (*MGST1L1*)

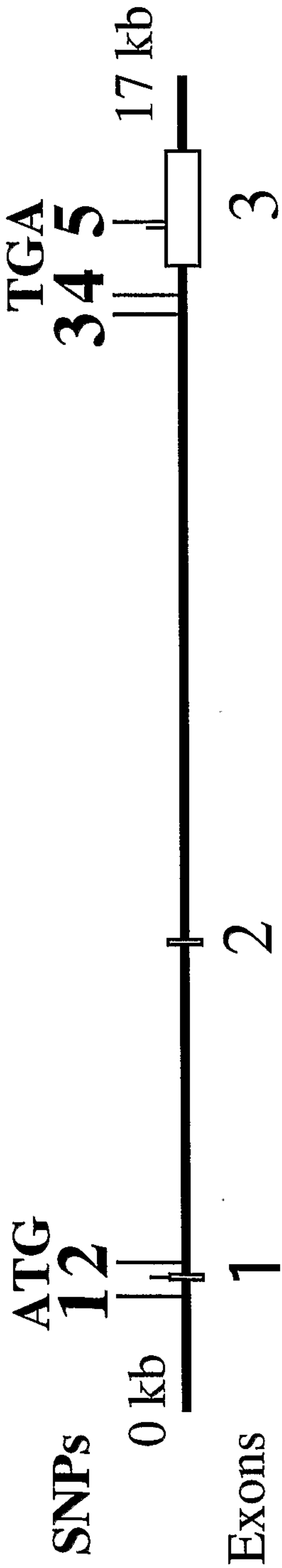


Fig.230
Microsomal glutathione S-transferase 2 (*MGST2*): AC019049.4

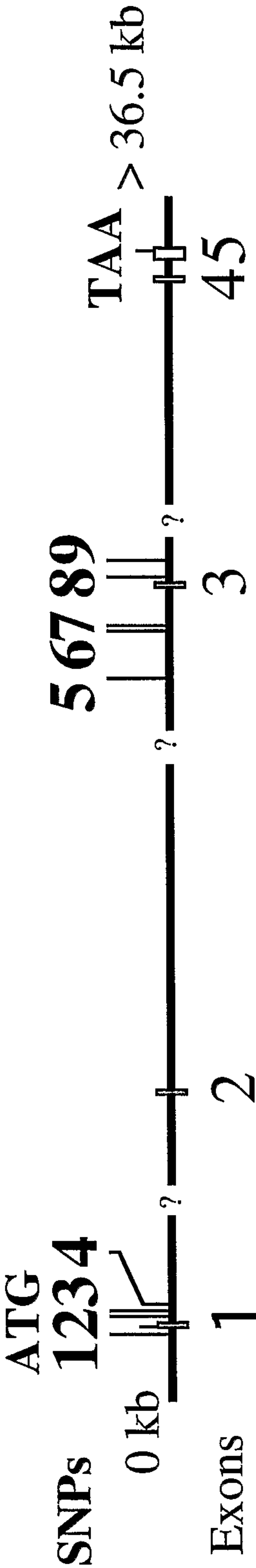


Fig.231
Microsomal glutathione S-transferase 3 (*MGST3*)

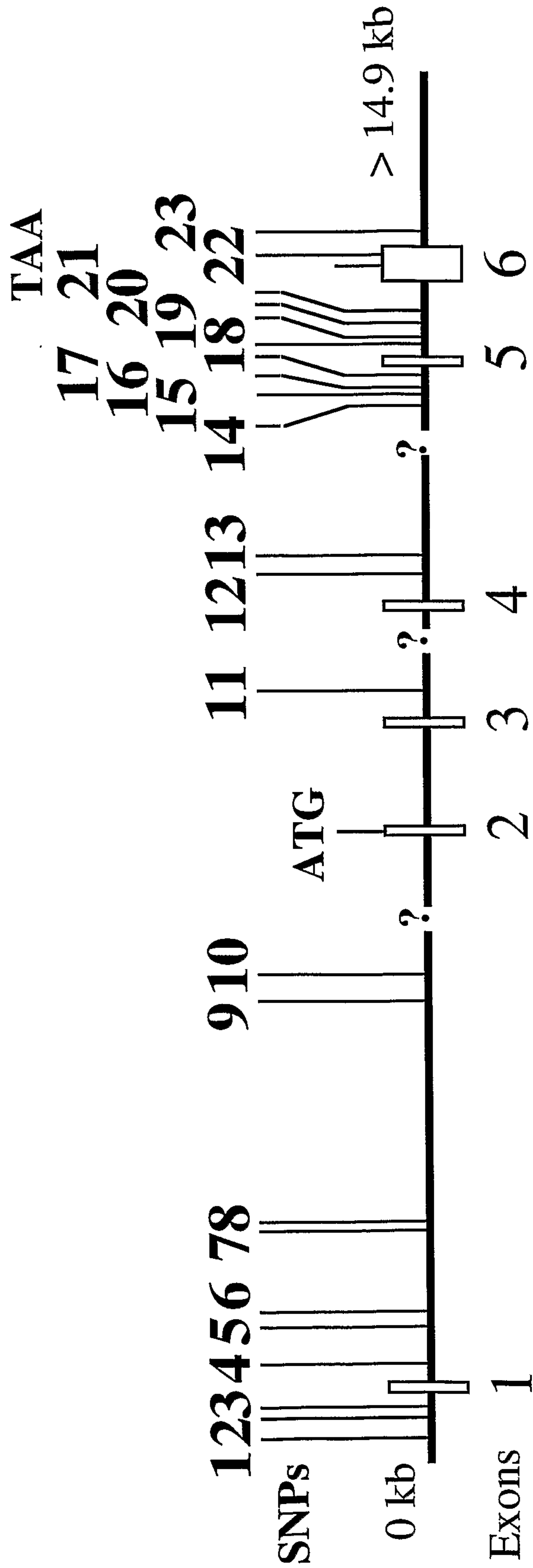


Fig.232

Sulfotransferase 1A1 (*SULT1A1/STP1*)

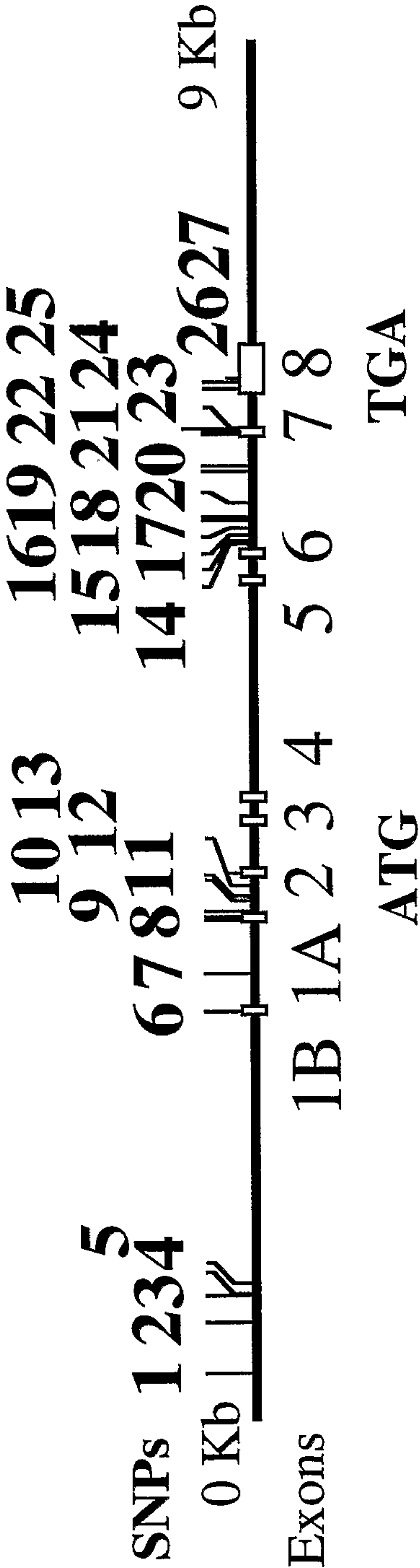


Fig.233

Sulfotransferase 1A2 (*SULT1A2/STP2*)

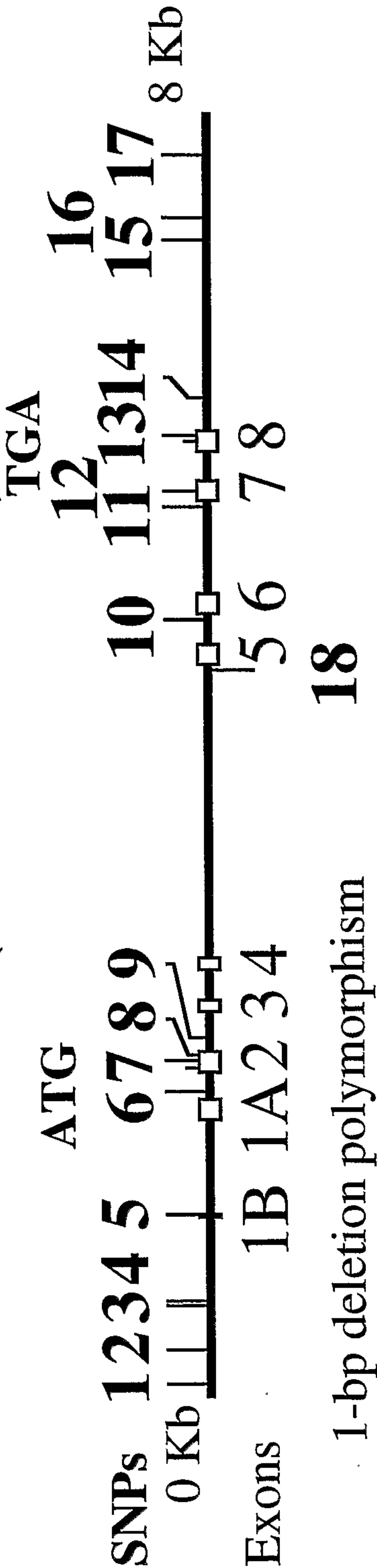


Fig.234
Sulfotransferase 1A3 (*SULT1A3/STM/ HAST*)

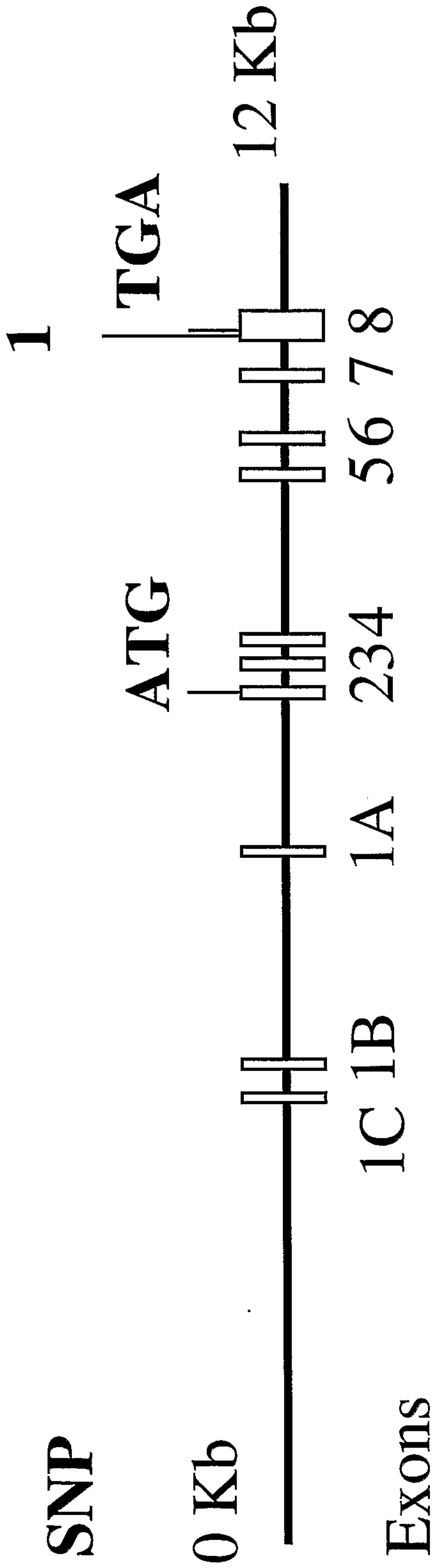


Fig.235 Sulfotransferase 1C1 (*SULT1C1*)

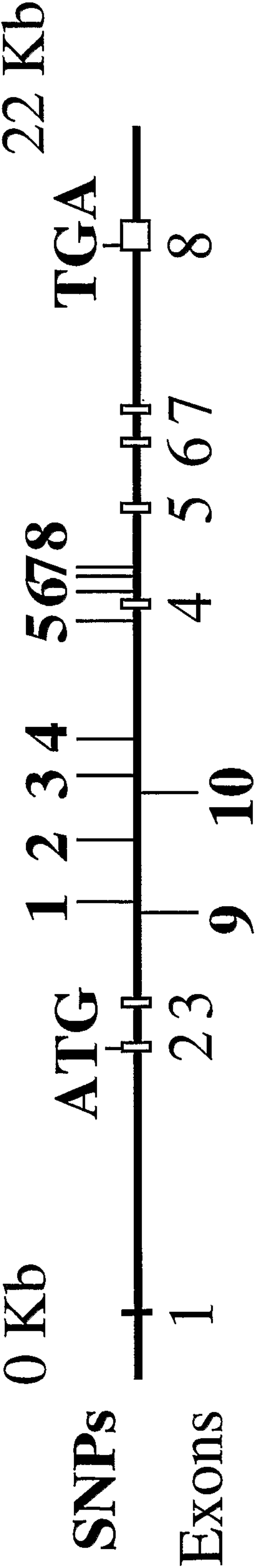


Fig.236 Sulfotransferase 1C2 (*SULT1C2*)

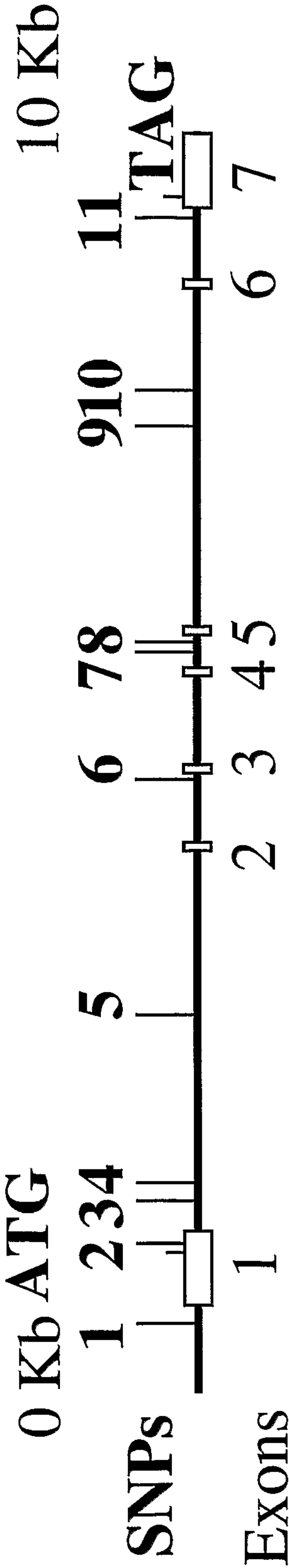


Fig.237 Sulfotransferase 2A1 (*SULT2A1*)

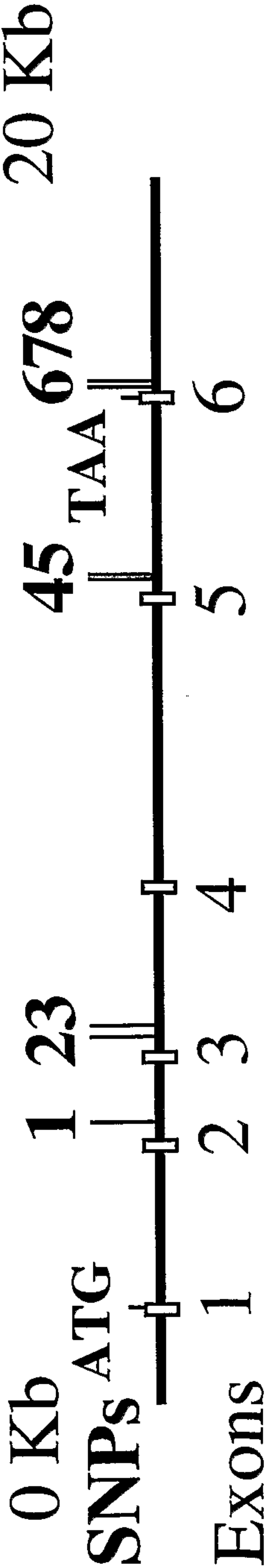
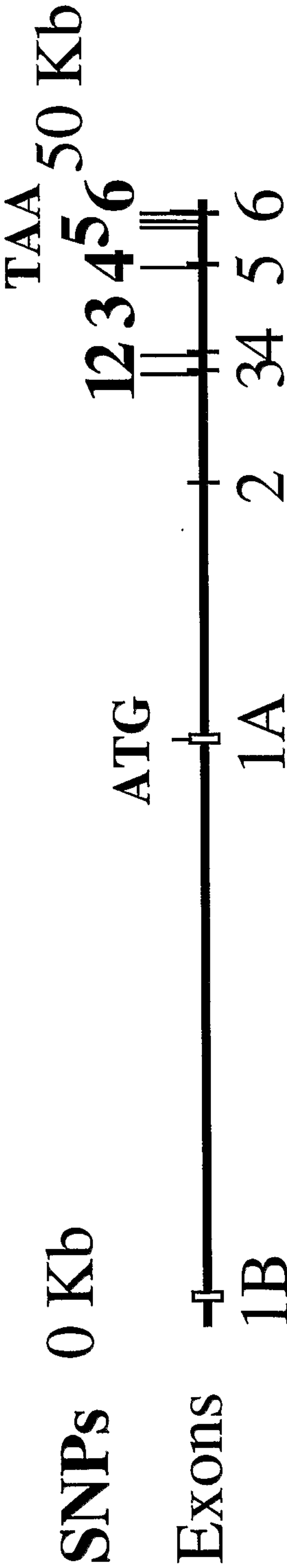


Fig.238 Sulfotransferase 2B1 (*SULT2B1*)



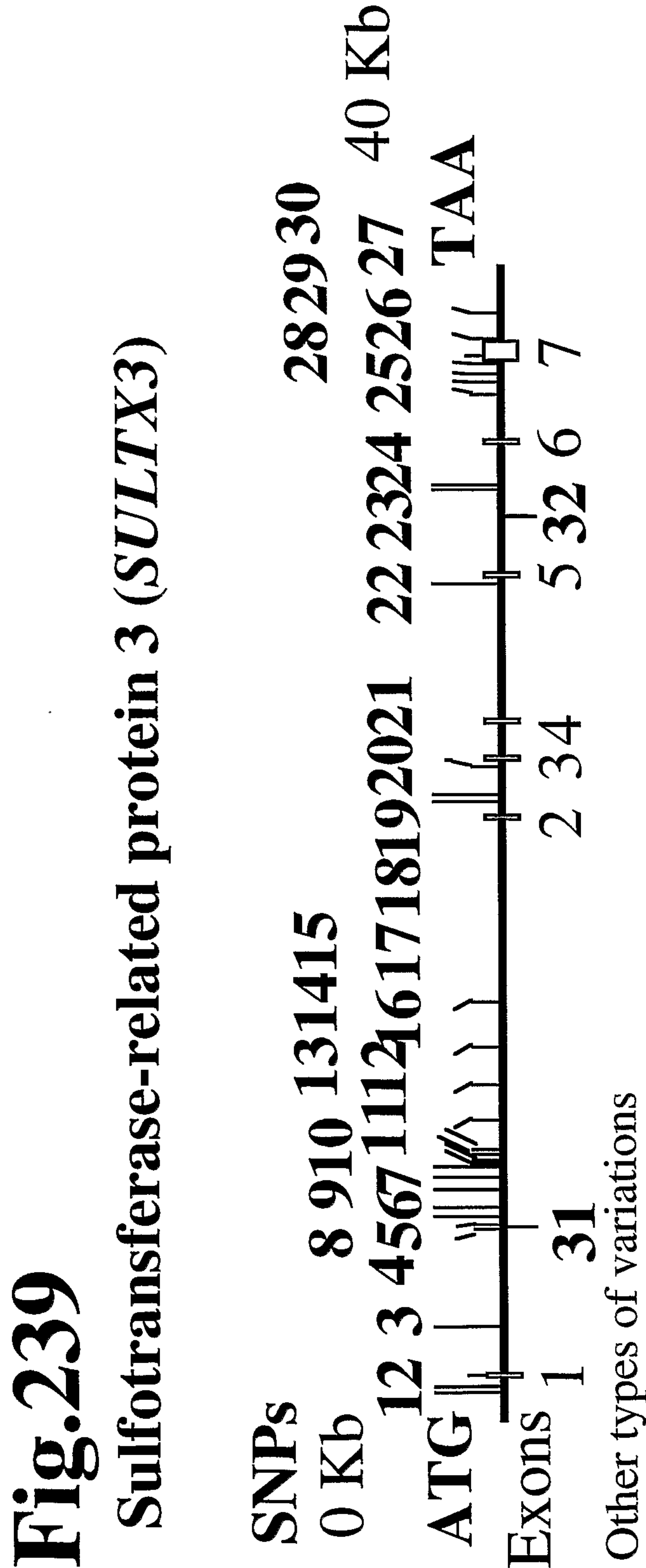


Fig.240 Tyrosylprotein sulfotransferase 1 (*TPST1*)

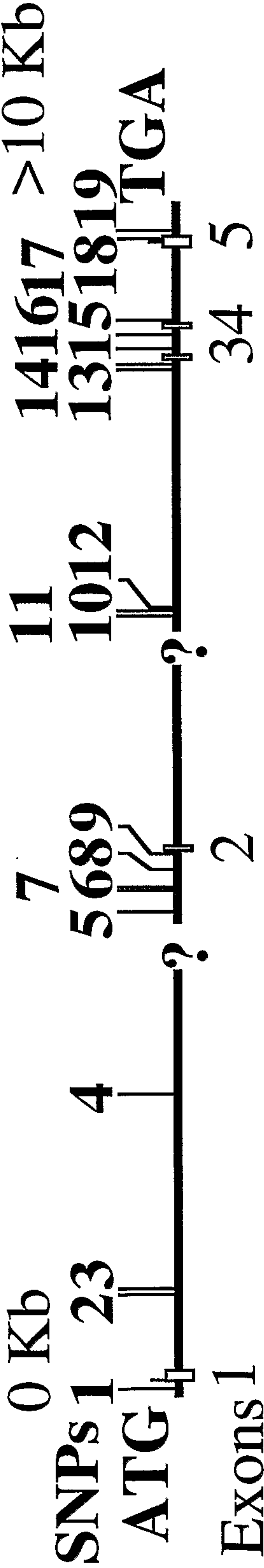


Fig.241 Tyrosylprotein sulfotransferase 2 (*TPST2*)

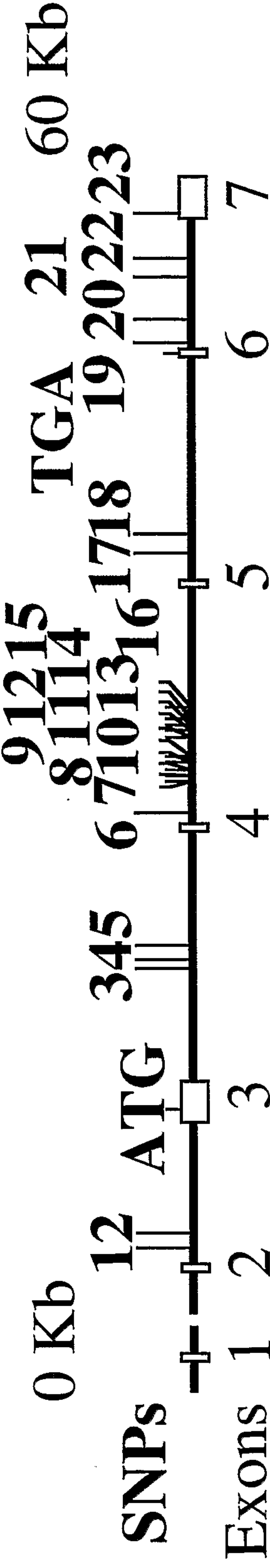
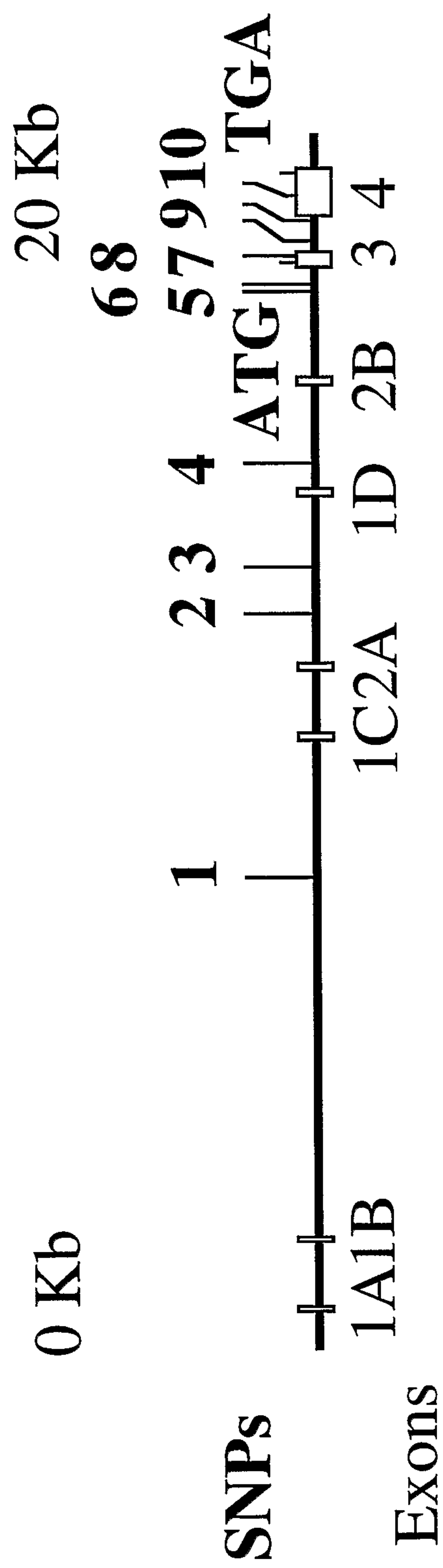


Fig. 242

Cerebroside Sulfotransferase (CST)



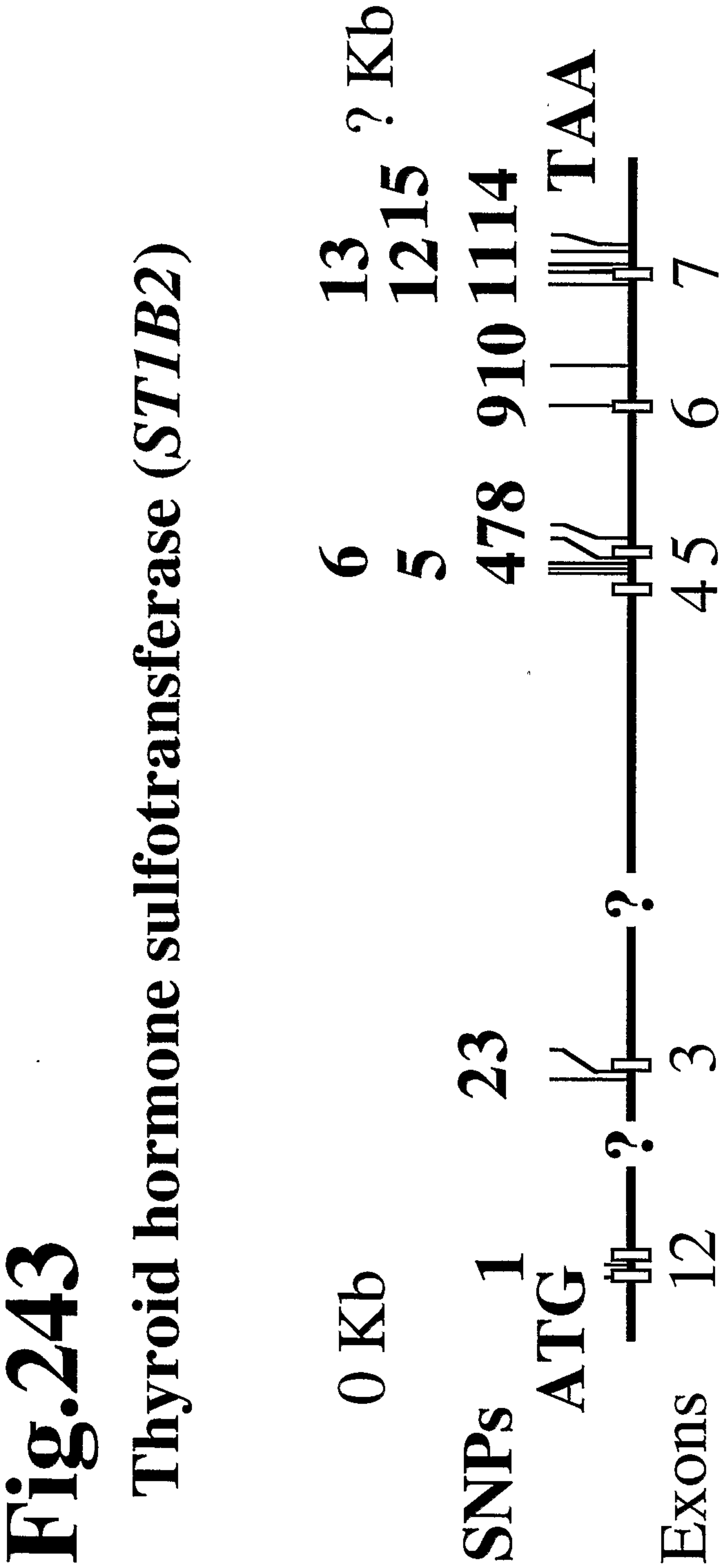


Fig.245
Carbohydrate sulfotransferase 2 (*CHST2*)

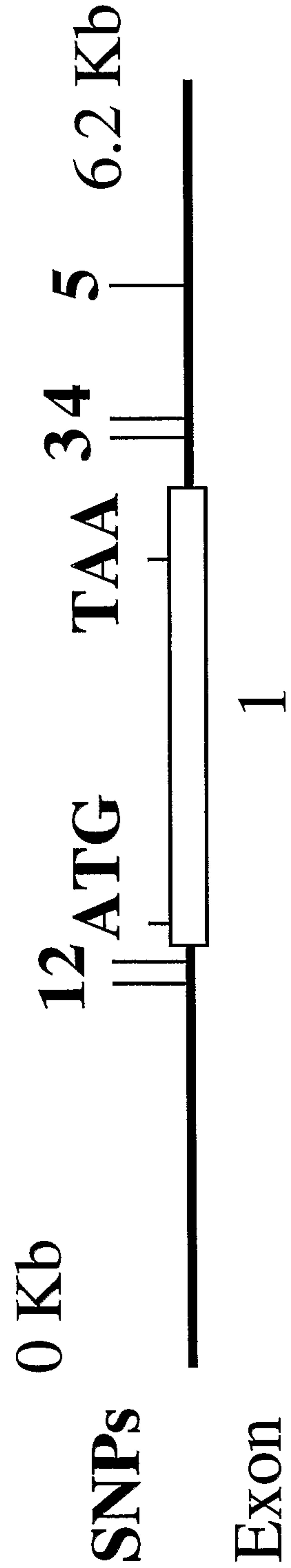
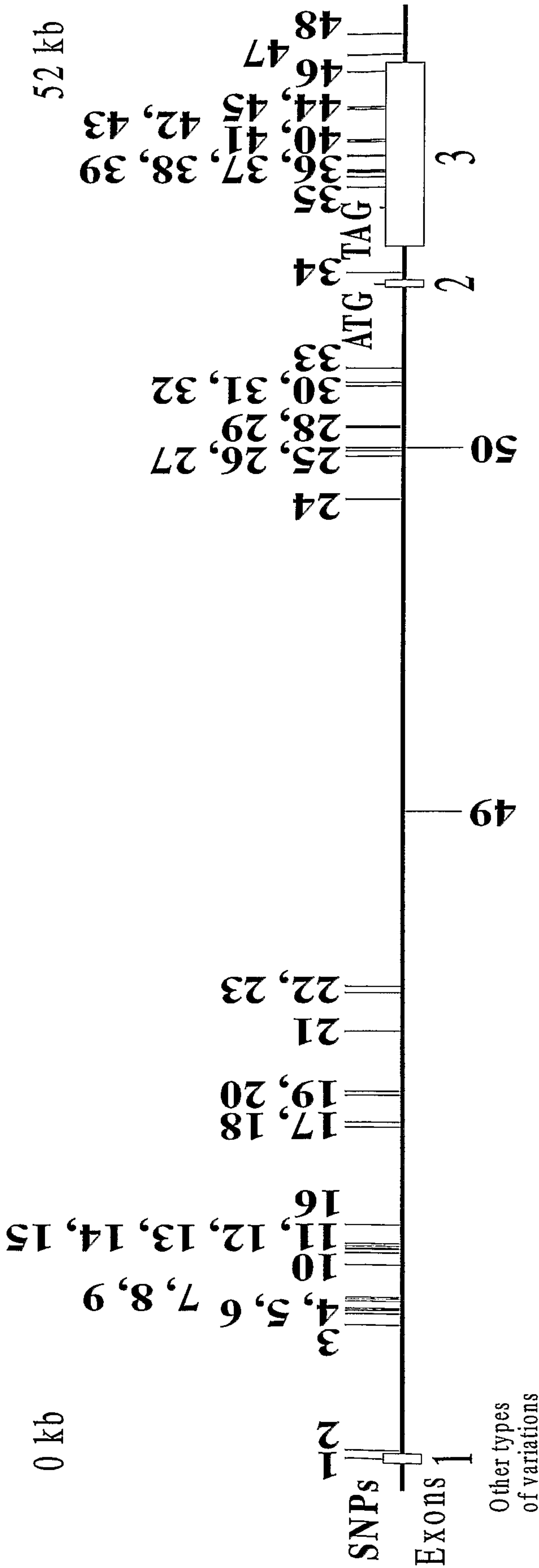


Fig. 246
Carbohydrate sulfotransferase 3 (*CHST3*)



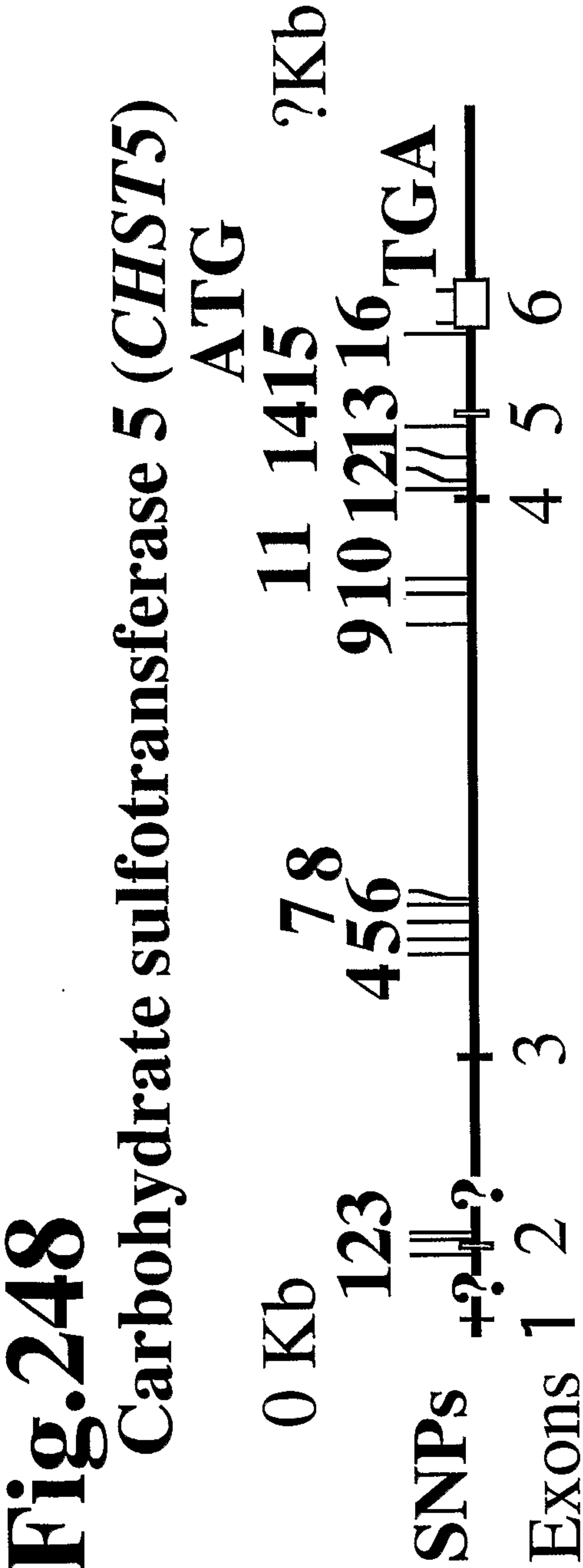
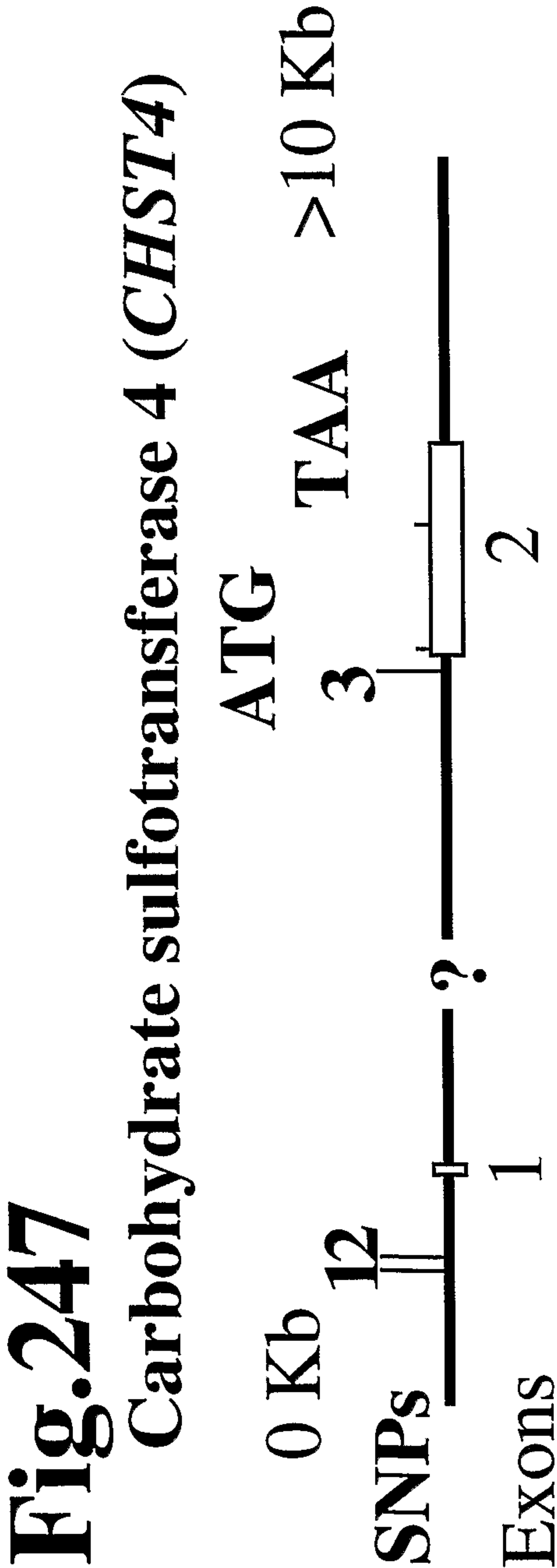


Fig. 249

HNK-sulfotransferase (*HNK-1ST*)

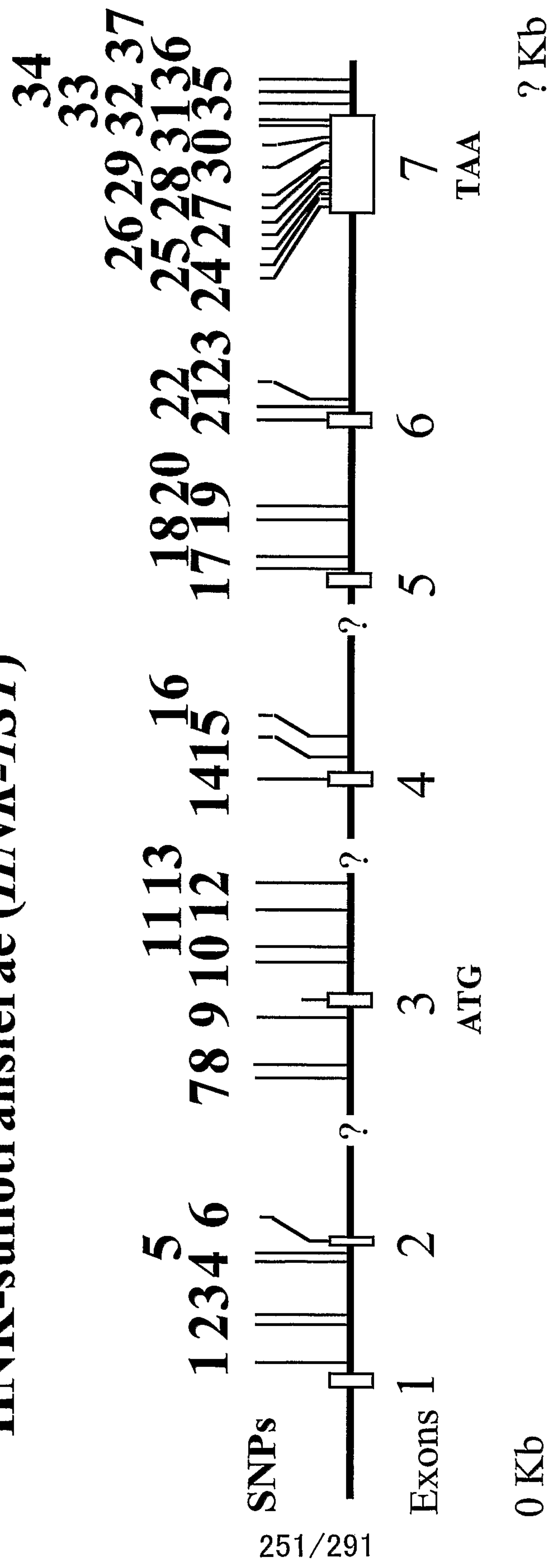


Fig. 250
Estrogen sulfotransferase (*STE*)

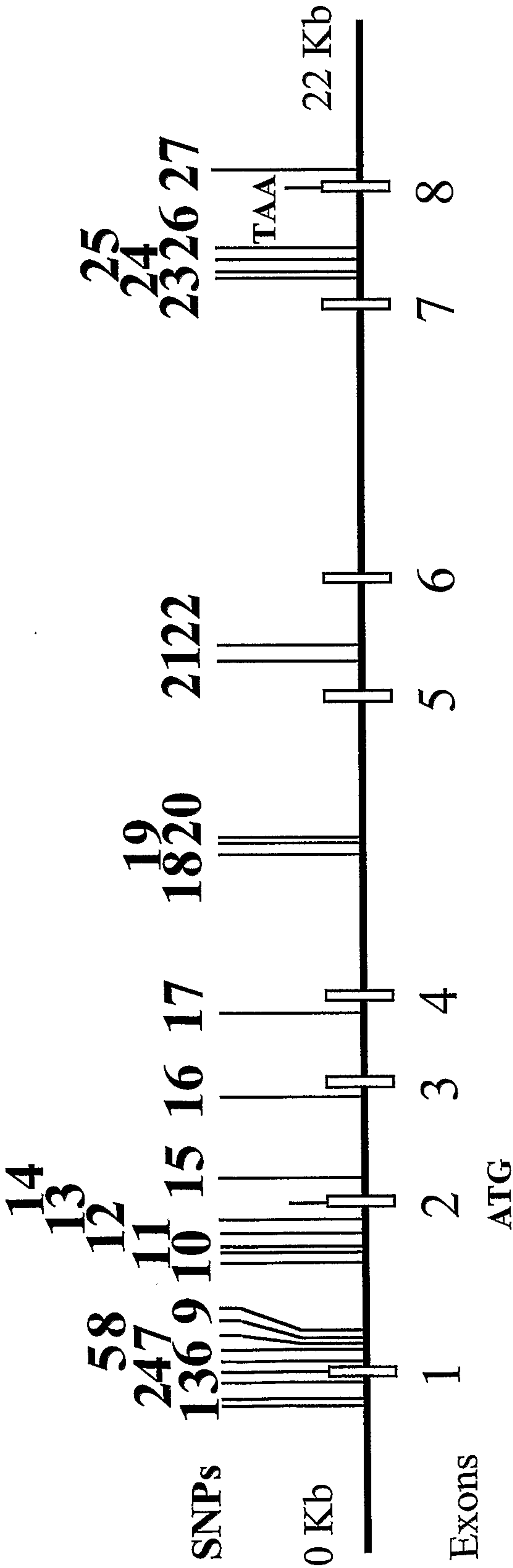


Fig. 251 NAD(P)H:quinone oxidoreductase 1 (*NQO1*)

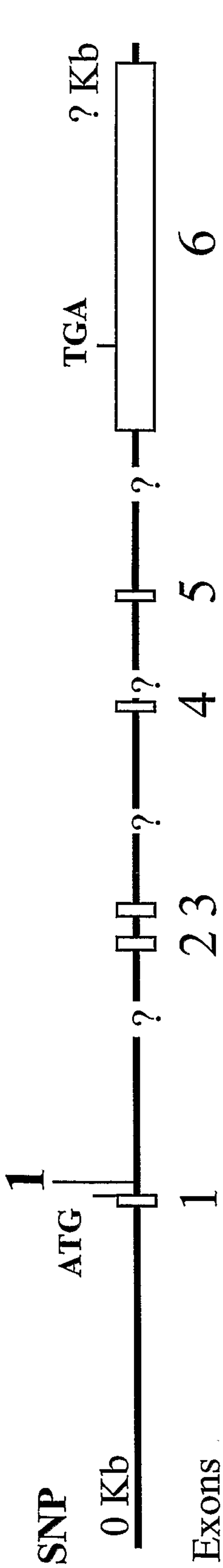


Fig. 252 NRH:quinone oxidoreductase 2 (*NQO2*)

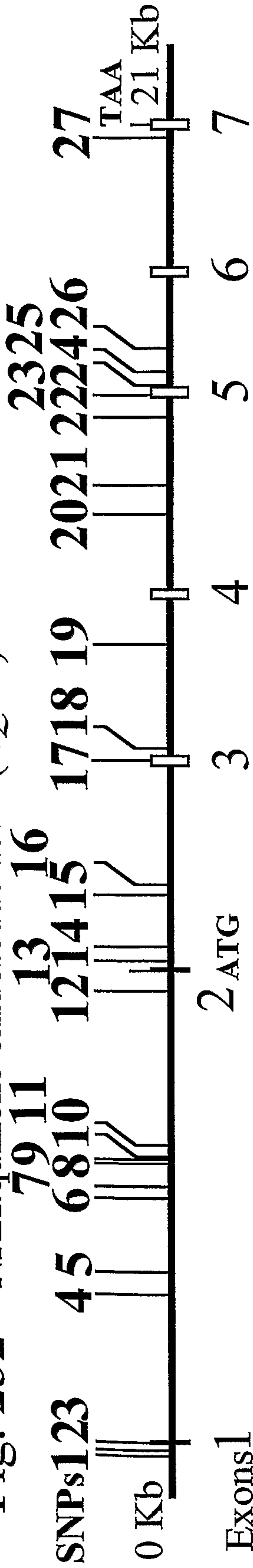


Fig. 253 p53-induced gene 3 (*PIG3*) / Quinone oxidoreductase homolog

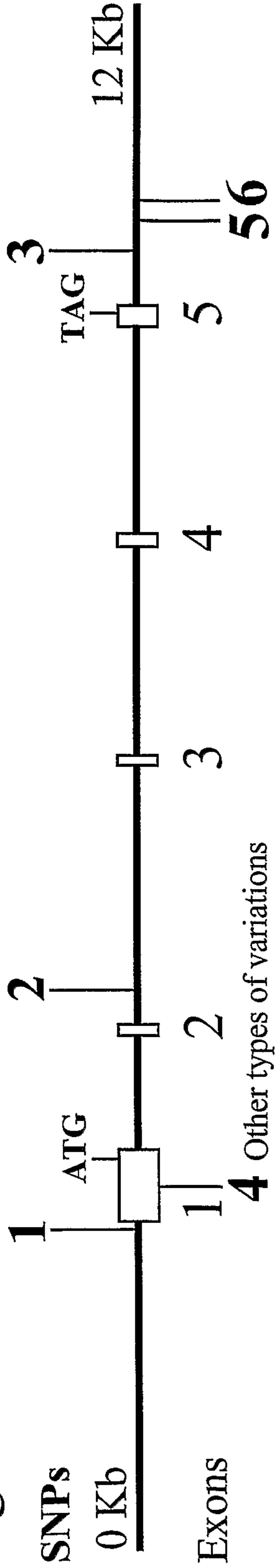


Fig. 254 NADH ubiquinone oxidoreductase 1 alpha subcomplex 1 (*NDUFA1*)

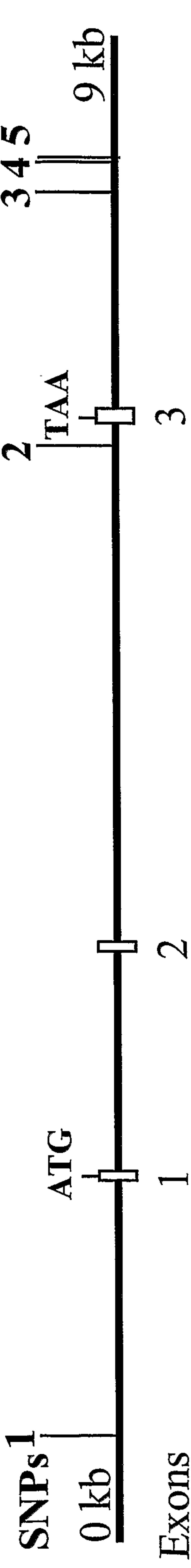


Fig. 255 NADH ubiquinone oxidoreductase 1 alpha subcomplex 2 (*NDUFA2*)

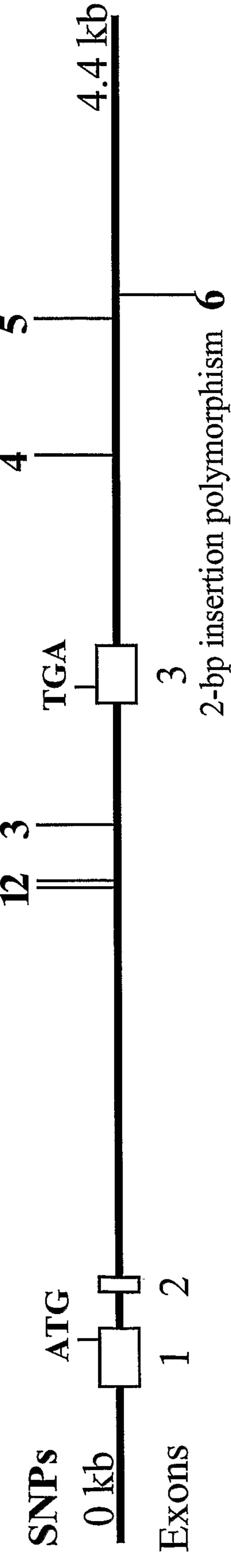


Fig. 256 NADH ubiquinone oxidoreductase 1 alpha subcomplex 3 (*NDUFA3*)

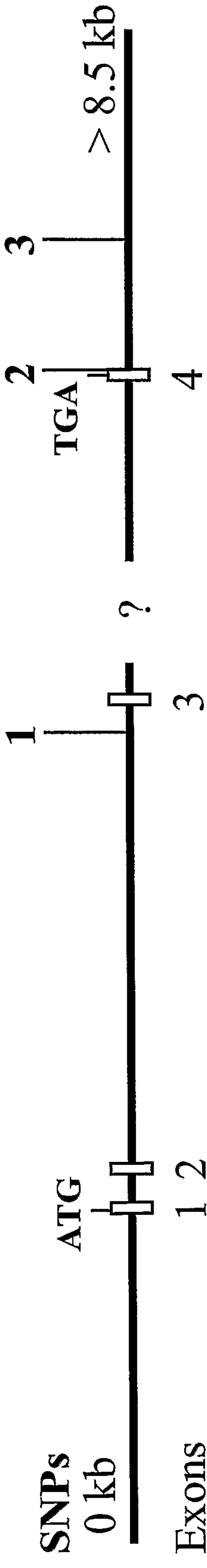


Fig. 257 NADH ubiquinone oxidoreductase 1 alpha subcomplex 5 (*NDUFA5*)

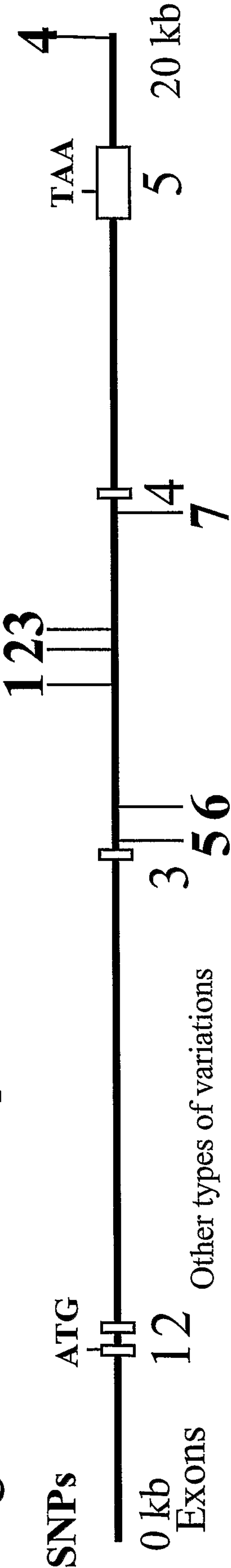


Fig. 258 NADH ubiquinone oxidoreductase 1 alpha subcomplex 6 (*NDUFA6*)

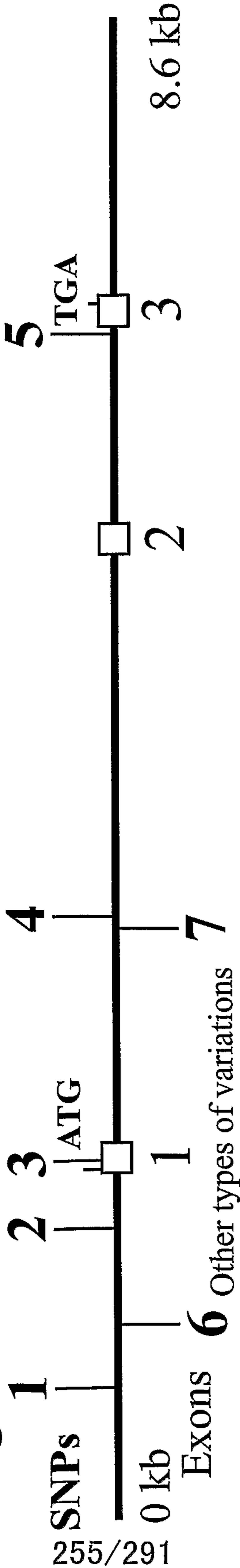


Fig. 259 NADH ubiquinone oxidoreductase 1 alpha subcomplex 7 (*NDUFA7*)

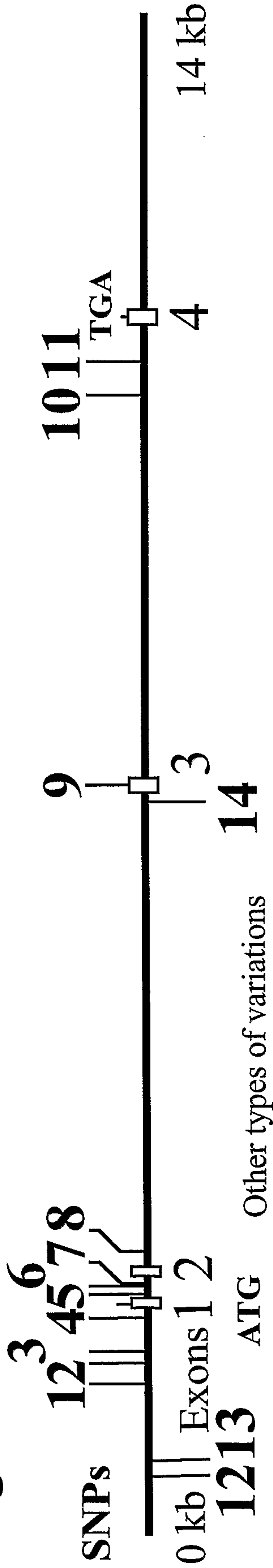


Fig. 260
NADH ubiquinone oxidoreductase 1 alpha subcomplex 8
(*NDUF A8*)

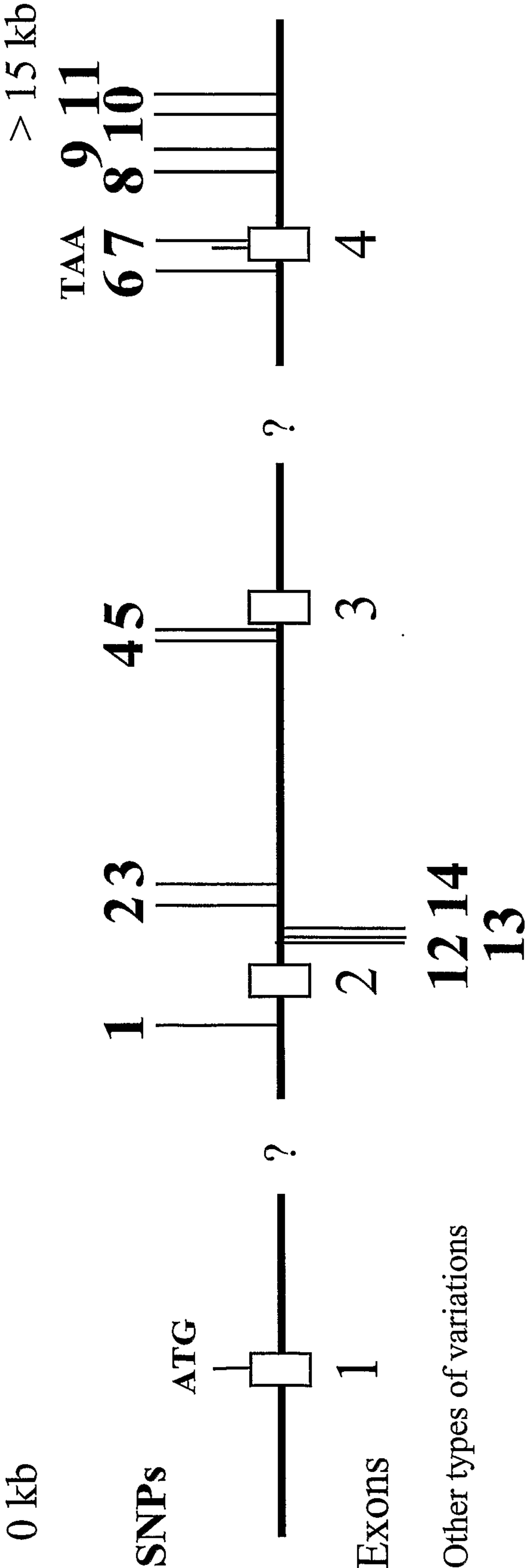


Fig. 261
NADH ubiquinone oxidoreductase 1 alpha subcomplex 9 (*NDUF A9*)

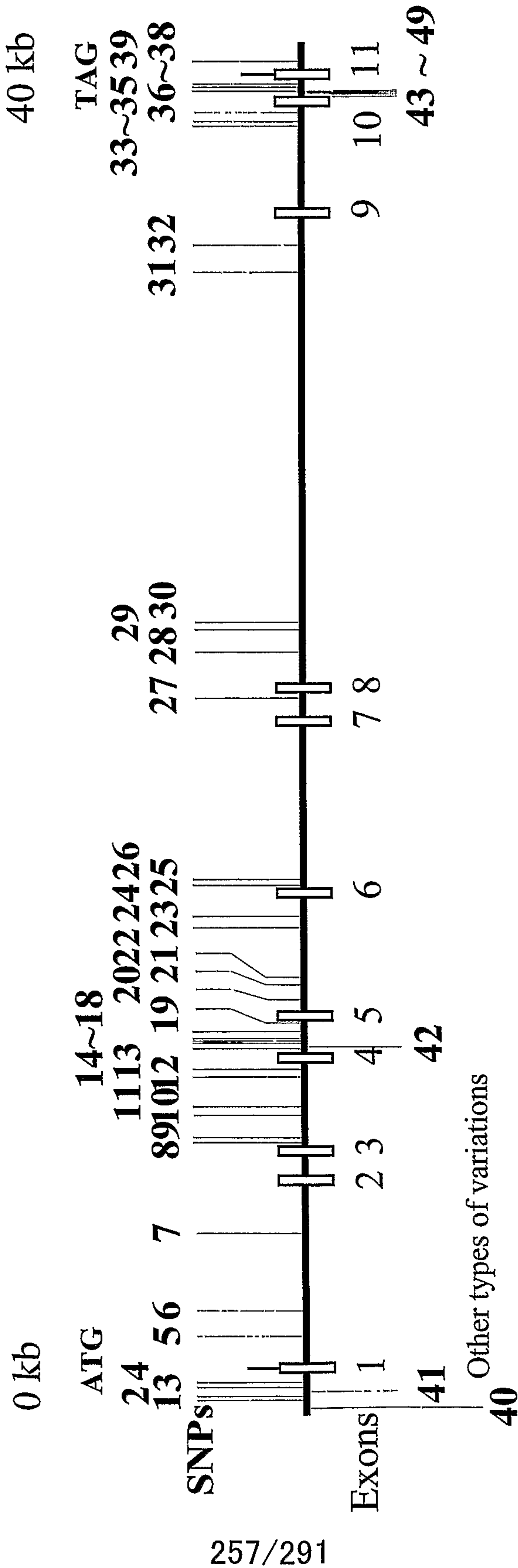


Fig. 262
NADH: ubiquinone oxidoreductase A 10 (*NDUFA10*)

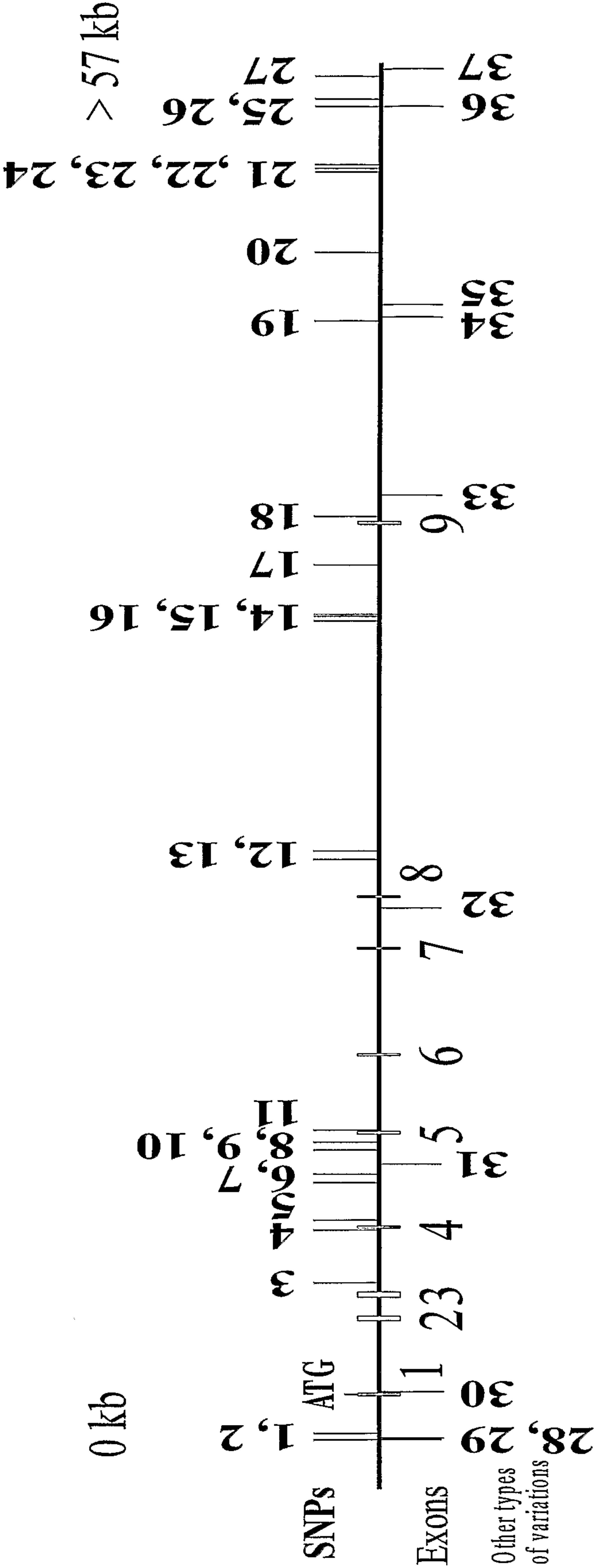
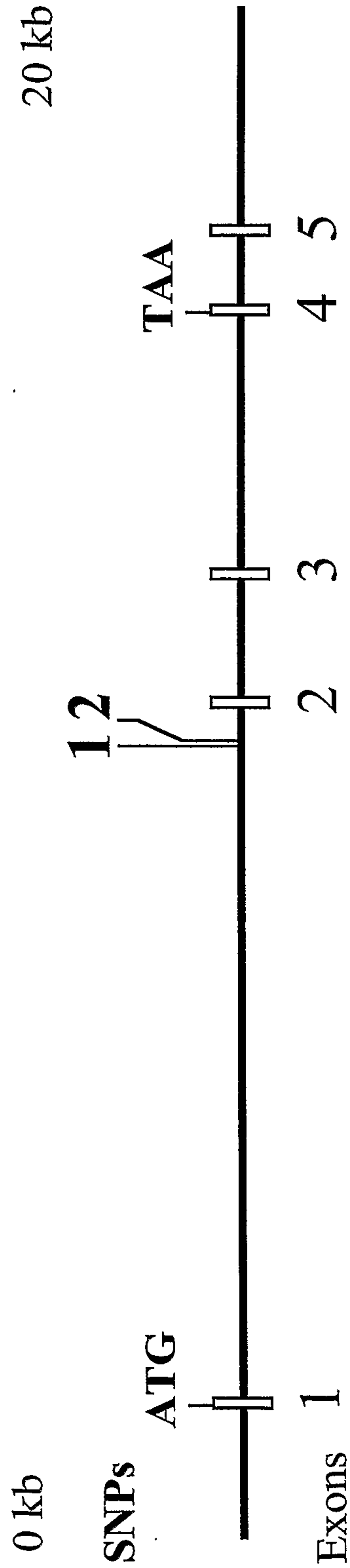


Fig. 263
NADH ubiquinone oxidoreductase 1 alpha/beta subcomplex 1
(*NDUFAB1*)



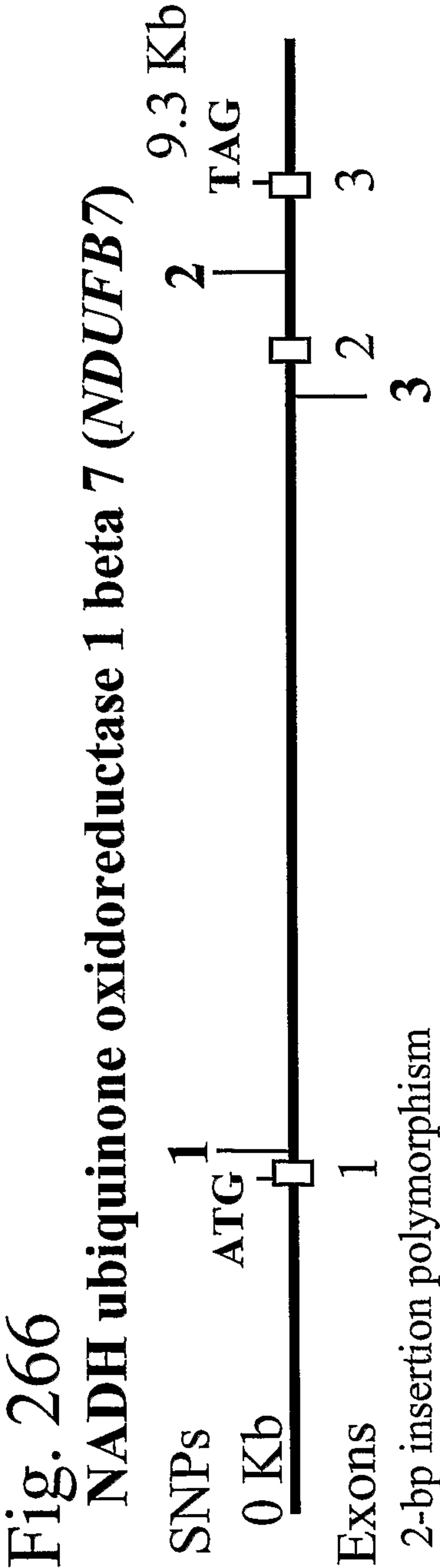
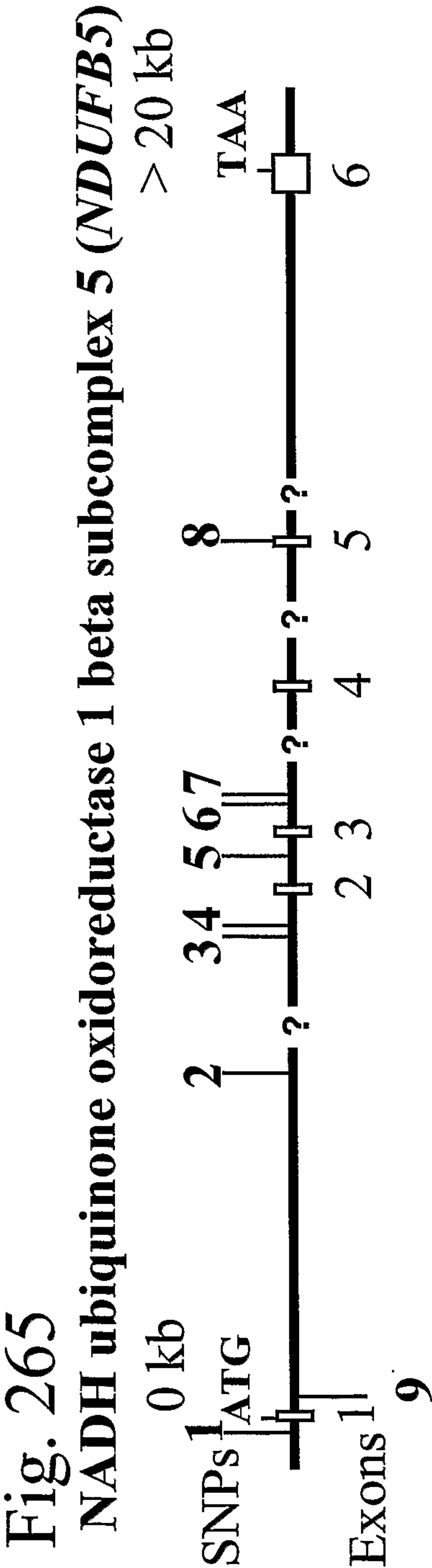
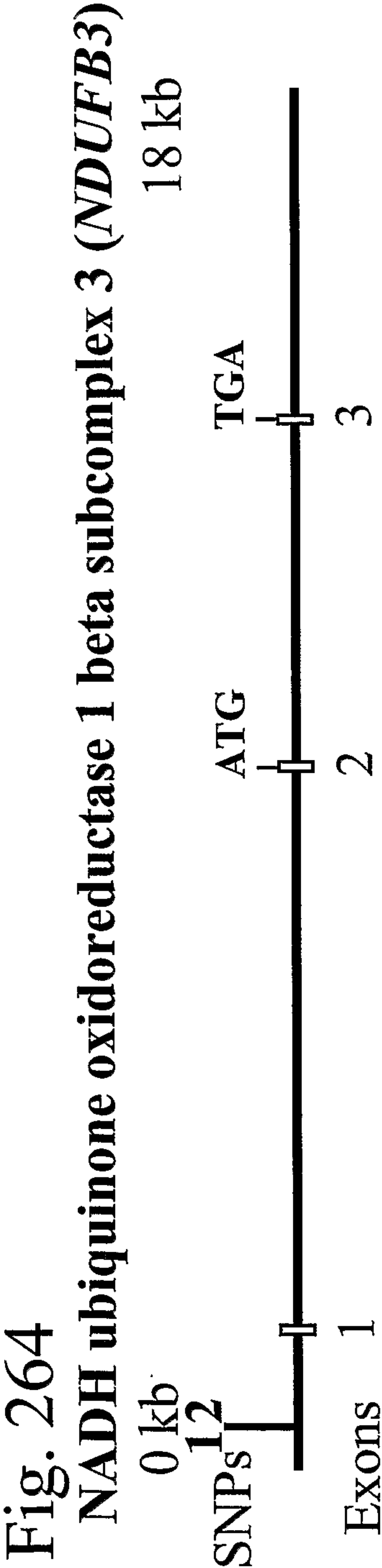


Fig. 267 NADH ubiquinone oxidoreductase Fe-S protein 1 (*NDUFS1*)

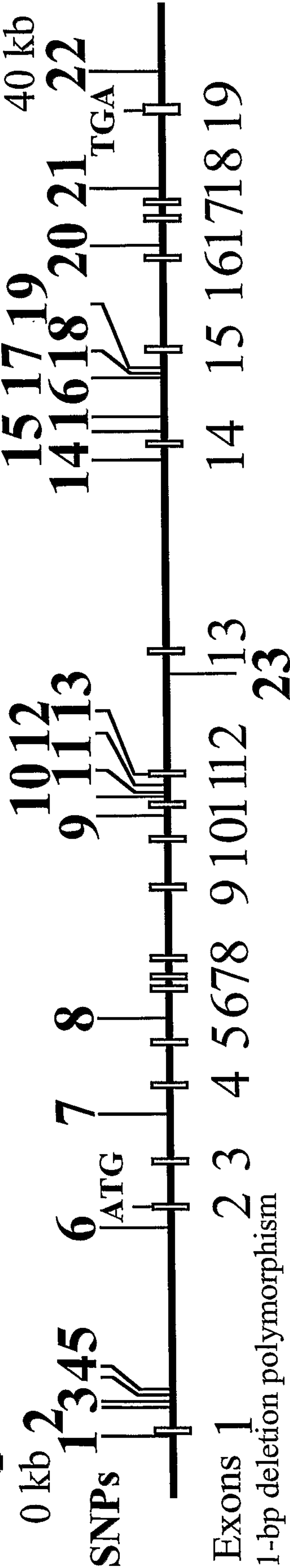


Fig. 268 NADH ubiquinone oxidoreductase Fe-S protein 3 (*NDUFS3*)

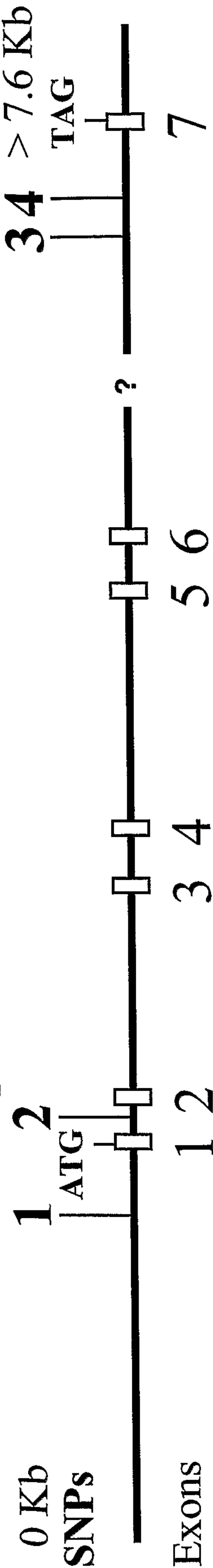
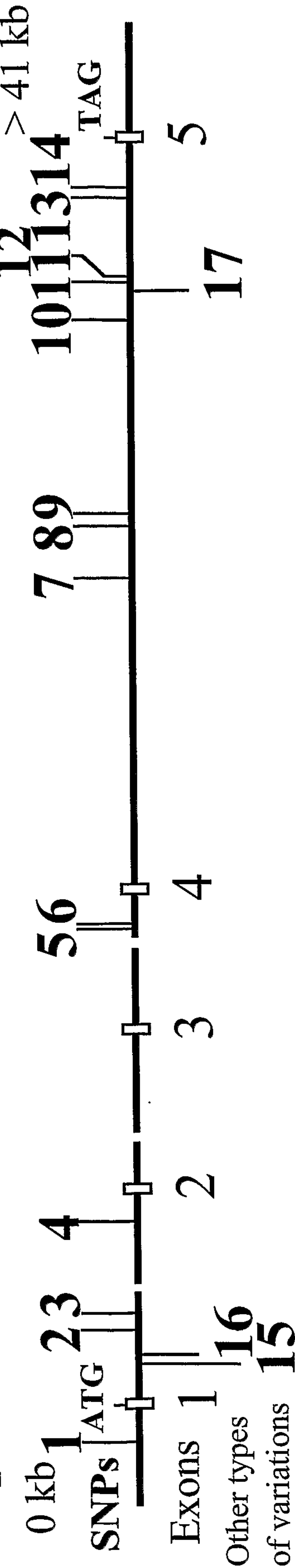


Fig. 269 NADH ubiquinone oxidoreductase Fe-S protein 4 (*NDUFS4*)



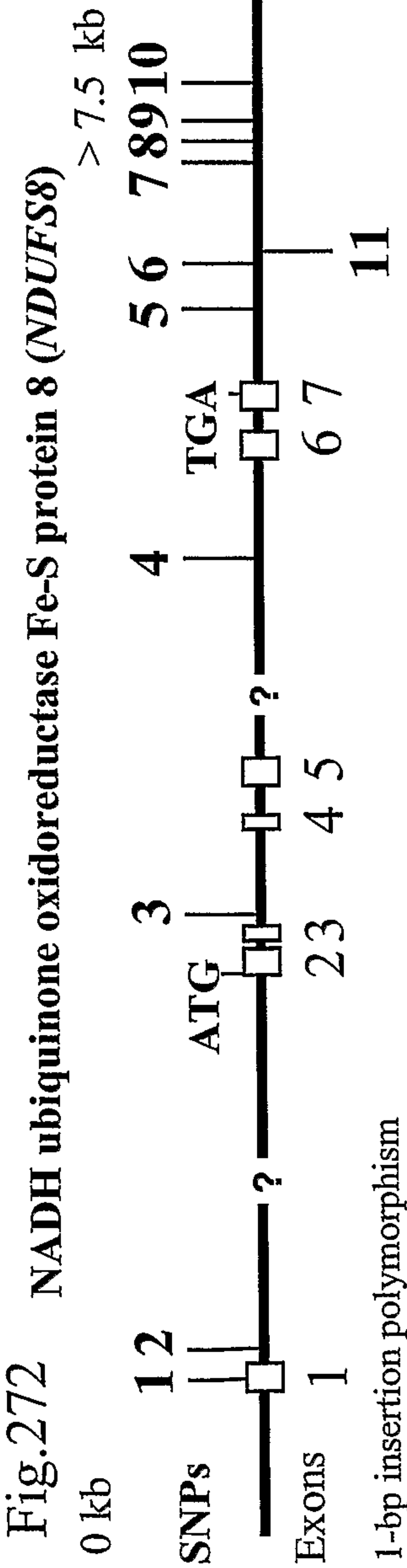
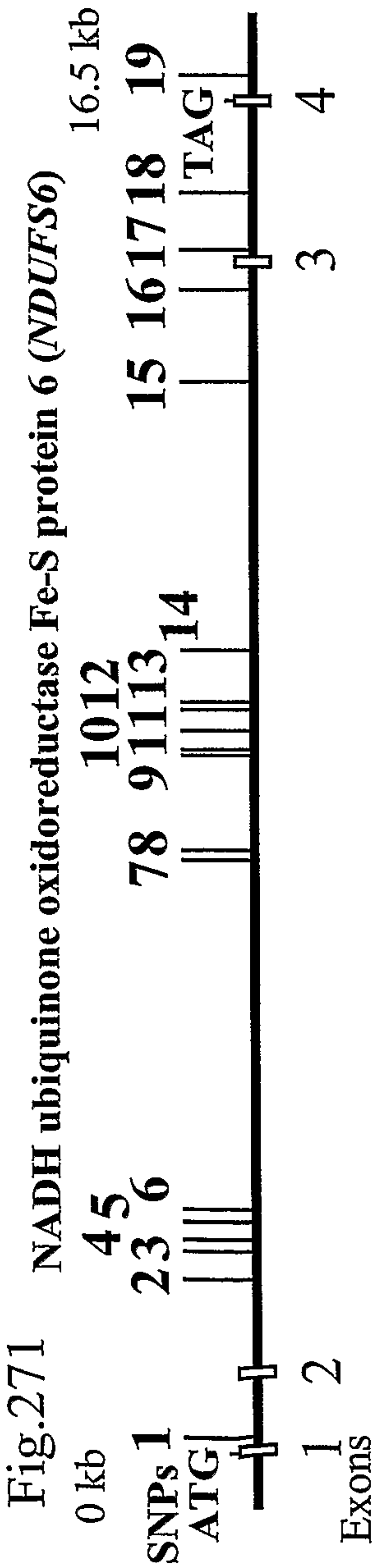
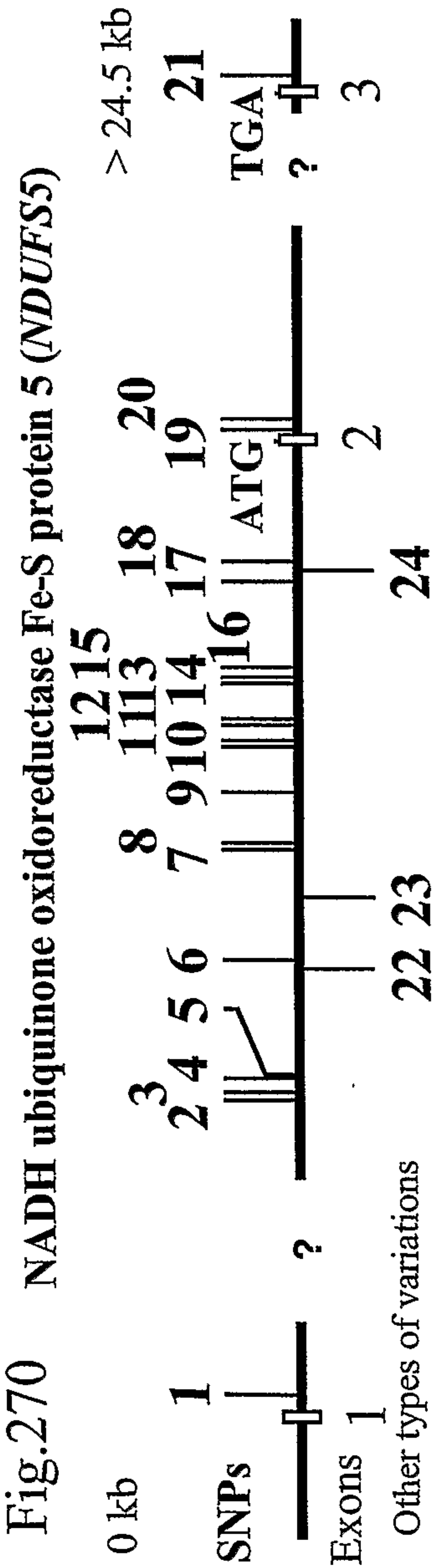


Fig. 273

NADH: ubiquinone dehydrogenase flavoprotein 1 (*NDUFV1*)

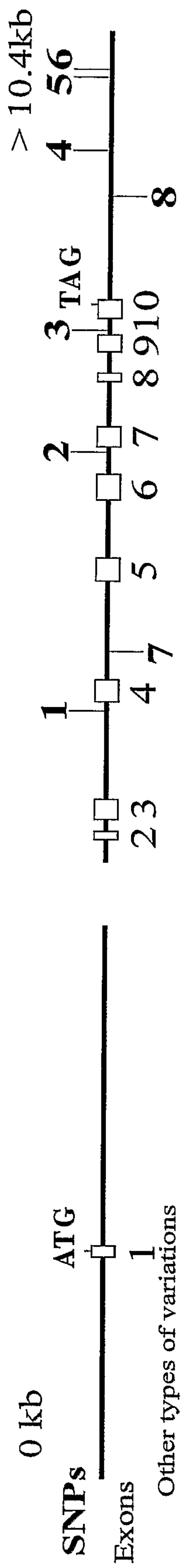


Fig. 274

NADH: ubiquinone oxidoreductase flavoprotein 2 (*NDUFV2*)

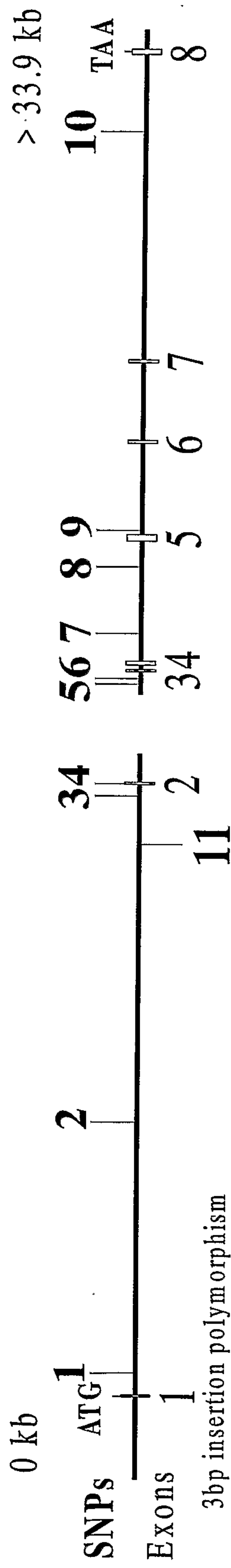


Fig. 275

NADH: ubiquinone oxidoreductase flavoprotein 3 (*NDUFV3*)

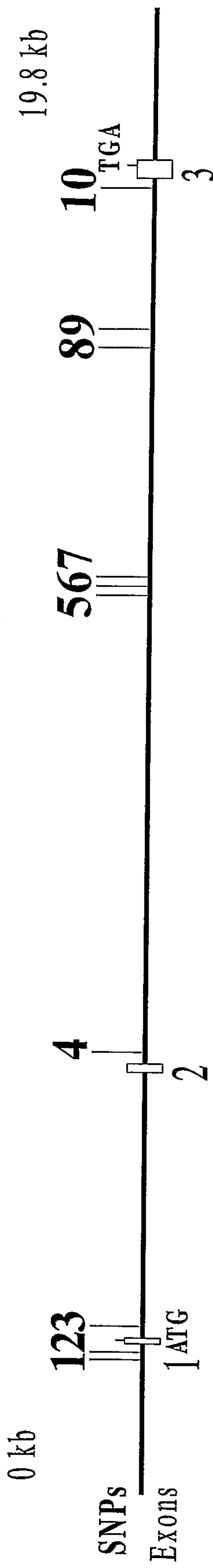


Fig. 276

Gamma- glutamyltransferase 1 (GGT1)

ACCESSION D87002.1

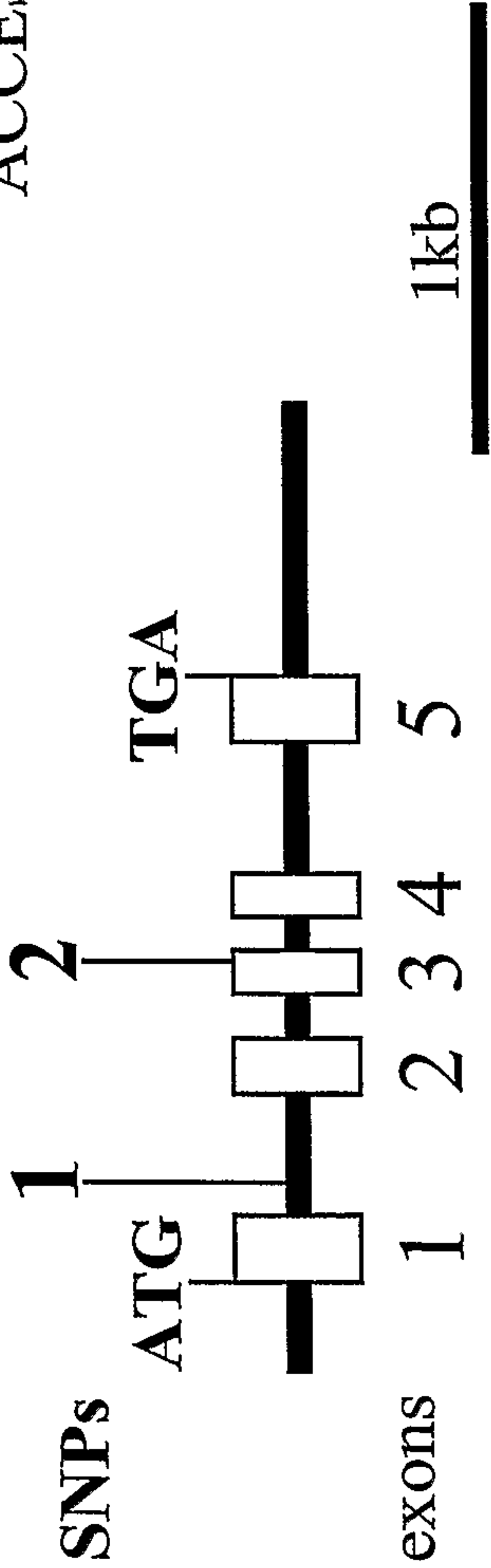


Fig. 277

Transglutaminase 1 (TGMI)

ACCESSION M98447.1

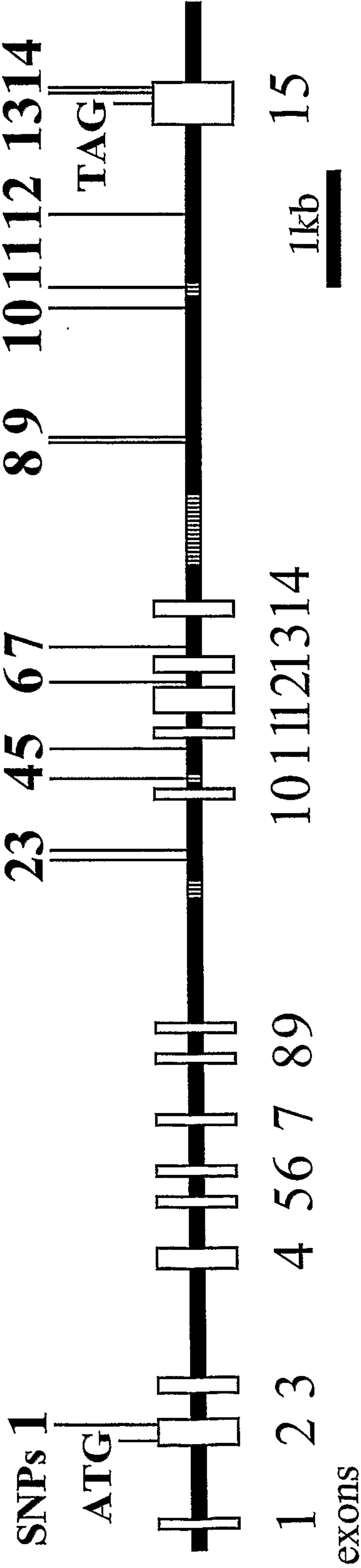


Fig. 278
Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)

ACCESSION X04300.1 AC020705.4

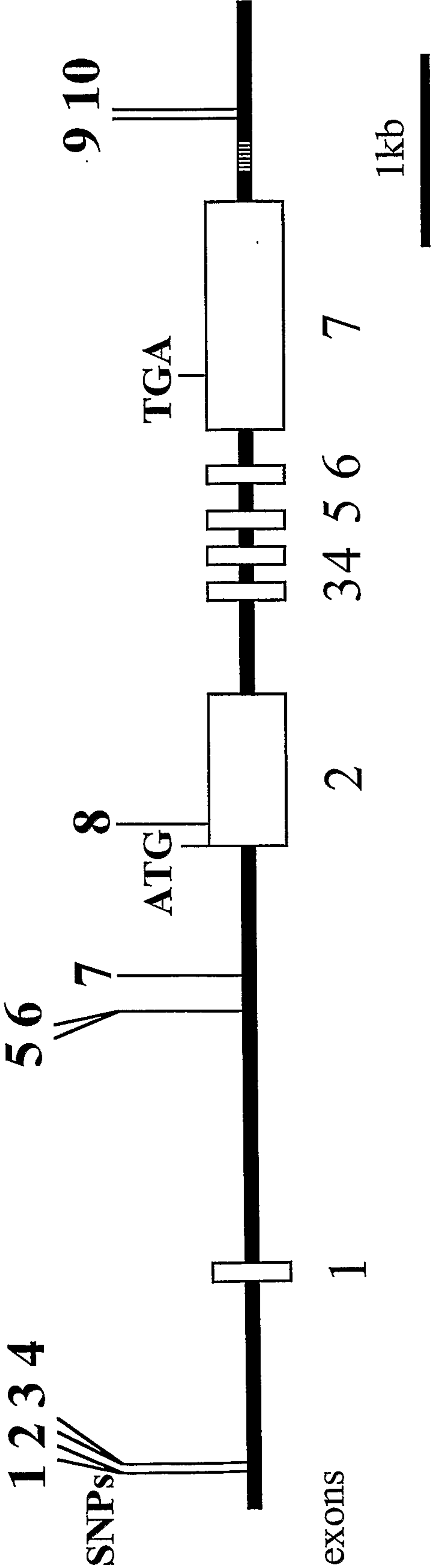


Fig. 279
Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)
ACCESSION AC020705.4

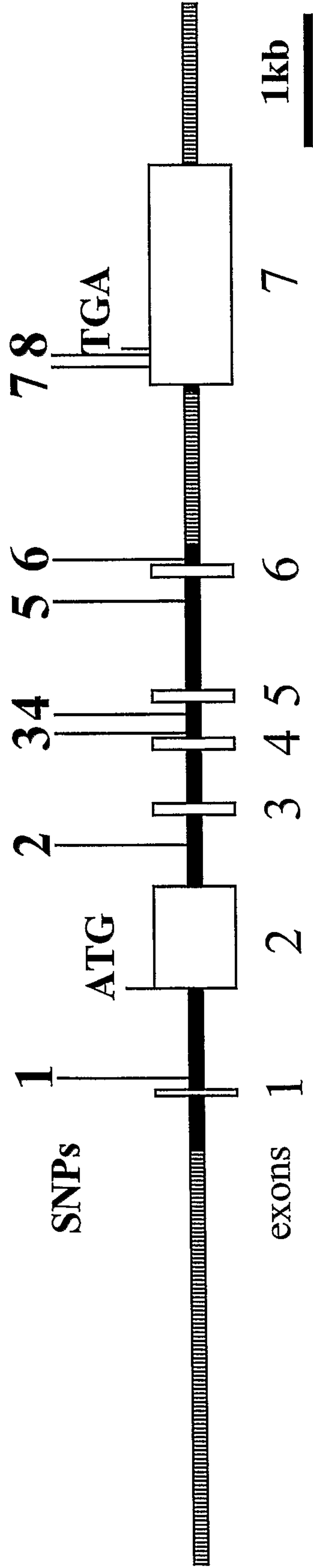


Fig. 280
Cytochrome P450, subfamily 1, polypeptide 1 (CYP1B1)
ACCESSION AC009229.4

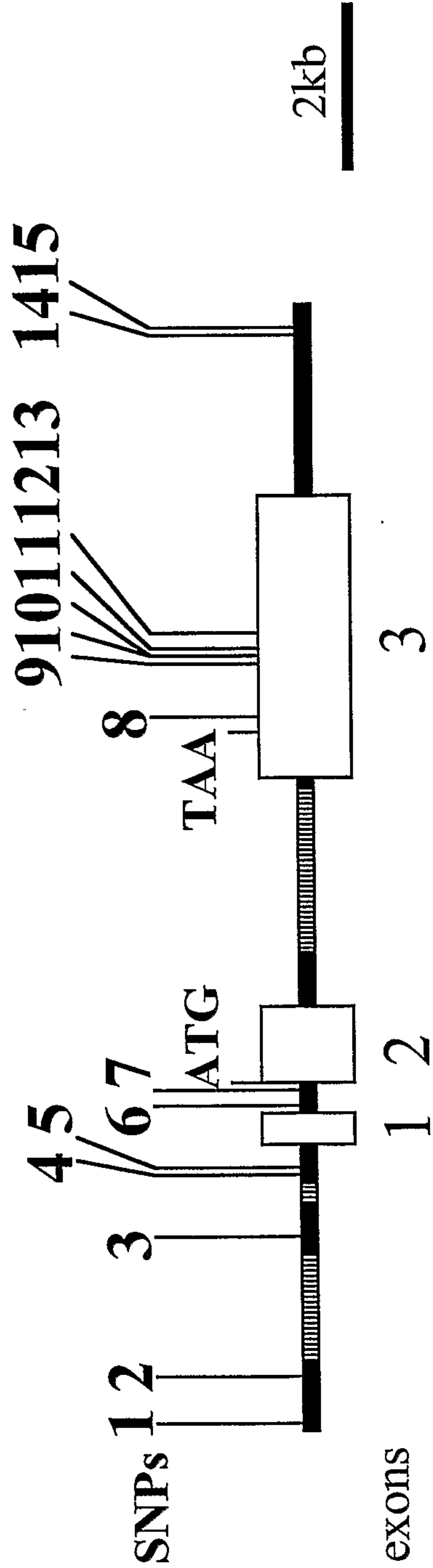
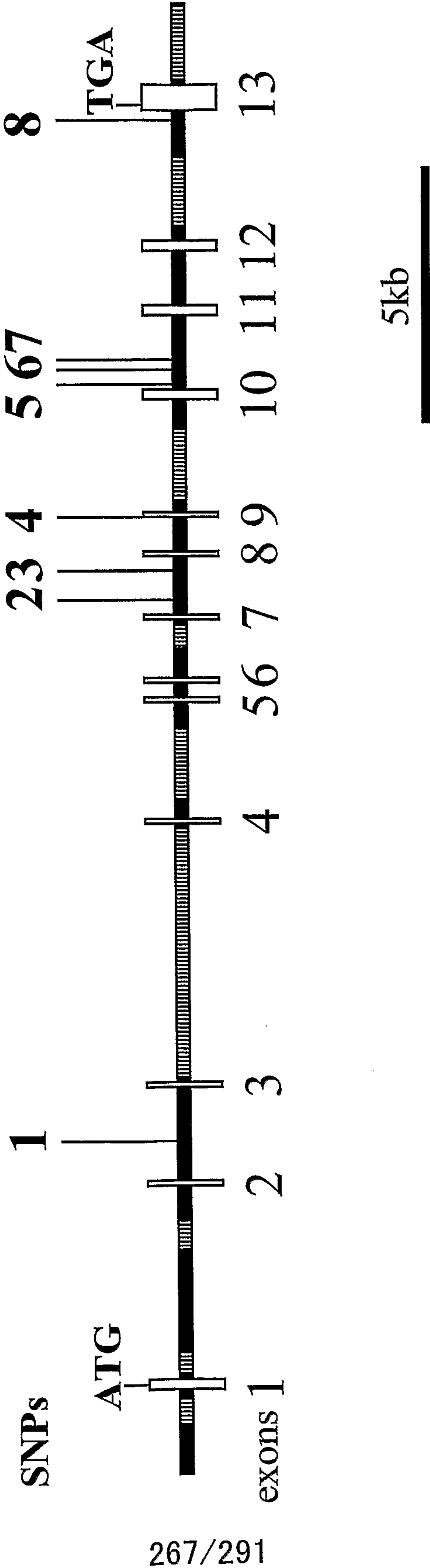


Fig. 281
Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)

ACCESSION AF280107.1



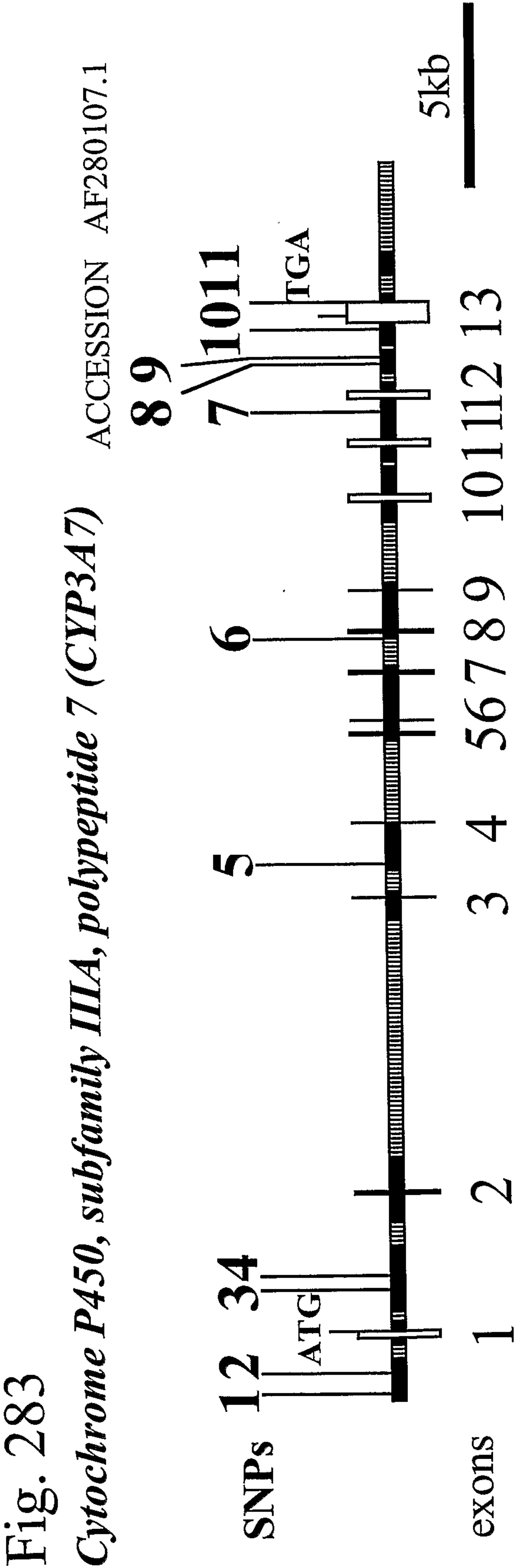
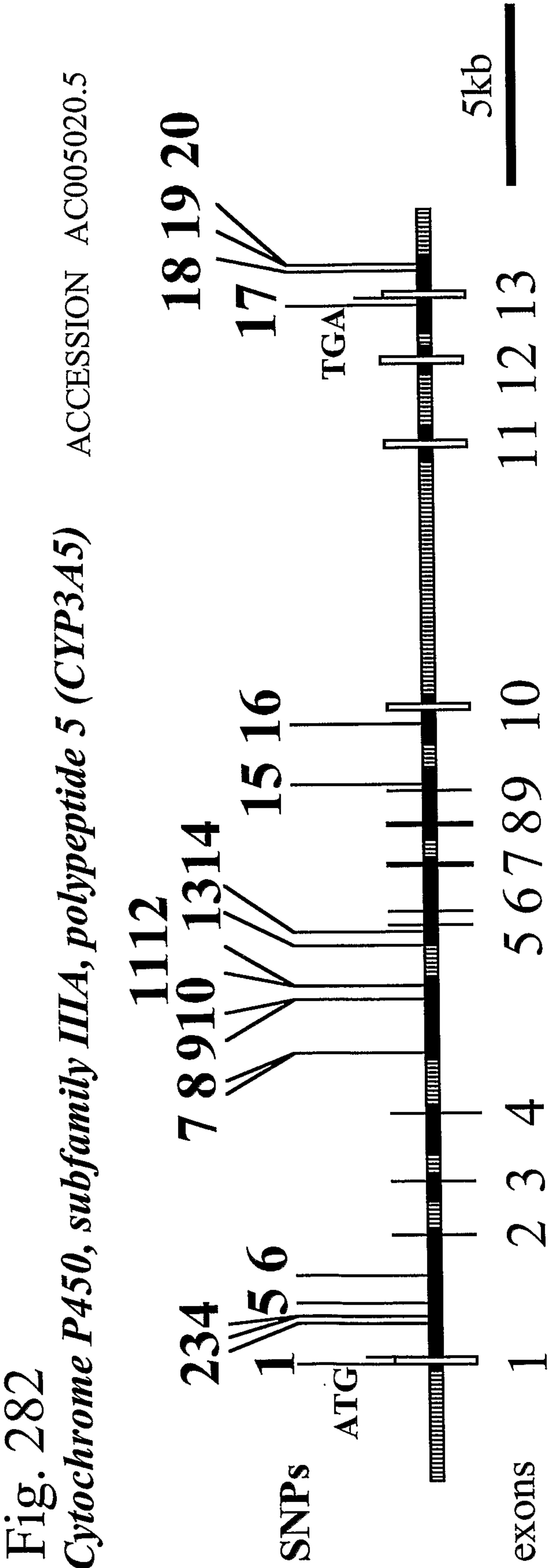
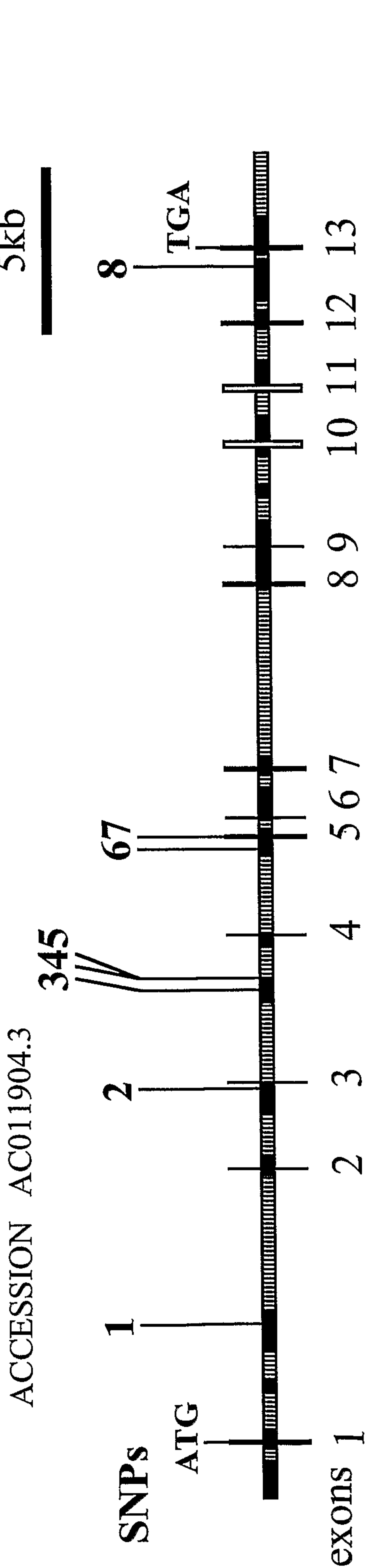


Fig. 284 *Cytochrome P450, subfamily IIIA, polypeptide 43 (CYP3A43)*



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Fig. 285 *Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)*

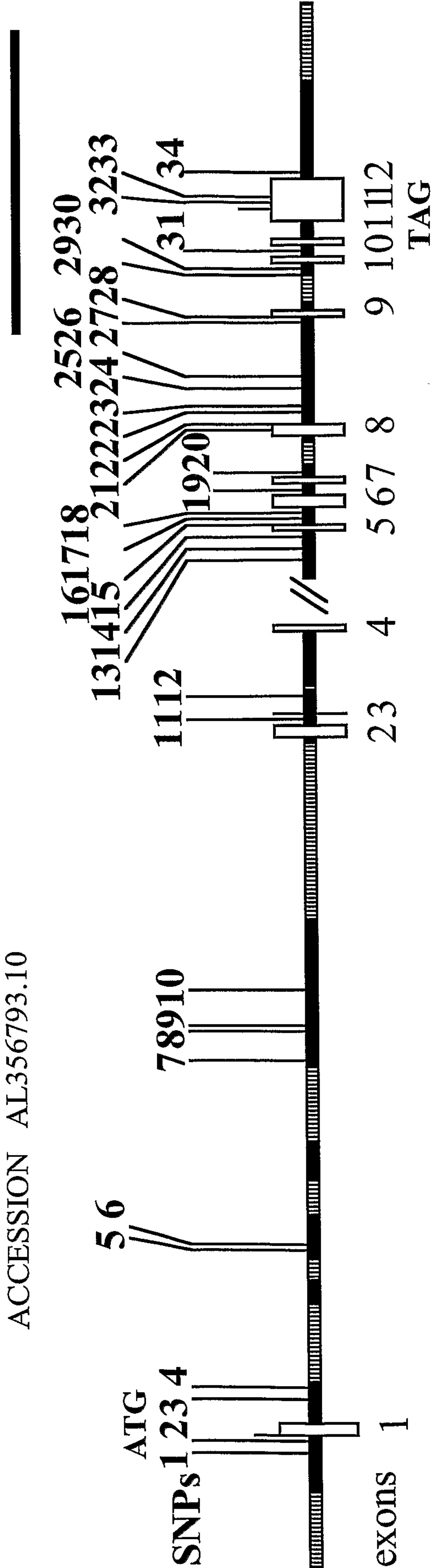


Fig. 286 *Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2)* ACCESSION AC005336.1

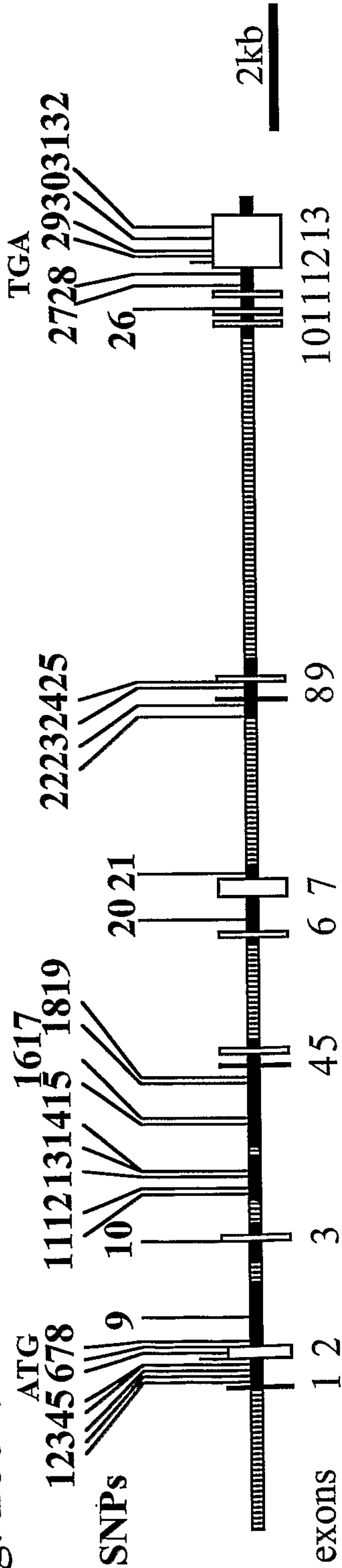


Fig. 287 *Cytochrome P450, subfamily IVF, polypeptide 3 (CYP4F3)* ACCESSION AD000685.1

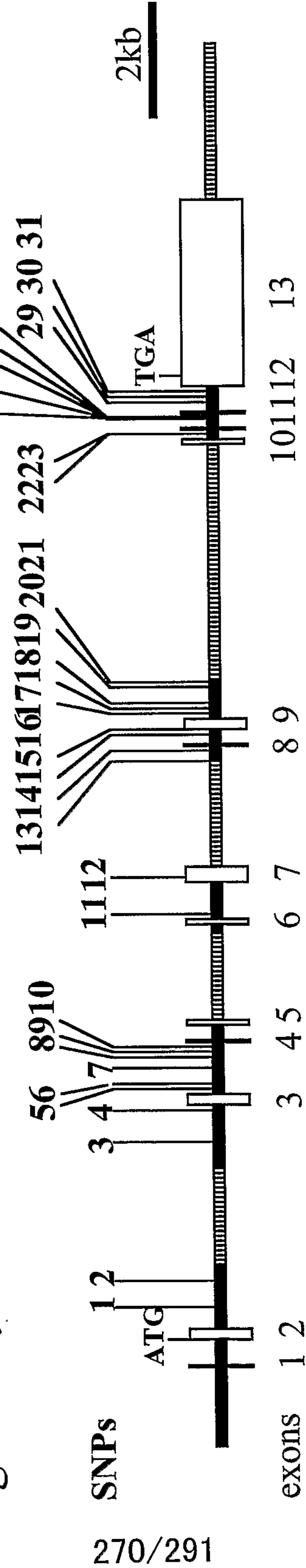


Fig. 288 *Cytochrome P450, subfamily IVF, polypeptide 8 (CYP4F8)* ACCESSION AC068845.3

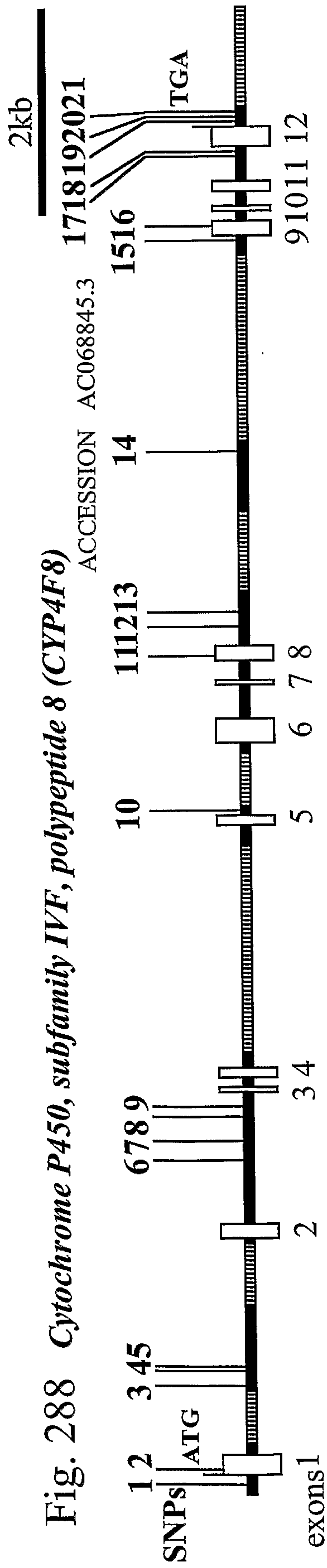


Fig. 289 *Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)*

ACCESSION AC009974.7

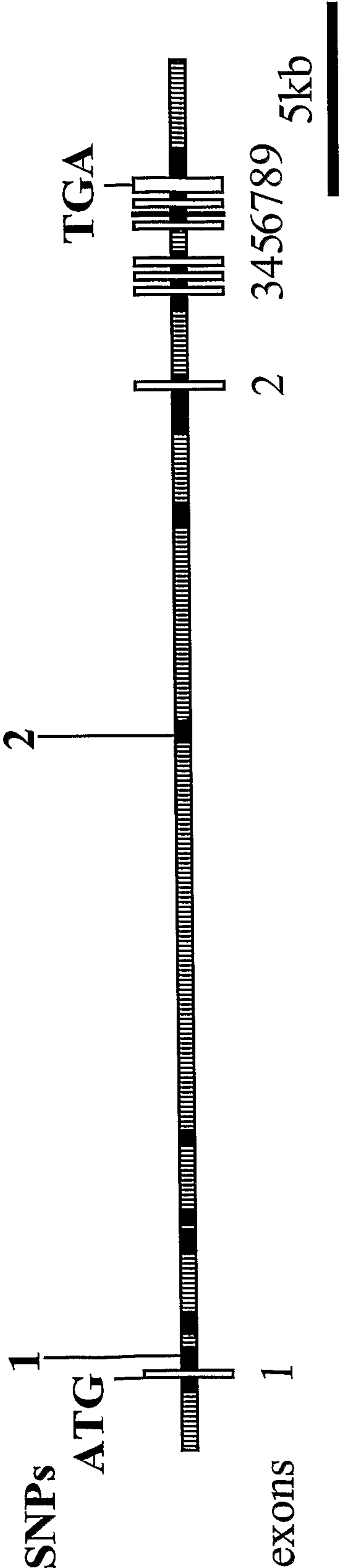


Fig. 290 *Cytochrome P450, subfamily XXVIIIB, polypeptide 1 (CYP27B1)*

ACCESSION AC025165.27

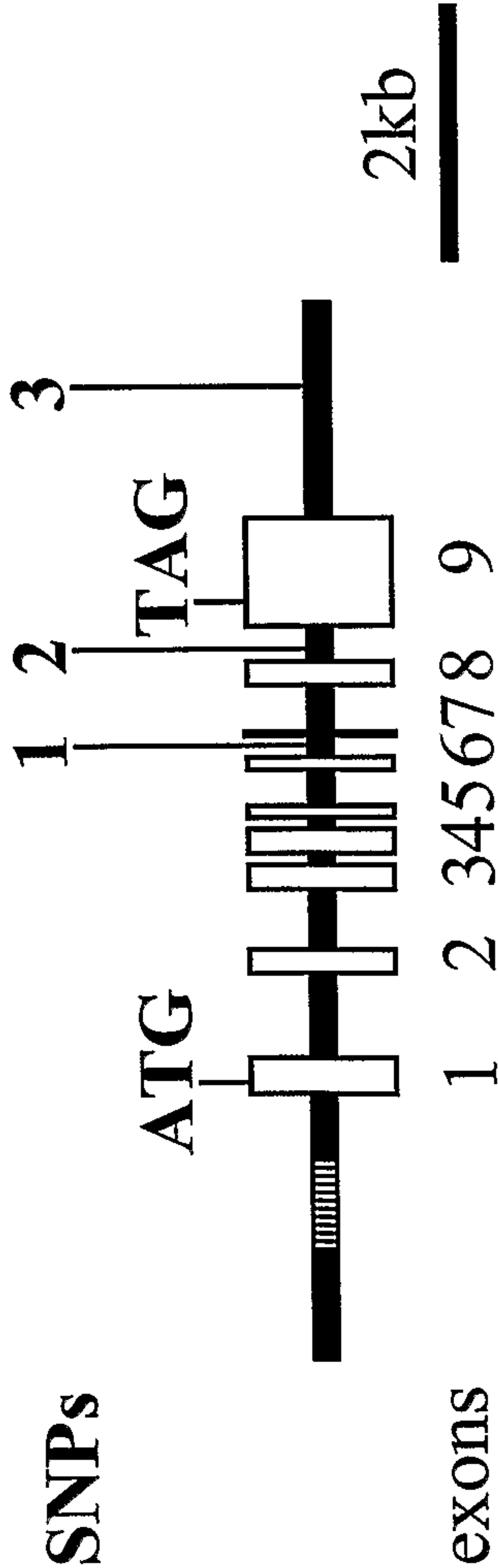


Fig.291 *Arylacetamide deacetylase (AADAC)* ACCESSION AC068647.4

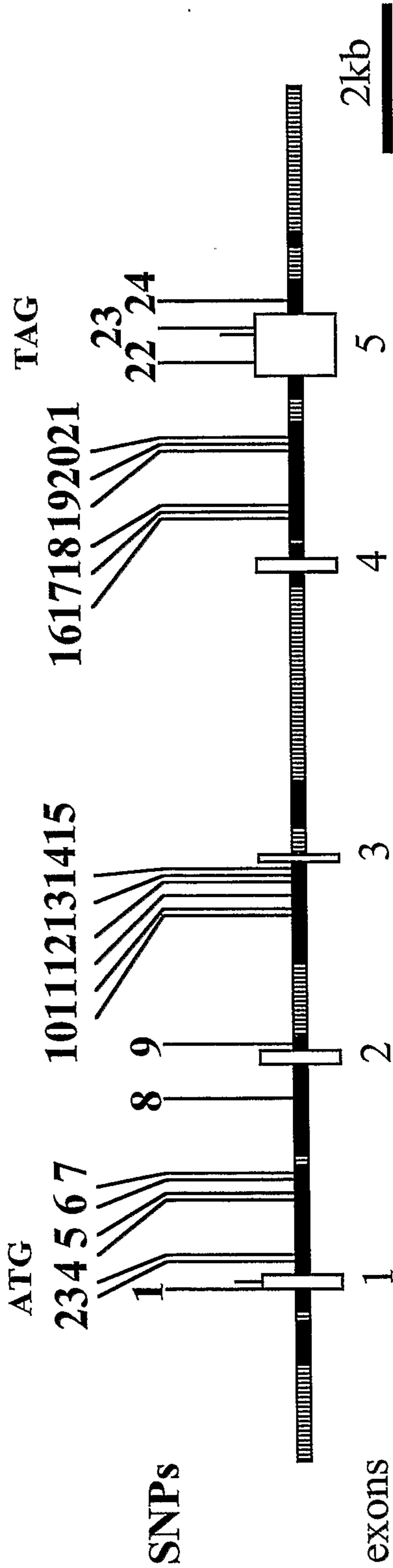


Fig. 292 *Carboxylesterase 1 (CES1)* ACCESSION AC007602.4

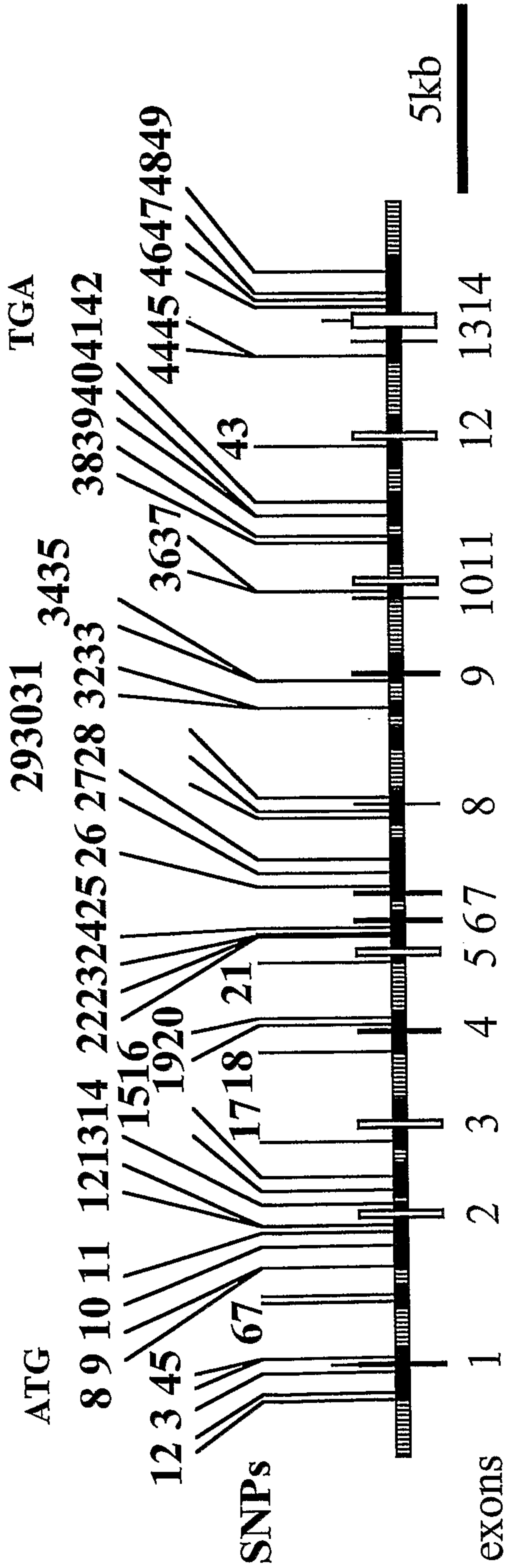


Fig. 293
Carboxylesterase 2 (CES2)

ACCESSION AC027131.4

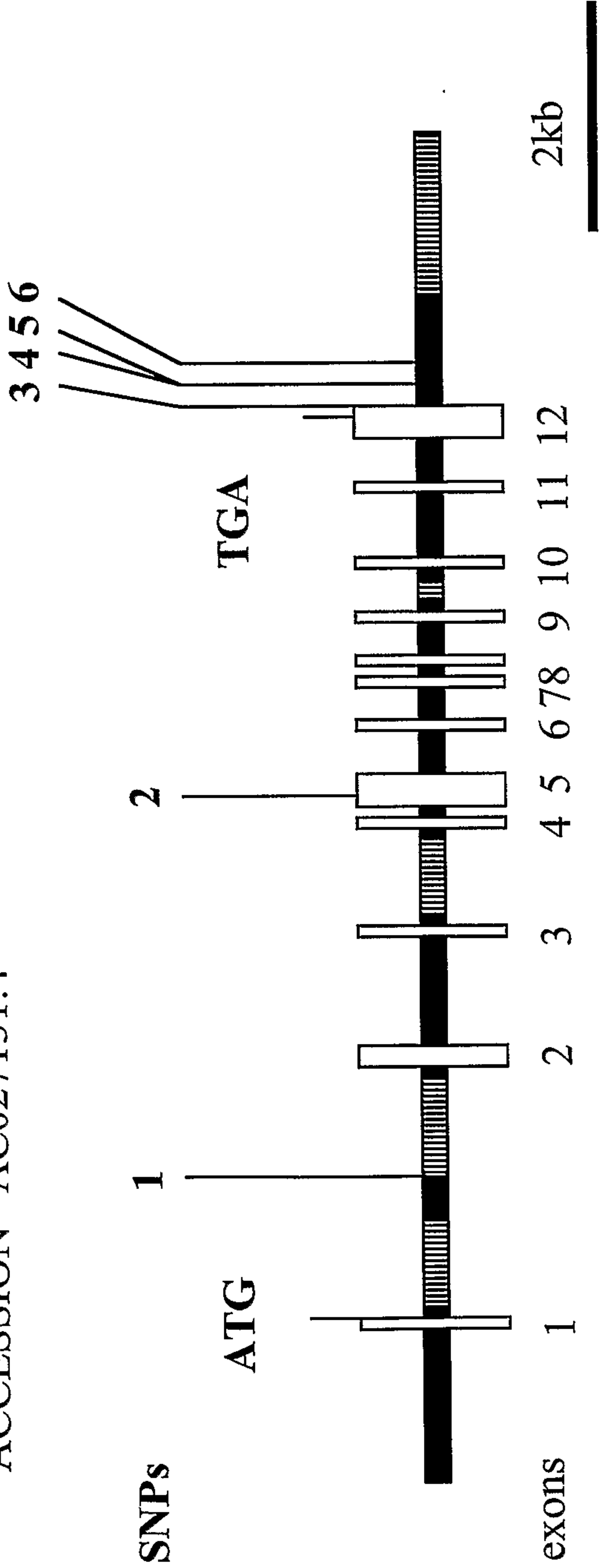


Fig. 294 *Granzyme A (GZMA)*

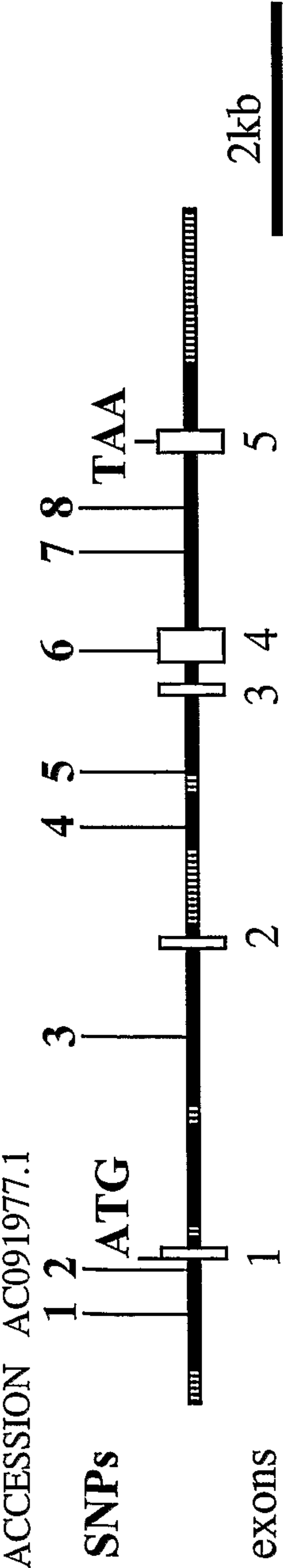


Fig. 295 *Granzyme B (GZMB)*

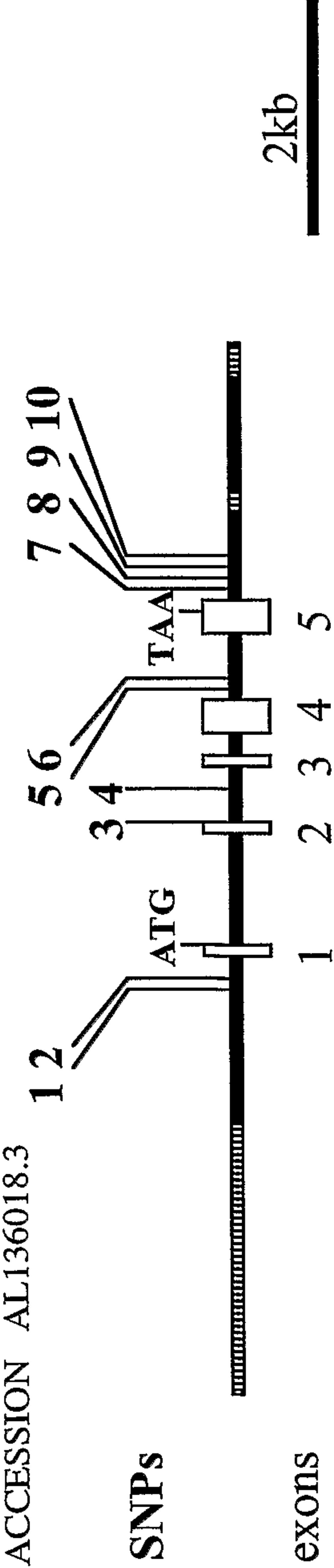


Fig. 296 *Esterase D (ESD)*

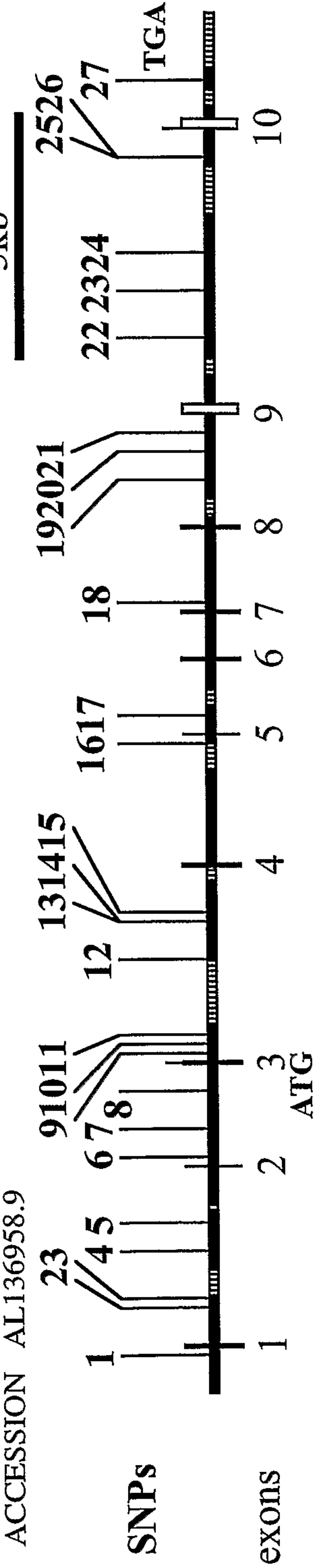


Fig. 297A *Carboxyl ester lipase (CEL)*
ACCESSION AL138750. AL162417.20 AF072711.1

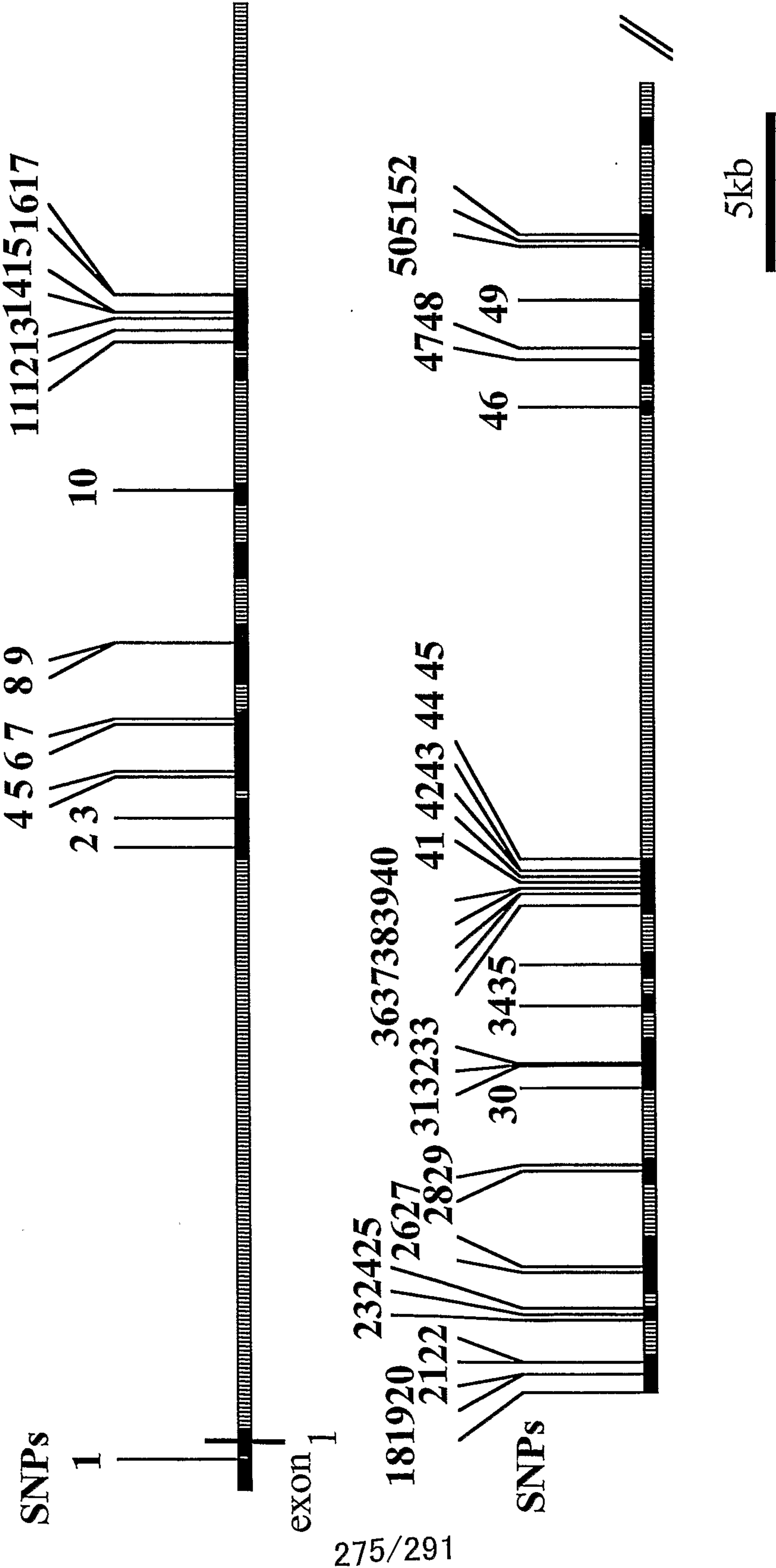


Fig. 297B

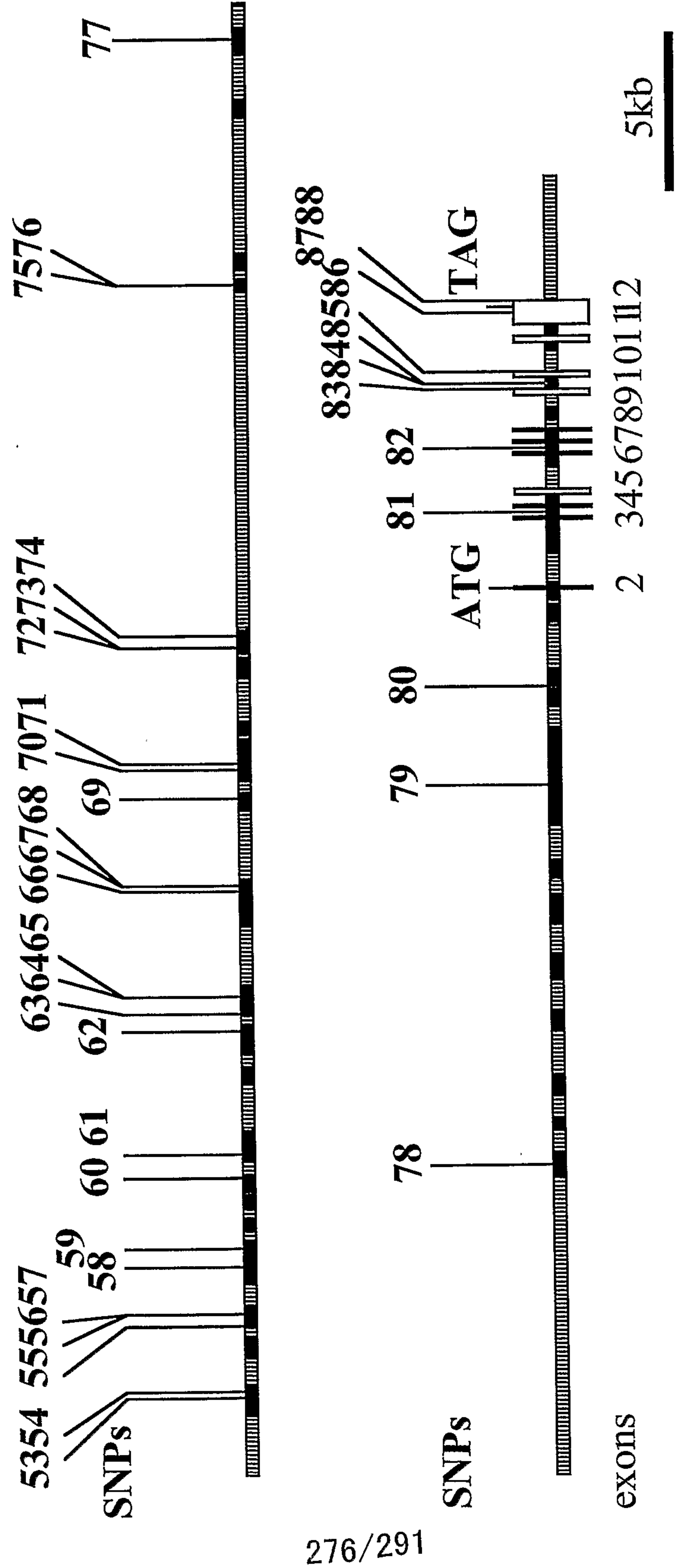


Fig. 298
Interleukin 17
(cytotoxic T-lymphocyte-associated serine esterase 8) (IL17)
ACCESSION AL355513.11

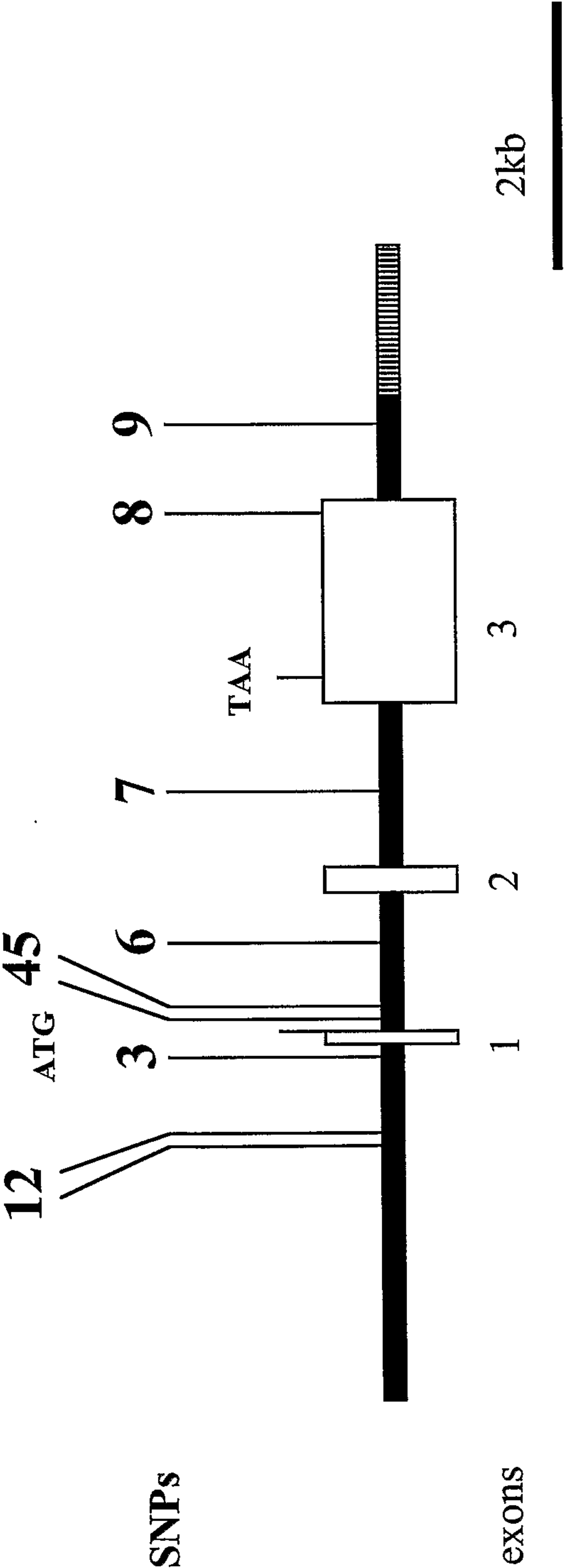


Fig. 299 *Ubiquitin carboxyl-terminal esterase L3 (UCHL3)*

ACCESSION AL137244.28

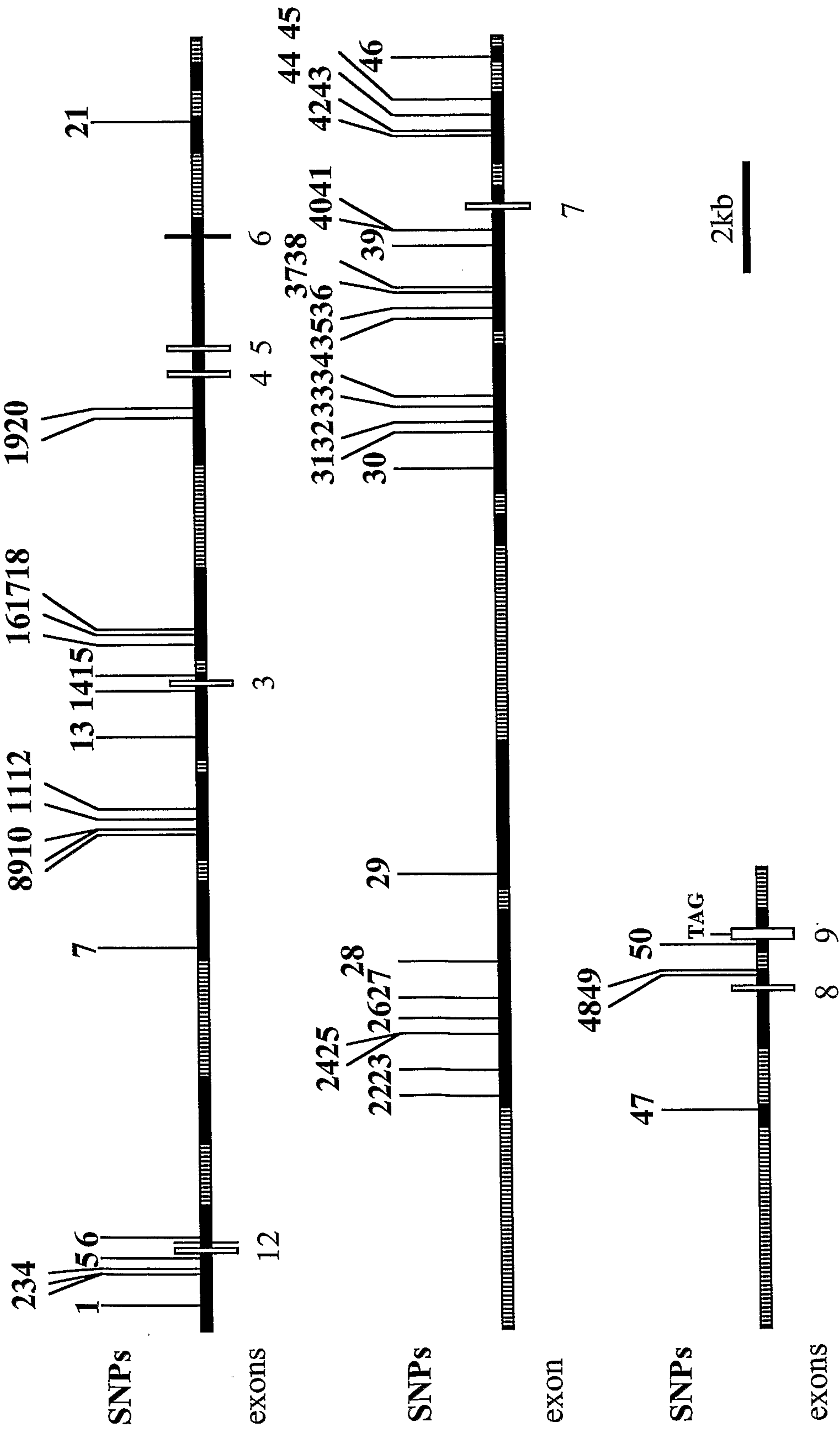
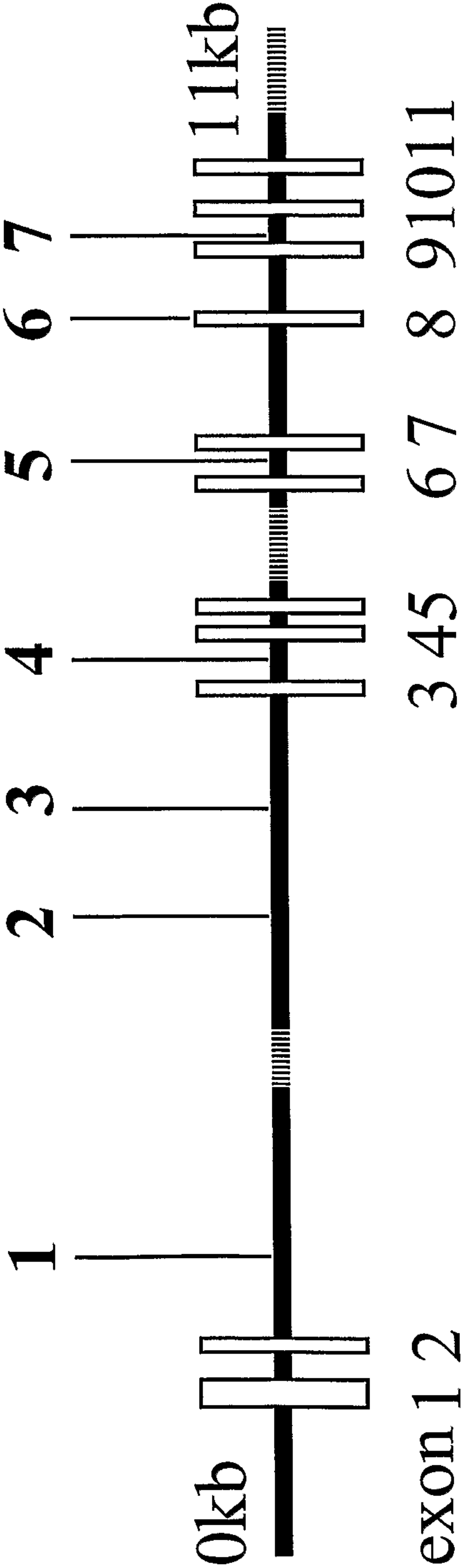


Fig. 300 *dolichyl-diphosphooligosaccharide-protein
glycosyltransferase (DDOST)*

Accession No. D89060



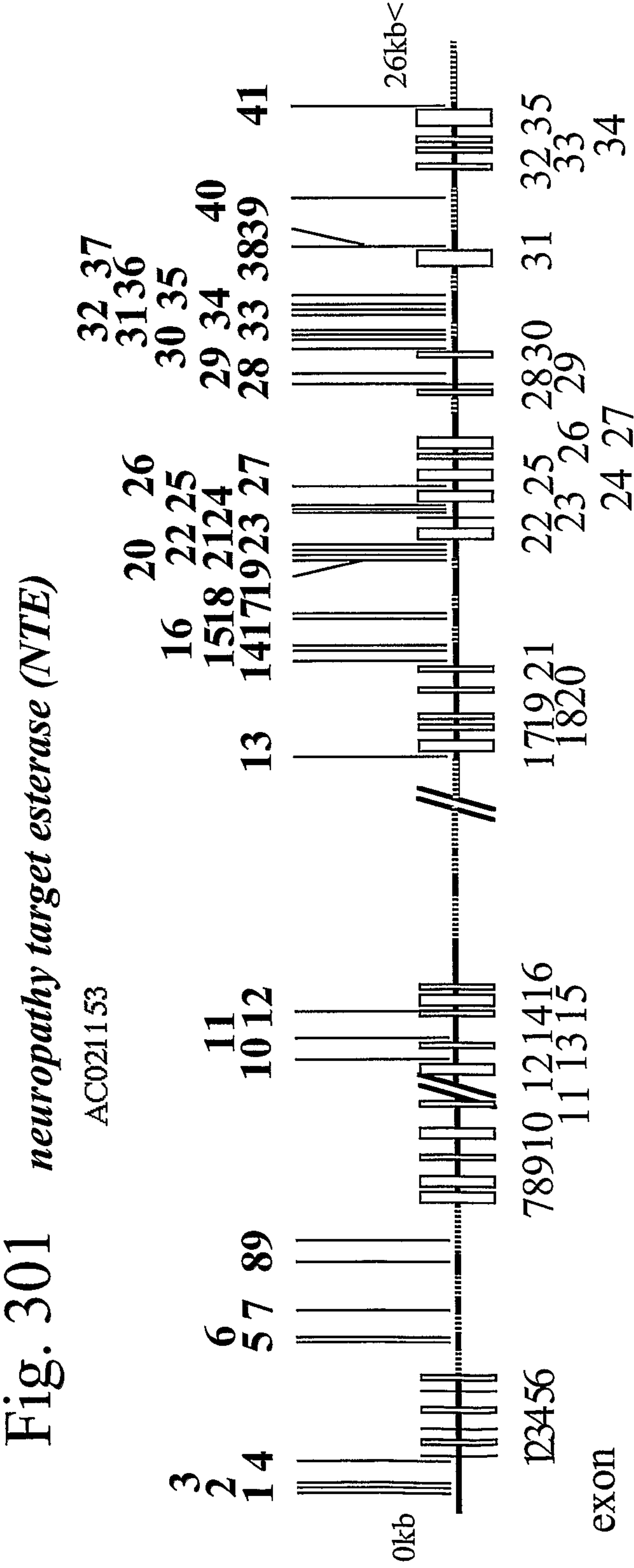


Fig. 302

L1 cell adhesion molecule (L1CAM)

Accession No. U52112

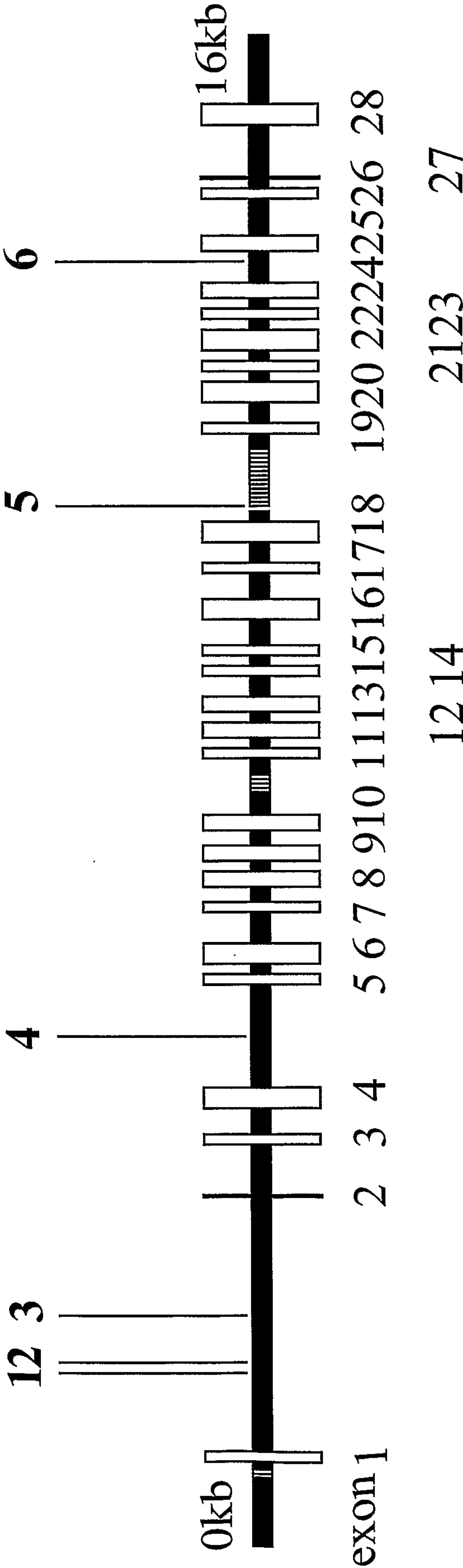


Fig. 303
arylalkylamine N-acetyltransferase(AANAT)

Accession No. U40391

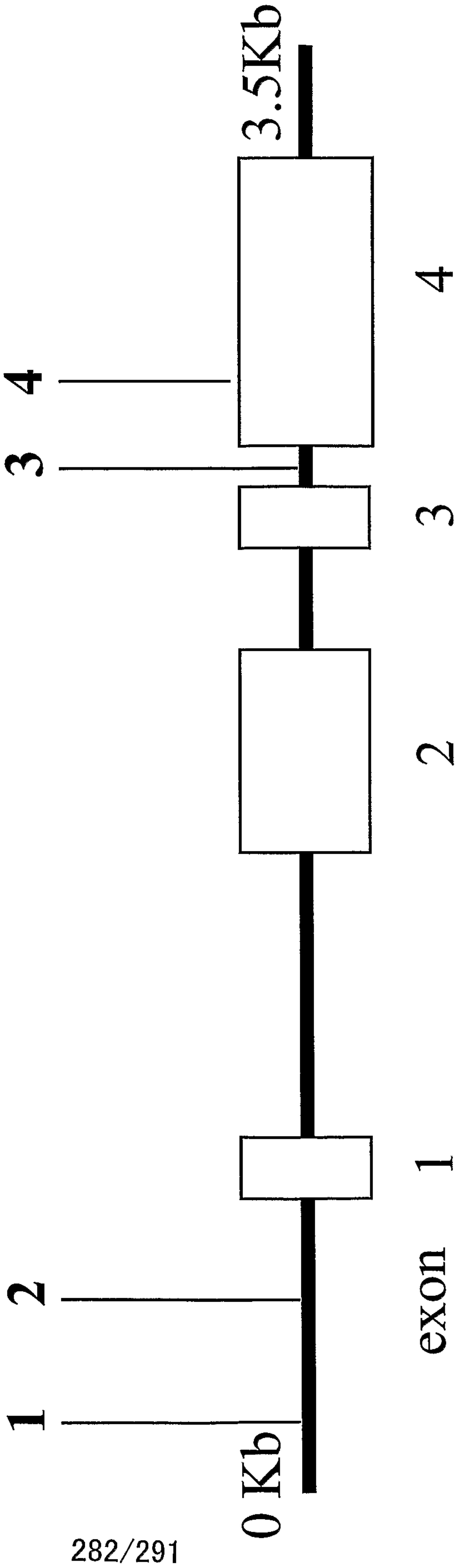


Fig. 304

N-acetyltransferase, homolog of S. cerevisiae (ARD1)

Accession No. U52112

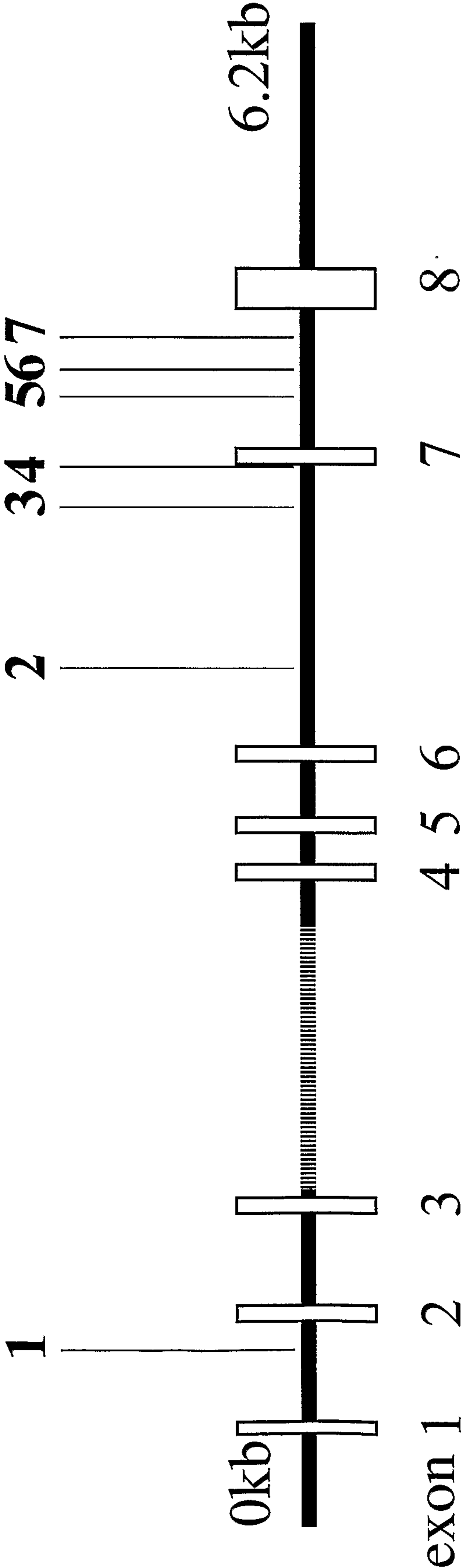
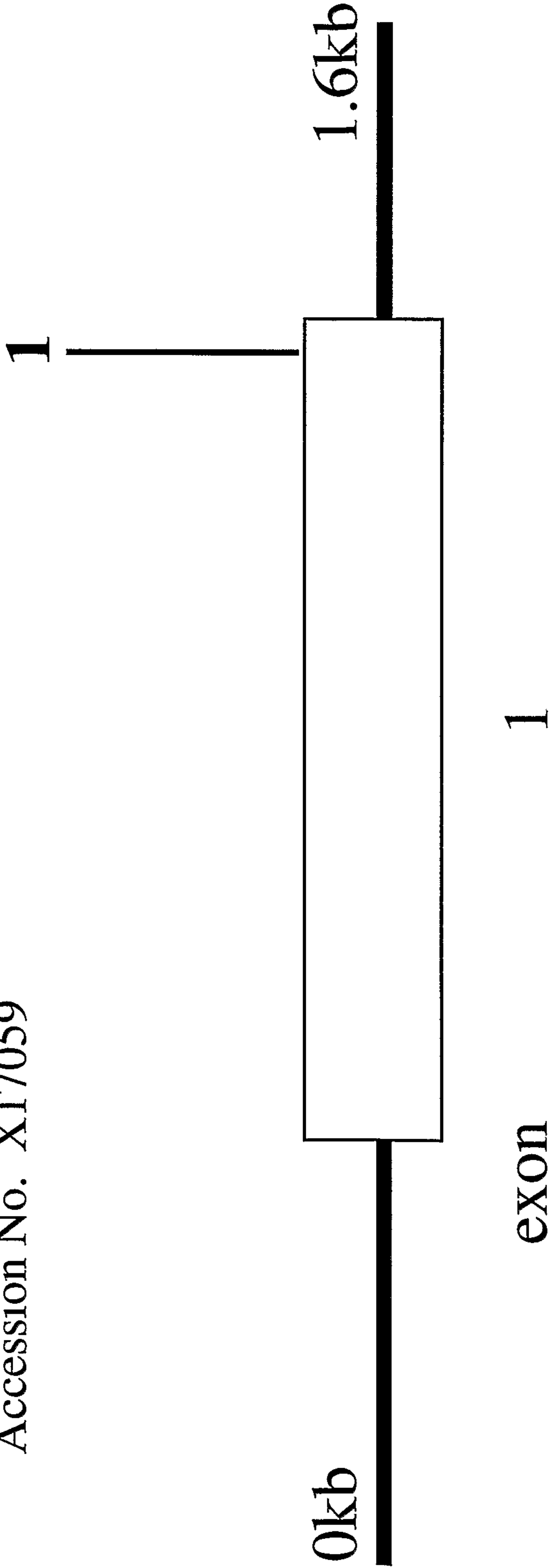


Fig. 305
N-acetyltransferase (NAT1)

Accession No. X17059



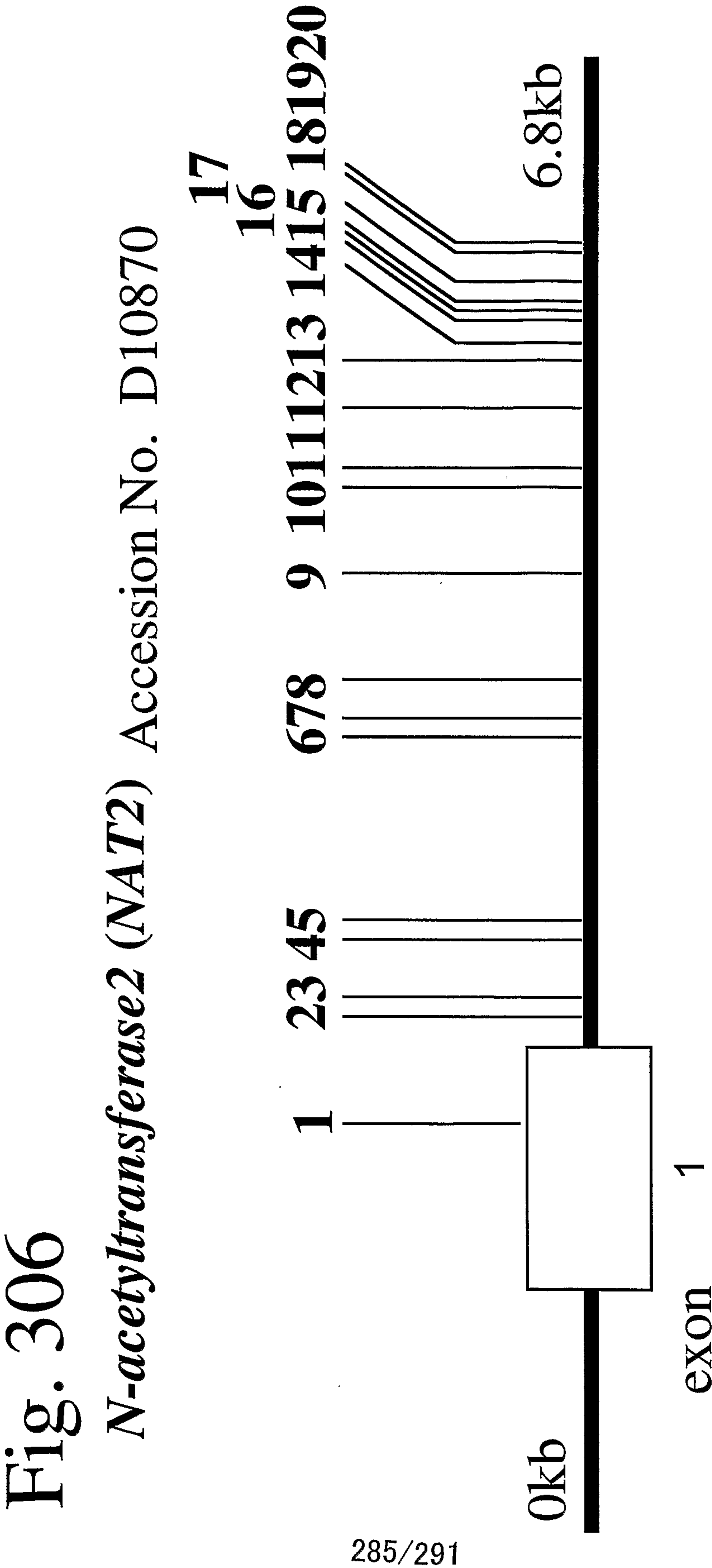


Fig. 307
ATP binding cassette, sub-family B, member 2 (ABCB2)
ACCESSION X66401

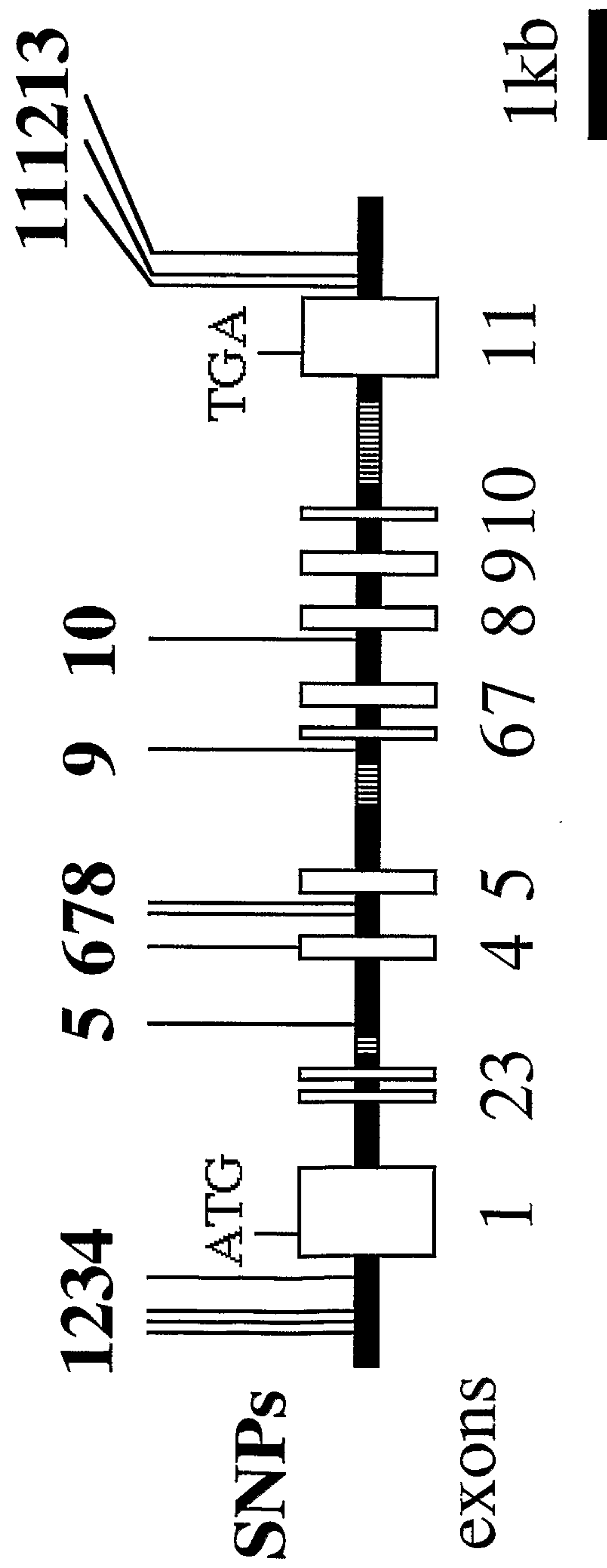


Fig. 308
ATP-binding cassette, sub-family B, member 3 (ABCB3)

ACCESSION X66401

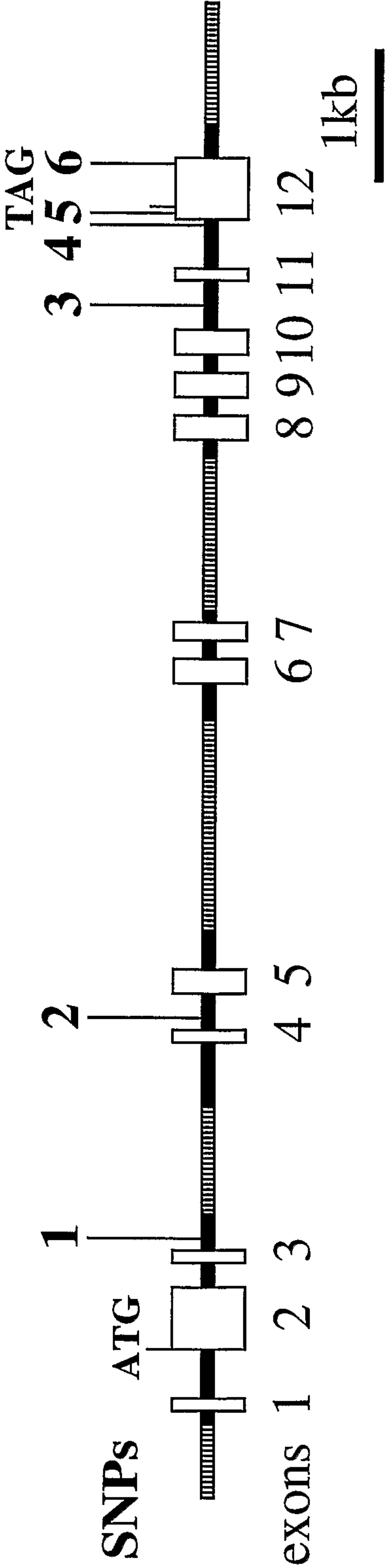


Fig. 309
Glutathione S transferase M3 (*GSTM3*): AF043105.1

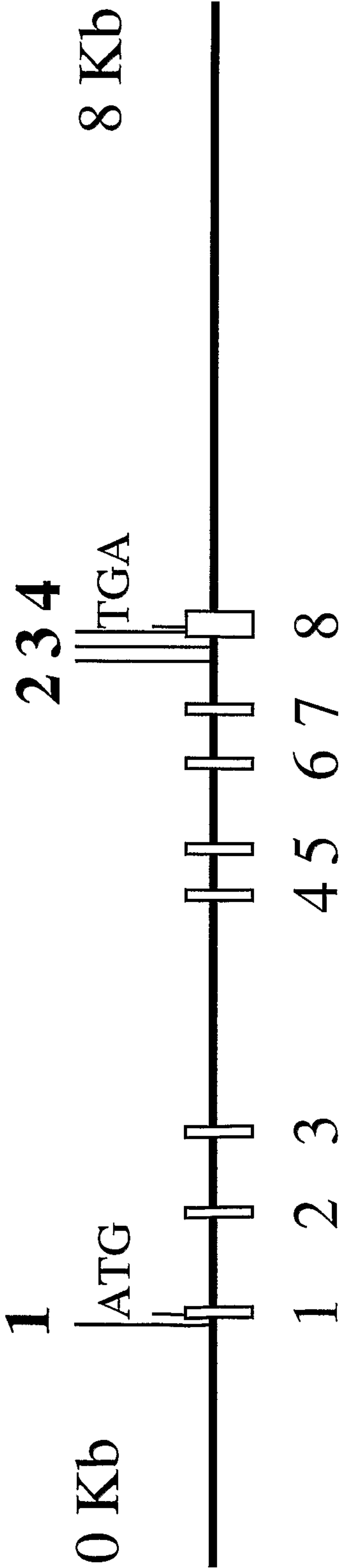


Fig. 310
Glutathione S transferase M4 (*GSTM4*): M96233.1

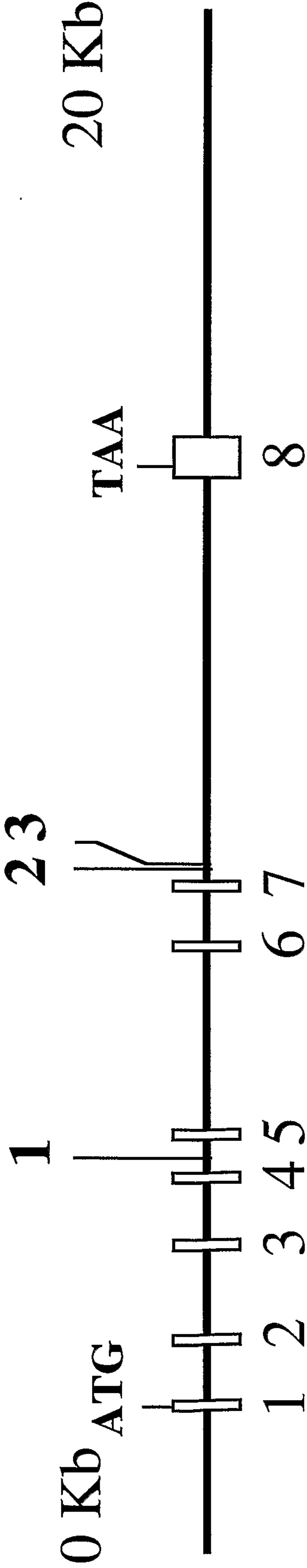


Fig. 311

Aldehyde dehydrogenase 7 (ALDH7)

ACCESSION AC004923

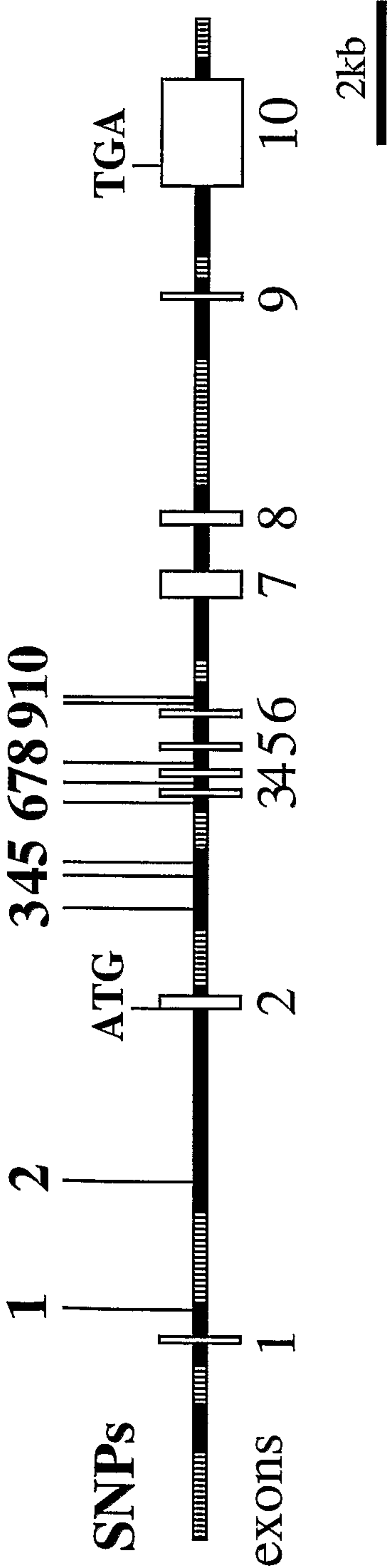


Fig. 312
High-mobility group protein 17-like 1 (*HMG17L1*)

