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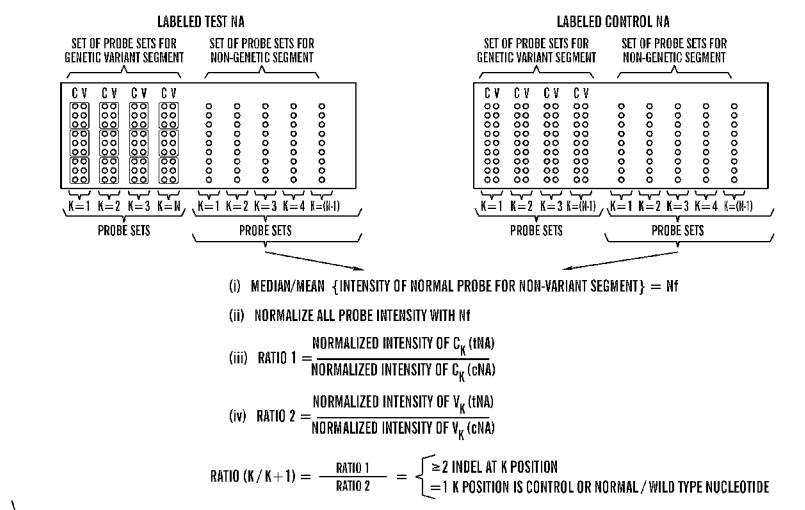


FIG. 6

(57) Abstract: The invention provides novel methods of making and designing nucleic acid probe libraries for accurate, reliable and specific detection and characterization of small nucleotide insertions or deletions (indels) or SNPs in any target nucleic acid sample. The invention further provides a probe library made by the methods and solid phase substrates coated with such probe libraries. The probe libraries of the invention allow detection of indels in a target nucleic acid segment also called a genetic variant segment. The invention further provides methods of using the probe library to detect the presence of indels in the test nucleic acid sample.

HIGH THROUGHPUT DETECTION OF SMALL GENOMIC DELETIONS AND INSERTIONS

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims benefit under 35 U.S.C. § 119(e) of the U.S. provisional application No. 61/239,872 filed September 4, 2009, the contents of which are expressly incorporated herein by reference in its entirety.

BACKGROUND OF INVENTION

[0002] The so-called "DNA-chips", also named "micro-arrays", "DNA-arrays" or "DNA bio-chips", and collections of beads with attached nucleic acids, are systems that functional genomics uses for large scale studies. One can also tailor these systems for specific mutation detection or detection of several mutations at the same time and thus for the use in functional genomics which studies the changes in the expression of genes due to environmental factors and to genetic characteristics of an individual.

[0003] Gene sequences present small inter-individual variations at one unique nucleotide called an SNP ("single nucleotide polymorphism"), which in a small percentage are involved in changes in the expression and/or function of genes that cause certain pathologies. The majority of studies which apply DNA-chips study gene expression, although chips are also used in the detection of SNPs. Other genetic variations such as differences in nucleotide repeat sequences are also involved in phenotypic variations. For example, aberrant numbers of trinucleotide repeats causes Huntington's disease, several ataxias, and fragile X syndrome. Large deletions and insertions are associated with multi-gene disorders, such as Down's syndrome.

[0004] The first DNA-chip was the "Southern blot" where labeled nucleic acid molecules were used to examine nucleic acid molecules attached to a solid support. The support was typically a nylon membrane.

[0005] Two breakthroughs marked the definitive beginning of DNA-chip. The use of a solid non-porous support, such as glass, enabled miniaturization of arrays thereby allowing a large number of individual probe features to be incorporated onto the surface of the support at a density of $>1,000$ probes per cm^2 . The adaptation of semiconductor photolithographic techniques enabled the production of DNA-chips containing more than 400,000 different oligonucleotides in a region of approximately $20 \mu\text{m}^2$, so-called high density DNA-chips.

[0006] For genetic expression studies, probes deposited on the solid surface, e.g. glass, are hybridized to cDNAs synthesized from mRNAs extracted from a given sample. In general the cDNA has been labeled with a fluorophore. The larger the number of cDNA molecules joined to their complementary sequence in the DNA-chip, the greater the intensity of the fluorescent signal detected, typically measured with a laser. This measure is therefore a reflection of the number of mRNA molecules in the analyzed sample and consequently, a reflection of the level of expression of each gene represented in the DNA-chip.

[0007] In the nucleic acid beads, a bead set is typically coated with a number of nucleic acid probes that are labeled such that different probes can be "seen" using visualization or capture of the beads after hybridization to a target nucleic acid.

[0008] Gene expression DNA-chips typically also contain probes for detection of expression of control genes, often referred to as "house-keeping genes", which allow experimental results to be standardized and multiple experiments to be compared in a quantitative manner. With the DNA-chip, the levels of expression of hundreds or thousands of genes in one cell can be determined in one single experiment. The cDNA of a test sample and that of a control sample can be labeled with two different fluorophores so that the same DNA-chip can be used to study differences in gene expression. DNA-chips for detection of genetic polymorphisms, changes or mutations (in general, genetic variations) in the DNA sequence, comprise a solid surface, typically glass, on which a high number of genetic sequences are deposited (the probes), complementary to the genetic variations to be studied. Using standard robotic printers to apply probes to the array a high density of individual probe features can be obtained, for example probe densities of 600 features per cm.² or more can be typically achieved. The positioning of probes on an array is precisely controlled by the printing device (robot, inkjet printer, photolithographic mask etc) and probes are aligned in a grid. The organization of probes on the array facilitates the subsequent identification of specific probe-target interactions. Additionally it is common, but not necessary to divide the array features into smaller sectors, also grid-shaped, that are subsequently referred to as sub-arrays. Sub-arrays typically comprise 32 individual probe features although lower (e.g. 16) or higher (e.g. 64 or more) features can comprise each sub-array.

[0009] One strategy used to detect genetic variations involves hybridization to sequences which specifically recognize the normal and the mutant allele in a fragment of DNA derived from a test sample. Typically, the fragment has been amplified, e.g. by using the polymerase chain reaction (PCR), and labeled e.g. with a fluorescent molecule. A laser can be used to detect bound labeled fragments on the chip and thus an individual who is homozygous for the normal allele can be specifically distinguished from heterozygous individuals (in the case of autosomal dominant conditions then these individuals are referred to as carriers) or those who are homozygous for the mutant allele.

[0010] Another strategy to detect genetic variations comprises carrying out an amplification reaction or extension reaction on the DNA-chip itself.

[0011] For differential hybridization based methods there are a number of methods for analyzing hybridization data for genotyping. For example, one can analyze an increase in hybridization level, wherein the hybridization level of complementary probes to the normal and mutant alleles are compared. One can also analyze a decrease in hybridization level, wherein differences in the sequence between a control sample and a test sample can be identified by a fall in the hybridization level of the totally complementary oligonucleotides with a reference sequence. A complete loss is produced in mutant homozygous individuals while there is only 50% loss in heterozygotes. In DNA-chips for examining all the bases of a sequence of "n" nucleotides ("oligonucleotide") of length in both strands, a

minimum of "2n" oligonucleotides that overlap with the previous oligonucleotide in all the sequence except in the nucleotide are necessary. Typically the size of the oligonucleotides is about 25 nucleotides. The increased number of oligonucleotides used to reconstruct the sequence reduces errors derived from fluctuation of the hybridization level. However, the exact change in sequence cannot be identified with this method; sequencing is later necessary in order to identify the mutation.

[0012] Where amplification or extension is carried out on the DNA-chip itself, three methods are presented by way of example:

[0013] In the mini-sequencing strategy, a mutation specific primer is fixed on the slide and after an extension reaction with fluorescent dideoxynucleotides, the image of the DNA-chip is captured with a scanner.

[0014] In the primer extension strategy, two oligonucleotides are designed for detection of the wild type and mutant sequences respectively. The extension reaction is subsequently carried out with one fluorescently labeled nucleotide and the remaining nucleotides unlabelled. In either case the starting material can be either an RNA sample or a DNA product amplified by PCR.

[0015] In the Tag arrays strategy, an extension reaction is carried out in solution with specific primers, which carry a determined 5' sequence or "tag". The use of DNA-chips with oligonucleotides complementary to these sequences or "tags" allows the capture of the resultant products of the extension. Examples of this include the high density DNA-chip "Flex-flex" (Affymetrix).

[0016] For genetic diagnosis, simplicity as well as accuracy must be taken into account. The need for amplification and purification reactions presents disadvantages for the on-chip extension/amplification methods compared to the differential hybridization based methods.

[0017] Small duplications, insertions and deletions are genetic variations that are quite difficult to automatically detect in resequencing assays because they are not automatically identified by the software analyzing the data. Small duplications, insertions and deletions that are generally less than or equal to 10 nucleotides are called indels. Only known indels can be detected because specific probes can be designed for their detection. In addition, novel indels are difficult to predict. In many diseases, indels represent from 10 to 40% of point mutations, and not detecting them can dramatically lead to the underestimation of the mutation rate and also the perceived mutation detection rate.

[0018] Alternative genotyping strategies for the detection of substitutions based mutations have been described, for example, in the International Patent application WO95/11995, but genotyping strategies for the detection of indels are lacking in general.

SUMMARY OF THE INVENTION

[0019] The present invention provides methods for the designing and using probe sets that allow detection of single nucleotide polymorphisms, small deletions and insertions of a small number of nucleotides referred to herein as "indels". The methods are based on a novel design system that allows rapid detection and characterization of the indels in any selected nucleic acid sequence.

[0020] Accordingly, in one embodiment, the invention provides a method of designing a library of probes for detecting at least one indel variation in a genetic variant segment, the method comprising the steps of (a) selecting a nucleic acid variant segment of N nucleotides long, wherein N can be any length between 25 and 5000; (b) selecting N number of probe sets each designed to hybridize to one of the N number of nucleotides in the nucleic acid variant segment; and (c) selecting at least one probe subset for the probe set, wherein the probe subset comprises at least two different probes forming a pair of probes, one designed to specifically hybridize to a normal/wild-type or a control sequence and one designed to specifically hybridize to a sequence with the at least one indel variation.

[0021] In some embodiments, the method further comprises a step of manufacturing the probe sets selected/designing through steps (a), (b) and (c).

[0022] In some embodiments, the method further comprises performing at least one of the steps (a), (b), or (c) with a computer. Such computer implemented system can be performed by setting forth an algorithm with the novel selection rules set forth in the method and allowing a computer to automatically select the probes using input parameters for the desired length of the probe, the type of an indel, the desired target variant sequence and so forth.

[0023] In some embodiments, the method further comprises a step of attaching the probe on a solid surface.

[0024] In some embodiments, the at least one pair of probes consist of a normal/control probe and a variant probe, both of which interrogate the about same region on the genetic variant segment, wherein the both probes forming the probe sub-set have the same sequence length and are of the same type of nucleic acids.

[0025] In some embodiments, the normal (N) or control (C) probe comprises the normal sequence (which is the wild type sequence) or a known SNP polymorphism (which is the control sequence) of genetic variant segment and the variant probe comprises an indel-containing variant sequence of genetic variant segment

[0026] In some embodiments, the at least two different probes has the difference between them located in position -4, -3, -2, -1, 0, +1, +2, +3 or +4 position of the probe, wherein the position 0 is the center nucleotide of the probe when the probe has an odd number of nucleotides; and wherein the position -1 and +1 are the two central nucleotides of the probe when the probe has an even number of nucleotides.

[0027] In other embodiments where the probes are longer than 25 nt, e. g. 40 or 50 nt long, or 25-50 bp, the position of the indel variation can be between -25 and +25 position (inclusive) from the center of the probe, e. g. -25, -24, -23, -22, -21, -20, -19, -18, -17, -16, -15, -14, -13, -12, -11, -10, -9, -8, -7, -6, -5, -4, -3, -2, -1, 0, +1, +2, +3, +4, +5, +6, +7, +8, +9, +10, +11, +12, +13, +14, +15, +16, +17, +18, +20, +21, +22, +23, +24 or +25.

[0028] In some embodiments the probes are DNA, RNA or PNA. Pairs of probes that are of the same type of nucleic acid means that the probe members constituting the pair of probes are all DNA,

RNA or PNA. The probe members constituting the pair of probes cannot be a mixture of one probe that is a DNA and the other probe is a RNA, a mixture of one probes that is a RNA and the other probe is a PNA, or a mixture of one probes that is a DNA and the other probe is a PNA. This ensures that the differences in the intensity are due to the presence of an indel and not due to the differences in binding affinity of the types of nucleic acid.

[0029] In some embodiments the indel variation is a deletion, an insertion or a duplication of nucleotide. The deletion, insertion or duplication can be 1-10, 1-20, 1-30, 1-40 or 1-50 nucleotides long. In some embodiments, the indel is 1-10 nucleotides long.

[0030] In other embodiments, the deletion can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0031] In other embodiments, the insertion can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0032] In other embodiments, the duplication can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0033] In some embodiments the deletion is selected from a group consisting of one, two, three, four, five, six, seven, eight, nine, and ten nucleotides. In some embodiments, deletion of 1-10, 1-15, 1-20, 1-50 nucleotides can be detected.

[0034] In some embodiments the insertion is selected from a group consisting of one, two, three, four, five, six, seven, eight, nine, and ten nucleotides.

[0035] In some embodiments the duplication is selected from a group consisting of one, two, three, four, five, six, seven, eight, nine, and ten nucleotides. In some embodiments, insertion of 1-10, 1-15, 1-20, 1-50 nucleotides can be detected.

[0036] In some embodiments the probes of the at least one probe sub-set is complementary to the sense strand of the genetic variant segment.

[0037] In some embodiments probes of the at least one probe sub-set is complementary to the anti-sense strand of the genetic variant segment.

[0038] In some embodiments only one kind of indel is detected, the method comprising a step of selecting one set of probe sets and as many probe sets as the length or number of nt (or base pairs) in the variant segment under interrogation, wherein each probe set comprises a single probe sub-set, wherein each probe sub-set comprises at least a pair of probes consisting of one control (C) or normal (N) /wild type probe and one variation probe (V).

[0039] In some embodiments at least two types of indels are designed to be detected, the method comprising the step of designing each probe set to comprise at least two probe sub-sets, wherein each probe sub-set comprises at least one pair of probes, wherein each pair of probes consists of one control or

normal or control probe and one variation probe, wherein the probes of each pair of probes making up the probe sub-set differ from each other in terms of length, indel variation location inside the probe and strand of interrogation of the variant segment.

[0040] In some embodiments more than two types of indels are designed to be detected, further comprising a step of designing as many probe sub-sets as there are indels that need to be detected, and wherein each pair of probes within a probe sub-set is designed to differ from each other in terms of length, interrogating position inside the probe and strand of interrogation of the variant segment.

[0041] The invention also provides a library of probes prepared by the methods described above.

[0042] In some embodiments, the probes are selected from the probes set forth in Table 1, SEQ ID NOS: 1-4575, and consist of or consist essentially of the probes set forth in Table 1, SEQ ID NOS: 1-4575.

[0043] In some embodiments the probes consist of, or consist essentially of SEQ ID NOS: 1-4575.

[0044] The invention also provides for methods of using or use of the library of probes designed/selected according to any one of methods described above. One can use the libraries to identify the location and the type of an indel in any target nucleic acid sequence, such as a genetic variant segment.

[0045] The invention also provides a DNA-chip comprising the library of probes set forth above and use of the DNA chips, and well as a collection of microbeads comprising the library of probes and uses thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

[0046] Figure 1A shows a pair of probes consisting of a control or normal/wild type probe and a variation probe (SEQ ID NOS: 4607 and 4608, respectively in the order of appearance); the pair of probes is used to investigate an indel located at nucleotide 16 which is the nucleotide of interest in a genetic variant segment. The indel here is a deletion of one base (G in position 16, illustrated in box) (Del1).

[0047] Figure 1B shows a pair of probes consisting of a control or normal/wild type probe and a variation probe (SEQ ID NOS: 4609 and 4610, respectively in the order of appearance); the pair of probes is used to investigate an indel consisting of a deletion of four nucleotides located at nucleotide 16 which is the nucleotide of interest in a genetic variant segment. The indel here is a deletion of the nucleotide 16 as well as the three nucleotides adjacent in 3' (boxed) (Del4).

[0048] Figure 2 shows the possible differences in various pairs of probes making up a indel probe sub-set: differences in probe length, 21 and 25 nucleotides long; differences in strand interrogated by the probes, the sense or anti-sense strand; and differences in the position of the indel location within

the probes such as at the 11th nucleotide (0 position) in a 21 nucleotide long probe or at the 13th nucleotide (0 position) in a 25 nucleotide long probe.

[0049] Figure 3 shows different pairs of probes making up a probe sub-set and a different probe sub-set make up a probe set (SEQ ID NOS: 4611-4615, 4612, 4616, 4614, 4617-4621, 4618, 4622, 4620 and 4623, respectively in the order of appearance).

[0050] Figure 4A shows an embodiment of a library of probes on a solid support for detecting a single indel. The library has N probe sets for interrogating a variant segment having a length of N basepair long, and each probe set comprises of one probe sub-set which comprises a pair of probes consisting of one control or normal/wild type probe (C) and one variation probe (V).

[0051] Figure 4B shows an embodiment of a library of probes on a solid support for detecting a single indel. The library has N probe sets for interrogating a variant segment having a length of N basepair long, and each probe set comprises of one probe sub-set which comprises several pair of probes, each of which consists of one control or normal/wild type probe (C) and one variation probe (V).

[0052] Figure 4C shows an embodiment of a library of probes on a solid support for detecting four distinct indels. The library has N probe sets for interrogating a variant segment having a length of N basepair long, and each probe set comprises of four probe sub-sets, one probe sub-set for each distinct indel, each probe sub-set comprises 32 pair of probes, each of which consists of one control or normal/wild type probe (C) and one variation probe (V).

[0053] Figure 5 shows one embodiment of the indel detection and analysis method.

[0054] Figure 6 shows one embodiment of the indel detection and analysis method.

[0055] Figure 7 shows one embodiment of the indel detection and analysis method.

[0056] Figure 8 illustrates three probes having 25, 23 and 20 nucleotide bases respectively showing the -3, -2, -1, 0, +1, +2, +3 positions of the indel within the probes.

[0057] Figure 9 shows a schematic presentation of an embodiment of replicate probe features of the pair of probes comprising the probe sub-sets on a flat solid support.

[0058] Figure 10 shows is a block diagram showing an exemplary system for detecting an indel type of genetic variation.

[0059] Figure 11 shows an exemplary set of instructions on a computer readable storage medium for use with the systems described herein.

DETAILED DESCRIPTION OF THE INVENTION

[0060] The present invention relates to an *in vitro* method of detecting genetic variations in an individual, specifically variations (e.g. duplications, insertions or deletions or loss of a small number of nucleotides collectively referred to as “indels”) in a sequence segment in the genome. The inventors have developed a sensitive, specific and reproducible computer implemented method for simultaneously detecting and characterizing indel variations in a genome. The method does not require prior knowledge of any indel in the segment. Therefore, novel indels can be discovered by the method described herein.

The inventors also developed methods for designing oligonucleotide probe sets for carrying out the method of detecting indel variations. Using the uniquely designed probe sets and analysis methods described herein, one can analyze any indels in a genome. The method is also useful for the development of products for commercial, fast and reliable genotyping methods to detect known indels. Such products, such as kits, can be used for, e.g., diagnostic and prognostic purposes and for the purposes of identifying individuals susceptible for, e.g., side effects associated with known indels or drug responsive individuals, wherein the drug response is associated with a known indel. In a preferred embodiment, the method is the detection of mutations responsible of the illness Hypercholesterolemia Familiar. The method is achieved with the use of a specially designed library of probes together with a computation algorithm for analysis of the data obtained from the library of probes.

[0061] Broadly, the invention provides methods and products for determining the presence of insertions or deletions of a small number of nucleotides (indels) in a genetic segment of interest, also named genetic variant segment, such as an exon, an intron or a promoter, in the target nucleic acid (NA) sample. The inventors showed that by using a specifically designed library of probes in hybridization experiments with a target NA sample to be genotyped, any indels harbored within a target NA sample can be detected with accuracy. Further, in the event that the indels are unknown, the type of indels found in the target NA sample can also be characterized. Because the method, in combination with the specially designed library of probes, facilitates simultaneous detection and characterization of the indels in a genetic variant segment, embodiments of the invention can therefore provide considerable efficiency in terms of savings in time and cost when compared to other methods of detecting and characterizing indels, for example, full NA sequencing of the genetic variant segment.

[0062] The method is unique in that it is based on a combination of (1) use of a solid support based array, such as NA-chips/microbeads genotyping strategy with some distinct modifications in the probe selection and array design, and (2) a sequential computation system (algorithm) amenable for electronically processing and interpreting the data generated by the genotyping strategy (based on a selection of the probes to be included in the computation of the genotype). This combination of genotyping strategy and a sequential computation system guarantees high level of specificity, sensitivity and reproducibility of results. This method is versatile because any solid support, such as, chips or microbeads that are coated with the selected unique probes can be used, for example, in clinical genetic diagnosis. The method is versatile for processing and interpreting of the data and it can be performed manually or by using a computer that is programmed to carry out the algorithm.

[0063] One specific advantage of the method is the availability of a library of probes for every nucleotide position of any genetic segment of interest. It is not necessary to have prior knowledge of the indels, for example, whether the indel variation is a deletion or an insertion, or the number of nucleotides (nt) deleted or inserted. The library of probes is specially designed to contain all probes that will detect all possible permutations of indels in a genetic variant segment. The genetic variant segment can be e.g., having a length of N nt, wherein N can be, for example, 100-2000 or 50-5000 nt long. In some

embodiments shorter than 50, such as 10-15, 25-50 nucleic acid fragments can be analyzed.

Alternatively, one can also analyze fragments that are larger, such as about 50 or 100 to 2000, to 3000, to 4000, to 5000, to 6000, to 7000, to 8000, to 9000 or up to about 10,000 nucleotides long.

[0064] Another specific advantage is the fact that direct identification of indel changes can be achieved, while previously used methods only detect the possible presence of an indel, without actually identifying the exact genetic change (i.e. the identity of the sequence variation).

Definitions

[0065] For convenience, certain terms employed herein, in the specification, examples and appended claims are collected here. Unless stated otherwise, or implicit from context, the following terms and phrases include the meanings provided below. Unless explicitly stated otherwise, or apparent from context, the terms and phrases below do not exclude the meaning that the term or phrase has acquired in the art to which it pertains. The definitions are provided to aid in describing particular embodiments, and are not intended to limit the claimed invention, because the scope of the invention is limited only by the claims. Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0066] The term "nucleic acid (NA)" refers to deoxyribonucleotides (DNA) or ribonucleotides (RNA) and polymers thereof ("polynucleotides") in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Where the NA is a double stranded, the term "base pairs" (bp) are used to refer to the building block bases. Where the NA is a single stranded such as an oligonucleotide probe, the term "nucleotides" (nt) are used to refer to the building block bases.

[0067] As used herein, the term "peptide-nucleic acid" or "PNA" refers to any synthetic nucleic acid analog (deoxyribonucleic acid (DNA) mimics with a pseudopeptide backbone) which can hybridize to form double-stranded structures with DNA in a similar fashion as naturally occurring nucleic acids. PNA is an extremely good structural mimic of DNA (or of ribonucleic acid (RNA)), and PNA oligomers are able to form very stable duplex structures with Watson-Crick complementary DNA and RNA (or PNA) oligomers, and they can also bind to targets in duplex DNA by helix invasion. Other type of complementary base pairing, such as the Hoogsteen pairing is possible too. PNA may be an oligomer, linked polymer or chimeric oligomer. Methods for the chemical synthesis and assembly of PNAs are well known in the art and are described in U. S. Patents Nos: 5,539,082, 5,527,675, 5,623,049, 5,714,331, 5,736,336, 5,773,571, and 5,786,571. Uses of the PNA technology are also well known in the art; see U. S. patents Nos. 6,265,166, 6,596,486, and 6,949,343. These references are hereby incorporated by reference in their entirety.

[0068] As used herein, the phrase "same type of nucleic acid" with regards to the probes constituting a pair of probes(also referred to as member probes), refers to the member probes being all

DNA, all RNA, or all PNA, and there is no mixture of RNA, DNA and/or PNA in a pair of probes. For this context of the make-up or composition of probes, the term “nucleic acid” also include PNA.

[0069] As used herein, the term “complementary base pair” refers to A:T and G:C in DNA and A:U in RNA. Most DNA consists of sequences of nucleotide only four nitrogenous bases: base or base adenine (A), thymine (T), guanine (G), and cytosine (C) or pseudocytosine (J). The pairing is based on the Watson-Crick pairing or the Hoogsteen pairing. Together these bases form the genetic alphabet, and long ordered sequences of them contain, in coded form, much of the information present in genes. Most RNA also consists of sequences of only four bases. However, in RNA, thymine is replaced by uridine (U).

[0070] As used herein, the term “indels” refers to small duplications, deletions and/or insertions which involve anywhere between one to ten nucleotides (nt) and in other embodiments, the indels are duplications, deletions and/or insertions involving up to 50 nt. In one embodiment, the indel is a one nt deletion indel. In another embodiment, the indel is a two nt deletion indel. In other embodiments, the indel is a three nt deletion indel, a four nt deletion indel, a five nt deletion indel, a six nt deletion indel, a seven nt deletion indel, an eight nt deletion indel, a nine nt deletion indel, or a ten nt deletion indel. In other embodiments, the indel is a one nt insertion indel, a two nt insertion indel, a three nt insertion indel, a four nt insertion indel, a five nt insertion indel, a six nt insertion indel, a seven nt insertion indel, an eight nt insertion indel, a nine nt insertion indel, or a ten nt insertion indel. In the embodiments where the indels are up to 50 nt, the duplication, deletion or insertion can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt. The term “indel” and “indel variation” are used interchangeably.

[0071] As used herein, the phrase “genetic variant segment” refers to a segment or region of nucleic acid (NA) wherein there may be or are commonly known sequence variations within a population of an animal species, including humans. Such allelic variations may be silent or causal, or disease or disease-risk causing mutations. In some embodiments, a “genetic variant segment” refers to or included a NA segment or NA region where there is a likelihood of sequence variations within a population of an animal species, e.g., a region prone to spontaneous mutations, a region of known genetic instability, and/or a region associated with a disease or disorder that is known to be linked to mutations in the gene. The NA can be DNA or RNA. The NA is typically a genomic DNA, but in some embodiments it can also be a primary transcript or fragments thereof or a messenger RNA or fragments thereof. In some embodiments, the sequence variation or genetic variant present in the “genetic variant segment” is an indel.

[0072] As used herein, the phrase “genetic non-variant segment” or “non-variant segment” refers to a segment or region of nucleic acid (NA) wherein the sequence is constant within a population of animal species, meaning that it is known that there is no allelic variation in the population in this region. While the “genetic non-variant segments” or “non-variant segment” do not have allelic variations among individuals in a population, they can have known mutations that result in very obvious and distinct

phenotypes. Two normal individuals who are of the same gender and do not exhibit any of the obvious and distinct phenotypes (e.g. Down syndrome) that are associated with known mutations at these "genetic non-variant segments" would have identical "genetic non-variant segments". "Genetic non-variant segments" function as the reference/control segments in the present invention in the analysis of indels. Mutations in non-variant segments can be selected from known disease-causing regions, such the DSCR1 locus on chromosome 21, the PLP locus and F9 locus on chromosome X, or any other region, which results in an unmistakable phenotype, wherein an absence of a phenotype, such as a Down syndrome, indicates that this region does not have variations in the subject, such as a human individual or an animal, whose nucleic acid is to be analyzed or in the sample from an individual or an animal whose sample is used as a control. A skilled artisan can easily select these regions based on these criteria and common knowledge of genetic diseases. The "genetic non-variant segments" can be DNA or RNA. The NA can be genomic DNA, a primary transcript or fragments thereof or a messenger RNA or fragments thereof.

[0073] In one embodiment, the non-variant segment selected for analysis of human samples is derived from the human chromosome 21. In another embodiment, the non-variant segment is derived from the Down Syndrome Critical Region 1 (DSCR1) on chromosome 21. The gene DSCR1 is also called RCAN1 for Regulator of Calcineurin 1. DSCR1/RCAN1 is located at position 21q22.1-q22.2; chromosome 21: 34,810,654-34,909,252 (SEQ ID NO: 4576) with respect to human genome assembly 18 March 2006 (GENBANK™ accession number for its mRNA: NM_004414.5, SEQ ID NO: 4577). It is involved in the development of the phenotype of the Down syndrome. Indeed a deletion of one copy this gene is lethal whereas the presence of an extra copy of this gene, i.e. a duplication of this gene, is responsible of the Down syndrome phenotype, which is easily recognizable. This gene, part of this gene or the region of the chromosome 21 wherein this gene is located can be used as the non-variant segment for the normalization in human samples in the presently claimed methods.

[0074] As used herein, the term "known genotype" when used in reference to control data of the genetic variant segment means that the type of indels, the number of nt involved, and the position or location, the bases or nt sequence(s) of the indel in the genetic variant segment are known, for example, one nt insertion at position K is the genetic variant in the segment. In some embodiments, the term "known genotype" when used in reference to control data means a SNP that is known, for example, it can be either a T nucleotide or a C nucleotide. In some embodiments, "known genotype" when used in reference to normal or wild type genotype data of the genetic variant segment which is the normal genotype in the population, meaning no indels at all in the genetic variant segment and the wild-type sequences are known.

[0075] As used herein, the term "a test nucleic acid (tNA)" refers to a nucleic acid (NA) sequence wherein the indels within the sequence is unknown. In some embodiments, the term "a test nucleic acid (tNA)" refers to a NA sequence wherein the indel within the sequence is of interest to the investigator and the tNA therefore is being studied, regardless of whether the indel is known or not. For

example, the investigator would like to verify that the indicated indel in the tNA is accurate and valid. A “test nucleic acid (tNA) sample” refers to a NA sample comprising at least one tNA.

[0076] As used herein, the term “a control nucleic acid (cNA)” refers to a nucleic acid (NA) sequence wherein the indel within the sequence is known. In one embodiment, a cNA is a NA sequence that is normal/wild type and has no known indel within the sequence. In another embodiment, a cNA is a NA sequence that has a SNP that is known, for example, it can be either a T or a C, within the control sequence. A control NA can be used in parallel with a tNA in the methods described herein for the detection and analysis of the indel in the tNA. A “control nucleic acid (cNA)” sample refers to a NA sample comprising at least one cNA.

[0077] As used herein, the term “target nucleic acids (target NAs)” refers to the nucleic acids that are to be hybridized to the probes immobilized on solid support(s) described herein. Target NAs can comprise both the control nucleic acid and the test nucleic acid. In some embodiments, target NAs can be detectably labeled or fragmented to smaller segments of nucleic acid sequences.

[0078] As used herein, the term “probe” refers to a short sequence of NA, typically consisting between 15nt-50nt, including all of the whole integers between 15-50, wherein the short sequence is complementary to a small portion of a genetic variant segment or complementary to a small portion of a non-variant segment (the control segment) that is under interrogation such that the probe can hybridize to the segment by complementary base pairing. For example, one can use probes that are 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 nucleic acids long. In some embodiments shorter, such as 10-15 Nt or longer probes, such as 50-100 nt, can be used, but typically, one uses about 25 nucleic acids as a standard probe. The probe can be a DNA, RNA, peptide nucleic acid (PNA) or hybrids thereof. Modifications to the backbone of the NA are encompassed within the definition. In one embodiment, the probe is a DNA-probe. In another embodiment, the probe is an RNA-probe. In another embodiment, the probe is a PNA-probe. Probes are preferably single-stranded probes, but double-stranded or partially double-stranded probes can also be used.

[0079] As used herein, the term “variation affecting one nucleotide” refers to any of a plurality of insertions or deletions affecting one nt of interest, exclusively, and/or one nt of interest together with an addition of one to nine nt located contiguously at its 3′ side. In other embodiments, the additional nt can be one and up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt. A deletion of only the nt of interest (one-nt deletion, or Del1) is an example of such a variation, i.e., affecting one nt. A deletion of the nt of interest together with one contiguous 3′ nucleotide (two-nt deletion, or Del2) is another example of such a variation affecting one nt. Other examples include Del3, a deletion of the nt of interest together with two contiguous 3′ nt; Del4, a deletion of the nt of interest together with three contiguous 3′ nt; Del5, a deletion of the nt of interest together with four contiguous 3′ nt; Del6, a deletion of the nt of interest together with five contiguous 3′ nt; Del7, a deletion of the nt of interest

together with six contiguous 3' nt; Del8, a deletion of the nt of interest together with seven contiguous 3' nt; Del9, a deletion of the nt of interest together with eight contiguous 3' nt; Del10, and a deletion of the nt of interest together with nine contiguous 3' nt.

[0080] A duplication of only the nt of interest (one-nt duplication, or Dup1) is another example of a variation affecting one nt. A duplication of the nt of interest together with one contiguous 3' nucleotide (two-nt duplication, or Dup2) is another example of such a variation affecting one nt. Other examples include Dup3, a duplication of the nt of interest together with two contiguous 3' nt; Dup4, a duplication of the nt of interest together with three contiguous 3' nt; Dup5, a duplication of the nt of interest together with four contiguous 3' nt; Dup6, a duplication of the nt of interest together with five contiguous 3' nt; Dup7, a duplication of the nt of interest together with six contiguous 3' nt; Dup8, a duplication of the nt of interest together with seven contiguous 3' nt; Dup9, a duplication of the nt of interest together with eight contiguous 3' nt; Dup10, and a duplication of the nt of interest together with nine contiguous 3' nt. The Fig. 1 shows graphically an example of Del1 and Del4 variations affecting one nt, at position 16, of the wild type sequence. In some embodiment, the duplications are insertions, where the sequences of the inserted nt are different from that of the nt of interest.

[0081] As used herein, the term "indel probe sub-set" or "probe sub-set" refers to a collection of probes interrogating one kind of indel variation affecting one nt. For example, a first probe sub-set investigates the presence of a single nt insertion at K position in variant segment, a second probe sub-set investigates the presence of a two- nt insertion at K position, a third probe sub-set investigates the presence of a three-nt insertion at K position, a fourth probe sub-set investigates the presence of a single nt deletion at K position, a fifth probe sub-set investigates the presence of a two-nt deletion at K position, a sixth probe sub-set investigates the presence of a three-nt deletion at K position, a seventh probe sub-set investigates the presence of a single nt duplication at K position, a probe sub-set investigates the presence of a two-nt duplication at K position, and a eighth probe sub-set investigates the presence of a three-nt duplication at K position. The collection of the entire eight probe sub-sets make up the probe set for the K position bp in the variant segment.

[0082] In one embodiment, an "indel probe sub-set" or "probe sub-set" comprises at least one pair of probes, wherein the pair of probes consist of one control or normal/wild type probe and one variation probe. In one embodiment, one control or normal/wild type probe and one variation probe making up a pair of probes that have the same length and sequence except for the indel variation, be it an insertion, deletion or duplication. For each kind of variation to be detected, probes can be designed with (1) different lengths, at (2) different positions in the probes wherein the indel variation to be detected are located; and (3) to hybridize to the sense strand solely, to the antisense strand solely, or to both strands. Any combination of the length, strand and position can be selected for a given indel probe sub-set. For example, a given indel probe sub-set can comprise probes of two different lengths, with sense and antisense probes of both lengths, and with two positions by which the variations will be detected in the

probes of one length and three positions by which the variations will be detected in the probes of the other length.

[0083] All indels probe sub-sets should include the normal (i.e., wild type) probes matching the variation probes in terms of length, strand and position of the variation in the probe. Fig. 2 shows an example of ten variations designed for the variation probes making up the pairs of probes that would make up an indel probe sub-set. The variation probes are of two different lengths (21 nt and 25 nt long). Variation probes of both lengths are designed for either the sense or antisense strands or both. Probes which are 21 nt-long carry the variation-detecting nt at positions 9 and 11, while probes which are 25-nt long carry the variation-detecting nt at positions 11, 13 and 15. In this example, positions of variation-detecting nt are the same for the sense and antisense probes, but do not necessarily have to be so in all embodiments.

[0084] In the Fig. 2 example, sense and antisense variation probes are designed for both lengths, but it does not necessarily have to be so in all embodiments. In this example, the indel probe sub-set includes the normal (i.e., wild type) probes that match the 10 variation probes. In another embodiment, the indel probe sub-set includes the control probes that match the 10 variation probes. The match of each variation probe with its normal or control probe forms a pair of probes. Any probe sub-set comprises at least two probes for the nucleotide of interest, a probe harboring a variation and the corresponding normal or control probe. The number of distinct probes in a probe sub-set can range from one (in the case of a non-variant segment) to about 10,000, typically one uses about 2-200 probes per probe sub-set. The probes are all distinct probes. In one embodiment, there is at least a duplicate or replicate of a probe. In another embodiment, one uses triplicates of a probe. In one embodiment, four or five replicates of each of the different probes making up a probe sub-set can be used. In other embodiments, more than five replicates of each different probe are used on a solid support, in some embodiment, up to 10, or up to 50 replicates are used. In the case of a non-variant segment, the probe sub-set is only composed of normal (i.e., wild type) or control probes.

[0085] As used herein, the term "an indel probe set" refers to the collection of all the probe sub-sets selected for interrogating a nucleotide or nucleotide of interest where an indel variation can occur, and detecting all the kinds of variation affecting this nucleotide of interest. Any combination of indel probe sub-sets can be selected for a given probe set. Probe sub-sets in a given probe set can have different number of probes, and different combinations of length, strand hybridization and position of the variation to be detected in the probe. However, the process of designing the probe sub-set and probe set follows the novel selection method claimed herein and remains the same.

[0086] As used herein, the term "a set of indel probe sets" refers to the collection of all the probe sets (thus, all the probes) selected for interrogating a genetic variant segment or a non-variant segment. For example, a genetic variant segment where indels are known to occur encompassing 0.7 kilobases (kb) long is selected for interrogation. The investigator can select any number of probe sets covering these regions. The full length of the segment of interest can be covered by designing indel

probe sets for all the nt of the variant segment, i. e. 700 nt. For example, one can decide to have 700 different indel probe sets. Each indel probe set can consist of any number of probes. In one embodiment, each indel probe set consists, for example, of 180 probes; each indel probe set interrogating one base of the 700 base pair long variant segment. This would result in $700 \times 180 = 126\,000$ different probes covering the variant segment. The number of distinct probes can be different for each probe set. The number of distinct probes in a set of probe sets can range from one to about 300,000, typically one uses about 25,000 – 200,000 probes per set of probe sets for a nucleic acid region covering 1 kb. The probes can be all distinct probes, and they complement and interrogate a single genetic variant segment or non-variant segment.

[0087] In one embodiment, "a set of indel probe sets" constitutes a library of probes. In one embodiment, the genetic variant segment where indels of interest can be found is between about 50 base-pair (bp) to about 5000 bp long. In one embodiment, the genetic variant segment where indels of interest can be found is between about 100 bp to about 2000 bp long.

[0088] In Fig. 3, a set of two probe sets is shown. The two probe sets affect respectively nt 16 and 17 of a variant segment which is 37 bp long. The first probe set is for interrogating variations of the 16th nt. Two probe sub-sets making up the probe set for nt 16 are shown: one designed to detect a one-nt deletion (Del1) of the nt of interest (nt 16), and the other designed to detect a deletion of nt 16 and the nt immediately 3' adjacent, i.e. nt 17 (Del2). The Del1 variation 1 probe length is 30 nt, and the position of the nt of interest is position 16 (of the 30 nt). The Del1 variation 2 probe also is 30 bp-long, but the position of the nt of interest is position 13 (of the 30 nt of the probe). The Del2 variation 1 of the second probe sub-set of this first probe set is the deletion of nt 16 and 17, the indel variation (16th bp) is placed at position 16 of a 30 nt long fragment. The Del2 variation 2 is designed to detect the deletion of nt 16 and 17, in other words, a two-nt deletion at the 16th nt position, but the indel variation is located in position 13 of a 30 nt long probe. The second probe set is designed to detect variations affecting the 17th bp of the same variant segment. Two probe sub-sets make up this second probe set for the 17th bp. As shown in Fig. 3, the same characteristics of probes have been designed, although this has not to be the case on other embodiments. Thus, for the variation 1 probe of the first probe sub- set (Del1), the nt of interest is in position 16 of a 30 nt-long probe. For the variation 2 probe, the indel variation is in position 13 of a 30 bp-long probe. In the second probe sub-set (Del2), deletions of 2 nt are interrogated, the indel variation is placed at position 16 of the 30 nt-long probe in variation 1, and in position 13 of the 30 nt-long probe in variation 2.

[0089] In some embodiments, probes are designed for the variant segment LDLR gene Exon 2, from position 68 -121, in intron 1, to nucleotide in position 190 +102 (reference sequence NM_000527.3, SEQ ID NO: 4579), a 345 nt- long sequence. The possible probes variety can be whether to have sense and antisense strands probes, have three different sizes of probes (probes of 21, 23 and 25 nt), 5 different positions of the indel variation in the probe , such as central (0), central-2 nt (-2), central-4 nt (-4), central+2 nt (+2), central+4 nt (+4) positions or more etc, for the detection of the deletion of one, two and

three nt and the detection of the insertion of one, two and three nt. For this variant segment, the number of probes to be designed can be 103,500, including both normal and variation probes.

[0090] As used herein, the term "normal probe" or "control probe" refers to a probe that has no indel genetic variation, meaning that the probe has the wild type sequence with no deletions, insertions or duplications or has a known SNP respectively. In one embodiment, the "normal probe" or "control probe" interrogates the control nucleic acid (cNA). In another embodiment, the "normal probe" or "control probe" interrogates the non-variant segment. In one embodiment, the wild type sequence with no deletions, insertions or duplications in the control or normal sequence of the cNA or non-variant segment.

[0091] As used herein, the term "variation probe" or "variant probe" refers to a probe that has an indel genetic variation with respect to the normal/wild type or control sequence, meaning that the probe has a deletion, insertion or duplication within the sequence. In one embodiment, the "variation probe" interrogates the test nucleic acid (tNA). In another embodiment, the "variation probe" interrogates the genetic variant segment.

[0092] As used herein, the term "probe feature" refers to a localized and concentrated deposit of multiple copies of the same probe on a solid support surface (a defined "spot" on the glass surface or oligonucleotides on one bead). For example, for a flat solid support such as on the glass-chip surface, a probe feature is a spot or dot printed with multiple copies of the same probe. The multiple copies can range from tens to hundreds to thousands, e.g., about 10-10,000, or 100-10,000. All of the whole integers numbering from 10 to 10,000 are included. Typically the concentration of the oligonucleotide solution and the droplet size will determine the approximate copies of oligonucleotides printed on a "probe feature spot" on a flat solid support. For a spherical surface such as a glass bead, "a probe feature" refers to a single bead coated with at least about 100 copies of the same oligonucleotides probe that complement and interrogate a single genetic variant segment or non-variant segment. In this case, typically the concentration of the oligonucleotide solution determines the approximate copies of oligonucleotides coating the bead. In one embodiment, the bead can have about 100-10,000 copies of the same probe. All of the whole integers running from 100 to 10,000 are included. The raw value or signal intensity of the hybridization reaction in the methods herein is obtained from a probe feature, meaning from a "dot" or a single probe-coated bead. In other words, measuring the signal intensity after hybridization of the test sample or the control sample gives a raw signal value.

[0093] As used herein, the phrases "replicate feature" or "replicate probe feature" refer to a replicate or multiples of a probe feature all having a single/same type of probe to genetic variant segment or non-variant segment (parallel dots or spots with same probe or oligonucleotide sequence on a solid surface or parallel numbers of beads coated with the same probe). For a flat solid support such as a glass-chip, all replicate features of one probe feature have one type of probe and the replicate features can be arranged, for example in a row but not close to each other on the glass-chip surface. For a spherical solid support such as a glass bead, "replicate feature" refers to number of probe-coated beads. For example,

100 probe-coated beads are 100 replicate features or replicate probe features. On a solid flat surface, for each probe, there are at least four replicate features, at least five, at least six, at least seven, at least eight, at least nine, and at least ten replicate features. However, one can also use 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 20-25, or even 25-50 replicates. In a typical analysis, one uses 10 replicate features. For a spherical solid surface, there are at least 100 replicate features, typically between about 100-5000 probe-coated beads. All of the whole integers going from 100 to 5,000 are included.

[0094] As used herein, the term "interrogation" refers to the examination, investigation or study of the nucleotide sequence information in a NA, i.e., the genotype.

[0095] As used herein, the term "comprising" means that other elements can also be present in addition to the defined elements presented. The use of "comprising" indicates inclusion rather than limitation.

[0096] The term "consisting" is a closed term, indicating that nothing else is considered to be included. The phrase "consisting essentially of" is intended to cover situations, wherein the operational parts are included but one can also include non-essential or non-active ingredients or steps.

[0097] As used herein, the term "median" when used in the analysis of the data obtained from the probe feature replicas refers to general meaning when used in statistical analysis. Median is the 'middle value' in a list of values when arranged in increasing order. For example, for a list of the following numbers: 9, 3, 44, 17, 15 (odd amount of numbers), after lining up these numbers: 3, 9, 15, 17, 44 in increasing order (smallest to largest), the median is 15 which is the number in the middle of the ordered list. In the situation, wherein an even number of replicates are present, a median is found by finding the middle pair of numbers, and then find the value that would be half way between them. This is easily done by adding them together and dividing by two. In the present methods, the analysis of median is performed using computer-implemented software with the signal intensity values from the replicate features as an input and median as an output.

[0098] As used herein, the term "mean" when used in the analysis of the data obtained from the probe feature replicas refers to general meaning when used in statistical analysis. Median is the average of a list of values, calculated by the formula:

$$\text{Average} = \frac{\text{Sum of the list of numbers}}{\text{Number in list}}$$

For example, for a list of the following five numbers: 9, 3, 44, 17, 15

$$\text{The mean} = \frac{(9+3+44+17+15)}{5} = 17.6$$

[0099] As used herein, the term "solid support", on which the plurality of probes is deposited, can be any solid support to which oligonucleotides can be attached. Practically any support, to which an oligonucleotide can be joined or immobilized, and which may be used in the production of DNA probe arrays and particle suspensions, can be used in the invention. For example, the said support can be of a non-porous material, for example, glass, silicone, plastic, or a porous material such as a membrane or filter (for example, nylon, nitrocellulose) or a gel. In one embodiment, the said support is a glass

support, such as a glass slide. In another embodiment, the support is a particle in suspension, as described above, such as a microparticle. Microparticles useful for the methods of the invention are commercially available for example from LUMINEX[®] Inc., INVITROGEN[™] (Carlsbad, Calif.), and Polysciences Inc. (Warrington, Pa.). In one embodiment, the solid support is a non-porous solid support. In one embodiment the solid support is a porous solid support. Such supports are well known to one skilled in the art.

Analysis methods

[0100] Embodiments of the invention provide (1) a library of probes which allows the detection of indels in a genetic variant segment; (2) a method of designing such a library of probes; (3) the use of the library of probes to detect the presence of indels in the test NA sample, the method comprises the immobilization of the probes on a solid support, the hybridization of test and optionally normal or control NA samples on the probes, the determination of the intensity for each NA-hybridized probe, and the analysis process and interpretation of the data generated by the hybridization; and (4) a solid support chip or spherical microbeads comprising a library of probes which allows the detection and analysis/characterization of indels in a genetic variant segment.

[0101] Accordingly, provided herein are method to design and a specifically designed library of probes for detecting at least one indel variation in a genetic variant segment having a length of N number of base pairs (wherein N is typically a number between 25 and 5000, for example 50-2000), the library comprising a set of probe sets which comprises N number of probe sets (i.e. the same number of probe sets as there are nucleotides in the segment to be analyzed), wherein there is one probe set for each nucleotide position of the genetic variant segment. Each probe set comprises at least one probe sub-set, wherein the at least one probe sub-set is for interrogating a single kind of indel; and further wherein the at least one probe sub-set comprises at least a pair of probes, a normal probe and a variant probe, both of which interrogate the same region on the genetic variant segment (i.e. are designed to bind to either to the normal or variant sequence in that specific location). These probes form a pair of probes that have the same sequence length and are of the same type of nucleic acids (except for the difference in the normal and variant sequence to be detected). The length of the probes is between 15-50 nucleotides. Thus, the normal probe comprises a sequence corresponding and binding to the normal / wild type or control sequence of genetic variant segment and the variant probe comprises an indel-containing variant sequence of genetic variant segment. Further, the indel in the variant probe is located at -4, -3, -2, -1, 0, +1, +2, +3 or +4 position in the variant probe or located up to 25 nt off the central nt for probes longer, e. g. up to 50nt, wherein the position 0 is the center nucleotide of the probe when the probe has an odd number of nucleotides; and wherein the position -1 and +1 are the two central nucleotides of the probe when the probe has an even number of nucleotides, e. g. -25, -24, -23, -22, -21, -20, -19, -18, -17, -16, -15, -14, -13, -12, -11, -10, -9, -8, -7, -6, -5, -4, -3, -2, -1, 0, +1, +2, +3, +4, +5, +6, +7, +8, +9, +10, +11, +12, +13, +14, +15, +16, +17, +18, +20, +21, +22, +23, +24 or +25.

[0102] Since the indel variations in the genetic variant segment are of various types, i. e. deletions, insertions and/or duplications, the library of probes can consist of the design of all the probes able to detect any one or all kinds of possible indels that one would desire or is likely to detect. If the indels are known indels that one looks for, e.g., as a disease screen or a drug resistance or tolerance screen, probes for only those specific indels can be included into the library. For example, if the genetic region of interest is 100 bp long in the genome, all possible indels for this region would encompass all indel types occurring at each of the 100 nt of this 100 bp-long sequence. For example, a deletion, an insertion and a duplication individually for the position 1 in this 100 bp-long sequence, and so forth for all the following 99 positions in this 100 bp-long sequence.

[0103] In one embodiment, the library of probes comprises or consists essentially of or consists of a control and/or a normal probe. In one embodiment, the control and/or normal probes are provided on a solid support. Control or normal/wild type probes for a known non-variant segment(s) on the X-chromosome exhibit gender dimorphism, meaning that the control, i.e. known nt at position x or the normal wild type nt at position x, is present depends on whether hybridization is performed on a male or female subject (one copy in males, two in females). Such control probes and their respective X chromosome non-variant segments can be used as controls to verify that the control nt, e.g. in SNP, or the normal/ wild type nt is detected in each hybridization, by comparing the test subject and a control subject of different gender. For example, an X chromosome non-variant segment(s) can be selected from two well characterized genes: the PLP locus and F9 locus on the human X-chromosome. These non-variant segments can be used for the normalization. The first gene is PLP (for Proteolipid Protein1, located Xq22), a gene whose duplications and deletions are responsible of the Pelizaeus-Merzbacher disease (PMD). This disease is an X-linked recessive hypomyelinating leukodystrophy (HLD1) in which myelin is not formed properly in the central nervous system. PMD is characterized clinically by nystagmus, spastic quadriplegia, ataxia, and developmental delay. PLP1 is located at position chromosome X: 102,927,195-102,934,703 (SEQ ID NO: 4580) with respect to human genome assembly 18 March 2006 (GENBANK™ accession number for its mRNA: NM_000533.3, SEQ ID NO: 4581). The second gene is the F9 (for coagulation factor IX, located Xq22) which is responsible of Hemophilia B. Deletions of this gene cause Hemophilia B. These genes or part of these genes are the genetic variant segments in test samples. F9 is located at position chromosome X: 138,440,061-138,473,783 (SEQ ID NO: 4582) with respect to human genome assembly 18 March 2006 (GENBANK™ accession number for its mRNA: NM_000133.3; SEQ ID NO: 4583).

[0104] In some embodiments, the indel variation can be deletion of one, two, three, four, five, six, seven, eight, nine or ten adjacent nucleotides (nts). In other embodiments, the deletion can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0105] In one embodiment, the indel variations also can be insertions of one, two, three, four, five, six, seven, eight, nine or ten adjacent nts. The insertions or deletions can be located at any of the nt

in the sequence. In other embodiments, the insertion can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0106] In some embodiments, the insertion of one or more nucleotides can be a duplication of one or more nt, up to ten nt, of the reference/control or wild type sequence, for example, two, three, four, five, six, seven, eight, nine or ten nts. In other embodiments, the duplication can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0107] Better detection of the many kinds of indel variations in a genetic variant segment can be achieved by using many different types of probes and/or a greater number of probes. While it is not possible to perform an “a priori” analysis to assess the best design of the probes for the detection of an indel, or for the detection of various indels, the inventors have designed a novel strategy which ensures that the library comprises at least one probe for each potential indel for each nt position in the genetic variant segment and that there is a better, if not best, probe for an indel at each nt position among all the probes that are designed of that indel at that nt position. The different types of probes encompassed for each nt position in the genetic variant segment include: (1) probes with different length, e. g. probes that are anywhere from 15- 50 nt long, such as 21, 23, 25, 27, 30 and 32 nt long; (2) the probes that have the indel variation located at different interrogating position inside the variant probe, e. g. located at the interrogating position-4, -3, -2, -1, 0, +1, +2, +3 or +4 position of the variant probe wherein the position 0 is the center nucleotide of the probe when the probe has an odd number of nts; and wherein the position -1 and +1 are the two central nts of the probe when the probe has an even number of nucleotides (see Fig. 8); and (3) probes that complement or hybridize to the sense strand or the anti-sense strand of the genetic variant segment. The strand to which the probe complements or hybridizes would be the strand interrogated by the probe of the variant segment. Thus, a great number of different types of probes can be designed for each specific indel at each specific nt position in the genetic variant segment according to the described novel design strategy. For example, for a deletion of a nt at a position k, the best probe for its detection might be a probe 25 bp long, interrogating the sense strand of the variant segment and the indel variation is located at the 0 position (i. e. nt number 13) of the 25 bp long probe (see Fig. 8), while for the deletion of one nt in position k+1, the best probe for its detection might be a probe 23 base-pair long, interrogating the anti-sense strand of the variant segment and with the indel variation is located at the -3 position (i. e. nt number 9) of the 23 bp-long probe (see Fig. 8).

[0108] In one embodiment of the at least one probe sub-set comprises more than one pair of probes, e. g. anywhere from 5-100 pairs of probes. Member probes constituting a pair of probes have the same length and interrogate the same region on the variant segment and they interrogate the same strand.

[0109] In one embodiment, the pairs of probes of the at least one probe set have different length, at least three different length, e. g. anywhere from 15-50 nt long. For example, there are pairs of probes

that are 15, 20, 25, 30, 35, 40, 45 and 50 nt long making up the at least one probe sub-set. For example, there are pairs of probes that are 21, 23 and 25 nt long making up the at least one probe sub-set.

[0110] In some embodiments, the pairs of probes of the at least one probe set interrogate a different strand of the genetic variant segment, e.g. some pairs of probes interrogate the sense strand of the genetic variant segment and other pairs of probes interrogate the anti-sense strand of the genetic variant segment. These pairs of probes can have the same length or different length. In some embodiments, the probes are all designed to hybridize to either the sense or the anti-sense strand.

[0111] In one embodiment, the pairs of probes of the at least one probe set have different positions of the indel variation located within the probe.

[0112] It is contemplated that in some embodiments, within a library of probes are probes for detecting and analysing/characterizing several combinations of indel variations in a genetic variant segment. This facilitates simultaneous detection and analysis of several indels in the genetic variant segment. For example, a library of probes can have probes for detecting and analysis/characterization insertions of one, two, and three nts at all the nt positions and probes for detecting and analysing/characterization deletions of one, two, and three nts at all the nt positions in the genetic variant segment. Another library of probes can have probes for insertions of four and five nts at all the nt positions and probes for deletions of four and five nts at all the nt positions in the genetic variant segment. Libraries can have probes that detecting and analysing/characterization all possible combinations of indel variations in a genetic variant segment described.

[0113] It is also contemplated that within a library of probes are probes for detecting and analysing/characterization of several combinations of indel variations if more than one indel is present in a genetic variant segment. In other embodiments, the library of probes can be used to detecting and analysing/characterization of several combinations of indel variations in more than one genetic variant segment, e. g. several genetic variant segments. For example, an investigator may wish to analyze several genetic variant segments found in a test NA sample. Such a library of probes will facilitate simultaneous detection and analysis of several indels in the test NA sample which may have only one or several genetic variant segments.

[0114] In one embodiment, only one kind of indel, for example, a deletion of one nt or an insertion of one nt located at an unknown position in a genetic variant segment, is investigated. For this embodiment, the library of probes comprises one set of probe sets and as many probe sets as the length or number of nt (or base pairs) in the variant segment under interrogation, wherein each probe set comprises a single probe sub-set, wherein each probe sub-set itself comprises a single pair of probes consisting of one control or normal/wild type probe (C) and one variation probe (V). Fig. 4A shows an example of this embodiment of the library of probes for a single indel detection whether it is a one nt deletion or a one nt-insertion. The library is for interrogating a variant segment having a length of N bp-long (where N can be any number of nucleotides, such as, 25-5000 or any size as described already above in connection with some embodiments), and each probe sub-set itself comprises a single pair of probes. For this N bp-long

segment, there should be N number of probe sets (i.e. as many probe sets as there are nucleotides in the segment that one wishes to analyze) making up the one set of probe sets. Replicas of each of the probes for each pair of probes can be placed on the solid support, e.g., replicas of the C and V probes (see Figure 4) of each pair of probes can be placed on the solid support.

[0115] In one embodiment, a library of probes is the set of probe sets or the entire collection of probe sets. The number of probe sets comprising in the library is as many as the length of nt (or base pairs) in the variant segment under interrogation. Each probe set comprises one or more probe sub-sets wherein each probe sub-set comprises one or more pairs of probes. A pair of probes consists of one control or normal/wild type probe and one variant probe. Each pair of probes making up a probe sub-set differ from the other pairs of probes within the same probe sub-set in term of the length, the location of the indel variation inside the variant probe, and/or the interrogation strand: sense strand or the anti-sense strand.

[0116] All pairs of probes making up a probe sub-set have the same type of indel variation under investigation, e. g. one deletion of one nt (see Fig. 3, probe sub-set nt 16 del1 or nt 17 del1) or one deletion of one nt at X position and one 3' contiguous nt (see Fig. 3, probe sub-set nt 16 del2 or nt 17 del2). Therefore, a probe sub-set is a collection of pairs of probes that investigates a single type of indel variation at a specific X position in a genetic variant segment.

[0117] A probe set is then a collection of probe sub-sets that investigates indel variations at a specific X position in a genetic variant segment (see Fig. 3, probe sub-set nt 16 del1 and nt 16 del2 make up the probe set for nt 16). In one embodiment, the collection of probe sub-sets (i. e. a probe set) investigates at least one type of indel variation at a specific X position in a genetic variant segment. In another embodiment, the collection of probe sub-sets investigates more than one type of indel variation at a specific X position in a genetic variant segment (e.g. when an insertion of 2 nt, an insertion of 3 nt and a deletion of 4 nt in the same genetic location). Where more than one indel variation at X position is desired, the probe set can be the collection of probe sub-sets that investigates all the desired types of indel variation at X position. For example, a probe sub-set comprises pairs of probes that investigate a deletion of one nt at the 16th position, probe sub-set nt 16, Del1. Another probe sub-set comprises pairs of probes that investigate an insertion of one nt at the 16th position, probe sub-set nt 16, Ins1. Another probe sub-set comprises pairs of probes that investigate a duplication of one nt at the 16th position, probe sub-set nt 16, Dup1. Another probe sub-set comprises pairs of probes that investigate a duplication of two nt at the 16th position, probe sub-set nt 16, Dup2. The collection of probe sub-sets for the 16th nt: Del1, Ins1, Dup1 and Dup2 make up a probe set for nt at the 16th position of the genetic variant segment.

[0118] In one embodiment, the control or normal/wild type probe and the variant probe making a pair of probe have the same length, i. e. both the normal and variant probes have the same number of bases or nt (Fig. 1 and Fig. 3).

[0119] In another embodiment, the control or normal/wild type probe and the variant probe making a pair of probe hybridize to the same strand of the genetic variant segment, i. e. both the normal

and variant probes hybridize to the sense strand of the genetic variant segment or both hybridize to the anti-sense strand of the genetic variant segment.

[0120] In another embodiment, the normal/control probe and the variant probe interrogate about the same region in the genetic variant segment.

[0121] In one embodiment, each of these probe sub-sets comprises at least a pair of probes consisting of one control or normal probe and one variant probe. In other embodiments, each probe sub-set comprises several pairs of probes wherein each pair consists of one control or normal probe and one variant probe. For the multiples pairs of probes comprising a probe sub-set interrogating any particular indel variation located at any particular nt position in the genetic variant segment, the probes of the different pairs of probes can differ from each other by the length, the location of the indel variation inside the variant probe or the interrogation strand: sense strand or the anti-sense strand.

[0122] For example, Fig. 3 shows two pairs of probes for the probe sub-set nt 16 del1, two pairs of probes for the probe sub-set nt 16 del2, two pairs of probes for the probe sub-set nt 17 del1 and two pairs of probes for the probe sub-set nt 17 del2. The two pairs of probes for the probe sub-set nt 16 del1 investigates a single nt deletion at nt position 16. All four probes of these two pairs are 30 mers, meaning they each consist of 30 nt. However, the probes from the two pairs differ by the location of the deletion on the probe; in nt 16 del1 variation 1, the deletion is located at position 16 of the 30 mer, or position +1, and in nt 16 del1 variation 2, the deletion is located at position 13 of the 30 mer, or position -3. The two pairs of probes for the probe sub-set nt 16 del2 investigates a single nt deletion at nt position 16 and a deletion of one 3' contiguous of nt position 16. All four probes of these two pairs are 30 mers, meaning they each consist of 30 nt. However, the probes from the two pairs differ by the location of the deletion on the probe; in nt 16 del1 variation 1, the deletion is located at position 16 of the 30 mer, or position +1, and in nt 16 del1 variation 2, the deletion is located at position 13 of the 30 mer, or position -3.

[0123] In one embodiment, one can decides to detect one kind of indel, for example, only deletions of one nt in a genetic variant segment. For this embodiment, the library of probes comprises one set of probe sets and as many probe sets as the length of the variant segment under interrogation (e.g., if the length of the segment to be analyzed is 2000 base pairs, 2000 probe sets are designed according the novel system or rules set forth in this specification), wherein each probe set comprises a single probe sub-set, wherein the probe sub-set comprises at least one pair of probes, wherein each pair of probes consists of one normal/wild type probe and one variant probe, wherein the probes of each pair of probes making up the probe sub-set differ from each other in terms of length, indel variation location inside the probe and strand of interrogation of the variant segment. Fig. 4B shows one exemplary system how to make a library of probes for detecting a single type of indel present in a variant segment having a length of N bp-long. For each probe set, there is a single probe sub-set consisting of ten pairs of probes. For this N bp-long segment, there are N numbers of probe sets making up the one set of probe sets. Replica of the C and V probes of each pair of probes can be placed on the solid support.

[0124] In this embodiment where there are only two probe sub-sets, one probe sub-set investigates the single nt deletion or insertion at position X in the genetic variant segment. The second probe sub-set investigates the single nt deletion or insertion plus another nt deletion or insertion 3' side of position X in the genetic variant segment.

[0125] In one embodiment, if one decides to detect more than one type of indel, for example, two types of indels; e.g., a deletion of only one nt in a genetic variant segment and an insertion of only one nt in a genetic variant segment. The only one-nt deletion in a genetic variant segment and the only one-nt insertion in a genetic variant segment represent two distinct kinds or types of indels that can occur for each and every nt position in the variant segment. For this embodiment, the library of probes comprises one set of probe sets and as many probe sets as the length of the variant segment under interrogation, wherein each probe set comprises two probe sub-sets, wherein each probe sub-set comprises at least one pair of probes, wherein each pair of probes consists of one control or normal/wild-type probe and one variation probe, wherein the probes of each pair of probes making up the probe sub-set differ from each other in terms of length, indel variation location inside the probe and strand of interrogation of the variant segment. There is one probe sub-set for each distinct indel being investigated. For example, for the two indels investigation described, there is a first and a second probe sub-set for the probe set that correspond to the nt at the X position in the genetic variant segment; the first probe sub-set that investigates the single nt deletion at position X in the genetic variant segment and the second probe sub-set investigates the single nt insertion at position X in the genetic variant segment.

[0126] The application therefore provides various combinations of indels that can be investigated simultaneously with a library of probes, where the library of probes is designed according to the rules set forth in this specification and examples.

[0127] In one embodiment, one decides to detect several kinds of indel variation in a genetic variant segment, for example, deletions of one, two, three, four and five nts. A library of probes for detecting and analysis of a genetic variant segment with one, two, three, four and five nts deletions has one set of probes sets. There are as many probe sets as the length of the variant segment under interrogation, each probe set comprising of five probe sub-set, each probe sub-set for investigating each of the different type of indel, i. e. deletions of one, two, three, four and five nts; each probe sub-set comprising at least one pair of probes which consist of one normal probe and one variant probe. The probes of each pair of probes within a probe sub-set differ from each other in terms of length, interrogating position inside the probe and strand of interrogation of the variant segment.

[0128] In one embodiment, one can detect several kinds of indel variations in a genetic variant segment simultaneously with a library of probes, for example, deletions of one, two and three nts and an insertion of one nt, i. e. four distinct indel variations. A library of probes for detecting and analysis of a genetic variant segment with one, two, and three nt deletions and one nt insertion will have one set of probes sets. There are again as many probe sets as the length of the variant segment under interrogation. Each probe set comprising four probe sub-sets, each probe sub-set for investigating each of the different

type of indel, i. e. deletions of one, two and three nt and insertion of one nt; each probe sub-set comprises at least one pair of probes which consist of one control or normal / wild type probe and one variant probe. The probes of each pair of probes within a probe sub-set differ from each other in terms of length, interrogating position inside the probe and strand of interrogation of the variant segment.

[0129] Fig. 4C shows one embodiment of the library of probes for detecting four types of indel present in a variant segment having a length of N bp-long. The library has four probe sub-sets, one probe sub-set for each of the different type of indel, i.e. deletions of one, two and three nt and insertion of one nt; each probe sub-set consisting of 32 pairs of probes. For this N bp-long segment, there are N numbers of probe sets making up the one set of probe sets. Replica of the C and V probes of a pair of probes can be placed on the solid support.

[0130] Methods of analysis for the detection of indels rely on, in general, comparisons of hybridization intensities among normal and variation probes, among tNA and cNA samples, among genetic variant and non-variant segments, and combinations thereof.

[0131] In one embodiment, the method of detection of indels relies solely on the hybridization intensities among normal and variation probes of at least one test sample. In this embodiment, probes comprising the probe sub sets should have the same characteristics (length, length, position of the indel variation of interest – i.e. at position +1 from the middle of the probe or as described above for other alternative positions, and strand hybridized – i.e., sense or anti-sense) across all probe sets. As used herein, the phrase "probe feature" refers to a localized and concentrated deposit of multiple copies of the same probe on a solid support surface (for example, a defined "spot" on the glass surface or oligonucleotides on one bead).

[0132] In one embodiment, the method of detecting and analyzing an least one indel in a genetic variant segment having a length of N nucleotide bases comprises:

- (a) designing and providing a library of probes on a solid support, wherein the library of probes comprises one set of probe sets for interrogating a genetic variant segment, wherein the set of probe sets comprise at least two probe sets, a first and a second probe set, wherein each the at least two probe sets comprises at least one probe sub-set, wherein the at least one probe sub-set comprise at least one pair of probes: a normal or control probe and a variation probe, wherein the normal probe of the pair is complementary to the normal (wild type) or control sequence of the genetic variant segment, and the variation probe is complementary to the normal sequence except for a position corresponding to the indel variation, wherein the type of indel variation probes of the at least two probe sets are the same, wherein the first probe set interrogates an indel located at position k in the genetic variant segment, and the second probe set interrogates the indel located position k+1 in the genetic variant segment, and wherein the probes are placed on the solid support as probe features;
- (b) providing at least a tNA sample;
- (c) amplifying the regions of interest of the at least one tNA sample ;

- (d) contacting the tNA with the solid support, thereby allowing NA hybridization between the tNA to the normal or control and variation probe features thereby forming NA-probe complexes, wherein each complex is detectably labeled;
- (e) measuring an intensity of the detectable label for NA-probe complex at each probe feature; and
- (f) applying an algorithm to the data from step (e), thereby determining the indel present in the genetic variant segment of the tNA sample, wherein algorithm comprises the steps of:

- (i). computing a first intensity ratio (Ratio 1) between the normal (N) or control (C) probe in the first probe set $IN_{(k)}$ and the corresponding normal probe in the corresponding pair in the second probe set $IN_{(k+1)}$

$$\text{Ratio 1} = IN_{(k)} \div IN_{(k+1)}$$

- (ii). computing a second intensity ratio (Ratio 2) between the variation probe in the first probe set $IV_{(k)}$ and the corresponding variation probe in the corresponding pair in the second probe set $IV_{(k+1)}$

$$\text{Ratio 2} = IV_{(k)} \div IV_{(k+1)}$$

wherein k has values from 1 to N-1 where 1 represent the first oligonucleotide of the variant segment and N is the last base;

- (iii). computing a $\text{Ratio}_{(k/k+1)}$ between the Ratio 1 and Ratio 2:

$$\text{Ratio}_{(k/k+1)} = \frac{IN_{(k)} / IN_{(k+1)}}{IV_{(k)} / IV_{(k+1)}} = \frac{\text{Ratio 1}}{\text{Ratio 2}}$$

wherein if the $\text{Ratio}_{(k/k+1)}$ is equal to about one, the genotype of the k nucleotide is normal (i.e. wild type) or the indel variation addressed by the probe sub-set of nucleotide base k is the same as that of the k+1 nucleotide of the variant segment; if the $\text{Ratio}_{(k/k+1)}$ is at least two, preferentially more than 5, preferentially more than 10, this indicates a heterozygote indel variation at the position k+1; if the $\text{Ratio}_{(k/k+1)}$ is more than 100, preferentially more than 200 fold, this indicates an homozygote indel variation at the position k+1.; Inversely, if the $\text{Ratio}_{(k/k+1)}$ is less than 0.5, preferentially less than 0.2, preferentially less than 0.1, this indicates an heterozygote indel variation at the position k, and if $\text{Ratio}_{(k/k+1)}$ is less than 0.01, preferentially less than 0.005, this indicates an homozygote indel variation at the position k.

[0133] It is understood that in the above described analysis method and other analysis methods described herein, when normal/wild type sequences are used in the analysis and comparison, the symbol (N) is used; and when the control known sequences are used in the analysis and comparison, the symbol (C) is used.

[0134] It is also understood that in the above described analysis method and other analysis methods described herein, when normal/wild type sequences are used in the analysis and comparison, normal/wild type probe sequences are designed/selected and used for the library. In the embodiments

wherein /selected and used control, known sequences are used in the analysis and comparison, control probe sequences are designed/selected and used for the library.

[0135] In embodiments where the probe sub-sets comprises more than one pair of probes, the method comprises comparing all the ratios of each probe sub-set to confirm that they all indicate the same indel variation. An example of this embodiment of method is shown in Fig. 5 and some exemplary intensity data generated by the hybridization of the test NA and the probe features and the calculation of the $\text{Ratio}_{(k/k+1)}$ can be found in Tables 2-5.

[0136] In one embodiment of the method, the probe sub-sets within the probe sets for each contiguous nt in the variant segment has the same number of pairs of probes and the same type of pair of probes in term of length, interrogating position inside the probe and strand of interrogation of the variant segment. The method compares results of a certain nucleotide with the results of the nucleotide to its right (k vs $k+1$). Thus the probes within each probe sub-set of a probe set must have matching probes in the probe sub-set of the adjacent probe set, matching in term of length, location of indel interrogation, and strand of interrogation between probe sub-sets in order to obtain the ratios for ratio comparison. The matching up is necessary for consecutive nt positions in the segment investigated. However, it is necessary for all the probe sub-sets have all the same number or variety of variation probes. For example, for a library with N number of probe sets, each with one probe sub-set, all the probe sub-set has two pairs of probes, one pair of 30 nt for the sense strand with the indel variation at the -2 position within the probe and the second pair of 25 nt for the sense strand with the indel variation at the -2 position within the probe. At the minimum, there should be at least one pair of probes for a probe sub-set for K position (in the K probe set) that matches up with at least one pair of probes of probe sub-set for $K+1$ position (in the $K+1$ probe set), and at least one pair of probes for a probe sub-set for K position that matches up with at least one pair of probes of probe sub-set for $K-1$ position (in the $K-1$ probe set). As used herein, matches up means that the matched pair of probes are of the same length, interrogate the approximately same region in the variant segment, interrogate the same type of indel and the indel is located at the same position within the probe (see Fig. 1 and 3).

[0137] In one embodiment, the method of detection and analysis of the indels relies on the hybridization of the tNA samples as well as one control NA sample. In this embodiment, the genetic variant segment and the non-variant segment from both the tNA and the cNA samples are used. The method of detecting and analyzing an indel in a genetic variant segment having a length of N nucleotide bases comprises:

- (a) providing at least a tNA sample;
- (b) providing one cNA sample;
- (c) amplifying at least one genetic variant segment from the at least a tNA and amplifying at least one genetic variant segment from the cNA samples, wherein the amplifications optionally use the same primers;

- (d) amplifying at least one genetic non-variant segment from the at least a tNA and amplifying at least one genetic non-variant segment from the cNA samples, wherein the amplifications optionally use the same primers;
- (d) providing one set of probe sets designed to hybridize to the at least one genetic variant segment and one set of probe sets designed to hybridize to at least one genetic non-variant segment, wherein the sets of probe sets are attached to a solid support, wherein each of the probe set for the genetic variant segment comprises at least one probe sub-set, wherein the at least one probe sub-set comprises at least one pair of probes: a normal or control probe and a variation probe, wherein the normal probe of the pair is complementary to the normal (wild type) or control (i. e. known variation) sequence of the genetic variant segment, and the variation probe is complementary to the normal sequence except for a position corresponding to the indel variation, wherein each of the probe set for the genetic non-variant comprises at least one probe sub-set, wherein the at least one probe sub-set comprises at least one probe: a normal (wild type) or control probe, and wherein the probes are placed on the solid support as probe features;
- (e) contacting, optionally in parallel reactions, the at least one genetic variant segment from the at least one tNA and the at least one genetic variant segment from the control NA with the solid support, thereby allowing NA hybridization between the genetic variant segments from tNA and the cNA to the probe features for the genetic variant segment and the probe features for the non-variant segment thereby forming NA-probe complexes, wherein each complex is detectably labeled.
- (f) measuring an intensity of the detectable label for NA-probe complex at each probe feature.
- (g) applying an algorithm to the data from step (f), thereby determining the indel variation present in the genetic variant segment of the tNA sample, wherein algorithm comprises the steps of:
- (i). computing a median or a mean of the intensity from step (f) for the normal or control probe features of all the probe sets of the set of probe sets interrogating the at least one non-variant segment wherein the median or mean is used as a normalization factor for intensities of step (f);
 - (ii). applying the normalization factor of step (i) to the intensities of step (f) to obtain a normalized intensity for all the probe features;
 - (iii). computing a normal or control ratio (Ratio 1) between $IN_{(k)t}$ over $IN_{(k)c}$ where k can have values from 1 to N where 1 represent the first nucleotide base of the variant segment and N the last nucleotide base, where $IN_{(k)t}$ represents the value of intensity of the normal probe from the tNA sample and $IN_{(k)c}$ represents the intensity of the normal (N) or control (C) probe from the c NA sample:

$$\text{Ratio 1} = IN_{(k)t} \div IN_{(k)c}$$

- (iv). pairing the probe feature of variation probes hybridized with the genetic variant segment from the tNA sample with the probe feature of variation probes hybridized with the genetic variant segment from the cNA sample for all the probe sub-sets of all probe sets; pairing of the normal or control probes are performed too;
- (v). computing a variation ratio (Ratio 2) between $IV_{(k)t}$ over $IV_{(k)c}$ where k can have values from 1 to N where 1 represent the first nucleotide base of the variant segment and n the last nucleotide base, where $IV_{(k)t}$ represents the value of intensity of the variation probe from the tNA sample and $IV_{(k)c}$ represents the intensity of the variation probe from the cNA sample:

$$\text{Ratio 2} = IV_{(k)t} \div IV_{(k)c}$$

- (vi). pairing the ratio 1 and its corresponding ratio 2 from steps (iii) and (v) for each indel probe sub-set of each indel probe set according to the length, position of the nucleotide of interest, and interrogation strand; and
- (vii). computing the ratio between the ratio N over the ratio V for each pair in step (vi):

$$\text{Ratio}_{(t/c)(k)} = \frac{IN_{(k)t} / IN_{(k)c}}{IV_{(k)t} / IV_{(k)c}} = \frac{\text{Ratio 1}}{\text{Ratio 2}}$$

wherein if a $\text{Ratio}_{(t/c)(k)}$ is equal to about one, the indel variation of the nucleotide k position is normal (i.e. wild type); if the $\text{Ratio}_{(t/c)(k)}$ is more than two, preferentially more than 5, preferentially more than 10, this indicates a heterozygote indel variation at the nucleotide k position; if the ratio is more than 100, preferentially more than 200 fold, this indicates an homozygote indel variation at the nucleotide in k position.

[0138] In this method, the comparison is between each probe set of the tNA and probe set of the control tNA (for instance, probe set for nt 16 for tNA versus the probe set control for nt 16 for cNA, and probe set for nt 17 for tNA versus probe set for nt 17 for cNA). Thus, all the probes in a sub-set for the tNA must have a corresponding probe in the cNA. The number of pairs of probes for the probe sub-set need not be the same, e. g. three pairs of probes in a sub-set of set 16, 4 totally different pairs of probes (in terms of length, location of indel interrogation, and strand of interrogation) in the corresponding sub-set of set 17, and compare both of them to the control as long as the corresponding pairs are in the control too, in this case, the control should have at least 7 probes, 3 matching the ones of set 16 and 4 matching the ones of set 17.

[0139] In some embodiments, the probe features of normal probes hybridized with the genetic variant segment from the tNA sample are paired with the probe features of normal probes hybridized with the genetic variant segment from the cNA sample for all the probe sub-sets of all probe sets.

[0140] In embodiments where the probe sub-sets comprises more than one pair of probes, the method comprises comparing all the ratios of each probe sub-set to confirm that they all indicate the same indel variation. An example of this embodiment of method is shown in Fig. 6.

[0141] In one embodiment, more than one control NA sample can be used for the method of detection and analysis of indels described. Those skilled in the art can readily adopt the above described

method to calculate the normalization factor of step (f) by using data from the various control NA samples, instead of data from just one cNA sample.

[0142] In one embodiment, the normalization factor is computed by the median or the mean of all the normal probe features of the variant segment when several, preferentially more than 10, preferentially more than 50, preferentially more than 100 probe sub sets are used.

[0143] In one embodiment, the method of detection of indels relies on the hybridization of the test samples as well as various control samples. In this embodiment, only the genetic variant segment is used. The method of detecting and analyzing an indel in a genetic variant segment having a length of N nucleotide bases comprises:

- (a) providing at least a tNA sample.
- (b) providing at least two cNA samples.
- (c) amplifying at least one genetic variant segment from the at least a test NA and amplifying at least one genetic variant segment from the at least two control NA samples, wherein the amplification of the genetic variant segments from the test NA samples and the control NA samples optionally use the same primers;
- (d) providing a set of probe sets designed to hybridize to the at least one genetic variant segment, wherein the set of probe sets comprising at least one probe set, wherein the at least one probe set for the genetic variant segment comprises at least one probe sub-set, wherein the at least one probe sub-sets comprise at least one pair of probes: a normal probe and a variation probe, wherein the normal probe of the pair is complementary to the normal (wild type or control) sequence of the genetic variant segment, and the variation probe is complementary to the normal sequence except for a position corresponding to the indel variation, and wherein the probes are placed on the solid support as probe features;
- (e) contacting optionally in parallel the at least one genetic variant segment from the at least tNA sample and the at least one genetic variant segment from the at least two cNA samples with the solid support, thereby allowing NA hybridization between the genetic variant segments from the tNA and the cNAs to the genetic variant probe features thereby forming NA-probe complexes, wherein each complex is detectably labeled;
- (f) measuring an intensity of the detectable label for NA-probe complex at each probe feature.
- (g) applying an algorithm to the data from step (f), thereby determining the indel present in the genetic variant segment of the tNA sample, wherein algorithm comprises the steps of:
 - (i). computing a ratio for each pair of probes:

$$\text{Ratio}_{(k)} = \frac{\text{intensity value for normal probe}}{(\text{intensity value for normal probe} + \text{intensity value for variation probe})}$$
 - (ii). computing the mean and the standard deviation of the ratios obtained for all the control NA samples; and

(iii). comparing the ratios obtained for each of the tNA sample with the mean ratio obtained for the cNA samples in step (ii), wherein if the ratio of the tNA sample is at least 5 standard deviations away from the mean ratio obtained with the cNA sample, the test NA has the indel variation at position k, either in an heterozygous or a homozygous state; wherein k has values from 1 to N-1 where 1 represent the first oligonucleotide of the variant segment and N is the last base.

[0144] An example of this embodiment of method is shown in Fig. 7.

[0145] In some embodiments of the methods, probes features of each pair of probes comprising the at least one probe sub-set are grouped together according to their length, position of the nucleotide of interest, and interrogation strand.

[0146] In some embodiments of the methods, the normal or control probe and their corresponding variation probe features are paired according to their length, position of the nucleotide of interest, and interrogation strand for the at least tNA sample and the cNA samples.

[0147] In one embodiment of the methods, there is as many probe sets as there are bp in the genetic variant segment under investigation. For example, if the genetic variant segment has N bp, then the library has N number of probe sets.

[0148] In some embodiments of the methods, probe features are grouped together according to their probe sub-set.

[0149] In some embodiments of the methods, the normal and their corresponding variation probe features are paired according to the probe feature groups.

[0150] In embodiments where the probe sub-sets comprise more than one pair of probes, the method comprises comparing all the ratios of each probe sub-set to confirm that they all indicate the same indel variation.

[0151] In some embodiments of the methods, one can use several test samples with the same control samples.

[0152] For any single indel, any of the method described can be used. It is contemplated that more than one described method is use for any given indel investigated. In some embodiments, one can use one of the four methods of indel detection. In some embodiments, two, three or all methods described are used for indel detection.

[0153] In some embodiments, one can use three of the four methods of indel detection.

[0154] In some embodiments, one can use four of the four methods of indel detection.

[0155] In some embodiments, one can use replicates of the probes or probe features.

[0156] In one embodiment, each probe of pairs of probes comprising the probe sub-sets are attached to a solid support to form probe features. In one embodiment, replicates of each probe features on the solid support are exemplified in Fig. 9. In some embodiments, the number of replicates for each probe is between 1-50, from 1 and up to 5, or from 1 up to 10. In one embodiment, there are four replicate features for each probe. In another embodiment, there are ten replicate features for each probe.

[0157] In one embodiment, the methods comprise measuring an intensity of the detectable label in non-probe positions of the solid support to obtain a background intensity value.

[0158] In one embodiment, the methods comprise transforming the intensity of the detectable label obtained into a raw value for each probe or probe feature and the solid support background using a quantitation software.

[0159] One embodiment of the methods comprises amending the raw value for each of the probe feature or replicate probe feature by deducting the background raw value, thereby obtaining a net value for the each probe feature or replicate probe feature for both the at least one genetic variant segment and the at least one genetic non-variant segment.

[0160] One embodiment of the methods comprises selecting for subsequent analysis the probe features whose net values pass quality control thresholds or values signal to noise ratio of, typically, over three ($SNR > 3$), in the probe feature positions wherein a signal is detected.

[0161] In one embodiment, one can use one or more control NA samples.

[0162] In one embodiment, the method is computer implemented.

[0163] The NA samples can be obtained from any appropriate biological sample which contains NA. The sample may be taken from a fluid or tissue, secretion, cell or cell line derived from the human body.

[0164] For example, samples may be taken from blood, including serum, lymphocytes, lymphoblastoid cells, fibroblasts, platelets, mononuclear cells or other blood cells, from saliva, liver, kidney, pancreas or heart, urine or from any other tissue, fluid, cell or cell line derived from the human body. For example, a suitable sample may be a sample of cells from the buccal cavity. One can also use hair follicle samples.

[0165] In one embodiment, the NA is obtained from a blood sample.

[0166] In general, NA can be extracted and isolated from the biological sample using conventional techniques. The nucleic acid to be extracted from the biological sample may be DNA, or RNA, typically total RNA. Typically RNA is extracted if the genetic variation to be studied is situated in the coding sequence of a gene. Where RNA is extracted from the biological sample, the methods further comprise a step of obtaining cDNA from the RNA. This may be carried out using conventional methods, such as reverse transcription using suitable primers. Subsequent procedures are then carried out on the extracted DNA or the cDNA obtained from extracted RNA. The term DNA, as used herein, may include both DNA and cDNA.

[0167] One can also use lab-on-a-chip methods wherein separate isolation step is not necessary because the raw sample, such as blood or urine sample, can be inserted into the micro-channel, the genetic variant and sos-variant segment amplified thereon and be hybridized to the designed chip either within the micro-channel or after exiting the micro-channel. Such lab-on-a-chip systems are well known to one skilled in the art.

[0168] In general, any genetic variant segment can be analyzed using the computer-implemented algorithm as described. The genetic variations to be tested are located within known nucleic acid sequences and well characterized.

[0169] In one aspect, the NA samples which contain the genetic segment or segments of interest are subjected to an amplification reaction prior to analysis in order to obtain amplification products which contain the genetic variations to be identified. The amplified nucleic acid regions are typically the variant and/or non-variant segment to be interrogated. Any suitable technique or method can be used for amplification. In general, the technique allows the multiplex amplification of all the DNA sequences containing the genetic variations to be identified. In other words, where multiple genetic variations are to be analyzed, it is preferable to simultaneously amplify all of the corresponding target DNA regions in one reaction (comprising the variations). Carrying out the amplification in a single step (or as few steps as possible) simplifies the method. PCR amplification conditions are such that the final copy number after amplification reflects the initial copy number of the segments in the NA samples.

[0170] For example, multiplex PCR can be carried out, using appropriate pairs of oligonucleotide PCR primers which are capable of amplifying the target regions containing the genetic variations to be identified. Here each genetic variant segment is amplified together with a genetic non-variant segment in the multiplex PCR reaction using the test or control NA sample as the DNA template. The genetic variant and the genetic non-variant segments amplified together form an amplification group. Any suitable pair of primers which allow specific amplification of a target DNA region may be used. In one aspect, the primers allow amplification in the least possible number of PCR reactions. Thus, by using appropriate pairs of oligonucleotide primers and appropriate conditions, all of the target DNA regions necessary for genotyping the genetic variations can be amplified for genotyping (e.g. DNA-array or particle suspension) analysis with the minimum number of reactions. . The present method can comprise the use of one or more of these primers or one or more of the listed primer pairs. Examples presented in the present application provide additional exemplary primers.

[0171] In one embodiment, several independent multiplex PCR amplification reactions are carried out for the test NA sample and the control sample. In one embodiment, at least four independent multiplex PCR amplification reactions are carried out for the test NA sample and the control sample. In one embodiment, about four independent multiplex PCR amplification reactions are carried out for the test NA sample and the control NA sample. The PCR products from the independent amplifications for the test NA sample are pooled together. Likewise, those of the control NA samples are pooled together.

[0172] In parallel with each genetic variant segment comprising the indel provided, no or at least one genetic non-variant segment can be selected. The genetic non-variant segment is encompassed within the test NA and control NA samples. For example, if neither the test nor the control exhibit Down syndrome, a test region from the Down syndrome region of chromosome 21 can be selected as a non-variant segment.

[0173] In one embodiment, the NA in the test NA and control samples are detectably-labeled. The aim is to be able to later detect hybridization between the genetic variant or non-variant segments and probe features fixed on a solid support. The greater the extent of hybridization of labeled segment to a probe feature, the greater the intensity of detectable label at that probe position. Methods of labeling NA are well known to one skill in the art, e. g. US Patent No. 6,573,374 and US Patent No. 5,700,647 describe suitable labeling methods. The attached label is detected by various methods known in the art, e.g. optically, wherein a photonic signal is converted to an electronic signal and registered by a computer, which outputs a signal in, for example, a numeric value. For example, a labeled nucleotide can be incorporated during the amplification reaction or labeled primers can be used for amplification. In some embodiments, the labeled nucleotide is a biotinylated nucleotide. In other embodiments, the labeled primer is a biotinylated primer.

[0174] Labeling can be direct using for example, fluorescent or radioactive markers or any other marker known by persons skilled in the art. Examples of fluorophores, include for example, Cy3 or Cy5. Alternatively enzymes may be used for sample labeling, for example alkaline phosphatase or peroxidase. Examples of radioactive isotopes which can be used include for example ^{33}P , ^{125}I , or any other marker known by persons skilled in the art. In one instance, labeling of amplification products is carried out using a nucleotide which has been labeled directly or indirectly with one or more fluorophores. In another example, labeling of amplification products is carried out using primers labeled directly or indirectly with one or more fluorophores.

[0175] Labeling may also be indirect, using, for example, chemical or enzymatic methods. For example, an amplification product may incorporate one member of a specific binding pair, for example avidin or streptavidin, conjugated with a fluorescent marker and the probe to which it will hybridize may be joined to the other member of the specific binding pair, for example biotin (indicator), allowing the probe/target binding signal to be measured by fluorimetry. In another example, an amplification product may incorporate one member of a specific binding pair, for example, an anti-dioxigenin antibody combined with an enzyme (marker) and the probe to which it will hybridise may be joined to the other member of the specific binding pair, for example dioxigenin (indicator). On hybridization of amplification product to probe the enzyme substrate is converted into a luminous or fluorescent product and the signal can be read by, for example, chemi-luminescence or fluorometry.

[0176] The NA or the amplification products can further undergo a fragmentation reaction, thereby obtaining some fragmentation products which comprise or contain the genetic variations to be identified or analyzed. Typically fragmentation increases the efficiency of the hybridization reaction. Fragmentation may be carried out by any suitable method known in the art, for example, by contacting the nucleic acid, e.g. the amplification products with a suitable enzyme such as a DNase.

[0177] In some embodiments, the PCR products are fragmented to smaller sizes and then detectably labeled prior to hybridization with probes on a solid support. In one embodiment, the PCR products are fragmented to between about 12 -250nt in size. In one embodiment, the PCR products are

fragmented to between about 25 -200nt in size. In one embodiment, the PCR products are fragmented to between about 25 -150nt in size. In one embodiment, the PCR products are fragmented to between about 25 -100nt in size. In one embodiment, the PCR products are fragmented to between about 25 -75nt in size. In one embodiment, the PCR products are fragmented to between about 25 -50nt in size.

[0178] On can also use method as described in U.S.S.N. 12/499,076 in the methods of the present application.

[0179] If the NA has not been previously labeled, e.g. during the amplification reaction, (and, typically, where no post-hybridization amplification or ligation is carried out on the solid support) then labeling with a detectable label may be carried out pre-hybridization by labeling the fragmentation products. Suitable labeling techniques are known in the art and may be direct or indirect as described herein. Direct labeling may comprise the use of, for example, fluorophores, enzymes or radioactive isotopes. In one embodiment, the direct labeling comprises the use of biotin. Indirect labeling may comprise the use of, for example, specific binding pairs that incorporate e.g. fluorophores, enzymes, etc. For example, if amplification products have not been labeled during the amplification reaction the fragmentation products may undergo a direct or indirect labeling with one or various markers, for example biotin or one or various fluorophores, although other known markers can be used by those skilled in the art.

[0180] In some embodiments, hybridization intensity values, for use in analysis methods, can be amended for each of the probe features by deducting the background raw value from the raw value, thereby obtaining a net value.

[0181] In one embodiment, at least one oligonucleotide probe is designed and synthesize for each of the variant and non-variant segment to be interrogated. In a preferred embodiment, at least two unique probes are designed and synthesize for each segment. In other embodiments, at least five, at least ten, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, and at least 100, including all the whole integers between 2-100,000 unique probes are designed and synthesize for each segment. All of the probes are unique, although they can have overlapping sequences.

[0182] In one embodiment, the collection of unique probes designed and synthesized for each segment constitutes a set of probe set. In one embodiment, the set of probe sets for a segment that is interrogated comprises at least two unique probe sets for that segment. In other embodiments, a set of probe sets for a segment that is interrogated comprises at least five, at least ten, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, and at least 100, including all the whole integers between 2-100, unique probe sets. In one embodiment, for the practice of the method described herein, a first set of probe sets is provided for a genetic variant segment (form the test NA sample) to be interrogated. In one embodiment, for the practice of the method, a second set of probe sets is provided for a genetic non-variant segment (from the control NA sample) to be interrogated.

DNA chips or microbeads

[0183] In one embodiment, the library of probe is attached to a solid support as probe features in a specific arrangement wherein the location of each probe feature is known. In one embodiment, a probe feature is provided on a solid support; the probe feature being a localized and concentrated sample having multiple copies of the same probe is deposited and attached on a solid surface. For example, for a flat solid support such as on the glass-chip surface, a probe feature is a minute spot or dot printed with multiple copies of the same probe (see Fig. 9). The multiple copies can range from hundreds to thousands, e.g. 100-10000. All of the whole integers between 100 to 10,000 are included is a single probe feature. For a spherical surface such as a glass bead, "a probe feature" refers to a single probe-coated bead. All the beads are coated with the multiple copies of same probe that complements and interrogates a single genetic variant segment or non-variant segment. The range of numbers of probe-coated beads in "a probe feature" is between 100-1000, including all of the whole integers between 10-10000.

[0184] In one embodiment, replicates of a probe feature are made on a solid support. For a flat solid support such as a glass-chip, all replicate features of one probe feature type have one type of probe and the replicates can be arranged in a row on the glass-chip surface. Multiple rows can be made and distributed in fix and known coordinates on the glass chip (see Fig. 9). For a spherical solid support such as a glass bead, replicate features of one probe are many probe-coated beads, about 100 probe-coated beads. These beads all have probes of a single type. For each probe on a flat solid support, there are at least four replicate features, at least five, at least six, at least seven, at least eight, at least nine, and at least ten replicate features, sometimes more. In some embodiments, the solid support has between 10- 50 replicate features for each unique probe. All whole integers between 10-50 are considered. For each probe on a spherical solid support, there are at least about 100 replicate features or probe-coated beads.

[0185] In one embodiment, for the practice of the methods, replicates of probe features of a first set of probe sets are provided for a genetic variant segment (from the test NA sample) to be interrogated. In one embodiment, for the practice of the methods, replicates of probe features of a second set of probe sets are provided for a genetic non-variant segment (from the control NA sample) to be interrogated. The replicates of probe features of the first and second set of probe sets are attached on same solid support.

[0186] In accordance with some methods, two or more identical solid supports are used, each solid support having probe features. One solid support is used to hybridize with the test NA sample and the other solid support is used to hybridize with the control NA sample (Fig. 6 and 7).

[0187] In accordance with the method where two identical solid supports are used, each solid support having all the replicates of a first and a second set of probe sets, wherein the first set of probe sets interrogates a genetic variant segment and the second set of probe sets interrogates a genetic non-variant segment. One solid support is used to hybridize with the test NA sample and the other solid support is used to hybridize with the control NA sample (see Fig. 6 and 7).

[0188] In one embodiment, each probe feature is provided in at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 9, at least 10 replicates and the probe features are attached to the flat

surface at positions according to a known uniform spatial distribution, i.e., a support or surface with an ordered array of binding (e.g. hybridization) sites or probes. In other embodiments, anywhere from 10-50 replicate probe features are provided. Thus, the arrangement of replicate features on the support is predetermined. Each probe replicate is located at a known predetermined position on the solid support such that the identity (i.e. the sequence) of each probe can be determined from its position on the array. Typically, the probes are uniformly distributed in a predetermined pattern.

[0189] In one embodiment, the solid support is a flat surface. For example, for a flat solid support is a glass-chip surface.

[0190] In addition to DNA-arrays in the form of DNA-chips to detect genetic variations, the present invention also contemplates the use of DNA particle or bead suspensions.

[0191] In one embodiment, the solid support is a micron-size particle. In one embodiment, the beads are uniquely identifiable. Examples of particle identifiers on a particle are a bar code and a fluorescent dye. In one embodiment, the beads are bar-coded. These beads such as polymer or magnetic beads have unique spectroscopic signatures. Beads can be synthesized by dispersion polymerization of a family of styrene monomers and methacrylic acid to generate a spectroscopically encoded bead library. Raman spectroscopy is used to monitor complexing events on the barcoded beads. The genotyping assays from ILLUMINA[®], Inc. uses the particles that are cylindrical beads encoded with a barcode, which are then read by a barcode scanner. Platforms such as the XMAP[™] technology from LUMINEX[®] is have the particles that are microspheres encoded with fluorescent dyes. The particles are read by a flow cytometer.

[0192] In one embodiment, the solid supports form particle suspensions. It has been found that these particle suspensions should comply with a number of requirements in order to be used in the present methods, for example in terms of the design of the probes, the number of probes provided for each genetic variation to be detected and the distribution of probes on the support. These are described in detail herein.

[0193] In one embodiment, wherein the solid support is a micron-size particle, each probe is attached to at least 10 units of each particle species, wherein each particle species is distinguishable by a unique code from all other particle species.

[0194] In one embodiment, wherein the solid support is a micron-size particle, each probe is attached to at least 1000 units of each particle species.

[0195] In practicing the method described herein, the labeled NA are contacted with a solid support having attached probes in a specified arrangement described herein as replicate features, allowing NA hybridization between the tNA and the cNA (collective hereby termed as target NA) with the probes in the replicate features and the formation of target-probe complexes. Under conditions which allow hybridization to occur between target NA and the corresponding probes, specific hybridization complexes are formed between target NA and corresponding probes. Since the NAs are labeled, the target-probe complexes formed can therefore be detected.

[0196] Typically, the hybridization conditions allow specific hybridization between probes and corresponding target NA to form specific probe/target hybridization complexes while minimizing hybridization between probes carrying one or more mismatches to the DNA. Such conditions may be determined empirically, for example by varying the time and/or temperature of hybridization and/or the number and stringency of the array washing steps that are performed following hybridization and are designed to eliminate all probe-DNA interactions that are non-specific. For example, the melting temperature of the probe/target complexes may occur at 75-85°C. In some embodiments, hybridizations can be for one hour, although higher and lower temperatures and longer or shorter hybridizations may also suffice. A skilled artisan can optimize these conditions using routine methods.

[0197] The hybridization can be carried out using conventional methods and devices. In one instance, hybridization is carried out using an automated hybridization station. For hybridization to occur, the segments are placed in contact with the probes under conditions which allow hybridization to take place. Using stable hybridization conditions allows the length and sequence of the probes to be optimized in order to maximize the discrimination between genetic variations A and B, e.g. between wild type and mutant sequences, as described herein.

[0198] In general a chip DNA array has from 300 to 40000 probe features, for example, from 400 to 30000 or 400 to 20000. The chip can have from 1000 to 20000 probes, such as 1000 to 15000 or 1000 to 10000, or 1000 to 5000. A suitable chip may have from 2000 to 20000, 2000 to 10000 or 2000 to 5000 probe features. For example, a chip may have 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 12000, 14000, 16000, 18000 or 20000 probes. Smaller chips 400 to 1000 probes, such as 400, 500, 600, 700, 800, 900 or 950 probes are also envisaged. The number of probes in a particle suspension will vary depending on the number of individually identifiable particles.

[0199] In general the chip DNA array of the invention comprises a support or surface with an ordered array of binding (e.g. hybridization) sites or probe features. Thus the arrangement of probes on the support is predetermined. Each probe (i.e. each replicate feature) is located at a known predetermined position on the solid support such that the identity (i.e. the sequence) of each probe can be determined from its position in the array. Typically the probes are uniformly distributed in a predetermined pattern.

[0200] Preferably, the probes deposited on the support, although they maintain a predetermined arrangement, are not grouped by genetic variation but have a random distribution. Typically they are also not grouped within the same genetic variation. If desired, this random distribution can be always the same. Therefore, typically the probes are deposited on the solid support (in an array) following a predetermined pattern so that they are uniformly distributed, for example, between the two areas that may constitute a DNA-chip, but not grouped according to the genetic variation to be characterized. Distributing probe replicates across the array in this way helps to reduce or eliminate any distortion of signal and data interpretation, e.g. arising from a non-uniform distribution of background noise across the array.

[0201] In some embodiments, probe features are arranged on the support in subarrays. Microarrays are in general prepared by selecting probes which comprise a given polynucleotide sequence, and then immobilizing such probes to a solid support or surface. Probes may be designed, tested and selected as described herein. In general, the probes can comprise DNA sequences. In some embodiments the probes may comprise RNA sequences, or copolymer sequences of DNA and RNA. The polynucleotide sequences of the probes may also comprise DNA and/or RNA analogues, or combinations thereof. For example, the polynucleotide sequences of the probes may be full or partial fragments of genomic DNA. The polynucleotide sequences of the probes may also be synthesized nucleotide sequences, such as synthetic oligonucleotide sequences. The probe sequences can be synthesized either enzymatically *in vivo*, enzymatically *in vitro* (e.g., by PCR), or non-enzymatically *in vitro*.

[0202] Microarrays or chips can be made in a number of ways. However produced, microarrays typically share certain characteristics. The arrays are reproducible, allowing multiple copies of a given array to be produced and easily compared with each other. Preferably, microarrays are made from materials that are stable under binding (e.g., nucleic acid hybridization) conditions. The microarrays are preferably small, e.g., between 0.25 to 25 or 0.5 to 20 cm², such 0.5 to 20 cm² or 0.5 to 15 cm², for example, 1 to 15 cm² or 1 to 10 cm², such as 2, 4, 6 or 9 cm².

[0203] Replicate probe features can be attached to the solid support using conventional techniques for immobilization of oligonucleotides on the surface of the supports. The techniques used depend, amongst other factors, on the nature of the support used - porous (membranes, micro-particles, etc.) or non-porous (glass, plastic, silicone, etc.) In general, the probes can be immobilized on the support either by using non-covalent immobilization techniques or by using immobilization techniques based on the covalent binding of the probes to the support by chemical processes.

[0204] Preparation of non-porous supports (e.g., glass, silicone, plastic) requires, in general, either pre-treatment with reactive groups (e.g., amino, aldehyde) or covering the surface of the support with a member of a specific binding pair (e.g. avidin, streptavidin). Likewise, in general, it is advisable to pre-activate the probes to be immobilized by means of corresponding groups such as thiol, amino or biotin, in order to achieve a specific immobilization of the probes on the support.

[0205] The immobilization of the probes on the support can be carried out by conventional methods, for example, by means of techniques based on the synthesis *in situ* of probes on the support (e.g., photolithography, direct chemical synthesis, etc.) or by techniques based on, for example, robotic arms which deposit the corresponding pre-synthesized probe (e.g. printing without contact, printing by contact) (See U. S. Patent No. 7,281,419 for example).

[0206] In one embodiment, the support is a glass slide and in this case, the probes, in the number of established replicates (for example, 6, 8 or 10) are printed on pre-treated glass slides, for example coated with aminosilanes, using equipment for automated production of DNA-chips by deposition of the oligonucleotides on the glass slides ("micro-arrayer"). Deposition is carried out under appropriate conditions, for example, by means of crosslinking with ultraviolet radiation and heating

(80°C), maintaining the humidity and controlling the temperature during the process of deposition, typically at a relative humidity of between 40-50% and typically at a temperature of 20°C.

[0207] The replicate probe features are distributed uniformly amongst the areas or sectors (sub-arrays), which typically constitute a DNA-chip. The number of replicas and their uniform distribution across the DNA-chip minimizes the variability arising from the printing process that can affect experimental results.

[0208] To control the quality of the manufacturing process of the DNA-chip, in terms of hybridization signal, background noise, specificity, sensitivity and reproducibility of each replica as well as differences caused by variations in the morphology of the spotted probe features after printing, a commercially synthesized NA can be used.

[0209] In contrast to chip DNA array technology, in which the probes are attached to the solid support at known locations, particle suspension technology allows for the detection of probes in a single vessel, with individual probes attached to a particle with a distinguishable characteristic. In some embodiments the particles are encoded with one or more optically distinguishable dyes, a detectable label, or other identifying characteristic such as a bar code. Other labeling methods include, but are not limited to a combination of fluorescent and non-fluorescent dyes, or avidin coating for binding of biotinylated ligands. Such methods of encoding particles are known in the art.

[0210] Once hybridization has taken place, the intensity of detectable label at each probe position (including control probes) can be determined. The intensity of the signal (the raw intensity value) is a measure of hybridization at each replicate feature.

[0211] The intensity of detectable label at each probe position (each probe feature replica) can be determined using any suitable means. The means chosen will depend upon the nature of the label. In general an appropriate device, for example, a scanner, collects the image of the hybridized and developed DNA-chip. An image is captured and quantified.

[0212] In one instance, e.g. where fluorescent labeling is used, after hybridization, the hybridized and developed DNA-chip is placed in a scanner in order to quantify the intensity of labeling at the points where hybridization has taken place. Although practically any scanner can be used, in one embodiment a fluorescence confocal scanner is used. In this case, the DNA-chip is placed in the said apparatus and the signal emitted by the fluorophore due to excitation by a laser is scanned in order to quantify the signal intensity at the points where hybridization has taken place. Non-limiting examples of scanners which can be used according to the present invention include scanners marketed by the following companies: Axon, Agilent, Perkin Elmer, etc.

[0213] In one aspect of the invention, the signal from the particles is detected by the use of a flow cytometer. In other embodiments, detection of fluorescent labels may also be carried out using a microscope or camera that will read the image on the particles. Flow cytometric software for detection and analysis of the signal is available for example from Luminex, Inc. (Austin, TX).

[0214] In one embodiment, wherein the measuring intensity of the detectable label for each probe is performed using scanning.

[0215] In one embodiment, wherein the measuring intensity of the detectable label for each probe is performed using flow measuring systems.

[0216] Typically, in determining the intensity of detectable label at each probe position (i.e. for each probe feature replica), account is taken of background noise, which is eliminated. Background noise arises because of non-specific binding to the probe array and can be determined by means of controls included in the array. Once the intensity of the background signal has been determined, this can be subtracted from the raw intensity value for each probe replica in order to obtain a clean intensity value. Typically the local background, based on the signal intensity detected in the vicinity of each individual feature is subtracted from the raw signal intensity value. This background is determined from the signal intensity in a predetermined area surrounding each feature (e.g. an area of X, Y or Z μm^2 centered on the position of the probe). The background signal is typically determined from the local signal of "blank" controls (solvent only). In many instances the device, e.g. scanner, which is used to determine signal intensities will provide means for determining background signal.

[0217] Thus, for example, where the label is a fluorescent label, absolute fluorescence values (raw intensity values) can be gathered for each probe replica and the background noise associated with each probe replica can also be assessed in order to produce "clean" values for signal intensity at each replicate feature position.

[0218] Once the test DNA has been hybridized to the chip and the intensity of detectable label has been determined at the probe feature replica positions on the chip (the raw intensity values), it is necessary to provide a method (model) which can relate the intensity data from the chip to the genotype of the individual.

[0219] The inventors have found that this can be done by applying a specific algorithm to the intensity data. The algorithm and computer software developed by the inventors allows analysis of the genetic variations with sufficient sensitivity and reproducibility as to allow use in a clinical setting.

[0220] Typically, amending the raw intensity value to obtain the clean intensity value for each probe replica comprises subtracting background noise from the raw value. Background noise is typically determined using appropriate controls such as area of chip with no NA or probe.

[0221] The inventors have found that the use of replicas and median calculated from replicas is important for reliable working of the invention.

[0222] The algorithm as described herein is designed to be computer implemented, and thus in some embodiments, the methods described herein comprise the use of a computer system and a computer program.

Systems for analysis of indel genetic variation

[0223] Embodiments of the invention can be described through functional modules, which are defined by computer executable instructions recorded on computer readable media and which cause a

computer to perform method steps when executed. The modules are segregated by function for the sake of clarity. However, it should be understood that the modules/systems need not correspond to discreet blocks of code and the described functions can be carried out by the execution of various code portions stored on various media and executed at various times. Furthermore, it should be appreciated that the modules may perform other functions, thus the modules are not limited to having any particular functions or set of functions.

[0224] The computer readable storage media can be any available tangible media that can be accessed by a computer. Computer readable storage media includes volatile and nonvolatile, removable and non-removable tangible media implemented in any method or technology for storage of information such as computer readable instructions, data structures, program modules or other data. Computer readable storage media includes, but is not limited to, RAM (random access memory), ROM (read only memory), EPROM (erasable programmable read only memory), EEPROM (electrically erasable programmable read only memory), flash memory or other memory technology, CD-ROM (compact disc read only memory), DVDs (digital versatile disks) or other optical storage media, magnetic cassettes, magnetic tape, magnetic disk storage or other magnetic storage media, other types of volatile and non-volatile memory, and any other tangible medium which can be used to store the desired information and which can be accessed by a computer including and any suitable combination of the foregoing.

[0225] Computer-readable data embodied on one or more computer-readable media may define instructions, for example, as part of one or more programs that, as a result of being executed by a computer, instruct the computer to perform one or more of the functions described herein, and/or various embodiments, variations and combinations thereof. Such instructions may be written in any of a plurality of programming languages, for example, Java, J#, Visual Basic, C, C#, C++, Fortran, Pascal, Eiffel, Basic, COBOL assembly language, and the like, or any of a variety of combinations thereof. The computer-readable media on which such instructions are embodied may reside on one or more of the components of either of a system, or a computer readable storage medium described herein, may be distributed across one or more of such components.

[0226] The computer-readable media can be transportable such that the instructions stored thereon can be loaded onto any computer resource to implement the aspects of the present invention discussed herein. In addition, it should be appreciated that the instructions stored on the computer-readable medium, described above, are not limited to instructions embodied as part of an application program running on a host computer. Rather, the instructions may be embodied as any type of computer code (e.g., software or microcode) that can be employed to program a computer to implement aspects of the present invention. The computer executable instructions may be written in a suitable computer language or combination of several languages. Basic computational biology methods are known to those of ordinary skill in the art and are described in, for example, Setubal and Meidanis et al., *Introduction to Computational Biology Methods* (PWS Publishing Company, Boston, 1997); Salzberg, Searles, Kasif, (Ed.), *Computational Methods in Molecular Biology*, (Elsevier, Amsterdam, 1998); Rashidi and

Buehler, Bioinformatics Basics: Application in Biological Science and Medicine (CRC Press, London, 2000) and Ouelette and Bzevanis Bioinformatics: A Practical Guide for Analysis of Gene and Proteins (Wiley & Sons, Inc., 2nd ed., 2001).

[0227] The functional modules of certain embodiments of the invention include at minimum a measuring module #40, a storage module #30, a comparison module #80, and an output module #110 (Fig. 10). The functional modules can be executed on one, or multiple, computers, or by using one, or multiple, computer networks. The measuring module has computer executable instructions to provide e.g., expression information in computer readable form.

[0228] The measuring module #40, can comprise any system for detecting a signal representing the detectable label from a target NA-probe complex (Fig. 10). Such systems can include DNA microarray readers, RNA expression array reader, flow cytometer or any other system which produces an electronic signal converted from the original label, such as a photonic signal or a radioactive signal. The original signal intensity or frequency determines the electronic signal intensity or frequency.

[0229] The information determined in the determination system can be read by the storage module #30 (Fig. 10). As used herein the "storage module" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus, data telecommunications networks, including local area networks (LAN), wide area networks (WAN), Internet, Intranet, and Extranet, and local and distributed computer processing systems. Storage modules also include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage media, magnetic tape, optical storage media such as CD-ROM, DVD, electronic storage media such as RAM, ROM, EPROM, EEPROM and the like, general hard disks and hybrids of these categories such as magnetic/optical storage media. The storage module is adapted or configured for having recorded thereon genetic variation information. Such information may be provided in digital form that can be transmitted and read electronically, e.g., via the Internet, on diskette, via USB (universal serial bus) or via any other suitable mode of communication.

[0230] As used herein, "stored" refers to a process for encoding information on the storage module. Those skilled in the art can readily adopt any of the presently known methods for recording information on known media to generate manufactures comprising genetic variation information.

[0231] In one embodiment, the reference data stored in the storage module to be read by the comparison module is e.g., genetic variation data from normal subjects.

[0232] The "comparison module" #80 (Fig. 10) can use a variety of available software programs and formats for the comparison operative to compare genetic variation data determined in the measuring module for the variant and non-variant segment. In one embodiment, the comparison module is configured to use pattern recognition techniques to compare information from one or more entries to one or more reference data patterns. The comparison module may be configured using existing commercially-available or freely-available software for comparing patterns, and may be optimized for

particular data comparisons that are conducted. The comparison module provides computer readable information related to normalized ratios of intensities, median $\log_2$ of intensities etc in the analysis and interpretation of the genetic variation in an individual.

[0233] The comparison module, or any other module of the invention, can include an operating system (e.g., UNIX) on which runs a relational database management system, a World Wide Web application, and a World Wide Web server. World Wide Web application includes the executable code necessary for generation of database language statements (e.g., Structured Query Language (SQL) statements). Generally, the executables will include embedded SQL statements. In addition, the World Wide Web application can include a configuration file which contains pointers and addresses to the various software entities that comprise the server as well as the various external and internal databases which must be accessed to service user requests. The Configuration file also directs requests for server resources to the appropriate hardware--as may be necessary should the server be distributed over two or more separate computers. In one embodiment, the World Wide Web server supports a TCP/IP protocol. Local networks such as this are sometimes referred to as "Intranets." An advantage of such Intranets is that they allow easy communication with public domain databases residing on the World Wide Web (e.g., the GENBANK™ or Swiss Pro World Wide Web site). Thus, in a particular preferred embodiment of the present invention, users can directly access data (via Hypertext links for example) residing on Internet databases using a HTML interface provided by Web browsers and Web servers.

[0234] The comparison module provides a computer readable comparison result that can be processed in computer readable form by predefined criteria, or criteria defined by a user, to provide a content-based in part on the comparison result that may be stored and output as requested by a user using an output module #110 (Fig. 10).

[0235] The content based on the comparison result, can be an expression value compared to a reference showing the $\text{Ratio}_{(k)}$ or $\text{Ratio}_{(k)/(k+1)}$ in a genetic variant segment of the test NA sample.

[0236] In one embodiment of the invention, the content based on the comparison result is displayed on a computer monitor #120. In one embodiment of the invention, the content based on the comparison result is displayed through printable media #130, #140. The display module can be any suitable device configured to receive from a computer and display computer readable information to a user. Non-limiting examples include, for example, general-purpose computers such as those based on Intel PENTIUM-type processor, Motorola PowerPC, Sun UltraSPARC, Hewlett-Packard PA-RISC processors, any of a variety of processors available from Advanced Micro Devices (AMD) of Sunnyvale, California, or any other type of processor, visual display devices such as flat panel displays, cathode ray tubes and the like, as well as computer printers of various types.

[0237] In one embodiment, a World Wide Web browser is used for providing a user interface for display of the content based on the comparison result. It should be understood that other modules of the invention can be adapted to have a web browser interface. Through the Web browser, a user may construct requests for retrieving data from the comparison module. Thus, the user will typically point

and click to user interface elements such as buttons, pull down menus, scroll bars and the like conventionally employed in graphical user interfaces.

[0238] The present invention therefore provides for systems (and computer readable media for causing computer systems) to perform methods for analyzing genetic variations in a tNA sample.

[0239] Systems and computer readable media described herein are merely illustrative embodiments of the invention for detecting indel genetic variation in an individual, and are not intended to limit the scope of the invention. Variations of the systems and computer readable media described herein are possible and are intended to fall within the scope of the invention.

[0240] The modules of the machine, or those used in the computer readable medium, may assume numerous configurations. For example, function may be provided on a single machine or distributed over multiple machines.

[0241] In one embodiment, provided herein is a system for detecting analyzing an indel variation in NA sample, comprising:

- a. a measuring module measuring the raw intensity comprising a detectable signal from a replicate feature indicating the presence or level of a NA-probe complex on a solid support comprising the replicate feature;
- b. a storage module configured to store data output from the measuring module;
- c. a comparison module adapted to compare the data stored on the storage module with reference and/or control data, and to provide a retrieved content, and
- d. an output module for displaying the retrieved content for the user, wherein the retrieved content the $\text{Ratio}_{(k)}$ or $\text{Ratio}_{(k)/(k+1)}$ for the kth nucleotide of the genetic variant segment indicates that the presence of an indel in the NA sample.

[0242] In one embodiment, provided herein is a computer readable storage medium comprising:

- a. a storing data module containing a detectable signal from a replicate feature indicating the presence or level of a NA-probe complex on a solid support comprising the replicate feature
- b. a comparison module that compares the data stored on the storing data module with a reference data and/or control data, and to provide a comparison content, and
- c. an output module displaying the comparison content for the user, wherein the retrieved content the $\text{Ratio}_{(k)}$ or $\text{Ratio}_{(k)/(k+1)}$ for the kth nucleotide of the genetic variant segment indicates that the presence of an indel in the NA sample..

[0243] In one embodiment, the control data comprises data from an individual with normal / wild type genotype at the genetic variant segment under interrogation.

Design and selection of probe sets and variant segments for indel analysis and an indel-chip

[0244] In one embodiment, genes or genetic variant segments are selected on the basis of the pathogenicity of indels they may contain. The probes for detecting indels are oligonucleotide NA ranging from 15 to 50 nt and are designed for interrogating genes or genetic variant segments. Indels to be

detected can be deletions of one nt, deletions of two nt, deletions of three nt, duplications of one nt, insertions of one nt, insertions of more than one nt. The deletion, insertions or duplications can be anywhere from one to ten nt at any of the nt positions in the genes or genetic variant segments. In other embodiments, the deletion insertions or duplications can be up to 50 nt, e. g. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nt.

[0245] As an exemplary, the gene having genetic variant segments to be interrogated is the gene encoding LDLR (for Low Density Lipoprotein Receptor, located 19p13.2). It is involved in the phenotype of Hypercholesterolemia, Autosomic Dominant (HAD mainly called Familial Hypercholesterolemia, hereafter named FH), all the regions known to be possibly affected by indels are selected as genetic variant segments for interrogations. These regions are listed below:

Genetic variant segment 1: Promoter and exon 1 of LDLR gene (SEQ ID NO: 4585).

[0246] From position (-377), considering the first nucleotide of the initiating methionine in position 1 of the protein as the origin, until 67+ 106, localized in intron 1 (reference sequence LDLR mRNA is NM_000527.3, SEQ ID NO: 4579). This region includes transcription regulatory elements (2 TATA box and 3 imperfect repetitions of elements regulated by sterol (SER elements).

Genetic variant segment 2: Exon 2 (SEQ ID NO: 4586).

[0247] From position 68 -121, in intron 1, until nucleotide in position 190 +102.

Genetic variant segment 3: Exon 3 (SEQ ID NO: 4587).

[0248] From position 191 -124, in intron 2, until nucleotide in position 313 +121.

Genetic variant segment 4: Exon 4 (SEQ ID NO: 4588).

[0249] From position 314 -77, in intron 3, until nucleotide in position 694 +81.

Genetic variant segment 5: Exon 5 (SEQ ID NO: 4589).

[0250] From position 695 -71, in intron 4, until nucleotide in position 817 +78.

Genetic variant segment 6: Exon 6 (SEQ. ID. NO: 4590).

[0251] From position 818 -71, in intron 5, until nucleotide in position 940 +83.

Genetic variant segment 7: Exon 7 (SEQ ID NO: 4591).

[0252] From position 941 -84, in intron 6, until nucleotide in position 1060 +146.

Genetic variant segment 8: Exon 8 (SEQ ID NO: 4592).

[0253] From position 1061- 94, in intron 7, until nucleotide in position 1186 +106.

Genetic variant segment 9: Exon 9, intron 9 and exon 10 (SEQ ID NO: 4593).

[0254] From position 1187 -93, in intron 8, until nucleotide in position 1586 +111. This region includes full intron 9.

Genetic variant segment 10: Exon 11 (SEQ ID NO: 4594).

[0255] From position 1587 -96, in intron 10, until nucleotide in position 1705 +107.

Genetic variant segment 11: Exon 12 (SEQ ID NO: 4595).

[0256] From position 1706 -130, in intron 11, until nucleotide in position 1845 +79.

Genetic variant segment 12: Exon 13, intron 13 and exon 14 (SEQ ID NO: 4596).

[0257] From position 1846 -78, in intron 12, until nucleotide in position 2140 +150. This region includes full intron 13.

Genetic variant segment 13: Exon 15 (SEQ ID NO: 4597).

[0258] From position 2141 -71, in intron 14, until nucleotide in position 2311 +84.

Genetic variant segment 14: Exon 16 (SEQ ID NO: 4598).

[0259] From position 2312 -116, in intron 15, until nucleotide in position 2389 +105.

Genetic variant segment 15: Exon 17 (SEQ ID NO: 4599).

[0260] From position 2390 -105, in intron 16, until nucleotide in position 2547 +80.

[0261] One embodiment of a library of probes designed according to the system described herein is found in Table 1, comprising SEQ ID NO: 1-4575. This library of probe is designed to detect all possible indels for the exon 2 of the human LDLR gene.

Genetic variant segment 16: Exon 18 (SEQ ID NO: 4600).

[0262] From position 2548 -146, in intron 17, until nucleotide in position 2580 +96.

[0263] Other genes having genetic variant segments that can be interrogated are the human apolipoprotein B (including Ag(x) antigen) (APOB) gene (SEQ ID NO: 4584), the various exons in PCSK9 (Proprotein convertase subtilisin/kexin type 9) gene, in particular, exons 2, 4, 7 and 10, as provided in SEQ ID NOS: 4602-4605, respectively and the cystic fibrosis transmembrane conductance regulator (CFTR) gene that is responsible for the genetic disorder cystic fibrosis. This gene is located on chromosome 7:116907153-117096054 (approx. 188kb) (SEQ ID NO: 4606).

Genetic variant segment 17: Exon 26 APOB (SEQ ID NO: 4601).

[0264] From position 10453, exon 26, until nucleotide in position 10740 (reference sequence NM_000384.2).

[0265] The nomenclature formula for the positions of the bases are as described in den Dunnen and Antonarakis, Human Mutation, 2000,15:7-12. The first number within each position formula XXX-YYY or XXX+YYY, e. g. position 2141 -71 or position 2547 +80 refers to the position of the base on the mRNA human LDLR sequence (SEQ ID NO: 4579) wherein the position number 1 is the "A" of the ATG of the signal peptide" in SEQ ID NO: 4576. In SEQ. ID. NO: 4, the "A" of the ATG of the signal peptide" or base position number 1 is the 469th nucleotide in the genomic sequence of human LDLR sequence (SEQ ID NO: 4579). In other words, the base position in the LDLR genomic sequence that corresponds to the 1st base position in the LDLR mRNA is 469. The second number within each position formula refers to the number of the bases that is to be added or subtracted from the base position in the genomic where that base position corresponds to the first number of the position formula which is that in the mRNA. The sequences of a number of indel oligonucleotide probes are selected from these variant segments. These probes are synthesized and then spotted on a solid support in an array as probe feature replicas.

[0266] The patient's NA, such as DNA, to be genotyped, called test NA sample, is amplified to produce various genetic variant segments as listed herein and can be complementary of the entire size of the probes. Together with the patient's DNA, one or more control NA sample is amplified under the same conditions of the test target NA.

[0267] Once amplified, the targets (test and control) are fragmented and labeled and then hybridized onto the probes that are immobilized on solid supports. Solid supports such as flat glass chips or beads are scanned to obtain intensities of each single probe.

[0268] Additional embodiments of the invention provides a DNA chip comprising a plurality of probe features deposited on a solid support, the chip being suitable for use in a method of the invention described herein; a computational method for obtaining a genotype from DNA-chip hybridization intensity data wherein the method comprises using ratios for each segment to be genotyped; a computer system comprising a processor and means for controlling the processor to carry out a computational method of the invention; and a computer program comprising computer program code which when run on a computer or computer network causes the computer or computer network to carry out a computational method of the invention.

Design and selection of probe sets for idel analysis

[0269] In one embodiment, the invention provides a library of probes for detecting at least one indel variation in a genetic variant segment having a length of N number of base pairs, the library comprising (a) a set of probe sets which comprises N number of probe sets, wherein there is one probe set for each nucleotide position of the genetic variant segment; wherein each probe set comprise of at least one probe sub-set, wherein the at least probe sub-set is for interrogating a single kind of indel; wherein the at least probe sub-set comprises at least a pair of probes, a normal or control probe and a variant probe, both of which interrogate a substantially similar region on the genetic variant segment, wherein the both probes forming the pair of probes have the same sequence length, interrogated the same strand of genetic variant segment and are of the same type of nucleic acids, and wherein the length of the probes are between 15-50 nucleotides; wherein the normal probe comprises the normal / wild type or control sequence of genetic variant segment and the variant probe comprises an indel-containing variant sequence of genetic variant segment; wherein the indel in the variant probe is located at -25, -24, -23, -22, -21, -20, -19, -18, -17, -16, -15, -14, -13, -12, -11, -10, -9, -8, -7, -6, -5, -4, -3, -2, -1, 0, +1, +2, +3, +4, +5, +6, +7, +8, +9, +10, +11, +12, +13, +14, +15, +16, +17, +18, +20, +21, +22, +23, +24 or +25 nucleotide position in the variant probe; wherein the position 0 is the center nucleotide of the probe when the probe has an odd number of nucleotides; and wherein the position -1 and +1 are the two central nucleotides of the probe when the probe has an even number of nucleotides.

[0270] This invention is further illustrated by the following example for selecting and designing a library of probes which should not be construed as limiting.

[0271] In one embodiment, control probes are designed and selected for the library.

[0272] In one embodiment, normal / wild type probes are designed and selected for the library.

[0273] In one embodiment, the library comprises only control probes and not normal probes, in addition to the corresponding variant probes.

[0274] In one embodiment, the library comprises only normal probes and not control probes, in addition to the corresponding variant probes.

[0275] In one embodiment, for the detection of indels, oligonucleotide probes are designed for each position to be tested in the genetic variant segment. In one embodiment, for each position of the segment to be interrogated, 36 probes are designed to detect changes from the normal or control sequence.

[0276] In one embodiment, all these probes are to be oriented in the 3' to 5' direction on the solid support. In another embodiment, all these probes are to be oriented in the 3' to 5' direction on the solid support.

[0277] In one embodiment, indels of 2 or more nts are always considered to the "right" (i.e., 3') of the nt interrogated in the genetic variant segment.

[0278] The following are the designs of these 36 probe sets for each indel position with reference to the probes in the 3' to 5' direction:

[0279] In one embodiment, the oligonucleotide probes can be about 15-50 nt long. The probes typically have the base to be examined (the site of the indel genetic variation) at the center of the probe, i.e., in the middle, such that for example a probe of 25 nucleotides long has the location of the genetic variation as nucleic acid 13 from the 5' end. In other words, the indel variation is located at the "0" position within the probe, "0" refers to the central nt in the oligonucleotide probe. In one embodiment, the indel variation can also be 2-4 nucleic acids 3' or 5' of the center of the probe, i. e. at the -4, -3, -2, -1, +1, +2, +3 or +4 position within the probe, wherein the probe oriented in the 3' to 5' direction on the solid support.

[0280] In one embodiment, one oligonucleotide probe where the base of interest (i. e. indel variation) located at the central base is deleted with respect to the normal or wild type allele. This probe detects a single nt deletion. The indel variation is located at the "0" position within the probe. The same oligonucleotide probe is also designed but on the other strand of the fragment is to be analyzed. Therefore, a pair of complementary probes is made. In this design, both the sense and anti-sense strand will be interrogated by this pair of complementary probes.

[0281] In one embodiment, one oligonucleotide probe where the base of interest is in an offset position of 4 nucleotides with respect to the central base towards the 5' end and is deleted compared to the normal or wild type allele. This probe detects a single nt deletion. This probe has the indel variation located at the -4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0282] In one embodiment, one oligonucleotide probe where the base of interest is in an offset position of 4 nucleotides with respect to the central base towards the 3' end and is deleted from the

normal or wild type allele. This probe detects a single nt deletion. This probe has the indel variation located at the +4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0283] In one embodiment, one oligonucleotide probe where the base of interest is located at the central base and its adjacent base on the 5' side is deleted with respect to the normal or wild type allele. This probe detects two nt deletion. The indel variation is located at the "0" position within the probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0284] In one embodiment, one oligonucleotide probe where the two bases of interest are in an offset position of 4 nucleotides towards the 5' with respect to the base in the central position and its adjacent base on the 5' side and are deleted respect to the normal or wild type allele. This probe detects two nt deletions. This probe has the indel variation located at the -4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0285] In one embodiment, one oligonucleotide probe where the two bases of interest are in an offset position of 4 nucleotides towards the 3' respect to the base in the central position and its adjacent base on the 5' side and are deleted respect to the normal or wild type allele. This probe detects two nt deletions. This probe has the indel variation located at the +4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0286] In one embodiment, one oligonucleotide probe where the bases of interest located the central base and its adjacent 2 base on the 5' side are deleted respect to the normal or wild type allele. This probe detects three nt deletions. The indel variation is located at the "0" position within the probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0287] In one embodiment, one oligonucleotide probe where the three bases of interest are in an offset position of 4 nucleotides towards the 5' respect to the base in the central position and its adjacent base on the 5' side and are deleted respect to the normal or wild type allele. This probe detects three nt deletions. This probe has the indel variation located at the -4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0288] In one embodiment, one oligonucleotide probe where the three bases of interest are in an offset position of 4 nucleotides towards the 3' respect to the base in the central position and its adjacent base on the 5' side and are deleted respect to the normal or wild type allele. This probe detects three nt deletions. This probe has the indel variation located at the +4 position with respect to the central nt in the

oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0289] In one embodiment, one oligonucleotide probe where the base of interest located at the central base is duplicated respect to the normal or wild type allele. This probe detects a single nt duplication. The indel variation is located at the "0" position within the probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0290] In one embodiment, one oligonucleotide probe where the base of interest is in an offset position of 4 nucleotides respects to the central base towards the 5' end and is duplicated respect from the normal or wild type allele. This probe detects a single nt duplication. This probe has the indel variation located at the -4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0291] In one embodiment, one oligonucleotide probe where the base of interest is in an offset position of 4 nucleotides respects to the central base towards the 3' end and is duplicated respect from the normal or wild type allele. This probe detects a single nt duplication. This probe has the indel variation located at the +4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0292] In one embodiment, one oligonucleotide probe where the bases of interest being the central base and its adjacent base on the 5' side are duplicated respect to the normal or wild type allele. This probe detects a two- nt duplication. The indel variation is located at the "0" position within the probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0293] In one embodiment, one oligonucleotide probe where the two bases of interest are in an offset position of 4 nucleotides towards the 5' respect to the base in the central position and its adjacent base on the 5' side and are duplicated respect to the normal or wild type allele. This probe detects a two- nt duplication. This probe has the indel variation located at the -4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0294] In one embodiment, one oligonucleotide probe where the two bases of interest are in an offset position of 4 nucleotides towards the 3' respect to the base in the central position and its adjacent base on the 5' side and are duplicated respect to the normal or wild type allele. This probe detects a two- nt duplication. This probe has the indel variation located at the +4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0295] In one embodiment, one oligonucleotide probe where the bases of interest being the central base and its adjacent 2 base on the 5' side are duplicated respect to the normal or wild type allele.

This probe detects a three-nt duplication. The indel variation is located at the “0” position within the probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0296] In one embodiment, one oligonucleotide probe where the three bases of interest are in an offset position of 4 nucleotides towards the 5’ respect to the base in the central position and its adjacent base on the 5’ side and are duplicated respect to the normal or wild type allele. This probe detects a three-nt duplication. This probe has the indel variation located at the -4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0297] In another embodiment, the library of probes comprises of oligonucleotide oligos of three different length, 21 nt, 23 nt, and 25 nt, all of which have the indel variation located in central (0) position and oligonucleotide probes interrogating the sense and the anti-sense strand are represented.

[0298] In one embodiment, one oligonucleotide probe where the three bases of interest are in an offset position of 4 nucleotides towards the 3’ respect to the base in the central position and its adjacent base on the 5’ side and are duplicated respect to the normal or wild type allele. This probe detects a three-nt duplication. This probe has the indel variation located at the +4 position with respect to the central nt in the oligonucleotide probe. A similar oligonucleotide probe is also designed but this probe hybridizes to the other strand of the fragment to be analyzed.

[0299] Unless otherwise explained, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Definitions of common terms in genomics and molecular biology can be found in The Encyclopedia of Molecular Biology, published by Blackwell Science Ltd., 1994 (ISBN 0-632-02182-9); Robert A. Meyers (ed.), Molecular Biology and Biotechnology: a Comprehensive Desk Reference, published by VCH Publishers, Inc., 1995 (ISBN 1-56081-569-8); and Discovering Genomics, Proteomics and Bioinformatics 2nd edition - by A. Malcolm Campbell and Laurie J. Heyer. (ISBN 0-8053-4722-4; published by Cold Spring Harbor Laboratory Press and Benjamin Cummings: 2006). Definitions of common terms in molecular biology may be found in Benjamin Lewin, Genes IX, published by Jones & Bartlett Publishing, 2007 (ISBN-13: 9780763740634); Kendrew et al. (eds.).

[0300] Unless otherwise stated, the present invention was performed using standard procedures, as described, for example in Microarrays Methods and Applications (Nuts & Bolts series) by Gary Hardiman (Ed.), DNA Press; 1st edition (2003; ISBN-13: 978-0966402766), Analytical Tools for DNA, Genes and Genomes : Nuts & Bolts (Nuts & Bolts series) by Arseni Markoff (Ed.), DNA Press, (2005, ISBN-13: 978-0974876511); and DNA Microarrays, Part B: Databases and Statistics, Volume 411 (Methods in Enzymology) by Alan R. Kimmel and Brian Oliver (Eds), Academic Press, 1st edition (2006; ISBN-13: 978-0121828165) which are all incorporated by reference herein in their entireties.

[0301] It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such may vary. The terminology used herein is for

the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims.

[0302] Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when used in connection with percentages may mean $\pm 1\%$.

[0303] The singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of this disclosure, suitable methods and materials are described below. The abbreviation, "e.g." is derived from the Latin *exempli gratia*, and is used herein to indicate a non-limiting example. Thus, the abbreviation "e.g." is synonymous with the term "for example."

[0304] All patents and other publications identified in the specification are expressly incorporated herein by reference for the purpose of describing and disclosing, for example, the methodologies described in such publications that might be used in connection with the present invention. These publications are provided solely for their disclosure prior to the filing date of the present application. Nothing in this regard should be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicants and does not constitute any admission as to the correctness of the dates or contents of these documents.

[0305] The contents of all references cited throughout this application, as well as the figures and tables are incorporated herein by reference.

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_100_d0_r	1	TCCCGTCTTGGCACTGGAACTCGTT	2	CCCGTCTTGGCACTGGAACTCGT	3	CCGTCTTGGCACTGGAACTCG
LDLRex2(27;68;123;30)_101_d0_f	4	ACGAGTTCCAGTGCCAAAGACGGGAA	5	CGAGTCCAGTGCCAAAGACGGGA	6	GAGTTCAGTGCCAAAGACGGG
LDLRex2(27;68;123;30)_101_d0_r	7	TTCCCGTCTTGGCACTGGAACTCGT	8	TCCCGTCTTGGCACTGGAACTCG	9	CCCGTCTTGGCACTGGAACTC
LDLRex2(27;68;123;30)_102_d0_f	10	CGAGTTCAGTGCCAAAGACGGGAAA	11	GAGTTCAGTGCCAAAGACGGGAA	12	AGTTCAGTGCCAAAGACGGGA
LDLRex2(27;68;123;30)_102_d0_r	13	TTTCCCGTCTTGGCACTGGAACTCG	14	TCCCGTCTTGGCACTGGAACTC	15	TCCCGTCTTGGCACTGGAACT
LDLRex2(27;68;123;30)_103_d0_f	16	GAGTTCAGTGCCAAAGACGGGAAAT	17	AGTTCAGTGCCAAAGACGGGAAA	18	GTTCCAGTGCCAAAGACGGGAA
LDLRex2(27;68;123;30)_103_d0_r	19	ATTTCCCGTCTTGGCACTGGAACTC	20	TTTCCCGTCTTGGCACTGGAACT	21	TTCCCGTCTTGGCACTGGAACT
LDLRex2(27;68;123;30)_104_d0_f	22	AGTTCAGTGCCAAAGACGGGAAATG	23	GTTCCAGTGCCAAAGACGGGAAAT	24	TTCAGTGCCAAAGACGGGAAA
LDLRex2(27;68;123;30)_104_d0_r	25	CATTTCCCGTCTTGGCACTGGAACT	26	ATTTCCCGTCTTGGCACTGGAACT	27	TTTCCCGTCTTGGCACTGGAA
LDLRex2(27;68;123;30)_105_d0_f	28	GTTCCAGTGCCAAAGACGGGAAATGC	29	TTCAGTGCCAAAGACGGGAAATG	30	TTCAGTGCCAAAGACGGGAAAT
LDLRex2(27;68;123;30)_105_d0_r	31	GCATTTCCCGTCTTGGCACTGGAACT	32	CATTTCCCGTCTTGGCACTGGAA	33	ATTTCCCGTCTTGGCACTGGAA
LDLRex2(27;68;123;30)_106_d0_f	34	TTCAGTGCCAAAGACGGGAAATGCA	35	TCCAGTGCCAAAGACGGGAAATGC	36	CCAGTGCCAAAGACGGGAAATG
LDLRex2(27;68;123;30)_106_d0_r	37	TGCATTTCCCGTCTTGGCACTGGAA	38	GCATTTCCCGTCTTGGCACTGGA	39	CATTTCCCGTCTTGGCACTGG
LDLRex2(27;68;123;30)_107_d0_f	40	TCCAGTGCCAAAGACGGGAAATGCAT	41	CCAGTGCCAAAGACGGGAAATGCA	42	CAGTGCCAAAGACGGGAAATGC
LDLRex2(27;68;123;30)_107_d0_r	43	ATGCATTTCCCGTCTTGGCACTGGA	44	TGCATTTCCCGTCTTGGCACTGG	45	GCATTTCCCGTCTTGGCACTG
LDLRex2(27;68;123;30)_108_d0_f	46	CCAGTGCCAAAGACGGGAAATGCATC	47	CAGTGCCAAAGACGGGAAATGCAT	48	AGTGCCAAAGACGGGAAATGCA
LDLRex2(27;68;123;30)_108_d0_r	49	GATGCATTTCCCGTCTTGGCACTGG	50	ATGCATTTCCCGTCTTGGCACTG	51	TGCATTTCCCGTCTTGGCACT
LDLRex2(27;68;123;30)_109_d0_f	52	CAGTGCCAAAGACGGGAAATGCATCT	53	AGTGCCAAAGACGGGAAATGCATC	54	GTGCCAAAGACGGGAAATGCAT
LDLRex2(27;68;123;30)_109_d0_r	55	AGATGCATTTCCCGTCTTGGCACTG	56	GATGCATTTCCCGTCTTGGCACT	57	ATGCATTTCCCGTCTTGGCAC
LDLRex2(27;68;123;30)_110_d0_f	58	AGTGCCAAAGACGGGAAATGCATCTC	59	GTGCCAAAGACGGGAAATGCATCT	60	TGCCAAAGACGGGAAATGCATC
LDLRex2(27;68;123;30)_110_d0_r	61	GAGATGCATTTCCCGTCTTGGCACT	62	AGATGCATTTCCCGTCTTGGCAC	63	GATGCATTTCCCGTCTTGGCA
LDLRex2(27;68;123;30)_111_d0_f	64	GTGCCAAAGACGGGAAATGCATCTCC	65	TGCCAAAGACGGGAAATGCATCTC	66	GCCAAAGACGGGAAATGCATCT
LDLRex2(27;68;123;30)_111_d0_r	67	GGAGATGCATTTCCCGTCTTGGCAC	68	GAGATGCATTTCCCGTCTTGGCA	69	AGATGCATTTCCCGTCTTGGC
LDLRex2(27;68;123;30)_112_d0_f	70	TGCCAAAGACGGGAAATGCATCTCT	71	GCCAAAGACGGGAAATGCATCTCC	72	CCAAGACGGGAAATGCATCTC
LDLRex2(27;68;123;30)_112_d0_r	73	AGGAGATGCATTTCCCGTCTTGGCA	74	GGAGATGCATTTCCCGTCTTGGC	75	GAGATGCATTTCCCGTCTTGG
LDLRex2(27;68;123;30)_113_d0_f	76	GCCAAAGACGGGAAATGCATCTCTCTA	77	CCAAGACGGGAAATGCATCTCTCT	78	CAAGACGGGAAATGCATCTCC
LDLRex2(27;68;123;30)_113_d0_r	79	TAGGAGATGCATTTCCCGTCTTGGC	80	AGGAGATGCATTTCCCGTCTTGG	81	GGAGATGCATTTCCCGTCTTG
LDLRex2(27;68;123;30)_114_d0_f	82	CCAAGACGGGAAATGCATCTCTCTAC	83	CAAGACGGGAAATGCATCTCTCTA	84	AAGACGGGAAATGCATCTCT
LDLRex2(27;68;123;30)_114_d0_r	85	GTAGGAGATGCATTTCCCGTCTTGG	86	TAGGAGATGCATTTCCCGTCTTG	87	AGGAGATGCATTTCCCGTCTT
LDLRex2(27;68;123;30)_115_d0_f	88	CAAGACGGGAAATGCATCTCTCTACA	89	AAGACGGGAAATGCATCTCTCTAC	90	AGACGGGAAATGCATCTCTCTA
LDLRex2(27;68;123;30)_115_d0_r	91	TGTAGGAGATGCATTTCCCGTCTTG	92	GTAGGAGATGCATTTCCCGTCTT	93	TAGGAGATGCATTTCCCGTCTT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_116_d0_f	94	AAGACGGGAAATGCATCTCTCTACAA	95	AGACGGGAAATGCATCTCTCTACAA	96	GACGGGAAATGCATCTCTCTAC
LDLRex2(27;68;123;30)_116_d0_r	97	TTGTAGGAGATGCATTTCCCGTCT	98	TGTAGGAGATGCATTTCCCGTCT	99	GTAGGAGATGCATTTCCCGTC
LDLRex2(27;68;123;30)_117_d0_f	100	AGACGGGAAATGCATCTCTCTACAA	101	GACGGGAAATGCATCTCTCTACAA	102	ACGGGAAATGCATCTCTCTACA
LDLRex2(27;68;123;30)_117_d0_r	103	CTTGTAGGAGATGCATTTCCCGTCT	104	TTGTAGGAGATGCATTTCCCGTC	105	TGTAGGAGATGCATTTCCCGT
LDLRex2(27;68;123;30)_118_d0_f	106	GACGGGAAATGCATCTCTCTACAA	107	ACGGGAAATGCATCTCTCTACAA	108	CGGGAAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_118_d0_r	109	ACTTGTAGGAGATGCATTTCCCGTC	110	CTTGTAGGAGATGCATTTCCCGT	111	TTGTAGGAGATGCATTTCCCG
LDLRex2(27;68;123;30)_119_d0_f	112	ACGGGAAATGCATCTCTCTACAA	113	CGGGAAATGCATCTCTCTACAA	114	GGGAAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_119_d0_r	115	CACTTGTAGGAGATGCATTTCCCGT	116	ACTTGTAGGAGATGCATTTCCCG	117	CTTGTAGGAGATGCATTTCC
LDLRex2(27;68;123;30)_120_d0_f	118	CGGGAAATGCATCTCTCTACAA	119	GGGAAATGCATCTCTCTACAA	120	GGAAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_120_d0_r	121	CCACTTGTAGGAGATGCATTTCCCG	122	CACCTGTAGGAGATGCATTTCC	123	ACTTGTAGGAGATGCATTTCC
LDLRex2(27;68;123;30)_121_d0_f	124	GGGAAATGCATCTCTCTACAA	125	GGAAATGCATCTCTCTACAA	126	GAAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_121_d0_r	127	CCCCTTGTAGGAGATGCATTTCC	128	CCACTTGTAGGAGATGCATTTCC	129	CACCTGTAGGAGATGCATTTCC
LDLRex2(27;68;123;30)_122_d0_f	130	GGAAATGCATCTCTCTACAA	131	GAAATGCATCTCTCTACAA	132	AAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_122_d0_r	133	ACCCACTTGTAGGAGATGCATTTCC	134	CCCACTTGTAGGAGATGCATTTCC	135	CCACTTGTAGGAGATGCATTT
LDLRex2(27;68;123;30)_123_d0_f	136	GAAATGCATCTCTCTACAA	137	AAATGCATCTCTCTACAA	138	AATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_123_d0_r	139	GACCCACTTGTAGGAGATGCATTTCC	140	ACCCACTTGTAGGAGATGCATTT	141	CCCCTTGTAGGAGATGCATTT
LDLRex2(27;68;123;30)_124_d0_f	142	AAATGCATCTCTCTACAA	143	AATGCATCTCTCTACAA	144	ATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_124_d0_r	145	AGACCCACTTGTAGGAGATGCATTT	146	GACCCACTTGTAGGAGATGCATTT	147	ACCCACTTGTAGGAGATGCAT
LDLRex2(27;68;123;30)_125_d0_f	148	AATGCATCTCTCTACAA	149	ATGCATCTCTCTACAA	150	TGCATCTCTCTACAA
LDLRex2(27;68;123;30)_125_d0_r	151	CAGACCCACTTGTAGGAGATGCATTT	152	AGACCCACTTGTAGGAGATGCAT	153	GACCCACTTGTAGGAGATGCA
LDLRex2(27;68;123;30)_126_d0_f	154	ATGCATCTCTCTACAA	155	TGCATCTCTCTACAA	156	GCATCTCTCTACAA
LDLRex2(27;68;123;30)_126_d0_r	157	GCAGACCCACTTGTAGGAGATGCAT	158	CAGACCCACTTGTAGGAGATGCA	159	AGACCCACTTGTAGGAGATGC
LDLRex2(27;68;123;30)_127_d0_f	160	TGCATCTCTCTACAA	161	GCATCTCTCTACAA	162	CATCTCTCTACAA
LDLRex2(27;68;123;30)_127_d0_r	163	CGCAGACCCACTTGTAGGAGATGCA	164	GCAGACCCACTTGTAGGAGATGC	165	CAGACCCACTTGTAGGAGATG
LDLRex2(27;68;123;30)_128_d0_f	166	GCATCTCTCTACAA	167	CATCTCTCTACAA	168	ATCTCTCTCTACAA
LDLRex2(27;68;123;30)_128_d0_r	169	TCGACACCCACTTGTAGGAGATGC	170	CGCAGACCCACTTGTAGGAGATG	171	GCAGACCCACTTGTAGGAGAT
LDLRex2(27;68;123;30)_129_d0_f	172	CATCTCTCTACAA	173	ATCTCTCTCTACAA	174	TCTCTCTCTACAA
LDLRex2(27;68;123;30)_129_d0_r	175	ATCGCAGACCCACTTGTAGGAGATG	176	TCGCAGACCCACTTGTAGGAGAT	177	CGCAGACCCACTTGTAGGAGA
LDLRex2(27;68;123;30)_130_d0_f	178	ATCTCTCTACAA	179	TCTCTCTCTACAA	180	CTCTCTCTCTACAA
LDLRex2(27;68;123;30)_130_d0_r	181	CATCGCAGACCCACTTGTAGGAGAT	182	ATCGCAGACCCACTTGTAGGAGA	183	TCGCAGACCCACTTGTAGGAG
LDLRex2(27;68;123;30)_131_d0_f	184	TCTCTCTCTACAA	185	CTCTCTCTCTACAA	186	TCCTCTCTCTCTACAA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_131_d0_r	187	CCATCGCAGACCCACTTGTAGGAGA	188	CATCGCAGACCCACTTGTAGGAG	189	ATCGCAGACCCACTTGTAGGA
LDLRex2(27;68;123;30)_132_d0_f	190	CTCCTACAAAGTGGTCTGCGATGGC	191	TCCTACAAAGTGGTCTGCGATGG	192	CCTACAAAGTGGTCTGCGATG
LDLRex2(27;68;123;30)_132_d0_r	193	GCCATCGCAGACCCACTTGTAGGAG	194	CCATCGCAGACCCACTTGTAGGA	195	CATCGCAGACCCACTTGTAGG
LDLRex2(27;68;123;30)_133_d0_f	196	TCCTACAAAGTGGTCTGCGATGGCA	197	CCTACAAAGTGGTCTGCGATGGC	198	CTACAAAGTGGTCTGCGATGG
LDLRex2(27;68;123;30)_133_d0_r	199	TGCCATCGCAGACCCACTTGTAGGA	200	GCCATCGCAGACCCACTTGTAGG	201	CCATCGCAGACCCACTTGTAG
LDLRex2(27;68;123;30)_134_d0_f	202	CCTACAAAGTGGTCTGCGATGGCAG	203	CTACAAAGTGGTCTGCGATGGCA	204	TACAAAGTGGTCTGCGATGGC
LDLRex2(27;68;123;30)_134_d0_r	205	CTGCCATCGCAGACCCACTTGTAGG	206	TGCCATCGCAGACCCACTTGTAG	207	GCCATCGCAGACCCACTTGTGA
LDLRex2(27;68;123;30)_135_d0_f	208	CTACAAAGTGGTCTGCGATGGCAGC	209	TACAAAGTGGTCTGCGATGGCAG	210	ACAAGTGGTCTGCGATGGCA
LDLRex2(27;68;123;30)_135_d0_r	211	GCTGCCATCGCAGACCCACTTGTAG	212	CTGCCATCGCAGACCCACTTGTGA	213	TGCCATCGCAGACCCACTTGT
LDLRex2(27;68;123;30)_136_d0_f	214	TACAAAGTGGTCTGCGATGGCAGCG	215	ACAAGTGGTCTGCGATGGCAGC	216	CAAGTGGTCTGCGATGGCAG
LDLRex2(27;68;123;30)_136_d0_r	217	CGCTGCCATCGCAGACCCACTTGTGA	218	GCTGCCATCGCAGACCCACTTGT	219	CTGCCATCGCAGACCCACTTG
LDLRex2(27;68;123;30)_137_d0_f	220	ACAAGTGGTCTGCGATGGCAGCGC	221	CAAGTGGTCTGCGATGGCAGCG	222	AAGTGGTCTGCGATGGCAGC
LDLRex2(27;68;123;30)_137_d0_r	223	GCGTGCCATCGCAGACCCACTTGT	224	CGCTGCCATCGCAGACCCACTTG	225	GCTGCCATCGCAGACCCACTT
LDLRex2(27;68;123;30)_138_d0_f	226	CAAGTGGTCTGCGATGGCAGCGCT	227	AAGTGGTCTGCGATGGCAGCGC	228	AGTGGTCTGCGATGGCAGCG
LDLRex2(27;68;123;30)_138_d0_r	229	AGCGCTGCCATCGCAGACCCACTTG	230	GCGCTGCCATCGCAGACCCACTT	231	CGCTGCCATCGCAGACCCACT
LDLRex2(27;68;123;30)_139_d0_f	232	AAGTGGTCTGCGATGGCAGCGCTG	233	AGTGGTCTGCGATGGCAGCGCT	234	GTGGTCTGCGATGGCAGCGC
LDLRex2(27;68;123;30)_139_d0_r	235	CAGCGTGCCATCGCAGACCCACTT	236	AGCGTGCCATCGCAGACCCACT	237	GCGTGCCATCGCAGACCCAC
LDLRex2(27;68;123;30)_140_d0_f	238	AGTGGTCTGCGATGGCAGCGCTGA	239	GTGGTCTGCGATGGCAGCGCTG	240	TGGTCTGCGATGGCAGCGCT
LDLRex2(27;68;123;30)_140_d0_r	241	TCAGCGCTGCCATCGCAGACCCACT	242	CAGCGCTGCCATCGCAGACCCAC	243	AGCGTGCCATCGCAGACCCCA
LDLRex2(27;68;123;30)_141_d0_f	244	GTGGGTCTGCGATGGCAGCGCTGAG	245	TGGGTCTGCGATGGCAGCGCTGA	246	GGGTCTGCGATGGCAGCGCTG
LDLRex2(27;68;123;30)_141_d0_r	247	CTCAGCGCTGCCATCGCAGACCCAC	248	TCAGCGCTGCCATCGCAGACCCA	249	CAGCGCTGCCATCGCAGACCC
LDLRex2(27;68;123;30)_142_d0_f	250	TGGGTCTGCGATGGCAGCGCTGAGT	251	GGGTCTGCGATGGCAGCGCTGAG	252	GGTCTGCGATGGCAGCGCTGA
LDLRex2(27;68;123;30)_142_d0_r	253	ACTCAGCGCTGCCATCGCAGACCCA	254	CTCAGCGCTGCCATCGCAGACCC	255	TCAGCGCTGCCATCGCAGACC
LDLRex2(27;68;123;30)_143_d0_f	256	GGGTCTGCGATGGCAGCGCTGAGTG	257	GGTCTGCGATGGCAGCGCTGAGT	258	GTCTGCGATGGCAGCGCTGAG
LDLRex2(27;68;123;30)_143_d0_r	259	CACCTCAGCGCTGCCATCGCAGACCC	260	ACTCAGCGCTGCCATCGCAGACC	261	CTCAGCGCTGCCATCGCAGAC
LDLRex2(27;68;123;30)_144_d0_f	262	GGTCTGCGATGGCAGCGCTGAGTGC	263	GTCTGCGATGGCAGCGCTGAGTG	264	TCTGCGATGGCAGCGCTGAGT
LDLRex2(27;68;123;30)_144_d0_r	265	GCACTCAGCGCTGCCATCGCAGACC	266	CACCTCAGCGCTGCCATCGCAGAC	267	ACTCAGCGCTGCCATCGCAGGA
LDLRex2(27;68;123;30)_145_d0_f	268	GTCTGCGATGGCAGCGCTGAGTGCC	269	TCTGCGATGGCAGCGCTGAGTGC	270	CTGCGATGGCAGCGCTGAGTG
LDLRex2(27;68;123;30)_145_d0_r	271	GGCACTCAGCGCTGCCATCGCAGAC	272	GCACTCAGCGCTGCCATCGCAGGA	273	CACTCAGCGCTGCCATCGCAG
LDLRex2(27;68;123;30)_146_d0_f	274	TCTGCGATGGCAGCGCTGAGTGCCA	275	CTGCGATGGCAGCGCTGAGTGCC	276	TGCGATGGCAGCGCTGAGTGC
LDLRex2(27;68;123;30)_146_d0_r	277	TGGCACTCAGCGCTGCCATCGCAGGA	278	GGCACTCAGCGCTGCCATCGCAG	279	GCACTCAGCGCTGCCATCGCA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_147_d0_f	280	CTGCGATGGCAGCGCTGAGTGCCAG	281	TGCGATGGCAGCGCTGAGTGCCA	282	GGATGGCAGCGCTGAGTGCC
LDLRex2(27;68;123;30)_147_d0_r	283	CTGGCACTACGCGCTGCCATCGAG	284	TGGCACTACGCGCTGCCATCGCA	285	GGCACTACGCGCTGCCATCGC
LDLRex2(27;68;123;30)_148_d0_f	286	TGCGATGGCAGCGCTGAGTGCCAGG	287	GCGATGGCAGCGCTGAGTGCCAG	288	CGATGGCAGCGCTGAGTGCCA
LDLRex2(27;68;123;30)_148_d0_r	289	CCTGGCACTACGCGCTGCCATCGCA	290	CTGGCACTACGCGCTGCCATCGC	291	TGGCACTACGCGCTGCCATCG
LDLRex2(27;68;123;30)_149_d0_f	292	GCGATGGCAGCGCTGAGTGCCAGGA	293	CGATGGCAGCGCTGAGTGCCAGG	294	GATGGCAGCGCTGAGTGCCAG
LDLRex2(27;68;123;30)_149_d0_r	295	TCCTGGCACTACGCGCTGCCATCGC	296	CCTGGCACTACGCGCTGCCATCG	297	CTGGCACTACGCGCTGCCATC
LDLRex2(27;68;123;30)_150_d0_f	298	CGATGGCAGCGCTGAGTGCCAGGAT	299	GATGGCAGCGCTGAGTGCCAGGA	300	ATGGCAGCGCTGAGTGCCAGG
LDLRex2(27;68;123;30)_150_d0_r	301	ATCCTGGCACTACGCGCTGCCATCG	302	TCCTGGCACTACGCGCTGCCATC	303	CCTGGCACTACGCGCTGCCAT
LDLRex2(27;68;123;30)_151_d0_f	304	GATGGCAGCGCTGAGTGCCAGGATG	305	ATGGCAGCGCTGAGTGCCAGGAT	306	TGGCAGCGCTGAGTGCCAGGA
LDLRex2(27;68;123;30)_151_d0_r	307	CATCTGGCACTACGCGCTGCCATC	308	ATCCTGGCACTACGCGCTGCCAT	309	TCCTGGCACTACGCGCTGCCA
LDLRex2(27;68;123;30)_152_d0_f	310	ATGGCAGCGCTGAGTGCCAGGATGG	311	TGGCAGCGCTGAGTGCCAGGATG	312	GGCAGCGCTGAGTGCCAGGAT
LDLRex2(27;68;123;30)_152_d0_r	313	CCATCTGGCACTACGCGCTGCCAT	314	CATCTGGCACTACGCGCTGCCA	315	ATCTGGCACTACGCGCTGCC
LDLRex2(27;68;123;30)_153_d0_f	316	TGGCAGCGCTGAGTGCCAGGATGGC	317	GGCAGCGCTGAGTGCCAGGATGG	318	GCAGCGCTGAGTGCCAGGATG
LDLRex2(27;68;123;30)_153_d0_r	319	GCCATCTGGCACTACGCGCTGCCA	320	CCATCTGGCACTACGCGCTGCC	321	CATCTGGCACTACGCGCTGC
LDLRex2(27;68;123;30)_154_d0_f	322	GGCAGCGCTGAGTGCCAGGATGGCT	323	GCAGCGCTGAGTGCCAGGATGGC	324	CAGCGCTGAGTGCCAGGATGG
LDLRex2(27;68;123;30)_154_d0_r	325	AGCCATCTGGCACTACGCGCTGCC	326	GCCATCTGGCACTACGCGCTGC	327	CCATCTGGCACTACGCGCTG
LDLRex2(27;68;123;30)_155_d0_f	328	GCAGCGCTGAGTGCCAGGATGGCTC	329	CAGCGCTGAGTGCCAGGATGGCT	330	AGCGCTGAGTGCCAGGATGGC
LDLRex2(27;68;123;30)_155_d0_r	331	GAGCCATCTGGCACTACGCGCTGC	332	AGCCATCTGGCACTACGCGCTG	333	GCCATCTGGCACTACGCGCT
LDLRex2(27;68;123;30)_156_d0_f	334	CAGCGCTGAGTGCCAGGATGGCTCT	335	AGCGCTGAGTGCCAGGATGGCTC	336	GCGCTGAGTGCCAGGATGGCT
LDLRex2(27;68;123;30)_156_d0_r	337	AGAGCCATCTGGCACTACGCGCTG	338	GAGCCATCTGGCACTACGCGCT	339	AGCCATCTGGCACTACGCGC
LDLRex2(27;68;123;30)_157_d0_f	340	AGCGCTGAGTGCCAGGATGGCTCTG	341	GCGCTGAGTGCCAGGATGGCTCT	342	CGCTGAGTGCCAGGATGGCTC
LDLRex2(27;68;123;30)_157_d0_r	343	CAGAGCCATCTGGCACTACGCGCT	344	AGAGCCATCTGGCACTACGCGC	345	GAGCCATCTGGCACTACGCG
LDLRex2(27;68;123;30)_158_d0_f	346	GCGCTGAGTGCCAGGATGGCTCTGA	347	CGCTGAGTGCCAGGATGGCTCTG	348	GCTGAGTGCCAGGATGGCTCT
LDLRex2(27;68;123;30)_158_d0_r	349	TCAGAGCCATCTGGCACTACGCGC	350	CAGAGCCATCTGGCACTACGCG	351	AGAGCCATCTGGCACTACAGC
LDLRex2(27;68;123;30)_159_d0_f	352	CGCTGAGTGCCAGGATGGCTCTGAT	353	GCTGAGTGCCAGGATGGCTCTGA	354	CTGAGTGCCAGGATGGCTCTG
LDLRex2(27;68;123;30)_159_d0_r	355	ATCAGAGCCATCTGGCACTACGCG	356	TCAGAGCCATCTGGCACTACAGC	357	CAGAGCCATCTGGCACTACAG
LDLRex2(27;68;123;30)_160_d0_f	358	GCTGAGTGCCAGGATGGCTCTGATG	359	CTGAGTGCCAGGATGGCTCTGAT	360	TGAGTGCCAGGATGGCTCTGA
LDLRex2(27;68;123;30)_160_d0_r	361	CATCAGAGCCATCTGGCACTACAGC	362	ATCAGAGCCATCTGGCACTCAG	363	TCAGAGCCATCTGGCACTCA
LDLRex2(27;68;123;30)_161_d0_f	364	CTGAGTGCCAGGATGGCTCTGATGA	365	TGAGTGCCAGGATGGCTCTGATG	366	GAGTGCCAGGATGGCTCTGAT
LDLRex2(27;68;123;30)_161_d0_r	367	TCATCAGAGCCATCTGGCACTCAG	368	CATCAGAGCCATCTGGCACTCA	369	ATCAGAGCCATCTGGCACTC
LDLRex2(27;68;123;30)_162_d0_f	370	TGAGTGCCAGGATGGCTCTGATGAG	371	GAGTGCCAGGATGGCTCTGATGA	372	AGTGCCAGGATGGCTCTGATG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_162_d0_r	373	CTCATCAGAGCCATCCTGGCACTCA	374	TCATCAGAGCCATCCTGGCACTC	375	CATCAGAGCCATCCTGGCACT
LDLRex2(27;68;123;30)_163_d0_f	376	GAGTGCCAGGATGGCTCTGATGAGT	377	AGTGCCAGGATGGCTCTGATGAG	378	GTGCCAGGATGGCTCTGATGA
LDLRex2(27;68;123;30)_163_d0_r	379	ACTCATCAGAGCCATCCTGGCACTC	380	CTCATCAGAGCCATCCTGGCACT	381	TCATCAGAGCCATCCTGGCAC
LDLRex2(27;68;123;30)_164_d0_f	382	AGTGCCAGGATGGCTCTGATGATC	383	GTGCCAGGATGGCTCTGATGAGT	384	TGCCAGGATGGCTCTGATGAG
LDLRex2(27;68;123;30)_164_d0_r	385	GACTCATCAGAGCCATCCTGGCACT	386	ACTCATCAGAGCCATCCTGGCAC	387	CTCATCAGAGCCATCCTGGCA
LDLRex2(27;68;123;30)_165_d0_f	388	GTGCCAGGATGGCTCTGATGATGCC	389	TGCCAGGATGGCTCTGATGATGC	390	GCCAGGATGGCTCTGATGAGT
LDLRex2(27;68;123;30)_165_d0_r	391	GGACTCATCAGAGCCATCCTGGCAC	392	GACTCATCAGAGCCATCCTGGCA	393	ACTCATCAGAGCCATCCTGGC
LDLRex2(27;68;123;30)_166_d0_f	394	TGCCAGGATGGCTCTGATGATCCC	395	GCCAGGATGGCTCTGATGATCC	396	CCAGGATGGCTCTGATGATGC
LDLRex2(27;68;123;30)_166_d0_r	397	GGGACTCATCAGAGCCATCCTGGCA	398	GGACTCATCAGAGCCATCCTGGC	399	GACTCATCAGAGCCATCCTGG
LDLRex2(27;68;123;30)_167_d0_f	400	GCCAGGATGGCTCTGATGATCCCA	401	CCAGGATGGCTCTGATGATCCC	402	CAGGATGGCTCTGATGATGCC
LDLRex2(27;68;123;30)_167_d0_r	403	TGGGACTCATCAGAGCCATCCTGGC	404	GGGACTCATCAGAGCCATCCTGG	405	GGACTCATCAGAGCCATCCTG
LDLRex2(27;68;123;30)_168_d0_f	406	CCAGGATGGCTCTGATGATCCAG	407	CAGGATGGCTCTGATGATCCCA	408	AGGATGGCTCTGATGATCCC
LDLRex2(27;68;123;30)_168_d0_r	409	CTGGGACTCATCAGAGCCATCCTGG	410	TGGGACTCATCAGAGCCATCCTG	411	GGGACTCATCAGAGCCATCCT
LDLRex2(27;68;123;30)_169_d0_f	412	CAGGATGGCTCTGATGATCCCAAG	413	AGGATGGCTCTGATGATCCCA	414	GGATGGCTCTGATGATCCCA
LDLRex2(27;68;123;30)_169_d0_r	415	CCTGGGACTCATCAGAGCCATCCTG	416	CTGGGACTCATCAGAGCCATCCT	417	TGGGACTCATCAGAGCCATCC
LDLRex2(27;68;123;30)_170_d0_f	418	AGGATGGCTCTGATGATCCCAAG	419	GGATGGCTCTGATGATCCCA	420	GATGGCTCTGATGATCCCA
LDLRex2(27;68;123;30)_170_d0_r	421	TCCTGGGACTCATCAGAGCCATCCT	422	CCTGGGACTCATCAGAGCCATCC	423	CTGGGACTCATCAGAGCCATC
LDLRex2(27;68;123;30)_171_d0_f	424	GGATGGCTCTGATGATCCCAAG	425	GATGGCTCTGATGATCCCA	426	ATGGCTCTGATGATCCCA
LDLRex2(27;68;123;30)_171_d0_r	427	CTCCTGGGACTCATCAGAGCCATCC	428	TCCTGGGACTCATCAGAGCCATC	429	CCTGGGACTCATCAGAGCCAT
LDLRex2(27;68;123;30)_172_d0_f	430	GATGGCTCTGATGATCCCAAG	431	ATGGCTCTGATGATCCCA	432	TGGCTCTGATGATCCCA
LDLRex2(27;68;123;30)_172_d0_r	433	TCTCCTGGGACTCATCAGAGCCATC	434	CTCCTGGGACTCATCAGAGCCAT	435	TCCTGGGACTCATCAGAGCCA
LDLRex2(27;68;123;30)_173_d0_f	436	ATGGCTCTGATGATCCCAAG	437	TGGCTCTGATGATCCCA	438	GGCTCTGATGATCCCA
LDLRex2(27;68;123;30)_173_d0_r	439	GTCTCCTGGGACTCATCAGAGCCAT	440	TCTCCTGGGACTCATCAGAGCCA	441	CTCCTGGGACTCATCAGAGCC
LDLRex2(27;68;123;30)_174_d0_f	442	TGGCTCTGATGATCCCAAG	443	GGCTCTGATGATCCCA	444	GCTCTGATGATCCCA
LDLRex2(27;68;123;30)_174_d0_r	445	CGTCTCCTGGGACTCATCAGAGCCA	446	GTCTCCTGGGACTCATCAGAGCC	447	TCTCCTGGGACTCATCAGAGC
LDLRex2(27;68;123;30)_175_d0_f	448	GGCTCTGATGATCCCAAG	449	GCTCTGATGATCCCA	450	CTCTGATGATCCCA
LDLRex2(27;68;123;30)_175_d0_r	451	ACGTCTCCTGGGACTCATCAGAGCC	452	CGTCTCCTGGGACTCATCAGAGC	453	GTCTCCTGGGACTCATCAGAG
LDLRex2(27;68;123;30)_176_d0_f	454	GCTCTGATGATCCCAAG	455	CTCTGATGATCCCA	456	TCTGATGATCCCA
LDLRex2(27;68;123;30)_176_d0_r	457	CACGTCTCCTGGGACTCATCAGAGC	458	ACGTCTCCTGGGACTCATCAGAG	459	CGTCTCCTGGGACTCATCAGAG
LDLRex2(27;68;123;30)_177_d0_f	460	CTCTGATGATCCCAAG	461	TCTGATGATCCCA	462	CTGATGATCCCA
LDLRex2(27;68;123;30)_177_d0_r	463	GCACGTCTCCTGGGACTCATCAGAG	464	CACGTCTCCTGGGACTCATCAGAG	465	ACGTCTCCTGGGACTCATCAGAG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_178_d0_f	466	TCTGATGATCCAGGAGACGTGCT	467	CTGATGATGCCAGGAGACGTGC	468	TGATGATCCAGGAGACGTG
LDLRex2(27;68;123;30)_178_d0_r	469	AGCACGTCTCTGGACTCATCAGA	470	GCACGTCTCTGGACTCATCAG	471	CACGTCTCTGGACTCATCA
LDLRex2(27;68;123;30)_179_d0_f	472	CTGATGATCCAGGAGACGTGCTG	473	TGATGATCCAGGAGACGTGCT	474	GATGATCCAGGAGACGTGC
LDLRex2(27;68;123;30)_179_d0_r	475	CAGCAGTCTCTGGACTCATCAG	476	AGCAGTCTCTGGACTCATCA	477	GCAGTCTCTGGACTCATC
LDLRex2(27;68;123;30)_180_d0_f	478	TGATGATCCAGGAGACGTGCTGT	479	GATGATCCAGGAGACGTGCTG	480	ATGATCCAGGAGACGTGCT
LDLRex2(27;68;123;30)_180_d0_r	481	ACAGCAGTCTCTGGACTCATCA	482	CAGCAGTCTCTGGACTCATC	483	AGCAGTCTCTGGACTCAT
LDLRex2(27;68;123;30)_181_d0_f	484	GATGATCCAGGAGACGTGCTGTG	485	ATGATCCAGGAGACGTGCTGT	486	TGATCCAGGAGACGTGCTG
LDLRex2(27;68;123;30)_181_d0_r	487	CACAGCAGTCTCTGGACTCATC	488	ACAGCAGTCTCTGGACTCAT	489	CAGCAGTCTCTGGACTCA
LDLRex2(27;68;123;30)_182_d0_f	490	ATGATCCAGGAGACGTGCTGTGA	491	TGATCCAGGAGACGTGCTGTG	492	GATCCAGGAGACGTGCTGT
LDLRex2(27;68;123;30)_182_d0_r	493	TCACAGCAGTCTCTGGACTCAT	494	CACAGCAGTCTCTGGACTCA	495	ACAGCAGTCTCTGGACTC
LDLRex2(27;68;123;30)_183_d0_f	496	TGATCCAGGAGACGTGCTGTGAG	497	GAGTCCAGGAGACGTGCTGA	498	AGTCCAGGAGACGTGCTGTG
LDLRex2(27;68;123;30)_183_d0_r	499	CTCAGCAGTCTCTGGACTCA	500	TCACAGCAGTCTCTGGACTC	501	CACAGCAGTCTCTGGACT
LDLRex2(27;68;123;30)_184_d0_f	502	GAGTCCAGGAGACGTGCTGTGAGT	503	AGTCCAGGAGACGTGCTGTGAG	504	GTCCAGGAGACGTGCTGTGA
LDLRex2(27;68;123;30)_184_d0_r	505	ACTCAGCAGTCTCTGGACTC	506	CTCAGCAGTCTCTGGACT	507	TCACAGCAGTCTCTGGGAC
LDLRex2(27;68;123;30)_185_d0_f	508	AGTCCAGGAGACGTGCTGTGATC	509	GTCCAGGAGACGTGCTGTGAGT	510	TCCAGGAGACGTGCTGTGAG
LDLRex2(27;68;123;30)_185_d0_r	511	GACTCAGCAGTCTCTGGACT	512	ACTCAGCAGTCTCTGGGAC	513	CTCAGCAGTCTCTCTGGGA
LDLRex2(27;68;123;30)_186_d0_f	514	GTCCAGGAGACGTGCTGTGATCC	515	TCCAGGAGACGTGCTGTGATC	516	CCCAGGAGACGTGCTGTGAGT
LDLRex2(27;68;123;30)_186_d0_r	517	GGACTCAGCAGTCTCTGGGAC	518	GACTCAGCAGTCTCTGGGA	519	ACTCAGCAGTCTCTCTGGG
LDLRex2(27;68;123;30)_187_d0_f	520	TCCAGGAGACGTGCTGTGATCCC	521	CCAGGAGACGTGCTGTGATCC	522	CCAGGAGACGTGCTGTGAGTC
LDLRex2(27;68;123;30)_187_d0_r	523	GGGACTCAGCAGTCTCTGGGA	524	GGACTCAGCAGTCTCTGGG	525	GACTCAGCAGTCTCTCTGG
LDLRex2(27;68;123;30)_188_d0_f	526	CCCAGGAGACGTGCTGTGATCCCC	527	CCAGGAGACGTGCTGTGATCCC	528	CAGGAGACGTGCTGTGAGTCC
LDLRex2(27;68;123;30)_188_d0_r	529	GGGGACTCAGCAGTCTCTGGG	530	GGGACTCAGCAGTCTCTGG	531	GGACTCAGCAGTCTCTCTG
LDLRex2(27;68;123;30)_189_d0_f	532	CCAGGAGACGTGCTGTGATCCCCCT	533	CAGGAGACGTGCTGTGATCCCC	534	AGGAGACGTGCTGTGATCCC
LDLRex2(27;68;123;30)_189_d0_r	535	AGGGACTCAGCAGTCTCTGG	536	GGGACTCAGCAGTCTCTCTG	537	GGGACTCAGCAGTCTCTCT
LDLRex2(27;68;123;30)_190 + 1_d0_f	538	AGGAGACGTGCTGTGATCCCCCTT	539	GGAGACGTGCTGTGATCCCCCT	540	GAGACGTGCTGTGATCCCCCT
LDLRex2(27;68;123;30)_190 + 1_d0_r	541	AAAGGGGACTCAGCAGTCTCTCT	542	AAGGGGACTCAGCAGTCTCTCC	543	AGGGGACTCAGCAGTCTCTC
LDLRex2(27;68;123;30)_190 + 10_d0_544	544	GCTGTGAGTCCCCCTTTGGGCATGAT	545	CTGTGAGTCCCCCTTTGGGCATGA	546	TGTGAGTCCCCCTTTGGGCATG
LDLRex2(27;68;123;30)_190 + 10_d0_547	547	ATCATGCCCAAGGGGACTCACAGC	548	TCATGCCCAAGGGGACTCACAG	549	CATGCCCAAGGGGACTCACCA
LDLRex2(27;68;123;30)_190 + 11_d0_550	550	CTGTGATCCCCCTTTGGGCATGATA	551	TGTGAGTCCCCCTTTGGGCATGAT	552	GTGATCCCCCTTTGGGCATGA
LDLRex2(27;68;123;30)_190 + 11_d0_553	553	TATCATGCCCAAGGGGACTCACAG	554	ATCATGCCCAAGGGGACTCACCA	555	TCATGCCCAAGGGGACTCAC
LDLRex2(27;68;123;30)_190 + 12_d0_556	556	TGTGATCCCCCTTTGGGCATGATAT	557	GTGAGTCCCCCTTTGGGCATGATA	558	TGAGTCCCCCTTTGGGCATGAT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_190 + 12_d0_559		ATATCATGCCAAAGGGGACTCACA	560	TATCATGCCAAAGGGGACTCAC	561	ATCATGCCAAAGGGGACTCA
LDLRex2(27;68;123;30)_190 + 13_d0_562		GTGAGTCCCTTTGGGCATGATATG	563	TGAGTCCCTTTGGGCATGATAT	564	GAGTCCCTTTGGGCATGATA
LDLRex2(27;68;123;30)_190 + 13_d0_565		CATATCATGCCAAAGGGGACTCAC	566	ATATCATGCCAAAGGGGACTCA	567	TATCATGCCAAAGGGGACTC
LDLRex2(27;68;123;30)_190 + 14_d0_568		TGAGTCCCTTTGGGCATGATATGC	569	GAGTCCCTTTGGGCATGATATG	570	AGTCCCTTTGGGCATGATAT
LDLRex2(27;68;123;30)_190 + 14_d0_571		GCATATCATGCCAAAGGGGACTCA	572	CATATCATGCCAAAGGGGACTC	573	ATATCATGCCAAAGGGGACT
LDLRex2(27;68;123;30)_190 + 15_d0_574		GAGTCCCTTTGGGCATGATATGCA	575	AGTCCCTTTGGGCATGATATGC	576	GTCCCTTTGGGCATGATATG
LDLRex2(27;68;123;30)_190 + 15_d0_577		TGCATATCATGCCAAAGGGGACTC	578	GCATATCATGCCAAAGGGGACT	579	CATATCATGCCAAAGGGGAC
LDLRex2(27;68;123;30)_190 + 2_d0_f 580		GGAGACGTGCTGTGAGTCCCTTTG	581	GAGACGTGCTGTGAGTCCCTTT	582	AGACGTGCTGTGAGTCCCTT
LDLRex2(27;68;123;30)_190 + 2_d0_r 583		CAAAGGGGACTCACAGCAGTCTCC	584	AAAGGGGACTCACAGCAGTCTC	585	AAGGGGACTCACAGCAGTCT
LDLRex2(27;68;123;30)_190 + 3_d0_f 586		GAGACGTGCTGTGAGTCCCTTTGG	587	AGACGTGCTGTGAGTCCCTTTG	588	GACGTGCTGTGAGTCCCTTT
LDLRex2(27;68;123;30)_190 + 3_d0_r 589		CCAAAGGGGACTCACAGCAGTCTC	590	CAAGGGGACTCACAGCAGTCT	591	AAAGGGGACTCACAGCAGTCT
LDLRex2(27;68;123;30)_190 + 4_d0_f 592		AGACGTGCTGTGAGTCCCTTTGGG	593	GACGTGCTGTGAGTCCCTTTGG	594	ACGTGCTGTGAGTCCCTTTG
LDLRex2(27;68;123;30)_190 + 4_d0_r 595		CCAAAGGGGACTCACAGCAGTCT	596	CCAAAGGGGACTCACAGCAGTCT	597	CAAGGGGACTCACAGCAGT
LDLRex2(27;68;123;30)_190 + 5_d0_f 598		GACGTGCTGTGAGTCCCTTTGGG	599	ACGTGCTGTGAGTCCCTTTGGG	600	CGTGTGTGAGTCCCTTTGG
LDLRex2(27;68;123;30)_190 + 5_d0_r 601		GCCCAAGGGGACTCACAGCAGTCT	602	CCCAAGGGGACTCACAGCAGT	603	CCAAAGGGGACTCACAGCAG
LDLRex2(27;68;123;30)_190 + 6_d0_f 604		ACGTGCTGTGAGTCCCTTTGGGCA	605	CGTGTGTGAGTCCCTTTGGGC	606	GTGTGTGAGTCCCTTTGGG
LDLRex2(27;68;123;30)_190 + 6_d0_r 607		TGCCAAAGGGGACTCACAGCAGT	608	GCCAAAGGGGACTCACAGCAG	609	CCCAAGGGGACTCACAGCAC
LDLRex2(27;68;123;30)_190 + 7_d0_f 610		CGTGTGTGAGTCCCTTTGGGCAT	611	GTGTGTGAGTCCCTTTGGGCA	612	TGCTGTGAGTCCCTTTGGGC
LDLRex2(27;68;123;30)_190 + 7_d0_r 613		ATGCCAAAGGGGACTCACAGCAG	614	TGCCAAAGGGGACTCACAGCAC	615	GCCCAAGGGGACTCACAGCA
LDLRex2(27;68;123;30)_190 + 8_d0_f 616		GTGTGTGAGTCCCTTTGGGCATG	617	TGTGTGTGAGTCCCTTTGGGCAT	618	GCTGTGAGTCCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 8_d0_r 619		CATGCCCAAGGGGACTCACAGCAC	620	ATGCCCAAGGGGACTCACAGCA	621	TGCCCAAGGGGACTCACAGC
LDLRex2(27;68;123;30)_190 + 9_d0_f 622		TGTGTGAGTCCCTTTGGGCATGA	623	GCTGTGAGTCCCTTTGGGCATG	624	CTGTGAGTCCCTTTGGGCAT
LDLRex2(27;68;123;30)_190 + 9_d0_r 625		TCATGCCCAAGGGGACTCACAGCA	626	CATGCCCAAGGGGACTCACAGC	627	ATGCCCAAGGGGACTCACAG
LDLRex2(27;68;123;30)_190_d0_f 628		CAGGAGACGTGCTGTGAGTCCCTT	629	AGGAGACGTGCTGTGAGTCCCT	630	GGAGACGTGCTGTGAGTCCCC
LDLRex2(27;68;123;30)_190_d0_r 631		AAGGGGACTCACAGCAGTCTCTCTG	632	AGGGGACTCACAGCAGTCTCT	633	GGGACTCACAGCAGTCTCC
LDLRex2(27;68;123;30)_68 - 1_d0_f 634		TCCTCTCTCTCAGTGGCGACAGAT	635	CCTCTCTCTCAGTGGCGACAGA	636	CTCTCTCTCAGTGGCGACAG
LDLRex2(27;68;123;30)_68 - 1_d0_r 637		ATCTGTGCCCACTGAGAGAGAGGA	638	TCTGTGCCCACTGAGAGAGAGG	639	CTGTGCCCACTGAGAGAGAG
LDLRex2(27;68;123;30)_68 - 10_d0_f 640		TTCTCTTTTCTCTCTCTCAGTGG	641	TCTCTTTTCTCTCTCTCAGTG	642	CTCCTTTTCTCTCTCTCAGT
LDLRex2(27;68;123;30)_68 - 10_d0_r 643		CCACTGAGAGAGAGAGAGAGAGAA	644	CACTGAGAGAGAGAGAGAGAGA	645	ACTGAGAGAGAGAGAGAGAG
LDLRex2(27;68;123;30)_68 - 11_d0_f 646		TTTCTCTTTTCTCTCTCTCAGTG	647	TTCTCTTTTCTCTCTCTCAGT	648	TCTCTTTTCTCTCTCTCAG
LDLRex2(27;68;123;30)_68 - 11_d0_r 649		CACTGAGAGAGAGAGAGAGAGAA	650	ACTGAGAGAGAGAGAGAGAGAA	651	CTGAGAGAGAGAGAGAGAGAA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_68 - 12_d0_f 652	652	CTTTCTCCTTTTCTCTCTCTCTCAGT	653	TTTCTCCTTTTCTCTCTCTCTCAG	654	TTCTCCTTTTCTCTCTCTCTCA
LDLRex2(27;68;123;30)_68 - 12_d0_r 655	655	ACTGAGAGAGAGGAAAGGAGAGAAAG	656	CTGAGAGAGAGGAAAGGAGAGAA	657	TGAGAGAGAGGAAAGGAGAGAA
LDLRex2(27;68;123;30)_68 - 13_d0_f 658	658	CCTTTCTCCTTTTCTCTCTCTCTCAG	659	CCTTCTCCTTTTCTCTCTCTCTCA	660	TTTCTCCTTTTCTCTCTCTCTC
LDLRex2(27;68;123;30)_68 - 13_d0_r 661	661	CTGAGAGAGAGGAAAGGAGAGAAAG	662	TGAGAGAGAGGAAAGGAGAGAAAG	663	GAGAGAGAGGAAAGGAGAGAA
LDLRex2(27;68;123;30)_68 - 14_d0_f 664	664	CCCTTTCTCCTTTTCTCTCTCTCTCA	665	CCTTCTCCTTTTCTCTCTCTCTC	666	CTTTCTCCTTTTCTCTCTCTCT
LDLRex2(27;68;123;30)_68 - 14_d0_r 667	667	TGAGAGAGAGGAAAGGAGAGAAAGG	668	GAGAGAGAGGAAAGGAGAGAAAGG	669	AGAGAGAGGAAAGGAGAGAAAG
LDLRex2(27;68;123;30)_68 - 15_d0_f 670	670	ACCCTTTCTCCTTTTCTCTCTCTCTC	671	CCCTTTCTCCTTTTCTCTCTCTCT	672	CTTTCTCCTTTTCTCTCTCTC
LDLRex2(27;68;123;30)_68 - 15_d0_r 673	673	GAGAGAGAGGAAAGGAGAGAAAGG	674	AGAGAGAGGAAAGGAGAGAAAGG	675	GAGAGAGGAAAGGAGAGAAAGG
LDLRex2(27;68;123;30)_68 - 2_d0_f 676	676	TTCTCTCTCTCTCAGTGGCGACAGA	677	TCCTCTCTCTCAGTGGCGACAG	678	CCTCTCTCTCAGTGGCGGACA
LDLRex2(27;68;123;30)_68 - 2_d0_r 679	679	TCTGTGCCCCACTGAGAGAGAGGAA	680	CTGTGCCCCACTGAGAGAGAGGA	681	TGTGCCCCACTGAGAGAGAGG
LDLRex2(27;68;123;30)_68 - 3_d0_f 682	682	TTTCTCTCTCTCTCAGTGGCGACAG	683	TTCTCTCTCTCTCAGTGGCGGACA	684	TCCTCTCTCTCAGTGGCGGAC
LDLRex2(27;68;123;30)_68 - 3_d0_r 685	685	CTGTGCCCCACTGAGAGAGAGGAAA	686	TGTGCCCCACTGAGAGAGAGGAA	687	GTCGCCCACTGAGAGAGAGGA
LDLRex2(27;68;123;30)_68 - 4_d0_f 688	688	TTTTCTCTCTCTCTCAGTGGCGGACA	689	TTCTCTCTCTCTCAGTGGCGGAC	690	TTCTCTCTCTCTCAGTGGCGGA
LDLRex2(27;68;123;30)_68 - 4_d0_r 691	691	TGTGCCCCACTGAGAGAGAGGAAAA	692	GTGCCCCACTGAGAGAGAGGAAA	693	TGCCCCACTGAGAGAGAGGAA
LDLRex2(27;68;123;30)_68 - 5_d0_f 694	694	CTTTTCTCTCTCTCTCAGTGGCGGAC	695	TTTTCTCTCTCTCAGTGGCGGA	696	TTTCTCTCTCTCAGTGGCGG
LDLRex2(27;68;123;30)_68 - 5_d0_r 697	697	GTGCCCCACTGAGAGAGAGGAAAA	698	TGCCCCACTGAGAGAGAGGAAAA	699	CGCCCCACTGAGAGAGAGGAAA
LDLRex2(27;68;123;30)_68 - 6_d0_f 700	700	CCTTTCTCTCTCTCTCAGTGGCGGA	701	CCTTCTCTCTCTCTCAGTGGCGG	702	TTTTCTCTCTCTCAGTGGGCG
LDLRex2(27;68;123;30)_68 - 6_d0_r 703	703	TGCCCCACTGAGAGAGAGGAAAAAG	704	CGCCCCACTGAGAGAGAGGAAAAAG	705	GCCCCACTGAGAGAGAGGAAAA
LDLRex2(27;68;123;30)_68 - 7_d0_f 706	706	TCCTTTTCTCTCTCTCTCAGTGGCGG	707	CTTTTCTCTCTCTCTCAGTGGCG	708	CTTTTCTCTCTCTCTCAGTGGG
LDLRex2(27;68;123;30)_68 - 7_d0_r 709	709	CGCCCCACTGAGAGAGAGGAAAAAGGA	710	GCCCCACTGAGAGAGAGGAAAAAGG	711	CCCCTGAGAGAGAGGAAAAAG
LDLRex2(27;68;123;30)_68 - 8_d0_f 712	712	CTCCTTTTCTCTCTCTCTCAGTGGCG	713	TCCTTTTCTCTCTCTCTCAGTGGG	714	CCTTTTCTCTCTCTCTCAGTGG
LDLRex2(27;68;123;30)_68 - 8_d0_r 715	715	GCCCCACTGAGAGAGAGGAAAAAGGAG	716	CCCACTGAGAGAGAGGAAAAAGGA	717	CCACTGAGAGAGAGGAAAAAGG
LDLRex2(27;68;123;30)_68 - 9_d0_f 718	718	TCTCCTTTTCTCTCTCTCTCAGTGGG	719	CTCCTTTTCTCTCTCTCTCAGTGG	720	TCCTTTTCTCTCTCTCTCAGTG
LDLRex2(27;68;123;30)_68 - 9_d0_r 721	721	CCCCTGAGAGAGAGGAAAAAGGAGA	722	CCACTGAGAGAGAGGAAAAAGGAG	723	CACTGAGAGAGAGGAAAAAGGA
LDLRex2(27;68;123;30)_68_d0_f 724	724	CCTCTCTCTCAGTGGCGGACAGATG	725	CTCTCTCTCAGTGGCGGACAGAT	726	TCTCTCTCAGTGGCGGACAGA
LDLRex2(27;68;123;30)_68_d0_r 727	727	CATCTGTGCCCCACTGAGAGAGAGG	728	ATCTGTGCCCCACTGAGAGAGAG	729	TCTGTGCCCCACTGAGAGAGA
LDLRex2(27;68;123;30)_69_d0_f 730	730	CTCTCTCTCAGTGGCGGACAGATGC	731	TCTCTCTCAGTGGCGGACAGATG	732	CTCTCTCAGTGGCGGACAGAT
LDLRex2(27;68;123;30)_69_d0_r 733	733	GCATCTGTGCCCCACTGAGAGAGAG	734	CATCTGTGCCCCACTGAGAGAGA	735	ATCTGTGCCCCACTGAGAGAG
LDLRex2(27;68;123;30)_70_d0_f 736	736	TCTCTCTCAGTGGCGGACAGATGCG	737	CTCTCTCAGTGGCGGACAGATGC	738	TCTCTCAGTGGCGGACAGATG
LDLRex2(27;68;123;30)_70_d0_r 739	739	CGCATCTGTGCCCCACTGAGAGAGA	740	GCATCTGTGCCCCACTGAGAGAG	741	CATCTGTGCCCCACTGAGAGA
LDLRex2(27;68;123;30)_71_d0_f 742	742	CTCTCTCAGTGGCGGACAGATGCGA	743	TCTCTCAGTGGCGGACAGATGCG	744	CTCTCAGTGGCGGACAGATGC

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_71_d0_r	745	TGCGATCTGTGCGCCCACTGAGAGAG	746	CGCATCTGTGCGCCCACTGAGAGA	747	GCATCTGTGCGCCCACTGAGAG
LDLRex2(27;68;123;30)_72_d0_f	748	TCTCTAGTGGGCGACAGATGCGAA	749	CTCTAGTGGGCGACAGATGCGA	750	TCTCAGTGGGCGACAGATGCGG
LDLRex2(27;68;123;30)_72_d0_r	751	TTGCGATCTGTGCGCCCACTGAGAGA	752	TGCGATCTGTGCGCCCACTGAGAG	753	CGCATCTGTGCGCCCACTGAGA
LDLRex2(27;68;123;30)_73_d0_f	754	CTCTAGTGGGCGACAGATGCGAAA	755	TCTCAGTGGGCGACAGATGCGAA	756	CTCAGTGGGCGACAGATGCGA
LDLRex2(27;68;123;30)_73_d0_r	757	TTTTCGATCTGTGCGCCCACTGAGAG	758	TTGCGATCTGTGCGCCCACTGAGA	759	TGCGATCTGTGCGCCCACTGAG
LDLRex2(27;68;123;30)_74_d0_f	760	TCTCAGTGGGCGACAGATGCGAAAG	761	CTCAGTGGGCGACAGATGCGAAA	762	TCAGTGGGCGACAGATGCGAA
LDLRex2(27;68;123;30)_74_d0_r	763	CTTTTCGATCTGTGCGCCCACTGAGA	764	TTTCGATCTGTGCGCCCACTGAG	765	TTGCGATCTGTGCGCCCACTGA
LDLRex2(27;68;123;30)_75_d0_f	766	CTCAGTGGGCGACAGATGCGAAAGA	767	TCAGTGGGCGACAGATGCGAAAG	768	CAGTGGGCGACAGATGCGAAA
LDLRex2(27;68;123;30)_75_d0_r	769	TCTTTTCGATCTGTGCGCCCACTGAG	770	CTTTTCGATCTGTGCGCCCACTG	771	TTTCGATCTGTGCGCCCACTG
LDLRex2(27;68;123;30)_76_d0_f	772	TCAGTGGGCGACAGATGCGAAAGAA	773	CAGTGGGCGACAGATGCGAAAGA	774	AGTGGGCGACAGATGCGAAAG
LDLRex2(27;68;123;30)_76_d0_r	775	TTCTTTTCGATCTGTGCGCCCACTGA	776	TCTTTTCGATCTGTGCGCCCACTG	777	CTTTTCGATCTGTGCGCCCACT
LDLRex2(27;68;123;30)_77_d0_f	778	CAGTGGGCGACAGATGCGAAAGAAA	779	AGTGGGCGACAGATGCGAAAGAA	780	GTGGGCGACAGATGCGAAAGA
LDLRex2(27;68;123;30)_77_d0_r	781	TTTCTTTTCGATCTGTGCGCCCACTG	782	TTCTTTTCGATCTGTGCGCCCACT	783	TCTTTTCGATCTGTGCGCCAC
LDLRex2(27;68;123;30)_78_d0_f	784	AGTGGGCGACAGATGCGAAAGAAAC	785	GTGGGCGACAGATGCGAAAGAAA	786	TGGGCGACAGATGCGAAAGAA
LDLRex2(27;68;123;30)_78_d0_r	787	GTTTCTTTTCGATCTGTGCGCCCACT	788	TTTCTTTTCGATCTGTGCGCCCA	789	TTCTTTTCGATCTGTGCGCCA
LDLRex2(27;68;123;30)_79_d0_f	790	GTGGGCGACAGATGCGAAAGAAACG	791	TGGGCGACAGATGCGAAAGAAAC	792	GGGCGACAGATGCGAAAGAAA
LDLRex2(27;68;123;30)_79_d0_r	793	CGTTTCTTTTCGATCTGTGCGCCAC	794	GTTTCTTTTCGATCTGTGCGCCA	795	TTTCTTTTCGATCTGTGCGCC
LDLRex2(27;68;123;30)_80_d0_f	796	TGGGCGACAGATGCGAAAGAAACGA	797	GGGCGACAGATGCGAAAGAAACG	798	GGCGACAGATGCGAAAGAAAC
LDLRex2(27;68;123;30)_80_d0_r	799	TCGTTTCTTTTCGATCTGTGCGCCA	800	CGTTTCTTTTCGATCTGTGCGCC	801	GTTTCTTTTCGATCTGTGCGCC
LDLRex2(27;68;123;30)_81_d0_f	802	GGGCGACAGATGCGAAAGAAACGAG	803	GGCGACAGATGCGAAAGAAACGA	804	GCGACAGATGCGAAAGAAACG
LDLRex2(27;68;123;30)_81_d0_r	805	CTCGTTTCTTTTCGATCTGTGCGCC	806	TCGTTTCTTTTCGATCTGTGCGC	807	CGTTTCTTTTCGATCTGTGCGC
LDLRex2(27;68;123;30)_82_d0_f	808	GGCGACAGATGCGAAAGAAACGAGT	809	GCGACAGATGCGAAAGAAACGAG	810	CGACAGATGCGAAAGAAACGA
LDLRex2(27;68;123;30)_82_d0_r	811	ACTCGTTTCTTTTCGATCTGTGCGC	812	CTCGTTTCTTTTCGATCTGTGCGC	813	TCGTTTCTTTTCGATCTGTGCG
LDLRex2(27;68;123;30)_83_d0_f	814	GCGACAGATGCGAAAGAAACGAGTT	815	CGACAGATGCGAAAGAAACGAGT	816	GACAGATGCGAAAGAAACGAG
LDLRex2(27;68;123;30)_83_d0_r	817	AACTCGTTTCTTTTCGATCTGTGCGC	818	ACTCGTTTCTTTTCGATCTGTGCG	819	CTCGTTTCTTTTCGATCTGTGTC
LDLRex2(27;68;123;30)_84_d0_f	820	CGACAGATGCGAAAGAAACGAGTTC	821	GACAGATGCGAAAGAAACGAGTT	822	ACAGATGCGAAAGAAACGAGT
LDLRex2(27;68;123;30)_84_d0_r	823	GAACTCGTTTCTTTTCGATCTGTGCG	824	AACTCGTTTCTTTTCGATCTGTGTC	825	ACTCGTTTCTTTTCGATCTGT
LDLRex2(27;68;123;30)_85_d0_f	826	GACAGATGCGAAAGAAACGAGTTCC	827	ACAGATGCGAAAGAAACGAGTTC	828	CAGATGCGAAAGAAACGAGTT
LDLRex2(27;68;123;30)_85_d0_r	829	GGAACTCGTTTCTTTTCGATCTGTGTC	830	GAACTCGTTTCTTTTCGATCTGT	831	AACTCGTTTCTTTTCGATCTG
LDLRex2(27;68;123;30)_86_d0_f	832	ACAGATGCGAAAGAAACGAGTTCCA	833	CAGATGCGAAAGAAACGAGTTCC	834	AGATGCGAAAGAAACGAGTTCC
LDLRex2(27;68;123;30)_86_d0_r	835	TGGAACTCGTTTCTTTTCGATCTGT	836	GGAACTCGTTTCTTTTCGATCTG	837	GAACTCGTTTCTTTTCGATCT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
normal						
LDLRex2(27;68;123;30)_87_d0_f	838	CAGATGCGAAAGAAACGAGTTCAG	839	AGATGCGAAAGAAACGAGTTCAC	840	GATGCGAAAGAAACGAGTTC
LDLRex2(27;68;123;30)_87_d0_r	841	CTGGAACCTGTTCTTCGCATCTG	842	TGGAACCTGTTCTTCGCATCT	843	GGAACCTGTTCTTCGCATC
LDLRex2(27;68;123;30)_88_d0_f	844	AGATGCGAAAGAAACGAGTTCAGT	845	GATGCGAAAGAAACGAGTTCAG	846	ATGCGAAAGAAACGAGTTC
LDLRex2(27;68;123;30)_88_d0_r	847	ACTGGAACCTGTTCTTCGCATCT	848	CTGGAACCTGTTCTTCGCATC	849	TGGAACCTGTTCTTCGCAT
LDLRex2(27;68;123;30)_89_d0_f	850	GATGCGAAAGAAACGAGTTCAGTG	851	ATGCGAAAGAAACGAGTTCAGT	852	TGCGAAAGAAACGAGTTCAG
LDLRex2(27;68;123;30)_89_d0_r	853	CACCTGGAACCTGTTCTTCGCATC	854	ACTGGAACCTGTTCTTCGCAT	855	CTGGAACCTGTTCTTCGC
LDLRex2(27;68;123;30)_90_d0_f	856	ATGCGAAAGAAACGAGTTCAGTGC	857	TGCGAAAGAAACGAGTTCAGTG	858	GCGAAAGAAACGAGTTCAGT
LDLRex2(27;68;123;30)_90_d0_r	859	GCACTGGAACCTGTTCTTCGCAT	860	CACCTGGAACCTGTTCTTCGC	861	ACTGGAACCTGTTCTTCGC
LDLRex2(27;68;123;30)_91_d0_f	862	TGCGAAAGAAACGAGTTCAGTGCC	863	GCGAAAGAAACGAGTTCAGTGC	864	CGAAAGAAACGAGTTCAGTG
LDLRex2(27;68;123;30)_91_d0_r	865	GGCACTGGAACCTGTTCTTCGC	866	GCACTGGAACCTGTTCTTCGC	867	CACTGGAACCTGTTCTTCG
LDLRex2(27;68;123;30)_92_d0_f	868	GCGAAAGAAACGAGTTCAGTGCCA	869	GCGAAAGAAACGAGTTCAGTGCC	870	GAAAGAAACGAGTTCAGTG
LDLRex2(27;68;123;30)_92_d0_r	871	TGGCACTGGAACCTGTTCTTCGC	872	GCGCACTGGAACCTGTTCTTCG	873	GCACTGGAACCTGTTCTTTC
LDLRex2(27;68;123;30)_93_d0_f	874	CGAAAGAAACGAGTTCAGTGCCAA	875	GAAAGAAACGAGTTCAGTGCCA	876	AAAGAAACGAGTTCAGTGCC
LDLRex2(27;68;123;30)_93_d0_r	877	TTGGCACTGGAACCTGTTCTTCG	878	TGGCACTGGAACCTGTTCTTTC	879	GGCACTGGAACCTGTTCTT
LDLRex2(27;68;123;30)_94_d0_f	880	GAAAGAAACGAGTTCAGTGCCAA	881	AAAGAAACGAGTTCAGTGCCAA	882	AAGAAACGAGTTCAGTGCCA
LDLRex2(27;68;123;30)_94_d0_r	883	CTTGGCACTGGAACCTGTTCTTTC	884	TTGGCACTGGAACCTGTTCTT	885	TGGCACTGGAACCTGTTCTT
LDLRex2(27;68;123;30)_95_d0_f	886	AAAGAAACGAGTTCAGTGCCAA	887	AAGAAACGAGTTCAGTGCCAA	888	AGAAACGAGTTCAGTGCCAA
LDLRex2(27;68;123;30)_95_d0_r	889	TCTTGGCACTGGAACCTGTTCTT	890	CTTGGCACTGGAACCTGTTCTT	891	TTGGCACTGGAACCTGTTCT
LDLRex2(27;68;123;30)_96_d0_f	892	AAGAAACGAGTTCAGTGCCAA	893	AGAAACGAGTTCAGTGCCAA	894	GAAACGAGTTCAGTGCCAA
LDLRex2(27;68;123;30)_96_d0_r	895	GTCTTGGCACTGGAACCTGTTCTT	896	TCTTGGCACTGGAACCTGTTCT	897	CTTGGCACTGGAACCTGTTCT
LDLRex2(27;68;123;30)_97_d0_f	898	AGAAACGAGTTCAGTGCCAA	899	GAAACGAGTTCAGTGCCAA	900	AAACGAGTTCAGTGCCAA
LDLRex2(27;68;123;30)_97_d0_r	901	CGTCTTGGCACTGGAACCTGTTCT	902	GTCTTGGCACTGGAACCTGTTT	903	TCTTGGCACTGGAACCTGTTT
LDLRex2(27;68;123;30)_98_d0_f	904	GAAACGAGTTCAGTGCCAA	905	AAACGAGTTCAGTGCCAA	906	AACGAGTTCAGTGCCAA
LDLRex2(27;68;123;30)_98_d0_r	907	CCGTCTTGGCACTGGAACCTGTTT	908	CGTCTTGGCACTGGAACCTGTTT	909	GTCTTGGCACTGGAACCTGTT
LDLRex2(27;68;123;30)_99_d0_f	910	AAACGAGTTCAGTGCCAA	911	AACGAGTTCAGTGCCAA	912	ACGAGTTCAGTGCCAA
LDLRex2(27;68;123;30)_99_d0_r	913	CCGTCTTGGCACTGGAACCTGTTT	914	CCGTCTTGGCACTGGAACCTGTT	915	CGTCTTGGCACTGGAACCTGTT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_100_d1_r	916	TTCCCGTCTTGGCCTGGAACCTCGTT	917	TCCCGTCTTGGCCTGGAACCTCGT	918	CCCGTCTTGGCCTGGAACCTCG
LDLRex2(27;68;123;30)_101_d1_f	919	ACGAGTCCAGTCCAAGACGGGAAA	920	CGAGTCCAGTCCAAGACGGGAA	921	GAGTTCAGTCCAAGACGGGA
LDLRex2(27;68;123;30)_101_d1_r	922	TTTCCCGTCTTGGACTGGAACCTCGT	923	TTCCCGTCTTGGACTGGAACCTCG	924	TCCCGTCTTGGACTGGAACCTC
LDLRex2(27;68;123;30)_102_d1_f	925	CGAGTTCAGTCCAAGACGGGAAAT	926	GAGTTCAGTCCAAGACGGGAAA	927	AGTTCAGTCCAAGACGGGAA
LDLRex2(27;68;123;30)_102_d1_r	928	ATTTCCCGTCTTGCACCTGGAACCTCG	929	TTCCCGTCTTGCACCTGGAACCTC	930	TTCCCGTCTTGCACCTGGAACCT
LDLRex2(27;68;123;30)_103_d1_f	931	GAGTTCAGTCCAAGACGGGAAATG	932	AGTTCAGTCCAAGACGGGAAAT	933	GTTCCAGTCCAAGACGGGAAA
LDLRex2(27;68;123;30)_103_d1_r	934	CATTTCCCGTCTTGCACCTGGAACCTC	935	ATTTCCCGTCTTGCACCTGGAACCT	936	TTTCCCGTCTTGCACCTGGAAC
LDLRex2(27;68;123;30)_104_d1_f	937	AGTTCAGTCCAAGACGGGAAATGC	938	GTTCCAGTCCAAGACGGGAAATG	939	TTCAGTCCAAGACGGGAAAT
LDLRex2(27;68;123;30)_104_d1_r	940	GCATTTCCCGTCTTGCACCTGGAACCT	941	CATTTCCCGTCTTGCACCTGGAAC	942	ATTTCCCGTCTTGCACCTGGA
LDLRex2(27;68;123;30)_105_d1_f	943	GTTCCAGTCCAAGACGGGAAATGCA	944	TTCAGTCCAAGACGGGAAATGC	945	TCCAGTCCAAGACGGGAAATG
LDLRex2(27;68;123;30)_105_d1_r	946	TGCATTTCCCGTCTTGCACCTGGAAC	947	GCATTTCCCGTCTTGCACCTGGA	948	CATTTCCCGTCTTGCACCTGGA
LDLRex2(27;68;123;30)_106_d1_f	949	TTCAGTCCAAGACGGGAAATGCAT	950	TCCAGTCCAAGACGGGAAATGCA	951	CCAGTCCAAGACGGGAAATGC
LDLRex2(27;68;123;30)_106_d1_r	952	ATGCATTTCCCGTCTTGCACCTGGA	953	TGCATTTCCCGTCTTGCACCTGGA	954	GCATTTCCCGTCTTGCACCTGG
LDLRex2(27;68;123;30)_107_d1_f	955	TCCAGTCCAAGACGGGAAATGCATC	956	CCAGTCCAAGACGGGAAATGCAT	957	CAGTCCAAGACGGGAAATGCA
LDLRex2(27;68;123;30)_107_d1_r	958	GATGCATTTCCCGTCTTGCACCTGGA	959	ATGCATTTCCCGTCTTGCACCTGG	960	TGCATTTCCCGTCTTGCACCTG
LDLRex2(27;68;123;30)_108_d1_f	961	CCAGTCCAAGACGGGAAATGCATCT	962	CAGTCCAAGACGGGAAATGCATC	963	AGTCCAAGACGGGAAATGCAT
LDLRex2(27;68;123;30)_108_d1_r	964	AGATGCATTTCCCTCTTGGCACTGG	965	GATGCATTTCCCTCTTGGCACTG	966	ATGCATTTCCCTCTTGGCACT
LDLRex2(27;68;123;30)_109_d1_f	967	CAGTCCAAGACGGGAAATGCATCTC	968	AGTCCAAGACGGGAAATGCATCT	969	GTGCAAGACGGGAAATGCATC
LDLRex2(27;68;123;30)_109_d1_r	970	GAGATGCATTTCCCTCTTGGCACTG	971	AGATGCATTTCCCTCTTGGCACT	972	GATGCATTTCCCTCTTGGCAC
LDLRex2(27;68;123;30)_110_d1_f	973	AGTCCAAGACGGGAAATGCATCTCC	974	GTGCAAGACGGGAAATGCATCTC	975	TGCAAGACGGGAAATGCATCT
LDLRex2(27;68;123;30)_110_d1_r	976	GGAGATGCATTTCCCTCTTGGCACT	977	GAGATGCATTTCCCTCTTGGCAC	978	AGATGCATTTCCCTCTTGGCA
LDLRex2(27;68;123;30)_111_d1_f	979	GTGCAAGACGGGAAATGCATCTCT	980	TGCAAGACGGGAAATGCATCTCC	981	GCAAGACGGGAAATGCATCTC
LDLRex2(27;68;123;30)_111_d1_r	982	AGGAGATGCATTTCCCTCTTGGCAC	983	GGAGATGCATTTCCCTCTTGGCA	984	GAGATGCATTTCCCTCTTGGC
LDLRex2(27;68;123;30)_112_d1_f	985	TGCAAGACGGGAAATGCATCTCTA	986	GCAAGACGGGAAATGCATCTCT	987	CCAAGACGGGAAATGCATCTCC
LDLRex2(27;68;123;30)_112_d1_r	988	TAGAGATGCATTTCCCTCTTGGCA	989	AGGAGATGCATTTCCCTCTTGGC	990	GGAGATGCATTTCCCTCTTGG
LDLRex2(27;68;123;30)_113_d1_f	991	GCCAAGACGGGAAATGCATCTCTAC	992	CCAAGACGGGAAATGCATCTCTA	993	CAAGACGGGAAATGCATCTCT
LDLRex2(27;68;123;30)_113_d1_r	994	GTAGGAGATGCATTTCCCTCTTGGC	995	TAGGAGATGCATTTCCCTCTTGG	996	AGGAGATGCATTTCCCTCTTG
LDLRex2(27;68;123;30)_114_d1_f	997	CCAAGACGGGAAATGCATCTCTACA	998	CAAGACGGGAAATGCATCTCTAC	999	AAGACGGGAAATGCATCTCTA
LDLRex2(27;68;123;30)_114_d1_r	1000	TGTAGGAGATGCATTTCCCTCTTGG	1001	GTAGGAGATGCATTTCCCTCTTG	1002	TAGGAGATGCATTTCCCTCTT
LDLRex2(27;68;123;30)_115_d1_f	1003	CAAGACGGGAAATGCATCTCTACA	1004	AAGACGGGAAATGCATCTCTACA	1005	AGACGGGAAATGCATCTCTAC
LDLRex2(27;68;123;30)_115_d1_r	1006	TTGTAGGAGATGCTTTCCCTCTTGG	1007	TGTAGGAGATGCTTTCCCTCTT	1008	GTAGGAGATGCTTTCCCTCTT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_116_d1_f	1009	AAGCGGGAATCATCTCTCTACAAG	1010	AGCGGGAATCATCTCTCTACAAG	1011	GACGGGAATCATCTCTCTACA
LDLRex2(27;68;123;30)_116_d1_r	1012	CTTGTAGGAGATGATTTCCCGTCT	1013	TTGTAGGAGATGATTTCCCGTCT	1014	TGTAGGAGATGATTTCCCGTC
LDLRex2(27;68;123;30)_117_d1_f	1015	AGACGGGAATGATCTCTACAAGT	1016	GACGGGAATGATCTCTACAAG	1017	ACGGGAATGATCTCTCTACAA
LDLRex2(27;68;123;30)_117_d1_r	1018	ACTTGTAGGAGATCATTTCCCGTCT	1019	CTTGTAGGAGATCATTTCCCGTC	1020	TTGTAGGAGATCATTTCCCGT
LDLRex2(27;68;123;30)_118_d1_f	1021	GACGGGAATGCTCTCTACAAGTG	1022	ACGGGAATGCTCTCTACAAGT	1023	CGGGAAATGCTCTCTCTACAAG
LDLRex2(27;68;123;30)_118_d1_r	1024	CATTGTAGGAGAGCATTTCCCGTC	1025	ACTTGTAGGAGAGCATTTCCCGT	1026	CTTGTAGGAGAGCATTTCCCG
LDLRex2(27;68;123;30)_119_d1_f	1027	ACGGGAATGCACTCTCTACAAGTGG	1028	CGGGAAATGCACTCTCTACAAGTG	1029	GGGAAATGCACTCTCTACAAGT
LDLRex2(27;68;123;30)_119_d1_r	1030	CCACTTGTAGGAGTGCAATTTCCCGT	1031	CACTTGTAGGAGTGCAATTTCCCG	1032	ACTTGTAGGAGTGCAATTTCCC
LDLRex2(27;68;123;30)_120_d1_f	1033	CGGGAAATGCATTCCTACAAGTGGG	1034	GGGAAATGCATTCCTACAAGTGG	1035	GGAAATGCATTCCTACAAGTG
LDLRex2(27;68;123;30)_120_d1_r	1036	CCCACTTGTAGGAATGCATTTCCCG	1037	CCACTTGTAGGAATGCATTTCCC	1038	CACCTTGTAGGAATGCATTTCC
LDLRex2(27;68;123;30)_121_d1_f	1039	GGGAAATGCATCCCTACAAGTGGGT	1040	GGAATGCATCCCTACAAGTGGG	1041	GAAATGCATCCCTACAAGTGG
LDLRex2(27;68;123;30)_121_d1_r	1042	ACCCACTTGTAGGGATGCATTTCCC	1043	CCCACTTGTAGGGATGCATTTCC	1044	CCACTTGTAGGGATGCATTTCC
LDLRex2(27;68;123;30)_122_d1_f	1045	GGAAATGCATCTCTACAAGTGGGTC	1046	GAAATGCATCTCTACAAGTGGGT	1047	AAATGCATCTCTACAAGTGGG
LDLRex2(27;68;123;30)_122_d1_r	1048	GACCACTTGTAGAGATGCATTTCC	1049	ACCACTTGTAGAGATGCATTTTC	1050	CCCACTTGTAGAGATGCATTTT
LDLRex2(27;68;123;30)_123_d1_f	1051	GAAATGCATCTCTACAAGTGGTCT	1052	AAATGCATCTCTACAAGTGGTCT	1053	AATGCATCTCTACAAGTGGGT
LDLRex2(27;68;123;30)_123_d1_r	1054	AGACCACTTGTAGAGATGCATTTCC	1055	GACCACTTGTAGAGATGCATTT	1056	ACCACTTGTAGAGATGCATT
LDLRex2(27;68;123;30)_124_d1_f	1057	AAATGCATCTCCACAAGTGGTCTG	1058	AATGCATCTCCACAAGTGGTCT	1059	ATGCATCTCCACAAGTGGTCT
LDLRex2(27;68;123;30)_124_d1_r	1060	CAGACCACTTGTGGAGATGCATTT	1061	AGACCACTTGTGGAGATGCATT	1062	GACCACTTGTGGAGATGCAT
LDLRex2(27;68;123;30)_125_d1_f	1063	AATGCATCTCTCAAGTGGTCTGC	1064	ATGCATCTCTCAAGTGGTCTG	1065	TGCATCTCTCAAGTGGGTCT
LDLRex2(27;68;123;30)_125_d1_r	1066	GCAGACCACTTGAAGAGATGCATT	1067	CAGACCACTTGAAGAGATGCAT	1068	AGACCACTTGAAGAGATGCA
LDLRex2(27;68;123;30)_126_d1_f	1069	ATGCATCTCTCAAGTGGTCTGCG	1070	TGCATCTCTCAAGTGGTCTGC	1071	GCATCTCTCAAGTGGTCTG
LDLRex2(27;68;123;30)_126_d1_r	1072	CGCAGACCACTTTAGGAGATGCAT	1073	GCAGACCACTTTAGGAGATGCA	1074	CAGACCACTTTAGGAGATGC
LDLRex2(27;68;123;30)_127_d1_f	1075	TGCATCTCTACAGTGGTCTGCGA	1076	GCATCTCTACAGTGGTCTGCG	1077	CATCTCTACAGTGGTCTGCG
LDLRex2(27;68;123;30)_127_d1_r	1078	TGCAGACCACTTAGGAGATGCA	1079	CGCAGACCACTTAGGAGATGC	1080	GCAGACCACTTAGGAGATG
LDLRex2(27;68;123;30)_128_d1_f	1081	GCATCTCTACAGTGGTCTGCGAT	1082	CATCTCTACAGTGGTCTGCGA	1083	ATCTCTACAGTGGTCTGCG
LDLRex2(27;68;123;30)_128_d1_r	1084	ATCGCAGACCACTTAGGAGATGC	1085	TGCAGACCACTTAGGAGATG	1086	CGCAGACCACTTAGGAGAT
LDLRex2(27;68;123;30)_129_d1_f	1087	CATCTCTACAATGGGTCTGCGATG	1088	ATCTCTACAATGGGTCTGCGAT	1089	TCTCTACAATGGGTCTGCGA
LDLRex2(27;68;123;30)_129_d1_r	1090	CATCGCAGACCACTTAGGAGATG	1091	ATCGCAGACCACTTAGGAGAT	1092	TCGCAGACCACTTAGGAGAG
LDLRex2(27;68;123;30)_130_d1_f	1093	ATCTCTACAAGGGGTCTGCGATGG	1094	TCTCTACAAGGGGTCTGCGATG	1095	CTCTACAAGGGGTCTGCGAT
LDLRex2(27;68;123;30)_130_d1_r	1096	CCATCGCAGACCCCTTAGGAGAT	1097	CATCGCAGACCCCTTAGGAGAG	1098	ATCGCAGACCCCTTAGGAGG
LDLRex2(27;68;123;30)_131_d1_f	1099	TCTCTACAAGTGGTCTGCGATGGC	1100	CTCTACAAGTGGTCTGCGATGG	1101	TCCTACAAGTGGTCTGCGATG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_131_d1_r	1102	GCCATCGCAGACCACTTGTAGGAGA	1103	CCATCGCAGACCACTTGTAGGAG	1104	CATCGCAGACCACTTGTAGGA
LDLRex2(27;68;123;30)_132_d1_f	1105	CTCTACAAGTGGTCTGCGATGGCA	1106	TCCTACAAGTGGTCTGCGATGGC	1107	CCTACAAGTGGTCTGCGATGG
LDLRex2(27;68;123;30)_132_d1_r	1108	TGCCATCGCAGACCACTTGTAGGAG	1109	GCCATCGCAGACCACTTGTAGGA	1110	CCATCGCAGACCACTTGTAGG
LDLRex2(27;68;123;30)_133_d1_f	1111	TCCTACAAGTGGTCTGCGATGGCAG	1112	CCTACAAGTGGTCTGCGATGGCA	1113	CTACAAGTGGTCTGCGATGGC
LDLRex2(27;68;123;30)_133_d1_r	1114	CTGCCATCGCAGACCACTTGTAGGA	1115	TGCCATCGCAGACCACTTGTAGG	1116	GCCATCGCAGACCACTTGTAG
LDLRex2(27;68;123;30)_134_d1_f	1117	CCTACAAGTGGGCTGCGATGGCAGC	1118	CTACAAGTGGGCTGCGATGGCAG	1119	TACAAGTGGGCTGCGATGGCA
LDLRex2(27;68;123;30)_134_d1_r	1120	GCTGCCATCGCAGCCCACTTGTAGG	1121	CTGCCATCGCAGCCCACTTGTAG	1122	TGCCATCGCAGCCCACTTGT
LDLRex2(27;68;123;30)_135_d1_f	1123	CTACAAGTGGGTTGCGATGGCAGCG	1124	TACAAGTGGGTTGCGATGGCAGC	1125	ACAAGTGGGTTGCGATGGCAG
LDLRex2(27;68;123;30)_135_d1_r	1126	CGCTGCCATCGCAACCCCACTTGTAG	1127	GCTGCCATCGCAACCCCACTTGT	1128	CTGCCATCGCAACCCCACTTGT
LDLRex2(27;68;123;30)_136_d1_f	1129	TACAAGTGGTCTGCGATGGCAGCGC	1130	ACAAGTGGTCTGCGATGGCAGCG	1131	CAAGTGGTCTGCGATGGCAGC
LDLRex2(27;68;123;30)_136_d1_r	1132	GCGTGCCATCGCGACCACTTGT	1133	CGCTGCCATCGCGACCACTTGT	1134	GCTGCCATCGCGACCACTTGT
LDLRex2(27;68;123;30)_137_d1_f	1135	ACAAGTGGGTTCTGATGGCAGCGCT	1136	CAAGTGGGTTCTGATGGCAGCGC	1137	AAGTGGGTTCTGATGGCAGCG
LDLRex2(27;68;123;30)_137_d1_r	1138	AGCGTGCCATCGAGACCACTTGT	1139	GCGTGCCATCGAGACCACTTGT	1140	CGCTGCCATCGAGACCACTT
LDLRex2(27;68;123;30)_138_d1_f	1141	CAAGTGGGTTCTGGATGGCAGCGCTG	1142	AAGTGGGTTCTGGATGGCAGCGCT	1143	AGTGGGTTCTGGATGGCAGCGC
LDLRex2(27;68;123;30)_138_d1_r	1144	CAGCGTGCCATCCAGACCACTTGT	1145	AGCGTGCCATCCAGACCACTT	1146	GCGTGCCATCCAGACCACT
LDLRex2(27;68;123;30)_139_d1_f	1147	AAGTGGGTTCTGATGGCAGCGCTGA	1148	AGTGGGTTCTGATGGCAGCGCTG	1149	GTGGGTTCTGATGGCAGCGCT
LDLRex2(27;68;123;30)_139_d1_r	1150	TCAGCGTGCCATGCAGACCACTT	1151	CAGCGTGCCATGCAGACCACT	1152	AGCGTGCCATGCAGACCACT
LDLRex2(27;68;123;30)_140_d1_f	1153	AGTGGGTTCTGCGTGGCAGCGCTGAG	1154	GTGGGTTCTGCGTGGCAGCGCTGA	1155	TGGGTTCTGCGTGGCAGCGCTG
LDLRex2(27;68;123;30)_140_d1_r	1156	CTCAGCGCTGCCACGCAGACCACT	1157	TCAGCGCTGCCACGCAGACCACT	1158	CAGCGTGCCACGCAGACCA
LDLRex2(27;68;123;30)_141_d1_f	1159	GTGGGTTCTGCGAGGCAGCGCTGAGT	1160	TGGGTTCTGCGAGGCAGCGCTGAG	1161	GGGTTCTGCGAGGCAGCGCTGA
LDLRex2(27;68;123;30)_141_d1_r	1162	ACTCAGCGCTGCCTCGCAGACCCAC	1163	CTCAGCGCTGCCTCGCAGACCCA	1164	TCAGCGCTGCCTCGCAGACCC
LDLRex2(27;68;123;30)_142_d1_f	1165	TGGGTTCTGCGATGCAGCGCTGAGTG	1166	GGGTTCTGCGATGCAGCGCTGAGT	1167	GGTCTGCGATGCAGCGCTGAG
LDLRex2(27;68;123;30)_142_d1_r	1168	CACTCAGCGCTGCATCGCAGACCCA	1169	ACTCAGCGCTGCATCGCAGACCC	1170	CTCAGCGCTGCATCGCAGACC
LDLRex2(27;68;123;30)_143_d1_f	1171	GGGTTCTGCGATGCAGCGCTGAGTGC	1172	GGTCTGCGATGCAGCGCTGAGTG	1173	GTCTGCGATGCAGCGCTGAGT
LDLRex2(27;68;123;30)_143_d1_r	1174	GCACTCAGCGCTGCATCGCAGACCC	1175	CACTCAGCGCTGCATCGCAGACC	1176	ACTCAGCGCTGCATCGCAGAC
LDLRex2(27;68;123;30)_144_d1_f	1177	GGTCTGCGATGGAGCGCTGAGTGCC	1178	GTCTGCGATGGAGCGCTGAGTGC	1179	TCTGCGATGGAGCGCTGAGTG
LDLRex2(27;68;123;30)_144_d1_r	1180	GGCACTCAGCGCTCCATCGCAGACC	1181	GCACCTCAGCGCTCCATCGCAGAC	1182	CACTCAGCGCTCCATCGCAGA
LDLRex2(27;68;123;30)_145_d1_f	1183	GTCTGCGATGGCGCGCTGAGTGCCA	1184	TCTGCGATGGCGCGCTGAGTGCC	1185	CTGCGATGGCGCGCTGAGTGC
LDLRex2(27;68;123;30)_145_d1_r	1186	TGGCACTCAGCGCGCCATCGCAGAC	1187	GGCACTCAGCGCGCCATCGCAGA	1188	GCACTCAGCGCGCCATCGCAG
LDLRex2(27;68;123;30)_146_d1_f	1189	TCTGCGATGGCAGCGCTGAGTGCCAG	1190	CTGCGATGGCAGCGCTGAGTGCCA	1191	TGCGATGGCAGCGCTGAGTGCC
LDLRex2(27;68;123;30)_146_d1_r	1192	CTGGCACTCAGCGTGCCATCGCAGA	1193	TGGCACTCAGCGTGCCATCGCAG	1194	GGCACTCAGCGTGCCATCGCA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_147_d1_f	1195	CTGCGATGGCAGGCTGAGTGCCAGG	1196	TGCGATGGCAGGCTGAGTGCCAG	1197	GCGATGGCAGGCTGAGTGCCA
LDLRex2(27;68;123;30)_147_d1_r	1198	CCTGGCACTCAGCCTGCCATCGCAG	1199	CTGGCACTCAGCCTGCCATCGCA	1200	TGGCACTCAGCCTGCCATCGC
LDLRex2(27;68;123;30)_148_d1_f	1201	TGCGATGGCAGCCTGAGTGCCAGGA	1202	GCGATGGCAGCCTGAGTGCCAGG	1203	CGATGGCAGCCTGAGTGCCAG
LDLRex2(27;68;123;30)_148_d1_r	1204	TCTGGCACTCAGGCTGCCATCGCA	1205	CCTGGCACTCAGGCTGCCATCGC	1206	CTGGCACTCAGGCTGCCATCG
LDLRex2(27;68;123;30)_149_d1_f	1207	GCGATGGCAGCGTGAGTGCCAGGAT	1208	CGATGGCAGCGTGAGTGCCAGGA	1209	GATGGCAGCGTGAGTGCCAGG
LDLRex2(27;68;123;30)_149_d1_r	1210	ATCCTGGCACTACGCTGCCATCGC	1211	TCCTGGCACTACGCTGCCATCG	1212	CCTGGCACTACGCTGCCATC
LDLRex2(27;68;123;30)_150_d1_f	1213	CGATGGCAGCGCGAGTGCCAGGATG	1214	GATGGCAGCGCGAGTGCCAGGAT	1215	ATGGCAGCGCGAGTGCCAGGA
LDLRex2(27;68;123;30)_150_d1_r	1216	CATCCTGGCACTCGCGTGCCATCG	1217	ATCCTGGCACTCGCGTGCCATC	1218	TCCTGGCACTCGCGTGCCAT
LDLRex2(27;68;123;30)_151_d1_f	1219	GATGGCAGCGCTAGTGCCAGGATGG	1220	ATGGCAGCGCTAGTGCCAGGATG	1221	TGGCAGCGCTAGTGCCAGGAT
LDLRex2(27;68;123;30)_151_d1_r	1222	CCATCCTGGCACTAGCGCTGCCATC	1223	CATCCTGGCACTAGCGCTGCCAT	1224	ATCCTGGCACTAGCGCTGCCA
LDLRex2(27;68;123;30)_152_d1_f	1225	ATGGCAGCGCTGGTGCCAGGATGGC	1226	TGGCAGCGCTGGTGCCAGGATGG	1227	GGCAGCGCTGGTGCCAGGATG
LDLRex2(27;68;123;30)_152_d1_r	1228	GCCATCCTGGCACCAGCGCTGCCAT	1229	CCATCCTGGCACCAGCGCTGCCA	1230	CATCCTGGCACCAGCGCTGCC
LDLRex2(27;68;123;30)_153_d1_f	1231	TGGCAGCGCTGATGCCAGGATGGCT	1232	GGCAGCGCTGATGCCAGGATGGC	1233	GCAGCGCTGATGCCAGGATGG
LDLRex2(27;68;123;30)_153_d1_r	1234	AGCCATCCTGGCATCAGCGCTGCCA	1235	GCCATCCTGGCATCAGCGCTGCC	1236	CCATCCTGGCATCAGCGCTGC
LDLRex2(27;68;123;30)_154_d1_f	1237	GGCAGCGCTGAGGCCAGGATGGCTC	1238	GCAGCGCTGAGGCCAGGATGGCT	1239	CAGCGCTGAGGCCAGGATGGC
LDLRex2(27;68;123;30)_154_d1_r	1240	GAGCCATCCTGGCCTCAGCGCTGCC	1241	AGCCATCCTGGCCTCAGCGCTGC	1242	GCCATCCTGGCCTCAGCGCTG
LDLRex2(27;68;123;30)_155_d1_f	1243	GCAGCGCTGAGTCCAGGATGGCTCT	1244	CAGCGCTGAGTCCAGGATGGCTC	1245	AGCGCTGAGTCCAGGATGGCT
LDLRex2(27;68;123;30)_155_d1_r	1246	AGAGCCATCCTGGACTCAGCGCTGC	1247	GAGCCATCCTGGACTCAGCGCTG	1248	AGCCATCCTGGACTCAGCGCT
LDLRex2(27;68;123;30)_156_d1_f	1249	CAGCGCTGAGTG CAGGATGGCTCTG	1250	AGCGCTGAGTG CAGGATGGCTCT	1251	GCCTGAGTG CAGGATGGCTC
LDLRex2(27;68;123;30)_156_d1_r	1252	CAGAGCCATCCTGCACTCAGCGCTG	1253	AGAGCCATCCTGCACTCAGCGCT	1254	GAGCCATCCTGCACTCAGCGC
LDLRex2(27;68;123;30)_157_d1_f	1255	AGCGCTGAGTG CAGGATGGCTCTGA	1256	GCCTGAGTG CAGGATGGCTCTG	1257	CGCTGAGTG CAGGATGGCTCT
LDLRex2(27;68;123;30)_157_d1_r	1258	TCAAGCCATCCTGCACTCAGCGCT	1259	CAGAGCCATCCTGCACTCAGCGC	1260	AGAGCCATCCTGCACTCAGCG
LDLRex2(27;68;123;30)_158_d1_f	1261	GCCTGAGTG CCGGATGGCTCTGAT	1262	CGCTGAGTG CCGGATGGCTCTGA	1263	GCTGAGTG CCGGATGGCTCTG
LDLRex2(27;68;123;30)_158_d1_r	1264	ATCAGAGCCATCCGGCACTCAGCGC	1265	TCAGAGCCATCCGGCACTCAGCG	1266	CAGAGCCATCCGGCACTCAGC
LDLRex2(27;68;123;30)_159_d1_f	1267	CGCTGAGTG CAGATGGCTCTGATG	1268	GCTGAGTG CAGATGGCTCTGAT	1269	CTGAGTG CAGATGGCTCTGA
LDLRex2(27;68;123;30)_159_d1_r	1270	CATCAGAGCCATCTGGCACTCAGCG	1271	ATCAGAGCCATCTGGCACTCAGC	1272	TCAGAGCCATCTGGCACTCAG
LDLRex2(27;68;123;30)_160_d1_f	1273	GCTGAGTG CAGATGGCTCTGATGA	1274	CTGAGTG CAGATGGCTCTGATG	1275	TGAGTG CAGATGGCTCTGAT
LDLRex2(27;68;123;30)_160_d1_r	1276	TCATCAGAGCCATCTGGCACTCAGC	1277	CATCAGAGCCATCTGGCACTCAG	1278	ATCAGAGCCATCTGGCACTCA
LDLRex2(27;68;123;30)_161_d1_f	1279	CTGAGTG CAGATGGCTCTGATGAG	1280	TGAGTG CAGATGGCTCTGATGA	1281	GAGTG CAGATGGCTCTGATG
LDLRex2(27;68;123;30)_161_d1_r	1282	CTCATGAGAGCCACTGGCACTCAG	1283	TCATGAGAGCCACTGGCACTCA	1284	CATCAGAGCCACTGGCACTC
LDLRex2(27;68;123;30)_162_d1_f	1285	TGAGTG CAGAGGCTCTGATGAGT	1286	GAGTG CAGAGGCTCTGATGAG	1287	AGTG CAGAGGCTCTGATGA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_162_d1_r	1288	ACTCATCAGAGCCTCTGGCACTCA	1289	CTCATCAGAGCCTCTGGCACTC	1290	TCATCAGAGCCTCTGGCACT
LDLRex2(27;68;123;30)_163_d1_f	1291	GAGTGCCAGGATGCTCTGATGATC	1292	AGTGCCAGGATGCTCTGATGAGT	1293	GTGCCAGGATGCTCTGATGAG
LDLRex2(27;68;123;30)_163_d1_r	1294	GACTCATCAGAGCATCTGGCACTC	1295	ACTCATCAGAGCATCTGGCACT	1296	CTCATCAGAGCATCTGGCAC
LDLRex2(27;68;123;30)_164_d1_f	1297	AGTGCCAGGATGCTCTGATGATCC	1298	GTGCCAGGATGCTCTGATGATC	1299	TGCCAGGATGCTCTGATGAGT
LDLRex2(27;68;123;30)_164_d1_r	1300	GGACTCATCAGAGCATCTGGCACT	1301	GACTCATCAGAGCATCTGGCAC	1302	ACTCATCAGAGCATCTGGCA
LDLRex2(27;68;123;30)_165_d1_f	1303	GTGCCAGGATGGTCTGATGATCCC	1304	TGCCAGGATGGTCTGATGATCC	1305	GCCAGGATGGTCTGATGATC
LDLRex2(27;68;123;30)_165_d1_r	1306	GGGACTCATCAGACCATCTCTGGCAC	1307	GGACTCATCAGACCATCTCTGGCA	1308	GACTCATCAGACCATCTCTGGC
LDLRex2(27;68;123;30)_166_d1_f	1309	TGCCAGGATGGCTGATGATCCCA	1310	GCCAGGATGGCTGATGATCCC	1311	CCAGGATGGCTGATGATGCC
LDLRex2(27;68;123;30)_166_d1_r	1312	TGGGACTCATCAGGCCATCTGGCA	1313	GGGACTCATCAGGCCATCTGGC	1314	GGAATCATCAGGCCATCTCTGG
LDLRex2(27;68;123;30)_167_d1_f	1315	GCCAGGATGGCTGATGATCCAG	1316	CCAGGATGGCTGATGATCCCA	1317	CAGGATGGCTGATGATCCC
LDLRex2(27;68;123;30)_167_d1_r	1318	CTGGGACTCATCAAGCCATCTGGC	1319	TGGGACTCATCAAGCCATCTGG	1320	GGGACTCATCAAGCCATCTG
LDLRex2(27;68;123;30)_168_d1_f	1321	CCAGGATGGCTCGATGATCCAGG	1322	CAGGATGGCTCGATGATCCAG	1323	AGGATGGCTCGATGATCCCA
LDLRex2(27;68;123;30)_168_d1_r	1324	CCTGGGACTCATCAGCCATCTCTGG	1325	CTGGGACTCATCAGCCATCTCTG	1326	TGGGACTCATCAGCCATCTCT
LDLRex2(27;68;123;30)_169_d1_f	1327	CAGGATGGCTCTATGATCCCA	1328	AGGATGGCTCTATGATCCCA	1329	GGATGGCTCTATGATCCCA
LDLRex2(27;68;123;30)_169_d1_r	1330	TCCTGGGACTCATAGGCCATCTCTG	1331	CCTGGGACTCATAGGCCATCTCT	1332	CTGGGACTCATAGGCCATCTC
LDLRex2(27;68;123;30)_170_d1_f	1333	AGGATGGCTCTGTGATCCCA	1334	GGATGGCTCTGTGATCCCA	1335	GATGGCTCTGTGATCCCA
LDLRex2(27;68;123;30)_170_d1_r	1336	CTCTGGGACTCATAGGCCATCTCT	1337	TCCTGGGACTCATAGGCCATCTC	1338	CCTGGGACTCATAGGCCATC
LDLRex2(27;68;123;30)_171_d1_f	1339	GGATGGCTCTGAGAGTCCCA	1340	GATGGCTCTGAGAGTCCCA	1341	ATGGCTCTGAGAGTCCCA
LDLRex2(27;68;123;30)_171_d1_r	1342	TCTCTGGGACTCTCAGAGCCATCC	1343	CTCTGGGACTCTCAGAGCCATC	1344	TCCTGGGACTCTCAGAGCCAT
LDLRex2(27;68;123;30)_172_d1_f	1345	GATGGCTCTGATAGTCCCA	1346	ATGGCTCTGATAGTCCCA	1347	TGGCTCTGATAGTCCCA
LDLRex2(27;68;123;30)_172_d1_r	1348	GTCTCTGGGACTATCAGAGCCATC	1349	TCTCTGGGACTATCAGAGCCAT	1350	CTCCTGGGACTATCAGAGCCA
LDLRex2(27;68;123;30)_173_d1_f	1351	ATGGCTCTGATGGTCCCA	1352	TGGCTCTGATGGTCCCA	1353	GGCTCTGATGGTCCCA
LDLRex2(27;68;123;30)_173_d1_r	1354	CGTCTCTGGGACCATCAGAGCCAT	1355	GTCTCTGGGACCATCAGAGCCA	1356	TCTCTGGGACCATCAGAGCC
LDLRex2(27;68;123;30)_174_d1_f	1357	TGGCTCTGATATCCCA	1358	GGCTCTGATATCCCA	1359	GCTCTGATATCCCA
LDLRex2(27;68;123;30)_174_d1_r	1360	ACGTCTCTGGGATCATCAGAGCCA	1361	CGTCTCTGGGATCATCAGAGCC	1362	GTCTCTGGGATCATCAGAGC
LDLRex2(27;68;123;30)_175_d1_f	1363	GGCTCTGATAGCCCA	1364	GCTCTGATAGCCCA	1365	CTCTGATAGCCCA
LDLRex2(27;68;123;30)_175_d1_r	1366	CACGTCTCTGGGCTCATCAGAGCC	1367	ACGTCTCTGGGCTCATCAGAGC	1368	CGTCTCTGGGCTCATCAGAG
LDLRex2(27;68;123;30)_176_d1_f	1369	GCTCTGATGATCCAGGACGCTG	1370	CTCTGATGATCCAGGACGCTG	1371	TCTGATGATCCAGGACGCT
LDLRex2(27;68;123;30)_176_d1_r	1372	GCAGTCTCTGGACTCATCAGAGC	1373	CAGTCTCTGGACTCATCAGAG	1374	ACGTCTCTGGACTCATCAGA
LDLRex2(27;68;123;30)_177_d1_f	1375	CTCTGATGATCCAGGACGCTGCT	1376	TCTGATGATCCAGGACGCTG	1377	CTGATGATCCAGGACGCTG
LDLRex2(27;68;123;30)_177_d1_r	1378	AGCAGTCTCTGGACTCATCAGAG	1379	GCAGTCTCTGGACTCATCAGA	1380	CACGTCTCTGGACTCATCAG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1	1381	TCTGATAGTCCAGGAGACGTGCTG	1382	CTGATAGTCCAGGAGACGTGCT	1383	TGATAGTCCAGGAGACGTGC
LDLRex2(27;68;123;30)_178_d1_f	1384	CAGCACGTCTCTGGACTCATCAGA	1385	AGCACGTCTCTGGACTCATCAG	1386	GCACGTCTCTGGACTCATCA
LDLRex2(27;68;123;30)_178_d1_r	1387	CTGATAGTCCCGGAGACGTGCTGT	1388	TGATAGTCCCGGAGACGTGCTG	1389	GATAGTCCCGGAGACGTGCT
LDLRex2(27;68;123;30)_179_d1_f	1390	ACAGCACGTCTCCGGACTCATCAG	1391	CAGCACGTCTCCGGACTCATCA	1392	AGCACGTCTCCGGACTCATC
LDLRex2(27;68;123;30)_179_d1_r	1393	TGATAGTCCAGAGACGTGCTGTG	1394	GATAGTCCAGAGACGTGCTGT	1395	ATGATCCCAGAGACGTGCTG
LDLRex2(27;68;123;30)_180_d1_f	1396	CACAGCACGTCTCTGGACTCATCA	1397	ACAGCACGTCTCTGGACTCATC	1398	CAGCACGTCTCTGGACTCAT
LDLRex2(27;68;123;30)_180_d1_r	1399	GATGATCCAGAGACGTGCTGTGA	1400	ATGATCCAGAGACGTGCTGTG	1401	TGATCCAGAGACGTGCTGT
LDLRex2(27;68;123;30)_181_d1_f	1402	TCACAGCACGTCTCTGGACTCATC	1403	CACAGCACGTCTCTGGACTCAT	1404	ACAGCACGTCTCTGGACTCA
LDLRex2(27;68;123;30)_181_d1_r	1405	ATGATCCAGGGACGTGCTGTGAG	1406	TGATCCAGGGACGTGCTGTGA	1407	GATCCAGGGACGTGCTGTG
LDLRex2(27;68;123;30)_182_d1_f	1408	CTCAGCACGTCTCTGGACTCAT	1409	TCACAGCACGTCTCTGGACTCA	1410	CACAGCACGTCTCTGGACTC
LDLRex2(27;68;123;30)_182_d1_r	1411	TGATCCAGGAACGTGCTGTGAGT	1412	GAGTCCAGGAACGTGCTGTGAG	1413	AGTCCAGGAACGTGCTGTGA
LDLRex2(27;68;123;30)_183_d1_f	1414	ACTCACAGCACGTCTCTGGACTCA	1415	CTCACAGCACGTCTCTGGACTC	1416	TCACAGCACGTCTCTGGACT
LDLRex2(27;68;123;30)_183_d1_r	1417	GAGTCCAGGAGCGTGTGTGAGTC	1418	AGTCCAGGAGCGTGTGTGAGT	1419	GTCCAGGAGCGTGTGTGAG
LDLRex2(27;68;123;30)_184_d1_f	1420	GACTCACAGCACGTCTCTGGACTC	1421	ACTCACAGCACGTCTCTGGACT	1422	CTCACAGCACGTCTCTGGGAC
LDLRex2(27;68;123;30)_184_d1_r	1423	AGTCCAGGAGAGTGTGTGAGTCC	1424	GTCCAGGAGAGTGTGTGAGTC	1425	TCCAGGAGAGTGTGTGAGT
LDLRex2(27;68;123;30)_185_d1_f	1426	GGACTCACAGCACTCTCTGGACT	1427	GACTCACAGCACTCTCTGGGAC	1428	ACTCACAGCACTCTCTCTGGGA
LDLRex2(27;68;123;30)_185_d1_r	1429	GTCCAGGAGAGTGTGTGAGTCCC	1430	TCCAGGAGAGTGTGTGAGTCC	1431	CCCAGGAGAGTGTGTGAGTC
LDLRex2(27;68;123;30)_186_d1_f	1432	GGGACTCACAGCACTCTCTGGGAC	1433	GGACTCACAGCACTCTCTGGGA	1434	GACTCACAGCACTCTCTCTGGG
LDLRex2(27;68;123;30)_186_d1_r	1435	TCCAGGAGACGGCTGTGAGTCCCC	1436	CCCAGGAGACGGCTGTGAGTCCC	1437	CCAGGAGACGGCTGTGAGTCC
LDLRex2(27;68;123;30)_187_d1_f	1438	GGGGACTCACAGCCGTCTCTCTGGGA	1439	GGGGACTCACAGCCGTCTCTCTGGG	1440	GGACTCACAGCCGTCTCTCTGG
LDLRex2(27;68;123;30)_187_d1_r	1441	CCCAGGAGACGTCTGTGAGTCCCT	1442	CCAGGAGACGTCTGTGAGTCCCC	1443	CAGGAGACGTCTGTGAGTCCC
LDLRex2(27;68;123;30)_188_d1_f	1444	AGGGGACTCACAGACGTCTCTCTGGG	1445	GGGGACTCACAGACGTCTCTCTGG	1446	GGGACTCACAGACGTCTCTCTG
LDLRex2(27;68;123;30)_188_d1_r	1447	CCAGGAGACGTGTGTGAGTCCCTT	1448	CAGGAGACGTGTGTGAGTCCCT	1449	AGGAGACGTGTGTGAGTCCCC
LDLRex2(27;68;123;30)_189_d1_f	1450	AAGGGACTCACACACGTCTCTCTGG	1451	AGGGACTCACACACGTCTCTCTG	1452	GGGGACTCACACACGTCTCTCT
LDLRex2(27;68;123;30)_190 + 1_d1_f	1453	AGGAGACGTGTGTGAGTCCCTTTG	1454	GGAGACGTGTGTGAGTCCCTTT	1455	GAGACGTGTGTGAGTCCCTTT
LDLRex2(27;68;123;30)_190 + 1_d1_r	1456	CAAAAGGGGACTCAAGCACGTCTCT	1457	AAAGGGGACTCAAGCACGTCTCC	1458	AAGGGGACTCAAGCACGTCTC
LDLRex2(27;68;123;30)_190 + 10_d1_f	1459	GCTGTGAGTCCCTTTGGGCATGATA	1460	CTGTGAGTCCCTTTGGGCATGAT	1461	TGTGAGTCCCTTTGGGCATGA
LDLRex2(27;68;123;30)_190 + 10_d1_r	1462	TATCATGCCCAAGGGACTCACAGC	1463	ATCATGCCCAAGGGACTCACAG	1464	TCATGCCCAAGGGACTCACACA
LDLRex2(27;68;123;30)_190 + 11_d1_f	1465	CTGTGAGTCCCTTTGGGCATGATAT	1466	TGTGAGTCCCTTTGGGCATGATA	1467	GTGAGTCCCTTTGGGCATGAT
LDLRex2(27;68;123;30)_190 + 11_d1_r	1468	ATATCATGCCCAAGGGACTCACAG	1469	TATCATGCCCAAGGGACTCACACA	1470	ATCATGCCCAAGGGAGACTCAC
LDLRex2(27;68;123;30)_190 + 12_d1_f	1471	TGTGAGTCCCTTTGGGCATGATATG	1472	GTGAGTCCCTTTGGGCATGATAT	1473	TGAGTCCCTTTGGGCATGATA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_190 + 12_d1_r	1474	CATATCATGCCCAAGGGGACTCACA	1475	ATATCATGCCCAAGGGGACTCAC	1476	TATCATGCCCAAGGGGACTCA
LDLRex2(27;68;123;30)_190 + 13_d1_f	1477	GTGAGTCCCTTGGGCATGATATGC	1478	TGAGTCCCTTGGGCATGATATG	1479	GAGTCCCTTGGGCATGATAT
LDLRex2(27;68;123;30)_190 + 13_d1_r	1480	GCATATCATGCCCAAGGGGACTCAC	1481	CATATCATGCCCAAGGGGACTCA	1482	ATATCATGCCCAAGGGGACTC
LDLRex2(27;68;123;30)_190 + 14_d1_f	1483	TGAGTCCCTTGGGCATGATATGCA	1484	GAGTCCCTTGGGCATGATATGC	1485	AGTCCCTTGGGCATGATATG
LDLRex2(27;68;123;30)_190 + 14_d1_r	1486	TGCATATCATGCCCAAGGGGACTCA	1487	GCATATCATGCCCAAGGGGACTC	1488	CATATCATGCCCAAGGGGACT
LDLRex2(27;68;123;30)_190 + 15_d1_f	1489	GAGTCCCTTGGGCATGATATGCAT	1490	AGTCCCTTGGGCATGATATGCA	1491	GTCCCTTGGGCATGATATGC
LDLRex2(27;68;123;30)_190 + 15_d1_r	1492	ATGCATATCATGCCCAAGGGGACTC	1493	TGCATATCATGCCCAAGGGGACT	1494	GCATATCATGCCCAAGGGGAC
LDLRex2(27;68;123;30)_190 + 2_d1_f	1495	GGAGACGTGCTGGAGTCCCTTTGG	1496	GAGACGTGCTGGAGTCCCTTTTG	1497	AGACGTGCTGGAGTCCCTTTT
LDLRex2(27;68;123;30)_190 + 2_d1_r	1498	CCAAAAGGGGACTCCAGCACGTCTCC	1499	CAAAAAGGGGACTCCAGCACGTCTC	1500	AAAGGGGACTCCAGCACGTCT
LDLRex2(27;68;123;30)_190 + 3_d1_f	1501	GAGACGTGCTAGTCCCTTTGGG	1502	AGACGTGCTAGTCCCTTTGG	1503	GACGTGCTAGTCCCTTTG
LDLRex2(27;68;123;30)_190 + 3_d1_r	1504	CCAAAAGGGGACTACAGCACGTCTC	1505	CCAAAAGGGGACTACAGCACGTCT	1506	CAAAGGGGACTACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 4_d1_f	1507	AGACGTGCTGGTCCCTTTGGG	1508	GACGTGCTGGTCCCTTTGGG	1509	ACGTGCTGGTCCCTTTGG
LDLRex2(27;68;123;30)_190 + 4_d1_r	1510	GCCAAAAGGGGACTACAGCACGTCT	1511	CCAAAAGGGGACTACAGCACGTCT	1512	CCAAAAGGGGACTACAGCACGT
LDLRex2(27;68;123;30)_190 + 5_d1_f	1513	GACGTGCTGATCCCTTTGGGCA	1514	ACGTGCTGATCCCTTTGGG	1515	CGTGTGCTGATCCCTTTGGG
LDLRex2(27;68;123;30)_190 + 5_d1_r	1516	TGCCCAAAGGGGACTACAGCACGTCT	1517	GCCCAAAGGGGACTACAGCACGT	1518	CCCAAAGGGGACTACAGCACG
LDLRex2(27;68;123;30)_190 + 6_d1_f	1519	ACGTGCTGAGCCCTTTGGGCAT	1520	CGTGTGAGCCCTTTGGGCA	1521	GTGTGTGAGCCCTTTGGGC
LDLRex2(27;68;123;30)_190 + 6_d1_r	1522	ATGCCCAAAGGGGCTCACAGCACGT	1523	TGCCCAAAGGGGCTCACAGCACG	1524	GCCCAAAGGGGCTCACAGCAC
LDLRex2(27;68;123;30)_190 + 7_d1_f	1525	CGTGTGAGTCCCTTTGGGCATG	1526	GTGTGTGAGTCCCTTTGGGCAT	1527	TGCTGTGAGTCCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 7_d1_r	1528	CATGCCCAAAGGGGACTCACAGCACG	1529	ATGCCCAAAGGGGACTCACAGCAC	1530	TGCCCAAAGGGGACTCACAGCA
LDLRex2(27;68;123;30)_190 + 8_d1_f	1531	GTGTGTGAGTCCCTTTGGGCATGA	1532	TGTGTGAGTCCCTTTGGGCATG	1533	GCTGTGAGTCCCTTTGGGCAT
LDLRex2(27;68;123;30)_190 + 8_d1_r	1534	TCATGCCCAAAGGGGACTCACAGCAC	1535	CATGCCCAAAGGGGACTCACAGCA	1536	ATGCCCAAAGGGGACTCACAGC
LDLRex2(27;68;123;30)_190 + 9_d1_f	1537	TGCTGTGAGTCCCTTTGGGCATGAT	1538	GCTGTGAGTCCCTTTGGGCATGA	1539	CTGTGAGTCCCTTTGGGCATG
LDLRex2(27;68;123;30)_190 + 9_d1_r	1540	ATCATGCCCAAAGGGGACTCACAGCA	1541	TCATGCCCAAAGGGGACTCACAGC	1542	CATGCCCAAAGGGGACTCACAG
LDLRex2(27;68;123;30)_190_d1_f	1543	CAGGACGTGCGTGAGTCCCTTT	1544	AGGACGTGCGTGAGTCCCTTT	1545	GGAGACGTGCGTGAGTCCCTT
LDLRex2(27;68;123;30)_190_d1_r	1546	AAAGGGGACTCACGCACGTCTCTCTG	1547	AAGGGGACTCACGCACGTCTCTCT	1548	AGGGGACTCACGCACGTCTCTC
LDLRex2(27;68;123;30)_68 - 1_d1_f	1549	TCCTCTCTCTCATGGGCGACAGATG	1550	CCCTCTCTCTCATGGGCGACAGAT	1551	CTCTCTCTCATGGGCGACAGA
LDLRex2(27;68;123;30)_68 - 1_d1_r	1552	CATCTGTGCGCCCATGAGAGAGAGGA	1553	ATCTGTGCGCCCATGAGAGAGAGG	1554	TCTGTGCGCCCATGAGAGAGAG
LDLRex2(27;68;123;30)_68 - 10_d1_f	1555	TTCTCTTTTCCCTCTCTCAGTGGG	1556	TCTCTTTTCCCTCTCTCAGTGG	1557	CTCCTTTTCCCTCTCTCAGTG
LDLRex2(27;68;123;30)_68 - 10_d1_r	1558	CCCACTGAGAGAGGGGAAAAGGAGAA	1559	CCACTGAGAGAGGGGAAAAGGAGA	1560	CACTGAGAGAGGGGAAAAGGAG
LDLRex2(27;68;123;30)_68 - 11_d1_f	1561	TTTCTCTTTTCTCTCTCTCAGTGG	1562	TTCTCTTTTCTCTCTCTCAGTG	1563	TCTCTTTTCTCTCTCTCAGT
LDLRex2(27;68;123;30)_68 - 11_d1_r	1564	CCCACTGAGAGAGAGAAAAGGAGAAA	1565	CACTGAGAGAGAGAAAAGGAGAA	1566	ACTGAGAGAGAGAAAAGGAGAA

del1	SEQ. ID			25 nt			SEQ. ID			23 nt			SEQ. ID		
	NO:			NO:			NO:			NO:			NO:		
LDLIRex2(27;68;123;30)_68 - 12_d1_f	1567			C T T T C C T T T T T C T C T C T C T C A G T G	1568			T T T C T C C T T T T T C T C T C T C T C A G T	1569			T T C T C C T T T T T C T C T C T C T C T C A G	1570		
LDLIRex2(27;68;123;30)_68 - 12_d1_r	1570			C A C T G A G A G A G A A A A G G A G A A A G	1571			A C T G A G A G A G A A A A A G G A A A A G	1572			C T G A G A G A G A A A A A G G A A A A G	1573		
LDLIRex2(27;68;123;30)_68 - 13_d1_f	1573			C T T T C C T T T C T C T C T C T C A G T	1574			C T T T C C T T T C T C T C T C T C A G T	1575			T T T C T C T T T C T C T C T C T C A	1576		
LDLIRex2(27;68;123;30)_68 - 13_d1_r	1576			A C T G A G A G A G A A A G G A G A A A G G	1577			C T G A G A G A G A A A A G G A G A A A G	1578			T G A G A G A G A A A A G G A A A A	1579		
LDLIRex2(27;68;123;30)_68 - 14_d1_f	1579			C C T T T C T C T T T C T C T C T C T C A G	1580			C C T T T C T C T T T C T C T C T C T C A	1581			C T T T C C T T T C T C T C T C T C T C	1582		
LDLIRex2(27;68;123;30)_68 - 14_d1_r	1582			C T G A G A G A G A A A G G A G A A A G G G	1583			T G A G A G A G A A A A G G A G A A A G G	1584			G A G A G A G A A A A G G A G A A A G	1585		
LDLIRex2(27;68;123;30)_68 - 15_d1_f	1585			A C C T T T C C T T T C T C T C T C T C A	1586			C C T T T C C T T T T C T C T C T C T C T C	1587			C C T T T C C T T T T C T C T C T C T C T	1588		
LDLIRex2(27;68;123;30)_68 - 15_d1_r	1588			T G A G A G A G A A A A G G A G A A A G G T	1589			G A G A G A G A A A A G G A G A A A G G G	1590			A G A G A G A A A A G G A G A A A G G	1589		
LDLIRex2(27;68;123;30)_68 - 2_d1_f	1591			T T C T C T C T C T G T G G G C G A C A G A T	1592			T C C T C T C T C T G T G G G C G A C A G A	1593			C C T C T C T C T G T G G G C G A C A G	1594		
LDLIRex2(27;68;123;30)_68 - 2_d1_r	1594			A T C T G C C C A C G A G A G A G A G G A A	1595			T C T G T C C C A C G A G A G A G A G A G A	1596			C T G T C C C A C G A G A G A G A G A G G	1595		
LDLIRex2(27;68;123;30)_68 - 3_d1_f	1597			T T T C T C T C T C T A G T G G G C G A C A G A	1598			T T C T C T C T C T A G T G G G C G A C A G	1599			T C C T C T C T A G T G G G C G A C A	1597		
LDLIRex2(27;68;123;30)_68 - 3_d1_r	1600			T C T G T C C C C A C T A G A G A G A G A A A	1601			C T G T C C C C A C T A G A G A G A G A A	1602			T G T C G C C C A C T A G A G A G A G A	1600		
LDLIRex2(27;68;123;30)_68 - 4_d1_f	1603			T T T T C T C T C C A G T G G G C G A C A G	1604			T T T C T C T C C A G T G G G C G A C A	1605			T T C C T C T C C A G T G G G C G A C	1603		
LDLIRex2(27;68;123;30)_68 - 4_d1_r	1606			C T G T C C C C A C T G G A G A G A G A A A A	1607			T G T C C C C A C T G G A G A G A G A A A	1608			G T C G C C C A C T G G A G A G A G A A	1606		
LDLIRex2(27;68;123;30)_68 - 5_d1_f	1609			C T T T T C T C T C T C A G T G G G C G A C A	1610			T T T T C T C T C T C A G T G G G C G A C	1611			T T T C T C T T C A G T G G G C G A	1609		
LDLIRex2(27;68;123;30)_68 - 5_d1_r	1612			T G T C G C C C A C T G A A G A G A G A A A A G	1613			G T C G C C C A C T G A A G A G A G A A A A	1614			T C G C C C A C T G A A G A G A G A A A	1612		
LDLIRex2(27;68;123;30)_68 - 6_d1_f	1615			C C T T T T C C T C T C T C A G T G G G C G A C	1616			C T T T T C T C T C T C A G T G G G C G A	1617			T T T T C T C T C T C A G T G G G C G	1615		
LDLIRex2(27;68;123;30)_68 - 6_d1_r	1618			G T C G C C C A C T G A G G A G A G A A A A G G	1619			T C G C C C A C T G A G G A G A G A A A A G	1620			C G C C C A C T G A G G A G A G A A A A	1618		
LDLIRex2(27;68;123;30)_68 - 7_d1_f	1621			T C C T T T C C T C T C T C A G T G G G C G A	1622			C C T T T C C T C T C T C A G T G G G C G	1623			C T T T T C C T C T C T C A G T G G C	1621		
LDLIRex2(27;68;123;30)_68 - 7_d1_r	1624			T C G C C C A C T G A A G A G A G A A A A G A	1625			C G C C C A C T G A A G A G A G A A A A G G	1626			G C C C A C T G A A G A G A G A A A A G	1624		
LDLIRex2(27;68;123;30)_68 - 8_d1_f	1627			C T C T T T T C T C T C T C A G T G G G C G	1628			T C C T T T T C T C T C T C A G T G G G C	1629			C C T T T T C C T C T C T C A G T G G G	1627		
LDLIRex2(27;68;123;30)_68 - 8_d1_r	1630			C G C C C A C T G A G A G A G A A A A G G A G	1631			G C C C A C T G A G A G A G A A A A G G A	1632			C C C A C T G A G A G A G A A A A A G G			

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1	1660	TTGCGCATCTGTGCGCACTGAGAGAG	1661	TGCGCATCTGTGCGCACTGAGAGA	1662	CGCATCTGTGCGCACTGAGAG
LDLRex2(27;68;123;30)_71_d1_r	1663	TCTCTCAGTGGGACAGATGCGAAA	1664	CTCTCAGTGGGACAGATGCGAA	1665	TCTCAGTGGGACAGATGCGA
LDLRex2(27;68;123;30)_72_d1_f	1666	TTTCGCACTGTGCGCACTGAGAGA	1667	TTTCGCACTGTGCGCACTGAGAG	1668	TGCGCATCTGTGCGCACTGAGA
LDLRex2(27;68;123;30)_72_d1_r	1669	CTCTCAGTGGGACAGATGCGAAAG	1670	TCTCAGTGGGACAGATGCGAAA	1671	CTCAGTGGGACAGATGCGAA
LDLRex2(27;68;123;30)_73_d1_f	1672	CTTCGCACTGTGCGCACTGAGAG	1673	TTTCGCACTGTGCGCACTGAGA	1674	TTTCGCACTGTGCGCACTGAG
LDLRex2(27;68;123;30)_73_d1_r	1675	TCTCAGTGGGCGCAGATGCGAAAGA	1676	CTCAGTGGGCGCAGATGCGAAAG	1677	TCAGTGGGCGCAGATGCGAAA
LDLRex2(27;68;123;30)_74_d1_f	1678	TCTTCGCACTGTGCGCACTGAGA	1679	CTTCGCACTGTGCGCACTGAG	1680	TTTCGCACTGTGCGCACTGA
LDLRex2(27;68;123;30)_74_d1_r	1681	CTCAGTGGGCGAAGATGCGAAAGAA	1682	TCAGTGGGCGAAGATGCGAAAGA	1683	CAGTGGGCGAAGATGCGAAAG
LDLRex2(27;68;123;30)_75_d1_f	1684	TTCTTCGCACTGTGCGCACTGAG	1685	TCTTCGCACTGTGCGCACTGA	1686	CTTCGCACTGTGCGCACTG
LDLRex2(27;68;123;30)_75_d1_r	1687	TACGTGGGCGACGATGCGAAAGAAA	1688	CAGTGGGCGACGATGCGAAAGAA	1689	AGTGGGCGACGATGCGAAAGA
LDLRex2(27;68;123;30)_76_d1_f	1690	TTCTTCGCACTGTGCGCACTGA	1691	TTCTTCGCACTGTGCGCACTG	1692	TCCTTCGCACTGTGCGCACT
LDLRex2(27;68;123;30)_76_d1_r	1693	CAGTGGGCGACAAATGCGAAAGAAC	1694	AGTGGGCGACAAATGCGAAAGAAA	1695	GTGGGCGACAAATGCGAAAGAA
LDLRex2(27;68;123;30)_77_d1_f	1696	GTTCTTCGCACTGTGCGCACTG	1697	TTCTTCGCACTGTGCGCACT	1698	TTCTTCGCACTGTGCGCCAC
LDLRex2(27;68;123;30)_77_d1_r	1699	AGTGGGCGACAGTGGGCGAAGAACG	1700	GTGGGCGACAGTGGGCGAAGAAC	1701	TGGGCGACAGTGGGCGAAGAAA
LDLRex2(27;68;123;30)_78_d1_f	1702	CGTTCTTCGCACTGTGCGCCACT	1703	GTTCTTCGCACTGTGCGCCAC	1704	TTCTTCGCACTGTGCGCCA
LDLRex2(27;68;123;30)_78_d1_r	1705	GTGGGCGACAGCGAAGAAACGA	1706	TGGGCGACAGCGAAGAAACG	1707	GGGCGACAGCGAAGAAAC
LDLRex2(27;68;123;30)_79_d1_f	1708	TCGTTCTTCGCTGTGCGCCAC	1709	CGTTCTTCGCTGTGCGCCA	1710	GTTCTTCGCTGTGCGCCC
LDLRex2(27;68;123;30)_79_d1_r	1711	TGGGCGACAGATCGAAGAAACGAG	1712	GGGCGACAGATCGAAGAAACGA	1713	GGCGACAGATCGAAGAAACG
LDLRex2(27;68;123;30)_80_d1_f	1714	CTCGTTTCTTCGATCTGTCGCCA	1715	TCGTTTCTTCGATCTGTCGCC	1716	CGTTTCTTCGATCTGTCGCC
LDLRex2(27;68;123;30)_80_d1_r	1717	GGGCGACAGATGGAAGAAACGAGT	1718	GGCGACAGATGGAAGAAACGAG	1719	GGCGACAGATGGAAGAAACGA
LDLRex2(27;68;123;30)_81_d1_f	1720	ACTCGTTTCTTCATCTGTGCC	1721	CTCGTTTCTTCATCTGTGCC	1722	TCGTTTCTTCATCTGTGCC
LDLRex2(27;68;123;30)_81_d1_r	1723	GGCGACAGATGCAAGAAACGAGTT	1724	GGCGACAGATGCAAGAAACGAGT	1725	CGACAGATGCAAGAAACGAG
LDLRex2(27;68;123;30)_82_d1_f	1726	AACTCGTTTCTTCATCTGTGCC	1727	ACTCGTTTCTTCATCTGTGCC	1728	CTCGTTTCTTCATCTGTCCG
LDLRex2(27;68;123;30)_82_d1_r	1729	GCGACAGATGCAAGAAACGAGTTC	1730	GCGACAGATGCAAGAAACGAGTT	1731	GACAGATGCAAGAAACGAGT
LDLRex2(27;68;123;30)_83_d1_f	1732	GAACTCGTTTCTTCGATCTGTGCC	1733	AACTCGTTTCTTCGATCTGTCCG	1734	ACTCGTTTCTTCGATCTGTC
LDLRex2(27;68;123;30)_83_d1_r	1735	CGACAGATGCAAGAAACGAGTTC	1736	GACAGATGCAAGAAACGAGTTC	1737	ACAGATGCAAGAAACGAGTT
LDLRex2(27;68;123;30)_84_d1_f	1738	GGAACCTCGTTTCTTCGATCTGTCCG	1739	GAACTCGTTTCTTCGATCTGTC	1740	AACTCGTTTCTTCGATCTGT
LDLRex2(27;68;123;30)_84_d1_r	1741	GACAGATGCAAGAAACGAGTCCA	1742	ACAGATGCAAGAAACGAGTTCC	1743	CAGATGCAAGAAACGAGTTC
LDLRex2(27;68;123;30)_85_d1_f	1744	TGGAACCTCGTTTCTTCGATCTGTCC	1745	GGAACCTCGTTTCTTCGATCTGT	1746	GAACTCGTTTCTTCGATCTG
LDLRex2(27;68;123;30)_85_d1_r	1747	ACAGATGCAAGAAACGAGTCCAG	1748	CAGATGCAAGAAACGAGTTCCA	1749	AGATGCAAGAAACGAGTTCC
LDLRex2(27;68;123;30)_86_d1_f	1750	CTGGAACCTCGTTTCTTCGATCTGT	1751	TGGAACCTCGTTTCTTCGATCTG	1752	GGAACCTCGTTTCTTCGATCT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del1						
LDLRex2(27;68;123;30)_87_d1_f	1753	CAGATGCGAAAGAACGAGTTCCAGT	1754	AGATGCGAAAGAACGAGTTCCAG	1755	GATGCGAAAGAACGAGTTCCA
LDLRex2(27;68;123;30)_87_d1_r	1756	ACTGGAACTCGTTCTTCGCATCTG	1757	CTGGAACTCGTTCTTCGCATCT	1758	TGGAACCTCGTTCTTCGCATC
LDLRex2(27;68;123;30)_88_d1_f	1759	AGATGCGAAAGAACGAGTTCCAGTG	1760	GATGCGAAAGAACGAGTTCCAGT	1761	ATGCGAAAGAACGAGTTCCAG
LDLRex2(27;68;123;30)_88_d1_r	1762	CAC TGGAAC TCGTTCTTCGCATCT	1763	ACTGGAAC TCGTTCTTCGCATC	1764	CTGGAAC TCGTTCTTCGCAT
LDLRex2(27;68;123;30)_89_d1_f	1765	GATGCGAAAGAACGAGTTCCAGTGC	1766	ATGCGAAAGAACGAGTTCCAGTG	1767	TGCGAAAGAACGAGTTCCAGT
LDLRex2(27;68;123;30)_89_d1_r	1768	GCAC TGGAAC TCGTTCTTCGCATC	1769	CACTGGAAC TCGTTCTTCGCAT	1770	ACTGGAAC TCGTTCTTCGCA
LDLRex2(27;68;123;30)_90_d1_f	1771	ATGCGAAAGAACGAGTTCCAGTGCC	1772	TGCGAAAGAACGAGTTCCAGTGC	1773	GCGAAAGAACGAGTTCCAGTG
LDLRex2(27;68;123;30)_90_d1_r	1774	GGCACTGGAAC TCTTCTTCGCAT	1775	GCAC TGGAAC TCTTCTTCGCA	1776	CACTGGAAC TCTTCTTCGC
LDLRex2(27;68;123;30)_91_d1_f	1777	TGCGAAAGAACGAGTTCCAGTGCCA	1778	GCGAAAGAACGAGTTCCAGTGCC	1779	CGAAAGAACGAGTTCCAGTGCC
LDLRex2(27;68;123;30)_91_d1_r	1780	TGGCACTGGAAC TGTTCCTTCGCA	1781	GGCACTGGAAC TGTTCCTTCGC	1782	GCACTGGAAC TGTTCCTTCG
LDLRex2(27;68;123;30)_92_d1_f	1783	GCGAAAGAACGAGTTCCAGTGCCAA	1784	CGAAAGAACGAGTTCCAGTGCCA	1785	GAAAGAACGAGTTCCAGTGCC
LDLRex2(27;68;123;30)_92_d1_r	1786	TTGGCACTGGAAC CCGTTCTTCGC	1787	TGGCACTGGAAC CCGTTCTTCG	1788	GGCACTGGAAC CCGTTCTTTC
LDLRex2(27;68;123;30)_93_d1_f	1789	CGAAAGAACGAGTTCCAGTGCCAAAG	1790	GAAAGAACGAGTTCCAGTGCCAA	1791	AAAGAACGAGTTCCAGTGCCA
LDLRex2(27;68;123;30)_93_d1_r	1792	CTTGGCACTGGAAC TCGTTCTTCG	1793	TTGGCACTGGAAC TCGTTCTTTC	1794	TGGCACTGGAAC TCGTTCTTTC
LDLRex2(27;68;123;30)_94_d1_f	1795	GAAAGAACGAGTTCCAGTGCCAAAGA	1796	AAAGAACGAGTTCCAGTGCCAAAG	1797	AAGAACGAGTTCCAGTGCCAA
LDLRex2(27;68;123;30)_94_d1_r	1798	TCTTGGCACTGGAC TCGTTCTTTC	1799	CTTGGCACTGGAC TCGTTCTTTC	1800	TTGGCACTGGAC TCGTTCTTTC
LDLRex2(27;68;123;30)_95_d1_f	1801	AAAGAACGAGTTCCAGTGCCAAAGAC	1802	AAGAACGAGTTCCAGTGCCAAAGA	1803	AGAACGAGTTCCAGTGCCAAAG
LDLRex2(27;68;123;30)_95_d1_r	1804	GTCTTGGCACTGGAC TCGTTCTTTC	1805	TCTTGGCACTGGAC TCGTTCTTTC	1806	CTTGGCACTGGAC TCGTTCTTTC
LDLRex2(27;68;123;30)_96_d1_f	1807	AAGAACGAGTTCCAGTGCCAAAGACG	1808	AGAACGAGTTCCAGTGCCAAAGAC	1809	GAAACGAGTTCCAGTGCCAAAGA
LDLRex2(27;68;123;30)_96_d1_r	1810	CGTCTTGGCACTGAACTCGTTTCTT	1811	GTCTTGGCACTGAACTCGTTTCT	1812	TCTTGGCACTGAACTCGTTTC
LDLRex2(27;68;123;30)_97_d1_f	1813	AGAACGAGTTCCAGTGCCAAAGACGG	1814	GAAACGAGTTCCAGTGCCAAAGACG	1815	AAACGAGTTCCAGTGCCAAAGAC
LDLRex2(27;68;123;30)_97_d1_r	1816	CCGTCCTTGGCACTGAACTCGTTTCT	1817	CGTCCTTGGCACTGAACTCGTTTC	1818	GTCTTGGCACTGAACTCGTTT
LDLRex2(27;68;123;30)_98_d1_f	1819	GAAACGAGTTCCGTCGCAAGACGGG	1820	AAACGAGTTCCGTCGCAAGACGGG	1821	AACGAGTTCCGTCGCAAGACG
LDLRex2(27;68;123;30)_98_d1_r	1822	CCGTCCTTGGCACTGAACTCGTTTC	1823	CCGTCCTTGGCACTGAACTCGTTT	1824	CGTCCTTGGCACTGAACTCGTT
LDLRex2(27;68;123;30)_99_d1_f	1825	AAACGAGTTCCATGCAAGACGGGA	1826	AAACGAGTTCCATGCAAGACGGG	1827	ACGAGTTCCATGCAAGACGGG
LDLRex2(27;68;123;30)_99_d1_r	1828	TCCGTCCTTGGCACTGAACTCGTTT	1829	CCGTCCTTGGCACTGAACTCGTT	1830	CCGTCCTTGGCACTGAACTCGT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del2	1831	TTTCCCGTCTTGGCTGGAACCTGTT	1832	TTCCCGTCTTGGCTGGAACCTCGT	1833	TCCCGTCTTGGCTGGAACCTCG
LDLRex2(27;68;123;30)_100_d2_r	1834	ACGAGTCCAGTCAAGACGGGAAAT	1835	CGAGTCCAGTCAAGACGGGAAA	1836	GAGTCCAGTCAAGACGGGAA
LDLRex2(27;68;123;30)_101_d2_f	1837	ATTCCCGTCTTGAAGTGAACCTCGT	1838	TTCCCGTCTTGAAGTGAACCTCG	1839	TTCCCGTCTTGAAGTGAACCTC
LDLRex2(27;68;123;30)_102_d2_f	1840	CGAGTCCAGTGAAGACGGGAAATG	1841	GAGTCCAGTGAAGACGGGAAAT	1842	AGTCCAGTGAAGACGGGAAA
LDLRex2(27;68;123;30)_102_d2_r	1843	CATTCCCGTCTTCACTGGAACCTCG	1844	ATTCCCGTCTTCACTGGAACCTC	1845	TTCCCGTCTTCACTGGAACCT
LDLRex2(27;68;123;30)_103_d2_f	1846	GAGTCCAGTGCAGACGGGAAATGC	1847	AGTCCAGTGCAGACGGGAAATG	1848	GTTCCAGTGCAGACGGGAAAT
LDLRex2(27;68;123;30)_103_d2_r	1849	GCATTTCGGTCTGCACTGGAACCTC	1850	CATTTCGGTCTGCACTGGAACCT	1851	ATTTCCCGTCTGCACTGGAAC
LDLRex2(27;68;123;30)_104_d2_f	1852	AGTTCAGTGCAGACGGGAAATGCA	1853	GTTCCAGTGCAGACGGGAAATGC	1854	TTCAGTGCAGACGGGAAATG
LDLRex2(27;68;123;30)_104_d2_r	1855	TGCATTTCCCGTTCGCACTGGAACCT	1856	GCATTTCCCGTTCGCACTGGAAC	1857	CATTTCCCGTTCGCACTGGA
LDLRex2(27;68;123;30)_105_d2_f	1858	GTTCCAGTGCAGACGGGAAATGCAT	1859	TTCAGTGCAGACGGGAAATGCA	1860	TCCAGTGCAGACGGGAAATGC
LDLRex2(27;68;123;30)_105_d2_r	1861	ATGCATTTCCCGTTCGCACTGGAAC	1862	TGCATTTCCCGTTCGCACTGGA	1863	GCATTTCCCGTTCGCACTGGA
LDLRex2(27;68;123;30)_106_d2_f	1864	TTCCAGTGCAGACGGGAAATGCATC	1865	TCCAGTGCAGACGGGAAATGCAT	1866	CCAGTGCAGACGGGAAATGCA
LDLRex2(27;68;123;30)_106_d2_r	1867	GATGCATTTCCCGTTCGCACTGGA	1868	ATGCATTTCCCGTTCGCACTGGA	1869	TGCATTTCCCGTTCGCACTGG
LDLRex2(27;68;123;30)_107_d2_f	1870	TCCAGTGCAGACGGGAAATGCATCT	1871	CCAGTGCAGACGGGAAATGCATC	1872	CAGTGCAGACGGGAAATGCAT
LDLRex2(27;68;123;30)_107_d2_r	1873	AGATGCATTTCCCGTTCGCACTGGA	1874	GATGCATTTCCCGTTCGCACTGG	1875	ATGCATTTCCCGTTCGCACTG
LDLRex2(27;68;123;30)_108_d2_f	1876	CCAGTGCAGACGGGAAATGCATCTC	1877	CAGTGCAGACGGGAAATGCATCT	1878	AGTGCAGACGGGAAATGCATC
LDLRex2(27;68;123;30)_108_d2_r	1879	GAGATGCATTTCTCTTGGCACTGG	1880	AGATGCATTTCTCTTGGCACTG	1881	GATGCATTTCTCTTGGCACT
LDLRex2(27;68;123;30)_109_d2_f	1882	CAGTGCAGACGGGAAATGCATCTCC	1883	AGTGCAGACGGGAAATGCATCTC	1884	GTGCCAAGACGGGAAATGCATCT
LDLRex2(27;68;123;30)_109_d2_r	1885	GGAGATGCATTTCTCTTGGCACTG	1886	GAGATGCATTTCTCTTGGCACT	1887	AGATGCATTTCTCTTGGCAC
LDLRex2(27;68;123;30)_110_d2_f	1888	AGTGCAGACGGGAAATGCATCTCCT	1889	GTGCCAAGACGGGAAATGCATCTCC	1890	TGCCAAGACGGGAAATGCATCTC
LDLRex2(27;68;123;30)_110_d2_r	1891	AGGAGATGCATTTCTCTTGGCACT	1892	GGAGATGCATTTCTCTTGGCAC	1893	GAGATGCATTTCTCTTGGCA
LDLRex2(27;68;123;30)_111_d2_f	1894	GTGCCAAGACGGGAAATGCATCTCCTA	1895	TGCCAAGACGGGAAATGCATCTCT	1896	GCCAAGACGGGAAATGCATCTCC
LDLRex2(27;68;123;30)_111_d2_r	1897	TAGGAGATGCATTTCTCTTGGCAC	1898	AGGAGATGCATTTCTCTTGGCA	1899	GGAGATGCATTTCTCTTGGC
LDLRex2(27;68;123;30)_112_d2_f	1900	TGCCAAGACGGGATGCATCTCTCTAC	1901	GCCAAGACGGGATGCATCTCTA	1902	CCAAGACGGGATGCATCTCTCT
LDLRex2(27;68;123;30)_112_d2_r	1903	GTAGGAGATGCATTTCTCTTGGCA	1904	TAGGAGATGCATTTCTCTTGGC	1905	AGGAGATGCATTTCTCTTGG
LDLRex2(27;68;123;30)_113_d2_f	1906	GCCAAGACGGGATGCATCTCTCTACA	1907	CCAAGACGGGATGCATCTCTCTAC	1908	CAAGACGGGATGCATCTCTCTA
LDLRex2(27;68;123;30)_113_d2_r	1909	TGTAGGAGATGCATTTCTCTTGGC	1910	GTAGGAGATGCATTTCTCTTGG	1911	TAGGAGATGCATTTCTCTTGG
LDLRex2(27;68;123;30)_114_d2_f	1912	CCAAGACGGGAAAGCATCTCTCTACAA	1913	CAAGACGGGAAAGCATCTCTCTACA	1914	AAGACGGGAAAGCATCTCTCTAC
LDLRex2(27;68;123;30)_114_d2_r	1915	TTGTAGGAGATGCTTTCCCGTCTTGG	1916	TGTAGGAGATGCTTTCCCGTCTTG	1917	GTAGGAGATGCTTTCCCGTCTT
LDLRex2(27;68;123;30)_115_d2_f	1918	CAAGACGGGAAACATCTCTCTACAAG	1919	AAGACGGGAAACATCTCTCTACAA	1920	AGACGGGAAACATCTCTCTACA
LDLRex2(27;68;123;30)_115_d2_r	1921	CTGTAGGAGATGTTTCCCGTCTTGG	1922	TTGTAGGAGATGTTTCCCGTCTT	1923	TGTAGGAGATGTTTCCCGTCT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del2	1924	AAGACGGGAAATATCTCTACAAGT	1925	AGACGGGAAATATCTCTACAAG	1926	GACGGGAAATATCTCTACAA
LDLRex2(27;68;123;30)_116_d2_f	1927	ACTTGTAGGAGATATTTCCGTCTT	1928	CTTGTAGGAGATATTTCCGTCT	1929	TTGTAGGAGATATTTCCGTC
LDLRex2(27;68;123;30)_116_d2_r	1930	AGACGGGAAATGCTCTACAAGTG	1931	GACGGGAAATGCTCTACAAGT	1932	ACGGGAAATGCTCTACAAG
LDLRex2(27;68;123;30)_117_d2_f	1933	CAC TTGTAGGAGACATTTCCGTCT	1934	ACTTGTAGGAGACATTTCCGTCT	1935	CTTGTAGGAGACATTTCCGT
LDLRex2(27;68;123;30)_117_d2_r	1936	GACGGGAAATGCTCTACAAGTG	1937	GACGGGAAATGCTCTACAAGT	1938	CGGGAAATGCTCTCTACAAGT
LDLRex2(27;68;123;30)_118_d2_f	1939	CCACTTGTAGGAGGCAATTTCCGTCT	1940	CAC TTGTAGGAGGCAATTTCCGT	1941	ACTTGTAGGAGGCAATTTCCG
LDLRex2(27;68;123;30)_118_d2_r	1942	ACGGGAAATGCATCTACAAGTGG	1943	ACGGGAAATGCATCTACAAGTG	1944	GGGAAATGCATCTACAAGTG
LDLRex2(27;68;123;30)_119_d2_f	1945	CCCACTTGTAGGATGCAATTTCCGT	1946	CCCACTTGTAGGATGCAATTTCCG	1947	CAC TTGTAGGATGCAATTTCCC
LDLRex2(27;68;123;30)_119_d2_r	1948	CGGGAAATGCATCTACAAGTGGT	1949	GGGAAATGCATCTACAAGTGG	1950	GGAAATGCATCTACAAGTGG
LDLRex2(27;68;123;30)_120_d2_f	1951	ACCACTTGTAGGATGCAATTTCCG	1952	CCCACTTGTAGGATGCAATTTCC	1953	CCACTTGTAGGATGCAATTTCC
LDLRex2(27;68;123;30)_120_d2_r	1954	GGGAAATGCATCTACAAGTGGTCT	1955	GGAAATGCATCTACAAGTGGT	1956	GAAATGCATCTACAAGTGG
LDLRex2(27;68;123;30)_121_d2_f	1957	GACCACTTGTAGGATGCAATTTCC	1958	ACCACTTGTAGGATGCAATTTCC	1959	CCCACTTGTAGGATGCAATTTCC
LDLRex2(27;68;123;30)_121_d2_r	1960	GGAAATGCATCTACAAGTGGTCT	1961	GAAATGCATCTACAAGTGGTCT	1962	AAATGCATCTACAAGTGGT
LDLRex2(27;68;123;30)_122_d2_f	1963	AGACCACTTGTAGGATGCAATTTCC	1964	GACCACTTGTAGGATGCAATTTCC	1965	ACCACTTGTAGGATGCAATTT
LDLRex2(27;68;123;30)_122_d2_r	1966	GAAATGCATCTACAAGTGGTCTG	1967	AAATGCATCTACAAGTGGTCT	1968	AAATGCATCTACAAGTGGTCT
LDLRex2(27;68;123;30)_123_d2_f	1969	CAGACCACTTGTAGGATGCAATTTCC	1970	AGACCACTTGTAGGATGCAATTT	1971	GACCACTTGTAGGATGCAATTT
LDLRex2(27;68;123;30)_123_d2_r	1972	AAATGCATCTCCAAGTGGTCTGC	1973	AATGCATCTCCAAGTGGTCTG	1974	ATGCATCTCCAAGTGGTCT
LDLRex2(27;68;123;30)_124_d2_f	1975	GCAGACCACTTGGGAGATGCAATTT	1976	CAGACCACTTGGGAGATGCAATTT	1977	AGACCACTTGGGAGATGCAAT
LDLRex2(27;68;123;30)_124_d2_r	1978	AATGCATCTCTAAGTGGTCTGCG	1979	ATGCATCTCTAAGTGGTCTGCG	1980	TGCATCTCTAAGTGGTCTG
LDLRex2(27;68;123;30)_125_d2_f	1981	CGCAGACCACTTAGGAGATGCAATTT	1982	GCAGACCACTTAGGAGATGCAAT	1983	CAGACCACTTAGGAGATGCA
LDLRex2(27;68;123;30)_125_d2_r	1984	ATGCATCTCTAAGTGGTCTGCGA	1985	TGCATCTCTAAGTGGTCTGCG	1986	GCACTCTCTAAGTGGTCTGCG
LDLRex2(27;68;123;30)_126_d2_f	1987	TCGACAGACCACTTAGGAGATGCAAT	1988	CGCAGACCACTTAGGAGATGCA	1989	GCAGACCACTTAGGAGATGCA
LDLRex2(27;68;123;30)_126_d2_r	1990	TGCATCTCTACGTGGTCTGCGAT	1991	GCATCTCTACGTGGTCTGCGA	1992	CATCTCTACGTGGTCTGCG
LDLRex2(27;68;123;30)_127_d2_f	1993	ATCGACAGACCACTTAGGAGATGCA	1994	TCGACAGACCACTTAGGAGATGCG	1995	CGCAGACCACTTAGGAGATG
LDLRex2(27;68;123;30)_127_d2_r	1996	GCATCTCTACATGGGTCTGCGATG	1997	CATCTCTACATGGGTCTGCGAT	1998	ATCTCTACATGGGTCTGCGA
LDLRex2(27;68;123;30)_128_d2_f	1999	CATCGCAGACCACTTAGGAGATGCG	2000	ATCGCAGACCACTTAGGAGATG	2001	TCGCAGACCACTTAGGAGAT
LDLRex2(27;68;123;30)_128_d2_r	2002	CATCTCTACAAGGTCTGCGATGG	2003	ATCTCTACAAGGTCTGCGATG	2004	TCTCTACAAGGTCTGCGAT
LDLRex2(27;68;123;30)_129_d2_f	2005	CCATCGCAGACCACTTAGGAGATG	2006	CATCGCAGACCACTTAGGAGAT	2007	ATCGCAGACCACTTAGGAGA
LDLRex2(27;68;123;30)_129_d2_r	2008	ATCTCTACAAGGTCTGCGATGGC	2009	TCTCTACAAGGTCTGCGATGG	2010	CTCCTACAAGGTCTGCGATG
LDLRex2(27;68;123;30)_130_d2_f	2011	GCCATCGCAGACCACTTAGGAGAT	2012	CCATCGCAGACCACTTAGGAGA	2013	CATCGCAGACCACTTAGGAG
LDLRex2(27;68;123;30)_130_d2_r	2014	TCTCTACAAGGTCTGCGATGGCA	2015	CTCCTACAAGGTCTGCGATGGC	2016	TCCTACAAGGTCTGCGATGG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del2						
LDLRex2(27;68;123;30)_131_d2_r	2017	TGCCATCGCAGACACTTGTAGGAGA	2018	GCCATCGCAGACACTTGTAGGAG	2019	CCATCGCAGACACTTGTAGGA
LDLRex2(27;68;123;30)_132_d2_f	2020	CTCTACAAAGTGTCTGCGATGGCAG	2021	TCCTACAAAGTGTCTGCGATGGCA	2022	CCTACAAAGTGTCTGCGATGGC
LDLRex2(27;68;123;30)_132_d2_r	2023	CTGCCATCGCAGACACTTGTAGGAG	2024	TGCCATCGCAGACACTTGTAGGA	2025	GCCATCGCAGACACTTGTAGG
LDLRex2(27;68;123;30)_133_d2_f	2026	TCTACAAAGTGGCTGGATGGCAGC	2027	CCTACAAAGTGGCTGGATGGCAG	2028	CTACAAAGTGGCTGGATGGCA
LDLRex2(27;68;123;30)_133_d2_r	2029	GCTGCCATCGCAGCCACTTGTAGGA	2030	CTGCCATCGCAGCCACTTGTAGG	2031	TGCCATCGCAGCCACTTGTAG
LDLRex2(27;68;123;30)_134_d2_f	2032	CCTACAAAGTGGGTGCGATGGCAGCG	2033	CTACAAAGTGGGTGCGATGGCAGC	2034	TACAAAGTGGGTGCGATGGCAG
LDLRex2(27;68;123;30)_134_d2_r	2035	CGCTGCCATCGCACCCTTGTAGG	2036	GCTGCCATCGCACCCTTGTAG	2037	CTGCCATCGCACCCTTGT
LDLRex2(27;68;123;30)_135_d2_f	2038	CTACAAAGTGGGTGCGATGGCAGCGC	2039	TACAAAGTGGGTGCGATGGCAGCG	2040	ACAAAGTGGGTGCGATGGCAGC
LDLRex2(27;68;123;30)_135_d2_r	2041	GCGCTGCCATCGCACCCTTGTAG	2042	CGCTGCCATCGCACCCTTGT	2043	GCTGCCATCGCACCCTTGT
LDLRex2(27;68;123;30)_136_d2_f	2044	TACAAAGTGGGTCCGATGGCAGCGCT	2045	ACAAAGTGGGTCCGATGGCAGCGC	2046	CAAGTGGGTCCGATGGCAGCG
LDLRex2(27;68;123;30)_136_d2_r	2047	AGCGCTGCCATCGGACCCTTGT	2048	GCGCTGCCATCGGACCCTTGT	2049	CGCTGCCATCGGACCCTTGT
LDLRex2(27;68;123;30)_137_d2_f	2050	ACAAAGTGGGTCTGATGGCAGCGCTG	2051	CAAGTGGGTCTGATGGCAGCGCT	2052	AAGTGGGTCTGATGGCAGCGC
LDLRex2(27;68;123;30)_137_d2_r	2053	CAGCGCTGCCATCAGACCCTTGT	2054	AGCGCTGCCATCAGACCCTTGT	2055	GCGCTGCCATCAGACCCTT
LDLRex2(27;68;123;30)_138_d2_f	2056	CAAGTGGGTCTGATGGCAGCGCTGA	2057	AAGTGGGTCTGATGGCAGCGCTG	2058	AGTGGGTCTGATGGCAGCGCT
LDLRex2(27;68;123;30)_138_d2_r	2059	TCAGCGCTGCCATCAGACCCTTGT	2060	CAGCGCTGCCATCAGACCCTT	2061	AGCGCTGCCATCAGACCCT
LDLRex2(27;68;123;30)_139_d2_f	2062	AAGTGGGTCTGCTGGCAGCGCTGAG	2063	AGTGGGTCTGCTGGCAGCGCTGA	2064	GTGGGTCTGCTGGCAGCGCTG
LDLRex2(27;68;123;30)_139_d2_r	2065	CTCAGCGCTGCCAGCAGACCCTT	2066	TCAGCGCTGCCAGCAGACCCT	2067	CAGCGCTGCCAGCAGACCCT
LDLRex2(27;68;123;30)_140_d2_f	2068	AGTGGGTCTGCGGGCAGCGCTGAGT	2069	GTGGGTCTGCGGGCAGCGCTGAG	2070	TGGGTCTGCGGGCAGCGCTGA
LDLRex2(27;68;123;30)_140_d2_r	2071	ACTCAGCGCTGCCCGCAGACCCT	2072	CTCAGCGCTGCCCGCAGACCCT	2073	TCAGCGCTGCCCGCAGACCCT
LDLRex2(27;68;123;30)_141_d2_f	2074	GTGGGTCTGCGAGCAGCGCTGAGTG	2075	TGGGTCTGCGAGCAGCGCTGAGT	2076	GGGTCTGCGAGCAGCGCTGAG
LDLRex2(27;68;123;30)_141_d2_r	2077	CACTCAGCGCTGCTCGCAGACCCT	2078	ACTCAGCGCTGCTCGCAGACCCT	2079	CTCAGCGCTGCTCGCAGACCCT
LDLRex2(27;68;123;30)_142_d2_f	2080	TGGGTCTGCGATCAGCGCTGAGTGC	2081	GGGTCTGCGATCAGCGCTGAGTG	2082	GGTCTGCGATCAGCGCTGAGT
LDLRex2(27;68;123;30)_142_d2_r	2083	GCACTCAGCGCTGATCGCAGACCCT	2084	CACTCAGCGCTGATCGCAGACCCT	2085	ACTCAGCGCTGATCGCAGACCCT
LDLRex2(27;68;123;30)_143_d2_f	2086	GGGTCTGCGATGAGCGCTGAGTGCC	2087	GGTCTGCGATGAGCGCTGAGTGC	2088	GTCTGCGATGAGCGCTGAGTG
LDLRex2(27;68;123;30)_143_d2_r	2089	GGCACTCAGCGCTCATCGCAGACCCT	2090	GCACTCAGCGCTCATCGCAGACCCT	2091	CACTCAGCGCTCATCGCAGACCCT
LDLRex2(27;68;123;30)_144_d2_f	2092	GGTCTGCGATGGGCGCTGAGTGCCA	2093	GTCTGCGATGGGCGCTGAGTGCC	2094	TCTGCGATGGGCGCTGAGTGC
LDLRex2(27;68;123;30)_144_d2_r	2095	TGGCACTCAGCGCCCTATCGCAGACCCT	2096	GGCACTCAGCGCCCTATCGCAGACCCT	2097	GCACTCAGCGCCCTATCGCAGACCCT
LDLRex2(27;68;123;30)_145_d2_f	2098	GTCTGCGATGGCCGCTGAGTGCCAG	2099	TCTGCGATGGCCGCTGAGTGCCA	2100	CTGCGATGGCCGCTGAGTGCC
LDLRex2(27;68;123;30)_145_d2_r	2101	CTGGCACTCAGCGGCCCTATCGCAGACCCT	2102	TGGCACTCAGCGGCCCTATCGCAGACCCT	2103	GGCACTCAGCGGCCCTATCGCAGACCCT
LDLRex2(27;68;123;30)_146_d2_f	2104	TCTGCGATGGCAGCTGAGTGCCAGG	2105	CTGCGATGGCAGCTGAGTGCCAG	2106	TGCGATGGCAGCTGAGTGCCA
LDLRex2(27;68;123;30)_146_d2_r	2107	CCTGGCACTCAGCTGCCATCGCAG	2108	CTGGCACTCAGCTGCCATCGCAG	2109	TGGCACTCAGCTGCCATCGCA

Table 1

del2	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_147_d2_f	2110	CTGCGATGGCAGCTGAGTGCCAGGA	2111	TGGATGGCAGCTGAGTGCCAGG	2112	GCGATGGCAGCTGAGTGCCAG
LDLRex2(27;68;123;30)_147_d2_r	2113	TCCTGGCACTCAGCTGCCATCGCAG	2114	CCTGGCACTCAGCTGCCATCGCA	2115	CTGGCACTCAGCTGCCATCGC
LDLRex2(27;68;123;30)_148_d2_f	2116	TGGATGGCAGCTGAGTGCCAGGAT	2117	GCGATGGCAGCTGAGTGCCAGGA	2118	CGATGGCAGCTGAGTGCCAGG
LDLRex2(27;68;123;30)_148_d2_r	2119	ATCTGGCACTCAGCTGCCATCGCA	2120	TCCTGGCACTCAGCTGCCATCGC	2121	CCTGGCACTCAGCTGCCATCG
LDLRex2(27;68;123;30)_149_d2_f	2122	GCGATGGCAGCGGAGTGCCAGGATG	2123	CGATGGCAGCGGAGTGCCAGGAT	2124	GATGGCAGCGGAGTGCCAGGA
LDLRex2(27;68;123;30)_149_d2_r	2125	CATCTGGCACTCGCTGCCATCGC	2126	ATCTGGCACTCGCTGCCATCG	2127	TCCTGGCACTCGCTGCCATC
LDLRex2(27;68;123;30)_150_d2_f	2128	CGATGGCAGCGCAGTGCCAGGATGG	2129	GATGGCAGCGCAGTGCCAGGATG	2130	ATGGCAGCGCAGTGCCAGGAT
LDLRex2(27;68;123;30)_150_d2_r	2131	CCATCTGGCACTGCGTGCCATCG	2132	CATCTGGCACTGCGTGCCATC	2133	ATCTGGCACTGCGTGCCAT
LDLRex2(27;68;123;30)_151_d2_f	2134	GATGGCAGCGCTGTGCCAGGATGG	2135	ATGGCAGCGCTGTGCCAGGATGG	2136	TGGCAGCGCTGTGCCAGGATG
LDLRex2(27;68;123;30)_151_d2_r	2137	GCCATCTGGCACAGCGCTGCCATC	2138	CCATCTGGCACAGCGTGCCAT	2139	CATCTGGCACAGCGTGCCA
LDLRex2(27;68;123;30)_152_d2_f	2140	ATGGCAGCGCTGTGCCAGGATGGCT	2141	TGGCAGCGCTGTGCCAGGATGGC	2142	GGCAGCGCTGTGCCAGGATGG
LDLRex2(27;68;123;30)_152_d2_r	2143	AGCCATCTGGCACAGCGCTGCCAT	2144	GCCATCTGGCACAGCGTGCCA	2145	CCATCTGGCACAGCGCTGCC
LDLRex2(27;68;123;30)_153_d2_f	2146	TGGCAGCGCTGAGCCAGGATGGCTC	2147	GGCAGCGCTGAGCCAGGATGGCT	2148	GCAAGCGCTGAGCCAGGATGGC
LDLRex2(27;68;123;30)_153_d2_r	2149	GAGCCATCTGGCTCAGCGTGCCA	2150	AGCCATCTGGCTCAGCGTGCC	2151	GCCATCTGGCTCAGCGTGCC
LDLRex2(27;68;123;30)_154_d2_f	2152	GGCAGCGCTGAGCCAGGATGGCTCT	2153	GCAAGCGCTGAGCCAGGATGGCTC	2154	CAGCGCTGAGCCAGGATGGCT
LDLRex2(27;68;123;30)_154_d2_r	2155	AGAGCCATCTGGCTCAGCGTGCC	2156	GAGCCATCTGGCTCAGCGTGCC	2157	AGCCATCTGGCTCAGCGCTG
LDLRex2(27;68;123;30)_155_d2_f	2158	GCAGCGTGAGTCAGGATGGCTCTG	2159	CAGCGTGAGTCAGGATGGCTCT	2160	AGCGTGAGTCAGGATGGCTC
LDLRex2(27;68;123;30)_155_d2_r	2161	CAGAGCCATCTGACTCAGCGCTGC	2162	AGAGCCATCTGACTCAGCGCTG	2163	GAGCCATCTGACTCAGCGCT
LDLRex2(27;68;123;30)_156_d2_f	2164	CAGCGCTGAGTGAGGATGGCTCTGA	2165	AGCGCTGAGTGAGGATGGCTCTG	2166	GCGTGAGTGAGGATGGCTCT
LDLRex2(27;68;123;30)_156_d2_r	2167	TCAGAGCCATCTCACTCAGCGCTG	2168	CAGAGCCATCTCACTCAGCGCT	2169	AGAGCCATCTCACTCAGCGC
LDLRex2(27;68;123;30)_157_d2_f	2170	AGCGCTGAGTGCGGATGGCTCTGAT	2171	GCGTGAGTGCGGATGGCTCTGA	2172	CGCTGAGTGCGGATGGCTCTG
LDLRex2(27;68;123;30)_157_d2_r	2173	ATCAGAGCCATCCGCACTCAGCGCT	2174	TCAGAGCCATCCGCACTCAGCGC	2175	CAGAGCCATCCGCACTCAGCG
LDLRex2(27;68;123;30)_158_d2_f	2176	GCGCTGAGTGCCGATGGCTCTGATG	2177	CGCTGAGTGCCGATGGCTCTGAT	2178	GCTGAGTGCCGATGGCTCTGA
LDLRex2(27;68;123;30)_158_d2_r	2179	CATCAGAGCCATCGGCACTCAGCGC	2180	ATCAGAGCCATCGGCACTCAGCG	2181	TCAGAGCCATCGGCACTCAGC
LDLRex2(27;68;123;30)_159_d2_f	2182	CGCTGAGTGCCAATGGCTCTGATGA	2183	GCTGAGTGCCAATGGCTCTGATG	2184	CTGAGTGCCAATGGCTCTGAT
LDLRex2(27;68;123;30)_159_d2_r	2185	TCATCAGAGCCATTGGCACTCAGCG	2186	CATCAGAGCCATTGGCACTCAGC	2187	ATCAGAGCCATTGGCACTCAG
LDLRex2(27;68;123;30)_160_d2_f	2188	GCTGAGTGCCAGTGCGCTCTGATGAG	2189	CTGAGTGCCAGTGCGCTCTGATGA	2190	TGAGTGCCAGTGCGCTCTGATG
LDLRex2(27;68;123;30)_160_d2_r	2191	CTCATCAGAGCCACTGGCACTCAGC	2192	TCATCAGAGCCACTGGCACTCAG	2193	CATCAGAGCCACTGGCACTCA
LDLRex2(27;68;123;30)_161_d2_f	2194	CTGAGTGCCAGGGGCTCTGATGATG	2195	TGAGTGCCAGGGGCTCTGATGAG	2196	GAGTGCCAGGGGCTCTGATGA
LDLRex2(27;68;123;30)_161_d2_r	2197	ACTCATCAGAGCCCTTGGCACTCAG	2198	CTCATCAGAGCCCTTGGCACTCA	2199	TCATCAGAGCCCTTGGCACTC
LDLRex2(27;68;123;30)_162_d2_f	2200	TGAGTGCCAGGAGCTCTGATGATGC	2201	GAGTGCCAGGAGCTCTGATGATG	2202	AGTGCCAGGAGCTCTGATGAG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del2						
LDLRex2(27;68;123;30)_162_d2_r	2203	GACTCATCAGAGCTCTGGCACTCA	2204	ACTCATCAGAGCTCTGGCACTC	2205	CTCATCAGAGCTCTGGCACT
LDLRex2(27;68;123;30)_163_d2_f	2206	GAGTGCCAGGATCTCTGATGATCC	2207	AGTGCCAGGATCTCTGATGATC	2208	GTGCCAGGATCTCTGATGAT
LDLRex2(27;68;123;30)_163_d2_r	2209	GGACTCATCAGAGATCCTGGCACTC	2210	GACTCATCAGAGATCCTGGCACT	2211	ACTCATCAGAGATCCTGGCAC
LDLRex2(27;68;123;30)_164_d2_f	2212	AGTGCCAGGATGCTCTGATGATCCC	2213	GTGCCAGGATGCTCTGATGATCC	2214	TGCCAGGATGCTCTGATGATC
LDLRex2(27;68;123;30)_164_d2_r	2215	GGGACTCATCAGACATCCTGGCACT	2216	GGACTCATCAGACATCCTGGCAC	2217	GACTCATCAGACATCCTGGCA
LDLRex2(27;68;123;30)_165_d2_f	2218	GTGCCAGGATGGCTGATGATGCCA	2219	TGCCAGGATGGCTGATGATGCC	2220	GCAGGATGGCTGATGATGCC
LDLRex2(27;68;123;30)_165_d2_r	2221	TGGGACTCATCAGCCATCCTGGCAC	2222	GGGACTCATCAGCCATCCTGGCA	2223	GGACTCATCAGCCATCCTGGC
LDLRex2(27;68;123;30)_166_d2_f	2224	TGCCAGGATGGCTGATGATGCCAG	2225	GCCAGGATGGCTGATGATGCCA	2226	CCAGGATGGCTGATGATGCC
LDLRex2(27;68;123;30)_166_d2_r	2227	CTGGGACTCATCAGCCATCCTGGCA	2228	TGGGACTCATCAGCCATCCTGGC	2229	GGGACTCATCAGCCATCCTGG
LDLRex2(27;68;123;30)_167_d2_f	2230	GCCAGGATGGCTGATGATGCCAGG	2231	CCAGGATGGCTGATGATGCCAG	2232	CAGGATGGCTGATGATGCCA
LDLRex2(27;68;123;30)_167_d2_r	2233	CCTGGGACTCATCAGCCATCCTGGC	2234	CTGGGACTCATCAGCCATCCTGG	2235	TGGGACTCATCAGCCATCCTG
LDLRex2(27;68;123;30)_168_d2_f	2236	CCAGGATGGCTCATGATGCCAGGA	2237	CAGGATGGCTCATGATGCCAGG	2238	AGGATGGCTCATGATGCCAG
LDLRex2(27;68;123;30)_168_d2_r	2239	TCCTGGGACTCATGAGCCATCCTGG	2240	CCTGGGACTCATGAGCCATCCTG	2241	CTGGGACTCATGAGCCATCCT
LDLRex2(27;68;123;30)_169_d2_f	2242	CAGGATGGCTCTTGATGCCAGGAG	2243	AGGATGGCTCTTGATGCCAGGA	2244	GGATGGCTCTTGATGCCAGG
LDLRex2(27;68;123;30)_169_d2_r	2245	CTCCTGGGACTCAAGAGCCATCCTG	2246	TCCTGGGACTCAAGAGCCATCCT	2247	CCTGGGACTCAAGAGCCATCC
LDLRex2(27;68;123;30)_170_d2_f	2248	AGGATGGCTCTGGAGTCCAGGAGA	2249	GGATGGCTCTGGAGTCCAGGAG	2250	GATGGCTCTGGAGTCCAGGA
LDLRex2(27;68;123;30)_170_d2_r	2251	TCCTCTGGGACTCCAGAGCCATCCT	2252	CTCCTGGGACTCCAGAGCCATCC	2253	TCCTGGGACTCCAGAGCCATC
LDLRex2(27;68;123;30)_171_d2_f	2254	GGATGGCTCTGAAGTCCAGGAGAC	2255	GATGGCTCTGAAGTCCAGGAGA	2256	ATGGCTCTGAAGTCCAGGAG
LDLRex2(27;68;123;30)_171_d2_r	2257	GTCTCTGGGACTTCAGAGCCATCC	2258	TCTCTGGGACTTCAGAGCCATC	2259	CTCTGGGACTTCAGAGCCAT
LDLRex2(27;68;123;30)_172_d2_f	2260	GATGGCTCTGATGTCCAGGAGACG	2261	ATGGCTCTGATGTCCAGGAGAC	2262	TGGCTCTGATGTCCAGGAGA
LDLRex2(27;68;123;30)_172_d2_r	2263	CGTCTCTGGGACATCAGAGCCATC	2264	GTCTCTGGGACATCAGAGCCAT	2265	TCTCTGGGACATCAGAGCCA
LDLRex2(27;68;123;30)_173_d2_f	2266	ATGGCTCTGATGTCCAGGAGACGT	2267	TGGCTCTGATGTCCAGGAGACG	2268	GGCTCTGATGTCCAGGAGAC
LDLRex2(27;68;123;30)_173_d2_r	2269	ACGTCTCTGGGACATCAGAGCCAT	2270	CGTCTCTGGGACATCAGAGCCA	2271	GTCTCTGGGACATCAGAGCC
LDLRex2(27;68;123;30)_174_d2_f	2272	TGGCTCTGATGACCCAGGAGACGTG	2273	GGCTCTGATGACCCAGGAGACGT	2274	GCTCTGATGACCCAGGAGACG
LDLRex2(27;68;123;30)_174_d2_r	2275	CACGTCTCTGGGTCATCAGAGCCA	2276	ACGTCTCTGGGTCATCAGAGCC	2277	CGTCTCTGGGTCATCAGAGC
LDLRex2(27;68;123;30)_175_d2_f	2278	GGCTCTGATGAGCCAGGAGACGTGC	2279	GCTCTGATGAGCCAGGAGACGTG	2280	CTCTGATGAGCCAGGAGACGT
LDLRex2(27;68;123;30)_175_d2_r	2281	GCACGTCTCTGGCTCATCAGAGCC	2282	CACGTCTCTGGCTCATCAGAGC	2283	ACGTCTCTGGCTCATCAGAG
LDLRex2(27;68;123;30)_176_d2_f	2284	GCTCTGATGATCAGGAGACGTGCT	2285	CTCTGATGATCAGGAGACGTGC	2286	TCTGATGATCAGGAGACGTG
LDLRex2(27;68;123;30)_176_d2_r	2287	AGCAGCTCTCTGACTCATCAGAGC	2288	GCAGTCTCTGACTCATCAGAG	2289	CAGTCTCTGACTCATCAGA
LDLRex2(27;68;123;30)_177_d2_f	2290	CTCTGATGATCAGGAGACGTGCTG	2291	TCTGATGATCAGGAGACGTGCT	2292	CTGATGATCAGGAGACGTGC
LDLRex2(27;68;123;30)_177_d2_r	2293	CAGCACGTCTCTGACTCATCAGAG	2294	AGCACGTCTCTGACTCATCAGA	2295	GCACGTCTCTGACTCATCAG

Table 1

del2	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_178_d2_f	2296	TCTGATGAGTCCGGAGACGTGCTGT	2297	CTGATGAGTCCGGAGACGTGCTG	2298	TGATGAGTCCGGAGACGTGCT
LDLRex2(27;68;123;30)_178_d2_r	2299	ACAGCAGTCTCCGGACTCATCAGA	2300	CAGCAGTCTCCGGACTCATCAG	2301	AGCAGTCTCCGGACTCATCA
LDLRex2(27;68;123;30)_179_d2_f	2302	CTGATGAGTCCGGAGACGTGCTGTG	2303	TGATGAGTCCGGAGACGTGCTGT	2304	GATGAGTCCGGAGACGTGCTG
LDLRex2(27;68;123;30)_179_d2_r	2305	CACAGCAGTCTCCGGACTCATCAG	2306	CACAGCAGTCTCCGGACTCATCA	2307	CAGCAGTCTCCGGACTCATC
LDLRex2(27;68;123;30)_180_d2_f	2308	TGATGAGTCCCAAGACGTGCTGTGA	2309	GATGAGTCCCAAGACGTGCTGTG	2310	ATGAGTCCCAAGACGTGCTGT
LDLRex2(27;68;123;30)_180_d2_r	2311	TCACAGCACGTCTTGGGACTCATCA	2312	CACAGCACGTCTTGGGACTCATC	2313	ACAGCACGTCTTGGGACTCAT
LDLRex2(27;68;123;30)_181_d2_f	2314	GATGAGTCCAGGACGTGCTGTGAG	2315	ATGAGTCCAGGACGTGCTGTGA	2316	TGAGTCCAGGACGTGCTGTG
LDLRex2(27;68;123;30)_181_d2_r	2317	CTCAGCAGCAGTCTCTGGGACTATC	2318	TCACAGCAGTCTCTGGGACTCAT	2319	CACAGCAGTCTCTGGGACTCA
LDLRex2(27;68;123;30)_182_d2_f	2320	ATGAGTCCAGGACGTGCTGTGAGT	2321	TGAGTCCAGGACGTGCTGTGAG	2322	GAGTCCAGGACGTGCTGTGA
LDLRex2(27;68;123;30)_182_d2_r	2323	ACTCAGCAGCAGTCTCTGGGACTCAT	2324	CTCAGCAGCAGTCTCTGGGACTCA	2325	TCACAGCAGTCTCTGGGACTC
LDLRex2(27;68;123;30)_183_d2_f	2326	TGAGTCCAGGACGTGCTGTGAGTC	2327	GAGTCCAGGACGTGCTGTGAGT	2328	AGTCCAGGACGTGCTGTGAG
LDLRex2(27;68;123;30)_183_d2_r	2329	GACTCAGCAGCAGTCTCTGGGACTCA	2330	ACTCAGCAGCAGTCTCTGGGACTC	2331	CTCAGCAGCAGTCTCTGGGACT
LDLRex2(27;68;123;30)_184_d2_f	2332	GAGTCCAGGAGGTGCTGTGAGTCC	2333	AGTCCAGGAGGTGCTGTGAGTC	2334	GTCCAGGAGGTGCTGTGAGT
LDLRex2(27;68;123;30)_184_d2_r	2335	GGACTCAGCAGCAGTCTCTGGGACTC	2336	GACTCAGCAGCAGTCTCTGGGACT	2337	ACTCAGCAGCAGTCTCTGGGAC
LDLRex2(27;68;123;30)_185_d2_f	2338	AGTCCAGGAGAGTGTGTGAGTCCC	2339	GTCCAGGAGAGTGTGTGAGTCC	2340	TCCAGGAGAGTGTGTGAGTC
LDLRex2(27;68;123;30)_185_d2_r	2341	GGGACTCAGCAGTCTCTCTGGGACT	2342	GGACTCAGCAGTCTCTCTGGGAC	2343	GACTCAGCAGTCTCTCTGGGA
LDLRex2(27;68;123;30)_186_d2_f	2344	GTCCAGGAGACGTGTGAGTCCCC	2345	TCCAGGAGACGTGTGAGTCCC	2346	CCAGGAGACGTGTGAGTCC
LDLRex2(27;68;123;30)_186_d2_r	2347	GGGACTCAGCAGTCTCTCTGGGAC	2348	GGGACTCAGCAGTCTCTCTGGGA	2349	GGACTCAGCAGTCTCTCTGGG
LDLRex2(27;68;123;30)_187_d2_f	2350	TCCAGGAGACGTGTGAGTCCCCT	2351	CCAGGAGACGTGTGAGTCCCC	2352	CCAGGAGACGTGTGAGTCCC
LDLRex2(27;68;123;30)_187_d2_r	2353	AGGGGACTCAGCAGTCTCTCTGGGA	2354	GGGGACTCAGCAGTCTCTCTGGG	2355	GGGACTCAGCAGTCTCTCTGG
LDLRex2(27;68;123;30)_188_d2_f	2356	CCCAGGAGACGTGTGAGTCCCCTT	2357	CCAGGAGACGTGTGAGTCCCCT	2358	CAGGAGACGTGTGAGTCCCC
LDLRex2(27;68;123;30)_188_d2_r	2359	AAGGGGACTCACAACGTCTCTCTGGG	2360	AGGGGACTCACAACGTCTCTCTGG	2361	GGGACTCACAACGTCTCTCTG
LDLRex2(27;68;123;30)_189_d2_f	2362	CCAGGAGACGTGGTGAAGTCCCCTT	2363	CAGGAGACGTGGTGAAGTCCCCTT	2364	AGGAGACGTGGTGAAGTCCCCT
LDLRex2(27;68;123;30)_189_d2_r	2365	AAAGGGGACTCACACGTCTCTCTGG	2366	AAAGGGGACTCACACGTCTCTCTG	2367	AGGGGACTCACACGTCTCTCT
LDLRex2(27;68;123;30)_190 + 1_d2_f	2368	AGGAGACGTGTGAGTCCCCTTTGG	2369	GGAGACGTGTGAGTCCCCTTTG	2370	GAGACGTGTGAGTCCCCTTT
LDLRex2(27;68;123;30)_190 + 1_d2_r	2371	CCAAAGGGGACTCAGCAGTCTCTCT	2372	CAAAGGGGACTCAGCAGTCTCTC	2373	AAAGGGGACTCAGCAGTCTC
LDLRex2(27;68;123;30)_190 + 10_d2_f	2374	GCTGTGAGTCCCCTTGGGCATGATAT	2375	CTGTGAGTCCCCTTGGGCATGATA	2376	TGTGAGTCCCCTTGGGCATGAT
LDLRex2(27;68;123;30)_190 + 10_d2_r	2377	ATATCATGCCCCAAGGGACTCACAGC	2378	TATCATGCCCCAAGGGACTCACAG	2379	ATCATGCCCCAAGGGACTCAC
LDLRex2(27;68;123;30)_190 + 11_d2_f	2380	CTGTGAGTCCCCTGGGCATGATATG	2381	TGTGAGTCCCCTGGGCATGATAT	2382	GTGAGTCCCCTGGGCATGATA
LDLRex2(27;68;123;30)_190 + 11_d2_r	2383	CATATCATGCCCCAAGGGACTCACAG	2384	ATATCATGCCCCAAGGGACTCAC	2385	TATCATGCCCCAAGGGACTCAC
LDLRex2(27;68;123;30)_190 + 12_d2_f	2386	TGTGAGTCCCCTGGGCATGATATGC	2387	GTGAGTCCCCTGGGCATGATATG	2388	TGAGTCCCCTGGGCATGATAT

Table 1

del2	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_190 + 12_d2_r	2389	GCATATCATGCCCCAGGGGACTCACA	2390	CATATCATGCCAGGGGACTCAC	2391	ATATCATGCCCCAGGGGACTCA
LDLRex2(27;68;123;30)_190 + 13_d2_f	2392	GTGAGTCCCTTGGCATGATGCA	2393	TGAGTCCCTTGGCATGATGCA	2394	GAGTCCCTTGGCATGATG
LDLRex2(27;68;123;30)_190 + 13_d2_r	2395	TGCATATCATGCCAAGGGGACTCAC	2396	GCATATCATGCCAAGGGGACTCA	2397	CATATCATGCCAAGGGGACTC
LDLRex2(27;68;123;30)_190 + 14_d2_f	2398	TGAGTCCCTTGGCATGATGCA	2399	GAGTCCCTTGGCATGATGCA	2400	AGTCCCTTGGCATGATG
LDLRex2(27;68;123;30)_190 + 14_d2_r	2401	ATGCATATCATGCAAGGGGACTCA	2402	TGCATATCATGCAAGGGGACTC	2403	GCATATCATGCAAGGGGACT
LDLRex2(27;68;123;30)_190 + 15_d2_f	2404	GAGTCCCTTGGCATGATGCA	2405	AGTCCCTTGGCATGATGCA	2406	GTCCCTTGGCATGATGCA
LDLRex2(27;68;123;30)_190 + 15_d2_r	2407	AATGCATATCATGCAAGGGGACTC	2408	ATGCATATCATGCAAGGGGACT	2409	TGCATATCATGCAAGGGGAC
LDLRex2(27;68;123;30)_190 + 2_d2_f	2410	GGAGACGTGCTGAGTCCCTTTGGG	2411	GAGACGTGCTGAGTCCCTTTGG	2412	AGACGTGCTGAGTCCCTTTG
LDLRex2(27;68;123;30)_190 + 2_d2_r	2413	CCCAAGGGGACTCAGCACGTCTC	2414	CCAAAGGGGACTCAGCACGTCTC	2415	CAAAAGGGGACTCAGCACGTCT
LDLRex2(27;68;123;30)_190 + 3_d2_f	2416	GAGACGTGCTGTGCCCTTTGGG	2417	AGACGTGCTGTGCCCTTTGGG	2418	GACGTGCTGTGCCCTTTGG
LDLRex2(27;68;123;30)_190 + 3_d2_r	2419	GCCCAAGGGGACACAGCACGTCTC	2420	CCAAAGGGGACACAGCACGTCT	2421	CCAAAGGGGACACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 4_d2_f	2422	AGACGTGCTGTGCCCTTTGGGCA	2423	GACGTGCTGTGCCCTTTGGG	2424	ACGTGCTGTGCCCTTTGGG
LDLRex2(27;68;123;30)_190 + 4_d2_r	2425	TGCCAAAGGGGACACAGCACGTCT	2426	GCCCAAGGGGACACAGCACGTCT	2427	CCCAAGGGGACACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 5_d2_f	2428	GACGTGCTGTGCCCTTTGGGCA	2429	ACGTGCTGTGCCCTTTGGGCA	2430	CGTGTGTGCCCTTTGGG
LDLRex2(27;68;123;30)_190 + 5_d2_r	2431	ATGCCCAAGGGGTACAGCACGTCT	2432	TGCCCAAGGGGTACAGCACGTCT	2433	GCCCAAGGGGTACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 6_d2_f	2434	ACGTGCTGTGCCCTTTGGGCA	2435	CGTGTGTGCCCTTTGGGCA	2436	GTGCTGTGCCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 6_d2_r	2437	CATGCCCAAGGGGTACAGCACGTCT	2438	ATGCCCAAGGGGTACAGCACGTCT	2439	TGCCCAAGGGGTACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 7_d2_f	2440	CGTGTGTGAGTCCTTTGGGCA	2441	GTGCTGTGAGTCCTTTGGGCA	2442	TGCTGTGAGTCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 7_d2_r	2443	TGATGCCCAAGGGGTACAGCACGTCT	2444	CATGCCCAAGGGGTACAGCACGTCT	2445	ATGCCCAAGGGGTACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 8_d2_f	2446	GTGCTGTGAGTCCTTTGGGCA	2447	TGCTGTGAGTCCTTTGGGCA	2448	GCTGTGAGTCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 8_d2_r	2449	ATCATGCCCAAGGGGTACAGCACGTCT	2450	TGATGCCCAAGGGGTACAGCACGTCT	2451	CATGCCCAAGGGGTACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 9_d2_f	2452	TGCTGTGAGTCCTTTGGGCA	2453	GCTGTGAGTCCTTTGGGCA	2454	CTGTGAGTCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 9_d2_r	2455	TATCATGCCCAAGGGGTACAGCACGTCT	2456	ATCATGCCCAAGGGGTACAGCACGTCT	2457	TCATGCCCAAGGGGTACAGCACGTCT
LDLRex2(27;68;123;30)_190_d2_f	2458	CAGGACGTGCTGAGTCCCTTTGGG	2459	AGGACGTGCTGAGTCCCTTTGGG	2460	GGAGACGTGCTGAGTCCCTTTGGG
LDLRex2(27;68;123;30)_190_d2_r	2461	CAAGGGGACTCAGCACGTCTCTCTG	2462	AAAGGGGACTCAGCACGTCTCTCT	2463	AAGGGGACTCAGCACGTCTCTCT
LDLRex2(27;68;123;30)_68 - 1_d2_f	2464	TCCTCTCTCAGGGGACAGATG	2465	CCCTCTCTCAGGGGACAGATG	2466	CTCTCTCTCAGGGGACAGATG
LDLRex2(27;68;123;30)_68 - 1_d2_r	2467	GCATCTGTGCCCTTGAGAGAGGGA	2468	CATCTGTGCCCTTGAGAGAGGGA	2469	ATCTGTGCCCTTGAGAGAGGGA
LDLRex2(27;68;123;30)_68 - 10_d2_f	2470	TTCTCTTTTCTCTCTCAGTGGG	2471	TCTCTTTTCTCTCTCAGTGGG	2472	CTCTTTTCTCTCTCAGTGGG
LDLRex2(27;68;123;30)_68 - 10_d2_r	2473	GCCCACTGAGAGGAAAGAGGAA	2474	CCCACTGAGAGGAAAGAGGAA	2475	CCACTGAGAGGAAAGAGGAA
LDLRex2(27;68;123;30)_68 - 11_d2_f	2476	TTTCTCTTTCTCTCTCAGTGGG	2477	TTTCTCTTTCTCTCTCAGTGGG	2478	TCTCTTTCTCTCTCTCAGTGGG
LDLRex2(27;68;123;30)_68 - 11_d2_r	2479	CCCACTGAGAGGAAAGAGGAA	2480	CCCACTGAGAGGAAAGAGGAA	2481	CACTGAGAGGAAAGAGGAA

Table 1

del2	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_68 - 12_d2_f	2482	CTTTCTCCTTTTCTCTCTCAGTGG	2483	TTTCTCCTTTTCTCTCTCAGTG	2484	TTCTCCTTTTCTCTCTCAGT
LDLRex2(27;68;123;30)_68 - 12_d2_r	2485	CCACTGAGAGAGAAAAGGAGAAAG	2486	CACTGAGAGAGAAAAGGAGAAA	2487	ACTGAGAGAGAAAAGGAGAAA
LDLRex2(27;68;123;30)_68 - 13_d2_f	2488	CCTTTCTCCTTTCTCTCTCAGTG	2489	CTTTCTCCTTTCTCTCTCAGT	2490	TTTCTCCTTTCTCTCTCAG
LDLRex2(27;68;123;30)_68 - 13_d2_r	2491	CACTGAGAGAGAAAAGGAGAAAG	2492	ACTGAGAGAGAAAAGGAGAAAG	2493	CTGAGAGAGAAAAGGAGAAA
LDLRex2(27;68;123;30)_68 - 14_d2_f	2494	CCCTTTCTCCTTCTCTCTCTCAGT	2495	CCTTTCTCCTTCTCTCTCTCAG	2496	CTTTCTCCTTCTCTCTCTCA
LDLRex2(27;68;123;30)_68 - 14_d2_r	2497	ACTGAGAGAGAGAAAGGAGAAAGGG	2498	CTGAGAGAGAGAAAGGAGAAAGG	2499	TGAGAGAGAGAAAGGAGAAAG
LDLRex2(27;68;123;30)_68 - 15_d2_f	2500	ACCCTTTCTCCTTCTCTCTCTCAG	2501	CCCTTTCTCCTTCTCTCTCTCTCA	2502	CCTTTCTCCTTCTCTCTCTCTC
LDLRex2(27;68;123;30)_68 - 15_d2_r	2503	CTGAGAGAGAGGAAAGGAGAAAGGGT	2504	TGAGAGAGAGGAAAGGAGAAAGGG	2505	GAGAGAGAGGAAAGGAGAAAGG
LDLRex2(27;68;123;30)_68 - 2_d2_f	2506	TTCTCTCTCTCTCTGGCGACAGATG	2507	TCCTCTCTCTCTGGCGACAGAT	2508	CCTCTCTCTCTGGCGACAGA
LDLRex2(27;68;123;30)_68 - 2_d2_r	2509	CATCTGTGCCCCAGAGAGAGAGGAA	2510	ATCTGTGCCCCAGAGAGAGAGGA	2511	TCTGTGCCCCAGAGAGAGAGG
LDLRex2(27;68;123;30)_68 - 3_d2_f	2512	TTTCTCTCTCTGTGGCGACAGAT	2513	TTCTCTCTCTGTGGCGACAGA	2514	TCCTCTCTCTGTGGCGACAG
LDLRex2(27;68;123;30)_68 - 3_d2_r	2515	ATCTGTGCCCCACAGAGAGAGGAAA	2516	TCTGTGCCCCACAGAGAGAGGAA	2517	CTGTGCCCCACAGAGAGAGGA
LDLRex2(27;68;123;30)_68 - 4_d2_f	2518	TTTTCTCTCTCTCAGTGGCGACAGA	2519	TTTCTCTCTCTCAGTGGCGACAG	2520	TTCTCTCTCTCAGTGGCGACA
LDLRex2(27;68;123;30)_68 - 4_d2_r	2521	TCTGTGCCCACTGAGAGAGGAAAA	2522	CTGTGCCCACTGAGAGAGGAAA	2523	TGTGCCCACTGAGAGAGGAA
LDLRex2(27;68;123;30)_68 - 5_d2_f	2524	CTTTCTCTCTCTCAGTGGCGACAG	2525	TTTTCTCTCTCAGTGGCGACA	2526	TTTCTCTCTCAGTGGCGAC
LDLRex2(27;68;123;30)_68 - 5_d2_r	2527	CTGTGCCCACTGAGAGAGGAAAAG	2528	TGTGCCCACTGAGAGAGGAAAA	2529	GTGCCCACTGAGAGAGGAAA
LDLRex2(27;68;123;30)_68 - 6_d2_f	2530	CCTTTCTCTCTCTCAGTGGCGACA	2531	CTTTTCTCTCTCAGTGGCGAC	2532	TTTTCTCTCTCAGTGGCGCA
LDLRex2(27;68;123;30)_68 - 6_d2_r	2533	TGTGCCCACTGAGAGAGGAAAAGG	2534	GTGCCCACTGAGAGAGGAAAAG	2535	TGCCCACTGAGAGAGGAAAA
LDLRex2(27;68;123;30)_68 - 7_d2_f	2536	TCCTTTTCTCTCTCAGTGGCGAC	2537	CCTTTCTCTCTCAGTGGCGCA	2538	CTTTTCTCTCTCAGTGGCGG
LDLRex2(27;68;123;30)_68 - 7_d2_r	2539	GTGCCCACTGAGAGAGGAAAAGGA	2540	TGCCCACTGAGAGAGGAAAAGG	2541	CGCCCACTGAGAGAGGAAAAG
LDLRex2(27;68;123;30)_68 - 8_d2_f	2542	CTCCTTTTCTCTCTCAGTGGCGCA	2543	TCCTTTTCTCTCTCAGTGGCGG	2544	CCTTTCTCTCTCTCAGTGGGC
LDLRex2(27;68;123;30)_68 - 8_d2_r	2545	TGCCCACTGAGAGAGGAAAAGGAG	2546	CGCCCACTGAGAGAGGAAAAGGA	2547	GCCCACTGAGAGAGGAAAAGG
LDLRex2(27;68;123;30)_68 - 9_d2_f	2548	TCCTCTTTTCTCTCTCAGTGGCGG	2549	CTCCTTTTCTCTCTCAGTGGGC	2550	TCCTTTTCTCTCTCAGTGGG
LDLRex2(27;68;123;30)_68 - 9_d2_r	2551	CGCCCACTGAGAGAGGAAAAGGAGA	2552	GCCCACTGAGAGAGGAAAAGGAG	2553	CCCACTGAGAGAGGAAAAGGA
LDLRex2(27;68;123;30)_68_d2_f	2554	CCCTCTCTCTCAGGCGACAGATGCG	2555	CTCTCTCTCAGGCGACAGATGC	2556	TCTCTCTCAGGCGACAGATG
LDLRex2(27;68;123;30)_68_d2_r	2557	CGCATCTGTGCCCCCTGAGAGAGAGG	2558	GCATCTGTGCCCCCTGAGAGAGAG	2559	CATCTGTGCCCCCTGAGAGAGA
LDLRex2(27;68;123;30)_69_d2_f	2560	CTCTCTCTCAGTGGCGACAGATGCGA	2561	TCTCTCTCAGTGGCGACAGATGCG	2562	CTCTCTCAGTGGCGACAGATGC
LDLRex2(27;68;123;30)_69_d2_r	2563	TCGCATCTGTGCGCACTGAGAGAGAG	2564	CGCATCTGTGCGCACTGAGAGAGA	2565	GCATCTGTGCGCACTGAGAGAG
LDLRex2(27;68;123;30)_70_d2_f	2566	TCTCTCTCAGTGGCGACAGATGCGAA	2567	CTCTCTCAGTGGCGACAGATGCGA	2568	TCTCTCAGTGGCGACAGATGCG
LDLRex2(27;68;123;30)_70_d2_r	2569	TTGCGATCTGTGCGCACTGAGAGAGA	2570	TGCGATCTGTGCGCACTGAGAGAG	2571	CGCATCTGTGCGCACTGAGAGA
LDLRex2(27;68;123;30)_71_d2_f	2572	CTCTCTCAGTGGGACAGATGCGAAA	2573	TCTCTCAGTGGGACAGATGCGAA	2574	CTCTCAGTGGGACAGATGCGA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del2	2575	TTTCGCATCTGTCCCACTGAGAG	2576	TTGCACTGTCCCACTGAGAGA	2577	TCGCATCTGTCCCACTGAGAG
LDLRex2(27;68;123;30)_71_d2_r	2578	TCTCTAGTGGGACAGATGCGAAAG	2579	CTCTAGTGGGACAGATGCGAAA	2580	TCTCAGTGGGACAGATGCGAA
LDLRex2(27;68;123;30)_72_d2_f	2581	CTTTCGCATCTGTCCCACTGAGAGA	2582	TTTCGCATCTGTCCCACTGAGAG	2583	TTTCGCATCTGTCCCACTGAGA
LDLRex2(27;68;123;30)_72_d2_r	2584	CTCTCAGTGGGCCAGATGCGAAAGA	2585	TCTCAGTGGGCCAGATGCGAAAG	2586	CTCAGTGGGCCAGATGCGAAA
LDLRex2(27;68;123;30)_73_d2_f	2587	TTCTTCGCATCTGGCCCACTGAGAG	2588	CTTTCGCATCTGGCCCACTGAGA	2589	TTTCGCATCTGGCCCACTGAG
LDLRex2(27;68;123;30)_73_d2_r	2590	TCTCAGTGGCGAGATGCGAAAGAA	2591	CTCAGTGGCGAGATGCGAAAGA	2592	TCAGTGGCGAGATGCGAAAG
LDLRex2(27;68;123;30)_74_d2_f	2593	TTCTTCGCATCTCGCCCACTGAGA	2594	TCTTCGCATCTCGCCCACTGAG	2595	CTTTCGCATCTCGCCCACTGA
LDLRex2(27;68;123;30)_74_d2_r	2596	CTCAGTGGCGAGATGCGAAAGAAA	2597	TCAGTGGCGAGATGCGAAAGAA	2598	CAGTGGCGAGATGCGAAAGA
LDLRex2(27;68;123;30)_75_d2_f	2599	TTTCTTCGCATCTCGCCCACTGAG	2600	TTCTTCGCATCTCGCCCACTGA	2601	TCCTTCGCATCTCGCCCACTG
LDLRex2(27;68;123;30)_75_d2_r	2602	TCAGTGGCGACATGCGAAAGAAC	2603	CAGTGGCGACATGCGAAAGAAA	2604	AGTGGCGACATGCGAAAGAA
LDLRex2(27;68;123;30)_76_d2_f	2605	GTTTCTTCGCATGTGCCCCACTGA	2606	TTTCTTCGCATGTGCCCCACTG	2607	TTCTTCGCATGTGCCCCACT
LDLRex2(27;68;123;30)_76_d2_r	2608	CAGTGGCGACATGCGAAAGAACG	2609	AGTGGCGACATGCGAAAGAAC	2610	GTGGCGACATGCGAAAGAAA
LDLRex2(27;68;123;30)_77_d2_f	2611	CGTTTCTTCGCATGTGCCCCACTG	2612	GTTTCTTCGCATGTGCCCCACT	2613	TTTCTTCGCATGTGCCCCAC
LDLRex2(27;68;123;30)_77_d2_r	2614	AGTGGCGACAGGCGAAAGAACGA	2615	GTGGCGACAGGCGAAAGAACG	2616	TGGCGACAGGCGAAAGAAC
LDLRex2(27;68;123;30)_78_d2_f	2617	TCGTTTCTTCGCCTGTGCCCCACT	2618	CGTTTCTTCGCCTGTGCCCCAC	2619	GTTTCTTCGCCTGTGCCCCA
LDLRex2(27;68;123;30)_78_d2_r	2620	GTGGCGACAGACGAAAGAACGAG	2621	TGGCGACAGACGAAAGAACGA	2622	GGGCGACAGACGAAAGAACG
LDLRex2(27;68;123;30)_79_d2_f	2623	CTCGTTTCTTCGTCTGTGCCCCAC	2624	TCGTTTCTTCGTCTGTGCCCCA	2625	CGTTTCTTCGTCTGTGCCCC
LDLRex2(27;68;123;30)_79_d2_r	2626	TGGCGACAGATGAAAGAACGAGT	2627	GGGCGACAGATGAAAGAACGAG	2628	GCGACAGATGAAAGAACGA
LDLRex2(27;68;123;30)_80_d2_f	2629	ACTCGTTTCTTCATCTGTGCCCCA	2630	CTCGTTTCTTCATCTGTGCCCC	2631	TCGTTTCTTCATCTGTGCGC
LDLRex2(27;68;123;30)_80_d2_r	2632	GGGCGACAGATGAAAGAACGAGTT	2633	GGCGACAGATGAAAGAACGAGT	2634	GCGACAGATGAAAGAACGAG
LDLRex2(27;68;123;30)_81_d2_f	2635	AACCTCGTTTCTTCATCTGTGCCCC	2636	ACTCGTTTCTTCATCTGTGCGC	2637	CTCGTTTCTTCATCTGTGCG
LDLRex2(27;68;123;30)_81_d2_r	2638	GGCGACAGATGCAAGAACGAGTTC	2639	GCGACAGATGCAAGAACGAGTT	2640	GACAGATGCAAGAACGAGT
LDLRex2(27;68;123;30)_82_d2_f	2641	GAACTCGTTTCTTCATCTGTGCGC	2642	AACCTCGTTTCTTCATCTGTGCG	2643	ACTCGTTTCTTCATCTGTGCG
LDLRex2(27;68;123;30)_82_d2_r	2644	GCGACAGATGCGAGAACGAGTTC	2645	GCGACAGATGCGAGAACGAGTTC	2646	GACAGATGCGAGAACGAGTT
LDLRex2(27;68;123;30)_83_d2_f	2647	GGAACCTGTTTCTTCGATCTGTGCG	2648	GAACTCGTTTCTTCGATCTGTGCG	2649	AACTCGTTTCTTCGATCTGTC
LDLRex2(27;68;123;30)_83_d2_r	2650	CGACAGATGCGAGAACGAGTTC	2651	GACAGATGCGAGAACGAGTTC	2652	ACAGATGCGAGAACGAGTTC
LDLRex2(27;68;123;30)_84_d2_f	2653	TGGAACCTGTTTCTTCGATCTGTGCG	2654	GGAACCTGTTTCTTCGATCTGTC	2655	GAACTCGTTTCTTCGATCTGT
LDLRex2(27;68;123;30)_84_d2_r	2656	GACAGATGCGAAAGAACGAGTTC	2657	ACAGATGCGAAAGAACGAGTTC	2658	CAGATGCGAAAGAACGAGTTC
LDLRex2(27;68;123;30)_85_d2_f	2659	CTGGAACCTGTTTCTTCGATCTGTC	2660	TGGAACCTGTTTCTTCGATCTGT	2661	GGAACCTGTTTCTTCGATCTG
LDLRex2(27;68;123;30)_85_d2_r	2662	ACAGATGCGAAAGAACGAGTTC	2663	CAGATGCGAAAGAACGAGTTC	2664	AGATGCGAAAGAACGAGTTC
LDLRex2(27;68;123;30)_86_d2_f	2665	ACTGGAACCTGTTTCTTCGATCTGT	2666	CTGGAACCTGTTTCTTCGATCTG	2667	TGGAACCTGTTTCTTCGATCT

Table 1

	del2	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
	LDLRex2(27;68;123;30)_87_d2_f	2668	CAGATGCGAAAGACGAGTTCAGTG	2669	AGATGCGAAAGACGAGTTCAGT	2670	GATGCGAAAGACGAGTTCAG
	LDLRex2(27;68;123;30)_87_d2_r	2671	CACTGGAACTCGTCTTCGCATCTG	2672	ACTGGAACTCGTCTTCGCATCT	2673	CTGGAACTCGTCTTCGCATC
	LDLRex2(27;68;123;30)_88_d2_f	2674	AGATGCGAAAGACGAGTTCAGTGC	2675	GATGCGAAAGACGAGTTCAGTG	2676	ATGCGAAAGACGAGTTCAGT
	LDLRex2(27;68;123;30)_88_d2_r	2677	GCACTGGAACCTCGTCTTCGCATCT	2678	CACTGGAACCTCGTCTTCGCATC	2679	ACTGGAACCTCGTCTTCGCAT
	LDLRex2(27;68;123;30)_89_d2_f	2680	GATGCGAAAGACGAGTTCAGTGCC	2681	ATGCGAAAGACGAGTTCAGTGC	2682	TGCGAAAGACGAGTTCAGTG
	LDLRex2(27;68;123;30)_89_d2_r	2683	GGCACTGGAACCTCTTCCTTCGCATC	2684	GCACTGGAACCTCTTCCTTCGCAT	2685	CACTGGAACCTCTTCCTTCGCA
	LDLRex2(27;68;123;30)_90_d2_f	2686	ATGCGAAAGAAAAAGTTCAGTGCCA	2687	TGCGAAAGAAAAAGTTCAGTGCC	2688	GCGAAAGAAAAAGTTCAGATGC
	LDLRex2(27;68;123;30)_90_d2_r	2689	TGGCACTGGAACCTTTCTTCGCAT	2690	GGCACTGGAACCTTTCTTCGCA	2691	GCACTGGAACCTTTCTTCGCG
	LDLRex2(27;68;123;30)_91_d2_f	2692	TGCGAAAGAAACGTTCCAGTGCCAA	2693	GCGAAAGAAACGTTCCAGTGCCA	2694	CGAAAGAAACGTTCCAGTGCC
	LDLRex2(27;68;123;30)_91_d2_r	2695	TTGGCACTGGAACGTTCTTCGCA	2696	TGGCACTGGAACGTTCTTCGCG	2697	GGCACTGGAACGTTCTTCG
	LDLRex2(27;68;123;30)_92_d2_f	2698	GCGAAAGAAACGTTCCAGTGCCAA	2699	CGAAAGAAACGTTCCAGTGCCAA	2700	GAAAGAAACGTTCCAGTGCCA
	LDLRex2(27;68;123;30)_92_d2_r	2701	CTTGGCACTGGAACGTTCTTCGCG	2702	TTGGCACTGGAACGTTCTTCG	2703	TGGCACTGGAACGTTCTTTC
	LDLRex2(27;68;123;30)_93_d2_f	2704	CGAAAGAAACGATCCAGTGCCAAAGA	2705	GAAAGAAACGATCCAGTGCCAAAG	2706	AAAGAAACGATCCAGTGCCAA
	LDLRex2(27;68;123;30)_93_d2_r	2707	TCTTGGCACTGGATCGTTCTTTCG	2708	CTTGGCACTGGATCGTTCTTTC	2709	TTGGCACTGGATCGTTCTT
	LDLRex2(27;68;123;30)_94_d2_f	2710	GAAAGAAACGAGCCAGTGCCAAAGAC	2711	AAAGAAACGAGCCAGTGCCAAAGA	2712	AAAGAAACGAGCCAGTGCCAAAG
	LDLRex2(27;68;123;30)_94_d2_r	2713	GTCTTGGCACTGGCTCGTTCTTTC	2714	TCTTGGCACTGGCTCGTTCTT	2715	CTTGGCACTGGCTCGTTCTT
	LDLRex2(27;68;123;30)_95_d2_f	2716	AAAGAAACGAGTCAGTGCCAAAGACG	2717	AAAGAAACGAGTCAGTGCCAAAGAC	2718	AGAAACGAGTCAGTGCCAAAGA
	LDLRex2(27;68;123;30)_95_d2_r	2719	CGTCTTGGCACTGACTCGTTTCTTT	2720	GTCTTGGCACTGACTCGTTTCTT	2721	TCTTGGCACTGACTCGTTTCT
	LDLRex2(27;68;123;30)_96_d2_f	2722	AAGAAACGAGTTAGTGCCAAAGACGG	2723	AGAAACGAGTTAGTGCCAAAGACG	2724	GAAACGAGTTAGTGCCAAAGAC
	LDLRex2(27;68;123;30)_96_d2_r	2725	CCGTCCTTGGCACTAACTCGTTTCTT	2726	CGTCCTTGGCACTAACTCGTTTCT	2727	GTCTTGGCACTAACTCGTTTC
	LDLRex2(27;68;123;30)_97_d2_f	2728	AGAAACGAGTTCTGTGCCAAGACGGG	2729	GAAACGAGTTCTGTGCCAAGACGG	2730	AAACGAGTTCTGTGCCAAGACG
	LDLRex2(27;68;123;30)_97_d2_r	2731	CCCGTCTTGGCACGAACTCGTTTCT	2732	CCGTCCTTGGCACGAACTCGTTTC	2733	CGTCCTTGGCACGAACTCGTTT
	LDLRex2(27;68;123;30)_98_d2_f	2734	GAAACGAGTTCTGTGCCAAGACGGGA	2735	AAACGAGTTCTGTGCCAAGACGGG	2736	AACGAGTTCTGTGCCAAGACGG
	LDLRex2(27;68;123;30)_98_d2_r	2737	TCCCGTCTTGGCAGAACTCGTTTC	2738	CCCGTCTTGGCAGAACTCGTTT	2739	CCGTCCTTGGCAGGAACTCGTT
	LDLRex2(27;68;123;30)_99_d2_f	2740	AAACGAGTTCCAGCCAAAGACGGGAA	2741	AACGAGTTCCAGCCAAAGACGGGA	2742	ACGAGTTCCAGCCAAAGACGGG
	LDLRex2(27;68;123;30)_99_d2_r	2743	TTCCCGTCTTGGCTGGAACCTCGTTT	2744	TCCCGTCTTGGCTGGAACCTCGTT	2745	CCCGTCTTGGCTGGAACCTCGT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del3						
LDLRex2(27;68;123;30)_100_d3_r	2746	ATTTCCTGCTTGTGAACTCGT	2747	TTTCCGCTTGTGAACTCGT	2748	TTCCCGTCTTGTGAACTCG
LDLRex2(27;68;123;30)_101_d3_f	2749	ACGAGTCCAGTAAGACGGGAAATG	2750	CGAGTCCAGTAAGACGGGAAAT	2751	GAGTCCAGTAAGACGGGAAA
LDLRex2(27;68;123;30)_101_d3_r	2752	CATTCCGCTTACTGGAACCTCGT	2753	ATTCCGCTTACTGGAACCTCG	2754	TTCCCGTCTTACTGGAACCTC
LDLRex2(27;68;123;30)_102_d3_f	2755	CGAGTCCAGTGAGACGGGAAATGC	2756	GAGTCCAGTGAGACGGGAAATG	2757	AGTCCAGTGAGACGGGAAAT
LDLRex2(27;68;123;30)_102_d3_r	2758	GCATTTCCGCTCTACTGGAACCTCG	2759	CATTCCGCTCTACTGGAACCTC	2760	ATTCCGCTCTACTGGAACCT
LDLRex2(27;68;123;30)_103_d3_f	2761	GAGTCCAGTGCGACGGGAAATGCA	2762	AGTCCAGTGCGACGGGAAATGC	2763	GTTCCAGTGCGACGGGAAATG
LDLRex2(27;68;123;30)_103_d3_r	2764	TGCATTTCCGCTCGCACTGGAACCTC	2765	GCATTTCCGCTCGCACTGGAAC	2766	CATTTCCGCTCGCACTGGAAC
LDLRex2(27;68;123;30)_104_d3_f	2767	AGTTCAGTGCCACGGGAAATGCA	2768	GTTCCAGTGCCACGGGAAATGCA	2769	TTCAGTGCCACGGGAAATGC
LDLRex2(27;68;123;30)_104_d3_r	2770	ATGCATTTCCGCTGGCACTGGAAC	2771	TGCATTTCCGCTGGCACTGGAAC	2772	GCATTTCCGCTGGCACTGGA
LDLRex2(27;68;123;30)_105_d3_f	2773	GTTCCAGTGCCACGGGAAATGCATC	2774	TTCAGTGCCACGGGAAATGCAT	2775	TCCAGTGCCACGGGAAATGCA
LDLRex2(27;68;123;30)_105_d3_r	2776	GATGCATTTCCGCTGGCACTGGAAC	2777	ATGCATTTCCGCTGGCACTGGA	2778	TGCATTTCCGCTGGCACTGGA
LDLRex2(27;68;123;30)_106_d3_f	2779	TTCAGTGCCACGGGAAATGCATCT	2780	TCCAGTGCCACGGGAAATGCATC	2781	CCAGTGCCACGGGAAATGCAT
LDLRex2(27;68;123;30)_106_d3_r	2782	AGATGCATTTCCCTTGGCACTGGAA	2783	GATGCATTTCCCTTGGCACTGGA	2784	ATGCATTTCCCTTGGCACTGG
LDLRex2(27;68;123;30)_107_d3_f	2785	TCCAGTGCCACGGGAAATGCATCTC	2786	CCAGTGCCACGGGAAATGCATCT	2787	CAGTGCCACGGGAAATGCATC
LDLRex2(27;68;123;30)_107_d3_r	2788	GAGATGCATTTCCCTTGGCACTGGA	2789	AGATGCATTTCCCTTGGCACTGG	2790	GATGCATTTCCCTTGGCACTG
LDLRex2(27;68;123;30)_108_d3_f	2791	CCAGTGCCACGGGAAATGCATCTCC	2792	CAGTGCCACGGGAAATGCATCTC	2793	AGTGCCACGGGAAATGCATCT
LDLRex2(27;68;123;30)_108_d3_r	2794	GGAGATGCATTTCTTGGCACTGG	2795	GAGATGCATTTCTTGGCACTG	2796	AGATGCATTTCTTGGCACT
LDLRex2(27;68;123;30)_109_d3_f	2797	CAGTGCCACGGGAAATGCATCTCCT	2798	AGTGCCACGGGAAATGCATCTCC	2799	GTGCCAAGACAAATGCATCTC
LDLRex2(27;68;123;30)_109_d3_r	2800	AGGAGATGCATTTGTCTTGGCACTG	2801	GGAGATGCATTTGTCTTGGCACT	2802	GAGATGCATTTGTCTTGGCAC
LDLRex2(27;68;123;30)_110_d3_f	2803	AGTGCCACGGGAAATGCATCTCCTA	2804	GTGCCAAGACGAATGCATCTCCT	2805	TGCCAAGACGAATGCATCTCC
LDLRex2(27;68;123;30)_110_d3_r	2806	TAGGAGATGCATTCGCTTGGCACT	2807	AGGAGATGCATTCGCTTGGCAC	2808	GGAGATGCATTCGCTTGGCA
LDLRex2(27;68;123;30)_111_d3_f	2809	GTGCCAAGACGGATGCATCTCCTAC	2810	TGCCAAGACGGATGCATCTCCTA	2811	GCCAAGACGGATGCATCTCCT
LDLRex2(27;68;123;30)_111_d3_r	2812	GTAGGAGATGCATCCGCTTGGCAC	2813	TAGGAGATGCATCCGCTTGGCA	2814	AGGAGATGCATCCGCTTGGC
LDLRex2(27;68;123;30)_112_d3_f	2815	TGCCAAGACGGGTGCATCTCCTACA	2816	GCCAAGACGGGTGCATCTCCTAC	2817	CCAAGACGGGTGCATCTCCTA
LDLRex2(27;68;123;30)_112_d3_r	2818	TGTAGGAGATGCACCCGCTTGGCA	2819	GTAGGAGATGCACCCGCTTGGC	2820	TAGGAGATGCACCCGCTTGG
LDLRex2(27;68;123;30)_113_d3_f	2821	GCCAAGACGGGAGCATCTCCTACAA	2822	CCAAGACGGGAGCATCTCCTACA	2823	CAAGACGGGAGCATCTCCTAC
LDLRex2(27;68;123;30)_113_d3_r	2824	TTGTAGGAGATGCTCCGCTTGGC	2825	TGTAGGAGATGCTCCGCTTGG	2826	GTAGGAGATGCTCCGCTTGG
LDLRex2(27;68;123;30)_114_d3_f	2827	CCAAGACGGGAAACATCTCCTACAAG	2828	CAAGACGGGAAACATCTCCTACAA	2829	AAGACGGGAAACATCTCCTACA
LDLRex2(27;68;123;30)_114_d3_r	2830	CTGTAGGAGATGTTCCCGTCTTGG	2831	TTGTAGGAGATGTTCCCGTCTTG	2832	TGTAGGAGATGTTCCCGTCTT
LDLRex2(27;68;123;30)_115_d3_f	2833	CAAGACGGGAAATCTCCTACAAGT	2834	AAGACGGGAAATCTCCTACAAG	2835	AGACGGGAAATCTCCTACAA
LDLRex2(27;68;123;30)_115_d3_r	2836	ACTGTAGGAGATTTCCCGTCTTG	2837	CTGTAGGAGATTTCCCGTCTT	2838	TTGTAGGAGATTTCCCGTCT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del3						
LDLRex2(27;68;123;30)_116_d3_f	2839	AAGACGGGAAATTTCTCTACAAGTG	2840	AGACGGGAAATTTCTCTACAAGT	2841	GACGGGAAATTTCTCTACAAG
LDLRex2(27;68;123;30)_116_d3_r	2842	CACCTGTAGGAGAAATTTCCCGTCT	2843	ACTTGTAGGAGAAATTTCCCGTCT	2844	CTTGTAGGAGAAATTTCCCGTC
LDLRex2(27;68;123;30)_117_d3_f	2845	AGACGGGAAATGCTCTACAAGTGG	2846	GACGGGAAATGCTCTACAAGTG	2847	ACGGGAAATGCTCTACAAGT
LDLRex2(27;68;123;30)_117_d3_r	2848	CCACTGTAGGAGCAATTTCCCGTCT	2849	CACCTGTAGGAGCAATTTCCCGTC	2850	ACTTGTAGGAGCAATTTCCCGT
LDLRex2(27;68;123;30)_118_d3_f	2851	GACGGGAAATGCTCTACAAGTGGG	2852	ACGGGAAATGCTCTACAAGTGG	2853	CGGGAAATGCTCTACAAGTG
LDLRex2(27;68;123;30)_118_d3_r	2854	CCCACTGTAGGAGCAATTTCCCGTC	2855	CCACTGTAGGAGCAATTTCCCGT	2856	CACCTGTAGGAGCAATTTCCCG
LDLRex2(27;68;123;30)_119_d3_f	2857	ACGGGAAATGCACCTACAAGTGGT	2858	CGGGAAATGCACCTACAAGTGGG	2859	GGGAAATGCACCTACAAGTGG
LDLRex2(27;68;123;30)_119_d3_r	2860	ACCCACTGTAGGTGCAATTTCCCGT	2861	CCCACTGTAGGTGCAATTTCCCG	2862	CCACTGTAGGTGCAATTTCCC
LDLRex2(27;68;123;30)_120_d3_f	2863	CGGGAAATGCATCTACAAGTGGTC	2864	GGGAAATGCATCTACAAGTGGT	2865	GGAAATGCATCTACAAGTGGG
LDLRex2(27;68;123;30)_120_d3_r	2866	GACCCACTGTAGTGCAATTTCCCG	2867	ACCCACTGTAGTGCAATTTCCC	2868	CCCACTGTAGTGCAATTTCC
LDLRex2(27;68;123;30)_121_d3_f	2869	GGGAAATGCATCTACAAGTGGTCT	2870	GGAAATGCATCTACAAGTGGTC	2871	GAAATGCATCTACAAGTGGT
LDLRex2(27;68;123;30)_121_d3_r	2872	AGACCCACTGTAGTGCAATTTCCC	2873	GACCCACTGTAGTGCAATTTCC	2874	ACCCACTGTAGTGCAATTTCC
LDLRex2(27;68;123;30)_122_d3_f	2875	GGAAATGCATCTACAAGTGGTCTG	2876	GAAATGCATCTACAAGTGGTCT	2877	AAATGCATCTACAAGTGGTCT
LDLRex2(27;68;123;30)_122_d3_r	2878	CAGACCCACTGTAGTGCAATTTCC	2879	AGACCCACTGTAGTGCAATTTCC	2880	GACCCACTGTAGTGCAATTT
LDLRex2(27;68;123;30)_123_d3_f	2881	GAAATGCATCTCCAAGTGGTCTGC	2882	AAATGCATCTCCAAGTGGTCTG	2883	AATGCATCTCCAAGTGGTCT
LDLRex2(27;68;123;30)_123_d3_r	2884	GCAGACCCACTTGGAGATGCATTTCC	2885	CAGACCCACTTGGAGATGCATTT	2886	AGACCCACTTGGAGATGCATT
LDLRex2(27;68;123;30)_124_d3_f	2887	AAATGCATCTCCAAGTGGTCTGCG	2888	AATGCATCTCCAAGTGGTCTGC	2889	ATGCATCTCCAAGTGGTCTG
LDLRex2(27;68;123;30)_124_d3_r	2890	CGCAGACCCACTTGGAGATGCATTT	2891	GCAGACCCACTTGGAGATGCATT	2892	CAGACCCACTTGGAGATGCAT
LDLRex2(27;68;123;30)_125_d3_f	2893	AATGCATCTCTAGTGGTCTGCGA	2894	ATGCATCTCTAGTGGTCTGCG	2895	TGCATCTCTAGTGGTCTGCG
LDLRex2(27;68;123;30)_125_d3_r	2896	TCGACAGACCCACTAGGAGATGCATT	2897	CGCAGACCCACTAGGAGATGCAT	2898	GCAGACCCACTAGGAGATGCA
LDLRex2(27;68;123;30)_126_d3_f	2899	ATGCACTCTCTAGTGGTCTGCGAT	2900	TGCATCTCTAGTGGTCTGCGA	2901	GCACTCTCTAGTGGTCTGCG
LDLRex2(27;68;123;30)_126_d3_r	2902	ATCGCAGACCCACTAGGAGATGCAT	2903	TCGCAGACCCACTAGGAGATGCA	2904	CGCAGACCCACTAGGAGATGC
LDLRex2(27;68;123;30)_127_d3_f	2905	TGCATCTCTACTGGTCTGCGATG	2906	GCATCTCTACTGGTCTGCGAT	2907	CATCTCTACTGGGTCTGCGA
LDLRex2(27;68;123;30)_127_d3_r	2908	CATCGCAGACCCAGTAGGAGATGCA	2909	ATCGCAGACCCAGTAGGAGATGC	2910	TCGCAGACCCAGTAGGAGATG
LDLRex2(27;68;123;30)_128_d3_f	2911	GCATCTCTACAGGGTCTGCGATGG	2912	CATCTCTACAGGGTCTGCGATG	2913	ATCTCTACAGGGTCTGCGAT
LDLRex2(27;68;123;30)_128_d3_r	2914	CCATCGCAGACCCCTGTAGGAGATGC	2915	CATCGCAGACCCCTGTAGGAGATG	2916	ATCGCAGACCCCTGTAGGAGAT
LDLRex2(27;68;123;30)_129_d3_f	2917	CATCTCTACAAGGTCTGCGATGGC	2918	ATCTCTACAAGGTCTGCGATGG	2919	TCTCTACAAGGTCTGCGATG
LDLRex2(27;68;123;30)_129_d3_r	2920	GCCATCGCAGACCTTGTAGGAGATG	2921	CCATCGCAGACCTTGTAGGAGAT	2922	CATCGCAGACCTTGTAGGAGA
LDLRex2(27;68;123;30)_130_d3_f	2923	ATCTCTACAAGGTCTGCGATGGCA	2924	TCTCTACAAGGTCTGCGATGGC	2925	CTCCTACAAGGTCTGCGATGG
LDLRex2(27;68;123;30)_130_d3_r	2926	TGCCATCGCAGACCTTGTAGGAGAT	2927	GCCATCGCAGACCTTGTAGGAGA	2928	CCATCGCAGACCTTGTAGGAG
LDLRex2(27;68;123;30)_131_d3_f	2929	TCTCTACAAGTCTGCGATGGCAG	2930	CTCCTACAAGTCTGCGATGGCA	2931	TCCTACAAGTCTGCGATGGC

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del3						
LDLRex2(27;68;123;30)_131_d3_r	2932	CTGCCATCGCAGAACTTGTAGGAGA	2933	TGCCATCGCAGAACTTGTAGGAG	2934	GCCATCGCAGAACTTGTAGGA
LDLRex2(27;68;123;30)_132_d3_f	2935	CTCTACAAAGTGCTGCGATGGCAGC	2936	TCCTACAAAGTGCTGCGATGGCAG	2937	CCTACAAAGTGCTGCGATGGCA
LDLRex2(27;68;123;30)_132_d3_r	2938	GCTGCCATCGCAGCACTTGTAGGAG	2939	CTGCCATCGCAGCACTTGTAGGA	2940	TGCCATCGCAGCACTTGTAGG
LDLRex2(27;68;123;30)_133_d3_f	2941	TCCTACAAAGTGGTGGATGGCAGCG	2942	CCTACAAAGTGGTGGATGGCAGC	2943	CTACAAAGTGGTGGATGGCAG
LDLRex2(27;68;123;30)_133_d3_r	2944	CGCTGCCATCGCAGCACTTGTAGGA	2945	GCTGCCATCGCAGCACTTGTAGG	2946	CTGCCATCGCAGCACTTGTAG
LDLRex2(27;68;123;30)_134_d3_f	2947	CCTACAAAGTGGGGCGATGGCAGCGC	2948	CTACAAAGTGGGGCGATGGCAGCG	2949	TACAAAGTGGGGCGATGGCAGC
LDLRex2(27;68;123;30)_134_d3_r	2950	GCGCTGCCATCGCCCCACTTGTAGG	2951	CGCTGCCATCGCCCCACTTGTAG	2952	GCTGCCATCGCCCCACTTGT
LDLRex2(27;68;123;30)_135_d3_f	2953	CTACAAAGTGGGTGCGATGGCAGCGCT	2954	TACAAAGTGGGTGCGATGGCAGCGC	2955	ACAAAGTGGGTGCGATGGCAGCG
LDLRex2(27;68;123;30)_135_d3_r	2956	AGCGCTGCCATCGACCCACTTGTAG	2957	GCGCTGCCATCGACCCACTTGT	2958	CGCTGCCATCGACCCACTTGT
LDLRex2(27;68;123;30)_136_d3_f	2959	TACAAAGTGGGTGCGATGGCAGCGCTG	2960	ACAAAGTGGGTGCGATGGCAGCGCT	2961	CAAGTGGGTGCGATGGCAGCGC
LDLRex2(27;68;123;30)_136_d3_r	2962	CAGCGCTGCCATCGACCCACTTGT	2963	AGCGCTGCCATCGACCCACTTGT	2964	GCGCTGCCATCGACCCACTTGT
LDLRex2(27;68;123;30)_137_d3_f	2965	ACAAAGTGGGTCTATGGCAGCGCTGA	2966	CAAGTGGGTCTATGGCAGCGCTG	2967	AAGTGGGTCTATGGCAGCGCT
LDLRex2(27;68;123;30)_137_d3_r	2968	TCAAGCGCTGCCATAGACCCACTTGT	2969	CAGCGCTGCCATAGACCCACTTGT	2970	AGCGCTGCCATAGACCCACTT
LDLRex2(27;68;123;30)_138_d3_f	2971	CAAGTGGGTCTGTGGCAGCGCTGAG	2972	AAGTGGGTCTGTGGCAGCGCTGA	2973	AGTGGGTCTGTGGCAGCGCTG
LDLRex2(27;68;123;30)_138_d3_r	2974	CTCAGCGCTGCCACAGACCCACTTG	2975	TCAAGCGCTGCCACAGACCCACTT	2976	CAGCGCTGCCACAGACCCACT
LDLRex2(27;68;123;30)_139_d3_f	2977	AAGTGGGTCTGCGGCGAGCGCTGAGT	2978	AGTGGGTCTGCGGCGAGCGCTGAG	2979	GTGGGTCTGCGGCGAGCGCTGA
LDLRex2(27;68;123;30)_139_d3_r	2980	ACTCAGCGCTGCCGAGACCCACTT	2981	CTCAGCGCTGCCGAGACCCACT	2982	TCAGCGCTGCCGAGACCCAC
LDLRex2(27;68;123;30)_140_d3_f	2983	AGTGGGTCTGCGGCGAGCGCTGAGTG	2984	GTGGGTCTGCGGCGAGCGCTGAGT	2985	TGGGTCTGCGGCGAGCGCTGAG
LDLRex2(27;68;123;30)_140_d3_r	2986	CACTCAGCGCTGCCGAGACCCACT	2987	ACTCAGCGCTGCCGAGACCCAC	2988	CTCAGCGCTGCCGAGACCCCA
LDLRex2(27;68;123;30)_141_d3_f	2989	GTGGGTCTGCGACAGCGCTGAGTGC	2990	TGGGTCTGCGACAGCGCTGAGTG	2991	GGGTCTGCGACAGCGCTGAGT
LDLRex2(27;68;123;30)_141_d3_r	2992	GCACTCAGCGCTGTCGAGACCCAC	2993	CACTCAGCGCTGTCGAGACCCCA	2994	ACTCAGCGCTGTCGAGACCC
LDLRex2(27;68;123;30)_142_d3_f	2995	TGGGTCTGCGATAGCGCTGAGTGCC	2996	GGGTCTGCGATAGCGCTGAGTGC	2997	GGTCTGCGATAGCGCTGAGTG
LDLRex2(27;68;123;30)_142_d3_r	2998	GGCACTCAGCGCTATCGCAGACCCA	2999	GCACTCAGCGCTATCGCAGACCC	3000	CACTCAGCGCTATCGCAGACC
LDLRex2(27;68;123;30)_143_d3_f	3001	GGGTCTGCGATGGCGCTGAGTGCCA	3002	GGTCTGCGATGGCGCTGAGTGCC	3003	GTCTGCGATGGCGCTGAGTGC
LDLRex2(27;68;123;30)_143_d3_r	3004	TGGCACTCAGCGCCATCGCAGACCC	3005	GGCACTCAGCGCCATCGCAGACC	3006	GCACTCAGCGCCATCGCAGAC
LDLRex2(27;68;123;30)_144_d3_f	3007	GGTCTGCGATGGCGCTGAGTGCCAG	3008	GTCTGCGATGGCGCTGAGTGCCA	3009	TCTGCGATGGCGCTGAGTGCC
LDLRex2(27;68;123;30)_144_d3_r	3010	CTGGCACTCAGCGCCATCGCAGACC	3011	TGGCACTCAGCGCCATCGCAGAC	3012	GGCACTCAGCGCCATCGCAGA
LDLRex2(27;68;123;30)_145_d3_f	3013	GTCTGCGATGGCGCTGAGTGCCAGG	3014	TCTGCGATGGCGCTGAGTGCCAG	3015	CTGCGATGGCGCTGAGTGCCA
LDLRex2(27;68;123;30)_145_d3_r	3016	CCTGGCACTCAGCGCCATCGCAGAC	3017	CTGGCACTCAGCGCCATCGCAGA	3018	TGGCACTCAGCGCCATCGCAG
LDLRex2(27;68;123;30)_146_d3_f	3019	TCTGCGATGGCACTGAGTGCCAGGA	3020	CTGCGATGGCACTGAGTGCCAGG	3021	TGGATGGCACTGAGTGCCAG
LDLRex2(27;68;123;30)_146_d3_r	3022	TCTGGCACTCAGTGCCATCGCAGA	3023	CCTGGCACTCAGTGCCATCGCAG	3024	CTGGCACTCAGTGCCATCGCA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del3	3025	CTGCGATGGCAGTGAGTGCCAGGAT	3026	TGCGATGGCAGTGAGTGCCAGGA	3027	GCGATGGCAGTGAGTGCCAGG
LDLRex2(27;68;123;30)_147_d3_f	3028	ATCTGGCACTCACTGCCATCGCAG	3029	TCCTGGCACTCACTGCCATCGCA	3030	CCTGGCACTCACTGCCATCGC
LDLRex2(27;68;123;30)_147_d3_r	3031	TGGATGGCAGCGAGTGCCAGGATG	3032	GCGATGGCAGCGAGTGCCAGGAT	3033	CGATGGCAGCGAGTGCCAGGA
LDLRex2(27;68;123;30)_148_d3_f	3034	CATCTGGCACTCGTGCCATCGCA	3035	ATCTGGCACTCGTGCCATCGC	3036	TCCTGGCACTCGTGCCATCG
LDLRex2(27;68;123;30)_148_d3_r	3037	GCGATGGCAGCGAGTGCCAGGATGG	3038	CGATGGCAGCGAGTGCCAGGATG	3039	GATGGCAGCGAGTGCCAGGAT
LDLRex2(27;68;123;30)_149_d3_f	3040	CCATCTGGCACTCGTGCCATCGC	3041	CATCTGGCACTCGTGCCATCG	3042	ATCTGGCACTCGTGCCATC
LDLRex2(27;68;123;30)_149_d3_r	3043	CGATGGCAGCGGTGCCAGGATGGC	3044	GATGGCAGCGGTGCCAGGATGG	3045	ATGGCAGCGGTGCCAGGATG
LDLRex2(27;68;123;30)_150_d3_f	3046	GCCATCTGGCAGCGCTGCCATCG	3047	CCATCTGGCAGCGCTGCCATC	3048	CATCTGGCAGCGCTGCCAT
LDLRex2(27;68;123;30)_150_d3_r	3049	GATGGCAGCGCTTGCCAGGATGGCT	3050	ATGGCAGCGCTTGCCAGGATGGC	3051	TGGCAGCGCTTGCCAGGATGG
LDLRex2(27;68;123;30)_151_d3_f	3052	AGCCATCTGGCAAGCGCTGCCATC	3053	GCCATCTGGCAAGCGCTGCCAT	3054	CCATCTGGCAAGCGCTGCCA
LDLRex2(27;68;123;30)_151_d3_r	3055	ATGGCAGCGCTGGCCAGGATGGCTC	3056	TGGCAGCGCTGGCCAGGATGGCT	3057	GGCAGCGCTGGCCAGGATGGC
LDLRex2(27;68;123;30)_152_d3_f	3058	GAGCCATCTGGCCAGCGCTGCCAT	3059	AGCCATCTGGCCAGCGCTGCCA	3060	GCCATCTGGCCAGCGCTGCC
LDLRex2(27;68;123;30)_152_d3_r	3061	TGGCAGCGCTGACCAGGATGGCTCT	3062	GGCAGCGCTGACCAGGATGGCTC	3063	GCAAGCGCTGACCAGGATGGCT
LDLRex2(27;68;123;30)_153_d3_f	3064	AGAGCCATCTGGTCAAGCGTGCCA	3065	GAGCCATCTGGTCAAGCGTGCC	3066	AGCCATCTGGTCAAGCGCTGC
LDLRex2(27;68;123;30)_153_d3_r	3067	GGCAGCGCTGAGCAGGATGGCTCTG	3068	GCAGCGCTGAGCAGGATGGCTCT	3069	CAGCGCTGAGCAGGATGGCTC
LDLRex2(27;68;123;30)_154_d3_f	3070	CAGAGCCATCTGTCAAGCGTGCC	3071	AGAGCCATCTGTCAAGCGTGCC	3072	GAGCCATCTGTCAAGCGCTG
LDLRex2(27;68;123;30)_154_d3_r	3073	GCAGCGCTGAGTAGGATGGCTCTGA	3074	CAGCGCTGAGTAGGATGGCTCTG	3075	AGCGCTGAGTAGGATGGCTCT
LDLRex2(27;68;123;30)_155_d3_f	3076	TCAGAGCCATCTACTACGCGCTGC	3077	CAGAGCCATCTACTACGCGCTG	3078	AGAGCCATCTACTACGCGCT
LDLRex2(27;68;123;30)_155_d3_r	3079	CAGCGCTGAGTGGGATGGCTCTGAT	3080	AGCGCTGAGTGGGATGGCTCTGA	3081	GCGCTGAGTGGGATGGCTCTG
LDLRex2(27;68;123;30)_156_d3_f	3082	ATCAGAGCCATCCCACTACGCGCTG	3083	TCAGAGCCATCCCACTACGCGCT	3084	CAGAGCCATCCCACTACGCGC
LDLRex2(27;68;123;30)_156_d3_r	3085	AGCGCTGAGTGCGATGGCTCTGATG	3086	GCGCTGAGTGCGATGGCTCTGAT	3087	CGCTGAGTGCGATGGCTCTGA
LDLRex2(27;68;123;30)_157_d3_f	3088	CATCAGAGCCATCGCACTACGCGCT	3089	ATCAGAGCCATCGCACTACGCGC	3090	TCAGAGCCATCGCACTACGCG
LDLRex2(27;68;123;30)_157_d3_r	3091	GCGCTGAGTGCCATGGCTCTGATGA	3092	CGCTGAGTGCCATGGCTCTGATG	3093	GCTGAGTGCCATGGCTCTGAT
LDLRex2(27;68;123;30)_158_d3_f	3094	TCATCAGAGCCATGGCACTACGCGC	3095	CATCAGAGCCATGGCACTACGCG	3096	ATCAGAGCCATGGCACTACGC
LDLRex2(27;68;123;30)_158_d3_r	3097	CGCTGAGTGCCATGGCTCTGATGAG	3098	GCTGAGTGCCATGGCTCTGATGA	3099	CTGAGTGCCATGGCTCTGATG
LDLRex2(27;68;123;30)_159_d3_f	3100	CTCATCAGAGCCATGGCACTACGCG	3101	TCATCAGAGCCATGGCACTACGC	3102	CATCAGAGCCATGGCACTCAG
LDLRex2(27;68;123;30)_159_d3_r	3103	GCTGAGTGCCAGGGCTCTGATGATG	3104	CTGAGTGCCAGGGCTCTGATGAG	3105	TGAGTGCCAGGGCTCTGATGA
LDLRex2(27;68;123;30)_160_d3_f	3106	ACTCATCAGAGCCCTGGCACTCAGC	3107	CTCATCAGAGCCCTGGCACTCAG	3108	TCATCAGAGCCCTGGCACTCA
LDLRex2(27;68;123;30)_160_d3_r	3109	CTGAGTGCCAGGGCTCTGATGATG	3110	TGAGTGCCAGGGCTCTGATGATG	3111	GAGTGCCAGGGCTCTGATGAG
LDLRex2(27;68;123;30)_161_d3_f	3112	GACTCATCAGAGCCCTGGCACTCAG	3113	ACTCATCAGAGCCCTGGCACTCA	3114	CTCATCAGAGCCCTGGCACTC
LDLRex2(27;68;123;30)_161_d3_r	3115	TGAGTGCCAGGACTCTGATGATCC	3116	GAGTGCCAGGACTCTGATGATC	3117	AGTGCCAGGACTCTGATGAGT

Table 1

	del3	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
	LDLRex2(27;68;123;30)_162_d3_r	3118	GGACTCATCAGAGTCTGGCACTCA	3119	GACTCATCAGAGTCTGGCACTC	3120	ACTCATCAGAGTCTGGCACT
	LDLRex2(27;68;123;30)_163_d3_f	3121	GAGTGCCAGGATTCTGATGAGTCCC	3122	AGTGCCAGGATTCTGATGAGTCC	3123	GTGCCAGGATTCTGATGAGTC
	LDLRex2(27;68;123;30)_163_d3_r	3124	GGGACTCATCAGAATCCTGGCACTC	3125	GGACTCATCAGAATCCTGGCACT	3126	GACTCATCAGAATCCTGGCAC
	LDLRex2(27;68;123;30)_164_d3_f	3127	AGTGCCAGGATGCTGATGAGTCCCA	3128	GTGCCAGGATGCTGATGAGTCCC	3129	TGCCAGGATGCTGATGAGTCC
	LDLRex2(27;68;123;30)_164_d3_r	3130	TGGGACTCATCAGCATCTGGCACT	3131	GGACTCATCAGCATCTGGCAC	3132	GGACTCATCAGCATCTGGCA
	LDLRex2(27;68;123;30)_165_d3_f	3133	GTGCCAGGATGGTGATGAGTCCACAG	3134	TGCCAGGATGGTGATGAGTCCCA	3135	GCCAGGATGGTGATGAGTCCC
	LDLRex2(27;68;123;30)_165_d3_r	3136	CTGGGACTCATCACCATCCTGGCAC	3137	TGGGACTCATCACCATCCTGGCA	3138	GGGACTCATCACCATCCTGGC
	LDLRex2(27;68;123;30)_166_d3_f	3139	TGCCAGGATGGCGATGAGTCCCAGG	3140	GCCAGGATGGCGATGAGTCCCAG	3141	CCAGGATGGCGATGAGTCCCA
	LDLRex2(27;68;123;30)_166_d3_r	3142	CCTGGGACTCATCGCCATCCTGGCA	3143	CTGGGACTCATCGCCATCCTGGC	3144	TGGGACTCATCGCCATCCTGG
	LDLRex2(27;68;123;30)_167_d3_f	3145	GCCAGGATGGCTATGAGTCCCAGGA	3146	CCAGGATGGCTATGAGTCCCAGG	3147	CAGGATGGCTATGAGTCCCAG
	LDLRex2(27;68;123;30)_167_d3_r	3148	TCTGGGACTCATAGCCATCCTGGC	3149	CCTGGGACTCATAGCCATCCTGG	3150	CTGGGACTCATAGCCATCCTG
	LDLRex2(27;68;123;30)_168_d3_f	3151	CCAGGATGGCTCTGAGTCCCAGGAG	3152	CAGGATGGCTCTGAGTCCCAGGA	3153	AGGATGGCTCTGAGTCCCAGG
	LDLRex2(27;68;123;30)_168_d3_r	3154	CTCTGGGACTCAGAGCCATCCTGG	3155	TCTGGGACTCAGAGCCATCCTG	3156	CCTGGGACTCAGAGCCATCCT
	LDLRex2(27;68;123;30)_169_d3_f	3157	CAGGATGGCTCTGAGTCCCAGGAGA	3158	AGGATGGCTCTGAGTCCCAGGAG	3159	GGATGGCTCTGAGTCCCAGGA
	LDLRex2(27;68;123;30)_169_d3_r	3160	TCTCTGGGACTCAGAGCCATCCTG	3161	CTCTGGGACTCAGAGCCATCCT	3162	TCCTGGGACTCAGAGCCATCC
	LDLRex2(27;68;123;30)_170_d3_f	3163	AGGATGGCTCTGAGTCCCAGGAGAC	3164	GGATGGCTCTGAGTCCCAGGAGA	3165	GATGGCTCTGAGTCCCAGGAG
	LDLRex2(27;68;123;30)_170_d3_r	3166	GTCTCTGGGACTCAGAGCCATCCT	3167	TCTCTGGGACTCAGAGCCATCC	3168	CTCTGGGACTCAGAGCCATC
	LDLRex2(27;68;123;30)_171_d3_f	3169	GGATGGCTCTGAGTCCCAGGAGACG	3170	GATGGCTCTGAGTCCCAGGAGAC	3171	ATGGCTCTGAGTCCCAGGAGA
	LDLRex2(27;68;123;30)_171_d3_r	3172	CGTCTCTGGGACTCAGAGCCATCC	3173	GTCTCTGGGACTCAGAGCCATC	3174	TCTCTGGGACTCAGAGCCAT
	LDLRex2(27;68;123;30)_172_d3_f	3175	GATGGCTCTGATTCCAGGAGACGT	3176	ATGGCTCTGATTCCAGGAGACG	3177	TGGCTCTGATTCCAGGAGAC
	LDLRex2(27;68;123;30)_172_d3_r	3178	ACGTCTCTGGGAAATCAGAGCCATC	3179	CGTCTCTGGGAAATCAGAGCCAT	3180	GTCTCTGGGAAATCAGAGCCA
	LDLRex2(27;68;123;30)_173_d3_f	3181	ATGGCTCTGATGCCAGGAGACGTG	3182	TGGCTCTGATGCCAGGAGACGT	3183	GGCTCTGATGCCAGGAGACG
	LDLRex2(27;68;123;30)_173_d3_r	3184	CACGTCTCTGGGCATCAGAGCCAT	3185	ACGTCTCTGGGCATCAGAGCCA	3186	CGTCTCTGGGCATCAGAGCC
	LDLRex2(27;68;123;30)_174_d3_f	3187	TGGCTCTGATGACCAGGAGACGTGC	3188	GGCTCTGATGACCAGGAGACGTG	3189	GCTCTGATGACCAGGAGACGT
	LDLRex2(27;68;123;30)_174_d3_r	3190	GCACGTCTCTGGTGCATCAGAGCCA	3191	CACGTCTCTGGTGCATCAGAGCC	3192	ACGTCTCTGGTGCATCAGAGC
	LDLRex2(27;68;123;30)_175_d3_f	3193	GGCTCTGATGAGCAGGAGACGTGCT	3194	GCTCTGATGAGCAGGAGACGTGC	3195	CTCTGATGAGCAGGAGACGTG
	LDLRex2(27;68;123;30)_175_d3_r	3196	AGCACGTCTCTGCTCATCAGAGCC	3197	GCACGTCTCTGCTCATCAGAGC	3198	CACGTCTCTGCTCATCAGAG
	LDLRex2(27;68;123;30)_176_d3_f	3199	GCTCTGATGAGTAGGAGACGTGCTG	3200	CTCTGATGAGTAGGAGACGTGCT	3201	TCTGATGAGTAGGAGACGTGC
	LDLRex2(27;68;123;30)_176_d3_r	3202	CAGCAGTCTCTACTATCATCAGAGC	3203	AGCAGTCTCTACTATCATCAGAG	3204	GCACGTCTCTACTATCATCAGA
	LDLRex2(27;68;123;30)_177_d3_f	3205	CTCTGATGAGTCGGAGACGTGCTGT	3206	TCTGATGAGTCGGAGACGTGCTG	3207	CTGATGAGTCGGAGACGTGCT
	LDLRex2(27;68;123;30)_177_d3_r	3208	ACAGCACGTCTCCGACTCATCAGAG	3209	CAGCACGTCTCCGACTCATCAGA	3210	AGCACGTCTCCGACTCATCAG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del3						
LDLRex2(27;68;123;30)_178_d3_f	3211	TCTGATGAGTCCGAGACGTGCTGTG	3212	CTGATGAGTCCGAGACGTGCTGT	3213	TGATGAGTCCGAGACGTGCTG
LDLRex2(27;68;123;30)_178_d3_r	3214	CACAGCACGTCTCGGACTCATCAGA	3215	ACAGCACGTCTCGGACTCATCAG	3216	CAGCACGTCTCGGACTCATCA
LDLRex2(27;68;123;30)_179_d3_f	3217	CTGATGAGTCCGAGACGTGCTGTGA	3218	TGATGAGTCCGAGACGTGCTGTG	3219	GATGAGTCCGAGACGTGCTGT
LDLRex2(27;68;123;30)_179_d3_r	3220	TCACAGACGTCTGGGACTCATCAG	3221	CACAGACGTCTGGGACTCATCA	3222	ACAGACGTCTGGGACTCATC
LDLRex2(27;68;123;30)_180_d3_f	3223	TGATGAGTCCGAGACGTGCTGTGAG	3224	GATGAGTCCGAGACGTGCTGTGA	3225	ATGATCCGAGACGTGCTGTG
LDLRex2(27;68;123;30)_180_d3_r	3226	CTCACAGCACGTCTGGGACTCATCA	3227	TCACAGCACGTCTGGGACTCATC	3228	CACAGCACGTCTGGGACTCAT
LDLRex2(27;68;123;30)_181_d3_f	3229	GATGAGTCCGAGACGTGCTGTGAGT	3230	ATGATCCGAGACGTGCTGTGAG	3231	TGATCCGAGACGTGCTGTGA
LDLRex2(27;68;123;30)_181_d3_r	3232	ACTCACAGCACGTCTGGGACTCATC	3233	CTCACAGCACGTCTGGGACTCAT	3234	TCACAGCACGTCTGGGACTCA
LDLRex2(27;68;123;30)_182_d3_f	3235	ATGATCCGAGACGTGCTGTGAGTC	3236	TGATCCGAGACGTGCTGTGAGT	3237	GAGTCCGAGACGTGCTGTGAG
LDLRex2(27;68;123;30)_182_d3_r	3238	GACTCACAGCACGTCTGGGACTCAT	3239	ACTCACAGCACGTCTGGGACTCA	3240	CTCACAGCACGTCTGGGACTC
LDLRex2(27;68;123;30)_183_d3_f	3241	TGATCCGAGACGTGCTGTGAGTCC	3242	GAGTCCGAGACGTGCTGTGAGTC	3243	AGTCCGAGACGTGCTGTGAGT
LDLRex2(27;68;123;30)_183_d3_r	3244	GGACTCACAGCACGTCTGGGACTCA	3245	GACTCACAGCACGTCTGGGACTC	3246	ACTCACAGCACGTCTGGGACT
LDLRex2(27;68;123;30)_184_d3_f	3247	GAGTCCGAGACGTGCTGTGAGTCCC	3248	AGTCCGAGACGTGCTGTGAGTCC	3249	GTCCCAGGAGTGTGTGAGTC
LDLRex2(27;68;123;30)_184_d3_r	3250	GGGACTCACAGCACGTCTGGGACTC	3251	GGACTCACAGCACGTCTGGGACT	3252	GACTCACAGCACGTCTGGGAC
LDLRex2(27;68;123;30)_185_d3_f	3253	AGTCCGAGACGTGCTGTGAGTCCCC	3254	GTCCCAGGAGACGTGTGAGTCCC	3255	TCCCAGGAGACGTGTGAGTCC
LDLRex2(27;68;123;30)_185_d3_r	3256	GGGACTCACAGCTCTCTGGGACT	3257	GGGACTCACAGCTCTCTGGGAC	3258	GGACTCACAGCTCTCTGGGA
LDLRex2(27;68;123;30)_186_d3_f	3259	GTCCAGGAGACCTGTGAGTCCCT	3260	TCCAGGAGACCTGTGAGTCCCT	3261	CCCAGGAGACCTGTGAGTCCC
LDLRex2(27;68;123;30)_186_d3_r	3262	AGGGGACTCACAGGTCTCTGGGAC	3263	GGGACTCACAGGTCTCTGGGA	3264	GGGACTCACAGGTCTCTGGG
LDLRex2(27;68;123;30)_187_d3_f	3265	TCCAGGAGACGTGTGAGTCCCTT	3266	CCCAGGAGACGTGTGAGTCCCT	3267	CCAGGAGACGTGTGAGTCCCC
LDLRex2(27;68;123;30)_187_d3_r	3268	AAGGGGACTCACACGTCTCTGGGA	3269	AGGGGACTCACACGTCTCTGGG	3270	GGGGACTCACACGTCTCTGG
LDLRex2(27;68;123;30)_188_d3_f	3271	CCCAGGAGACGTGTGAGTCCCTTT	3272	CCAGGAGACGTGTGAGTCCCTT	3273	CAGGAGACGTGTGAGTCCCT
LDLRex2(27;68;123;30)_188_d3_r	3274	AAAGGGGACTCACACGTCTCTGGG	3275	AAGGGGACTCACACGTCTCTGG	3276	AGGGGACTCACACGTCTCTG
LDLRex2(27;68;123;30)_189_d3_f	3277	CCAGGAGACGTGTGAGTCCCTTTG	3278	CAGGAGACGTGTGAGTCCCTTT	3279	AGGAGACGTGTGAGTCCCTT
LDLRex2(27;68;123;30)_189_d3_r	3280	CAAGGGGACTCACACGTCTCTGG	3281	AAAGGGGACTCACACGTCTCTG	3282	AAGGGGACTCACACGTCTCT
LDLRex2(27;68;123;30)_190 + 1_d3_f	3283	AGGAGACGTGTAGTCCCTTTGGG	3284	GGAGACGTGTAGTCCCTTTGG	3285	GAGACGTGTAGTCCCTTTG
LDLRex2(27;68;123;30)_190 + 1_d3_r	3286	CCCAAGGGGACTAGCACGTCTCT	3287	CCAAAGGGGACTAGCACGTCTCC	3288	CAAAAGGGGACTAGCACGTCTC
LDLRex2(27;68;123;30)_190 + 10_d3_f	3289	GCTGTGAGTCCCTGGGATGATG	3290	CTGTGAGTCCCTGGGATGATAT	3291	TGTGAGTCCCTGGGATGATA
LDLRex2(27;68;123;30)_190 + 10_d3_r	3292	CATATCATGCCAGGAGACTCACAGC	3293	ATATCATGCCAGGAGACTCACAG	3294	TATCATGCCAGGAGACTCACA
LDLRex2(27;68;123;30)_190 + 11_d3_f	3295	CTGTGAGTCCCGGGATGATATGC	3296	TGTGAGTCCCGGGATGATATG	3297	GTGAGTCCCGGGATGATAT
LDLRex2(27;68;123;30)_190 + 11_d3_r	3298	GCATATCATGCCCGGGAGACTCACAG	3299	CATATCATGCCCGGGAGACTCACA	3300	ATATCATGCCCGGGAGACTCAC
LDLRex2(27;68;123;30)_190 + 12_d3_f	3301	TGTGAGTCCCTGGCATGATGCA	3302	GTGAGTCCCTGGCATGATGTC	3303	TGAGTCCCTGGCATGATATG

del3	SEQ_ID		25 nt		SEQ_ID		23 nt		SEQ_ID		21 nt	
	NO:		NO:		NO:		NO:		NO:		NO:	
LDLRex2(27;68;123;30)_190 + 12_d3_1	3304	TGCATATCATGCCAGGGGACTCAC	3305	GCATATCATGCCAGGGGACTCAC	3306	CATATCATGCCAGGGGACTCA						
LDLRex2(27;68;123;30)_190 + 13_d3_1	3307	GTGAGTCCCCTTGCCATGATGCAT	3308	TGAGTCCCCTTGCCATGATGCA	3309	GAGTCCCCTTGCCATGATATGC						
LDLRex2(27;68;123;30)_190 + 13_d3_1	3310	ATGCATATCATGCAAGGGGACTCAC	3311	TGCATATCATGCAAGGGGACTCA	3312	GCATATCATGCAAGGGGACTC						
LDLRex2(27;68;123;30)_190 + 14_d3_1	3313	TGAGTCCCCTTGCCATGATGCATT	3314	GAGTCCCCTTGCCATGATGCAT	3315	AGTCCCCTTGCCATGATATGCA						
LDLRex2(27;68;123;30)_190 + 14_d3_1	3316	AATGCATATCATGAAAGGGGACTCA	3317	ATGCATATCATGAAAGGGGACTC	3318	TGCATATCATGAAAGGGGACT						
LDLRex2(27;68;123;30)_190 + 15_d3_1	3319	GAGTCCCCTTGCCATGATGCATT	3320	AGTCCCCTTGCCATGATGCATT	3321	GTCCCCTTGATGATATGCAT						
LDLRex2(27;68;123;30)_190 + 15_d3_1	3322	AAATGCATATCATAAAGGGGACTC	3323	GAATGCATATCATAAAGGGGACT	3324	ATGCATATCATAAAGGGGAC						
LDLRex2(27;68;123;30)_190 + 2_d3_f	3325	GGAGACGTGCTGCTCCCTTTGGGC	3326	GAGACGTGCTGGTCCCTTTGGG	3327	AGACGTGCTGCTCCCTTTGG						
LDLRex2(27;68;123;30)_190 + 2_d3_r	3328	GCCAAAGGGGACAGCAGCTCTCC	3329	CCAAAGGGGACAGCAGCTCTC	3330	CCAAAGGGGACAGCAGCTCT						
LDLRex2(27;68;123;30)_190 + 3_d3_f	3331	GAGACGTGCTGTTCCCTTTGGGCA	3332	GAGACGTGCTTCCCTTTGGGCA	3333	GACGTGCTTCCCTTTGGG						
LDLRex2(27;68;123;30)_190 + 3_d3_r	3334	TGCCAAAGGGGAACAGCAGCTCTC	3335	TGCCAAAGGGGAACAGCAGCTCTC	3336	CCAAAGGGGAACAGCAGCTC						
LDLRex2(27;68;123;30)_190 + 4_d3_f	3337	AGACGTGCTGTGCCCTTTGGGCAT	3338	AGACGTGCTGTGCCCTTTGGGCAT	3339	ACGTGCTGTGCCCTTTGGGC						
LDLRex2(27;68;123;30)_190 + 4_d3_r	3340	ATGCCAAAGGGGACAGCAGCTCT	3341	ATGCCAAAGGGGACAGCAGCTCT	3342	GCCCAAGGGGACAGCAGCAGT						
LDLRex2(27;68;123;30)_190 + 5_d3_f	3343	GACGTGCTGTACCCTTTGGGCATG	3344	GACGTGCTGTACCCTTTGGGCATG	3345	CGTGTGTGACCTTTGGGCA						
LDLRex2(27;68;123;30)_190 + 5_d3_r	3346	CATGCCAAAGGGTCACAGCAGCTC	3347	CATGCCAAAGGGTCACAGCAGCTC	3348	TGCCAAAGGGTCACAGCAGC						
LDLRex2(27;68;123;30)_190 + 6_d3_f	3349	ACGTGCTGTGAGCCTTTGGGCATGA	3350	ACGTGCTGTGAGCCTTTGGGCATGA	3351	GTGCTGTGAGCCTTTGGGCAT						
LDLRex2(27;68;123;30)_190 + 6_d3_r	3352	TCATGCCAAAGGGTCACAGCAGCT	3353	TCATGCCAAAGGGTCACAGCAGCT	3354	ATGCCAAAGGGTCACAGCAGC						
LDLRex2(27;68;123;30)_190 + 7_d3_f	3355	CGTGTGTGAGTCTTTGGGCATGAT	3356	CGTGTGTGAGTCTTTGGGCATGAT	3357	TGCTGTGAGTCTTTGGGCATG						
LDLRex2(27;68;123;30)_190 + 7_d3_r	3358	ATCATGCCAAAGACTCACAGCAGC	3359	ATCATGCCAAAGACTCACAGCAGC	3360	CATGCCAAAGACTCACAGCA						
LDLRex2(27;68;123;30)_190 + 8_d3_f	3361	GTGTGTGAGTCTTTGGGCATGATA	3362	GTGTGTGAGTCTTTGGGCATGAT	3363	GCTGTGAGTCTTTGGGCATGA						
LDLRex2(27;68;123;30)_190 + 8_d3_r	3364	TATCATGCCAAAGACTCACAGCAC	3365	TATCATGCCAAAGACTCACAGCA	3366	TCATGCCAAAGACTCACAGC						
LDLRex2(27;68;123;30)_190 + 9_d3_f	3367	TGCTGTGAGTCTTTGGGCATGATAT	3368	TGCTGTGAGTCTTTGGGCATGAT	3369	CTGTGAGTCTTTGGGCATGAT						
LDLRex2(27;68;123;30)_190 + 9_d3_r	3370	ATATCATGCCAAAGACTCACAGCA	3371	ATATCATGCCAAAGACTCACAGCA	3372	ATCATGCCAAAGACTCACAG						
LDLRex2(27;68;123;30)_190_d3_f	3373	CAGGAGACGTGCGAGTCCCCTTTGG	3374	CAGGAGACGTGCGAGTCCCCTTTG	3375	GGAGACGTGCGAGTCCCCTTT						
LDLRex2(27;68;123;30)_190_d3_r	3376	CCAAAGGGGACTCGCACGCTCTCTG	3377	CCAAAGGGGACTCGCACGCTCTCT	3378	AAAGGGGACTCGCACGCTCTC						
LDLRex2(27;68;123;30)_68 - 1_d3_f	3379	TCCTCTCTCAGCGCACAGATGCG	3380	TCCTCTCTCAGCGCACAGATGC	3381	CTCTCTCAGCGCACAGATG						
LDLRex2(27;68;123;30)_68 - 1_d3_r	3382	CGCATCTGTGCTGCTGAGAGAGGA	3383	CGCATCTGTGCTGCTGAGAGAGG	3384	CATCTGTGCTGCTGAGAGAG						
LDLRex2(27;68;123;30)_68 - 10_d3_f	3385	TTCTCCTTTTCCCTCTCAGTGGCG	3386	TTCTCCTTTTCCCTCTCAGTGGCG	3387	CTCCTTTTCCCTCTCAGTGGG						
LDLRex2(27;68;123;30)_68 - 10_d3_r	3388	CGCCCACTGAGAGGGAAAAGGAGAA	3389	CGCCCACTGAGAGGGAAAAGGAGA	3390	CCCACTGAGAGGGAAAAGGAG		</				

Table 1

del3	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_68 - 12_d3_f	3397	CTTTCTCCTTTTCTCTCTCAGTGGG	3398	TTTCTCCTTTTCTCTCTCAGTGG	3399	TTTCTCCTTTTCTCTCTCAGTG
LDLRex2(27;68;123;30)_68 - 12_d3_r	3400	CCCACTGAGAGAGAAAGGAGAAAG	3401	CCCACTGAGAGAGAAAGGAGAAA	3402	CACTGAGAGAGAAAGGAGAA
LDLRex2(27;68;123;30)_68 - 13_d3_f	3403	CCTTTCTCCTTTCTCTCTCAGTGG	3404	CTTTCTCCTTTCTCTCTCAGTG	3405	TTTCTCCTTTCTCTCTCAGT
LDLRex2(27;68;123;30)_68 - 13_d3_r	3406	CCCACTGAGAGAGAAAGGAGAAAG	3407	CACTGAGAGAGAAAGGAGAAAG	3408	ACTGAGAGAGAAAGGAGAAA
LDLRex2(27;68;123;30)_68 - 14_d3_f	3409	CCCTTTCTCCTTCTCTCTCTCAGTG	3410	CCCTTCTCCTTCTCTCTCTCAGT	3411	CTTTCTCCTTCTCTCTCTCAG
LDLRex2(27;68;123;30)_68 - 14_d3_r	3412	CACTGAGAGAGAGAAAGGAGAAAGG	3413	CACTGAGAGAGAGAAAGGAGAAAG	3414	CTGAGAGAGAGAAAGGAGAAAG
LDLRex2(27;68;123;30)_68 - 15_d3_f	3415	ACCCTTTCTCCTCTCTCTCTCAGT	3416	CCCTTTCTCCTCTCTCTCTCAG	3417	CCCTTCTCCTCTCTCTCTCTCA
LDLRex2(27;68;123;30)_68 - 15_d3_r	3418	ACTGAGAGAGAGAGAGAGAAAGGGT	3419	CTGAGAGAGAGAGAGAGAAAGGG	3420	TGAGAGAGAGAGAGAGAAAGG
LDLRex2(27;68;123;30)_68 - 2_d3_f	3421	TTCTCTCTCTCTCGGGCGACAGTGC	3422	TCCTCTCTCTCGGGCGACAGATG	3423	CCTCTCTCTCGGGCGACAGAT
LDLRex2(27;68;123;30)_68 - 2_d3_r	3424	GCATCTGTGCGCCCGAGAGAGAGAA	3425	CATCTGTGCGCCCGAGAGAGAGGA	3426	ATCTGTGCGCCCGAGAGAGAGG
LDLRex2(27;68;123;30)_68 - 3_d3_f	3427	TTTCTCTCTCTTGGGCGACAGATG	3428	TTCTCTCTCTTGGGCGACAGAT	3429	TCCTCTCTTGGGCGACAGA
LDLRex2(27;68;123;30)_68 - 3_d3_r	3430	CATCTGTGCGCCCAAGAGAGAGAGAA	3431	ATCTGTGCGCCCAAGAGAGAGAGAA	3432	TCTGTGCGCCCAAGAGAGAGGA
LDLRex2(27;68;123;30)_68 - 4_d3_f	3433	TTTTCTCTCTCTGTGGCGACAGAT	3434	TTTTCTCTCTCTGTGGCGACAGA	3435	TTCTCTCTCTGTGGCGACAG
LDLRex2(27;68;123;30)_68 - 4_d3_r	3436	ATCTGTGCGCCACGAGAGAGAGAAA	3437	TCTGTGCGCCACGAGAGAGAGAAA	3438	CTGTGCGCCACGAGAGAGAGAA
LDLRex2(27;68;123;30)_68 - 5_d3_f	3439	CTTTCTCTCTCTAGTGGCGACAGA	3440	TTTTCTCTCTCTAGTGGCGACAG	3441	TTTCTCTCTAGTGGCGACA
LDLRex2(27;68;123;30)_68 - 5_d3_r	3442	TCTGTGCGCCACTAGAGAGAGAGAAA	3443	CTGTGCGCCACTAGAGAGAGAGAAA	3444	TGTGCGCCACTAGAGAGAGAAA
LDLRex2(27;68;123;30)_68 - 6_d3_f	3445	CCTTTCTCTCTCCAGTGGCGACAG	3446	CTTTCTCTCTCCAGTGGCGACA	3447	TTTCTCTCTCCAGTGGCGAC
LDLRex2(27;68;123;30)_68 - 6_d3_r	3448	CTGTGCGCCACTGGAGAGAGAGAGAA	3449	TGTGCGCCACTGGAGAGAGAGAGAA	3450	GTCGCCCACTGGAGAGAGAGAAA
LDLRex2(27;68;123;30)_68 - 7_d3_f	3451	TCCTTTTCTCTCTCAGTGGCGACA	3452	CCCTTTCTCTCTCAGTGGCGCAC	3453	CTTTTCTCTCTCAGTGGCGCA
LDLRex2(27;68;123;30)_68 - 7_d3_r	3454	TGTGCGCCCACTGAAGAGAGAGAGAA	3455	GTCGCCCACTGAAGAGAGAGAGAA	3456	TGCGCCCACTGAAGAGAGAGAAAG
LDLRex2(27;68;123;30)_68 - 8_d3_f	3457	CTCCTTTTCTCTCTCAGTGGCGAC	3458	TCCTTTTCTCTCTCAGTGGCGCA	3459	CCCTTTTCTCTCTCAGTGGCGG
LDLRex2(27;68;123;30)_68 - 8_d3_r	3460	GTCGCCCACTGAGAGAGAGAGAGAGG	3461	TGCGCCCACTGAGAGAGAGAGAGG	3462	CGCCCACTGAGAGAGAGAGAGG
LDLRex2(27;68;123;30)_68 - 9_d3_f	3463	TCTCCTTTTCTCTCTCAGTGGCGCA	3464	CTCCTTTTCTCTCTCAGTGGCGG	3465	TCCTTTTCTCTCTCAGTGGGC
LDLRex2(27;68;123;30)_68 - 9_d3_r	3466	TGCGCCCACTGAGAGAGAGAGAGAGG	3467	CGCCCACTGAGAGAGAGAGAGAGG	3468	GCCCACTGAGAGAGAGAGAGG
LDLRex2(27;68;123;30)_68_d3_f	3469	CCCTCTCTCTCAGCGACAGATGCGA	3470	CTCTCTCTCAGCGACAGATGCG	3471	TCTCTCTCAGCGACAGATGCG
LDLRex2(27;68;123;30)_68_d3_r	3472	TCGCATCTGTGCGCTGAGAGAGAGG	3473	CGCATCTGTGCGCTGAGAGAGAG	3474	GCATCTGTGCGCTGAGAGAGA
LDLRex2(27;68;123;30)_69_d3_f	3475	CTCTCTCTCAGTCGACAGATGCGAA	3476	TCCTCTCTCAGTCGACAGATGCGA	3477	CTCTCTCAGTCGACAGATGCGG
LDLRex2(27;68;123;30)_69_d3_r	3478	TTGCGCATCTGTGCGACTGAGAGAGAG	3479	TGCGCATCTGTGCGACTGAGAGAGA	3480	CGCATCTGTGCGACTGAGAGAG
LDLRex2(27;68;123;30)_70_d3_f	3481	TCTCTCTCAGTGGACAGATGCGAAA	3482	CTCTCTCAGTGGACAGATGCGAA	3483	TCTCTCAGTGGACAGATGCGA
LDLRex2(27;68;123;30)_70_d3_r	3484	TTTGGCATCTGTCCACTGAGAGAGA	3485	TTGCGCATCTGTCCACTGAGAGAG	3486	TGCGCATCTGTCCACTGAGAGA
LDLRex2(27;68;123;30)_71_d3_f	3487	CTCTCTCAGTGGACAGATGCGAAA	3488	TCCTCTCAGTGGACAGATGCGAAA	3489	CTCTCAGTGGACAGATGCGAA

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
del3	3490	CTTTGCGACTGTCCACTGAGAG	3491	TTTTCGACTGTCCACTGAGAGA	3492	TTGCGATCTGCCACTGAGAG
LDLRex2(27;68;123;30)_71_d3_r	3493	TCTCTAGTGGGCAGATGCGAAAGA	3494	CTCTAGTGGGCAGATGCGAAAG	3495	TCTCAGTGGGCAGATGCGAAA
LDLRex2(27;68;123;30)_72_d3_f	3496	TCTTCGACTGTCCACTGAGAGA	3497	CTTTCGACTGTCCACTGAGAG	3498	TTTCGATCTGCCACTGAGA
LDLRex2(27;68;123;30)_72_d3_r	3499	CTCTAGTGGGCAGATGCGAAAGAA	3500	TCTCAGTGGGCAGATGCGAAAGA	3501	CTCAGTGGGCAGATGCGAAAG
LDLRex2(27;68;123;30)_73_d3_f	3502	TTCTTTGCGACTGTCCACTGAGAG	3503	TCTTCGACTGTCCACTGAGA	3504	CTTTCGATCTGCCACTGAG
LDLRex2(27;68;123;30)_73_d3_r	3505	TCTCAGTGGCGGATGCGAAAGAAA	3506	CTCAGTGGCGGATGCGAAAGAA	3507	TCAGTGGCGGATGCGAAAGA
LDLRex2(27;68;123;30)_74_d3_f	3508	TTTCTTTGCGATCCGCCACTGAGA	3509	TTCTTTGCGATCCGCCACTGAG	3510	TCCTTCGATCCGCCCACTGA
LDLRex2(27;68;123;30)_74_d3_r	3511	CTCAGTGGCGGAATGCGAAAGAAC	3512	TCAGTGGCGGAATGCGAAAGAA	3513	CAGTGGCGGAATGCGAAAGAA
LDLRex2(27;68;123;30)_75_d3_f	3514	GTTTCTTTGCGATTGCCCACTGAG	3515	TTTCTTTGCGATTGCCCACTGA	3516	TTCTTTGCGATTGCCCACTG
LDLRex2(27;68;123;30)_75_d3_r	3517	TCAGTGGCGACTGCGAAAGAACG	3518	CAGTGGCGACTGCGAAAGAAC	3519	AGTGGCGACTGCGAAAGAAA
LDLRex2(27;68;123;30)_76_d3_f	3520	CGTTTCTTTGCGATCGCCCACTGA	3521	GTTTCTTTGCGATCGCCCACTG	3522	TTTCTTTGCGATCGCCCACT
LDLRex2(27;68;123;30)_76_d3_r	3523	CAGTGGCGACAGCGAAAGAACGA	3524	AGTGGCGACAGCGAAAGAACG	3525	GTGGCGACAGCGAAAGAAC
LDLRex2(27;68;123;30)_77_d3_f	3526	TCGTTTCTTTGCTGTGCCCACTG	3527	CGTTTCTTTGCTGTGCCCACT	3528	GTTTCTTTGCTGTGCCCAC
LDLRex2(27;68;123;30)_77_d3_r	3529	AGTGGCGACAGCGAAAGAACGAG	3530	GTGGCGACAGCGAAAGAACGA	3531	TGGCGACAGCGAAAGAACG
LDLRex2(27;68;123;30)_78_d3_f	3532	CTCGTTTCTTTGCTGTGCCCACT	3533	TCGTTTCTTTGCTGTGCCCAC	3534	CGTTTCTTTGCTGTGCCCA
LDLRex2(27;68;123;30)_78_d3_r	3535	GTGGCGACAGAGAAAGAACGAGT	3536	TGGCGACAGAGAAAGAACGAG	3537	GGCGACAGAGAAAGAACGA
LDLRex2(27;68;123;30)_79_d3_f	3538	ACTCGTTTCTTTCTGTGCCCAC	3539	CTCGTTTCTTTCTGTGCCCA	3540	TCGTTTCTTTCTGTGCCCC
LDLRex2(27;68;123;30)_79_d3_r	3541	TGGCGACAGATAAAGAACGAGTT	3542	GGCGACAGATAAAGAACGAGT	3543	GGCGACAGATAAAGAACGAG
LDLRex2(27;68;123;30)_80_d3_f	3544	AACTCGTTTCTTTATCTGTGCCCA	3545	ACTCGTTTCTTTATCTGTGCCCC	3546	CTCGTTTCTTTATCTGTGCC
LDLRex2(27;68;123;30)_80_d3_r	3547	GGCGACAGATGAAGAACGAGTTC	3548	GGCGACAGATGAAGAACGAGTT	3549	GCGACAGATGAAGAACGAGT
LDLRex2(27;68;123;30)_81_d3_f	3550	GAACCTCGTTTCTTCTGTGCCCC	3551	AACTCGTTTCTTCTGTGCCCC	3552	ACTCGTTTCTTCTGTGCC
LDLRex2(27;68;123;30)_81_d3_r	3553	GGCGACAGATGCGAAACGAGTTC	3554	GCGACAGATGCGAAACGAGTTC	3555	GCGACAGATGCGAAACGAGTT
LDLRex2(27;68;123;30)_82_d3_f	3556	GGAACCTCGTTTCTGTGCCCC	3557	GAACTCGTTTCTGTGTGCC	3558	AACTCGTTTCTGTGTGCC
LDLRex2(27;68;123;30)_82_d3_r	3559	GCGACAGATGCGAAACGAGTTC	3560	GCGACAGATGCGAAACGAGTTC	3561	GACAGATGCGAAACGAGTTC
LDLRex2(27;68;123;30)_83_d3_f	3562	TGGAACCTCGTTTCCGATCTGTGC	3563	GGAACCTCGTTTCCGATCTGTGC	3564	GAACTCGTTTCCGATCTGT
LDLRex2(27;68;123;30)_83_d3_r	3565	CGACAGATGCGAAACGAGTTCAG	3566	GACAGATGCGAAACGAGTTC	3567	ACAGATGCGAAACGAGTTC
LDLRex2(27;68;123;30)_84_d3_f	3568	CTGGAACCTCGTTTCCGATCTGTGC	3569	TGGAACCTCGTTTCCGATCTGT	3570	GGAACCTCGTTTCCGATCTGT
LDLRex2(27;68;123;30)_84_d3_r	3571	GACAGATGCGAAACGAGTTCAGT	3572	ACAGATGCGAAACGAGTTCAG	3573	CAGATGCGAAACGAGTTC
LDLRex2(27;68;123;30)_85_d3_f	3574	ACTGGAACCTCGTTTCCGATCTGT	3575	CTGGAACCTCGTTTCCGATCTGT	3576	TGGAACCTCGTTTCCGATCTGT
LDLRex2(27;68;123;30)_85_d3_r	3577	ACAGATGCGAAACGAGTTCAGTG	3578	CAGATGCGAAACGAGTTCAGT	3579	AGATGCGAAACGAGTTCAG
LDLRex2(27;68;123;30)_86_d3_f	3580	CACCTGGAACCTCGTTTCCGATCTGT	3581	ACTGGAACCTCGTTTCCGATCTGT	3582	CTGGAACCTCGTTTCCGATCT

Table 1

	del3	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
	LDLRex2(27;68;123;30)_87_d3_f	3583	CAGATGCGAAAGCGAGTCCAGTGC	3584	AGATGCGAAAGCGAGTCCAGTG	3585	GATGCGAAAGCGAGTCCAGT
	LDLRex2(27;68;123;30)_87_d3_r	3586	GCACTGGAACTCGCTTCGCATCTG	3587	CACTGGAACTCGCTTCGCATCT	3588	ACTGGAACTCGCTTCGCATC
	LDLRex2(27;68;123;30)_88_d3_f	3589	AGATGCGAAAGAGAGTCCAGTGCC	3590	GATGCGAAAGAGAGTCCAGTGC	3591	ATGCGAAAGAGAGTCCAGTG
	LDLRex2(27;68;123;30)_88_d3_r	3592	GGCACTGGAACTCTCTTCGCATCT	3593	GCACTGGAACTCTCTTCGCATC	3594	CACTGGAACTCTCTTCGCAT
	LDLRex2(27;68;123;30)_89_d3_f	3595	GATGCGAAAGAAAGTCCAGTGCCA	3596	ATGCGAAAGAAAGTCCAGTGCC	3597	TGCGAAAGAAAGTCCAGTGC
	LDLRex2(27;68;123;30)_89_d3_r	3598	TGGCACTGGAACTTCTTCGCATC	3599	GGCACTGGAACTTCTTCGCAT	3600	GCACTGGAACTTCTTCGCA
	LDLRex2(27;68;123;30)_90_d3_f	3601	ATGCGAAAGAAAGTCCAGTGCCAA	3602	TGCGAAAGAAAGTCCAGTGCCA	3603	GCGAAAGAAAGTCCAGTGCC
	LDLRex2(27;68;123;30)_90_d3_r	3604	TTGGCACTGGAACTTCTTCGCAT	3605	TGGCACTGGAACTTCTTCGCA	3606	GGCACTGGAACTTCTTCGCG
	LDLRex2(27;68;123;30)_91_d3_f	3607	TGCGAAAGAACTCCAGTGCCAAG	3608	GCGAAAGAACTCCAGTGCCAA	3609	CGAAAGAACTCCAGTGCCA
	LDLRex2(27;68;123;30)_91_d3_r	3610	CTTGGCACTGGAAAGTTCCTTCGCA	3611	TTGGCACTGGAAAGTTCCTTCGC	3612	TGGCACTGGAAAGTTCCTTCG
	LDLRex2(27;68;123;30)_92_d3_f	3613	GCGAAAGAAACGCCAGTGCCAAGA	3614	CGAAAGAAACGCCAGTGCCAAG	3615	GAAAGAAACGCCAGTGCCA
	LDLRex2(27;68;123;30)_92_d3_r	3616	TCTTGGCACTGGACGTTCTTCGCG	3617	CTTGGCACTGGACGTTCTTCG	3618	TTGGCACTGGACGTTCTTTC
	LDLRex2(27;68;123;30)_93_d3_f	3619	CGAAAGAAACGACCAGTGCCAAGAC	3620	GAAAGAAACGACCAGTGCCAAGA	3621	AAAGAAACGACCAGTGCCAAG
	LDLRex2(27;68;123;30)_93_d3_r	3622	GTCTTGGCACTGGTCTTCTTCG	3623	TCTTGGCACTGGTCTTCTTTC	3624	CTTGGCACTGGTCTTCTTT
	LDLRex2(27;68;123;30)_94_d3_f	3625	GAAAGAAACGAGCAGTGCCAAGACG	3626	AAAGAAACGAGCAGTGCCAAGAC	3627	AAGAAACGAGCAGTGCCAAGA
	LDLRex2(27;68;123;30)_94_d3_r	3628	CGTCTTGGCACTGCTGTTCTTTC	3629	GTCTTGGCACTGCTGTTCTTT	3630	TCTTGGCACTGCTGTTCTT
	LDLRex2(27;68;123;30)_95_d3_f	3631	AAAGAAACGAGTAGTGCCAAGACGG	3632	AAGAAACGAGTAGTGCCAAGACG	3633	AGAAACGAGTAGTGCCAAGAC
	LDLRex2(27;68;123;30)_95_d3_r	3634	CCGTCTTGGCACTACTCGTTCTTT	3635	CGTCTTGGCACTACTCGTTCTT	3636	GTCTTGGCACTACTCGTTCT
	LDLRex2(27;68;123;30)_96_d3_f	3637	AAGAAACGAGTTGTGCCAAGACGGG	3638	AGAAACGAGTTGTGCCAAGACGG	3639	GAAACGAGTTGTGCCAAGACG
	LDLRex2(27;68;123;30)_96_d3_r	3640	CCCGTCTTGGCACAACTCGTTCTT	3641	CCGTCTTGGCACAACTCGTTCT	3642	CGTCTTGGCACAACTCGTTTC
	LDLRex2(27;68;123;30)_97_d3_f	3643	AGAAACGAGTTCTGCCAAGACGGGA	3644	GAAACGAGTTCTGCCAAGACGGG	3645	AAACGAGTTCTGCCAAGACGG
	LDLRex2(27;68;123;30)_97_d3_r	3646	TCCCGTCTTGGCAGAACTCGTTCT	3647	CCCGTCTTGGCAGAACTCGTTTC	3648	CCGTCTTGGCAGAACTCGTTT
	LDLRex2(27;68;123;30)_98_d3_f	3649	GAAACGAGTTCCGCCAAGACGGGAA	3650	AAACGAGTTCCGCCAAGACGGGA	3651	AACGAGTTCCGCCAAGACGGG
	LDLRex2(27;68;123;30)_98_d3_r	3652	TTCCCGTCTTGGCGAACTCGTTTC	3653	TCCCGTCTTGGCGAACTCGTTT	3654	CCCGTCTTGGCGAACTCGTT
	LDLRex2(27;68;123;30)_99_d3_f	3655	AAACGAGTTCCACCAAGACGGGAAA	3656	AACGAGTTCCACCAAGACGGGAA	3657	ACGAGTTCCACCAAGACGGGA
	LDLRex2(27;68;123;30)_99_d3_r	3658	TTTCCCGTCTTGGTGGAACTCGTTT	3659	TTCCCGTCTTGGTGGAACTCGTT	3660	TCCCGTCTTGGTGGAACTCGT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
ins1						
LDLRex2(27;68;123;30)_100_i1_r	3661	CCCGTCTTGGCAACTGGAACCTGTT	3662	CCGTCTTGGCAACTGGAACCTG	3663	CGTCTTGGCAACTGGAACCTCG
LDLRex2(27;68;123;30)_101_i1_f	3664	ACGAGTTCAGTGGCCAAAGACGGGA	3665	CGAGTTCAGTGGCCAAAGACGGG	3666	GAGTTCAGTGGCCAAAGACGGG
LDLRex2(27;68;123;30)_101_i1_r	3667	TCCCGTCTTGGCAACTGGAACCTG	3668	CCCGTCTTGGCAACTGGAACCTG	3669	CCGTCTTGGCAACTGGAACCTC
LDLRex2(27;68;123;30)_102_i1_f	3670	CGAGTTCAGTGCCCAAGACGGGAA	3671	GAGTTCAGTGCCCAAGACGGGGA	3672	AGTTCAGTGCCCAAGACGGGG
LDLRex2(27;68;123;30)_102_i1_r	3673	TCCCGTCTTGGCAACTGGAACCTG	3674	TCCCGTCTTGGCAACTGGAACCTC	3675	CCCGTCTTGGCAACTGGAACCT
LDLRex2(27;68;123;30)_103_i1_f	3676	GAGTTCAGTGCCCAAGACGGGAAA	3677	GAGTTCAGTGCCCAAGACGGGAA	3678	GTTCCAGTGCCCAAGACGGGA
LDLRex2(27;68;123;30)_103_i1_r	3679	TTCCCGTCTTGGCAACTGGAACCTC	3680	TTCCCGTCTTGGCAACTGGAAC	3681	TCCCGTCTTGGCAACTGGAAC
LDLRex2(27;68;123;30)_104_i1_f	3682	AGTTCAGTGCCAAAGACGGGAAAT	3683	AGTTCAGTGCCAAAGACGGGAAA	3684	TTCAGTGCCAAAGACGGGAA
LDLRex2(27;68;123;30)_104_i1_r	3685	ATTTCCCGTCTTGGCACTGGAAC	3686	TTTCCCGTCTTGGCACTGGAAC	3687	TTCCCGTCTTGGCACTGGAA
LDLRex2(27;68;123;30)_105_i1_f	3688	GTTCCAGTGCCAAAGACGGGAAATG	3689	TTCAGTGCCAAAGACGGGAAAT	3690	TCCAGTGCCAAAGACGGGAAA
LDLRex2(27;68;123;30)_105_i1_r	3691	CATTTCCCGTCTTGGCACTGGAAC	3692	ATTTCCCGTCTTGGCACTGGA	3693	TTTCCCGTCTTGGCACTGGA
LDLRex2(27;68;123;30)_106_i1_f	3694	TTCAGTGCCAAAGACGGGAAATGC	3695	TCCAGTGCCAAAGACGGGAAATG	3696	CCAGTGCCAAAGACGGGAAAT
LDLRex2(27;68;123;30)_106_i1_r	3697	GCATTTCCCGTCTTGGCACTGGAA	3698	CATTTCCCGTCTTGGCACTGGA	3699	ATTTCCCGTCTTGGCACTGG
LDLRex2(27;68;123;30)_107_i1_f	3700	TCCAGTGCCAAAGACGGGAAATGCA	3701	CCAGTGCCAAAGACGGGAAATGC	3702	CAGTGCCAAAGACGGGAAATG
LDLRex2(27;68;123;30)_107_i1_r	3703	TGCAATTTCCCGTCTTGGCACTGGA	3704	GCATTTCCCGTCTTGGCACTGG	3705	CATTTCCCGTCTTGGCACTG
LDLRex2(27;68;123;30)_108_i1_f	3706	CCAGTGCCAAAGACGGGAAATGCAT	3707	CAGTGCCAAAGACGGGAAATGCA	3708	AGTGCCAAAGACGGGAAATGC
LDLRex2(27;68;123;30)_108_i1_r	3709	ATGCATTTCCCGTCTTGGCACTGG	3710	TGCATTTCCCGTCTTGGCACTG	3711	GCATTTCCCGTCTTGGCACT
LDLRex2(27;68;123;30)_109_i1_f	3712	CAGTGCCAAAGACGGGAAATGCATC	3713	AGTGCCAAAGACGGGAAATGCAT	3714	GTGCCAAGACGGGAAATGCA
LDLRex2(27;68;123;30)_109_i1_r	3715	GATGCATTTCCCGTCTTGGCACTG	3716	ATGCATTTCCCGTCTTGGCACT	3717	TGCATTTCCCGTCTTGGCAC
LDLRex2(27;68;123;30)_110_i1_f	3718	AGTGCCAAAGACGGGAAATGCATCT	3719	GTGCCAAGACGGGAAATGCATC	3720	TGCCAAGACGGGAAATGCAT
LDLRex2(27;68;123;30)_110_i1_r	3721	AGATGCATTTCCCGTCTTGGCACT	3722	GATGCATTTCCCGTCTTGGCAC	3723	ATGCATTTCCCGTCTTGGCA
LDLRex2(27;68;123;30)_111_i1_f	3724	GTGCCAAGACGGGAAATGCATCTC	3725	TGCCAAGACGGGAAATGCATCT	3726	GCCAAGACGGGAAATGCATC
LDLRex2(27;68;123;30)_111_i1_r	3727	GAGATGCATTTCCCGTCTTGGCAC	3728	AGATGCATTTCCCGTCTTGGCA	3729	GATGCATTTCCCGTCTTGGC
LDLRex2(27;68;123;30)_112_i1_f	3730	TGCCAAGACGGGAAATGCATCTCC	3731	GCCAAGACGGGAAATGCATCTC	3732	CCAAGACGGGAAATGCATCT
LDLRex2(27;68;123;30)_112_i1_r	3733	GGAGATGCATTTCCCGTCTTGGCA	3734	GAGATGCATTTCCCGTCTTGGC	3735	AGATGCATTTCCCGTCTTGG
LDLRex2(27;68;123;30)_113_i1_f	3736	GCCAAGACGGGAAATGCATCTCCT	3737	CCAAGACGGGAAATGCATCTCC	3738	CAAGACGGGAAATGCATCTC
LDLRex2(27;68;123;30)_113_i1_r	3739	AGGAGATGCATTTCCCGTCTTGGC	3740	GGAGATGCATTTCCCGTCTTGG	3741	GAGATGCATTTCCCGTCTTG
LDLRex2(27;68;123;30)_114_i1_f	3742	CCAAGACGGGAAATGCATCTCCTA	3743	CAAGACGGGAAATGCATCTCT	3744	AAGACGGGAAATGCATCTCC
LDLRex2(27;68;123;30)_114_i1_r	3745	TAGGAGATGCATTTCCCGTCTTGG	3746	AGGAGATGCATTTCCCGTCTTG	3747	GGAGATGCATTTCCCGTCTT
LDLRex2(27;68;123;30)_115_i1_f	3748	CAAGACGGGAAATGCATCTCTAC	3749	AAGACGGGAAATGCATCTCCTA	3750	AGACGGGAAATGCATCTCT
LDLRex2(27;68;123;30)_115_i1_r	3751	GTAGGAGATGCAATTTCCCGTCTTG	3752	TAGGAGATGCAATTTCCCGTCTT	3753	AGGAGATGCAATTTCCCGTCT

Table 1

ins1	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_116_i1_f	3754	AAGACGGGAAATGGCATCTCTCTACA	3755	AGACGGGAAATGGCATCTCTCTAC	3756	GACGGGAAATGGCATCTCTCTA
LDLRex2(27;68;123;30)_116_i1_r	3757	TGTAGGAGATGCCATTTCCGCTCT	3758	GAGGAGATGCCATTTCCGCTCT	3759	TAGGAGATGCCATTTCCGCTC
LDLRex2(27;68;123;30)_117_i1_f	3760	AGACGGGAAATGCCATCTCTACAA	3761	GACGGGAAATGCCATCTCTACA	3762	ACGGGAAATGCCATCTCTCTAC
LDLRex2(27;68;123;30)_117_i1_r	3763	TTGTAGGAGATGCCATTTCCGCTCT	3764	TGTAGGAGATGCCATTTCCGCTC	3765	GTAGGAGATGCCATTTCCGCT
LDLRex2(27;68;123;30)_118_i1_f	3766	GACGGGAAATGCAATCTCTACAA	3767	ACGGGAAATGCAATCTCTACAA	3768	CGGAAATGCAATCTCTCTACA
LDLRex2(27;68;123;30)_118_i1_r	3769	CTGTAGGAGATTCGATTTCCCGTCT	3770	TTGTAGGAGATTCGATTTCCCGT	3771	TGTAGGAGATTCGATTTCCCG
LDLRex2(27;68;123;30)_119_i1_f	3772	ACGGGAAATGCATTTCTCTACAA	3773	CGGGAAATGCATTTCTCTACAA	3774	GGGAAATGCATTTCTCTACAA
LDLRex2(27;68;123;30)_119_i1_r	3775	ACTGTAGGAGATGCATTTCCCGT	3776	CTGTAGGAGATGCATTTCCCG	3777	TTGTAGGAGATGCATTTCC
LDLRex2(27;68;123;30)_120_i1_f	3778	CGGGAAATGCATCTCTCTACAA	3779	GGGAAATGCATCTCTCTACAA	3780	GGAAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_120_i1_r	3781	CACCTGTAGGAGATGCATTTCCCG	3782	ACTGTAGGAGATGCATTTCC	3783	CTGTAGGAGATGCATTTCC
LDLRex2(27;68;123;30)_121_i1_f	3784	GGGAAATGCATCTCTCTACAA	3785	GGAAATGCATCTCTCTACAA	3786	GAAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_121_i1_r	3787	CCACTGTAGGAGATGCATTTCC	3788	CACCTGTAGGAGATGCATTTCC	3789	ACTGTAGGAGATGCATTTCC
LDLRex2(27;68;123;30)_122_i1_f	3790	GGAAATGCATCTCTCTACAA	3791	GAAATGCATCTCTCTACAA	3792	AAATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_122_i1_r	3793	CCCACTGTAGGAGATGCATTTCC	3794	CCACTGTAGGAGATGCATTTCC	3795	CACCTGTAGGAGATGCATTT
LDLRex2(27;68;123;30)_123_i1_f	3796	GAAATGCATCTCTCTACAA	3797	AAATGCATCTCTCTACAA	3798	AATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_123_i1_r	3799	ACCCACTGTAGGAGATGCATTTCC	3800	CCCCTGTAGGAGATGCATTT	3801	CCACTGTAGGAGATGCATTT
LDLRex2(27;68;123;30)_124_i1_f	3802	AAATGCATCTCTCTACAA	3803	AATGCATCTCTCTACAA	3804	ATGCATCTCTCTACAA
LDLRex2(27;68;123;30)_124_i1_r	3805	GACCCACTGTAGGAGATGCATTT	3806	ACCCTGTAGGAGATGCATTT	3807	CCCCTGTAGGAGATGCATTT
LDLRex2(27;68;123;30)_125_i1_f	3808	AATGCATCTCTCTACAA	3809	ATGCATCTCTCTACAA	3810	TGCATCTCTCTACAA
LDLRex2(27;68;123;30)_125_i1_r	3811	AGACCCACTGTAGGAGATGCATTT	3812	GACCCACTGTAGGAGATGCAT	3813	ACCCACTGTAGGAGATGCA
LDLRex2(27;68;123;30)_126_i1_f	3814	ATGCATCTCTCTACAA	3815	TGCATCTCTCTACAA	3816	GCATCTCTCTACAA
LDLRex2(27;68;123;30)_126_i1_r	3817	CAGACCCACTGTAGGAGATGCAT	3818	AGACCCACTGTAGGAGATGCA	3819	GACCCACTGTAGGAGATGC
LDLRex2(27;68;123;30)_127_i1_f	3820	TGCATCTCTCTACAA	3821	GCATCTCTCTACAA	3822	CATCTCTCTACAA
LDLRex2(27;68;123;30)_127_i1_r	3823	GCAGACCCACTGTAGGAGATGCA	3824	CAGACCCACTGTAGGAGATGC	3825	AGACCCACTGTAGGAGATG
LDLRex2(27;68;123;30)_128_i1_f	3826	GCATCTCTCTACAA	3827	CATCTCTCTACAA	3828	ATCTCTCTACAA
LDLRex2(27;68;123;30)_128_i1_r	3829	CGCAGACCCACTGTAGGAGATGC	3830	GCAGACCCACTGTAGGAGATG	3831	CAGACCCACTGTAGGAGAT
LDLRex2(27;68;123;30)_129_i1_f	3832	CATCTCTACAA	3833	ATCTCTACAA	3834	TCTCTACAA
LDLRex2(27;68;123;30)_129_i1_r	3835	TGCAGACCCACTGTAGGAGATG	3836	CGCAGACCCACTGTAGGAGAT	3837	GCAGACCCACTGTAGGAGA
LDLRex2(27;68;123;30)_130_i1_f	3838	ATCTCTACAA	3839	TCTCTACAA	3840	CTCTACAA
LDLRex2(27;68;123;30)_130_i1_r	3841	ATCGCAGACCCAACTGTAGGAGAT	3842	TCGCAGACCCAACTGTAGGAGA	3843	CGCAGACCCAACTGTAGGAG
LDLRex2(27;68;123;30)_131_i1_f	3844	TCTCTACAA	3845	CTCTACAA	3846	TCCTACAA

Table 1

ins1	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_131_i1_r	3847	CATCGCAGACCCCACTTGTAGGAGA	3848	ATCGCAGACCCCACTTGTAGGAG	3849	TCGCAGACCCCACTTGTAGGA
LDLRex2(27;68;123;30)_132_i1_f	3850	CTCCTACAAAGTGGGGTCTGCGATGG	3851	TCCTACAAAGTGGGGTCTGCGATG	3852	CCTACAAAGTGGGGTCTGCGAT
LDLRex2(27;68;123;30)_132_i1_r	3853	CCATCGCAGACCCCACTTGTAGGAG	3854	CATCGCAGACCCCACTTGTAGGA	3855	ATCGCAGACCCCACTTGTAGG
LDLRex2(27;68;123;30)_133_i1_f	3856	TCCTACAAAGTGGGGTCTGCGATGGC	3857	CCTACAAAGTGGGGTCTGCGATGG	3858	CTACAAAGTGGGGTCTGCGATG
LDLRex2(27;68;123;30)_133_i1_r	3859	GCATCGCAGACCCCACTTGTAGGA	3860	CCATCGCAGACCCCACTTGTAGG	3861	CATCGCAGACCCCACTTGTAG
LDLRex2(27;68;123;30)_134_i1_f	3862	CCTACAAAGTGGGTCTGCGATGGCA	3863	CTACAAAGTGGGTCTGCGATGGC	3864	TACAAAGTGGGTCTGCGATGG
LDLRex2(27;68;123;30)_134_i1_r	3865	TGCCATCGCAGAACCCCACTTGTAGG	3866	GCCATCGCAGAACCCCACTTGTAG	3867	CCATCGCAGAACCCCACTTGTGA
LDLRex2(27;68;123;30)_135_i1_f	3868	CTACAAAGTGGGTCTGCGATGGCAG	3869	TACAAAGTGGGTCTGCGATGGCA	3870	ACAAGTGGGTCTGCGATGGC
LDLRex2(27;68;123;30)_135_i1_r	3871	CTGCCATCGCAGGACCCCACTTGTAG	3872	TGCCATCGCAGGACCCCACTTGTGA	3873	GCCATCGCAGGACCCCACTTGT
LDLRex2(27;68;123;30)_136_i1_f	3874	TACAAAGTGGGTCTGCGATGGCAGC	3875	ACAAGTGGGTCTGCGATGGCAG	3876	CAAGTGGGTCTTGGATGGCA
LDLRex2(27;68;123;30)_136_i1_r	3877	GCTGCCATCGCAAGACCCCACTTGTGA	3878	CTGCCATCGCAAGACCCCACTTGT	3879	TGCCATCGCAAGACCCCACTTG
LDLRex2(27;68;123;30)_137_i1_f	3880	ACAAGTGGGTCTGGCGATGGCAGCG	3881	CAAGTGGGTCTGGCGATGGCAGC	3882	AAGTGGGTCTGGCGATGGCAG
LDLRex2(27;68;123;30)_137_i1_r	3883	CGCTGCCATCGCCAGACCCCACTTGT	3884	GCTGCCATCGCCAGACCCCACTTG	3885	CTGCCATCGCCAGACCCCACTT
LDLRex2(27;68;123;30)_138_i1_f	3886	CAAGTGGGTCTGCCGATGGCAGCGC	3887	AAGTGGGTCTGCCGATGGCAGCG	3888	AGTGGGTCTGCCGATGGCAGC
LDLRex2(27;68;123;30)_138_i1_r	3889	GCGCTGCCATCGGCAGACCCCACTTG	3890	CGCTGCCATCGGCAGACCCCACTT	3891	GCTGCCATCGGCAGACCCCACT
LDLRex2(27;68;123;30)_139_i1_f	3892	AAGTGGGTCTGCGGATGGCAGCGCT	3893	AGTGGGTCTGCGGATGGCAGCGC	3894	GTGGGTCTGCGGATGGCAGCG
LDLRex2(27;68;123;30)_139_i1_r	3895	AGCGCTGCCATCGCAGACCCCACTT	3896	GCGCTGCCATCGCAGACCCCACT	3897	CGCTGCCATCGCAGACCCCACT
LDLRex2(27;68;123;30)_140_i1_f	3898	AGTGGGTCTGCGAATGGCAGCGCTG	3899	GTGGGTCTGCGAATGGCAGCGCT	3900	TGGGTCTGCGAATGGCAGCGC
LDLRex2(27;68;123;30)_140_i1_r	3901	CAGCGCTGCCATTTCGCAGACCCCACT	3902	AGCGCTGCCATTTCGCAGACCCCACT	3903	GCGCTGCCATTTCGCAGACCCCA
LDLRex2(27;68;123;30)_141_i1_f	3904	GTGGGTCTGCGATTGGCAGCGCTGA	3905	TGGGTCTGCGATTGGCAGCGCTG	3906	GGGTCTGCGATTGGCAGCGCT
LDLRex2(27;68;123;30)_141_i1_r	3907	TCAGCGCTGCCAATCGCAGACCCCACT	3908	CAGCGCTGCCAATCGCAGACCCCA	3909	AGCGCTGCCAATCGCAGACCC
LDLRex2(27;68;123;30)_142_i1_f	3910	TGGGTCTGCGATGGGCAGCGCTGAG	3911	GGGTCTGCGATGGGCAGCGCTGA	3912	GGTCTGCGATGGGCAGCGCTG
LDLRex2(27;68;123;30)_142_i1_r	3913	CTCAGCGCTGCCATCGCAGACCCCA	3914	TCAGCGCTGCCATCGCAGACCC	3915	CAGCGCTGCCATCGCAGACCC
LDLRex2(27;68;123;30)_143_i1_f	3916	GGGTCTGCGATGGGCAGCGCTGAGT	3917	GGTCTGCGATGGGCAGCGCTGAG	3918	GTCTGCGATGGGCAGCGCTGA
LDLRex2(27;68;123;30)_143_i1_r	3919	ACTCAGCGCTGCCATCGCAGACCC	3920	CTCAGCGCTGCCATCGCAGACC	3921	TCAGCGCTGCCATCGCAGAC
LDLRex2(27;68;123;30)_144_i1_f	3922	GGTCTGCGATGGCCAGCGCTGAGTG	3923	GTCTGCGATGGCCAGCGCTGAGT	3924	TCTGCGATGGCCAGCGCTGAG
LDLRex2(27;68;123;30)_144_i1_r	3925	CACTCAGCGCTGGCCATCGCAGACC	3926	ACTCAGCGCTGGCCATCGCAGAC	3927	CTCAGCGCTGGCCATCGCAGA
LDLRex2(27;68;123;30)_145_i1_f	3928	GTCTGCGATGGCAAGCGCTGAGTGC	3929	TCTGCGATGGCAAGCGCTGAGTG	3930	CTGCGATGGCAAGCGCTGAGT
LDLRex2(27;68;123;30)_145_i1_r	3931	GCACTCAGCGCTTGGCCATCGCAGAC	3932	CACCTCAGCGCTTGGCCATCGCAGA	3933	ACTCAGCGCTTGGCCATCGCAG
LDLRex2(27;68;123;30)_146_i1_f	3934	TCTGCGATGGCAGGCGCTGAGTGCC	3935	CTGCGATGGCAGGCGCTGAGTGC	3936	TGCGATGGCAGGCGCTGAGTG
LDLRex2(27;68;123;30)_146_i1_r	3937	GGCACTCAGCGCTTGGCCATCGCAGA	3938	GCACTCAGCGCTTGGCCATCGCAG	3939	CACCTCAGCGCTTGGCCATCGCA

Table 1

ins1	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_147_i1_f	3940	CTGCGATGGCAGCGCTGAGTGCCA	3941	TGCGATGGCAGCGCTGAGTGCC	3942	GCGATGGCAGCGCTGAGTGC
LDLRex2(27;68;123;30)_147_i1_r	3943	TGGCACTCAGCGGCTGCCATCGCAG	3944	GGCACTCAGCGGCTGCCATCGCA	3945	GCACTCAGCGGCTGCCATCGC
LDLRex2(27;68;123;30)_148_i1_f	3946	TGCGATGGCAGCGGCTGAGTGCCAG	3947	GCGATGGCAGCGGCTGAGTGCCA	3948	CGATGGCAGCGGCTGAGTGCC
LDLRex2(27;68;123;30)_148_i1_r	3949	CTGGCACTCAGCGCTGCCATCGCA	3950	TGGCACTCAGCGGCTGCCATCGC	3951	GGCACTCAGCGGCTGCCATCG
LDLRex2(27;68;123;30)_149_i1_f	3952	GCGATGGCAGCGCTGAGTGCCAGG	3953	CGATGGCAGCGCTGAGTGCCAG	3954	GATGGCAGCGCTGAGTGCCA
LDLRex2(27;68;123;30)_149_i1_r	3955	CCTGGCACTCAGCGCTGCCATCGC	3956	CTGGCACTCAGCGCTGCCATCG	3957	TGGCACTCAGCGCTGCCATC
LDLRex2(27;68;123;30)_150_i1_f	3958	CGATGGCAGCGCTTGAAGTGCCAGGA	3959	GATGGCAGCGCTTGAAGTGCCAGG	3960	ATGGCAGCGCTTGAAGTGCCAG
LDLRex2(27;68;123;30)_150_i1_r	3961	TCCTGGCACTCAAGCGCTGCCATCG	3962	CCTGGCACTCAAGCGCTGCCATC	3963	CTGGCACTCAAGCGCTGCCAT
LDLRex2(27;68;123;30)_151_i1_f	3964	GATGGCAGCGCTGGAGTGCCAGGAT	3965	ATGGCAGCGCTGGAGTGCCAGGA	3966	TGGCAGCGCTGGAGTGCCAGG
LDLRex2(27;68;123;30)_151_i1_r	3967	ATCCTGGCACTCCAGCGCTGCCATC	3968	TCCTGGCACTCCAGCGCTGCCAT	3969	CCTGGCACTCCAGCGCTGCCA
LDLRex2(27;68;123;30)_152_i1_f	3970	ATGGCAGCGCTGAAGTGCCAGGATG	3971	TGGCAGCGCTGAAGTGCCAGGAT	3972	GGCAGCGCTGAAGTGCCAGGA
LDLRex2(27;68;123;30)_152_i1_r	3973	CATCCTGGCACTTCAGCGCTGCCAT	3974	ATCCTGGCACTTCAGCGCTGCCA	3975	TCCTGGCACTTCAGCGCTGCC
LDLRex2(27;68;123;30)_153_i1_f	3976	TGGCAGCGCTGAGGTGCCAGGATGG	3977	GGCAGCGCTGAGGTGCCAGGATG	3978	GCAGCGCTGAGGTGCCAGGAT
LDLRex2(27;68;123;30)_153_i1_r	3979	CCATCCTGGCACTTCAGCGCTGCCA	3980	CATCCTGGCACTTCAGCGCTGCC	3981	ATCCTGGCACTTCAGCGCTGC
LDLRex2(27;68;123;30)_154_i1_f	3982	GGCAGCGCTGAGTTGCCAGGATGGC	3983	GCAGCGCTGAGTTGCCAGGATGG	3984	CAGCGCTGAGTTGCCAGGATG
LDLRex2(27;68;123;30)_154_i1_r	3985	GCCATCTGGCACTCAGCGCTGCC	3986	CCATCTGGCACTCAGCGCTGC	3987	CATCTGGCACTCAGCGCTG
LDLRex2(27;68;123;30)_155_i1_f	3988	GCAGCGCTGAGTGCCAGGATGGCT	3989	CAGCGCTGAGTGCCAGGATGGC	3990	AGCGCTGAGTGCCAGGATGG
LDLRex2(27;68;123;30)_155_i1_r	3991	AGCCATCTGGCCACTCAGCGCTGC	3992	GCCATCTGGCCACTCAGCGCTG	3993	CCATCTGGCCACTCAGCGCT
LDLRex2(27;68;123;30)_156_i1_f	3994	CAGCGCTGAGTGCCAGGATGGCTC	3995	AGCGCTGAGTGCCAGGATGGCT	3996	GCGCTGAGTGCCAGGATGGC
LDLRex2(27;68;123;30)_156_i1_r	3997	GAGCCATCTGGGCACTCAGCGCTG	3998	AGCCATCTGGGCACTCAGCGCT	3999	GCCATCTGGGCACTCAGCGC
LDLRex2(27;68;123;30)_157_i1_f	4000	AGCGCTGAGTGCCAGGATGGCTCT	4001	GCGCTGAGTGCCAGGATGGCTC	4002	CGCTGAGTGCCAGGATGGCT
LDLRex2(27;68;123;30)_157_i1_r	4003	AGAGCCATCTGGGCACTCAGCGCT	4004	GAGCCATCTGGGCACTCAGCGC	4005	AGCCATCTGGGCACTCAGCG
LDLRex2(27;68;123;30)_158_i1_f	4006	GCGCTGAGTGCCAGGATGGCTCTG	4007	CGCTGAGTGCCAGGATGGCTCT	4008	GCTGAGTGCCAGGATGGCTC
LDLRex2(27;68;123;30)_158_i1_r	4009	CAGAGCCATCTTGGCACTCAGCGC	4010	AGAGCCATCTTGGCACTCAGCG	4011	GAGCCATCTTGGCACTCAGC
LDLRex2(27;68;123;30)_159_i1_f	4012	CGCTGAGTGCCAGGATGGCTCTGA	4013	GCTGAGTGCCAGGATGGCTCTG	4014	CTGAGTGCCAGGATGGCTCT
LDLRex2(27;68;123;30)_159_i1_r	4015	TCAGAGCCATCCCTGGCACTCAGCG	4016	CAGAGCCATCCCTGGCACTCAGC	4017	AGAGCCATCCCTGGCACTCAG
LDLRex2(27;68;123;30)_160_i1_f	4018	GCTGAGTGCCAGGATGGCTCTGAT	4019	CTGAGTGCCAGGATGGCTCTGA	4020	TGAGTGCCAGGATGGCTCTG
LDLRex2(27;68;123;30)_160_i1_r	4021	ATCAGAGCCATCCCTGGCACTCAGC	4022	TCAGAGCCATCCCTGGCACTCAG	4023	CAGAGCCATCCCTGGCACTCA
LDLRex2(27;68;123;30)_161_i1_f	4024	CTGAGTGCCAGGATGGCTCTGATG	4025	TGAGTGCCAGGATGGCTCTGAT	4026	GAGTGCCAGGATGGCTCTGA
LDLRex2(27;68;123;30)_161_i1_r	4027	CATCAGAGCCATTCCTGGCACTCAG	4028	ATCAGAGCCATTCCTGGCACTCA	4029	TCAGAGCCATTCCTGGCACTC
LDLRex2(27;68;123;30)_162_i1_f	4030	TGAGTGCCAGGATGGCTCTGATGA	4031	GAGTGCCAGGATGGCTCTGATG	4032	AGTGCCAGGATGGCTCTGAT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
ins1						
LDLRex2(27;68;123;30)_162_i1_r	4033	TCATCAGAGCCAAATCCTGGCACTCA	4034	CATCAGAGCCAAATCCTGGCACTC	4035	ATCAGAGCCAAATCCTGGCACT
LDLRex2(27;68;123;30)_163_i1_f	4036	GAGTGCCAGGATGGGCTCTGATGAG	4037	AGTGCCAGGATGGGCTCTGATGA	4038	GTGCCAGGATGGGCTCTGATG
LDLRex2(27;68;123;30)_163_i1_r	4039	CTCATCAGAGCCATCCTGGCACTC	4040	TCATCAGAGCCCATCCTGGCACT	4041	CATCAGAGCCCATCCTGGCAC
LDLRex2(27;68;123;30)_164_i1_f	4042	AGTGCCAGGATGGGCTCTGATGAGT	4043	GTGCCAGGATGGGCTCTGATGAG	4044	TGCCAGGATGGGCTCTGATGA
LDLRex2(27;68;123;30)_164_i1_r	4045	ACTCATCAGAGCCCATCCTGGCACT	4046	CTCATCAGAGCCCATCCTGGCAC	4047	TCATCAGAGCCCATCCTGGCA
LDLRex2(27;68;123;30)_165_i1_f	4048	GTGCCAGGATGGCCTCTGATGAGTC	4049	TGCCAGGATGGCCTCTGATGAGT	4050	GCCAGGATGGCCTCTGATGAG
LDLRex2(27;68;123;30)_165_i1_r	4051	GACTCATCAGAGGCCATCCTGGCAC	4052	ACTCATCAGAGGCCATCCTGGCA	4053	CTCATCAGAGGCCATCCTGGC
LDLRex2(27;68;123;30)_166_i1_f	4054	TGCCAGGATGGCTTCTGATGAGTCC	4055	GCCAGGATGGCTTCTGATGAGTC	4056	CCAGGATGGCTTCTGATGAGT
LDLRex2(27;68;123;30)_166_i1_r	4057	GGACTCATCAGAAAGCCATCCTGGCA	4058	GACTCATCAGAAAGCCATCCTGGC	4059	ACTCATCAGAAAGCCATCCTGG
LDLRex2(27;68;123;30)_167_i1_f	4060	GCCAGGATGGCTCTGATGAGTCCC	4061	CCAGGATGGCTCTGATGAGTCC	4062	CAGGATGGCTCTGATGAGTC
LDLRex2(27;68;123;30)_167_i1_r	4063	GGGACTCATCAGGAGCCATCCTGGC	4064	GGACTCATCAGGAGCCATCCTGG	4065	GACTCATCAGGAGCCATCCTG
LDLRex2(27;68;123;30)_168_i1_f	4066	CCAGGATGGCTCTTGTGATGATCCCA	4067	CAGGATGGCTCTTGTGATGATCCC	4068	AGGATGGCTCTTGTGATGATCC
LDLRex2(27;68;123;30)_168_i1_r	4069	TGGGACTCATCAAGAGCCATCCTGG	4070	GGGACTCATCAAGAGCCATCCTG	4071	GGACTCATCAAGAGCCATCCT
LDLRex2(27;68;123;30)_169_i1_f	4072	CAGGATGGCTCTGGATGATGCCAG	4073	AGGATGGCTCTGGATGATGCCCA	4074	GGATGGCTCTGGATGATGCC
LDLRex2(27;68;123;30)_169_i1_r	4075	CTGGGACTCATCCAGAGCCATCCTG	4076	TGGGACTCATCCAGAGCCATCCT	4077	GGGACTCATCCAGAGCCATCC
LDLRex2(27;68;123;30)_170_i1_f	4078	AGGATGGCTCTGAATGATGCCAGG	4079	GGATGGCTCTGAATGATGCCAG	4080	GATGGCTCTGAATGATGCCCA
LDLRex2(27;68;123;30)_170_i1_r	4081	CCTGGGACTCATTCAGAGCCATCCT	4082	CTGGGACTCATTCAGAGCCATCC	4083	TGGGACTCATTCAGAGCCATC
LDLRex2(27;68;123;30)_171_i1_f	4084	GGATGGCTCTGATTGATGCCAGGA	4085	GATGGCTCTGATTGATGCCAGG	4086	ATGGCTCTGATTGATGCCCAG
LDLRex2(27;68;123;30)_171_i1_r	4087	TCCTGGGACTCAATCAGAGCCATCC	4088	CCTGGGACTCAATCAGAGCCATC	4089	CTGGGACTCAATCAGAGCCAT
LDLRex2(27;68;123;30)_172_i1_f	4090	GATGGCTCTGATGGAGTCCCAGGAG	4091	ATGGCTCTGATGGAGTCCCAGGA	4092	TGGCTCTGATGGAGTCCCAGG
LDLRex2(27;68;123;30)_172_i1_r	4093	CTCCTGGGACTCCATCAGAGCCATC	4094	TCCTGGGACTCCATCAGAGCCAT	4095	CCTGGGACTCCATCAGAGCCA
LDLRex2(27;68;123;30)_173_i1_f	4096	ATGGCTCTGATGAAGTCCCAGGAGA	4097	TGGCTCTGATGAAGTCCCAGGAG	4098	GGCTCTGATGAAGTCCCAGGA
LDLRex2(27;68;123;30)_173_i1_r	4099	TCTCCTGGGACTTCATCAGAGCCAT	4100	CTCCTGGGACTTCATCAGAGCCA	4101	TCCTGGGACTTCATCAGAGCC
LDLRex2(27;68;123;30)_174_i1_f	4102	TGGCTCTGATGAGTCCCAGGAGAC	4103	GGCTCTGATGAGTCCCAGGAGA	4104	GCTCTGATGAGTCCCAGGAG
LDLRex2(27;68;123;30)_174_i1_r	4105	GTCTCCTGGGACCTCATCAGAGCCA	4106	TCTCCTGGGACCTCATCAGAGCC	4107	CTCCTGGGACCTCATCAGAGC
LDLRex2(27;68;123;30)_175_i1_f	4108	GGCTCTGATGAGTCCCAGGAGACG	4109	GCTCTGATGAGTCCCAGGAGAC	4110	CTCTGATGAGTCCCAGGAGA
LDLRex2(27;68;123;30)_175_i1_r	4111	CGTCTCTGGGAACTCATCAGAGCC	4112	GTCTCTGGGAACTCATCAGAGC	4113	TCTCTGGGAACTCATCAGAG
LDLRex2(27;68;123;30)_176_i1_f	4114	GCTCTGATGAGTCCCCAGGAGACGT	4115	CTCTGATGAGTCCCCAGGAGACG	4116	TCTGATGAGTCCCCAGGAGAC
LDLRex2(27;68;123;30)_176_i1_r	4117	ACGTCTCTGGGGACTCATCAGAGC	4118	CGTCTCTGGGGACTCATCAGAG	4119	GTCTCTGGGGACTCATCAGAG
LDLRex2(27;68;123;30)_177_i1_f	4120	CTCTGATGAGTCCCCAGGAGACGTG	4121	TCTGATGAGTCCCCAGGAGACGT	4122	CTGATGAGTCCCCAGGAGAGG
LDLRex2(27;68;123;30)_177_i1_r	4123	CACGTCTCTGGGACTCATCAGAG	4124	ACGTCTCTGGGACTCATCAGAG	4125	CGTCTCTGGGACTCATCAG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
ins1						
LDLRex2(27;68;123;30)_178_i1_f	4126	TCTGATGAGTCCCAGGAGACGTGC	4127	CTGATGAGTCCCAGGAGACGTG	4128	TGATGAGTCCCAGGAGACGT
LDLRex2(27;68;123;30)_178_i1_r	4129	GCACGTCTCTGGGACTCATCAGA	4130	CACGTCTCTGGGACTCATCAG	4131	ACGTCTCTGGGACTCATCA
LDLRex2(27;68;123;30)_179_i1_f	4132	CTGATGAGTCCCAAGGAGACGTGCT	4133	TGATGAGTCCCAAGGAGACGTGC	4134	GATGAGTCCCAAGGAGACGTG
LDLRex2(27;68;123;30)_179_i1_r	4135	AGCACGTCTCTGGACTCATCAG	4136	GCAGTCTCTTGGGACTCATCA	4137	CACGTCTCTTGGGACTCATC
LDLRex2(27;68;123;30)_180_i1_f	4138	TGATGAGTCCCAGGAGACGTGCTG	4139	GATGAGTCCCAGGAGACGTGCT	4140	ATGATCCCAGGAGACGTGC
LDLRex2(27;68;123;30)_180_i1_r	4141	CAGCACGTCTCTGGACTCATCA	4142	AGCACGTCTCTGGGACTCATC	4143	GCAGTCTCTCTGGGACTCAT
LDLRex2(27;68;123;30)_181_i1_f	4144	GATGAGTCCCAGGAGACGTGCTGT	4145	ATGATCCCAGGAGACGTGCTG	4146	TGATCCCAGGAGACGTGCT
LDLRex2(27;68;123;30)_181_i1_r	4147	ACAGCACGTCTCTCTGGACTCATC	4148	CAGCACGTCTCTCTGGGACTCAT	4149	AGCACGTCTCTCTGGGACTCA
LDLRex2(27;68;123;30)_182_i1_f	4150	ATGAGTCCCAGGAAGACGTGCTGTG	4151	TGAGTCCCAGGAAGACGTGCTGT	4152	GAGTCCCAGGAAGACGTGCTG
LDLRex2(27;68;123;30)_182_i1_r	4153	CACAGCACGTCTCTGGGACTCAT	4154	ACAGCACGTCTCTGGGACTCA	4155	CAGCACGTCTCTCTGGGACTC
LDLRex2(27;68;123;30)_183_i1_f	4156	TGAGTCCCAGGAGACGTGCTGTGA	4157	GAGTCCCAGGAGACGTGCTGTG	4158	AGTCCCAGGAGACGTGCTGT
LDLRex2(27;68;123;30)_183_i1_r	4159	TCACAGCACGTCTCTCTGGGACTCA	4160	CACAGCACGTCTCTCTGGGACTC	4161	ACAGCACGTCTCTCTGGGACT
LDLRex2(27;68;123;30)_184_i1_f	4162	GAGTCCCAGGAGAACGTGCTGTGAG	4163	AGTCCCAGGAGAACGTGCTGTGA	4164	GTCCCAGGAGAACGTGCTGTG
LDLRex2(27;68;123;30)_184_i1_r	4165	CTCACAGCACGTCTCTCTGGGACTC	4166	TCACAGCACGTCTCTCTGGGACT	4167	CACAGCACGTCTCTCTGGGAC
LDLRex2(27;68;123;30)_185_i1_f	4168	AGTCCCAGGAGACCGTGTGTGAGT	4169	GTCCCAGGAGACCGTGTGTGAG	4170	TCCCAGGAGACCGTGTGTGA
LDLRex2(27;68;123;30)_185_i1_r	4171	ACTCACAGCACGTCTCTCTGGGACT	4172	CTCACAGCACGTCTCTCTGGGAC	4173	TCACAGCACGTCTCTCTGGGA
LDLRex2(27;68;123;30)_186_i1_f	4174	GTCCCAGGAGACGGTGTGTGAGTC	4175	TCCCAGGAGACGGTGTGTGAGT	4176	CCCAGGAGACGGTGTGTGAG
LDLRex2(27;68;123;30)_186_i1_r	4177	GACTCACAGCACCGTCTCTCTGGGAC	4178	ACTCACAGCACCGTCTCTCTGGGA	4179	CTCACAGCACCGTCTCTCTGGG
LDLRex2(27;68;123;30)_187_i1_f	4180	TCCCAGGAGACGTTGCTGTGAGTCC	4181	CCCAGGAGACGTTGCTGTGAGTC	4182	CCAGGAGACGTTGCTGTGAGT
LDLRex2(27;68;123;30)_187_i1_r	4183	GGACTCACAGCAACGTCTCTCTGGGA	4184	GACTCACAGCAACGTCTCTCTGGG	4185	ACTCACAGCAACGTCTCTCTGG
LDLRex2(27;68;123;30)_188_i1_f	4186	CCAGGAGACGTGGCTGTGAGTCCC	4187	CCAGGAGACGTGGCTGTGAGTCC	4188	CAGGAGACGTGGCTGTGAGTC
LDLRex2(27;68;123;30)_188_i1_r	4189	GGGACTCACAGCCACGTCTCTCTGGG	4190	GGACTCACAGCCACGTCTCTCTGG	4191	GACTCACAGCCACGTCTCTCTG
LDLRex2(27;68;123;30)_189_i1_f	4192	CCAGGAGACGTGCCTGTGAGTCCCC	4193	CAGGAGACGTGCCTGTGAGTCCC	4194	AGGAGACGTGCCTGTGAGTCC
LDLRex2(27;68;123;30)_189_i1_r	4195	GGGACTCACAGGACGTCTCTCTGG	4196	GGGACTCACAGGACGTCTCTCTG	4197	GGACTCACAGGACGTCTCTCT
LDLRex2(27;68;123;30)_190 + 1_i1_f	4198	AGGAGACGTGCTGTTGAGTCCCCTT	4199	GGAGACGTGCTGTTGAGTCCCCT	4200	GAGACGTGCTGTTGAGTCCCC
LDLRex2(27;68;123;30)_190 + 1_i1_r	4201	AAGGGGACTCACACGACACGTCTCT	4202	AGGGGACTCACACGACACGTCTCC	4203	GGGGACTCACACGACACGTCTC
LDLRex2(27;68;123;30)_190 + 10_i1_f	4204	GCTGTGAGTCCCCCTTTGGGCATGA	4205	CTGTGAGTCCCCCTTTGGGCATG	4206	TGTGAGTCCCCCTTTGGGCAT
LDLRex2(27;68;123;30)_190 + 10_i1_r	4207	TCATGCCCAAAAGGGGACTCACAGC	4208	CATGCCCAAAAGGGGACTCACAG	4209	ATGCCCAAAAGGGGACTCACAC
LDLRex2(27;68;123;30)_190 + 11_i1_f	4210	CTGTGAGTCCCCCTTTGGGCATGAT	4211	TGTGAGTCCCCCTTTGGGCATGA	4212	GTGAGTCCCCCTTTGGGCATG
LDLRex2(27;68;123;30)_190 + 11_i1_r	4213	ATCATGCCCAAAAGGGGACTCACAG	4214	TCATGCCCAAAAGGGGACTCACAC	4215	CATGCCCAAAAGGGGACTCAC
LDLRex2(27;68;123;30)_190 + 12_i1_f	4216	TGTGAGTCCCCCTTTGGGCATGATA	4217	GTGAGTCCCCCTTTGGGCATGAT	4218	TGAGTCCCCCTTTGGGCATGA

Table 1

ins1	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_190 + 12_i1_r 4219		TATCATGCCCAAAAGGGGACTCACA	4220	ATCATGCCCAAAAGGGGACTCAC	4221	TCATGCCCAAAAGGGGACTCA
LDLRex2(27;68;123;30)_190 + 13_i1_f 4222		GTGAGTCCCTTTTGGGCATGATAT	4223	TGAGTCCCTTTTGGGCATGATA	4224	GAGTCCCTTTTGGGCATGAT
LDLRex2(27;68;123;30)_190 + 13_i1_r 4225		ATATCATGCCCAAAAGGGGACTCAC	4226	TATCATGCCCAAAAGGGGACTCA	4227	ATCATGCCCAAAAGGGGACTC
LDLRex2(27;68;123;30)_190 + 14_i1_f 4228		TGAGTCCCTTTTGGGCATGATATG	4229	GAGTCCCTTTTGGGCATGATAT	4230	AGTCCCTTTTGGGCATGATA
LDLRex2(27;68;123;30)_190 + 14_i1_r 4231		CATATCATGCCCAAAAGGGGACTCA	4232	ATATCATGCCCAAAAGGGGACTC	4233	TATCATGCCCAAAAGGGGACT
LDLRex2(27;68;123;30)_190 + 15_i1_f 4234		GAGTCCCTTTTGGGCATGATATGC	4235	AGTCCCTTTTGGGCATGATATG	4236	GTCCCTTTTGGGCATGATAT
LDLRex2(27;68;123;30)_190 + 15_i1_r 4237		GCAATATCATGCCCAAAAGGGGACTC	4238	CATATCATGCCCAAAAGGGGACT	4239	ATATCATGCCCAAAAGGGGAC
LDLRex2(27;68;123;30)_190 + 2_i1_f 4240		GGAGACGTGCTGTTGAGTCCCTTT	4241	GAGACGTGCTGTTGAGTCCCTT	4242	AGACGTGCTGTTGAGTCCCT
LDLRex2(27;68;123;30)_190 + 2_i1_r 4243		AAAGGGGACTCAACAGCACGTCTCC	4244	AAGGGGACTCAACAGCACGTCTC	4245	AGGGGACTCAACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 3_i1_f 4246		GAGACGTGCTGGAGTCCCTTTG	4247	AGACGTGCTGGAGTCCCTTT	4248	GACGTGCTGGAGTCCCTT
LDLRex2(27;68;123;30)_190 + 3_i1_r 4249		CAAAGGGGACTCCACAGCACGTCTC	4250	AAAGGGGACTCCACAGCACGTCT	4251	AAGGGGACTCCACAGCACGTCT
LDLRex2(27;68;123;30)_190 + 4_i1_f 4252		AGACGTGCTGGAAGTCCCTTTGG	4253	GACGTGCTGGAAGTCCCTTTG	4254	ACGTGCTGGAAGTCCCTTT
LDLRex2(27;68;123;30)_190 + 4_i1_r 4255		CCAAAGGGGACTTCAACAGCACGTCT	4256	CAAAGGGGACTTCAACAGCACGTCT	4257	AAAGGGGACTTCAACAGCACGT
LDLRex2(27;68;123;30)_190 + 5_i1_f 4258		GACGTGCTGAGGTCCCTTTGGG	4259	ACGTGCTGAGGTCCCTTTGG	4260	CGTGTGAGGTCCCTTTGG
LDLRex2(27;68;123;30)_190 + 5_i1_r 4261		CCCAAGGGGACCTCACAGCACGTCT	4262	CCAAAGGGGACCTCACAGCACGT	4263	CAAAGGGGACCTCACAGCACG
LDLRex2(27;68;123;30)_190 + 6_i1_f 4264		ACGTGCTGAGTTCCTTTGGGC	4265	CGTGTGAGTTCCTTTGGG	4266	GTGTGTGAGTTCCTTTGG
LDLRex2(27;68;123;30)_190 + 6_i1_r 4267		GCCCAAGGGGAACTCACAGCACGT	4268	CCCAAGGGGAACTCACAGCACG	4269	CCAAAGGGGAACTCACAGCAC
LDLRex2(27;68;123;30)_190 + 7_i1_f 4270		CGTGTGAGTCCCTTTGGGCA	4271	GTGTGTGAGTCCCTTTGGGC	4272	TGCTGTGAGTCCCTTTGGG
LDLRex2(27;68;123;30)_190 + 7_i1_r 4273		TGCCCAAGGGGAACTCACAGCACG	4274	GCCCAAGGGGAACTCACAGCAC	4275	CCCAAGGGGAACTCACAGCA
LDLRex2(27;68;123;30)_190 + 8_i1_f 4276		GTGCTGTGAGTCCCTTTGGGCAT	4277	TGCTGTGAGTCCCTTTGGGCA	4278	GCTGTGAGTCCCTTTGGGC
LDLRex2(27;68;123;30)_190 + 8_i1_r 4279		ATGCCCAAGGGGAACTCACAGCAC	4280	TGCCCAAGGGGAACTCACAGCA	4281	GCCCAAGGGGAACTCACAGC
LDLRex2(27;68;123;30)_190 + 9_i1_f 4282		TGCTGTGAGTCCCTTTGGGCATG	4283	GCTGTGAGTCCCTTTGGGCA	4284	CTGTGAGTCCCTTTGGGCA
LDLRex2(27;68;123;30)_190 + 9_i1_r 4285		CATGCCCAAGGGGAACTCACAGCA	4286	ATGCCCAAGGGGAACTCACAGC	4287	TGCCCAAGGGGAACTCACAG
LDLRex2(27;68;123;30)_190_i1_f 4288		CAGGAGACGTCTTGTGAGTCCCT	4289	AGGAGACGTCTTGTGAGTCCCC	4290	GGAGACGTCTTGTGAGTCCC
LDLRex2(27;68;123;30)_190_i1_r 4291		AGGGGAACTCAAGACAGCTCTCTG	4292	GGGAACTCAAGACAGCTCTCT	4293	GGGAACTCAAGACAGCTCTCC
LDLRex2(27;68;123;30)_68 - 1_i1_f 4294		TCCTCTCTCTCAGGTGGGCGACAGA	4295	CCTCTCTCTCAGGTGGGCGACAG	4296	CTCTCTCTCAGGTGGGCGACA
LDLRex2(27;68;123;30)_68 - 1_i1_r 4297		TCTGTGCCCACTGAGAGAGAGGA	4298	CTGTGCCCACTGAGAGAGAGG	4299	TGTGCCCACTGAGAGAGAG
LDLRex2(27;68;123;30)_68 - 10_i1_f 4300		TTCTCTTTTCTCTCTCTCTCAGTG	4301	TCTCTTTTCTCTCTCTCTCAGT	4302	CTCTTTTCTCTCTCTCTCAG
LDLRex2(27;68;123;30)_68 - 10_i1_r 4303		CACGTGAGAGAGAGAGAGAGAGAA	4304	ACTGAGAGAGAGAGAGAGAGAA	4305	CTGAGAGAGAGAGAGAGAGG
LDLRex2(27;68;123;30)_68 - 11_i1_f 4306		TTTCTCTTTTCTCTCTCTCTCAGT	4307	TTCTCTTTTCTCTCTCTCTCAG	4308	TCTCTTTTCTCTCTCTCTCA
LDLRex2(27;68;123;30)_68 - 11_i1_r 4309		ACTGAGAGAGAGAGAGAGAGAA	4310	CTGAGAGAGAGAGAGAGAGAA	4311	TGAGAGAGAGAGAGAGAGAA

Table 1

ins1	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
LDLRex2(27;68;123;30)_68 - 12_i1_f	4312	CTTTCTCCTTTTCCCTCTCTCTCAG	4313	TTTCTCCTTTTCCCTCTCTCTCA	4314	TTCTCCTTTTCCCTCTCTCTC
LDLRex2(27;68;123;30)_68 - 12_i1_r	4315	CTGAGAGAGAGGGAAGGAGAGAAAG	4316	TGAGAGAGAGGGAAGGAGAGAAA	4317	GAGAGAGAGGGAAGGAGAGAAA
LDLRex2(27;68;123;30)_68 - 13_i1_f	4318	CCTTTCTCCTTTTCCCTCTCTCTCA	4319	CTTTCTCCTTTTCCCTCTCTCTC	4320	TTTCTCCTTTTCCCTCTCTCT
LDLRex2(27;68;123;30)_68 - 13_i1_r	4321	TGAGAGAGAGGGAAGGAGAGAAAG	4322	GAGAGAGAGGGAAGGAGAGAAAG	4323	AGAGAGAGGGAAGGAGAGAAA
LDLRex2(27;68;123;30)_68 - 14_i1_f	4324	CCCTTTCTCCTTTTCCCTCTCTCTC	4325	CCTTTCTCCTTTTCCCTCTCTCT	4326	CTTTCTCCTTTTCCCTCTCTC
LDLRex2(27;68;123;30)_68 - 14_i1_r	4327	GAGAGAGAGGGAAGGAGAGAAAGG	4328	AGAGAGAGGGAAGGAGAGAAAGG	4329	GAGAGAGGGAAGGAGAGAAAAG
LDLRex2(27;68;123;30)_68 - 15_i1_f	4330	ACCTTTCTCCTTTTCCCTCTCTCT	4331	CCCTTTCTCCTTTTCCCTCTCTC	4332	CTTTCTCCTTTTCCCTCTCT
LDLRex2(27;68;123;30)_68 - 15_i1_r	4333	AGAGAGAGGGAAGGAGAGAAAGGT	4334	GAGAGAGGGAAGGAGAGAAAGG	4335	AGAGAGGGAAGGAGAGAAAAG
LDLRex2(27;68;123;30)_68 - 2_i1_f	4336	TTCTCTCTCTCAAGTGGCGACAG	4337	TCCTCTCTCAAGTGGCGACA	4338	CCTCTCTCAAGTGGCGGAC
LDLRex2(27;68;123;30)_68 - 2_i1_r	4339	CTGTGCCCCACTTGAGAGAGAGAA	4340	TGTGCCCCACTTGAGAGAGAGGA	4341	GTCGCCACTTGAGAGAGAGG
LDLRex2(27;68;123;30)_68 - 3_i1_f	4342	TTCTCTCTCTCCAGTGGCGACA	4343	TTCTCTCTCTCCAGTGGCGAC	4344	TCCTCTCTCCAGTGGCGGA
LDLRex2(27;68;123;30)_68 - 3_i1_r	4345	TGTGCCCCACTTGAGAGAGAGGAAA	4346	GTCGCCACTTGAGAGAGAGAGAA	4347	TGCCCCACTTGAGAGAGAGGA
LDLRex2(27;68;123;30)_68 - 4_i1_f	4348	TTTCTCTCTCTTCCAGTGGCGAC	4349	TTTCTCTCTCTTCCAGTGGCGA	4350	TTCTCTCTCTTCCAGTGGCG
LDLRex2(27;68;123;30)_68 - 4_i1_r	4351	GTCGCCACTGAAGAGAGAGGAAAA	4352	TGCCCCACTGAAGAGAGAGGAAA	4353	CGCCCCACTGAAGAGAGAGGAA
LDLRex2(27;68;123;30)_68 - 5_i1_f	4354	CTTTCTCTCTCTCCAGTGGCGCA	4355	TTTTCTCTCTCTCCAGTGGCG	4356	TTTCTCTCTCTCCAGTGGGC
LDLRex2(27;68;123;30)_68 - 5_i1_r	4357	TGCCCCACTGAGGAGAGAGGAAAA	4358	CGCCCCACTGAGGAGAGAGGAAAA	4359	GCCCCACTGAGGAGAGAGGAAA
LDLRex2(27;68;123;30)_68 - 6_i1_f	4360	CCTTTCTCTCTCTCCAGTGGCG	4361	CTTTCTCTCTCTTCCAGTGGGC	4362	TTTTCTCTCTTCTCAGTGGG
LDLRex2(27;68;123;30)_68 - 6_i1_r	4363	CGCCCCACTGAGAGAGAGGAAAAAG	4364	GCCCCACTGAGAGAGAGGAAAAAG	4365	CCCACTGAGAGAGAGAGGAAAA
LDLRex2(27;68;123;30)_68 - 7_i1_f	4366	TCCTTTCTCTCTCTCTCAGTGGC	4367	CCTTTCTCTCTCTCTCAGTGGG	4368	CTTTCTCTCTCTCTCAGTGG
LDLRex2(27;68;123;30)_68 - 7_i1_r	4369	GCCCCACTGAGAGAGAGGAAAAAGGA	4370	CCCACTGAGAGAGAGGAAAAAGG	4371	CCCACTGAGAGAGAGGAAAAAG
LDLRex2(27;68;123;30)_68 - 8_i1_f	4372	CTCCTTTCTCTCTCTCTCAGTGG	4373	TCCTTTTCTCTCTCTCTCAGTGG	4374	CCTTTTCTCTCTCTCTCAGTG
LDLRex2(27;68;123;30)_68 - 8_i1_r	4375	CCCACTGAGAGAGAGGAAAAAGGAG	4376	CCCACTGAGAGAGAGGAAAAAGGA	4377	CACCTGAGAGAGAGGAAAAAGG
LDLRex2(27;68;123;30)_68 - 9_i1_f	4378	TCTCCTTTCTCTCTCTCTCAGTGG	4379	CTCCTTTCTCTCTCTCTCAGTG	4380	TCCTTTTCTCTCTCTCTCAGT
LDLRex2(27;68;123;30)_68 - 9_i1_r	4381	CCCACTGAGAGAGGAGGAAAAAGGAGA	4382	CACCTGAGAGAGGAGGAAAAAGGAG	4383	ACTGAGAGAGGAGGAAAAAGGA
LDLRex2(27;68;123;30)_68_i1_f	4384	CTCTCTCTCAGTTGGCGACAGAT	4385	CTCTCTCTCAGTTGGCGACAGA	4386	TCTCTCAGTTGGCGGACAG
LDLRex2(27;68;123;30)_68_i1_r	4387	ATCTGTGCCCCAACTGAGAGAGAGG	4388	TCTGTGCCCCAACTGAGAGAGAG	4389	CTGTGCCCCAACTGAGAGAGA
LDLRex2(27;68;123;30)_69_i1_f	4390	CTCTCTCTCAGTGGGCGACAGATG	4391	TCTCTCTCAGTGGGCGACAGAT	4392	CTCTCTCAGTGGGCGGACAGA
LDLRex2(27;68;123;30)_69_i1_r	4393	CATCTGTGCCCCAACTGAGAGAGAG	4394	ATCTGTGCCCCAACTGAGAGAGA	4395	TCTGTGCCCCAACTGAGAGAG
LDLRex2(27;68;123;30)_70_i1_f	4396	TCTCTCTCAGTGGGCGACAGATGC	4397	CTCTCTCAGTGGGCGACAGATG	4398	TCTCTCAGTGGGCGGACAGAT
LDLRex2(27;68;123;30)_70_i1_r	4399	GCATCTGTGCCCCAACTGAGAGAGA	4400	CATCTGTGCCCCAACTGAGAGAG	4401	ATCTGTGCCCCAACTGAGAGA
LDLRex2(27;68;123;30)_71_i1_f	4402	CTCTCTCAGTGGGCGACAGATGCG	4403	TCTCTCAGTGGGCGACAGATGC	4404	CTCTCAGTGGGCGGACAGATG

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
ins1						
LDLRex2(27;68;123;30)_71_i1_r	4405	CGCATCTGTGCGCCCACTGAGAG	4406	GCATCTGTGCGCCCACTGAGAGA	4407	CATCTGTGCGCCCACTGAGAG
LDLRex2(27;68;123;30)_72_i1_f	4408	TCTCTCAGTGGGCGGACAGATGCGA	4409	CTCTCAGTGGGCGGACAGATGCG	4410	TCTCAGTGGGCGGACAGATGC
LDLRex2(27;68;123;30)_72_i1_r	4411	TGCGCATCTGTGCGCCCACTGAGAGA	4412	CGCATCTGTGCGCCCACTGAGAG	4413	GCATCTGTGCGCCCACTGAGA
LDLRex2(27;68;123;30)_73_i1_f	4414	CTCTCAGTGGGCGGACAGATGCGAA	4415	TCTCAGTGGGCGGACAGATGCGA	4416	CTCAGTGGGCGGACAGATGGG
LDLRex2(27;68;123;30)_73_i1_r	4417	TTGCGATCTGTGCGCCCACTGAGAG	4418	TCGATCTGTGCGCCCACTGAGA	4419	CGCATCTGTGCGCCCACTGAG
LDLRex2(27;68;123;30)_74_i1_f	4420	TCTCAGTGGGCGAACAAGATGCGAAA	4421	CTCAGTGGGCGAACAAGATGCGAA	4422	TCAGTGGGCGAACAAGATGCGA
LDLRex2(27;68;123;30)_74_i1_r	4423	TTTCGATCTGTGCGCCCACTGAGA	4424	TTGCGATCTGTGCGCCCACTGAG	4425	TCGATCTGTGCGCCCACTGA
LDLRex2(27;68;123;30)_75_i1_f	4426	CTCAGTGGGCGACCAAGATGCGAAA	4427	TCAGTGGGCGACCAAGATGCGAAA	4428	CAGTGGGCGACCAAGATGCGAA
LDLRex2(27;68;123;30)_75_i1_r	4429	CTTCGATCTGTGCGCCCACTGAG	4430	TTTCGATCTGTGCGCCCACTGA	4431	TTGCGATCTGTGCGCCCACTG
LDLRex2(27;68;123;30)_76_i1_f	4432	TCAGTGGGCGACAAGATGCGAAA	4433	CAGTGGGCGACAAGATGCGAAAG	4434	AGTGGGCGACAAGATGCGAAA
LDLRex2(27;68;123;30)_76_i1_r	4435	TCTTCGATCTGTGCGCCCACTGA	4436	CTTCGATCTGTGCGCCCACTG	4437	TTTCGATCTGTGCGCCCACT
LDLRex2(27;68;123;30)_77_i1_f	4438	CAGTGGGCGACAGGATGCGAAAGAA	4439	AGTGGGCGACAGGATGCGAAAGA	4440	GTGGGCGACAGGATGCGAAAG
LDLRex2(27;68;123;30)_77_i1_r	4441	TTCTTCGATCTGTGCGCCCACTG	4442	TCTTCGATCTGTGCGCCCACT	4443	CTTTCGATCTGTGCGCCCACT
LDLRex2(27;68;123;30)_78_i1_f	4444	AGTGGGCGACAGAATGCGAAAGAAA	4445	GTGGGCGACAGAATGCGAAAGAA	4446	TGGGCGACAGAATGCGAAAGA
LDLRex2(27;68;123;30)_78_i1_r	4447	TTCTTCGATCTGTGCGCCCACT	4448	TTCTTCGATCTGTGCGCCCACT	4449	TCTTCGATCTGTGCGCCCA
LDLRex2(27;68;123;30)_79_i1_f	4450	GTGGGCGACAGATGCGAAAGAAAC	4451	TGGGCGACAGATGCGAAAGAAA	4452	GGGCGACAGATGCGAAAGAA
LDLRex2(27;68;123;30)_79_i1_r	4453	GTTTCTTCGCAATCTGTGCGCCAC	4454	TTTCTTCGCAATCTGTGCGCCA	4455	TTCTTCGCAATCTGTGCGCCC
LDLRex2(27;68;123;30)_80_i1_f	4456	TGGGCGACAGATGCGAAAGAAACG	4457	GGGCGACAGATGCGAAAGAAAC	4458	GGCGACAGATGCGAAAGAAA
LDLRex2(27;68;123;30)_80_i1_r	4459	CGTTTCTTCGCCATCTGTGCGCCA	4460	GTTTCTTCGCCATCTGTGCGCCC	4461	TTTCTTCGCCATCTGTGCGCC
LDLRex2(27;68;123;30)_81_i1_f	4462	GGGCGACAGATGCGAAAGAAACGA	4463	GGCGACAGATGCGAAAGAAACG	4464	GCGACAGATGCGAAAGAAAC
LDLRex2(27;68;123;30)_81_i1_r	4465	TCGTTTCTTCGGCATCTGTGCGCC	4466	CGTTTCTTCGGCATCTGTGCGCC	4467	GTTTCTTCGGCATCTGTGCGC
LDLRex2(27;68;123;30)_82_i1_f	4468	GGCGACAGATGCGAAAGAAACGAG	4469	GCGACAGATGCGAAAGAAACGA	4470	CGACAGATGCGAAAGAAACG
LDLRex2(27;68;123;30)_82_i1_r	4471	CTCGTTTCTTCGGCATCTGTGCGCC	4472	TCGTTTCTTCGGCATCTGTGCGC	4473	CGTTTCTTCGGCATCTGTGCG
LDLRex2(27;68;123;30)_83_i1_f	4474	GCGACAGATGCGAAAGAAACGAGT	4475	CGACAGATGCGAAAGAAACGAG	4476	GACAGATGCGAAAGAAACGA
LDLRex2(27;68;123;30)_83_i1_r	4477	ACTCGTTTCTTCGCATCTGTGCGC	4478	CTCGTTTCTTCGCATCTGTGCG	4479	TCGTTTCTTCGCATCTGTGTC
LDLRex2(27;68;123;30)_84_i1_f	4480	CGACAGATGCGAAAGAAACGAGTT	4481	GACAGATGCGAAAGAAACGAGT	4482	ACAGATGCGAAAGAAACGAG
LDLRex2(27;68;123;30)_84_i1_r	4483	AACTCGTTTCTTCGCATCTGTGCG	4484	ACTCGTTTCTTCGCATCTGTG	4485	CTCGTTTCTTCGCATCTGT
LDLRex2(27;68;123;30)_85_i1_f	4486	GACAGATGCGAAAGAAACGAGTTC	4487	ACAGATGCGAAAGAAACGAGTT	4488	CAGATGCGAAAGAAACGAGT
LDLRex2(27;68;123;30)_85_i1_r	4489	GAACTCGTTTCTTCGCATCTGTC	4490	AACCTCGTTTCTTCGCATCTGT	4491	ACTCGTTTCTTCGCATCTG
LDLRex2(27;68;123;30)_86_i1_f	4492	ACAGATGCGAAAGAAACGAGTTC	4493	CAGATGCGAAAGAAACGAGTTC	4494	AGATGCGAAAGAAACGAGTT
LDLRex2(27;68;123;30)_86_i1_r	4495	GAACTCGTTTCTTCGCATCTGT	4496	GAACTCGTTTCTTCGCATCTG	4497	AACCTCGTTTCTTCGCATCT

Table 1

	SEQ ID NO:	25 nt	SEQ ID NO:	23 nt	SEQ ID NO:	21 nt
ins1						
LDLRex2(27;68;123;30)_87_i1_f	4498	CAGATGCGAAAGAAACGAGTTCCA	4499	AGATGCGAAAGAAACGAGTTCC	4500	GATCGAAAGAAACGAGTTTC
LDLRex2(27;68;123;30)_87_i1_r	4501	TGGAACCTGTTTCTTTCGCATCTG	4502	GGAACCTGTTTCTTTCGCATCT	4503	GAACTCGTTTCTTTCGCATC
LDLRex2(27;68;123;30)_88_i1_f	4504	AGATGCGAAAGAAACGAGTTCCAG	4505	GATGCGAAAGAAACGAGTTCCA	4506	ATGCGAAAGAAACGAGTTCC
LDLRex2(27;68;123;30)_88_i1_r	4507	CTGGAACCTGTTTCTTTCGCATCT	4508	TGGAACCTGTTTCTTTCGCATC	4509	GGAACCTGTTTCTTTCGCAT
LDLRex2(27;68;123;30)_89_i1_f	4510	GATGCGAAAGAAACGAGTTCCAGT	4511	ATGCGAAAGAAACGAGTTCCAG	4512	TGCGAAAGAAACGAGTTCCA
LDLRex2(27;68;123;30)_89_i1_r	4513	ACTGGAACCTGTTTCTTTCGCATC	4514	CTGGAACCTGTTTCTTTCGCAT	4515	TGGAACCTGTTTCTTTCGCA
LDLRex2(27;68;123;30)_90_i1_f	4516	ATGCGAAAGAAACGAGTTCCAGTG	4517	TGCGAAAGAAACGAGTTCCAGT	4518	GCGAAAGAAACGAGTTCCAG
LDLRex2(27;68;123;30)_90_i1_r	4519	CACTGGAACCTGTTTCTTTCGCAT	4520	ACTGGAACCTGTTTCTTTCGCA	4521	CTGGAACCTGTTTCTTTCGC
LDLRex2(27;68;123;30)_91_i1_f	4522	TGCGAAAGAAACGAGTTCCAGTGC	4523	GCGAAAGAAACGAGTTCCAGTG	4524	CGAAAGAAACGAGTTCCAGT
LDLRex2(27;68;123;30)_91_i1_r	4525	GCACTGGAACCTCGTTTCTTTCGCA	4526	CACTGGAACCTCGTTTCTTTCGC	4527	ACTGGAACCTCGTTTCTTTCG
LDLRex2(27;68;123;30)_92_i1_f	4528	GCGAAAGAAACGAGTTCCAGTGCC	4529	CGAAAGAAACGAGTTCCAGTGC	4530	GAAAGAAACGAGTTCCAGTG
LDLRex2(27;68;123;30)_92_i1_r	4531	GGCACTGGAACCTCGTTTCTTTCGC	4532	GCACTGGAACCTCGTTTCTTTCG	4533	CACCTGGAACCTCGTTTCTTTC
LDLRex2(27;68;123;30)_93_i1_f	4534	CGAAAGAAACGAGTTCCAGTGCCA	4535	GAAAGAAACGAGTTCCAGTGCC	4536	AAAGAAACGAGTTCCAGTGCC
LDLRex2(27;68;123;30)_93_i1_r	4537	TGGCACTGGAACCTCGTTTCTTTCG	4538	GGCACTGGAACCTCGTTTCTTTC	4539	GCACTGGAACCTCGTTTCTTTC
LDLRex2(27;68;123;30)_94_i1_f	4540	GAAAGAAACGAGTTCCAGTGCCAA	4541	AAAGAAACGAGTTCCAGTGCCA	4542	AAGAAACGAGTTCCAGTGCC
LDLRex2(27;68;123;30)_94_i1_r	4543	TGGCACTGGAACCTCGTTTCTTTC	4544	TGGCACTGGAACCTCGTTTCTT	4545	GGCACTGGAACCTCGTTTCTT
LDLRex2(27;68;123;30)_95_i1_f	4546	AAAGAAACGAGTTCCAGTGCCAAG	4547	AAGAAACGAGTTCCAGTGCCAA	4548	AGAAACGAGTTCCAGTGCCA
LDLRex2(27;68;123;30)_95_i1_r	4549	CTTGGCACTGGAACCTCGTTTCTT	4550	TTGGCACTGGAACCTCGTTTCTT	4551	TGGCACTGGAACCTCGTTTCT
LDLRex2(27;68;123;30)_96_i1_f	4552	AAGAAACGAGTTCCAGTGCCAAGA	4553	AGAAACGAGTTCCAGTGCCAAG	4554	GAAACGAGTTCCAGTGCCA
LDLRex2(27;68;123;30)_96_i1_r	4555	TCTTGGCACTGGGAACCTCGTTTCTT	4556	CTTGGCACTGGGAACCTCGTTTCT	4557	TTGGCACTGGGAACCTCGTTTC
LDLRex2(27;68;123;30)_97_i1_f	4558	AGAAACGAGTTCCAGTGCCAAGAC	4559	GAAACGAGTTCCAGTGCCAAGA	4560	AAACGAGTTCCAGTGCCAAG
LDLRex2(27;68;123;30)_97_i1_r	4561	GTCCTGGCACTGGGAACCTCGTTTCT	4562	TCTTGGCACTGGGAACCTCGTTTC	4563	CTTGGCACTGGGAACCTCGTTT
LDLRex2(27;68;123;30)_98_i1_f	4564	GAAACGAGTTCCAAGTGCCAAGACG	4565	AAACGAGTTCCAAGTGCCAAGAC	4566	AACGAGTTCCAAGTGCCAAGA
LDLRex2(27;68;123;30)_98_i1_r	4567	CGTCTTGGCACTTGGAACTCGTTTC	4568	GTCTTGGCACTTGGAACTCGTTT	4569	TCTTGGCACTTGGAACTCGTT
LDLRex2(27;68;123;30)_99_i1_f	4570	AAACGAGTTCCAGTGCCAAGACGG	4571	AACGAGTTCCAGTGCCAAGACG	4572	ACGAGTTCCAGTGCCAAGAC
LDLRex2(27;68;123;30)_99_i1_r	4573	CCGTCTTGGCACCTGGAACTCGTTT	4574	CGTCTTGGCACCTGGAACTCGTT	4575	GTCTTGGCACCTGGAACTCGT

Table 2

Type of probes	mut HTZ en K			
	lk	lk+1	ratios IN(k)/IN(k+1) y IV(k)/IV(k+1)	ratios IN(k)/IN(k+1) / IV(k)/IV(k+1)
Wild type or normal	250	600	0.42	0.031
Nt 16 Del1 variation 1	400	30	13.33	
Wild type or normal	250	400	0.63	0.042
Nt 16 Del1 variation 2	150	10	15.00	
Wild type or normal	550	500	1.10	0.550
NT 16 Del2 variation 1	20	10	2.00	
Wild type or normal	400	550	0.73	2.182
Nt 16 Del2 variation 2	10	30	0.33	
Wild type or normal	450	600	0.75	1.500
Nt 17 Del1 variation 1	10	20	0.50	
Wild type or normal	500	650	0.77	1.154
Nt 17 Del1 variation 2	20	30	0.67	
Wild type or normal	650	500	1.30	0.433
Nt 17 Del2 variation 2	30	10	3.00	
Wild type or normal	550	400	1.38	2.063
Nt 17 Del2 variation 2	20	30	0.67	

Table 3

Type of probes	mut HMZ en K			
	lk	lk+1	ratios IN(k)/IN(k+1) y IV(k)/IV(k+1)	ratios IN(k)/IN(k+1) / IV(k)/IV(k+1)
Wild type or normal	20	600	0.03	0.003
Nt 16 Del1 variation 1	400	30	13.33	
Wild type or normal	30	400	0.08	0.001
Nt 16 Del1 variation 2	550	10	55.00	
Wild type or normal	550	500	1.10	0.550
NT 16 Del2 variation 1	20	10	2.00	
Wild type or normal	400	550	0.73	2.182
Nt 16 Del2 variation 2	10	30	0.33	
Wild type or normal	450	600	0.75	1.500
Nt 17 Del1 variation 1	10	20	0.50	
Wild type or normal	500	650	0.77	1.154
Nt 17 Del1 variation 2	20	30	0.67	
Wild type or normal	650	500	1.30	0.433
Nt 17 Del2 variation 2	30	10	3.00	
Wild type or normal	550	400	1.38	2.063
Nt 17 Del2 variation 2	20	30	0.67	

Table 4

Type of probes	mut HTZ en K+1			
	lk	lk+1	ratios IN(k)/IN(k+1) y IV(k)/IV(k+1)	ratios IN(k)/IN(k+1) / IV(k)/IV(k+1)
Wild type or normal	600	300	2.00	23.333
Nt 16 Del1 variation 1	30	350	0.09	
Wild type or normal	400	250	1.60	32.000
Nt 16 Del1 variation 2	10	200	0.05	
Wild type or normal	500	550	0.91	1.818
NT 16 Del2 variation 1	10	20	0.50	
Wild type or normal	550	400	1.38	0.458
Nt 16 Del2 variation 2	30	10	3.00	
Wild type or normal	600	450	1.33	0.667
Nt 17 Del1 variation 1	20	10	2.00	
Wild type or normal	650	500	1.30	0.867
Nt 17 Del1 variation 2	30	20	1.50	
Wild type or normal	500	650	0.77	2.308
Nt 17 Del2 variation 2	10	30	0.33	
Wild type or normal	400	550	0.73	0.485
Nt 17 Del2 variation 2	30	20	1.50	

Table 5

Type of probes	mut HMZ en K+1			
	lk	lk+1	ratios IN(k)/IN(k+1) y IV(k)/IV(k+1)	ratios IN(k)/IN(k+1) / IV(k)/IV(k+1)
Wild type or normal	600	20	30.00	400.000
Nt 16 Del1 variation 1	30	400	0.08	
Wild type or normal	400	30	13.33	733.333
Nt 16 Del1 variation 2	10	550	0.02	
Wild type or normal	500	550	0.91	1.818
NT 16 Del2 variation 1	10	20	0.50	
Wild type or normal	550	400	1.38	0.458
Nt 16 Del2 variation 2	30	10	3.00	
Wild type or normal	600	450	1.33	0.667
Nt 17 Del1 variation 1	20	10	2.00	
Wild type or normal	650	500	1.30	0.867
Nt 17 Del1 variation 2	30	20	1.50	
Wild type or normal	500	650	0.77	2.308
Nt 17 Del2 variation 2	10	30	0.33	
Wild type or normal	400	550	0.73	0.485
Nt 17 Del2 variation 2	30	20	1.50	

CLAIMS

What is claimed is:

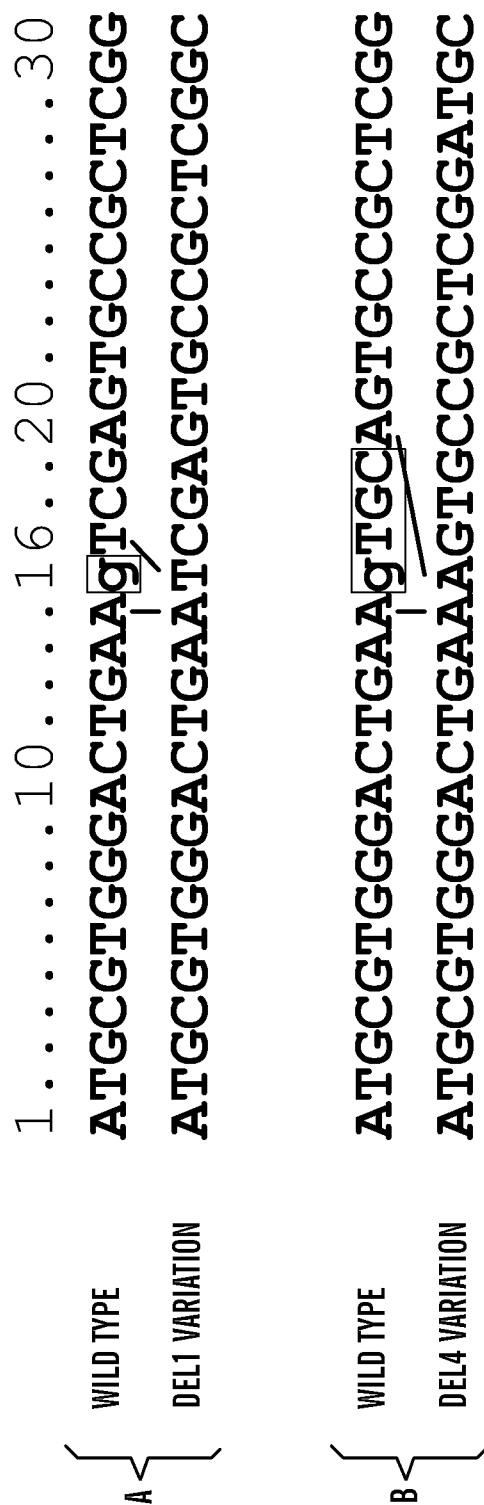
1. A method of designing a library of probes for detecting at least one indel variation in a genetic variant segment, the method comprising the steps of (a) selecting a nucleic acid variant segment of N nucleotides long, wherein N can be any length between 25 and 5000; (b) selecting N number of probe sets each designed to hybridize to each of the N number of nucleotides in the nucleic acid variant segment; and (c) selecting at least one probe subset for the probe set, wherein the probe subset comprises at least two different probes forming a pair of probes, one designed to specifically hybridize to a normal/wild-type or a control sequence and one designed to specifically hybridize to a sequence with the at least one indel variation.
2. The method of claim 1, further comprising a step of manufacturing the probe sets selected/designed through steps (a), (b) and (c).
3. The method of any one of the preceding claims, wherein at least one of the steps (a), (b), or (c) is performed using a computer implemented system.
4. The method of any one of the preceding claims, further comprising a step of attaching the probe on a solid surface.
5. The method of any one of the preceding claims, wherein the at least one pair of probes consist of a normal/control probe and a variant probe, both of which interrogate the about same region on the genetic variant segment, wherein the both probes forming the at least one pair of probe sub-set have the same sequence length and are of the same type of nucleic acids.
6. The method of any one of the preceding claims, wherein the normal/control probe comprises the normal sequence or the known SNP polymorphism of genetic variant segment and the variant probe comprises an indel-containing variant sequence of genetic variant segment
7. The method of any one of the preceding claims, wherein each of the at least two different probes has the difference between them located in position -25, -24, -23, -22, -21, -20, -19, -18, -17, -16, -15, -14, -13, -12, -11, -10, -9, -8, -7, -6, -5, -4, -3, -2, -1, 0, +1, +2, +3, +4, +5, +6, +7, +8, +9, +10, +11, +12, +13, +14, +15, +16, +17, +18, +20, +21, +22, +23, +24 or +25 of the probe, wherein the position 0 is the center nucleotide of the probe when the probe has an odd number of nucleotides; and wherein the position -1 and +1 are the two central nucleotides of the probe when the probe has an even number of nucleotides.
8. The method of any one of the preceding claims, wherein the probes are 15-50 nucleotides long.
9. The method of any one of the preceding claims, wherein each of the at least two different probes has the difference between them located in position -4, -3, -2, -1, 0, +1, +2, +3 or +4 of the probe, wherein the position 0 is the center nucleotide of the probe when the probe has an odd number of nucleotides; and wherein the position -1 and +1 are the two central nucleotides of the probe when the probe has an even number of nucleotides.
10. The method of any one of the preceding claims, wherein the probes are DNA, RNA or PNA.

11. The method of any one of the preceding claims, wherein the indel variation is a deletion, an insertion or a duplication of nucleotide.
12. The method of any one of the preceding claims, wherein the deletion is selected from a group consisting of one, two, three, four, five, six, seven, eight, nine, ten, and up to fifty nucleotides.
13. The method of any one of the preceding claims, wherein the insertion is selected from a group consisting of one, two, three, four, five, six, seven, eight, nine, ten, and up to fifty nucleotides.
14. The method of any one of the preceding claims, wherein the duplication is selected from a group consisting of one, two, three, four, five, six, seven, eight, nine, ten, and up to fifty nucleotides.
15. The method of any one of the preceding claims, wherein the probes of the at least one probe sub-set is complementary to the sense strand of the genetic variant segment.
16. The method of any one of the preceding claims, wherein probes of the at least one probe sub-set is complementary to the anti-sense strand of the genetic variant segment.
17. The method of any one of the preceding claims, wherein only one kind of indel is detected, the method comprising a step of selecting one set of probe sets and as many probe sets as the length or number of nt (or base pairs) in the variant segment under interrogation, wherein each probe set comprises a single probe sub-set, wherein each probe sub-set comprises at least a pair of probes consisting of one control or normal/wild type probe (C) and one variation probe (V).
18. The method of any one of the preceding claims, wherein at least two types of indels are designed to be detected, the method comprising the step of designing each probe set to comprise at least two probe sub-sets, wherein each probe sub-set comprises at least one pair of probes, wherein each pair of probes consists of one control or normal probe and one variation probe, wherein the member probes of each pair of probes within each probe sub-set is designed to differ from each other in terms of length, indel variation location inside the probe and strand of interrogation of the variant segment.
19. The method of any one of the preceding claims, wherein more than two types of indels are to be detected, further comprising a step of designing as many probe sub-sets as there are indels that need to be detected, and wherein each pair of probes within a probe sub-set is designed to differ from each other in terms of length, interrogating position inside the probe and strand of interrogation of the variant segment.
20. A library of probes prepared by the method of any one of the preceding claims.
21. A library of probes, wherein the probes are selected from the probes set forth in Table 1, SEQ ID NO: 1-4575.
22. The library of probes according to claim 20, wherein the probes consist of SEQ ID No: 1-4575.
23. Use of the library of probes according to any one of claims 20-22.
24. A DNA-chip comprising the library of probes of any one of claims 20-22.
25. Use of the DNA chip of claim 24.
26. A collection of microbeads comprising the library of probes of any one of claims 20-22.
27. Use of the collection of microbeads of claim 26.

28. The method of detecting and analyzing an indel in a genetic variant segment having a length of N nucleotide bases comprises:
- (a) providing at least a tNA sample.
 - (b) providing at least two cNA samples.
 - (c) amplifying at least one genetic variant segment from the at least a test NA and amplifying at least one genetic variant segment from the at least two control NA samples, wherein the amplification of the genetic variant segments from the test NA samples and the control NA samples optionally use the same primers;
 - (d) providing a set of probe sets designed to hybridize to the at least one genetic variant segment, wherein the set of probe sets comprising at least one probe set, wherein the at least one probe set for the genetic variant segment comprises at least one probe sub-set, wherein the at least one probe sub-sets comprise at least one pair of probes: a normal probe and a variation probe, wherein the normal probe of the pair is complementary to the normal (wild type or control) sequence of the genetic variant segment, and the variation probe is complementary to the normal sequence except for a position corresponding to the indel variation, and wherein the probes are placed on the solid support as probe features;
 - (e) contacting optionally in parallel the at least one genetic variant segment from the at least tNA sample and the at least one genetic variant segment from the at least two cNA samples with the solid support, thereby allowing NA hybridization between the genetic variant segments from the tNA and the cNAs to the genetic variant probe features thereby forming NA-probe complexes, wherein each complex is detectably labeled;
 - (f) measuring an intensity of the detectable label for NA-probe complex at each probe feature.
 - (g) applying an algorithm to the data from step (f), thereby determining the indel present in the genetic variant segment of the tNA sample, wherein algorithm comprises the steps of:
 - (i). computing a ratio for each pair of probes:

$$\text{Ratio}_{(k)} = \frac{\text{intensity value for normal probe}}{(\text{intensity value for normal probe} + \text{intensity value for variation probe})}$$
 - (ii). computing the mean and the standard deviation of the ratios obtained for all the control NA samples; and
 - (iii). comparing the ratios obtained for each of the tNA sample with the mean ratio obtained for the cNA samples in step (ii), wherein if the ratio of the tNA sample is at least 5 standard deviations away from the mean ratio obtained with the cNA sample, the test NA has the indel variation at position k, either in an heterozygous or a homozygous state; wherein k has values from 1 to N-1 where 1 represent the first oligonucleotide of the variant segment and N is the last base.

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**FIG. 1**

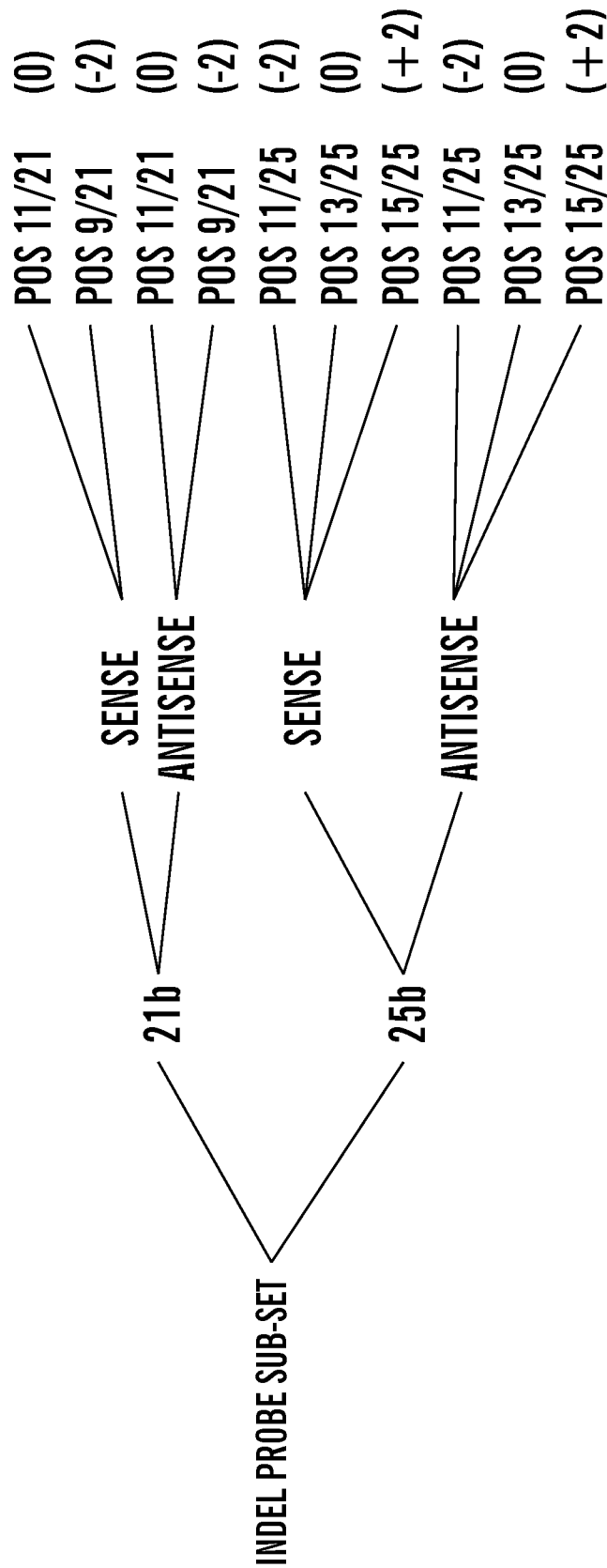
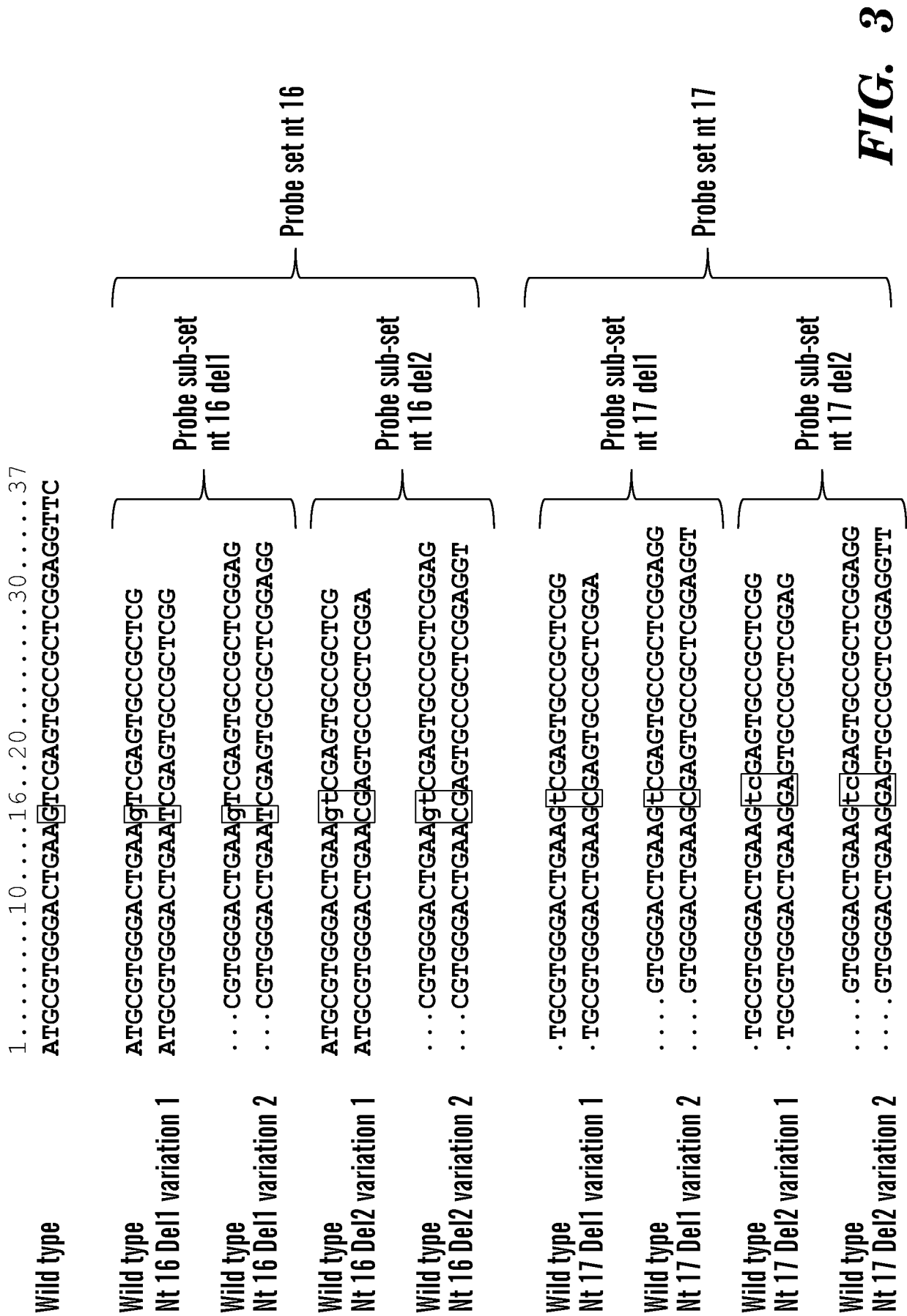


FIG. 2



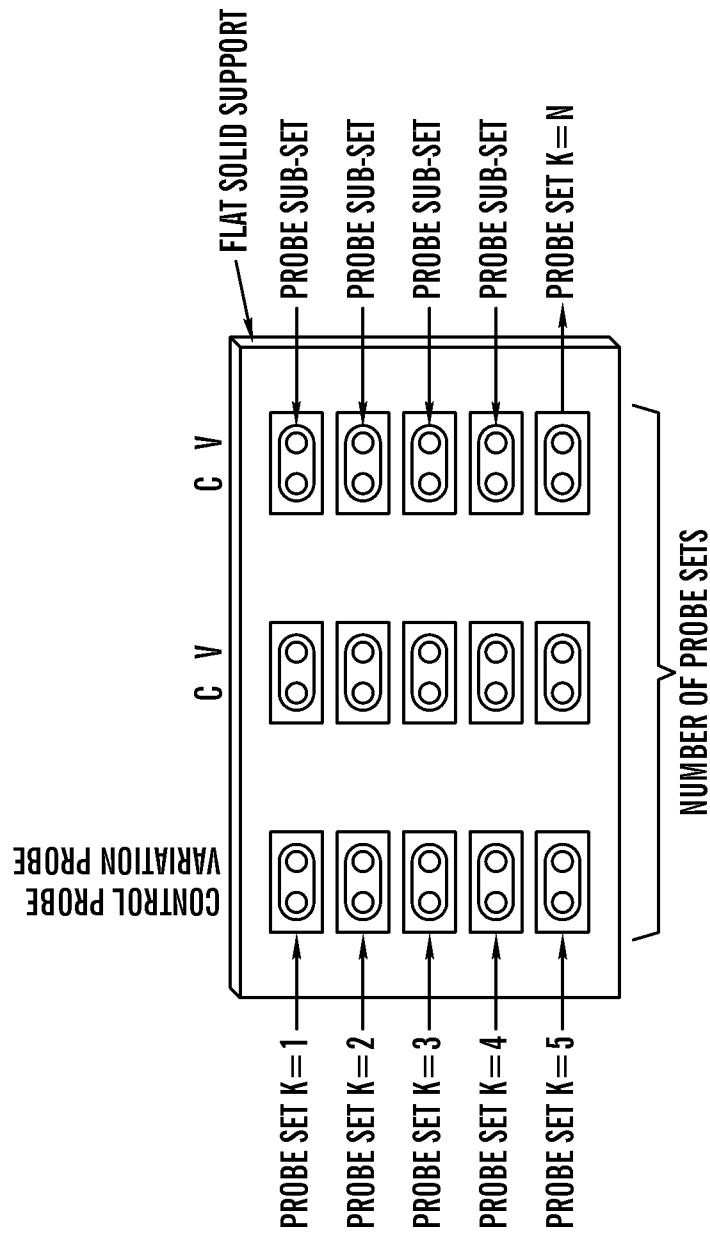


FIG. 4A

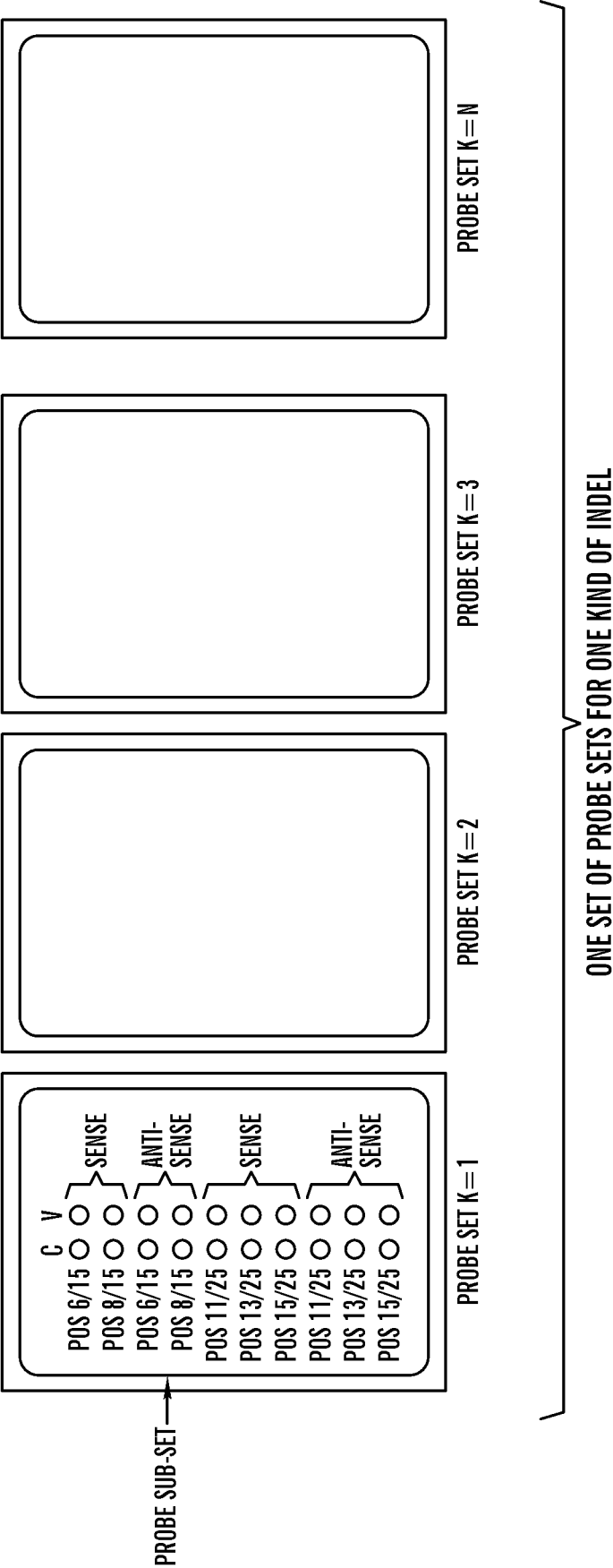


FIG. 4B

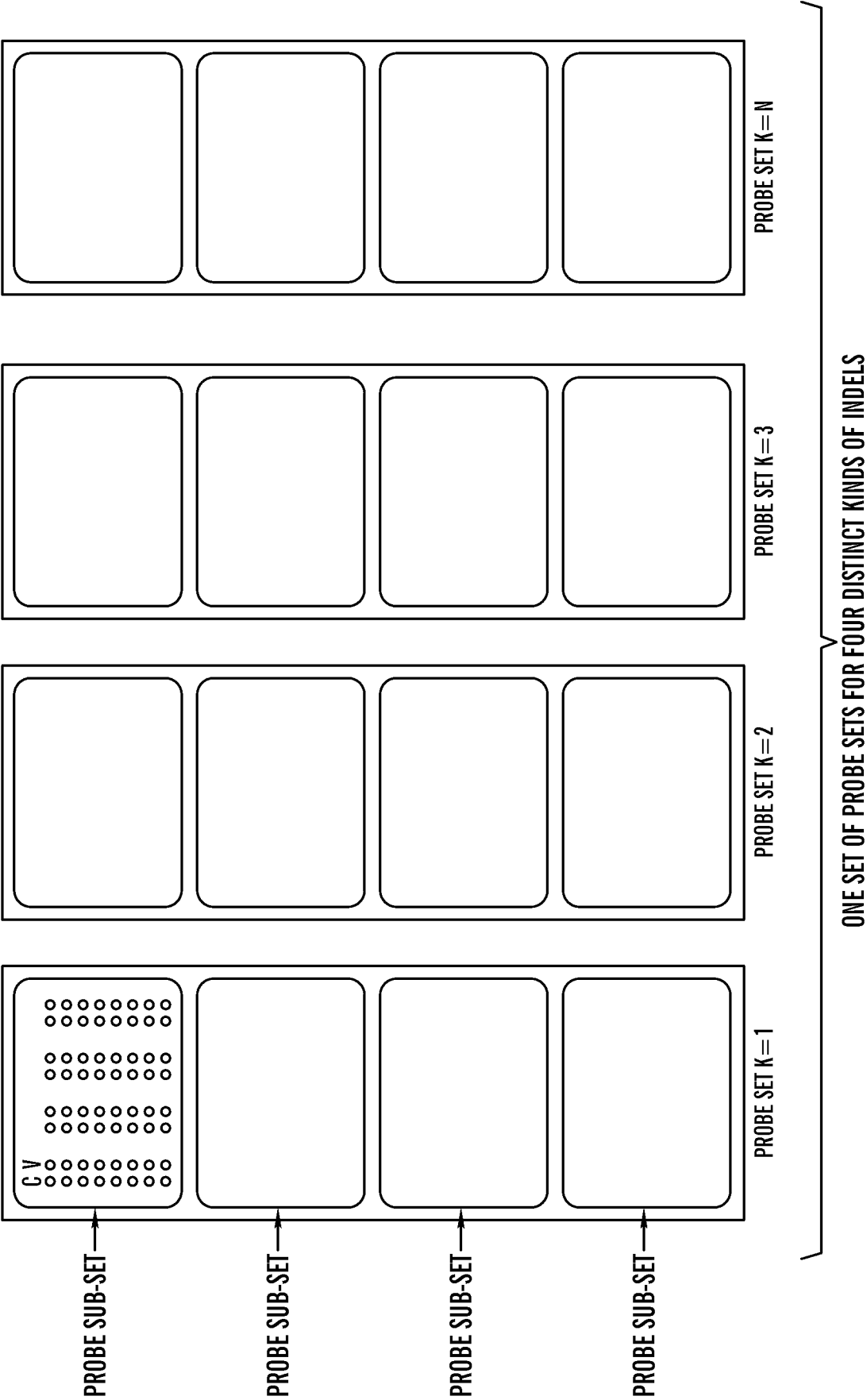
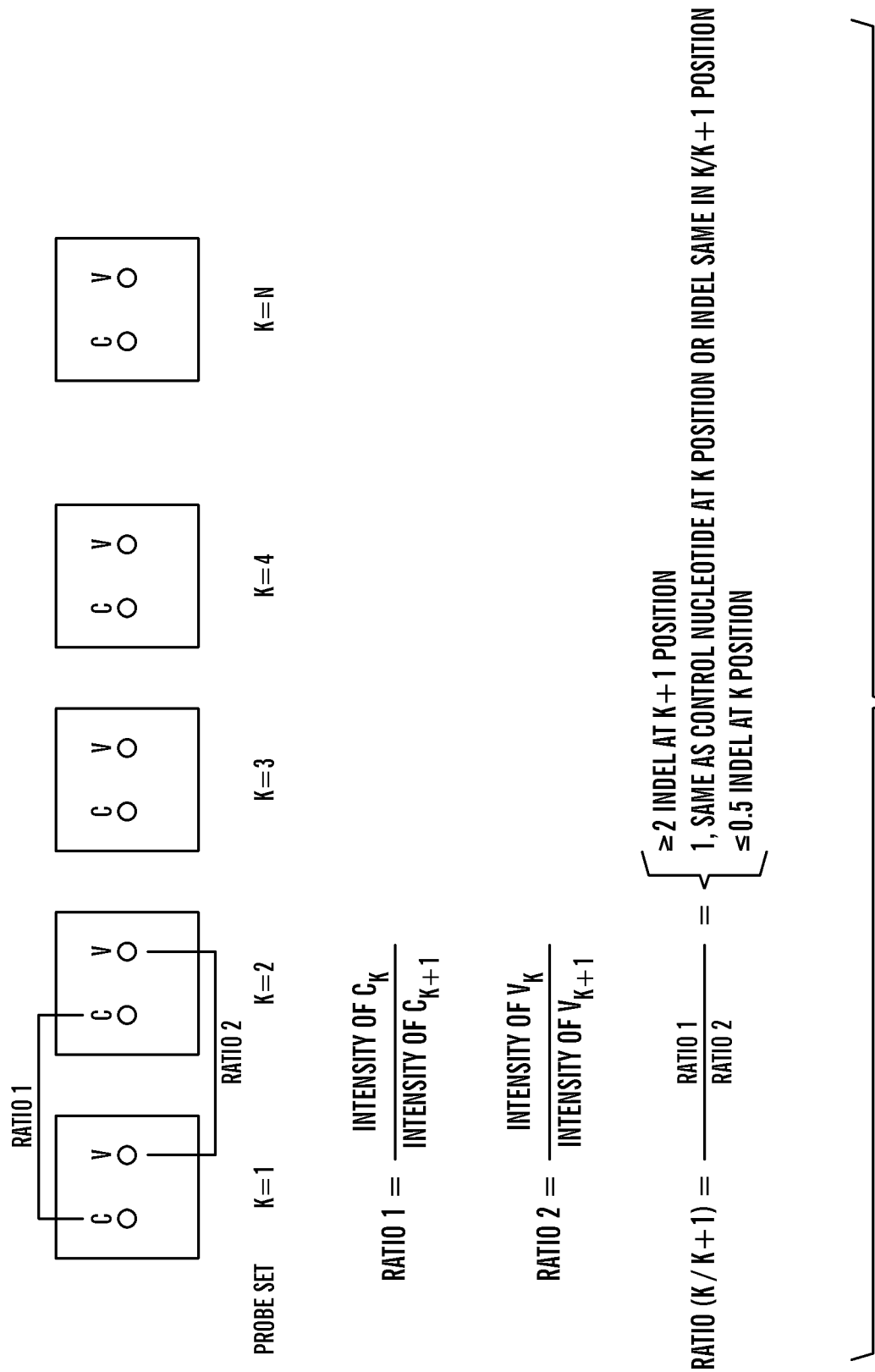


FIG. 4C



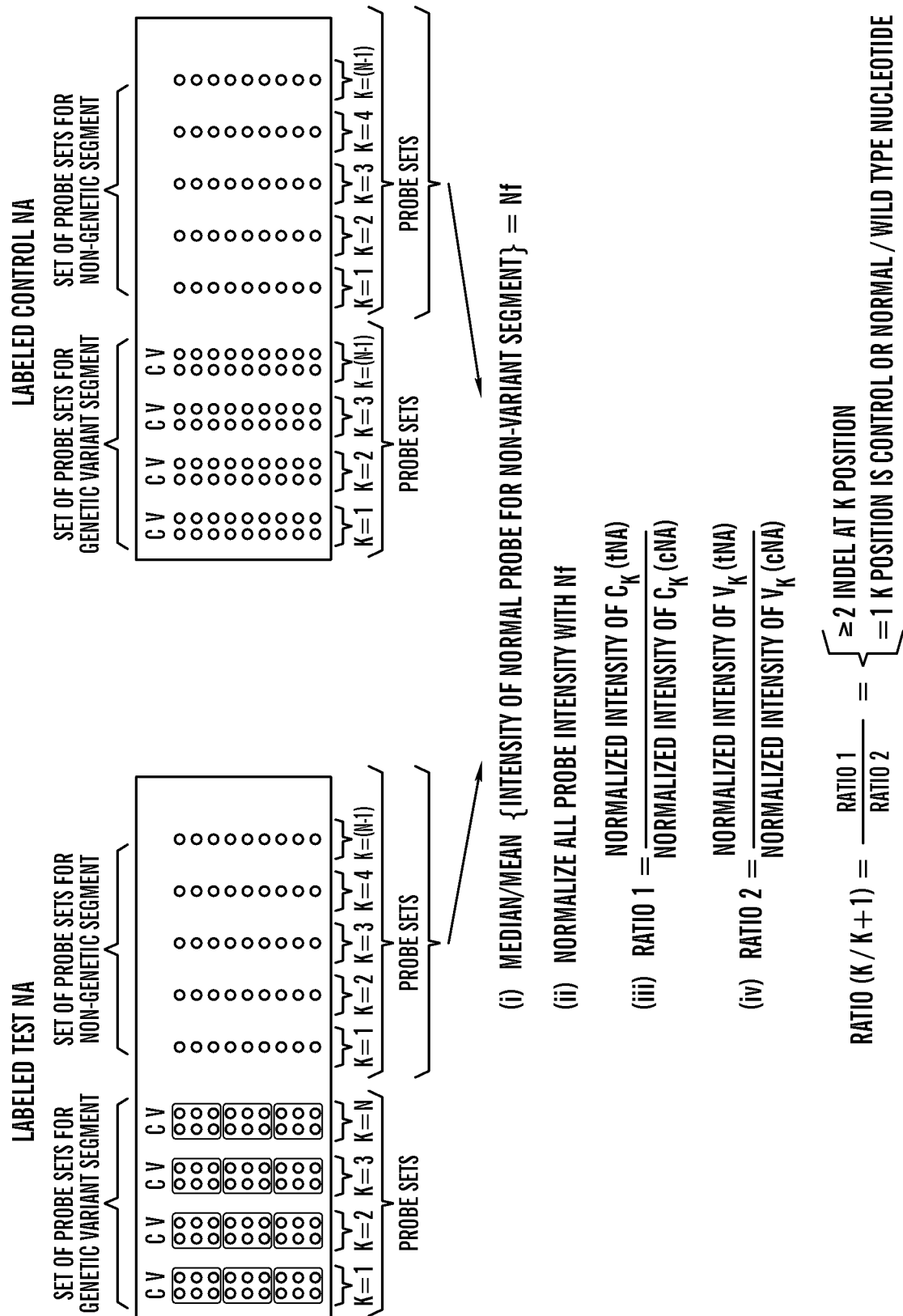
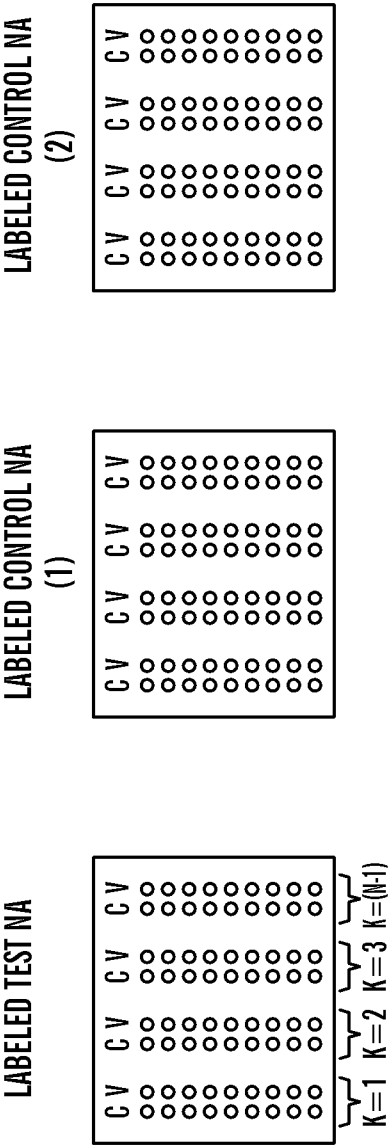


FIG. 6



RATIO (K) = $\frac{\text{INTENSITY OF } C_K}{(\text{INTENSITY OF } C_K + \text{INTENSITY OF } V_K)}$
(for tNA & cNA)

MEAN + STANDARD DEVIATION {RATIO (K) FOR CONTROL NA (1) + CONTROL NA (2) }

RATIO (K) (for tNA) $\begin{cases} \geq \text{MEAN} + 5 \times \text{SD, INDEL AT K POSITION} \\ < \text{MEAN} + 5 \times \text{SD, K POSITION IS CONTROL OR NORMAL / WILD TYPE NUCLEOTIDE} \end{cases}$

FIG. 7

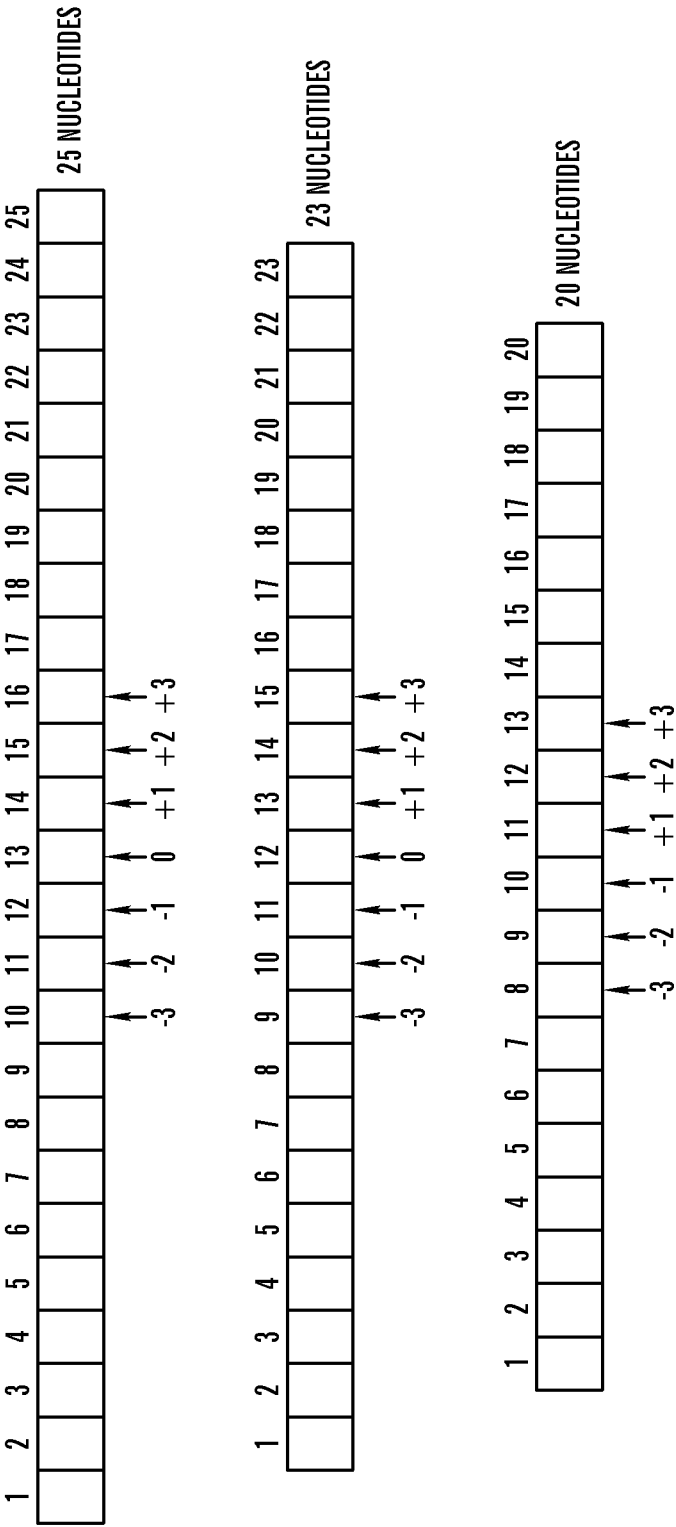


FIG. 8

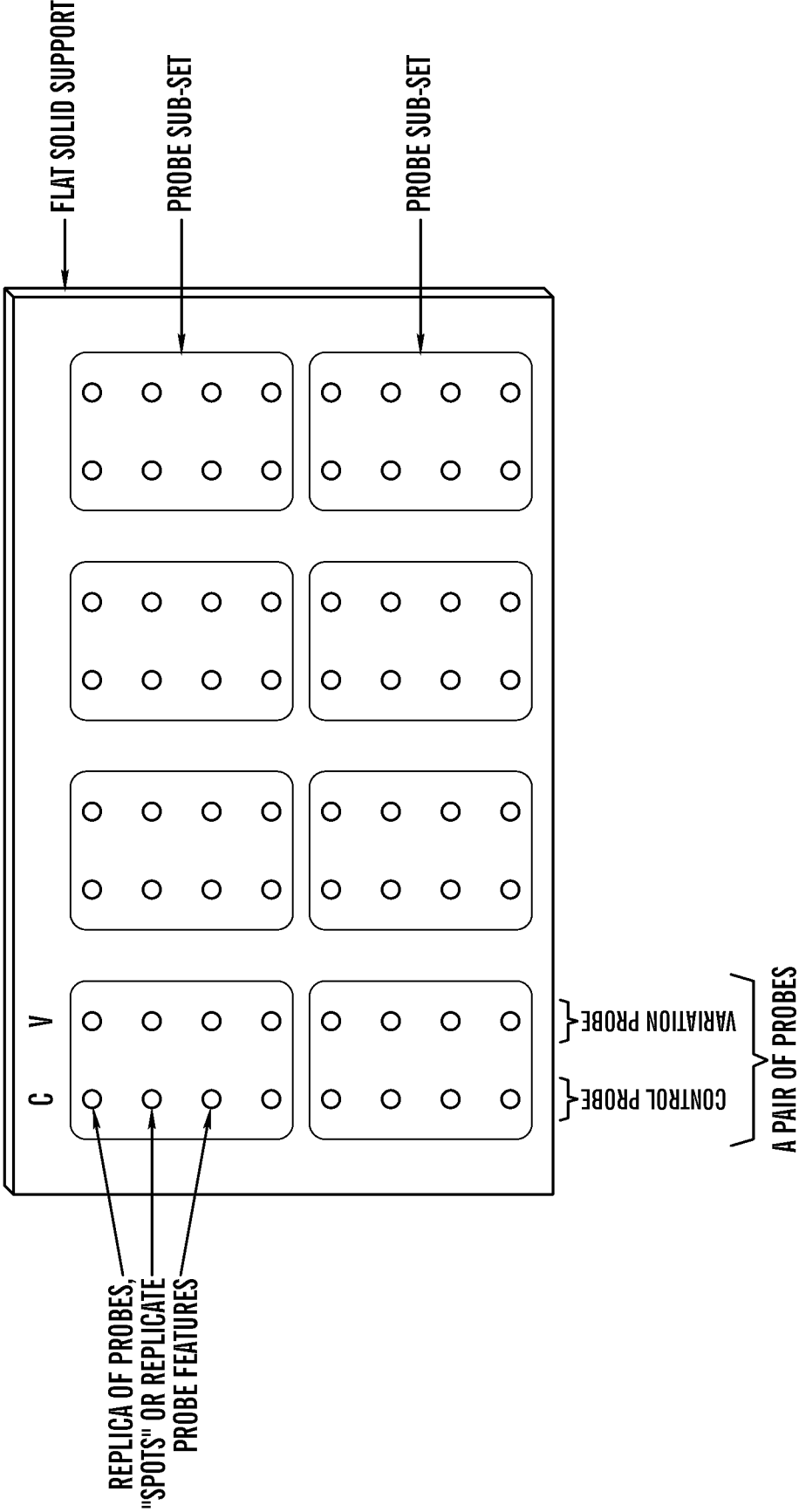
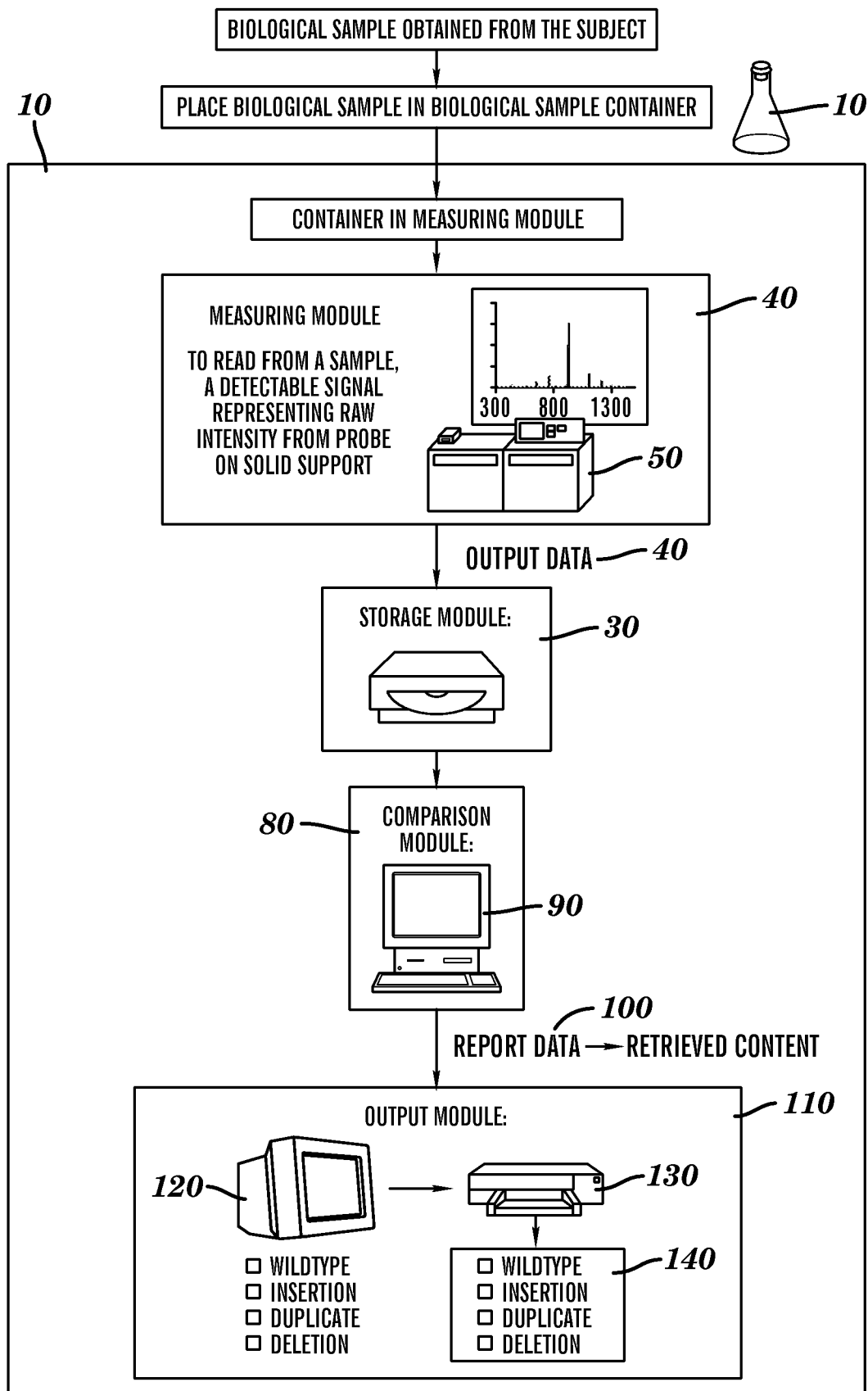
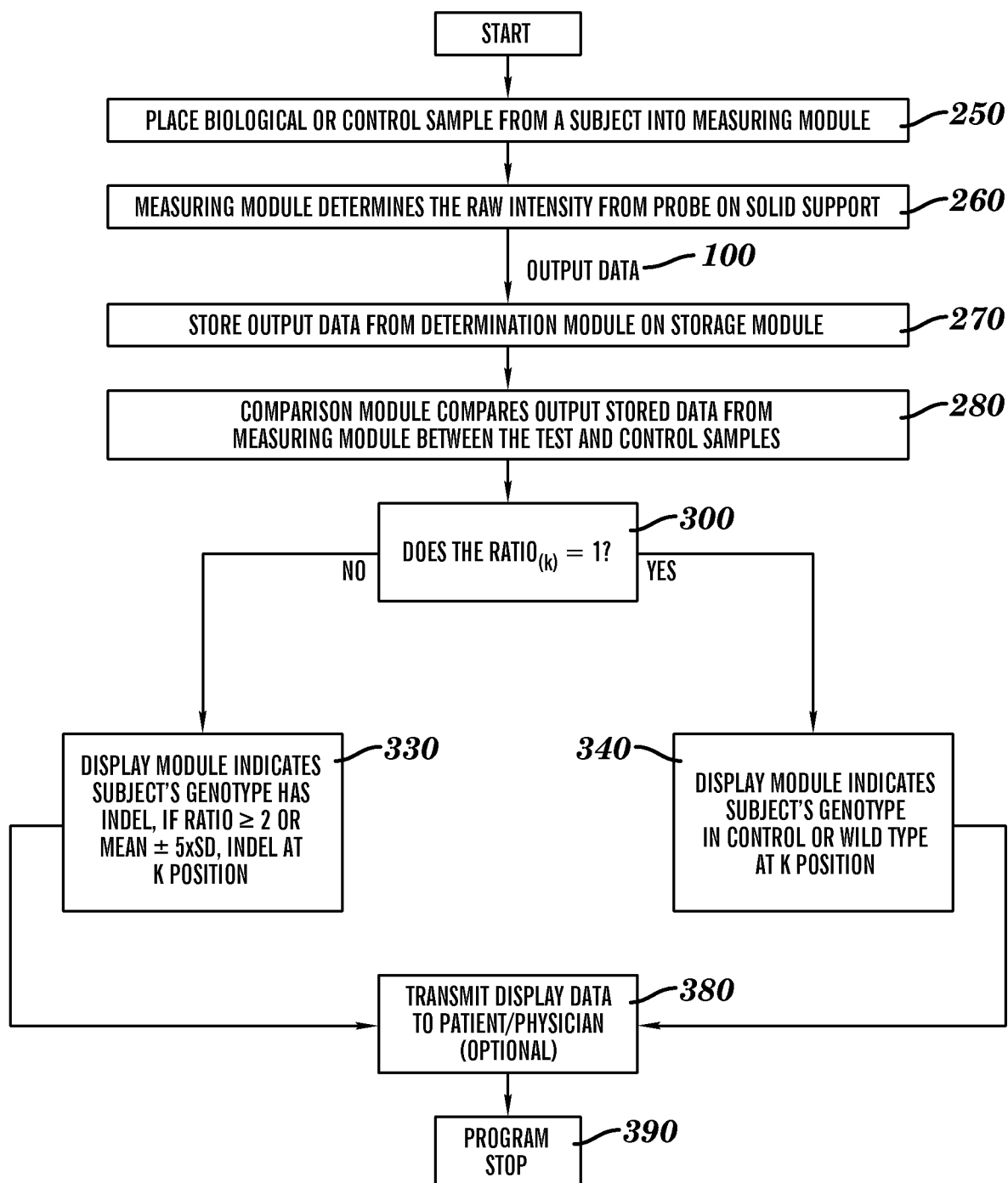


FIG. 9

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**FIG. 10**

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**FIG. 11**

INTERNATIONAL SEARCH REPORT

International application No
PCT/IB2010/002354

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, WPI Data

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2003/165823 A1 (CRONIN MAUREEN T [US] ET AL) 4 September 2003 (2003-09-04)	1-16, 19, 20, 23-28
Y	the whole document	17, 18, 21, 22
Y	DE 102 42 206 A1 (MAX DELBRUECK CENTRUM [DE]) 3 April 2003 (2003-04-03) the whole document	21, 22
Y	WO 2006/075039 A2 (LACER SA [ES]; LOPEZ MARTINEZ MONICA [ES]; MARTIN AZNAR BEATRIZ [ES];) 20 July 2006 (2006-07-20) the whole document	21, 22
Y	US 6 461 816 B1 (WOLBER PAUL K [US] ET AL) 8 October 2002 (2002-10-08) example 2	17, 18
	- / - -	



Further documents are listed in the continuation of Box C.



See patent family annex.

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Date of the actual completion of the international search

21 January 2011

Date of mailing of the international search report

07/02/2011

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Authorized officer

Cornelis, Karen

INTERNATIONAL SEARCH REPORT

International application No

PCT/IB2010/002354

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
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A	----- SALATHIA N ET AL: "Indel arrays: An affordable alternative for genotyping", PLANT JOURNAL, BLACKWELL SCIENTIFIC PUBLICATIONS, OXFORD, GB, vol. 51, no. 4, 1 August 2007 (2007-08-01), pages 727-737, XP002563916, ISSN: 0960-7412, DOI: DOI:10.1111/J.1365-313X.2007.03194.X [retrieved on 2007-07-20] the whole document	1-28
A	----- MAHARJAN RAM P ET AL: "Genome-wide analysis of single nucleotide polymorphisms in Bordetella pertussis using comparative genomic sequencing", RESEARCH IN MICROBIOLOGY, vol. 159, no. 9-10, November 2008 (2008-11), pages 602-608, XP002617797, ISSN: 0923-2508 the whole document	1-28
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Information on patent family members

International application No

PCT/IB2010/002354

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