DESCRIPTION

METHOD FOR DETERMINATION OF ONSET RISK OF GLAUCOMA

TECHNICAL FIELD

[0001] The present invention relates to a method of detecting the presence of a single nucleotide polymorphism associated with the onset of glaucoma, or a single nucleotide polymorphism with a high onset risk of glaucoma, and a kit used in the detection method.

BACKGROUND ART

[0002] Glaucoma is a disease which causes a characteristic optic nerve cupping and an impairment in a visual field by retinal ganglion cell death. An elevation in an intraocular pressure is considered to be a major cause for the nerve cupping and the impairment in the visual field in glaucoma. On the other hand, there is also glaucoma in which an intraocular pressure is held within a normal range in statistical calculation, and even in this case, it is considered that glaucoma develops because the intraocular pressure is at a sufficiently high level for causing the impairment in a visual field for an individual.

[0003] The basic treatment for glaucoma is to maintain an intraocular pressure at a low level, and it is necessary to consider the causes for a high intraocular pressure in order to maintain a low intraocular pressure.

Therefore, in the diagnosis of glaucoma, it is important to classify the types of glaucoma in accordance with the levels of intraocular pressures and causes therefor. As the causes for an elevation in an intraocular pressure, the presence or absence of closure of angle which is a major drainage pathway for an aqueous humor filling an eye is important. From these viewpoints, the primary glaucoma is roughly classified into the two groups of closed-angle glaucoma accompanying angle closure and open-angle glaucoma without accompanying angle closure. Among them, the open-angle glaucoma is classified into open-angle glaucoma, in a narrow sense, accompanying an elevation in an intraocular pressure, i.e. primary open-angle glaucoma, and normal tension glaucoma in which an intraocular pressure is held within a normal range.

[0004] It is known from old times that glaucoma is associated with inheritance. It is reported that 5 to 50% of individuals with open-angle glaucoma have a family history, and it is generally understood that 20 to 25% of individuals have hereditary causes. Based on these reports, studies on a search for a gene responsible for glaucoma are performed. As a result, it is reported that a mutation in *myocilin* (MYOC) gene is associated with open-angle glaucoma (See Patent Publication: 1), and that a mutation in *optineurin* gene (OPTN) is associated with normal tension glaucoma (See Non-Patent Publication: 1). However, all the genetic causes of glaucoma cannot be explained only by these genes, and the presence of unknown glaucoma-related genes is expected.

[0005] On the other hand, a single nucleotide polymorphism means that a substitution mutation in which a single base is changed into another base is

found in base sequences of the genome of an individual, and the mutation exists in a certain frequency, generally a frequency of about 1% or more, in the population of an organism species. A single nucleotide polymorphism exists at intron or exon on genes, or any of the regions of the genome other than these.

Patent Publication 1: Japanese Patent-Laid Open No. 2000-306165

Non Patent Publication 1: Rezaie T and eleven others, *Science*, 2002, **295(5557)**, 1077-1079.

DISCLOSURE OF INVENTION

PROBLEMS TO BE SOLVED BY THE INVENTION

[0006] Generally, an intraocular pressure or an ocular fundus photograph is used as a simple examination for glaucoma; however, these examinations do not necessarily lead to a definite diagnosis for glaucoma. Usually, in addition to these, visual field examinations are performed; however, there are some disadvantages that the examination is carried out for a long period of time, causing burdens on patients, and that one must be accustomed to the examination, so that initial examination results have low reliability.

[0007] On the other hand, as mentioned above, the involvement of hereditary causes is strongly suspected in the onset of glaucoma, but critical responsible genes are not identified. On the other hand, even if the involvement of a single gene to the disease cannot be explained by a mutation or polymorphism, it is considered that there are numerous mutations or polymorphisms of a gene of which involvement to glaucoma is relatively moderate, and the involvement of hereditary causes to the onset of

glaucoma can be explained by a combined action of each of these mutations or polymorphisms.

[0008] The inventors have remarked on a polymorphism on the genome, especially a single nucleotide polymorphism, in order to find a gene associated with glaucoma.

[0009] By finding polymorphisms involved in the onset of glaucoma, a person having the polymorphisms which are found in a high frequency in glaucoma patients is predicted to have a high onset risk of glaucoma in future even before the onset thereof. Also, the polymorphisms can be applied to screening of whether or not a visual field examination is required, in an early stage of glaucoma which is difficult to be detected by the simple determination of glaucoma, i.e. a method such as a measurement of intraocular pressure or an ocular fundus photograph, which is available to be diagnosed only by carrying out the visual field examination. In other words, a sample donor can take a preventive measure for the onset of glaucoma by knowing the onset risk of glaucoma, and in addition, a necessary measure for preventing visual constriction such as a definite diagnosis and an initiation of treatment at an early stage according to a precision examination can be taken; therefore, it is important to find a polymorphism involved in the onset of glaucoma.

[0010] An object of the present invention is to provide a method of detecting a single nucleotide polymorphism involved in the onset of glaucoma, thereby predicting an onset risk of glaucoma, and a kit used in the detection method.

MEANS TO SOLVE THE PROBLEMS

[0011] The present inventors have found a single nucleotide polymorphism associated with the onset of glaucoma by a comprehensive analysis of known polymorphic sites existing on the genome (autosome) in glaucoma patients and non-patients without a family history of glaucoma, and further found an allele identified in a high frequency in glaucoma patients and an opposite allele thereof, and a genotype identified in a high frequency in glaucoma patients, which is a combination of each of the alleles, in the single nucleotide polymorphism. Furthermore, the present inventors have found that a determination on whether or not a sample donor is a person who is more likely to suffer from the onset of glaucoma can be made at an even higher precision by performing the determination in a combination of these plural single nucleotide polymorphisms associated with the onset of glaucoma. Thus, the present invention has been perfected thereby.

[0012] Concretely, the present invention relates to:

[1] a method of determining the presence or the absence of a glaucoma risk, including the steps of:

detecting *in vitro* an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence, in a sample from a subject, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto (step A), and

comparing the allele and/or the genotype detected in the step A with at least one of an allele and/or a genotype, containing a high-risk allele, in

the base sequences shown in SEQ ID NOs: 203 to 514 (step B),
wherein the presence of a glaucoma risk is determined in a case where the allele detected in the step A is the high-risk allele, or
wherein the presence of a glaucoma risk is determined in a case where the genotype detected in the step A is a homozygote of the genotype containing the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or
wherein the presence of a glaucoma risk is determined in a case where the genotype detected in the step A is a homozygote of the genotype containing the high-risk allele when the high-risk allele complies with a recessive genetic model;

[2] a method of determining the presence or the absence of a glaucoma risk, including the steps of:

detecting *in vitro*, in a sample from a subject, an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence in a nucleic acid molecule, wherein the nucleic acid molecule comprises at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto (step C1), or

detecting *in vitro*, in a sample from a subject, an allele and/or a genotype of a single nucleotide polymorphism, using a nucleic acid molecule comprising a base sequence containing at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto (step C2), and

comparing the allele and/or the genotype detected in the step C1 or C2 with at least one nucleic acid molecule comprising an allele and/or a genotype, containing a high-risk allele, in the base sequences shown in the SEQ ID NOs: 203 to 514 (step D),

wherein the presence of a glaucoma risk is determined in a case where the allele detected in the step C1 or C2 is the high-risk allele, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in the step C1 or C2 is a homozygote of the genotype containing the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in the step C1 or C2 is a homozygote of the genotype containing the high-risk allele when the high-risk allele complies with a recessive genetic model;

[3] a kit of determining the presence or the absence of a glaucoma risk, containing

a nucleic acid molecule comprising at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, wherein the nucleic acid molecule comprises a single nucleotide polymorphism which is located on a 31st base of a base sequence, and/or

a nucleic acid molecule comprising a base sequence containing at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence

thereto,

wherein the kit is for use in detecting *in vitro* an allele and/or a genotype of a single nucleotide polymorphism in a sample from a subject;

[4] a method of determining the presence or the absence of a glaucoma risk, including the following steps of:

step (i): extracting a nucleic acid molecule from a sample from a subject,

step (ii): detecting an allele of a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, for the nucleic acid molecule extracted in the step (i), and

step (iii): determining the presence or the absence of a glaucoma risk, based on the allele detected in the step (ii);

[5] use of a nucleic acid molecule for determining a glaucoma risk, wherein the nucleic acid molecule comprises at least one base sequence, the base sequence being a base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, wherein the nucleic acid molecule comprises an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence;

[6] a method of diagnosing glaucoma, including the steps of:

detecting *in vitro* an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence, in a sample from a subject, wherein the base sequence is at least one base

sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto (step E), and

comparing the allele and/or the genotype detected in the step E with at least one of an allele and/or a genotype, containing a high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 514 (step F),

wherein the subject is diagnosed as glaucoma in a case where the allele detected in the step E is the high-risk allele, or

wherein the subject is diagnosed as glaucoma in a case where the genotype detected in the step E is a homozygote of the genotype containing the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or

wherein the subject is diagnosed as glaucoma in a case where the genotype detected in the step E is a homozygote of the genotype containing the high-risk allele when the high-risk allele complies with a recessive genetic model; and

[7] a method of determining an onset risk of glaucoma, including the following steps of:

step (I): determining the presence or the absence of the onset risk of glaucoma, with the method as defined in claim 3,

step (II): determining that a further risk determination is needed, in a case where the presence of the onset risk is determined in the step (I) for any one of single nucleotide polymorphisms, and

step (III): further determining the presence or the absence of the onset risk of glaucoma, with the method as defined in claim 5, in a case of being

determined that a further risk determination is needed in the step (II).

EFFECTS OF THE INVENTION

[0013] According to the method of the present invention, the presence or the absence of the onset risk of glaucoma in a sample donor can be determined, and further the level of the risk can be predicted, by analyzing an allele or a genotype of a single nucleotide polymorphism in the present invention contained in a nucleic acid molecule derived from the genome existing in a sample. A sample donor can be provided with a preventive measure for glaucoma, or can receive appropriate treatments, on the basis of this risk. In addition, according to the method of the present invention, a sample donor who is suspected of glaucoma, having an allele or a genotype containing a single nucleotide polymorphism in the genome that is identified in a high frequency in glaucoma patients, can be given a detailed examination on whether or not the donor is with early glaucoma, which is difficult to be determined sufficiently by an intraocular pressure or an ocular fundus photograph, and can be started with a treatment at an early stage in a case where the donor is diagnosed as glaucoma.

BEST MODE FOR CARRYING OUT THE INVENTION

[0014] The present invention is a method of determining the presence or the absence of a glaucoma risk, including the step of detecting *in vitro* an allele and/or a genotype having at least one single nucleotide polymorphism using at least one single nucleotide polymorphism (hereinafter may be referred to as SNP) contained in a base sequence selected from the group consisting of

specified base sequences or a complementary sequence thereto, wherein the method of determining the presence or the absence of a glaucoma risk further includes the step of:

comparing the allele and/or the genotype detected in the step with at least one of an allele and/or a genotype, containing a high-risk allele, in the specified base sequences, in a sample from a subject,

wherein the presence of a glaucoma risk is determined in a case where the detected allele is the high-risk allele, or

wherein the presence of a glaucoma risk is determined in a case where the detected genotype is a homozygote of the genotype containing the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the detected genotype is a homozygote of the genotype containing the high-risk allele when the high-risk allele complies with a recessive genetic model.

A great feature of the present invention resides in that a single nucleotide polymorphism associated with the onset of glaucoma is found, further that in the single nucleotide polymorphism, an allele identified in a high frequency in glaucoma patients and an opposite allele thereof, and a genotype, which is a combination of each of the alleles identified in a high frequency in glaucoma patients are found, and used. The polymorphism as used herein refers to a matter that a diversity is found in sequences of a specified location on the genome in a certain organism species, and a site at which the polymorphism exists (hereinafter also referred to as polymorphic

site) refers to a site on the genome that a single nucleotide polymorphism is found.

[0015] In addition, the allele as used herein refers to each of types having a different base from each other that can be taken in a certain polymorphic site. The genotype as used herein refers to a combination of opposite alleles in a certain polymorphic site. Further, in a certain polymorphic site, there are three types for a genotype which is a combination of opposite alleles, wherein a combination of the same alleles is referred to as a homozygote, and a combination of different alleles is referred to as a heterozygote.

[0016] The opposite allele as used herein refers to another allele corresponding to a specified allele among the alleles constituting a certain single nucleotide polymorphism.

[0017] In the present invention, the single nucleotide polymorphism associated with glaucoma refers to a single nucleotide polymorphism associated with the onset of glaucoma or a single nucleotide polymorphism associated with the progression of glaucoma. In other words, the single nucleotide polymorphism associated with the onset of glaucoma refers to a single nucleotide polymorphism in which each allele or each genotype frequency in the single nucleotide polymorphism significantly differs in a statistical analysis at a given p-value between glaucoma patients and non-patients; and the single nucleotide polymorphism associated with the progression of glaucoma refers to a single nucleotide polymorphism in which each allele or each genotype frequency in the single nucleotide polymorphism significantly differs in a statistical analysis at a given p-value

between the progressive glaucoma cases and the nonprogressive glaucoma cases.

[0018] In the present invention, the high-risk allele refers to an allele having a higher frequency in a glaucoma patient group than that of a non-patient group among each of the alleles of the single nucleotide polymorphism associated with glaucoma. On the other hand, in the present invention, the low-risk allele refers to an allele opposite to the high-risk allele in a certain polymorphic site.

[0019] In addition, the homozygote and the heterozygote of a genotype are defined in the same manner as in the high-risk allele and the low-risk allele. In other words, in certain polymorphic sites, a combination of high-risk alleles or low-risk alleles themselves is referred to a homozygote, and a combination of a high-risk allele and a low-risk allele is referred to as a heterozygote.

[0020] An embodiment where allele frequencies of the glaucoma patient group and the non-patient group are statistically compared is referred to as an allele model, and an embodiment where genotype frequencies thereof are compared is referred to as a genotype model. There are a dominant genetic model and a recessive genetic model in the genotype models, wherein the former means an embodiment where both a homozygote of high-risk alleles and a heterozygote are involved with the onset risk, and the latter means an embodiment where a homozygote of a high-risk allele is involved with the onset risk.

[0021] In the present invention, the glaucoma risk refers to a risk concerning glaucoma. The onset risk of glaucoma refers to a possibility of the future

onset of glaucoma determined by susceptibility to a disease. In the present invention, the prediction of a risk refers to a determination of the presence or the absence of a future risk at the present stage, or determining the level of a future risk at the present stage.

[0022] Also, the glaucoma as used herein means preferably open-angle glaucoma (OAG) or normal tension glaucoma (NTG), and the open-angle glaucoma, when used without specifying otherwise, means primary open-angle glaucoma (POAG) in a narrow sense, without embracing normal tension glaucoma.

[0023] A method of identifying a single nucleotide polymorphism associated with glaucoma will be explained hereinbelow.

[0024] In the present invention, in selecting the single nucleotide polymorphism associated with glaucoma, in particular, a candidate single nucleotide polymorphism is selected by the steps including extracting a total DNA from blood of each of glaucoma patients diagnosed as primary open-angle glaucoma or normal tension glaucoma and non-patients diagnosed as not being with glaucoma and determined to have no family history of glaucoma according to a medical interview (also referred to as control individuals), and comparing allele or genotype frequencies of individual single nucleotide polymorphisms in the glaucoma patients and the non-patients using known single nucleotide polymorphisms of about 500,000 on the human genome as an index. Further, the allele or genotype frequencies of individual single nucleotide polymorphisms for the single nucleotide polymorphisms that are selected as candidates are obtained for glaucoma patients and non-patients that are different from the sample

groups mentioned above. By combining these results, a single nucleotide polymorphism of which difference in frequencies is recognized with high statistical significance is found. Here, a group composed of the glaucoma patients is referred to as a glaucoma patient group, and a group composed of the non-patients is referred to as a non-patient group. By using the alleles or genotypes having a single nucleotide polymorphism associated with the onset of glaucoma found according to these analyses, the determination of the presence or the absence of the onset risk of glaucoma, and the prediction of the level of an onset risk can be enabled. Although the details will be explained in the section of Examples, a single nucleotide polymorphism associated with glaucoma disclosed in the present invention can be identified according to a method given below.

[0025] (Identification of Single Nucleotide Polymorphism Associated with Glaucoma)

First, a total DNA is extracted from blood of each of patients diagnosed as glaucoma and non-patients determined to have no family history of glaucoma. The total DNA in blood can be extracted by any known methods; for example, a DNA can be extracted by binding a DNA eluted by lysing cells to surfaces of magnetic beads coated with silica, and separating and collecting the DNA utilizing a magnetic force.

[0026] The kind of a base in a single nucleotide polymorphism in the extracted DNA sample, i.e. an allele having a single nucleotide polymorphism can be identified by any methods, including, for example, a method using an immobilized probe described later, or the like. Upon the identification, a probe used in the detection can be designed on the basis of

the sequence information of a single nucleotide polymorphism of interest and surrounding sequences thereof. When the probe is designed, the sequence information obtained from the database for known single nucleotide polymorphisms such as dbSNP can be used as a reference. As to a probe used in the detection of a single nucleotide polymorphism, the detection can be made with either a probe complementary to a sense strand of the genome, or a probe complementary to an antisense strand. Although the details will be described later, a kit in which probes capable of detecting single nucleotide polymorphisms existing on the human genome are immobilized in large amounts, thereby making it possible to determine alleles of numerous single nucleotide polymorphisms in a single operation is commercially available, and whereby an allele in a sample can be efficiently determined using the kit. Many of the kits also have the constitution that the alleles that are opposite to each other contained in one sample are detected in a single operation, so that a genotype can be determined.

[0027] The single nucleotide polymorphism associated with glaucoma can be determined by previously identifying an allele existing on DNA from glaucoma patients and non-patients according to the method as mentioned above, statistically comparing each of the allele frequencies and the genotype frequencies in a glaucoma patient group against a non-patient group, and determining whether or not a difference that a p-value is below the significance level as defined by a given standard is caused in at least one of the allele frequencies and the genotype frequencies. In a case where the difference is caused, the allele frequencies or genotype frequencies for these

factors in the glaucoma patient group and the non-patient group are compared to determine whether any of the alleles or genotypes are identified in a high frequency in the glaucoma patient group.

[0028] In the statistical analysis, for example, a chi-square test can be used. Type I error caused by multiple comparisons can be corrected by a known correction method, for example, Bonferroni method. In a case where a correction is based on Bonferroni correction, for example, a significance level can be obtained by dividing a p-value of 5×10^{-2} by the number of multiple comparisons, i.e. the number of polymorphisms to be compared in the chi-square test. A single nucleotide polymorphism below the significance level determined in the manner described above can be selected as a more preferred single nucleotide polymorphism, and a method used in other known multiple corrections, for example, an FDR method or a permutation method may also be used in the selection of a preferred single nucleotide polymorphism. However, a known multiple correction method such as Bonferroni correction is a method presupposing that the phenomenon of carrying out multiple analyses is completely independent; on the other hand, there are some cases where the phenomenon is not completely independent because linkage disequilibrium is found in a single nucleotide polymorphism as described later. In other words, in the case as mentioned above, it is considered that overcorrection takes place when correction is carried out according to Bonferroni method. Especially, in the analysis of a single nucleotide polymorphism over the whole genome as in the present invention, factors to be statistically compared are highly enormous in number; therefore, a p-value serving as a standard is drastically

lowered when multiple corrections are performed, so that a possibility of an oversight of a single nucleotide polymorphism associated with a disease becomes high (Schymick J C et al., *Lancet Neurology*. 2007: **6**: 322-8; Van Steen K et al., *Nature Genetics*. 2005: **37**: 683-691). An academically preferred multiple correction method is not yet established, and as other correction methods, correction by another known correction method can be carried out, or a significance level can be set at any appropriate levels within the range that would not be below the significance level according to the Bonferroni correction. When any appropriate level is set, for example, the significance level in a case where about 500,000 single nucleotide polymorphisms are analyzed repeatedly of 5×10^{-2} is used, more preferably 1×10^{-2}, even more preferably 1×10^{-3}, even more preferably 1×10^{-4}, even more preferably 3×10^{-5}, and even more preferably 1×10^{-5}. As described later, the adjustment of the significance level as described above is useful from the fact that it is confirmed that a single nucleotide polymorphism identified to be associated with glaucoma in the present invention exists continuously in a certain region on the genome.

[0029] In addition, in general, it is known that type I error and the statistical power are inversely proportional. A method of maintaining the statistical power while lowering type I error includes a method of performing a single nucleotide polymorphism analysis in two divided steps (Skol A.D. et al., *Nature Genetics*. 2006: **38:** 209-213). For example, in a case where a single nucleotide polymorphism analysis is carried out for a fixed number of samples, firstly, analysis of enormous single nucleotide polymorphisms over the whole genome for a part of samples thereof is carried out as

primary analysis, and secondly, analysis of single nucleotide polymorphisms narrowed down in the first analysis to some degree is carried out for the remainder samples as secondary analysis. In this case, in both of the analyses, a single nucleotide polymorphism may be selected so as to have a relatively low p-value, for example, 0.05; preferably, a single nucleotide polymorphism serving as a candidate in the first analysis may be selected at a given significance level, and the selected single nucleotide polymorphism may be further analyzed using another sample. On the other hand, it is more preferable that the results of the first analysis and the secondary analysis are not individually statistically analyzed but these results are combined and analyzed. In the case as mentioned above, the two analytical results can be combined by a known method of meta-analysis, for example, Mantel-Haenszel method (Mantel N et al., *Journal of the National Cancer Institute* 1959: **22:** 719-748). When the analytical results are combined according to a meta-analysis method such as Mantel-Haenszel method, the significance level for the selection of a single nucleotide polymorphism in individual analysis is not needed to be at the level of Bonferroni correction, and the significance level may be set by taking narrowing-down efficiency or the like into consideration. On the other hand, upon determination of whether or not a single nucleotide polymorphism is significant by a p-value combined by a meta-analysis method such as Mantel-Haenszel method, it is preferable to use a significance level with considering multiple comparisons. Here, the Mantel-Haenszel method refers to a method of combining analytical results by weighting the results obtained by multiple analyses when a chi-square test or the like is carried

out. A statistical parameter combined by Mantel-Haenszel method includes, in addition to the p-value, an odds ratio described later or the like.

[0030] A single nucleotide polymorphism for the detection of the allele or genotype associated with glaucoma is preferably a single nucleotide polymorphism having a p-value of 1×10^{-3} or less, more preferably a single nucleotide polymorphism having a p-value of 3×10^{-4} or less, even more preferably a single nucleotide polymorphism having a p-value of 1×10^{-4} or less, and even more preferably a single nucleotide polymorphism having a p-value of 3×10^{-5} or less, when the single nucleotide polymorphism for the detection is based on the results obtained in a single analysis using, for example, a microarray in which about 500,000 single nucleotide polymorphisms are detected in a single operation. When the results are obtained by combining multiple analytical results according to a meta-analysis method such as Mantel-Haenszel method, the single nucleotide polymorphism for the detection is preferably a single nucleotide polymorphism having a p-value of 1×10^{-2} or less, more preferably a single nucleotide polymorphism having a p-value of 3×10^{-3} or less, even more preferably a single nucleotide polymorphism having a p-value of 1×10^{-4} or less, and even more preferably a single nucleotide polymorphism having a p-value of 3×10^{-4} or less.

[0031] It is preferable that a sufficient number of single nucleotide polymorphisms are analyzed, in order to obtain highly reliable results upon analysis. For example, a polymorphic site having a low determination rate of each single nucleotide polymorphism to the whole sample, i.e. a low call rate, is likely to have a high rate of typing errors, so that the reliability is not

high. Therefore, it is preferable that the analysis is performed using a single nucleotide polymorphism having a sufficiently high call rate. As to the call rate that serves as a standard of accepting or rejecting a single nucleotide polymorphism, for example, it is preferable that a single nucleotide polymorphism showing a call rate of preferably 70%, more preferably 75%, even more preferably 80%, even more preferably 85%, and even more preferably 90% or more is employed.

[0032] Besides them, factors that can be considered upon analysis are Hardy-Weinberg's equilibrium and minor allele frequency.

[0033] The Hardy-Weinberg's equilibrium means that a distribution frequency of the opposite alleles in a certain gene locus is constant even after generations, in a genetically homogeneous population having a sufficient number of individuals formed by panmixia without a mutation or selection pressure. Whether or not the Hardy-Weinberg's equilibrium is established can be confirmed by some known methods, for example, a chi-square test and a direct probability calculation method of Fischer. In a population of a sufficient number, it is considered that the Hardy-Weinberg's equilibrium is established by a single panmixia, i.e. the Hardy-Weinberg's equilibrium is established as long as inbreeding does not exist. Therefore, generally, under the assumption that the Hardy-Weinberg's equilibrium is established in the general population, analysis of the Hardy-Weinberg's equilibrium is used for the purpose of detecting errors of genotype determination of a sample. However, even if the Hardy-Weinberg's equilibrium is established as a whole, when a certain genotype is unevenly distributed in a disease group or a control group in a

certain gene locus, for example, there are some cases where a certain genotype has a predominant influence on a disease, or the like; therefore, said analysis can be omitted, in a case where a search for disease-associated genes is carried out.

[0034] The minor allele frequency refers to an allele frequency with a lower frequency of the frequencies of two alleles in a case where single nucleotide polymorphisms are contained in two alleles. It is possible that a threshold thereof is arbitrarily set. As mentioned above, it is preferable that a single nucleotide polymorphism having a minor allele frequency of below 1% is rejected, because the concept of a single nucleotide polymorphism is in that the single nucleotide polymorphism has a minor allele frequency exceeding about 1%. On the other hand, there is a possibility that an allele having a very high or very low allele frequency in a disease group has a predominant influence on a disease. It is considered that polymorphisms of which relative involvement to a disease is relatively low are multiply involved in search of polymorphisms causative of multi-factorial diseases; therefore, for the purpose of searching the polymorphisms as mentioned above, an analysis excluding a frequency of a certain level or lower, for example, a minor allele of less than 5% can be a preferred means. On the other hand, in order to search polymorphisms that have predominant influences on a disease, it is effective not to reject the polymorphisms of the minor allele frequency.

[0035] From the allele or genotype associated with glaucoma thus obtained, the information such as a location on the genome at which a single nucleotide polymorphism exists, the sequence information, a gene in which

a single nucleotide polymorphism exists or a gene existing in the neighborhood, discrimination of intron or exon or a function thereof in a case where the single nucleotide polymorphism exists on the gene, and a homologous gene in other organism species can be obtained, by referring to the database of known sequences such as GenBank, or the database of known single nucleotide polymorphisms such as dbSNP, whereby a nucleic acid molecule used in the present invention is obtained, on the basis of the information, and a probe or the like used in the present invention can be designed.

[**0036**] As the criteria for determining the presence or the absence of a risk in a single nucleotide polymorphism associated with glaucoma determined as mentioned above, a high-risk allele is defined. As mentioned above, in the present invention, the high-risk allele refers to an allele having a higher frequency in a glaucoma patient group than that of a non-patient group among each of the alleles of single nucleotide polymorphisms associated with glaucoma, and in the present invention, the low-risk allele refers to an allele opposite to a high-risk allele in a certain polymorphic site.

[**0037**] The determination of the presence or the absence of an onset risk can be carried out according to an allele or a genotype.

[**0038**] In a case where the determination is carried out according to an allele, the presence of the onset risk is determined for the single nucleotide polymorphism because of having a high-risk allele.

[**0039**] In a case where the determination is carried out according to a genotype, the onset risk is determined by taking into consideration whether the high-risk allele complies with a dominant genetic model, or with a

recessive genetic model. In a certain polymorphic site, when the frequency of a homozygote of the high-risk allele and a heterozygote is significantly high in a glaucoma patient group as compared to that of a non-patient group, it is said that these genotypes comply with a dominant genetic model. The presence of an onset risk is determined for the single nucleotide polymorphism in a case where the genotype is a homozygote of the high-risk allele or a heterozygote, when the high-risk allele complies with a dominant genetic model. On the other hand, when the frequency of a homozygote of the high-risk allele is significantly high in a glaucoma patient group as compared to that of a non-patient group, it is said that these genotypes comply with a recessive genetic model. The presence of an onset risk is determined for the single nucleotide polymorphism in a case where the genotype is a homozygote of the high-risk allele, when the high-risk allele complies with a recessive genetic model.

[0040] The determination of the presence or the absence of an onset risk can be also carried out according to a low-risk allele. As mentioned above, the low-risk allele is an allele opposite to a high-risk allele, i.e. an allele identified in a high frequency in a non-patient group. In a case where the determination is carried out according to an allele, the presence of an onset risk is determined for the single nucleotide polymorphism because of not having a low-risk allele.

[0041] The same applies to a case of a genotype as well. When the determination is carried out according to a genotype, an onset risk is determined by taking into consideration whether the low-risk allele complies with a dominant genetic model, or with a recessive genetic model.

In a certain polymorphic site, when the frequency of a homozygote of the low-risk allele and a heterozygote is significantly high in a non-patient group as compared to that of a glaucoma patient group, it is said that these genotypes comply with a dominant genetic model. The presence of an onset risk is determined for the single nucleotide polymorphism in a case where the genotype is not a homozygote of the low-risk allele or a heterozygote, when the low-risk allele complies with a dominant genetic model. On the other hand, when the frequency of a homozygote of the low-risk allele is significantly high in a non-patient group as compared to that of a glaucoma patient group, it is said that these genotypes comply with a recessive genetic model. The presence of an onset risk is determined for the single nucleotide polymorphism in a case where the genotype is not a homozygote of the low-risk allele, when the low-risk allele complies with a recessive genetic model.

[0042] As to whether the determination is carried out using a method for any of an allele, a dominant genetic model, and a recessive genetic model, the same method as in a method where a p-value judged to be significant is obtained can be used. In a case where the methods where a p-value judged to be significant is obtained exist in a plurality for one single nucleotide polymorphism, any of these methods may be used, and preferably, the same method as in a method where the lowest p-value is calculated is used.

[0043] Generally, in a single nucleotide polymorphism associated with a disease, a relative risk or an odds ratio is used as an index of an extent of the strength of the association that exists between one allele or genotype and the presence or the absence of a disease.

[0044] Generally, the relative risk refers to a ratio of an incidence rate in a group with a risk factor to an incidence rate in a group without a risk factor. On the other hand, the odds ratio generally refers to a ratio obtained by dividing odds, which is a ratio of a proportion of individuals with a risk factor to a proportion of individuals without a risk factor in a patient group, by odds obtained in a non-patient group in the same manner, which is in many cases used in a case-control study as in the present invention. The odds ratio in the present invention is determined on the basis of the allele frequency or the genotype frequency. In other words, the odds ratio of a single nucleotide polymorphism associated with the onset refers to a value obtained by calculating a quotient obtained in a ratio of an allele or genotype frequency to another allele or genotype frequency in a glaucoma patient group, over a ratio of frequencies obtained in the same manner in a non-patient group. In the present invention, an extent to which an onset risk of glaucoma increases can be predicted by comparing a case of having a certain allele or genotype to a case of having an allele or genotype other than the above, using these indices. For example, when an odds ratio of a certain allele in a certain single nucleotide polymorphism is greater than 1, the allele is an allele found in a high frequency in a glaucoma patient group, in which the larger the odds ratio, the higher the onset risk of glaucoma for a sample donor having the allele. On the other hand, when an odds ratio of an allele is less than 1, the allele is an opposite allele of the allele that is identified in a high frequency in a disease, in which the smaller the odds ratio, the lower the onset risk of glaucoma for a sample donor having the

allele. The risk of a disease can also be predicted in the same manner for a genotype.

[0045] In the present invention, the value of the odds ratio would be always greater than 1 by obtaining an odds ratio based on the high-risk allele. The risk prediction in a combination of plural single nucleotide polymorphisms is facilitated by defining so that the odds ratio is greater than 1 when having the high-risk allele as mentioned above.

[0046] Although the details are shown by the numerical formulas in the section of Examples, in a case where an odds ratio is obtained for an allele, the odds ratio may be a value obtained by calculating a quotient obtained in a ratio of the high-risk allele frequency to the low-risk allele frequency in a glaucoma patient group, over a ratio of the high-risk allele frequency to the low-risk allele frequency in a non-patient group. In order to obtain an odds ratio in a genotype, the odds ratio is obtained by taking into consideration whether the high-risk allele complies with a dominant genetic model, or with a recessive genetic model. In other words, a homozygote of the high-risk allele and a heterozygote becomes a risk factor when the high-risk allele complies with a dominant genetic model, and a homozygote of the high-risk allele becomes a risk factor when the high-risk allele complies with a recessive genetic model. Therefore, when the high-risk allele complies with a dominant genetic model, the odds ratio may be obtained by obtaining the sum of the homozygote frequency of the high-risk allele and the heterozygote frequency in a glaucoma patient group, and calculating a quotient obtained in a ratio of the above sum to the homozygote frequency of the low-risk allele, over a ratio of frequencies obtained in the same

manner in a non-patient group. When the high-risk allele complies with a recessive genetic model, the odds ratio may be obtained by obtaining the sum of the homozygote frequency of the low-risk allele and the heterozygote frequency in a glaucoma patient group, and calculating a quotient obtained in a ratio of the homozygote frequency of the high-risk allele to the above sum, over a ratio of frequencies obtained in the same manner in a non-patient group.

[0047] Further, the reliability of a single nucleotide polymorphism used in the prediction of a risk can be confirmed with an odds ratio. As mentioned above, the meaning for the prediction of a risk reverses in a case where the odds ratio is 1 or more and a case where the odds ratio is 1 or less. Therefore, in a case where a calculated 95% confidence interval of the odds ratio includes 1, it cannot be said that the reliability for the prediction of a risk for the odds ratio as mentioned above would be high.

[0048] In addition, in a case where an onset risk of glaucoma is predicted by a combination of single nucleotide polymorphisms of the present invention, the level of the risk can be predicted by using the level of the odds ratio.

[0049] In the odds ratio according to an allele, the odds ratio of combined two or more single nucleotide polymorphisms can be calculated according to the following formula:

$$(RA1_{comb}RA2_{comb})/(RA3_{comb}RA4_{comb})$$

wherein

$RA1_{comb}$: an allele frequency in a case where at least one allele is a high-risk allele in a glaucoma patient group;

$RA2_{comb}$: an allele frequency in a case where all the alleles are low-risk alleles in the glaucoma patient group;

$RA3_{comb}$: an allele frequency corresponding to $RA1_{comb}$ in a non-patient group; and

$RA4_{comb}$: an allele frequency in a case where all the alleles are low-risk alleles in the non-patient group.

[0050] For example, in a case where two single nucleotide polymorphisms associated with the onset risk of glaucoma are combined, an odds is determined by dividing the frequencies in a glaucoma patient group all having high-risk alleles of a single nucleotide polymorphism, or having any one of high-risk alleles, by the frequency in the glaucoma patient group not having any one of high-risk alleles. The odds ratio in a case of a combination of the single nucleotide polymorphisms can be determined by calculating a ratio of said odds to the odds of that in a non-patient group obtained in the same manner.

[0051] In order to obtain an odds ratio according to a combination in cases of genotypes, the odds ratio is obtained by taking into consideration whether the high-risk allele complies with a dominant genetic model, or with a recessive genetic model, in the same manner as that alone.

[0052] In the odds ratio according to a dominant genetic model, the odds ratio of combined two or more single nucleotide polymorphisms can be calculated according to the following formula:

$$(RGd1_{comb}RGd2_{comb})/(RGd3_{comb}RGd4_{comb})$$

wherein

$RGd1_{comb}$: a frequency at which at least one genotype is a homozygote of a high-risk allele or a heterozygote, in a glaucoma patient group;

$RGd2_{comb}$: a frequency at which all the genotypes are homozygotes of a low-risk allele in the glaucoma patient group;

$RGd3_{comb}$: a frequency of the genotype corresponding to $RGd1_{comb}$ in a non-patient group; and

$RGd4_{comb}$: a frequency at which all the genotypes are homozygotes of a low-risk allele in the non-patient group.

[0053] For example, in a case where both the high-risk alleles of the two single nucleotide polymorphisms comply with a dominant genetic model, the odds ratio may be obtained by calculating a quotient obtained in a ratio of the frequency at which any of the two single nucleotide polymorphisms are a homozygote of a high-risk allele or a heterozygote in a glaucoma patient group to the frequency at which both the two single nucleotide polymorphisms are a homozygote of a low-risk allele in the glaucoma patient group, over a ratio of frequencies of those obtained in the same manner in a non-patient group.

[0054] In the odds ratio according to a recessive genetic model, the odds ratio of combined two or more single nucleotide polymorphisms can be calculated according to the following formula:

$$(RGr1_{comb}RGr2_{comb})/(RGr3_{comb}RGr4_{comb})$$

wherein

$RGr1_{comb}$: a frequency at which at least one genotype is a homozygote of a high-risk allele, in a glaucoma patient group;

$RGr2_{comb}$: a frequency at which all the genotypes are homozygotes of a low-risk allele in the glaucoma patient group;

$RGr3_{comb}$: a frequency of the genotype corresponding to $RGr1_{comb}$ in a non-patient group; and

$RGr4_{comb}$: a frequency at which all the genotypes are homozygotes of a low-risk allele in the non-patient group.

[0055] For example, in a case where both the high-risk alleles of the two single nucleotide polymorphisms comply with a recessive genetic model, the odds ratio may be obtained by calculating a quotient obtained in a ratio of the frequency at which any of the two single nucleotide polymorphisms are a homozygote of a high-risk allele in a glaucoma patient group to the frequency at which both the two single nucleotide polymorphisms are a homozygote of a low-risk allele in the glaucoma patient group, over a ratio of frequencies of those obtained in the same manner in a non-patient group. Here, the odds ratio for a combination of single nucleotide polymorphisms can also be calculated by combining single nucleotide polymorphisms having different genetic forms.

[0056] Generally, the odds ratio increases by combining two or more single nucleotide polymorphisms, as compared to a case where these single nucleotide polymorphisms are used alone. Therefore, by a combination of two or more single nucleotide polymorphisms, a sample donor with a higher onset risk of glaucoma would be identified, whereby the improvement in the precision of the prediction can be made possible, as compared to the case where a single nucleotide polymorphism is used alone.

[0057] In order to confirm the improvement of the precision of the prediction of an onset risk of glaucoma according to a combination of single nucleotide polymorphisms in the present invention, a multivariate analysis can be employed. As the multivariate analysis method, a method well known to one of ordinary skill in the art such as logistic regression analysis method, discriminant analysis method, multiple linear regression analysis method, or proportional hazard analysis method can be employed, among which the logistic regression analysis method is effective in a case where a dichotomous variable such as the presence or the absence of an onset risk of glaucoma is handled.

[0058] The logistic regression analysis method refers to a method of analyzing a degree to which multiple independent variables (Π) contribute in order to describe a single dependent variable (Φ) (*Wakariyasui Igaku Tokeigaku (Easy Medical Statistics)*, pp. 148-179, Toshio MORIZANE, Medical Tribune). By performing the logistic regression analysis, a regression coefficient (λ) for each independent variable can be obtained, and this regression coefficient can be utilized as an index showing a degree to which each independent variable describes a dependent variable. In addition, a dependent variable on each obtained independent variable can be calculated by substituting this regression coefficient into the following formula:

$$\Phi = 1 / \{1 + \exp[- (\lambda 0 + \lambda 1 \Pi 1 + \lambda 2 \Pi 2 + \lambda 3 \Pi 3 + \ldots)]\}$$

Here, when the logistic regression analysis is performed, the independent variables Π used in analysis can be previously narrowed down using a

stepwise method or the like. The stepwise method refers to a method for selecting independent variables Π so as to maximize the regression coefficients by adding an optional independent variable Π. In other words, it means that after the regression coefficient is maximized by adding an arbitrary independent variable Π, the same outcome is obtained even if another independent variable Π is further added.

[0059] In the present invention, by combining any two or more single nucleotide polymorphisms determined to be involved in the onset of glaucoma, the extent to which the precision of the prediction of an onset risk is improved can be known, as compared to that where each of the single nucleotide polymorphisms is used alone. Concretely, the above formula is obtained according to logistic regression analysis by using each of any two or more single nucleotide polymorphisms as an independent variable Π (homozygote of one allele = 0, heterozygote = 1, homozygote of an opposite allele = 2). In each sample, a dependent variable Φ is calculated by substituting a variable for each single nucleotide polymorphism into this formula. When a dependent variable Φ is greater than a given threshold (for example, 0.5), this sample donor is determined to be a glaucoma patient. The determination results are collated with the matter of whether the sample donor having a single nucleotide polymorphism was actually the glaucoma patient. According to the combination of the two or more single nucleotide polymorphisms in the present invention, an improvement in a concordance proportion is confirmed, whereby the precision improvement by the combination can be confirmed.

[0060] In addition, the single nucleotide polymorphisms which exist in genetically sufficiently close locations to each other are inherited in linkage, not inherited independently, in some cases. In a certain population, a state in which a linkage as described above is held regardless of occurrence of a recombination by mating is referred to as a linkage disequilibrium, and a unit holding the linkage is referred to a haplotype block or an LD block.

[0061] In the experiment results by the present inventors, it is found that a single nucleotide polymorphism associated with glaucoma actually may exist in clusters in a relatively closely on the genome in some cases. It is considered that these regions belong to an LD block associated with glaucoma. In order to determine an LD block associated with glaucoma, the LD block can be determined by analyzing single nucleotide polymorphisms which exist in the region as many as possible by the method mentioned above, and applying an algorithm to determine an LD block, for example, an EM algorithm. In addition, when the single nucleotide polymorphism associated with glaucoma in the present invention belongs to a known LD block, the LD block can be considered as an LD block associated with glaucoma. Genome Browser provided on the internet web sites by California University at Santa Cruz, or the like can be consulted for a known LD block.

[0062] Because a single nucleotide polymorphism that belongs to an LD block associated with glaucoma is linked to a single nucleotide polymorphism associated with glaucoma identified according to the experiments of the present inventors, it can be considered that the single nucleotide polymorphism that belongs to an LD block associated with

glaucoma also associates with glaucoma in the same manner; therefore, the single nucleotide polymorphism is used in the prediction of an onset risk or progressive risk of glaucoma. In addition, by re-determining a sequence within the LD block associated with glaucoma, or a sequence surrounding the single nucleotide polymorphism associated with glaucoma that is identified according to the experiments by the present inventors, there is a possibility that an unknown single nucleotide polymorphism which is linked with the single nucleotide polymorphism, in other words, which is associated with the onset of glaucoma or the progression thereof, is found. Whether or not the found single nucleotide polymorphism is actually associated with the onset of glaucoma or the progress thereof can be determined by comparing an allele or genotype frequency of a disease group with that of a control group in the same manner as explained above.

[0063] In the present invention, an intronic single nucleotide polymorphism (iSNP) refers to one in which a single nucleotide polymorphism is identified in intron. A coding single nucleotide polymorphism (cSNP) refers to one that is accompanied by a change in an amino acid sequence, such as a codon in which the single nucleotide polymorphism is mutated to a codon encoding other amino acids or a termination codon, among those in which single nucleotide polymorphisms exist in regions translated in a protein. A silent single nucleotide polymorphism (sSNP) refers to one without accompanying a change in an amino acid sequence, among those in which a single nucleotide polymorphism is identified in a coding region. A genomic single nucleotide polymorphism (gSNP) refers to one in which a single nucleotide polymorphism exists in a region not encoding the gene on the

genome. A regulatory polymorphism (rSNP) refers to a single nucleotide polymorphism existing in a site that is thought to be involved in the transcriptional regulation.

[0064] As described above, a single nucleotide polymorphism may exist in any location on the genome, any cases of which can be associated with a disease. In a case where a single nucleotide polymorphism exists in the intron or a non-coding region, there may be some cases where the single nucleotide polymorphism may influence a gene expression control, or splicing that takes place after the gene transcription or stability of mRNA. In a case where a single nucleotide polymorphism exists in the coding region, by substitution of its base, a codon corresponding to a certain amino acid may be changed to a codon corresponding to a different amino acid, or may undergo a change, for example, a change to a termination codon, or the like, which may lead to a change in the structure of a protein encoded thereby. Changes in expression levels or functions of genes by these changes consequently lead to changes in expression levels or functions of proteins encoded by the genes, which can be causes for various diseases. In a case where the genomic single nucleotide polymorphism is associated with a disease, there is a possibility that a region including the polymorphic site is actually translated, and influences in some way to other gene expressions. In a case where a silent single nucleotide polymorphism is associated with a disease, it is considered that a different polymorphism associating with the disease exists in the surrounding of the single nucleotide polymorphism, and the polymorphism and the silent single nucleotide polymorphism are linked, so that the association with the disease

is found. Similarly, in a single nucleotide polymorphism other than the silent single nucleotide polymorphism, even when the single nucleotide polymorphism itself is not a direct cause for glaucoma but links to a polymorphism which is the true cause for glaucoma existing in the surrounding, the association of these single nucleotide polymorphisms and glaucoma may be found in some cases. In the case as described above, as described later, a polymorphism which is causative of glaucoma can be found by re-sequencing the surrounding of the single nucleotide polymorphism in the present invention. However, in any case, these single nucleotide polymorphisms can be also used for the purpose of predicting an onset risk of glaucoma, regardless of whether or not these would be the true causes for the disease.

[0065] (Nucleic Acid Molecule Comprising Allele Associated with Glaucoma)

In an embodiment of the present invention, there are provided a nucleic acid molecule comprising a single nucleotide polymorphism associated with glaucoma, and a nucleic acid molecule having a sequence complementary to the nucleic acid molecule comprising a single nucleotide polymorphism associated with glaucoma.

[0066] The nucleic acid molecule comprising a single nucleotide polymorphism associated with glaucoma or the nucleic acid molecule having a sequence complementary to the nucleic acid molecule can be used as a marker for determining the level of the onset risk of glaucoma. Further, these nucleic acid molecules can be used as a probe for detecting an allele or

an opposite allele thereof identified in a high frequency in glaucoma patients, or determining a genotype, in the single nucleotide polymorphism. In addition, in a case where the single nucleotide polymorphism exists on exon or in the neighborhood thereof, these nucleic acid molecules can be used in the detection of transcripts of genes.

[0067] The nucleic acid molecule constituting the genome of an eukaryote is constituted by double strands of a sense strand and an antisense strand complementary to the sense strand. In other words, the single nucleotide polymorphism also exists on the sense strand and the antisense strand, and the nucleic acid molecule of the present invention embraces both of these strands because the detection of a single nucleotide polymorphism of both the strands is equally significant.

[0068] Nucleic acid molecules comprising any one of single nucleotide polymorphisms listed in Tables 1 and 2, Tables 5 to 25, Tables 26 to 28 and Tables 29 to 51 shown later, nucleic acid molecules comprising any single nucleotide polymorphisms existing in a region or on a gene determined by the linkage disequilibrium data or the like listed in Tables 3 and 4 shown later, and nucleic acid molecules complementary to these nucleic acid molecules are all embraced in the nucleic acid molecule of the present invention.

[0069] In an embodiment of the present invention, the nucleic acid molecule of the present invention is preferably nucleic acid molecules comprising a single nucleotide polymorphism listed in Tables 1 and 2, Tables 26 to 28 or Tables 52 to 62 shown later, or nucleic acid molecules complementary thereto, wherein

in a case where the single nucleotide polymorphism is gSNP, the nucleic acid molecule is a nucleic acid molecule comprising a sequence from a next base of a known single nucleotide polymorphism on an upstream side of the sense strand to a base before a known single nucleotide polymorphism on a downstream side, or a nucleic acid molecule comprising a sequence complementary thereto,

in a case where the single nucleotide polymorphism is iSNP, sSNP or cSNP, the nucleic acid molecule is a nucleic acid molecule comprising a full length of the gene on the genome including the single nucleotide polymorphism, a nucleic acid molecule comprising a sequence complementary thereto, and a nucleic acid molecule containing a complementary DNA (cDNA) molecule comprising the single nucleotide polymorphism or a sequence complementary thereto,

in a case where the single nucleotide polymorphism is rSNP, the nucleic acid molecule is a nucleic acid molecule comprising a sequence from a next base of a known single nucleotide polymorphism on an upstream side of the sense strand to a full length of the gene existing downstream of a promoter region in which the single nucleotide polymorphism exists, or a nucleic acid molecule comprising a sequence complementary thereto.

[0070] The nucleic acid molecule in the present invention is not limited whether it is a deoxyribonucleic acid, a ribonucleic acid, or a peptide nucleic acid, and a nucleic acid molecule comprising a mixed sequence thereof is also embraced in the present invention. In a case where a ribonucleic acid is used in the nucleic acid molecule in the present invention,

in the sequence of the nucleic acid molecule in the present invention (including a sequence complementary thereto), thymine may be read as uracil. In addition, these nucleic acid molecules may be subjected to chemical modifications as occasion demands, within the range that would not impair a function to be used in the present invention. In this case, the function refers to a function of accomplishing the purpose of using the nucleic acid molecule.

[0071] The nucleic acid molecule in the present invention can be synthesized by a known method, for example, a phosphoramidite method, on the basis of the sequence information disclosed herein, or the sequence information obtained by searching the information disclosed herein with the database. The nucleic acid molecule can be synthesized using a commercially available DNA synthesizer. In addition, the nucleic acid molecule in the present invention can be obtained from a sample comprising DNA from human according to a known method such as a PCR method, or in some nucleic acid molecules, can be obtained from a sample containing RNA from human according to a known method such as an RT-PCR method. As to primers that are necessary for the obtainment, one of ordinary skill in the art can design the primers on the basis of the sequence information disclosed herein, or the sequence information that can be searched from ID of the database disclosed herein. For example, in a case where a PCR method is used, primers having about 10 to about 30 bases that have sequences homologous to a part of the sequences of the nucleic acid molecule of interest can be used, and in a case where an RT-PCR method is used, the nucleic acid molecule can be obtained by carrying out reverse

transcription reaction using an oligo dT primer, or a random hexamer, or the like to prepare cDNA, and amplifying a sequence of interest in the cDNA by the PCR method mentioned above.

[0072] The nucleic acid molecule has a length of preferably from 16 to 55 bases, and more preferably from 23 to 27 bases or 47 to 53 bases. It is preferable that the nucleic acid molecule is a nucleic acid molecule containing the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto.

[0073] When a nucleic acid molecule comprising a single nucleotide polymorphism associated with the onset of glaucoma is selected, in a case where the nucleic acid molecule is selected based on the results obtained in a single analysis using a microarray in which, for example, 500,000 nucleic acid molecules are detected in a single operation, the nucleic acid molecule in the present invention is preferably a nucleic acid molecule having a p-value of 1×10^{-3} or less, more preferably a nucleic acid molecule having a p-value of 3×10^{-4} or less, even more preferably a nucleic acid molecule having a p-value of 1×10^{-4} or less, and even more preferably a nucleic acid molecule having a p-value of 3×10^{-5} or less. In a case where plural analytic results are combined and obtained according to a method of meta-analysis, such as Mantel-Haenszel method, the nucleic acid molecule is preferably a nucleic acid molecule having a p-value of 1×10^{-2} or less, more preferably a nucleic acid molecule having a p-value of 3×10^{-3} or less, even more preferably a nucleic acid molecule having a p-value of 1×10^{-3} or less, even more preferably a nucleic acid molecule having a p-value of 3×10^{-4} or less,

and even more preferably a nucleic acid molecule having a p-value of 1×10^{-4} or less.

[0074] As a different means of selecting a preferred nucleic acid molecule, a significance level is set according to a known multiple correction method, whereby a preferred nucleic acid molecule can be selected. In a case where a correction is based on Bonferroni correction, for example, a significance level can be obtained by dividing a p-value of 5×10^{-2} by the number of multiple comparisons, i.e. the number of polymorphisms to be compared in the chi-square test. A nucleic acid molecule having a single nucleotide polymorphism below the significance level thus obtained may be selected as a more preferred nucleic acid molecule. Upon the selection, Bonferroni correction may be performed using a p-value that is combined according to a method of meta-analysis, such as Mantel-Haenszel method, and the number of single nucleotide polymorphisms to be subject for the meta-analysis. Other known methods used in multiple corrections, for example, an FDR method or a permutation method may be used in the selection of a preferred nucleic acid molecule.

[0075] (Method of Detecting Single Nucleotide Polymorphism Associated with Glaucoma and Method of Predicting Onset Risk of Glaucoma)

Another embodiment of the present invention provides a method of detecting the presence or absence of an allele or genotype having a high frequency in glaucoma patients in a sample containing a nucleic acid molecule from the genome. The samples may be any ones so long as the nucleic acid molecules from the genome can be extracted, and for example, blood, white blood cells, hair root, hair, saliva, oral mucosa cells, skin,

tissues such as muscles or organs obtained by biopsy, or the like can be used.

[0076] As mentioned above, the nucleic acid molecule constituting the genome of an eukaryote is constituted by a sense strand and an antisense strand that are complementary to each other, and the determination of the allele of the single nucleotide polymorphism in the present invention can also be performed by detecting any one of the bases of the sense strand and the antisense strand of the polymorphic site.

[0077] As mentioned above, in the method of determining the presence or the absence of the allele or genotype in a sample containing a nucleic acid molecule, any means can be used. For example, hybridization is carried out using a probe specific to each of the alleles, preferably a probe in the present invention described later, which is designed based on the sequence information disclosed in the present invention, and each of the alleles can be detected by detecting signals therefor. In addition, each of the alleles opposite to each other, in other words, an allele having a high association to a disease for a certain single nucleotide polymorphism and an allele having a low association thereto are each provided with different labels, and a probe capable of hybridizing these alleles to a polymorphic site, or an immobilized probe such as a microarray in which each of alleles opposite to each other is immobilized is used, whereby each of the alleles opposite to each other contained in the same sample can be detected. In the constitution as described above, not only the alleles of the sample, but also the genotypes can be determined. In addition, in a case where an immobilized probe such as a microarray in which each of the alleles opposite to each other is

immobilized on the same carrier is used, a constitution that the hybridization is carried out in a single operation, and that the detection is carried out in a single operation can be also taken.

[0078] As another method of detecting a single nucleotide polymorphism in the present invention, the following method can be utilized. Examples of a method of hybridization using a probe are Taqman method, Invader (registered trademark) method, LightCycler method, cyclin probe method, MPSS method, beads-array method, and the like, and any of these methods can be employed. As to the probe for detecting the same allele, a more preferred probe may differ in some cases depending upon a method used in the detection. The determination of the allele or genotype of the single nucleotide polymorphism in the present invention does not depend upon the detection method, and it is preferable to use a suitable probe depending upon the detection method.

[0079] The Taqman method is a method of detecting a genetic polymorphism using an oligoprobe having a given length in which a fluorescent substance is bound to a 5'-side, and a quencher is bound to a 3'-side. The presence or absence of the polymorphism is determined by hybridizing a probe to a nucleic acid molecule having a polymorphism of interest, cutting off a part of the probe on the 5'-side by a PCR reaction, and measuring a fluorescent amount emitted by a fluorescent substance.

[0080] The Invader method is a method of detecting a genetic polymorphism using a probe (reporter) which has a sequence common to a 3'-side of a nucleic acid molecule having a polymorphism, but the sequence on a 5'-side being completely different therefrom, and a probe (invader) having only a

sequence common to a 5'-side. The nucleic acid molecules of interest and these two probes are hybridized, a product is then treated with a nuclease, a part of the cut-out reporter probe is hybridized with a probe for detection having a fluorescent substance and a quencher, a hybridization product is treated with a nuclease, and the fluorescent substance is released, whereby the presence or absence of the polymorphism is determined by a fluorescent amount thereof.

[0081] The LightCycler method is a method of detecting a polymorphism including the step of hybridizing a polymorphic detection probe having a fluorescent substance and an anchor probe having a quencher, to a nucleic acid molecule having a polymorphism previously amplified by PCR. If the hybridized DNA is gradually heated, the polymorphic detection probe is released when a given temperature is reached, and the presence or absence of the polymorphism is determined by measuring this fluorescent amount.

[0082] The cyclin probe method is a polymorphic analysis method utilizing a probe having a fluorescent substance or a quencher on each end of a DNA (DRD probe), wherein DNA sequences are bound in a manner that both ends of an RNA sequence having a sequence complementary to a polymorphic site of a nucleic acid molecule of interest are sandwiched. A DRD probe is hybridized to a nucleic acid molecule of interest previously amplified by PCR or the like, RNase is allowed to act on this complex, and a fluorescent dye is released, whereby the presence or absence of the polymorphism is determined by measuring this fluorescent amount.

[0083] The MPSS method is a method of performing polymorphic analysis using an encoded adaptor probe and a decoder probe. The encoded adaptor

probe is an oligo DNA having a 4-bases long protruding end on a 5'-side, subsequently a recognition sequence for a restriction enzyme BbvI, and a single-stranded sequence bound to a decoder probe on a 3'-side. On the other hand, the decoder probe is a single-stranded oligo DNA having a fluorescent substance on a 3'-side, and the decoder probe containing 4 different sequences, each sequence specifically hybridizing to a single encoded adaptor probe. The nucleic acid molecule having a polymorphism is previously immobilized on beads, and an initiation adaptor containing a recognition sequence for BbvI is bound thereto, to digest with BbvI to form a 4-bases long protruding end. The ligation with the encoded adaptor probe is carried out sequentially from a 3'-side of the protruding 4 bases, and the sequence of the bound encoded adaptor is detected with a specified decoder probe.

[**0084**] The beads array method is a method of performing the determination of a genotype including the step of combining beads to which a probe for allele detection and an oligonucleotide (address sequence) specifying the location information on the array of signals detected by the probe for allele detection are bound. For example, there are Golden Gate Assay using beads immobilized with only an address sequence (23 bases) of Illumina, and Infinium (registered trademark) Assay using beads in which probes (50 bases) for allele detection are bound to an address sequence (30 bases). In both the methods, which location on an array the probes for allele detection are bound can be known for each of the beads arranged arbitrarily on the array, on the basis of the address sequence.

[0085] The method of the Golden Gate Assay will be shown hereinbelow. In the detection of a single nucleotide polymorphism, two kinds of probes (allele-specific probes) specifically hybridizing to each allele, and a probe capable of specifically hybridizing to a sequence located 1 to 20 bases downstream on the 3'-side of the single nucleotide polymorphism (downstream sequence recognition probe) are used. In the downstream sequence recognition probe, an address sequence for specifying the location on the array is provided. In addition, these three probes contain a sequence to which universal primers described later are bound. The three probes are annealed with a genomic DNA, and a DNA polymerase and a ligase are added thereto. By carrying out an extension reaction and a ligation reaction, an allele-specific product ligating a gap between the allele-specific probe and the downstream sequence recognition probe is formed. A reaction for PCR is carried out with this allele-specific product as a template using two kinds of fluorescent-labeled universal primers, each being specific to each allele, and a universal primer bound to the downstream sequence recognition probe. A labeled PCR product is hybridized to an oligonucleotide immobilized on beads via an address sequence. The fluorescence on the beads is detected with a confocal laser scanner, thereby determining an allele and a genotype.

[0086] The method of the Infinium Assay will be shown hereinbelow. An array by Illumina [Illumina, iSelect™ Genotyping BeadChip] described later is in accordance with this method. There are two methods in the detection of an allele by this array. In one method, two kinds of probes (probes for allele detection of 50 bases long, Infinium I type) only differing

by a base at a 3'-end, wherein the 3'-end is a site for detecting a single nucleotide polymorphism, are used. Whole genome amplification for a genomic DNA is previously carried out, and fragmentation with an enzyme is carried out. The probe and the fragmented genomic DNA are hybridized, and thereafter an allele-specific extension reaction takes place, whereby a base on the downstream (3'-side) by a single base of a polymorphic site labeled with a single kind of a fluorescent dye is incorporated corresponding to the probe. In another method, one kind of probe without having an allele-specific sequence of a single nucleotide polymorphism in the probe is used (probe for allele detection of 50 bases, Infinium II type). A 3'-end of this probe has a sequence up to a single base upstream (5'-side) from a polymorphic site. The probe and the fragmented genomic DNA are hybridized, and according to a single base extension reaction, a base labeled with either one of two kinds of fluorescent dyes is incorporated corresponding to a single nucleotide polymorphic site of interest. In both the methods, the fluorescence is detected by a confocal laser scanner, thereby determining an allele and a genotype.

[0087] Here, the details of properties for length, modification and the like of probes used in the hybridization method mentioned above will be described later.

[0088] In addition, a method without carrying out hybridization with a probe includes PCR-RFLP method, SSCP method, mass spectrometry and direct sequencing method.

[0089] The PCR-RFLP method is a method including the steps of forming different DNA fragments according to enzymatic digestion of a nucleic acid

molecule having a polymorphism due to the existence of a polymorphism in a cleavage site of the restriction enzyme in the nucleic acid molecule, and determining the presence or absence of a polymorphism from a difference in electrophoretic patterns thereof. A nucleic acid molecule of interest is amplified by PCR, this amplified fragment is cleaved with a restriction enzyme, and a fragment formed electrophoretically is analyzed. The length of the nucleic acid molecule comprising an amplified polymorphism is usually from 50 to 10,000 base pairs, and more preferably from 100 to 1,000 base pairs.

[0090] The SSCP method is a method including the steps of amplifying a nucleic acid molecule having a polymorphism by PCR, forming a single-stranded DNA, electrophoresing the product, and determining the presence or absence of a polymorphism from a difference in the electrophoretic patterns thereof. The nucleic acid molecule of interest is amplified by PCR, and a single-stranded DNA is formed by subjecting this amplified fragment to heat or an alkali treatment. This single-stranded DNA forms a base sequence-specific higher-order structure; therefore, if these amplified fragments are electrophoresed, a difference in the electrophoretic mobility is found due to the difference in its structure. The primer used in PCR is labeled with a radioisotope or fluorescent substance. In addition, the length of the nucleic acid molecule comprising an amplified polymorphism is usually from 50 to 10,000 base pairs, and more preferably from 100 to 1,000 base pairs.

[0091] The mass spectrometry is a method including the steps of ionizing a polymer with a matrix and a laser or the like, accelerating the ionized

polymer in a high electric field to allow a flight to a detector, and identifying mass from a difference in the flight time, or the like. This mass spectrometry is combined with the above primer extension method or the like to detect a polymorphism. Concretely, a single base extension reaction is carried out with a primer complementary to a sequence up to a single base upstream of a polymorphic site of a nucleic acid molecule having a polymorphism, any one of 4 kinds of dideoxyribonucleotides, and deoxyribonucleic acids other than those corresponding the above, and a difference in mass of nucleic acid products having different sequences incorporated in a 3'-end is determined, whereby a polymorphism can be identified.

[0092] The direct sequencing method is a method of directly reading off a base sequence of a nucleic acid molecule having a polymorphism. Representative methods are called Sanger method (dideoxy method). A primer that is unlabeled or labeled with a radioisotope or a fluorescent substance is bound to a nucleic acid molecule of interest, an extension reaction with Klenow enzyme or the like is stopped with four kinds of dideoxyribonucleotides that are unlabeled or labeled with a radioisotope or a fluorescent substance, the product is digested with a restriction enzyme, and a DNA fragment generated is separated by electrophoresis. The base sequence of a 3'-end is read off in the order of fragments having a lower molecular weight on the basis of an electrophoretic image, thereby a base sequence containing a few bases before and after a polymorphism is determined. As a modified method thereof, there is a method called a primer extension method. This is a method including the steps of carrying

out a single base extension reaction using a primer complementary to a sequence up to a single base upstream of a polymorphic site of a nucleic acid molecule having a polymorphism, and reading off any one of the sequences of the 4 kinds of dideoxyribonucleotides incorporated in the 3-end. There are various methods in the identification of this dideoxyribonucleotides; for example, 4 kinds of nucleotides are labeled with different fluorescent substances, and separated and identified electrophoretically. In addition, a method of converting pyrophosphoric acid formed during an extension reaction to ATP, and identifying its ATP from luminescence of luciferase is also employed. The length of the primer used in the extension reaction is usually from 10 to 300 base pairs, and preferably from 15 to 25 base pairs.

[0093] In the present invention, the hybridization means that a nucleic acid molecule having a certain sequence is associated with a nucleic acid molecule complementary to at least a part of the nucleic acid molecule via a hydrogen bond on the basis of base sequences that are complementary to each other. The kind of the complementary nucleic acid molecule associated with the original nucleic acid molecule may be identical or different, and a nucleic acid constituting these nucleic acid molecules can be a deoxyribonucleic acid, a ribonucleic acid, or a peptide nucleic acid. In these nucleic acid molecules, when referred to the ribonucleic acid, in the sequence of the nucleic acid molecule (including a complementary sequence), thymine may be read as uracil.

[0094] The stringent conditions in the present invention mean conditions in which a nucleic acid molecule having a sequence complementary to a

partial sequence of a nucleic acid molecule having a certain sequence is specifically hybridized to the nucleic acid molecule (Fred M. Ausuble et al., *Current Protocols in Molecular Biology*, 2.10.1-2.10.16, John Wiley and Sons, Inc). Concrete examples of the conditions as described above include conditions such as a temperature lower than a melting temperature (Tm) of a complex formed between a nucleic acid molecule having a certain sequence and a complementary nucleic acid molecule hybridized to the nucleic acid molecule by preferably from about 5° to about 30°C, and by more preferably about 10° to about 25°C, a reaction solution for hybridization, such as SSC (mixed solution of sodium chloride and sodium citrate) in a concentration of 0.01 to 6-folds, SSPE (mixed solution of sodium chloride, sodium dihydrogenphosphate, and EDTA) or MES (a mixed solution of 2-(N-morpholino)ethanesulfonic acid and tetramethylammonium chloride) buffer, and hydrogen ion concentrations of a pH of from 6 to 8. For example, the stringent conditions in a case where an immobilized probe is prepared by immobilizing a 25 bp DNA probe include conditions of hybridization at 49°C in the MES buffer (hydrogen ion concentrations being from 6.5 to 6.7) in a 1-fold concentration, and sequentially washing with SSC (hydrogen ion concentrations being 8.0) in a 6-fold concentration at 25°C, and thereafter SSC (hydrogen ion concentrations being 8.0) in a 0.6-fold concentration at 45°C.

[0095] In the present invention, the term allele-specific (or specific to allele) means that the allele is contained in a sequence from the genome including the polymorphic site or in a prepared nucleic acid molecule including the polymorphic site, or a certain nucleic acid molecule is capable of

specifically hybridizing under stringent conditions to a nucleic acid molecule having a sequence containing the allele in the polymorphic site, in other words, in the manner of being capable of discriminating the allele and the opposite allele.

[0096] Base sequences of 61 bases in length including a single nucleotide polymorphism associated with the onset of glaucoma, disclosed in the present invention, are composed of two pairs of base sequences which differ only by a base in the center (i.e. 31st base) (i.e. those pairs are consisting of a sequence having odd number of SEQ ID No. and a sequence having even number of SEQ ID No.), and the 31st base is a polymorphic site. The high-risk alleles in the polymorphic sites are listed in Tables 1 and 2 or Tables 52 to 63 given later. In any of these single nucleotide polymorphisms, in a case where the existence of an allele that exists in a high frequency in glaucoma patients is determined, a high-risk allele in a sample is detected, whereby the existence of the allele that exists in a high frequency in glaucoma patients can be determined.

[0097] In addition, as to any single nucleotide polymorphisms associated with the onset of glaucoma identified above, the genotype can be determined by detecting the presence or the absence of each of the alleles opposite to each other contained in one sample. In detail, in a case where only a certain allele is detected, the genotype is a homozygote of the allele, and in a case where two alleles are detected, the genotype is a heterozygote having the two alleles. In at least one of these single nucleotide polymorphisms, by detecting a genotype, it is determined whether or not the genotype that is identified in a higher frequency in a glaucoma patient group

than that of a non-patient group exists in a sample. In other words, in the single nucleotide polymorphism mentioned above, when the high-risk allele complies with a dominant genetic model, a homozygote of the high-risk allele or a heterozygote is a genotype that is identified in a higher frequency in a glaucoma patient group than that of a non-patient group, and when the high-risk allele complies with a recessive genetic model, a homozygote of the high-risk allele is a genotype that is identified in a higher frequency in a glaucoma patient group than that of a non-patient group. It is preferable that each of the opposite alleles is measured in a single operation, from the viewpoint of reducing judgmental error.

[0098] The sample is analyzed in the manner described above, and in a case where the allele or genotype that is identified in a higher frequency in a glaucoma patient group than that of a non-patient group exists in the sample, there are some high probabilities that an individual donating the sample not having glaucoma at the present point is predicted to have a high onset risk of glaucoma, or is determined that a precision examination for glaucoma such as visual field examination is necessary, and that an individual donating the sample who is suspected of having glaucoma should be diagnosed as glaucoma.

[0099] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting an onset risk of glaucoma in the present invention, the single nucleotide polymorphism used in the detection is a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base

sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto,
more preferably a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto,
even more preferably a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of pairs of base sequences containing a single nucleotide polymorphism listed below or a complementary sequence thereto,
wherein, as mentioned above, in the pairs of SEQ ID NOs: shown in **a** to **r**, each of the pairs of sequences corresponds to one single nucleotide polymorphism, and each of the base sequences is a base sequence containing an allele opposite to each other of the single nucleotide polymorphism in a 31st base:

a: SEQ ID NO: 203 and/or SEQ ID NO: 204,

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

c: SEQ ID NO: 207 and/or SEQ ID NO: 208,

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

e: SEQ ID NO: 211 and/or SEQ ID NO: 212,

f: SEQ ID NO: 213 and/or SEQ ID NO: 214,

g: SEQ ID NO: 215 and/or SEQ ID NO: 216,

h: SEQ ID NO: 217 and/or SEQ ID NO: 218,

i: SEQ ID NO: 219 and/or SEQ ID NO: 220,

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224,

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

m: SEQ ID NO: 227 and/or SEQ ID NO: 228,

n: SEQ ID NO: 229 and/or SEQ ID NO: 230,

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238.

[0100] In a case where any one of the single nucleotide polymorphisms is used, especially, it is preferable that an allele of a single nucleotide polymorphism located on a 31st base of a base sequence is used, wherein the base sequence is at least one base sequence selected from the group consisting of the following base sequences containing a single nucleotide polymorphism:

SEQ ID NO: 203, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 234, SEQ ID NO: 235, and SEQ ID NO: 238,

or a complementary sequence thereto.

Here, these sequences are sequences containing a high-risk allele in each of polymorphic sites.

[0101] Further, the precision of the determination of a future onset risk of glaucoma can be improved by detecting a combination of two or more of

alleles or genotypes associated with glaucoma in the present invention, using one sample.

[**0102**] For the single nucleotide polymorphisms to be combined, any ones can be used so long as they are a single nucleotide polymorphism in the present invention, preferably a single nucleotide polymorphism having a low p-value, and more preferably a single nucleotide polymorphism of which p-value obtained by combining the results obtained in two analyses by a meta-analysis method, such as Mantel-Haenszel method, is determined to be significant even below the level of Bonferroni correction. In addition, from a different viewpoint, it is preferable to use a single nucleotide polymorphism that is confirmed to contribute to the improvement in the precision of the risk prediction by a combination according to the logistic regression analysis described later. On the other hand, since the single nucleotide polymorphisms in a state of linkage disequilibrium mentioned above show the same behavior, in a case where plural single nucleotide polymorphisms in a state of linkage disequilibrium are combined, risks of glaucoma based on the same region may be evaluated unnecessarily seriously in some cases. In a case where a risk of a disease is predicted by combining the single nucleotide polymorphisms in the present invention, when it is intended to evaluate all the risks in even weighting, it is preferable that the prediction is carried out employing only one of the single nucleotide polymorphisms in the state of linkage disequilibrium, in a case that the plural single nucleotide polymorphisms that are in the state of linkage disequilibrium mentioned above are contained.

[0103] In a case where a risk is predicted according to a combination of any two or more single nucleotide polymorphisms in the present invention, an onset risk of glaucoma can be predicted using the regression formula obtained by the logistic regression analysis. Concretely, the regression formula according to the logistic regression analysis is obtained by respectively using each of the any two or more single nucleotide polymorphisms as an independent variable Π (homozygote of one allele = 0, heterozygote = 1, homozygote of an opposite allele = 2). In each sample, a dependent variable Φ is calculated by substituting a value corresponding to each single nucleotide polymorphism into this formula. When a dependent variable Φ is greater than a given threshold (for example, 0.5), the determination can be made that this sample donor has an onset risk.

[0104] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting an onset risk of glaucoma in the present invention, in a case where any two or more single nucleotide polymorphisms are combined, the single nucleotide polymorphisms used in the detection are preferably single nucleotide polymorphisms which are located on 31st bases of base sequences, wherein the base sequences are base sequences containing two or more different single nucleotide polymorphisms, selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto,

more preferably single nucleotide polymorphisms which are located on 31st bases of base sequences, wherein the base sequences are base sequences containing two or more different single nucleotide polymorphisms, selected

from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto,

even more preferably single nucleotide polymorphisms which are located on 31st bases of base sequences, wherein the base sequences are base sequences containing two or more different single nucleotide polymorphisms, selected from the group consisting of pairs of base sequences containing a single nucleotide polymorphism listed below or a complementary sequence thereto,

wherein, as mentioned above, in the pairs of SEQ ID NOs: shown in **a** to **r**, each of the pairs of sequences corresponds to one single nucleotide polymorphism, and each of the base sequences is a base sequence containing an allele opposite to each other of the single nucleotide polymorphism in a 31st base:

a: SEQ ID NO: 203 and/or SEQ ID NO: 204,

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

c: SEQ ID NO: 207 and/or SEQ ID NO: 208,

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

e: SEQ ID NO: 211 and/or SEQ ID NO: 212,

f: SEQ ID NO: 213 and/or SEQ ID NO: 214,

g: SEQ ID NO: 215 and/or SEQ ID NO: 216,

h: SEQ ID NO: 217 and/or SEQ ID NO: 218,

i: SEQ ID NO: 219 and/or SEQ ID NO: 220,

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224,

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

m: SEQ ID NO: 227 and/or SEQ ID NO: 228,

n: SEQ ID NO: 229 and/or SEQ ID NO: 230,

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238, and

even more preferably single nucleotide polymorphisms which are located on 31st bases of base sequences, wherein the base sequences are base sequences containing 10 or more different single nucleotide polymorphisms, selected from the group consisting of pairs of base sequences containing a single nucleotide polymorphism listed above or a complementary sequence thereto, and

even more preferably single nucleotide polymorphisms which are located on 31st bases of base sequences, wherein the base sequences are base sequences containing all the different single nucleotide polymorphisms, selected from the group consisting of pairs of base sequences containing a single nucleotide polymorphism listed above or a complementary sequence thereto.

[0105] In addition, it is preferable that the single nucleotide polymorphisms to be used in combination are those that are not in the state of linkage disequilibrium, and from this viewpoint, in all the embodiments of the combinations mentioned above, supposing that

a group composed of a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

a: SEQ ID NO: 203 and/or SEQ ID NO: 204, and

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

or a complementary sequence thereto, is named as a single nucleotide polymorphism of Group 1,

a group composed of a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

c: SEQ ID NO: 207 and/or SEQ ID NO: 208, and

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

or a complementary sequence thereto, is named as a single nucleotide polymorphism of Group 2,

a group composed of a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224, and

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

or a complementary sequence thereto, is named as a single nucleotide polymorphism of Group 3,

a group composed of a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238,

or a complementary sequence thereto, is named as a single nucleotide polymorphism of Group 4,

it is preferable to use

any one of the single nucleotide polymorphisms in Group 1 in a case that the single nucleotide polymorphisms belonging to Group 1 are used,

any one of the single nucleotide polymorphisms in Group 2 in a case that the single nucleotide polymorphisms belonging to Group 2 are used,

any one of the single nucleotide polymorphisms in Group 3 in a case that the single nucleotide polymorphisms belonging to Group 3 are used, and/or

any one of the single nucleotide polymorphisms in Group 4 in a case that the single nucleotide polymorphisms belonging to Group 4 are used.

[0106] Further, in all the embodiments of the combinations mentioned above, it is preferable that an allele of a single nucleotide polymorphism located on a 31st base of a base sequence is used, wherein the base sequence is a base sequence containing two or more different single nucleotide polymorphisms, selected from the group consisting of the following base sequences containing a single nucleotide polymorphism:

SEQ ID NO: 203, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 234, SEQ ID NO: 235, and SEQ ID NO: 238,

or a complementary sequence thereto.

Here, these base sequences are sequences containing a high-risk allele in each of polymorphic sites.

[0107] (Probe Capable of Detecting Allele Associated with Glaucoma)

In another embodiment of the present invention, an allele-specific nucleic acid molecule or probe (hereinafter referred to as probe) capable of detecting an allele associated with glaucoma, and a method of detecting an allele or a genotype associated with glaucoma using the probe are provided.

[0108] Any probes may be used so long as the probe is capable of hybridizing under the stringent conditions to an allele-specific sequence, in a polymorphic site of the single nucleotide polymorphism associated with glaucoma in the present invention. The determination of the allele in a polymorphic site can be made by detecting any one of polymorphic sites of the sense strand and the antisense strand on the genome; therefore, the probe in the present invention embraces any one of sequences complementary to a sequence specific to an allele of the sense strand and sequences complementary to a sequence specific to an allele of the antisense strand, in other words, sequences specific to an allele of the sense strand. The probe in the present invention can also be used in the detection of cDNA or mRNA, containing a single nucleotide polymorphism in the present invention. In a case where the probe is used in the detection of cDNA or mRNA, a probe in which the single nucleotide polymorphism exists in exon or neighborhood thereof is used.

[0109] The probes capable of detecting each of alleles of the single nucleotide polymorphisms listed in Tables 1 and 2, Tables 5 to 25, Tables 26 to 28, Tables 29 to 51, or Tables 52 to 62 given later or a complementary

strand thereto, and the probes capable of specifically detecting each of alleles of any single nucleotide polymorphisms that exist in a region associated with glaucoma listed in Tables 3 and 4 or Tables 63 to 70 given later or a complementary strand thereto are all embraced in the probe in the present invention. In a case where, for example, the obtained results are based on a single analysis using a microarray in which a probe capable of specifically detecting each of alleles of 500,000 single nucleotide polymorphisms, or a complementary strand thereto, is detected in a single operation, the probe of the present invention is preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 1×10^{-3} or less, more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 3×10^{-4} or less, even more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 1×10^{-4} or less, and even more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 3×10^{-5} or less. In a case where plural analytical results are combined and obtained according to a method of meta-analysis, such as Mantel-Haenszel method, the probe is preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 1×10^{-2} or less, more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of

which p-value is 3×10^{-3} or less, even more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 1×10^{-3} or less, even more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 3×10^{-4} or less, and even more preferably a probe capable of specifically detecting each of alleles of a single nucleotide polymorphism or a complementary strand thereto, of which p-value is 1×10^{-4} or less.

[0110] The probe in the present invention preferably contains an allele-specific sequence or a complementary strand thereto, and even more preferably in the probe in the present invention, a sequence contributing to an allele-specific hybridization consists only of an allele-specific sequence or a complementary strand thereto. To the probe in the present invention, a spacer or any sequences of several bases that are not from an allele-specific sequence for the purpose of providing stabilization or the like can be added in an end, within the range that the probe is capable of hybridizing to the sequence under the stringent conditions. The added sequence is preferably a sequence that does not take a three-dimensional structure, such as a hairpin structure.

[0111] The probe can be provided with any labels for use in the detection. Any labels to be provided to the probe that are ordinarily used can be used, and in general, a fluorescent label such as FITC or Cy3, biotin, an enzyme label such as an alkaline phosphatase and horseradish peroxidase, or the like is usable. In a case where a biotin label is used, streptavidin capable of specifically binding to biotin is previously provided with a further

detectable label, and the labeled streptavidin is used as a secondary label. A labeled anti-biotin antibody can also be used in place of the labeled streptavidin. As a method of providing a label to a probe, any known methods may be used, and the methods are well known to one of ordinary skill in the art. An arbitrary sequence which serves as a spacer as mentioned above may be added to the probe, and the spacer may be provided with a label. A reagent for labeling a probe, a labeled streptavidin, a labeled anti-biotin antibody or the like is commercially available as a reagent, and can also be purchased.

[0112] The probe in the present invention is not limited whether it is a deoxyribonucleic acid, a ribonucleic acid, or a peptide nucleic acid, and a probe containing a mixed sequence thereof is also embraced in the present invention, so long as the probe is capable of specifically hybridizing to a nucleic acid molecule having an allele of interest. In a case where a probe containing a ribonucleic acid is used as the probe in the present invention, in the sequence of the probe in the present invention (including a sequence complementary thereto), thymine may read as uracil. In addition, the probe in the present invention may be subjected to chemical modifications as needed, so long as the probe is capable of specifically hybridizing under stringent conditions to a nucleic acid molecule having an allele of interest. As the method of providing a chemical label, any known methods may be used.

[0113] The probe for the detection can be reacted with the sample in the state of solution and then detected by a known method, or previously immobilized to a carrier. The probe can take the form of an immobilized

probe obtained by previously immobilizing a probe corresponding to each of the alleles of several to several hundred-thousand different single nucleotide polymorphisms to a location defined on a solid carrier in the number of from one to dozen probes per one single nucleotide polymorphism, reacting a sample to the immobilized probes, scanning a signal generated from a hybridized probe, and analyzing the scanned data with a computer, which is a so-called microarray. In a case where the probe takes the form of an immobilized probe, the largest number of the immobilized probes are limited by immobilization density and area of immobilized sites for the probes.

[0114] In a case where the probe takes the form of an immobilized probe as described above, signals on the solid phase from the nucleic acid molecule having a labeled target allele can be detected by previously labeling a nucleic acid molecule in a sample by a known method, and binding the labeled nucleic acid molecule with an immobilized unlabeled probe in the present invention, or by binding a nucleic acid molecule having an allele to be detected to an immobilized unlabeled probe in the present invention, and thereafter labeling the product according to a known method.

[0115] The immobilization can be carried out by any of known method, and for example, a method such as synthetic oligoprint or spotting photolithograph can be used. Also, the material for the carrier is not limited, and a generally used material, for example, a polymer such as a polycarbonate or a polystyrene, glass, silicon crystal or the like can be used. In addition, in order to enhance adhesive strength of the nucleic acids, a carrier may be provided with a coating such as cationization before the

immobilization. In addition, in order to prevent nonspecific nucleic acids from being adsorbed to a carrier, blocking can be carried out with a known blocking agent after the immobilization. The blocking agent as mentioned above may be any ones so long as the blocking agent is capable of controlling the nonspecific nucleic acids from being adsorbed to the carrier, and for example, salmon sperm DNA, Denhardt's solution, Cot-I DNA extracted from human placenta, an anionic surfactant such as sodium dodecyl sulfate, a nonionic surfactant such as polyoxyethylene sorbitan monolaurate, or the like can be used.

[0116] In addition, in a case where the probe is immobilized, it is possible to construct that each of the opposite alleles contained in one sample is detected under the same operation by immobilizing a probe specific to each of the alleles opposite to each other on the same carrier. In the construction as described above, not only the alleles but also the genotypes in the samples can be determined.

[0117] It is preferable that the probe used in the detection of the allele is a probe having a length of preferably from 16 to 55 bases, more preferably from 23 to 27 bases or 47 to 53 bases, and even more preferably 25 bases in total of a length of the polymorphic site and some bases before and after the polymorphic site, the probe containing the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, that the probe is a probe containing the polymorphic site mentioned above and a 5'-upstream side thereof, preferably a sequence of 49 bases (i.e. a sequence of 50 bases), the probe containing the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence

complementary thereto, or that the probe is a probe containing a sequence of 50 bases on a 5'-upstream side of the polymorphic site mentioned above, the probe having a sequence adjoining the polymorphic site mentioned above, or a sequence complementary thereto.

[0118] An even more preferred probe used in the detection of the allele is:

1) a probe capable of specifically detecting an allele of the single nucleotide polymorphism, containing the polymorphic site mentioned above and a sequence of 12 bases each before and after the polymorphic site, i.e. a sequence of 25 bases in length, and the probe containing the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, or

2a) a probe capable of specifically detecting an allele of the single nucleotide polymorphism, containing the polymorphic site mentioned above and a sequence of 49 bases on the 5'-upstream side thereof (i.e. sequence of 50 bases), and the probe containing a sequence containing the polymorphic site mentioned above or a sequence complementary thereto, or

2b) a probe capable of specifically detecting an allele of the single nucleotide polymorphism, having a sequence of 50 bases on a 5'-upstream side of the polymorphic site mentioned above, and the probe having a sequence adjoining the polymorphic site mentioned above, or a sequence complementary thereto.

[0119] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting an onset risk of glaucoma in the present invention, the probe usable in the detection is a probe containing a single nucleotide polymorphism which is located on a

31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, and/or a probe having a base sequence containing at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto, more preferably a probe containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto, or a partial sequence thereof, and/or a probe having a base sequence containing at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 535 or a complementary sequence thereto, and

even more preferably a probe containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from following Group A consisting of pairs of base sequences **a** to **r** containing a single nucleotide polymorphism or a complementary sequence thereto, or a partial sequence thereof, and/or a probe containing a base sequence, wherein the base sequence is at least one base sequence or a pair of base sequences, selected from Group B consisting of base sequences **aa** to **rr** or pairs of the base sequences, or a complementary sequence thereto,

wherein in pairs of SEQ ID NOs: shown in **a** to **r**, each of the pairs of sequences corresponds to one single nucleotide polymorphism, and each of

the base sequences is a base sequence containing an allele opposite to each other of the single nucleotide polymorphism on a 31st base, and

in SEQ ID NOs: shown in **aa** to **rr** or pairs of the SEQ ID NOs:, each of the base sequences or the pairs of the base sequences is a sequence for the probe or a pair of sequences for the probes, used in the detection of one single nucleotide polymorphism,

wherein **a** and **aa**, **b** and **bb**, **c** and **cc**, **d** and **dd**, **e** and **ee**, **f** and **ff**, **g** and **gg**, **h** and **hh**, **i** and **ii**, **j** and **jj**, **k** and **kk**, **l** and **ll**, **m** and **mm**, **n** and **nn**, **o** and **oo**, **p** and **pp**, **q** and **qq**, and **r** and **rr** respectively correspond to the same single nucleotide polymorphism,

Group A

a: SEQ ID NO: 203 and/or SEQ ID NO: 204,

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

c: SEQ ID NO: 207 and/or SEQ ID NO: 208,

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

e: SEQ ID NO: 211 and/or SEQ ID NO: 212,

f: SEQ ID NO: 213 and/or SEQ ID NO: 214,

g: SEQ ID NO: 215 and/or SEQ ID NO: 216,

h: SEQ ID NO: 217 and/or SEQ ID NO: 218,

i: SEQ ID NO: 219 and/or SEQ ID NO: 220,

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224,

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

m: SEQ ID NO: 227 and/or SEQ ID NO: 228,

n: SEQ ID NO: 229 and/or SEQ ID NO: 230,

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238, and

Group B

aa: SEQ ID NO: 515 and/or SEQ ID NO: 533,

bb: SEQ ID NO: 516,

cc: SEQ ID NO: 517,

dd: SEQ ID NO: 518 and/or SEQ ID NO: 534,

ee: SEQ ID NO: 519,

ff: SEQ ID NO: 520,

gg: SEQ ID NO: 521,

hh: SEQ ID NO: 522,

ii: SEQ ID NO: 523,

jj: SEQ ID NO: 524,

kk: SEQ ID NO: 525,

ll: SEQ ID NO: 526,

mm: SEQ ID NO: 527,

nn: SEQ ID NO: 528,

oo: SEQ ID NO: 529,

pp: SEQ ID NO: 530 and/or SEQ ID NO: 535,

qq: SEQ ID NO: 531, and

rr: SEQ ID NO: 532.

[0120] In a case where any one of the single nucleotide polymorphisms is used, especially, it is preferable that in Group A, a probe containing an allele

of a single nucleotide polymorphism located on a 31st base of a base sequence is used, wherein the base sequence is at least one base sequence selected from the group consisting of the following base sequences containing a single nucleotide polymorphism:

SEQ ID NO: 203, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 234, SEQ ID NO: 235, and SEQ ID NO: 238,

or a complementary sequence thereto, or a partial sequence thereof, and in Group B, a probe containing a base sequence containing at least one base sequence selected from the group consisting of the following base sequences:

SEQ ID NO: 533, SEQ ID NO: 516, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 535, SEQ ID NO: 531, and SEQ ID NO: 532,

or a complementary sequence thereto is used.

Here, these base sequences are sequences corresponding to a probe used in the detection of a high-risk allele.

[0121] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting an onset risk of glaucoma in the present invention, in a case where any two or more single nucleotide polymorphisms are combined, the probes usable in the detection

are preferably probes containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, and/or probes having a base sequence containing a base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto, wherein the probes are probes corresponding to two or more different single nucleotide polymorphisms thereof,

more preferably probes containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto, or a partial sequence thereof, and/or probes having a base sequence containing a base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 535 or a complementary sequence thereto, wherein the probes are probes corresponding to two or more different single nucleotide polymorphisms thereof, and

even more preferably probes containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism selected from following Group A consisting of pairs of base sequences **a** to **r** containing a single nucleotide polymorphism or a complementary

sequence thereto, or a partial sequence thereof, and/or two or more different probes having a base sequence, wherein the base sequence contains base sequences or a pair of base sequences, selected from Group B consisting of base sequences **aa** to **rr** or pairs of the base sequences, or a complementary sequence thereto,

wherein in pairs of SEQ ID NOs: shown in **a** to **r**, each of the pairs of sequences corresponds to one single nucleotide polymorphism, and each of the base sequences is a base sequence containing an allele opposite to each other of the single nucleotide polymorphism on a 31st base, and

in SEQ ID NOs: shown in **aa** to **rr** or pairs of the SEQ ID NOs:, each of the base sequences or the pairs of the base sequences is a sequence for the probe or a pair of sequences for the probes, used in the detection of one single nucleotide polymorphism,

wherein **a** and **aa**, **b** and **bb**, **c** and **cc**, **d** and **dd**, **e** and **ee**, **f** and **ff**, **g** and **gg**, **h** and **hh**, **i** and **ii**, **j** and **jj**, **k** and **kk**, **l** and **ll**, **m** and **mm**, **n** and **nn**, **o** and **oo**, **p** and **pp**, **q** and **qq**, and **r** and **rr** respectively correspond to the same single nucleotide polymorphism,

Group A

a: SEQ ID NO: 203 and/or SEQ ID NO: 204,

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

c: SEQ ID NO: 207 and/or SEQ ID NO: 208,

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

e: SEQ ID NO: 211 and/or SEQ ID NO: 212,

f: SEQ ID NO: 213 and/or SEQ ID NO: 214,

g: SEQ ID NO: 215 and/or SEQ ID NO: 216,

h: SEQ ID NO: 217 and/or SEQ ID NO: 218,

i: SEQ ID NO: 219 and/or SEQ ID NO: 220,

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224,

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

m: SEQ ID NO: 227 and/or SEQ ID NO: 228,

n: SEQ ID NO: 229 and/or SEQ ID NO: 230,

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238, and

Group B

aa: SEQ ID NO: 515 and/or SEQ ID NO: 533,

bb: SEQ ID NO: 516,

cc: SEQ ID NO: 517,

dd: SEQ ID NO: 518 and/or SEQ ID NO: 534,

ee: SEQ ID NO: 519,

ff: SEQ ID NO: 520,

gg: SEQ ID NO: 521,

hh: SEQ ID NO: 522,

ii: SEQ ID NO: 523,

jj: SEQ ID NO: 524,

kk: SEQ ID NO: 525,

ll: SEQ ID NO: 526,

mm: SEQ ID NO: 527,

nn: SEQ ID NO: 528,

oo: SEQ ID NO: 529,

pp: SEQ ID NO: 530 and/or SEQ ID NO: 535,

qq: SEQ ID NO: 531, and

rr: SEQ ID NO: 532,

even more preferably probes containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism selected from Group A listed above consisting of pairs of the base sequences containing the single nucleotide polymorphism or a complementary sequence thereto, or a partial sequence thereof, and/or probes having a base sequence, wherein the base sequence contains a base sequence selected from Group B listed above consisting of pairs of the base sequences or a complementary sequence thereto, wherein the probes are probes corresponding to 10 or more different single nucleotide polymorphisms thereof, and

even more preferably probes containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism selected from Group A listed above consisting of pairs of the base sequences containing the single nucleotide polymorphism or a complementary sequence thereto, or a partial sequence thereof, and/or probes having a base sequence, wherein the base sequence contains a base sequence selected from Group B listed above consisting of pairs of the base sequences or a complementary sequence thereto, wherein the probes are

probes corresponding to all the different single nucleotide polymorphisms thereof.

[0122] In addition, it is preferable that the single nucleotide polymorphisms to be used in combination are those that are not in the state of linkage disequilibrium, and from this viewpoint, in all the embodiments of the combinations mentioned above, supposing that, in Group A,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

a: SEQ ID NO: 203 and/or SEQ ID NO: 204, and

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 1,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

c: SEQ ID NO: 207 and/or SEQ ID NO: 208, and

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 2,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224, and

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 3,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 4, and

that in Group B,

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

aa: SEQ ID NO: 515 and/or SEQ ID NO: 533, and

bb: SEQ ID NO: 516,

or a complementary sequence thereto, is named as a base sequence of Group 1,

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

cc: SEQ ID NO: 517, and

dd: SEQ ID NO: 518 and/or SEQ ID NO: 534

or a complementary sequence thereto, is named as a base sequence of Group 2,

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

jj: SEQ ID NO: 524,

kk: SEQ ID NO: 525, and

ll: SEQ ID NO: 526,

or a complementary sequence thereto, is named as a base sequence of Group 3, and

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

oo: SEQ ID NO: 529,

pp: SEQ ID NO: 530 and/or SEQ ID NO: 535,

qq: SEQ ID NO: 531, and

rr: SEQ ID NO: 532,

or a complementary sequence thereto, is named as a base sequence of Group 4,

it is preferable to use

a probe containing any one of the base sequences in Group 1 in a case that the base sequences belonging to Group 1 are used,

a probe containing any one of the base sequences in Group 2 in a case that the base sequences belonging to Group 2 are used,

a probe containing any one of the base sequences in Group 3 in a case that the base sequences belonging to Group 3 are used, and/or

a probe containing any one of the base sequences in Group 4 in a case that the base sequences belonging to Group 4 are used.

[0123] Further, in all the embodiment of the combinations mentioned above, in Group A, a probe containing an allele of a single nucleotide polymorphism located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism selected from the group consisting of the following base sequences containing a single nucleotide polymorphism:

SEQ ID NO: 203, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 234, SEQ ID NO: 235, and SEQ ID NO: 238,

or a complementary sequence thereto, or a partial sequence thereof, is preferred, and

in Group B, a probe containing a base sequence containing a base sequence selected from the group consisting of the following base sequences:

SEQ ID NO: 533, SEQ ID NO: 516, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 535, SEQ ID NO: 531, and SEQ ID NO: 532,

or a complementary sequence thereto is preferred.

Here, these base sequences are sequences corresponding to a probe used in the detection of a high-risk allele.

[0124] The probe in a case where a Taqman method is used in the detection of an allele usually has a length of preferably from 10 to 300 bases, and

contains the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, and the probe also contains a fluorescent substance and a quencher. More preferably, the probe has a length of 20 to 60 bases, and contains the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, and the probe contains a fluorescent substance and a quencher.

[0125] The probes in a case where an Invader method is used in the detection of an allele comprise a probe (reporter) which have a common sequence to a 3'-side of the polymorphic site mentioned above and a sequence on a 5'-side being completely different therefrom, and a probe (invader) only composed of the common sequence to a 5'-side. These probes usually have a length of preferably from 10 to 300 bases, and more preferably a length of from 20 to 60 bases.

[0126] The probe in a case where a LightCycler method is used in the detection of an allele, usually has a length of preferably from 10 to 300 bases, and contains the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, and the probe contains a fluorescent substance and a quencher. More preferably, the probe has a length of 20 to 60 bases, and contains the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, and the probe contains a fluorescent substance and a quencher.

[0127] The probe in a case where a cyclin probe method is used in the detection of an allele is a probe in which DNA sequences are bound in a manner that both ends of an RNA sequence having the polymorphic site and

a surrounding sequence thereof, or a sequence complementary thereto, are sandwiched, and each of DNA ends has a fluorescent substance or a quencher. These probes usually have a length of preferably from 10 to 300 bases, and contain the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto. More preferably, the probe has a length of 20 to 60 bases, and contains the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto.

[0128] The probes in a case where an MPSS method is used in the detection of an allele comprise an oligo DNA (encoded adaptor probe) having a protruding end of 4 bases on a 5'-side, subsequently a recognition sequence for a restriction enzyme BbvI, and a single-stranded sequence to which a decoder probe is bound on a 3'-side, and a single strand oligo DNA (decoder probe) which has fluorescent substance on a 3'-side, and containing 4 different sequences, each sequence specifically hybridizing to one of the encoded adaptor probes. Here, a DNA sequence is bound in a manner that both ends of an RNA sequence having the polymorphic site mentioned above and a surrounding sequence thereof, or a sequence complementary thereto, are sandwiched, and each of DNA ends has a fluorescent substance or a quencher. The encoded adaptor probe usually has a length of preferably from 10 to 300 base pairs, and more preferably from 15 to 40 base pairs. On the other hand, the decoder probe usually has a length of preferably from 10 to 300 base pairs, and more preferably from 5 to 30 base pairs.

[0129] (Kit of Detecting Allele Associated with Glaucoma)

In another embodiment of the present invention, a kit of detecting a single nucleotide polymorphism associated with glaucoma is provided.

[0130] The kit of the present invention (or a composition for predicting a risk) embraces all those kits so long as the allele or genotype of any one of single nucleotide polymorphisms associated with glaucoma disclosed in the present invention can be detected in a nucleic acid molecule in a sample. As mentioned above, the kit of the present invention may be those that detect a base of either the sense strand or the antisense strand of the single nucleotide polymorphism, or those that detect bases of both the strands. In a case where the kit of the present invention is based on the results obtained in a single analysis using a microarray for a kit of detecting an allele or genotype associated with glaucoma for detecting, for example, 500,000 single nucleotide polymorphisms in a single operation, the kit is preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 1×10^{-4} or less listed in Tables 1 and 2 set forth below, more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 3×10^{-4} or less, even more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 1×10^{-4} or less, and even more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 3×10^{-5} or less. In a case where the plural analytic results are combined and obtained according to a method of meta-analysis, such as Mantel-Haenszel method, the kit is preferably a kit of detecting an allele or genotype associated with

glaucoma for single nucleotide polymorphisms having a p-value listed in Tables 52 to B set forth below of 1×10^{-2} or less, more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 3×10^{-3} or less, even more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 1×10^{-3} or less, even more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 3×10^{-4} or less, and even more preferably a kit of detecting an allele or genotype associated with glaucoma for single nucleotide polymorphisms having a p-value of 1×10^{-4} or less.

[0131] A kit of detecting both an allele identified in a high frequency in the glaucoma patient group mentioned above and an allele opposite to the allele is also one embodiment of the present invention. In a case where a kit as described above is used, as already explained, a genotype of each of the alleles can also be determined.

[0132] By detecting the presence of an allele or a genotype that is identified in a high frequency in glaucoma patients in the sample using the kit of the present invention, a future onset risk of glaucoma of an individual not having glaucoma at the present stage can be predicted, whether or not precise visual field examinations for glaucoma are required can be determined, or the diagnosis of an individual who is suspected of glaucoma can be made for glaucoma.

[0133] In addition, as mentioned above, a kit for determining alleles that are opposite to each other in a single operation can be prepared by using a probe

specific to each of the alleles that are opposite to each other, and providing different labels to the probes, or providing in the form of a microarray or beads array as mentioned above.

[0134] The precision for the prediction of the onset risk of glaucoma or the determination of whether or not precise visual field examinations are required can also be improved by providing a kit having the constitution of detecting these plural alleles or genotypes using one sample. Even in the constitution as described above, a constitution can be taken that the detection is carried out in a single operation by having the form of probes provided with different labels, or the form of the microarray or beads array mentioned above.

[0135] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting an onset risk of glaucoma in the present invention, the kit usable in detecting or predicting a risk is

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing at least one

base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto,

more preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 535 or a complementary sequence thereto,

even more preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from following Group A consisting of pairs of base sequences **a** to **r** containing a single nucleotide polymorphism or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing at least one

base sequence or a pair of base sequences, selected from Group B consisting of base sequences **aa** to **rr** or pairs of the base sequences, or a complementary sequence thereto,

wherein in pairs of SEQ ID NOs: shown in **a** to **r**, each of the pairs of sequences corresponds to one single nucleotide polymorphism, and each of the base sequences is a base sequence containing an allele opposite to each other of the single nucleotide polymorphism on a 31st base, and

in SEQ ID NOs: shown in **aa** to **rr** or pairs of the SEQ ID NOs:, each of the base sequences or the pairs of the base sequences is a sequence for the nucleic acid molecule or a pair of sequences for the nucleic acid molecule, used in the detection of one single nucleotide polymorphism,

wherein **a** and **aa**, **b** and **bb**, **c** and **cc**, **d** and **dd**, **e** and **ee**, **f** and **ff**, **g** and **gg**, **h** and **hh**, **i** and **ii**, **j** and **jj**, **k** and **kk**, **l** and **ll**, **m** and **mm**, **n** and **nn**, **o** and **oo**, **p** and **pp**, **q** and **qq**, and **r** and **rr** respectively correspond to the same single nucleotide polymorphism,

Group A

a: SEQ ID NO: 203 and/or SEQ ID NO: 204,

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

c: SEQ ID NO: 207 and/or SEQ ID NO: 208,

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

e: SEQ ID NO: 211 and/or SEQ ID NO: 212,

f: SEQ ID NO: 213 and/or SEQ ID NO: 214,

g: SEQ ID NO: 215 and/or SEQ ID NO: 216,

h: SEQ ID NO: 217 and/or SEQ ID NO: 218,

i: SEQ ID NO: 219 and/or SEQ ID NO: 220,

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224,

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

m: SEQ ID NO: 227 and/or SEQ ID NO: 228,

n: SEQ ID NO: 229 and/or SEQ ID NO: 230,

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238, and

Group B

aa: SEQ ID NO: 515 and/or SEQ ID NO: 533,

bb: SEQ ID NO: 516,

cc: SEQ ID NO: 517,

dd: SEQ ID NO: 518 and/or SEQ ID NO: 534,

ee: SEQ ID NO: 519,

ff: SEQ ID NO: 520,

gg: SEQ ID NO: 521,

hh: SEQ ID NO: 522,

ii: SEQ ID NO: 523,

jj: SEQ ID NO: 524,

kk: SEQ ID NO: 525,

ll: SEQ ID NO: 526,

mm: SEQ ID NO: 527,

nn: SEQ ID NO: 528,

oo: SEQ ID NO: 529,

pp: SEQ ID NO: 530 and/or SEQ ID NO: 535,

qq: SEQ ID NO: 531, and

rr: SEQ ID NO: 532.

[0136] In a case where any one of the single nucleotide polymorphisms is used, especially, in Group A, preferred is a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or predicting an onset risk of glaucoma, using a nucleic acid molecule containing an allele of a single nucleotide polymorphism located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from the group consisting of the following base sequences containing a single nucleotide polymorphism:

SEQ ID NO: 203, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 234, SEQ ID NO: 235, and SEQ ID NO: 238,

or a complementary sequence thereto, or a partial sequence thereof, and in Group B, preferred is a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing a base sequence selected from the group consisting of the following base sequences:

SEQ ID NO: 533, SEQ ID NO: 516, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526,

SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 535, SEQ ID NO: 531, and SEQ ID NO: 532,

or a complementary sequence thereto.

Here, these base sequences are sequences corresponding to a nucleic acid molecule used in the detection of a high-risk allele.

[**0137**] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting an onset risk of glaucoma in the present invention, in a case where any two or more single nucleotide polymorphisms are combined, the kit usable in detecting or predicting a risk is

preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing a base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto, wherein the kit is a kit corresponding to two or more different single nucleotide polymorphisms thereof,

more preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 218 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing a base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 535 or a complementary sequence thereto, wherein the kit is a kit corresponding to two or more different single nucleotide polymorphisms thereof,

even more preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from the group consisting of the following pairs of base sequences containing a single nucleotide polymorphism or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a

nucleic acid molecule comprising a base sequence, wherein the base sequence contains a base sequence or a pair of base sequences, selected from Group B consisting of base sequences **aa** to **rr** or pairs of the base sequences, or a complementary sequence thereto, wherein the kit is a kit corresponding to two or more different single nucleotide polymorphisms thereof,

wherein in pairs of SEQ ID NOs: shown in **a** to **r**, each of the pairs of sequences corresponds to one single nucleotide polymorphism, and each of the base sequences is a base sequence containing an allele opposite to each other of the single nucleotide polymorphism on a 31st base, and

in SEQ ID NOs: shown in **aa** to **rr** or pairs of the SEQ ID NOs:, each of the base sequences or the pair of base sequences is a sequence for the nucleic acid molecule or a pair of sequences for the nucleic acid molecule, used in the detection of one single nucleotide polymorphism,

wherein **a** and **aa**, **b** and **bb**, **c** and **cc**, **d** and **dd**, **e** and **ee**, **f** and **ff**, **g** and **gg**, **h** and **hh**, **i** and **ii**, **j** and **jj**, **k** and **kk**, **l** and **ll**, **m** and **mm**, **n** and **nn**, **o** and **oo**, **p** and **pp**, **q** and **qq**, and **r** and **rr** respectively correspond to the same single nucleotide polymorphism,

Group A

a: SEQ ID NO: 203 and/or SEQ ID NO: 204,

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

c: SEQ ID NO: 207 and/or SEQ ID NO: 208,

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

e: SEQ ID NO: 211 and/or SEQ ID NO: 212,

f: SEQ ID NO: 213 and/or SEQ ID NO: 214,

g: SEQ ID NO: 215 and/or SEQ ID NO: 216,

h: SEQ ID NO: 217 and/or SEQ ID NO: 218,

i: SEQ ID NO: 219 and/or SEQ ID NO: 220,

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224,

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

m: SEQ ID NO: 227 and/or SEQ ID NO: 228,

n: SEQ ID NO: 229 and/or SEQ ID NO: 230,

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238, and

Group B

aa: SEQ ID NO: 515 and/or SEQ ID NO: 533,

bb: SEQ ID NO: 516,

cc: SEQ ID NO: 517,

dd: SEQ ID NO: 518 and/or SEQ ID NO: 534,

ee: SEQ ID NO: 519,

ff: SEQ ID NO: 520,

gg: SEQ ID NO: 521,

hh: SEQ ID NO: 522,

ii: SEQ ID NO: 523,

jj: SEQ ID NO: 524,

kk: SEQ ID NO: 525,

ll: SEQ ID NO: 526,

mm: SEQ ID NO: 527,

nn: SEQ ID NO: 528,

oo: SEQ ID NO: 529,

pp: SEQ ID NO: 530 and/or SEQ ID NO: 535,

qq: SEQ ID NO: 531, and

rr: SEQ ID NO: 532,

even more preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from Group A consisting of pairs of the base sequences containing a single nucleotide polymorphism listed above or a complementary sequence thereto, or a partial sequence thereof, and/or a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing a base sequence selected from Group B consisting of pairs of the base sequences listed above or a complementary sequence thereto, wherein the kit is a kit corresponding to ten or more different single nucleotide polymorphisms thereof, and

even more preferably a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein

the base sequence is a base sequence containing a single nucleotide polymorphism, selected from Group A consisting of pairs of the base sequences containing a single nucleotide polymorphism listed above or a complementary sequence thereto, or a partial sequence thereof, and/or a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing a base sequence selected from Group B consisting of pairs of the base sequences listed above or a complementary sequence thereto, wherein the kit is a kit corresponding to all the different single nucleotide polymorphisms thereof.

[0138] In addition, it is preferable that the single nucleotide polymorphisms to be used in combination are those that are not in the state of linkage disequilibrium, and from this viewpoint, in all the embodiments of the combinations mentioned above, supposing that, in Group A,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

a: SEQ ID NO: 203 and/or SEQ ID NO: 204, and

b: SEQ ID NO: 205 and/or SEQ ID NO: 206,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 1,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

c: SEQ ID NO: 207 and/or SEQ ID NO: 208, and

d: SEQ ID NO: 209 and/or SEQ ID NO: 210,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 2,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

j: SEQ ID NO: 221 and/or SEQ ID NO: 222,

k: SEQ ID NO: 223 and/or SEQ ID NO: 224, and

l: SEQ ID NO: 225 and/or SEQ ID NO: 226,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 3,

a group composed of a base sequence containing a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is a base sequence belonging to the group consisting of:

o: SEQ ID NO: 231 and/or SEQ ID NO: 232,

p: SEQ ID NO: 233 and/or SEQ ID NO: 234,

q: SEQ ID NO: 235 and/or SEQ ID NO: 236, and

r: SEQ ID NO: 237 and/or SEQ ID NO: 238,

or a complementary sequence thereto, or a partial sequence thereof, is named as a base sequence of Group 4, and

that in Group B,

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

aa: SEQ ID NO: 515 and/or SEQ ID NO: 533, and

bb: SEQ ID NO: 516,

or a complementary sequence thereto, is named as a base sequence of Group 1,

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

cc: SEQ ID NO: 517, and

dd: SEQ ID NO: 518 and/or SEQ ID NO: 534

or a complementary sequence thereto, is named as a base sequence of Group 2,

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

jj: SEQ ID NO: 524,

kk: SEQ ID NO: 525, and

ll: SEQ ID NO: 526,

or a complementary sequence thereto, is named as a base sequence of Group 3, and

a group composed of a base sequence containing a base sequence belonging to the group consisting of:

oo: SEQ ID NO: 529,

pp: SEQ ID NO: 530 and/or SEQ ID NO: 535,

qq: SEQ ID NO: 531, and

rr: SEQ ID NO: 532,

or a complementary sequence thereto, is named as a base sequence of Group 4,

it is preferable to use

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising any one of the base sequences in Group 1 when the base sequences belonging to Group 1 are used,

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising any one of the base sequences in Group 2 when the base sequences belonging to Group 2 are used,

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising any one of the base sequences in Group 3 when the base sequences belonging to Group 3 are used, and/or

a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising any one of the base sequences in Group 4 when the base sequences belonging to Group 4 are used.

[0139] In all the combinations mentioned above, in Group A, preferred is a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising an allele of a single nucleotide polymorphism located on a 31st base of a base sequence, wherein the base sequence is a base sequence containing a single nucleotide polymorphism, selected from the group consisting of the following base sequences containing a single nucleotide polymorphism:

SEQ ID NO: 203, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 234, SEQ ID NO: 235, and SEQ ID NO: 238,

or a complementary sequence thereto, or a partial sequence thereof, and in Group B, preferred is a kit of detecting a single nucleotide polymorphism associated with the onset of glaucoma or a kit of predicting an onset risk of glaucoma, using a nucleic acid molecule comprising a base sequence containing a base sequence selected from the group consisting of the following base sequences:

SEQ ID NO: 533, SEQ ID NO: 516, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 535, SEQ ID NO: 531, and SEQ ID NO: 532,

or a complementary sequence thereto.

Here, these base sequences are sequences corresponding to a nucleic acid molecule used in the detection of a high-risk allele.

[0140] (Method of Predicting Onset Risk of Glaucoma, Including Performing the Predicting Risk in Two-Steps or Multi-Steps)

When a prediction of an onset risk of glaucoma using a single nucleotide polymorphism in the present invention is carried out, it can be performed in two or more steps as follows; candidates who are considered

that precise prediction of an onset risk of glaucoma is necessary are selected, and the candidates are subjected to detailed prediction of a risk.

[0141] In a case where prediction of a risk is performed in two or more multi-steps, first, prediction of an onset risk of glaucoma mentioned above is preformed on at least one single nucleotide polymorphism in the present invention, preferably any one or several single nucleotide polymorphisms, and subsequently, prediction of detailed risks may be performed using a combination of the single nucleotide polymorphisms of the present invention mentioned above. The number of combinations may be further increased as occasion demands, whereby precision of the prediction of a risk can also be improved. As described above, by performing prediction of a risk in two or more multi-steps, the reduction in costs for performing the prediction of a risk and the prediction of a risk in a high precision can be both accomplished.

[0142] The prediction of a risk in an initial step may be a convenient method of predicting a risk. For example, a method of predicting a risk so that an immobilized probe capable of detecting at least one of the single nucleotide polymorphisms, preferably any one or several single nucleotide polymorphisms, is immobilized in a manner that at least one of the single nucleotide polymorphisms in the present invention is detectable is a convenient method, and can be realized at a low cost. Here, as to a method for nucleic acid extraction in this case, a kit that can be realized according to a known technique, or a commercially available simple kit for nucleic acid extraction can be used. It is convenient to use a method including the steps of using, for example, an enzyme-labeled probe as the immobilized probe

used in the prediction of a risk as described above, and detecting the probe according to a colorimetric method. As to the samples used in the detection, those that are obtained in a relatively low penetration, such as saliva, oral mucosa cells, urine, hair root, blood or white blood cells are preferred.

[0143] The prediction of a risk in a next step may be a method of predicting a risk with an emphasis on precision. For example, the detection of a single nucleotide polymorphism associated with the onset of glaucoma is carried out by combining two or more single nucleotide polymorphisms in the present invention mentioned above, whereby prediction of a risk may be performed in a high precision.

[0144] By performing prediction of a risk in two or more multi-steps, the precision for prediction of a risk can be improved, while reducing the costs or lowering a burden on a subject at an initial step to a minimum level.

[0145] According to the method disclosed in the present invention, the determination can be made that an individual who has an allele or genotype on the genome that is identified in a high frequency in glaucoma patients disclosed in the present invention has a high risk of the onset of glaucoma in future, and that an individual who does not have an allele or genotype that is identified in a high frequency in the glaucoma patients has a low risk of the onset of glaucoma in future.

[0146] In addition, an individual having an allele or genotype on the genome that is identified in a high frequency in glaucoma patients disclosed in the present invention has a possibility of being in an early stage of glaucoma that is difficult to be diagnosed according to a simple method of determination of glaucoma, such as measurement of intraocular pressure or

examination of ocular fundus, and that is diagnosed for the first time after performing visual field examination. Therefore, a single nucleotide polymorphism in the present invention is detected, whereby whether or not the visual field examination is required can be screened. On the other hand, in a case where an individual who is suspected of being glaucoma has an allele or genotype associated with glaucoma in the present invention on the genome, there is a high probability that the individual who is suspected of being glaucoma is to be diagnosed as glaucoma.

EXAMPLES

[0147] The present invention will be specifically described hereinbelow by Examples, and Examples are given for illustration purposes for a better comprehension of the present invention, without intending to limit the scope of the present invention thereto. Here, in the following Examples, as to generally used molecular biological methods that are not specifically described in detail, methods and conditions described in a textbook such as *Molecular Cloning* (Joseph Sambrook et al., *Molexular Cloning - A Laboratory Manual, 3rd Edition*, Cold Spring Harbor Laboratory Press, 2001) or the like are used.

[0148] In the present invention, a total DNA was extracted from blood of each of patients diagnosed as glaucoma, and non-patients diagnosed as being not with glaucoma and determined not to have any family history in glaucoma according to a medical interview, and gene loci associated with the disease were analyzed based on about 500,000 known single nucleotide polymorphisms on the human genome as an index to determine an

association of a single nucleotide polymorphism and the disease. In addition, patients with fast progression of glaucoma, i.e. progressive glaucoma cases, and patients with slow progression of glaucoma, i.e. nonprogressive glaucoma cases were subjected to the identification of a single nucleotide polymorphism and the association of the single nucleotide polymorphism with the progression in the same manner as above.

[0149] Example 1 DNA Extraction from Specimens

In DNA extraction from specimens, a commercially available automated nucleic acid extraction apparatus (QUIAGEN, BIOROBOT (registered trademark) EZ1), and a kit for extraction of a nucleic acid (EZ1 DNA Blood 350 μl Kit) compatible to the extraction apparatus and in which nucleic acids absorbed to magnetic beads were collected by a magnetic force were used. A total DNA was extracted in accordance with the instruction manuals of the apparatus and kit. According to the present method, a total DNA of about 5 μg was obtained from 350 μL of a blood specimen.

[0150] Example 2 Analysis of Single Nucleotide Polymorphism

In the analysis of single nucleotide polymorphisms, a commercially available microarray type single nucleotide polymorphism analysis kit (Affimetrix (GeneChip(registered trademark)Human Mapping 500K) (hereinafter also referred to as microarray) capable of analyzing about 500,000 known single nucleotide polymorphisms on the human genome was used. In the detection of single nucleotide polymorphisms, a scanner (Affimetrix (GeneChip(registered trademark) Scanner 3000)) compatible to the kit was used. In the analysis of single nucleotide polymorphisms, a

specialized analysis software (Affimetrix (GTYPE(registered trademark))) was used.

[0151] The total DNA extracted in Example 1 was treated in accordance with the instruction manuals of the kit and apparatus, and applied to a microarray, and a single nucleotide polymorphism existing on the DNA extracted from the specimen was analyzed. Briefly explaining, a sample obtained by treating 250 ng of a total DNA with a restriction enzyme NspI and a sample obtained by treating 250 ng of a total DNA with a restriction enzyme StyI were prepared, and amplified by a PCR method with adaptors bound to the protruding ends of each of the samples. A PCR product was collected, and fragmented with DNaseI, and the ends of the fragmented PCR products were biotin-labeled using the labeling reagent contained in the kit. A buffer for hybridization was added to the PCR products that were already fragmented at both ends and labeled, the mixture was heat-treated at 99°C for 10 minutes, and incubated at 49°C for 1 minute, and the resulting mixture was injected to a microarray for NspI-treated sample or a microarray for StyI-treated sample depending on a firstly treated restriction enzyme, and hybridized at 49°C for 16 to 18 hours. After the termination of hybridization, the microarray was stained with streptavidin-phycoerythrin. A fluorescence from phycoerythrin bound via biotin and streptavidin to DNA ends of samples hybridized with an immobilized allele-specific probe was read using the scanner mentioned above, and analyzed with the software mentioned above. Probes corresponding to about 250,000 single nucleotide polymorphisms each are previously immobilized to the microarray for NspI-treated sample and the microarray for StyI-treated

sample, respectively, and analytical results for about 500,000 single nucleotide polymorphisms per one sample were obtained by combination of both the results. According to the present method, opposite alleles of each of the single nucleotide polymorphisms were read with a single operation, and consequently, a genotype was determined. In this case, it was determined that the genotype was a heterozygote in a case where both signals from each of the alleles constituting a single nucleotide polymorphism were detected, and that the genotype was a homozygote of the detected allele in a case where only either one of the signals was detected.

[0152] Here, in accordance with the instruction manual of the kit, as the probe immobilized to the kit, a probe for a sense strand or a probe for an antisense strand of the genome is used. In addition, according to the datasheet of the kit, the determination results for the present kit using 270 samples and those in HapMap are compared for single nucleotide polymorphisms overlapping between single nucleotide polymorphisms reported in the HapMap project and single nucleotide polymorphisms in the kit. As a result, a concordance rate of the single nucleotide polymorphisms shows 99% or more.

[0153] Example 3 Comparison of Single Nucleotide Polymorphisms Between Glaucoma Patients and Non-Patients

The comparison on single nucleotide polymorphisms associated with a disease was made in accordance with the method used in the studies on genes responsible for age-related macular degeneration by Klein et al (*Science*, **308**, 385, 2005).

[0154] Primary open-angle glaucoma patients and normal tension glaucoma patients that were diagnosed on the basis of Guidelines offered by Japan Glaucoma Society were assigned to a glaucoma patient group, and healthy individuals that were confirmed to have no family history of glaucoma according to a medical interview were assigned to a non-patient group. Blood donated under the consent on free will of the participants after having sufficiently explained the contents of studies from 418 cases of the glaucoma patient group and 300 controls of the non-patient group was used as specimens, a total DNA was extracted from the specimens according to the method described in Example 1, and the analysis of single nucleotide polymorphisms was performed according to the method described in Example 2. The analytical results of a single nucleotide polymorphism obtained in each of the patients were stored in the Laboratory Information Management System (World Fusion, LaboServer) adopting a relational database. A specialized analysis program for a single nucleotide polymorphism was created and loaded within the system, and the analysis was performed as follows: A single nucleotide polymorphism considered to have a high experimental reliability was extracted by rejecting a single nucleotide polymorphism having a call rate of less than 90% in both the glaucoma patient group and the non-patient group, a single nucleotide polymorphism having a difference in call rates between the glaucoma patient group and the non-patient group by 5% or more, a single nucleotide polymorphism having a minor allele frequency of less than 5%, and a single nucleotide polymorphism that is determined to deviate from the Hardy-Weinberg's equilibrium under conditions of a p-value of 1×10^{-4} or

less according to a chi-square test, and allele frequencies and genotype frequencies of the single nucleotide polymorphisms were compared between the groups. The allele frequencies and the genotype frequencies were statistically compared according to the chi-square test. As to single nucleotide polymorphisms showing a p-value of 1×10^{-3} or less, cluster images serving as a basis for the determination of a genotype were confirmed. In a case where the determination of a genotype was made regardless of unclearness of the separation among clusters, the single nucleotide polymorphism was considered to be a non-subject of the analysis. In other words, the errors in the determination of a genotype were excluded by this step. The evaluation of the cluster was performed without informing the names of single nucleotide polymorphisms and the critical rates. Single nucleotide polymorphisms of which allele or genotype shows association with glaucoma at a p-value of 1×10^{-4} or less, i.e. -log P of 4 or more are listed in Tables 1 to 2. Here, the odds ratio for association of an allele with a disease, and the odds ratio for association of a genotype with a disease in each of the tables, respectively, were calculated on the basis of the following formulas (1) to (5).

Allele Frequency = Number of Detection of an Allele in Group/Total Number of Detection of Alleles in Group

formula (1)

Genotype Frequency = Number of Detection of a Genotype in Group/Total Number of Detection of Genotypes in Group formula (2)

Odds Ratio for Allele

= [(Number of Detection of an Allele Identified in High Frequency in Glaucoma Patient Group, in Glaucoma Patient Group)/(Number of Detection of an Allele Opposite to the Allele Identified in High Frequency in Glaucoma Patient Group, in Glaucoma Patient Group)]/

[(Number of Detection of the Allele Identified in High Frequency in Glaucoma Patient Group, in Non-Patient Group)/(Number of Detection of the Allele Opposite to the Allele Identified in High Frequency in Glaucoma Patient Group, in Non-Patient Group)] formula (3)

Odds Ratio for Genotype of Homozygote =

[(Number of Detection of a Genotype Having Homozygote of an Allele Identified in High Frequency in Glaucoma Patient Group, in Glaucoma Patient Group)/(Number of Detection of a Genotype Having Homozygote of an Allele Identified in High Frequency in Non-Patient Group, in Glaucoma Patient Group)]/

[(Number of Detection of the Genotype Having Homozygote of the Allele Identified in High Frequency in Glaucoma Patient Group, in Non-Patient Group)/(Number of Detection of the Genotype Having Homozygote of the Allele Identified in High Frequency in Non-Patient Group, in Non-Patient Group)] formula (4)

Odds Ratio for Genotype of Heterozygote

= [(Number of Detection of a Genotype of Heterozygote in Glaucoma Patient Group)/(Number of Detection of a Genotype Having Homozygote of an Allele Identified in High Frequency in Non-Patient Group, in Glaucoma Patient Group)]/

[(Number of Detection of the Genotype Having Homozygote in Non-Patient Group)/(Number of Detection of the Genotype Having Homozygote of the Allele Identified in High Frequency in Non-Patient Group, in Non-Patient Group)] formula (5)

[0155] [Table 1]

dbSNP ID	Allele1 / Allele2	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	High-Risk Allele	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote1) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)	Sequence Containing Allele 1	Sequence Containing Allele 2
rs12632110	A/G	SEMA3F Intron18 (NM_004186.2)	3	50199229	4.27	0.54	0.44	Allele 1	1.54	3.60	2.34	1.71	SEQ ID No:1	SEQ ID No:2
rs2233476	A/C	CYB561D2 Exon1 (NM_007022.3)	3	50363387	5.57	0.55	0.42	Allele 1	1.66	4.91	2.75	1.84	SEQ ID No:3	SEQ ID No:4
rs9852677	C/T	GNAI2 Intron4 (NM_002070.1)	3	50266621	5.27	0.56	0.44	Allele 2	1.63	4.62	2.70	1.80	SEQ ID No:5	SEQ ID No:6
rs2236944	G/T	GNAI2 Intron4 (NM_002070.1)	3	50267197	5.00	0.55	0.43	Allele 2	1.61	4.41	2.60	1.84	SEQ ID No:7	SEQ ID No:8
rs6786523	A/G	CACNA2D2 Intron2 (NM_006030.1)	3	50499225	4.05	0.60	0.49	Allele 1	1.53	3.60	2.46	1.80	SEQ ID No:9	SEQ ID No:10
rs1467913	G/T	CACNA2D2 Intron2 (NM_006030.1)	3	50500021	4.22	0.60	0.50	Allele 2	1.54	3.73	2.49	1.79	SEQ ID No:11	SEQ ID No:12
rs2004243	A/G	LOC51337 +641bp (NM_016647.1)	8	143815988	4.46	0.45	0.34	Allele 1	1.58	3.85	2.25	1.78	SEQ ID No:13	SEQ ID No:14
rs3761980	C/T	SLC26A8 -1529bp (NM_052961.2), SLC26A8 -1636bp (NM_138718.1)	6	36101884	4.12	0.93	0.87	Allele 2	2.05	3.48	6.40	3.13	SEQ ID No:15	SEQ ID No:16
rs16884919	A/G	MAPK14 Intron10 (NM_001315.1), MAPK14 Intron10 (NM_139012.1), MAPK14 Intron9 (NM_139014.1), MAPK14 +982bp (NM_139013.1)	6	36179495	4.12	0.93	0.87	Allele 2	2.05	3.48	6.40	3.13	SEQ ID No:17	SEQ ID No:18
rs16883860	C/T	MAPK14 Intron1 (NM_139013.1), MAPK14 Intron1 (NM_001315.1), MAPK14 Intron1 (NM_139012.1), MAPK14 Intron1 (NM_139014.1)	6	36110440	4.42	0.94	0.87	Allele 2	2.14	3.74	6.41	3.00	SEQ ID No:19	SEQ ID No:20
rs10513095	G/T	CLSTN2 Intron1 (NM_022131.1)	3	141219021	4.52	0.84	0.75	Allele 2	1.73	3.73	3.02	1.74	SEQ ID No:21	SEQ ID No:22
rs7081455	A/C	PLXDC2 +69770bp (NM_032812.7)	10	20678891	4.33	0.83	0.74	Allele 1	1.70	3.91	1.91	0.98	SEQ ID No:23	SEQ ID No:24
rs7850541	C/T	GBGT1 -11253bp (NM_021996.3)	9	133080108	4.15	0.76	0.66	Allele 1	1.60	3.89	3.35	2.33	SEQ ID No:25	SEQ ID No:26
rs10116267	C/T	PSAT1 Intron5 (NM_021154.3), PSAT1 Intron5 (NM_058179.2)	9	78151286	4.24	0.78	0.69	Allele 1	1.63	3.50	2.18	1.24	SEQ ID No:27	SEQ ID No:28
rs10116231	A/G	PSAT1 Intron5 (NM_021154.3), PSAT1 Intron5 (NM_058179.2)	9	78151153	4.11	0.78	0.69	Allele 2	1.61	3.37	2.18	1.26	SEQ ID No:29	SEQ ID No:30
rs6813301	G/T	MGC45800 +203455bp (NM_178838.2)	4	183234501	4.16	0.12	0.06	Allele 2	2.24	3.67	2.07	2.45	SEQ ID No:31	SEQ ID No:32
rs11945595	C/T	MGC45800 +201900bp (NM_178838.2)	4	183236056	4.07	0.12	0.06	Allele 2	2.24	3.57	2.04	2.45	SEQ ID No:33	SEQ ID No:34
rs2049723	A/G	SPON1 -17894bp (NM_006108.1)	11	13922920	4.78	0.76	0.65	Allele 1	1.66	3.96	2.87	1.83	SEQ ID No:35	SEQ ID No:36
rs1159623	C/G	CNTN5 Intron2 (NM_014361.2), CNTN5 Intron2 (NM_175566.1)	11	98877941	4.18	0.45	0.34	Allele 2	1.55	3.88	2.21	1.84	SEQ ID No:37	SEQ ID No:38
rs7109406	A/C	CNTN5 Intron2 (NM_014361.2), CNTN5 Intron2 (NM_175566.1)	11	98867701	4.17	0.45	0.35	Allele 2	1.55	4.01	2.17	1.89	SEQ ID No:39	SEQ ID No:40

[0156] [Table 2]

dbSNP ID	Allele1 / Allele2	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	High-Risk Allele	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote1) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)	Sequence Containing Allele 1	Sequence Containing Allele 2
rs4763559	C/G	KLRA1 +10130bp (NM_006611.1)	12	10622909	4.48	0.75	0.65	Allele 2	1.62	3.70	2.32	1.34	SEQ ID No:41	SEQ ID No:42
rs4763531 (rs9739469)	A/G	KLRA1 +3474bp (NM_006611.1)	12	10629565	4.11	0.74	0.65	Allele 1	1.58	3.31	2.29	1.39	SEQ ID No:43	SEQ ID No:44
rs2125094	C/T	KLRA1 +11027bp (NM_006611.1)	12	10622012	4.38	0.74	0.64	Allele 1	1.61	3.59	2.34	1.37	SEQ ID No:45	SEQ ID No:46
rs2233476	A/C	CYB561D2 Exon1 (NM_007022.3)	3	50363387	5.57	0.55	0.42	Allele 1	1.66	4.91	2.75	1.84	SEQ ID No:47	SEQ ID No:48
rs9852677	C/T	GNAI2 Intron4 (NM_002070.1)	3	50266621	5.27	0.56	0.44	Allele 2	1.63	4.62	2.70	1.80	SEQ ID No:49	SEQ ID No:50
rs2236944	G/T	GNAI2 Intron4 (NM_002070.1)	3	50267197	5.00	0.55	0.43	Allele 2	1.61	4.41	2.60	1.84	SEQ ID No:51	SEQ ID No:52
rs4430902	A/G	GULP1 Intron1 (NM_016315.1)	2	189010443	3.57	0.85	0.77	Allele 1	1.64	4.48	1.14	0.54	SEQ ID No:53	SEQ ID No:54
rs10804020	C/T	GULP1 Intron1 (NM_016315.1)	2	189028382	2.93	0.84	0.77	Allele 1	1.54	4.10	1.02	0.50	SEQ ID No:55	SEQ ID No:56
rs13137759	C/T	DKFZp686L1814 Intron2 (NM_194282.1)	4	84262335	3.39	0.82	0.74	Allele 2	1.58	4.23	1.32	0.64	SEQ ID No:57	SEQ ID No:58
rs11737784	A/C	DKFZp686L1814 -11708bp (NM_194282.1)	4	84300869	3.15	0.81	0.74	Allele 2	1.54	4.14	1.25	0.61	SEQ ID No:59	SEQ ID No:60
rs9498701	C/T	GRIK2 Intron6 (NM_021956.2), GRIK2 Intron6 (NM_175768.1)	6	102336911	0.93	0.59	0.55	Allele 2	1.19	4.10	1.17	0.57	SEQ ID No:61	SEQ ID No:62
rs9322609	A/G	GRIK2 Intron8 (NM_021956.2), GRIK2 Intron8 (NM_175768.1)	6	102357540	0.67	0.58	0.55	Allele 2	1.14	4.04	1.11	0.55	SEQ ID No:63	SEQ ID No:64
rs10130333	A/C	CHES1 Intron2 (NM_005197.1)	14	88929499	3.97	0.69	0.59	Allele 1	1.54	4.36	2.73	2.46	SEQ ID No:65	SEQ ID No:66
rs11133030	C/T	FBXO8 +139977bp (NM_012180.1)	4	175392565	2.16	0.70	0.63	Allele 1	1.36	4.01	2.46	2.79	SEQ ID No:67	SEQ ID No:68
rs2220757	A/C	BARX2 +108243bp (NM_003658.3)	11	128935268	1.34	0.71	0.66	Allele 2	1.26	4.03	0.95	0.50	SEQ ID No:69	SEQ ID No:70
rs7109406	A/C	CNTN5 Intron2 (NM_014361.2), CNTN5 Intron2 (NM_175566.1)	11	98867701	4.17	0.45	0.35	Allele 2	1.55	4.01	2.17	1.89	SEQ ID No:71	SEQ ID No:72
rs2347897	C/T	LOC402300 Intron2 (XM_377974), CALD1 Intron1 (NM_004342.5), CALD1 Intron1 (NM_033138.2), CALD1 Intron1 (NM_033157.2), CALD1 -95572bp (NM_033139.2), CALD1 -95572bp (NM_033140.2)	7	133937842	2.98	0.39	0.31	Allele 1	1.45	4.05	1.58	2.02	SEQ ID No:73	SEQ ID No:74
rs7794696	A/G	LOC402300 Intron1 (XM_377974), CALD1 Intron1 (NM_004342.5), CALD1 Intron1 (NM_033138.2), CALD1 Intron1 (NM_033157.2), CALD1 -72140bp (NM_033139.2), CALD1 -72140bp (NM_033140.2)	7	133961274	3.29	0.39	0.30	Allele 2	1.49	4.01	1.67	1.99	SEQ ID No:75	SEQ ID No:76
rs803594	C/G	VGLL2 -7136bp (NM_153453.1), VGLL2 -7152bp (NM_182645.2)	6	117686278	0.94	0.21	0.18	Allele 2	1.24	4.31	0.49	1.90	SEQ ID No:77	SEQ ID No:78
rs762164	A/C	RUNX1 Intron5 (NM_001754.2)	21	35140644	0.52	0.44	0.42	Allele 2	1.12	4.02	1.05	1.98	SEQ ID No:79	SEQ ID No:80

[0157] Tables 1 and 2 list dbSNP ID number or Affimetrix Array ID number specifying known single nucleotide polymorphisms obtained, each of bases constituting Allele 1 and Allele 2, the exon, intron information (in a case where a single nucleotide polymorphism exists on a gene, the gene name and the exon or intron in which SNP exists are shown, and in a case where a single nucleotide polymorphism does not exist on a gene, neighboring genes and a distance between the gene and the single nucleotide polymorphism are shown), the chromosome number at which a single nucleotide polymorphism exists, the physical location of a single nucleotide polymorphism, the p-value for an allele according to a chi-square test (-log P), the high-risk allele frequencies in the glaucoma patient group and the non-patient group, the type of the high-risk allele (indicating whether the high-risk allele is Allele 1 or Allele 2), the odds ratio for an allele, the p-value for a genotype according to a chi-square test (-log P), the odds ratio for a genotype of a homozygote and the odds ratio for a genotype of a heterozygote, and SEQ ID NO of the sequence containing Allele 1 and Allele 2 in each of the polymorphic sites. Here, one of ordinary skill in the art can obtain the information for sequences or alleles of the single nucleotide polymorphisms from dbSNP ID number or Affimetrix array ID number mentioned above.

[0158] When the allele or genotype frequencies listed in Tables 1 to 2 were compared between the non-patients without family history and the glaucoma patients, a statistical difference was found. By determining an allele of any one of these single nucleotide polymorphisms, whether or not an allele that is identified in a higher frequency in the glaucoma patient

group than that of the non-patient group exists in the sample can be determined.

[0159] Specifically, when a first single nucleotide polymorphism listed in Tables 1 and 2 is explained as an example, one polymorphic site exists in a nucleic acid molecule shown in SEQ ID NO: 1 or 2 occupying a gene locus homologous to each other. In detail, a single nucleotide polymorphism is associated with the onset of glaucoma, of which 31st base is either A (Allele 1) or G (Allele 2), wherein Allele 1 indicated as a high-risk allele, that is, an allele of being A in the single nucleotide polymorphism is identified in a high frequency in the glaucoma patient group. Further, using the odds ratio for an allele, or the odds ratio for a genotype of a homozygote and the odds ratio for a genotype of a heterozygote, the degree of which the risk of a disease increases can be predicted in a case of having the allele or genotype. Similarly, all the sequences disclosed in Tables 1 and 2 have a polymorphic site associated with glaucoma in the sequence, and one allele or at least one genotype in the polymorphic site is identified in a high frequency in the glaucoma patient group.

[0160] According to the above studies, 40 single nucleotide polymorphisms of which alleles or genotypes were associated with glaucoma at a p-value of 1×10^{-4} or less existing in clusters in relatively adjacent regions on the genome were found in 21 regions.

[0161] The allele or genotype identified in a high frequency in the glaucoma patient group of a single nucleotide polymorphism listed in Tables 1 and 2 can be used as a marker showing that an onset risk of glaucoma is high. On the other hand, an allele that is opposite to the allele or a genotype other than

the genotype can be used as a marker showing that an onset risk of glaucoma is low.

[0162] Next, the surrounding regions and/or genes of the single nucleotide polymorphisms listed in Tables 1 and 2 were determined on the basis of the database provided by the HapMap project. In detail, regions in which single nucleotide polymorphisms that were considered to be in a linkage disequilibrium with the single nucleotide polymorphisms listed in Tables 1 and 2 exist were determined, on the basis of the linkage disequilibrium data in combination of the Japanese and the Chinese in the HapMap project.

[0163] Also, in a case where the single nucleotide polymorphism listed in Tables 1 and 2 exists in the linkage disequilibrium region containing the gene, the physical location and the gene name of the region were determined. On the other hand, in a case where the single nucleotide polymorphism listed in Tables 1 and 2 exists in the linkage disequilibrium region without containing the gene, only the physical location of the region was determined. In addition, in a case where the single nucleotide polymorphism listed in Tables 1 and 2 exists on one gene beyond the linkage disequilibrium region, only the gene name was determined.

[0164] A single nucleotide polymorphism of which p-value is lowest in each region is considered to be a single nucleotide polymorphism representing the region. Tables 3 and 4 list a single nucleotide polymorphism representing the region, the chromosome number at which the region exists, the physical location of the region (start point and end point) and the gene name contained in the region.

[0165] [Table 3]

Representative SNP (SNP with Lowest p-value of the Region)	Chromosome	Start Point of Physical Location	End Point of Physical Location	Genes Contained in the Region
rs16883860	6	36,014,367	36,248,614	SLC26A8
				DPRXP2
				MAPK14
				MAPK13
rs2233476	3	49,952,596	50,516,561	RBM6
				RBM5
				SEMA3F
				GNAT1
				SLC38A3
				GNAI2
				SEMA3B
				FLJ38608
				C3orf45
				IFRD2
				HYAL3
				NAT6
				HYAL1
				HYAL2
				TUSC2
				RASSF1
				ZMYND10
				TUSC4
				CYB561D2
				TMEM115
				CACNA2D2
rs2004243	8	143,691,186	143,902,698	ARC
				AK092432
				JRK
				PSCA
				LY6K
				LOC51337
				C8orf55
				SLURP1
				LYPDC2
				LYNX1
				AK126845
				LY6D
				LYPD2
rs10513095	3	-	-	CLSTN2
rs7081455	10	20,663,479	20,716,201	no gene
rs7850541	9	134,756,557	135,192,865	TSC1
				GFI1B
				LOC158078
				GTF3C5
				CEL
				CELP
				RALGDS
				GBGT1
				OBP2B
				LOC286310
				ABO
				LOC653163
				SURF6

[0166] [Table 4]

Representative SNP (SNP with Lowest p-value of the Region)	Chromosome	Start Point of Physical Location	End Point of Physical Location	Genes Contained in the Region
rs7109406	11	-	-	CNTN5
rs4763559	12	10,535,930	10,724,935	LOC255308
				KLRA1
				FLJ10292
				STYK1
rs10116267	9	-	-	PSAT1
rs6813301	4	183,058,962	183,243,277	LOC643296
rs2049723	11	13,851,048	14,245,926	SPON1
rs9498701	6	-	-	GRIK2
rs2233476	3	49,952,596	50,516,561	RBM6
				RBM5
				SEMA3F
				GNAT1
				SLC38A3
				GNAI2
				SEMA3B
				FLJ38608
				C3orf45
				IFRD2
				HYAL3
				NAT6
				HYAL1
				HYAL2
				TUSC2
				RASSF1
				ZMYND10
				TUSC4
				CYB561D2
				TMEM115
				CACNA2D2
rs10130333	14	88,697,458	89,155,209	CHES1
				LOC646224
				CAP2P1
				LOC400236
rs4430902	2	188,904,662	189,286,159	GULP1
rs13137759	4	83,800,064	84,215,995	SCD4
				SEC31L1
				THAP9
				DKFZp686L1814
				COPS4
rs11133030	4	175,234,727	175,450,910	FBXO8
				KIAA1712
rs762164	21	35,049,200	35,343,511	RUNX1
rs7109406	11	-	-	CNTN5
rs2220757	11	128,920,427	128,953,084	no gene
rs803594	6	117,682,814	117,853,711	VGLL2
				ROS1
rs2347897	7	-	-	CALD1

[0167] The region listed in Tables 3 and 4 is a region or gene considered to be linked with a single nucleotide polymorphism listed in Tables 3 and 4 which is associated with glaucoma in the present invention, and a single nucleotide polymorphism which exists in these regions or genes is considered to be linked with a single nucleotide polymorphism in the present invention. In other words, any single nucleotide polymorphisms which exist in these regions are linked with the single nucleotide polymorphism which exists in the region as listed in Tables 3 and 4, and any of these single nucleotide polymorphisms can be used in the prediction of a risk of glaucoma in the same manner.

[0168] Also, a single nucleotide polymorphism of which allele or genotype shows association with glaucoma at a p-value of 1×10^{-3} or less, i.e. -log P of 3 or more, is also listed in Tables 5 to 25.

[0169] [Table 5]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs2139539	COL16A1 +69bp (NM_001856.2)	1	31,786,872	3.99	0.87	0.80	1.75	3.81	7.12	4.52
rs693421	ZP4 -45155bp (NM_021186.2)	1	234,425,131	3.53	0.55	0.45	1.48	3.77	2.14	2.02
rs2038845	CACNA1S Intron2 (NM_000069.1)	1	197,799,070	0.57	0.41	0.39	1.13	3.76	1.00	1.89
rs4040617	LOC284591 Intron2 (XM_211529)	1	819,185	0.24	0.17	0.15	1.09	3.68 ND		0.75
rs540782	ZP4 -43104bp (NM_021186.2)	1	234,423,080	3.43	0.56	0.46	1.47	3.52	2.09	1.96
rs2040073	LOC339442 -148785bp (XM_378855)	1	38,498,317	3.58	0.38	0.29	1.52	3.38	1.93	1.80
rs547984	ZP4 -42951bp (NM_021186.2)	1	234,422,927	3.48	0.55	0.46	1.47	3.35	2.10	1.88
rs10798882	PEF Intron1 (NM_012392.1)	1	31,777,640	3.52	0.86	0.79	1.67	3.35	6.05	3.84
rs2499601	ZP4 -50960bp (NM_021186.2)	1	234,430,936	3.24	0.55	0.46	1.45	3.23	2.05	1.89
rs909002	COL16A1 Intron44 (NM_001856.2)	1	31,808,728	3.47	0.84	0.77	1.63	3.19	4.38	2.94
rs2147798	CACNA1S Intron3 (NM_000069.1)	1	197,793,475	1.22	0.56	0.51	1.22	3.14	1.58	2.09
rs10752589	CSF3R -53414bp (NM_000760.2), CSF3R -53414bp (NM_156038.2), CSF3R -53414bp (NM_156039.2), CSF3R -53414bp (NM_172313.1)	1	36,671,016	3.61	0.18	0.11	1.77	3.13	2.06	1.92
rs2236913	PSEN2 Intron5 (NM_000447.1), PSEN2 Intron5 (NM_012486.1)	1	223,380,860	0.61	0.35	0.33	1.14	3.13	0.88	1.74
rs10518601	ELTD1 -94220bp (XM_371262)	1	79,312,758	0.27	0.79	0.78	1.08	3.08	3.51	4.57
rs17102821	ELTD1 -89304bp (XM_371262)	1	79,307,842	0.28	0.80	0.78	1.09	3.08	3.52	4.57
rs7525498	ELTD1 -102412bp (XM_371262)	1	79,320,950	0.30	0.80	0.78	1.09	3.04	3.53	4.54
rs2359112	MGC15882 +194951bp (NM_032884.2)	1	34,548,776	0.58	0.30	0.27	1.15	3.03	5.23	0.86
rs1892116	ELYS Intron2 (NM_175865.1), ELYS Intron2 (NM_015446.1)	1	243,406,363	3.15	0.75	0.67	1.49	2.91	2.89	2.07
rs7524405	PEF Intron1 (NM_012392.1)	1	31,777,672	3.27	0.84	0.77	1.59	2.89	3.77	2.54
rs704709	MGC39558 Intron8 (NM_152490.1)	1	231,947,005	3.45	0.61	0.52	1.48	2.83	2.20	1.39
rs1951626	SERPINC1 -5704bp (NM_000488.1)	1	170,623,758	3.34	0.38	0.30	1.49	2.66	2.33	1.43
rs11163089	MGC34032 Intron4 (NM_152697.2)	1	75,490,567	3.31	0.85	0.77	1.61	2.55	2.70	1.75
rs10430126	LOC388630 +220720bp (XM_371250)	1	47,934,070	3.10	0.64	0.55	1.45	2.54	2.08	1.33

[0170] [Table 6]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs16865980	RNF144 +1203466bp (NM_014746.2)	2	7,255,254	1.98	0.24	0.18	1.41	3.96	0.84	1.99
rs4953262	PRKCE Intron1 (NM_005400.2)	2	45,952,444	0.15	0.53	0.52	1.04	3.75	1.01	0.53
rs10170220	GULP1 Intron2 (NM_016315.1)	2	189,123,624	2.80	0.84	0.78	1.53	3.68	1.03	0.53
rs6717705	VIT Intron1 (NM_053276.2)	2	36,838,198	2.80	0.88	0.82	1.60	3.62	18.77	14.09
rs759428	VIT Intron1 (NM_053276.2)	2	36,844,694	2.76	0.88	0.82	1.59	3.58	18.68	14.12
rs4670589	VIT Intron1 (NM_053276.2)	2	36,840,872	2.72	0.88	0.82	1.59	3.57	18.77	14.29
rs10931358	GULP1 Intron2 (NM_016315.1)	2	189,096,087	2.69	0.84	0.77	1.52	3.55	1.02	0.53
rs11124532	VIT Intron1 (NM_053276.2)	2	36,840,580	2.65	0.88	0.82	1.58	3.50	18.48	14.14
rs828868	MGC22014 Intron8 (XM_371501)	2	74,236,159	3.37	0.66	0.57	1.47	3.48	2.06	1.10
rs11677028	LOC339789 Intron9 (NM_207358.1)	2	8,309,297	1.34	0.71	0.66	1.26	3.45	2.50	2.92
rs6431929	LOC339789 +418778p (NM_207358.1) SLC4A5 Intron5 (NM_033323.2),	2	8,255,994	1.22	0.69	0.65	1.24	3.43	2.32	2.78
rs2421844	SLC4A5 Intron5 (NM_133478.1), SLC4A5 Intron5 (NM_133479.1), SLC4A5 Intron1 (NM_021196.2)	2	74,451,749	3.42	0.48	0.38	1.48	3.43	2.39	1.13
rs7559118	FLJ34870 Intron4 (NM_207481.1)	2	133,706,762	2.37	0.64	0.56	1.37	3.34	2.15	2.25
rs17754672	PELI1 -61125bp (NM_020651.2)	2	64,312,259	2.49	0.24	0.17	1.49	3.27	6.36	1.11
rs7584987	QPCT +1296898p (NM_012413.2)	2	37,641,805	2.56	0.44	0.37	1.39	3.26	2.40	1.03
rs7571760	CDC42EP3 +1279858p (NM_006449.3)	2	37,654,409	3.06	0.40	0.31	1.46	3.13	2.69	1.17
rs6724538	QPCT +1275538p (NM_012413.2) SLC4A5 Intron2 (NM_033323.2),	2	37,639,669	3.33	0.42	0.32	1.48	3.12	2.49	1.16
rs13387588	SLC4A5 Intron2 (NM_133478.1), SLC4A5 Intron2 (NM_133479.1), SLC4A5 -19990bp (NM_021196.2) SP110 Intron3 (NM_004509.2),	2	74,473,795	3.27	0.48	0.39	1.46	3.10	2.29	1.15
rs7601299	SP110 Intron3 (NM_080424.1), SP110 Intron3 (NM_004510.2)	2	230,903,499	1.26	0.91	0.88	1.39	3.08	ND	ND

[0171] [Table 7]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs1198825	RAMP1 -3950bp (NM_005855.1)	2	238,546,337	3.82	0.44	0.34	1.52	3.07	2.23	1.57
rs10930321	STK39 -102538bp (NM_013233.1)	2	169,032,150	3.70	0.44	0.34	1.51	3.04	2.42	1.40
SNP_A-2170785	LTBP1 Intron2 (NM_206943.1), LTBP1 -181297bp (NM_000627.2)	2	33,090,031	1.24	0.78	0.73	1.27	3.01	3.21	3.52
rs12611812	CNTNAP5 Intron3 (NM_130773.2), CNTNAP5 Intron3 (NM_138996.1)	2	124,776,344	1.80	0.59	0.52	1.30	3.00	1.52	0.79
rs11123034	CNTNAP5 Intron3 (NM_130773.2), CNTNAP5 Intron3 (NM_138996.1)	2	124,776,617	1.80	0.59	0.52	1.30	3.00	1.52	0.79
rs7581836	SLC4A5 -7735bp (NM_033323.2), SLC4A5 -7735bp (NM_133478.1), SLC4A5 -7735bp (NM_133479.1), SLC4A5 -35247bp (NM_021196.2)	2	74,489,052	3.18	0.49	0.40	1.45	2.95	2.24	1.17
rs4430896	KBTBD9 -239670bp (XM_496546)	2	23,246,431	3.58	0.75	0.66	1.54	2.94	1.91	1.12
rs7574012	QPCT +126765bp (NM_012413.2)	2	37,638,881	3.04	0.41	0.32	1.45	2.81	2.49	1.22
rs9309484	DCTN1 +1471bp (NM_023019.1), DCTN1 +1471bp (NM_004082.2)	2	74,498,466	3.06	0.49	0.40	1.44	2.77	2.16	1.16
rs4666488	ODD -128777bp (NM_145260.1)	2	19,608,777	3.13	0.36	0.28	1.48	2.67	1.90	1.65
rs3771738	SLC4A5 Intron5 (NM_033323.2), SLC4A5 Intron5 (NM_133478.1), SLC4A5 Intron5 (NM_133479.1), SLC4A5 Intron1 (NM_021196.2)	2	74,452,572	3.04	0.48	0.40	1.43	2.65	2.14	1.19
rs4848607	FLJ14816 -60027bp (NM_032845.1)	2	120,999,954	3.28	0.75	0.66	1.50	2.58	2.33	1.61
rs4668312	LOC389059 -20365bp (XM_374017)	2	171,432,334	3.04	0.74	0.65	1.47	2.58	1.80	1.08
rs4411759	HTLF Intron2 (NM_002158.2)	2	48,468,133	3.16	0.55	0.46	1.44	2.57	2.07	1.57
rs2268794	SRD5A2 Intron1 (NM_000348.2)	2	31,691,055	3.01	0.20	0.13	1.63	2.55	5.02	1.46
rs11676168	HTLF Intron1 (NM_002158.2)	2	48,465,842	3.15	0.55	0.46	1.44	2.52	2.07	1.54

[0172] [Table 8]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)		Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs4667649	SP5 +8390bp (XM_371581)	2	171,408,395	3.21	0.73	0.65	1.49	2.43		1.93	1.23
rs6745010	LRP1B +648365bp (NM_018557.1)	2	140,174,363	3.09	0.91	0.86	1.75	2.42		3.69	2.17
rs2356232	SP5 +12276bp (XM_371581)	2	171,412,281	3.19	0.73	0.65	1.49	2.41		1.92	1.23
rs7608898	SP5 +23719bp (XM_371581)	2	171,423,724	3.19	0.73	0.65	1.48	2.41		1.92	1.23
rs10184230	LOC389059 -25058bp (XM_374017)	2	171,427,641	3.19	0.73	0.65	1.48	2.41		1.92	1.23
rs6433243	LOC389059 -21697bp (XM_374017)	2	171,431,002	3.19	0.73	0.65	1.48	2.41		1.92	1.23
rs10930437	SP5 +6843bp (XM_371581)	2	171,406,848	3.15	0.73	0.64	1.48	2.40		1.92	1.22
rs1566993	DPP10 +503127bp (NM_020868.1)	2	116,821,290	3.13	0.96	0.91	2.10	2.40		4.55	2.22
rs1990702	LRP2 +8346bp (NM_004525.1)	2	169,802,022	3.04	0.71	0.63	1.46	2.36		2.00	1.32
rs10183959	NEDL2 Intron1 (XM_038999)	2	197,139,030	3.15	0.93	0.88	1.89	2.35		3.17	1.72
rs6746374	LOC389059 -7686bp (XM_374017)	2	171,445,013	3.03	0.74	0.66	1.47	2.34		1.95	1.25
rs6599252	SCN10A Intron12 (NM_006514.1)	3	38,764,695	0.14	0.48	0.47	1.04	3.94		1.17	0.56
rs7612549	LOC285307 +209732bp (XM_211837)	3	34,789,105	2.18	0.44	0.36	1.35	3.93		2.38	0.88
rs1012728	FLJ22419 Intron4 (NM_024697.1)	3	21,519,300	2.60	0.49	0.41	1.39	3.84		1.76	2.08
rs13097360	GBE1 -805292bp (NM_000158.1)	3	82,698,727	1.55	0.82	0.77	1.34	3.22		0.56	0.32
rs33954719	SGEF Intron6 (NM_015595.2)	3	155,359,077	1.70	0.65	0.58	1.30	3.07		2.09	2.33
rs1462840	LOC285194 +426618bp (XM_379207)	3	118,345,185	2.84	0.63	0.54	1.42	3.07		2.23	2.03
rs17013665	LOC440947 -8774bp (XM_496633)	3	23,718,507	3.79	0.71	0.62	1.53	3.05		2.42	1.69
rs2044757	SGEF Intron5 (NM_015595.2)	3	155,352,950	1.58	0.65	0.59	1.28	3.05		2.03	2.32
rs1503075	ALCAM -279337bp (NM_001627.1)	3	106,289,543	3.46	0.13	0.07	1.93	3.01	ND		1.84
rs6550308	LOC285307 +332200bp (XM_211837)	3	34,911,573	3.08	0.48	0.39	1.44	2.98		1.90	1.78
rs12494849	CACNA2D2 Intron2 (NM_006030.1)	3	50,499,562	3.61	0.59	0.49	1.48	2.89		2.20	1.52
rs3755827	ZNF312 -13500bp (NM_018008.2)	3	62,335,411	3.69	0.81	0.73	1.61	2.88		2.43	1.51
rs9881866	ALCAM -264171bp (NM_001627.1)	3	106,304,709	3.32	0.15	0.09	1.81	2.87		1.97	1.97
rs34329202	LOC389099 -54783bp (XM_371621)	3	22,240,837	3.37	0.92	0.86	1.83	2.82		1.99	1.01
rs10935365	CLSTN2 Intron1 (NM_022131.1)	3	141,227,766	3.47	0.84	0.76	1.61	2.77		2.61	1.62

[0173] [Table 9]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs2138789	GRK7 Intron2 (NM_139209.1)	3	142,991,449	3.33	0.14	0.08	1.86	2.67	3.28	1.88
rs6550783	LOC440947 -8191bp (XM_496633)	3	23,719,090	3.18	0.69	0.61	1.47	2.48	2.18	1.51
rs779701	GRM7 Intron7 (NM_181875.1), GRM7 Intron7 (NM_000844.2), GRM7 Intron7 (NM_181874.1)	3	7,493,772	3.03	0.33	0.25	1.48	2.48	1.80	1.64
rs2216524	IL1RAP Intron7 (NM_134470.2), IL1RAP Intron7 (NM_002182.2)	3	191,824,803	3.03	0.86	0.79	1.59	2.47	1.99	1.18
rs3922704	FLJ31579 Intron3 (NM_153268.1)	3	112,983,875	3.06	0.88	0.82	1.66	2.44	2.09	1.20
rs7641653	LOC389105 -266407bp (XM_374037)	3	35,093,422	3.06	0.40	0.32	1.45	2.43	2.08	1.50
rs2193877	IL1RAP Intron7 (NM_134470.2), IL1RAP Intron7 (NM_002182.2)	3	191,825,144	3.05	0.85	0.79	1.59	2.41	2.15	1.30
rs4624606	IL1RAP Intron9 (NM_002182.2), IL1RAP +6172bp (NM_134470.2)	3	191,836,948	3.07	0.84	0.78	1.58	2.40	2.50	1.59
rs4858594	THRB Intron2 (NM_000461.2)	3	24,248,858	3.02	0.69	0.61	1.45	2.21	1.95	1.33
rs10454254	LOC285441 Intron1 (XM_379295)	4	187,735,925	1.17	0.81	0.77	1.27	3.70	0.60	0.33
rs13110551	CCRN4L -116225bp (NM_012118.2)	4	140,178,323	2.59	0.58	0.50	1.38	3.56	2.22	2.18
rs1503539	MAD2L1 +168679bp (NM_002358.2)	4	121,169,516	3.91	0.38	0.28	1.56	3.53	3.05	1.40
rs3804100	TLR2 Exon2 (NM_003264.2)	4	154,983,014	3.96	0.74	0.64	1.57	3.37	2.72	1.84
rs4516662	CCRN4L -116103bp (NM_012118.2)	4	140,178,445	2.22	0.57	0.50	1.34	3.27	2.08	2.12
rs10009731	STX18 -141961bp (NM_016930.2)	4	4,803,808	2.34	0.83	0.77	1.46	3.23	6.58	5.41
rs7676755	CYP4V2 Intron2 (NM_207352.1)	4	187,490,196	0.68	0.80	0.78	1.18	3.22	3.26	4.09
rs10517556	LOC391656 -135832bp (XM_373027)	4	62,947,647	2.42	0.51	0.43	1.37	3.21	1.75	1.96
rs16996478	UNC5C -11150bp (NM_003728.2)	4	96,838,490	3.98	0.20	0.12	1.80	3.17	3.11	1.79
rs10517578	LOC285533 Intron4 (NM_173662.1)	4	155,005,757	3.89	0.74	0.65	1.56	3.15	2.47	1.61
rs34415360	LOC132391 -118159bp (XM_497978)	4	117,081,308	3.45	0.29	0.21	1.57	3.01	3.26	1.28
rs930438	CENPC1 +97050bp (NM_001812.1)	4	68,069,912	3.27	0.82	0.75	1.57	2.84	3.33	2.31

[0174] [Table 10]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs17279573	KIAA0922 +22425bp (NM_015196.2)	4	154,937,893	3.34	0.68	0.60	1.48	2.74	2.31	1.66
rs11727442	TLR2 -23144bp (NM_003264.2)	4	154,943,527	3.42	0.69	0.60	1.49	2.73	2.22	1.49
rs1027690	MAD2L1 +191047bp (NM_002358.2)	4	121,147,148	3.22	0.43	0.34	1.46	2.63	2.24	1.45
rs16891164	LOC441009 +88767bp (XM_498965)	4	14,590,288	3.15	0.96	0.92	2.12	2.63 ND	ND	
rs13107767	LOC152519 +6607bp (NM_207330.1)	4	47,886,619	3.44	0.60	0.50	1.47	2.62	2.07	1.39
rs1980391	LOC389239 -207565bp (XM_371714)	4	165,986,419	3.18	0.62	0.53	1.45	2.60	1.99	1.23
rs7376639	LOC132391 -82192bp (XM_497978)	4	117,117,275	3.04	0.29	0.21	1.52	2.56	2.90	1.27
rs4256218	SCD4 Intron1 (NM_024906.1)	4	84,047,858	3.28	0.89	0.82	1.69	2.55	2.70	1.59
rs972469	FSTL5 +959616bp (NM_020116.2)	4	161,703,038	3.06	0.40	0.32	1.45	2.47	2.27	1.36
rs6829490	TXK +894bp (NM_003328.1)	4	47,908,795	3.23	0.57	0.48	1.45	2.46	2.04	1.46
rs3804099	TLR2 Exon2 (NM_003264.2)	4	154,982,261	3.07	0.71	0.63	1.46	2.45	2.24	1.57
rs4392496	KIAA0922 Intron3 (NM_015196.2)	4	154,800,110	3.10	0.46	0.37	1.44	2.41	2.04	1.47
rs4568220	LOC344988 Intron2 (XM_293671)	4	121,413,055	3.23	0.11	0.06	2.04	2.40	3.19	2.00
rs33964061	TXK +1806bp (NM_003328.1)	4	47,907,883	3.11	0.57	0.48	1.43	2.34	2.00	1.46
rs6447614	TXK +804bp (NM_003328.1)	4	47,908,885	3.11	0.57	0.48	1.43	2.34	2.00	1.46
rs12655405	PDZK3 -33552bp (NM_015022.2), PDZK3 -33552bp (NM_178140.1)	5	31,801,198	0.80	0.93	0.91	1.33	3.88	0.13	0.06
rs4515309	NNT +296580bp (NM_012343.2), NNT +296836bp (NM_182977.1)	5	44,037,927	1.77	0.12	0.08	1.56	3.74	0.00	2.02
rs1377489	MTRR +135148bp (NM_024010.1), MTRR +135148bp (NM_002454.1)	5	8,089,385	1.15	0.82	0.78	1.28	3.56	20.15	19.82
rs309593	CSPG2 Intron10 (NM_004385.2)	5	82,884,337	3.95	0.43	0.33	1.54	3.45	2.43	1.64
rs6579788	TCOF1 -25018bp (NM_000356.1)	5	149,692,410	1.15	0.37	0.32	1.23	3.43	2.27	0.80
rs6451268	FLJ25422 Intron11 (NM_145000.2)	5	36,291,121	1.39	0.61	0.56	1.25	3.38	1.85	2.30
rs529279	C5orf13 -5941bp (NM_004772.1)	5	111,126,776	3.20	0.30	0.22	1.53	2.90	3.30	1.31
rs298091	PDE4D -114328bp (NM_006203.3)	5	59,032,360	3.58	0.82	0.74	1.61	2.86	2.37	1.43
rs3097776	FAT2 Intron2 (NM_001447.1)	5	150,916,554	3.34	0.72	0.63	1.49	2.77	2.01	1.23
rs11750584	FLJ40243 -22454bp (NM_173489.2)	5	41,129,616	3.13	0.20	0.13	1.64	2.68	1.86	1.80

[0175] [Table 11]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs11748095	FBXL17 -103066bp (NM_022824.1)	5	107,848,076	3.18	0.50	0.41	1.45	2.66	1.95	1.66
rs1428470	LY64 -8157bp (NM_005582.1)	5	66,536,525	3.15	0.80	0.72	1.53	2.64	1.93	1.16
rs11167493	CSF1R +19417bp (NM_005211.2)	5	149,393,634	3.02	0.12	0.07	1.92	2.52	ND	1.77
rs6891720	LY64 -7944bp (NM_005582.1)	5	66,536,312	3.04	0.80	0.72	1.51	2.52	1.91	1.16
rs4246764	LY64 -384319bp (NM_005582.1)	5	66,912,687	3.00	0.29	0.21	1.51	2.46	2.43	1.54
rs429419	ADAMTS12 Intron17 (NM_030955.1)	5	33,624,092	3.12	0.91	0.85	1.76	2.44	3.75	2.20
rs298063	PDE4D -88343bp (NM_006203.3)	5	59,006,375	3.15	0.82	0.75	1.55	2.44	2.11	1.32
rs818725	ADAMTS12 Intron17 (NM_030955.1)	5	33,624,060	3.05	0.91	0.86	1.74	2.37	3.66	2.17
rs4285312	NEDD9 -191677bp (NM_006403.2), NEDD9 -191687bp (NM_182966.1)	6	11,532,564	3.28	0.16	0.10	1.76	3.87	1.07	2.27
rs4840196	GRIK2 Intron8 (NM_021956.2), GRIK2 Intron8 (NM_175768.1)	6	102,359,520	0.96	0.60	0.55	1.19	3.72	1.19	0.60
rs4075603	NEDD9 -191609bp (NM_006403.2), NEDD9 -191619bp (NM_182966.1)	6	11,532,496	3.09	0.16	0.10	1.73	3.67	1.04	2.22
rs2764236	GRIK2 Intron9 (NM_021956.2), GRIK2 Intron9 (NM_175768.1)	6	102,389,150	0.83	0.59	0.56	1.17	3.61	1.15	0.59
rs4840195	GRIK2 Intron8 (NM_021956.2), GRIK2 Intron8 (NM_175768.1)	6	102,359,490	0.84	0.59	0.55	1.17	3.55	1.18	0.60
rs372534	AOF1 Intron8 (XM_173173)	6	18,295,895	3.02	0.68	0.59	1.45	3.50	2.40	2.31
rs6907963	LOC442154 Intron1 (XM_498036)	6	4,903,481	2.45	0.88	0.83	1.56	3.18	16.95	13.09
rs6916915	EGFL11 -135926bp (NM_198283.1)	6	66,398,533	3.44	0.54	0.45	1.47	3.08	2.18	1.20
rs3857597	LOC442216 -86680bp (XM_498099)	6	51,020,014	3.84	0.22	0.14	1.73	3.07	2.60	1.76
rs902287	EGFL11 -127786bp (NM_198283.1)	6	66,390,393	3.31	0.51	0.42	1.46	3.05	2.19	1.16
rs7761118	MAPK14 Intron9 (NM_139013.1), MAPK14 Intron9 (NM_001315.1), MAPK14 Intron9 (NM_139012.1), MAPK14 Intron9 (NM_139014.1)	6	36,176,281	3.63	0.93	0.87	1.95	3.05	4.77	2.39

[0176] [Table 12]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs9473926	LOC442216 -10440bp (XM_498099)	6	50,943,774	3.30	0.54	0.45	1.46	2.90	2.17	1.69
rs1206153	KIAA1900 Intron6 (NM_052904.1)	6	97,652,757	3.02	0.56	0.47	1.43	2.80	1.95	1.08
rs16871306	NEDD9 -153598bp (NM_006403.2), NEDD9 -153608bp (NM_182966.1)	6	11,494,485	3.04	0.09	0.04	2.17	2.52	ND	2.22
rs9398995	ENPP1 Intron1 (NM_006208.1)	6	132,181,896	3.12	0.58	0.48	1.44	2.51	2.06	1.59
rs9358578	LOC389370 Intron1 (XM_374162)	6	22,810,626	3.27	0.44	0.35	1.47	2.46	2.12	1.39
rs10488281	PRES Intron2 (NM_206883.1), PRES Intron2 (NM_206884.1), PRES Intron2 (NM_206885.1), PRES Intron2 (NM_198999.1)	7	102,663,783	1.13	0.48	0.44	1.21	3.64	1.66	0.72
rs2215164	COBL Intron1 (NM_015198.2)	7	51,093,537	1.75	0.88	0.83	1.44	3.60	0.32	0.17
rs2299257	PON1 Intron4 (NM_000446.3)	7	94,587,416	3.65	0.37	0.28	1.54	3.43	2.01	1.80
rs1075737	PRES Intron2 (NM_206883.1), PRES Intron2 (NM_206884.1), PRES Intron2 (NM_206885.1), PRES Intron2 (NM_198999.1)	7	102,665,144	0.99	0.48	0.44	1.19	3.41	1.60	0.72
rs10232532	CPA5 -3205bp (NM_080385.2)	7	129,575,431	0.30	0.52	0.50	1.07	3.24	1.18	1.94
rs3917538	PON1 Intron5 (NM_000446.3)	7	94,582,544	3.50	0.51	0.42	1.47	3.16	2.20	1.16
rs1222418	FLJ32786 Intron12 (NM_144648.1)	7	133,334,253	3.72	0.17	0.10	1.89	3.14	10.10	1.72
rs2966701	TAS2R41 +27695bp (NM_176883.1)	7	142,720,419	3.59	0.13	0.07	2.01	3.13	2.48	2.15
rs10271531	HGF +217504bp (NM_000601.3)	7	80,758,592	3.78	0.42	0.33	1.52	3.11	2.46	1.41
rs12700287	DNAH11 Intron8 (NM_003777.1)	7	21,385,860	3.76	0.96	0.92	2.39	3.10	ND	ND
rs10228385	LOC401324 +47600bp (XM_379484)	7	35,236,926	3.79	0.84	0.76	1.65	3.07	2.21	1.26
rs4726533	PRSS1 -172004bp (NM_002769.2)	7	141,771,615	0.57	0.39	0.36	1.13	3.07	1.71	0.72

[0177] [Table 13]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
	OSBPL3 Intron22 (NM_015550.2), OSBPL3 Intron21 (NM_145320.1),									
rs2285652	OSBPL3 Intron21 (NM_145321.1), OSBPL3 Intron20 (NM_145322.1), OSBPL3 Intron22 (NM_145323.1), OSBPL3 Intron21 (NM_145324.1)	7	24,617,110	3.56	0.84	0.77	1.64	3.02	3.55	2.33
rs10250170	TPK1 Intron8 (NM_022445.2)	7	143,650,537	0.69	0.12	0.10	1.24	3.02	0.11	1.67
rs2966712	TAS2R41 -7843bp (NM_176883.1)	7	142,683,960	3.22	0.11	0.06	1.97	3.02	0.82	2.20
rs1001148	COBL Intron1 (NM_015198.2)	7	51,094,084	1.40	0.88	0.84	1.37	3.01	0.32	0.18
rs17167646	FLJ32786 Intron16 (NM_144648.1)	7	133,365,708	3.50	0.15	0.09	1.84	2.93	9.85	1.66
rs930688	FLJ32786 Intron16 (NM_144648.1)	7	133,366,047	3.50	0.15	0.09	1.84	2.93	9.85	1.66
rs991162	FLJ32110 -9270bp (NM_181646.2)	7	88,024,134	3.55	0.15	0.09	1.89	2.91	2.49	1.98
rs2592845	LOC401324 +94391bp (XM_379484)	7	35,283,717	3.07	0.77	0.69	1.51	2.90	3.17	2.30
rs10228514	LOC401324 +47709bp (XM_379484)	7	35,237,035	3.55	0.83	0.75	1.62	2.86	2.20	1.30
rs10488110	LOC340268 Intron1 (XM_294634)	7	9,827,710	3.41	0.11	0.06	2.07	2.81 ND		1.89
rs975910	HIC +252683bp (NM_199072.2)	7	114,505,890	3.53	0.94	0.88	1.98	2.72	5.49	3.05
rs2893506	LOC401324 +25585bp (XM_379484)	7	35,214,911	3.52	0.83	0.75	1.60	2.69	2.47	1.58
rs10236415	LOC401324 +28462bp (XM_379484)	7	35,217,788	3.52	0.83	0.75	1.60	2.69	2.47	1.58
rs9640055	GLCCI1 Intron1 (XM_166529)	7	7,802,756	3.27	0.82	0.75	1.57	2.65	2.55	1.62
rs2592860	LOC401324 +14726bp (XM_379484)	7	35,204,052	3.25	0.71	0.63	1.48	2.52	2.15	1.45
rs6961391	NUP205 -1742bp (XM_371954)	7	134,698,206	3.12	0.73	0.65	1.47	2.52	2.11	1.36
rs115357	FLJ13842 +130801bp (NM_024645.1)	8	40,376,469	1.62	0.31	0.25	1.32	3.49	1.01	1.90
rs2977752	LOC441352 +55834bp (XM_499115)	8	72,715,809	1.84	0.58	0.52	1.30	3.39	1.87	2.19
rs10504440	LOC389667 +50257bp (XM_372046)	8	70,255,391	2.06	0.70	0.64	1.35	3.32	2.77	2.73
rs2470722	GEM -2381bp (NM_005261.2), GEM -2381bp (NM_181702.1)	8	95,346,114	1.12	0.77	0.73	1.25	3.28	0.79	0.45

[0178] [Table 14]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
	CTSB +629bp (NM_001908.2), CTSB +629bp (NM_147780.1),									
rs12898	CTSB +629bp (NM_147781.1), CTSB +629bp (NM_147782.1), CTSB +629bp (NM_147783.1)	8	11,738,607	2.92	0.49	0.40	1.42	3.27	1.81	1.90
rs6991723	ZNF596 +33933bp (NM_173539.1)	8	221,272	2.75	0.58	0.49	1.40	3.25	2.08	2.04
rs16904092	MGC27434 Intron1 (NM_145050.2)	8	130,571,112	1.05	0.90	0.87	1.33	3.19	0.16	0.09
rs6468360	LOC286135 -35034bp (XM_379573)	8	29,863,536	2.01	0.55	0.48	1.32	3.16	1.78	0.86
rs4736872	FLJ13842 Intron5 (NM_024645.1)	8	40,570,858	0.36	0.63	0.61	1.09	3.12	1.54	2.26
rs10958627	FLJ13842 Intron5 (NM_024645.1)	8	40,594,675	0.03	0.47	0.47	1.01	3.08	0.96	1.75
rs16935718	LOC389667 +60391bp (XM_372046)	8	70,265,525	1.87	0.74	0.68	1.34	3.07	3.16	3.04
rs1605950	PXMP3 -574113bp (NM_000318.1)	8	78,649,107	0.82	0.28	0.25	1.19	3.07	0.78	1.73
rs2513858	STARS -43515bp (NM_139166.2)	8	107,895,164	0.07	0.65	0.65	1.02	3.05	1.49	2.29
rs16935744	LOC389667 +75414bp (XM_372046)	8	70,280,548	1.80	0.74	0.68	1.33	3.04	3.05	2.98
rs2272767	CTSB Intron1 (NM_001908.2), CTSB Intron3 (NM_147780.1), CTSB Intron2 (NM_147781.1), CTSB Intron2 (NM_147782.1), CTSB Intron2 (NM_147783.1)	8	11,748,468	2.69	0.48	0.40	1.40	3.01	1.75	1.85
rs705998	LOC389667 +90010bp (XM_372046)	8	70,295,144	1.55	0.71	0.65	1.29	3.01	2.51	2.69
rs12545915	SNTG1 Intron2 (NM_018967.1)	8	51,329,479	3.39	0.85	0.77	1.62	2.91	1.82	1.01
rs6999627	SNTG1 Intron2 (NM_018967.1)	8	51,340,728	3.27	0.85	0.78	1.61	2.77	1.81	1.02
rs3757916	RBPMS Intron9 (NM_006867.1)	8	30,545,447	3.10	0.43	0.34	1.45	2.62	1.96	1.62
rs2729482	LOC169355 Intron9 (NM_194294.1)	8	39,975,804	3.50	0.11	0.06	2.07	2.61	3.62	2.00
rs7823902	LOC286129 Intron2 (XM_209910)	8	26,963,854	3.20	0.34	0.26	1.50	2.58	2.12	1.56
rs11783765	GTF2E2 Intron7 (NM_002095.3)	8	30,556,550	3.12	0.40	0.32	1.46	2.55	2.17	1.51

[0179] [Table 15]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs17758599	SNTG1 Intron1 (NM_018967.1)	8	51,109,255	3.14	0.85	0.78	1.59	2.49	2.77	1.78
rs2468705	KCNK9 +75721bp (NM_016601.2)	8	140,618,265	3.08	0.28	0.20	1.53	2.45	2.48	1.52
rs6474298	FLJ13842 -168006bp (NM_024645.1)	8	41,042,506	3.23	0.81	0.73	1.55	2.45	2.27	1.48
rs17473451	TUSC3 -73601bp (NM_006765.2), TUSC3 -73601bp (NM_178234.1)	8	15,368,500	3.05	0.79	0.71	1.51	2.43	1.98	1.24
rs6559770	SLC28A3 +1167111bp (NM_022127.1)	9	84,005,935	2.83	0.47	0.38	1.41	3.55	1.82	1.96
rs10984339	LOC442434 +1827466bp (XM_498343)	9	118,798,668	1.63	0.42	0.36	1.28	3.18	1.34	1.89
rs920753	LOC389771 -178380bp (XM_374296)	9	89,862,442	0.11	0.27	0.26	1.04	3.13	0.55	1.55
rs411102	LOC347265 +480760bp (XM_294590)	9	99,196,524	3.28	0.16	0.10	1.79	3.06	1.50	2.03
rs1342022	ANXA1 -61274bp (NM_000700.1)	9	72,935,061	1.37	0.60	0.54	1.24	3.05	1.34	0.70
rs10972299	VCP +4230bp (NM_007126.2)	9	35,042,331	3.54	0.95	0.89	2.09	3.01	2.57	15.88
rs303612	LOC340511 -47888bp (XM_295261)	9	103,142,991	0.20	0.61	0.59	1.05	3.01	1.39	2.12
rs1316814	BARX1 -25445bp (NM_021570.2)	9	93,822,273	3.20	0.57	0.48	1.45	2.80	2.27	1.60
rs1538844	JMJD2C Intron8 (NM_015061.1)	9	6,953,799	3.07	0.41	0.33	1.46	2.78	1.91	1.70
rs2148591	PCSK5 -63459bp (NM_006200.2)	9	75,671,716	3.11	0.45	0.36	1.45	2.72	2.28	1.21
rs932881	JMJD2C +18496bp (NM_015061.1)	9	7,167,496	3.25	0.78	0.70	1.52	2.53	2.37	1.61
rs10764881	MGMT -70674bp (NM_002412.1)	10	131,153,821	0.91	0.72	0.68	1.20	3.94	5.56	6.03
rs1649035	TFAM +176804bp (NM_003201.1), TFAM +187289bp (NM_012251.1)	10	60,002,707	3.82	0.61	0.51	1.51	3.94	2.56	2.09
rs782394	LOC387721 -251645bp (XM_370585)	10	130,349,442	2.06	0.54	0.47	1.33	3.70	1.75	0.80
rs1649048	TFAM +168385bp (NM_003201.1), TFAM +178870bp (NM_012251.1)	10	59,994,288	3.54	0.60	0.51	1.48	3.54	2.36	1.99
rs7477330	TFAM +162217bp (NM_003201.1), TFAM +172702bp (NM_012251.1)	10	59,988,120	3.63	0.60	0.51	1.49	3.52	2.38	1.95
rs17157033	LOC439960 -30545bp (XM_498478)	10	44,613,470	2.88	0.96	0.92	2.14	3.45 ND	ND	
rs10458653	PCBD -540766bp (NM_000281.1)	10	72,369,768	0.63	0.25	0.22	1.16	3.45	5.56	0.82

[0180] [Table 16]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs3849969	SEC24C Intron12 (NM_004922.2), SEC24C Intron11 (NM_198597.1)	10	75,196,005	3.36	0.27	0.19	1.57	3.44	1.58	1.92
rs1658438	TFAM +170686bp (NM_003201.1), TFAM +181171bp (NM_012251.1)	10	59,996,589	3.56	0.60	0.51	1.48	3.43	2.35	1.92
rs1649039	TFAM +174144bp (NM_003201.1), TFAM +184629bp (NM_012251.1)	10	60,000,047	3.59	0.60	0.50	1.48	3.43	2.34	1.91
rs1658456	TFAM +148429bp (NM_003201.1), TFAM +158914bp (NM_012251.1)	10	59,974,332	3.54	0.60	0.51	1.48	3.40	2.33	1.91
rs1649060	TFAM +154583bp (NM_003201.1), TFAM +165068bp (NM_012251.1)	10	59,980,486	3.54	0.60	0.51	1.48	3.40	2.33	1.91
rs17130394	HABP2 -103263bp (NM_004132.2)	10	115,199,512	3.18	0.84	0.77	1.59	3.40	1.38	0.71
rs10763558	TFAM +186037bp (NM_003201.1), TFAM +196522bp (NM_012251.1)	10	60,011,940	3.62	0.60	0.50	1.49	3.36	2.33	1.87
rs10763556	TFAM +185501bp (NM_003201.1), TFAM +195986bp (NM_012251.1)	10	60,011,404	3.53	0.60	0.50	1.48	3.34	2.33	1.89
rs7902091	CTNNA3 Intron7 (NM_013266.1)	10	68,268,298	2.66	0.51	0.43	1.39	3.33	1.98	0.94
rs1210065	TMEM23 Intron5 (NM_147156.3)	10	51,882,795	2.61	0.41	0.34	1.40	3.31	1.59	1.89
rs10994838	ACF Intron1 (NM_014576.2), ACF Intron1 (NM_138932.1), ACF Intron1 (NM_138933.1)	10	52,312,506	1.16	0.36	0.32	1.23	3.31	2.21	0.80
rs11189912	SH2D4B +793340bp (NM_207372.1)	10	83,189,636	3.27	0.92	0.86	1.83	3.15	1.07	0.52
rs1028534	TMEM23 Intron3 (NM_147156.3)	10	51,898,627	2.47	0.66	0.59	1.38	3.10	2.22	2.21
rs1203392	TMEM23 Intron5 (NM_147156.3)	10	51,874,999	2.46	0.41	0.34	1.38	3.08	1.57	1.85
rs7910849	LOC220929 +29028bp (NM_182755.1)	10	31,144,546	3.06	0.74	0.66	1.48	3.08	1.69	0.93
rs7904101	TMEM23 -7099bp (NM_147156.3)	10	52,060,842	1.38	0.37	0.32	1.26	3.05	1.12	1.81
rs4474374	LOC439991 -14752bp (XM_495838)	10	85,647,711	0.14	0.33	0.32	1.04	3.05	1.98	0.69
rs11016249	MKI67 -323870bp (NM_002417.2)	10	130,138,328	3.24	0.69	0.60	1.47	2.90	2.42	1.91

[0181] [Table 17]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs2092832	SH2D4B +843746bp (NM_207372.1)	10	83,240,042	3.58	0.94	0.88	1.99	2.88	3.15	1.55
rs4934425	ANKRD22 Intron1 (NM_144590.1)	10	90,599,698	3.05	0.64	0.55	1.44	2.83	2.29	1.86
rs2688612	PLAU -17730bp (NM_002658.1)	10	75,323,211	3.57	0.42	0.33	1.50	2.81	2.28	1.45
rs10883820	CNNM2 Intron1 (NM_017649.3), CNNM2 Intron1 (NM_199076.1), CNNM2 +77286bp (NM_199077.1)	10	104,754,651	3.37	0.90	0.84	1.76	2.78	2.47	1.34
rs7074084	TFAM +146618bp (NM_003201.1), TFAM +157103bp (NM_012251.1)	10	59,972,521	3.20	0.59	0.49	1.44	2.77	2.16	1.69
rs1649023	TFAM +129923bp (NM_003201.1), TFAM +140408bp (NM_012251.1)	10	59,955,826	3.11	0.59	0.50	1.44	2.69	2.13	1.69
rs1649080	TFAM +137397bp (NM_003201.1), TFAM +147882bp (NM_012251.1)	10	59,963,300	3.11	0.59	0.50	1.44	2.69	2.13	1.69
rs1303970	TFAM +142580bp (NM_003201.1), TFAM +153065bp (NM_012251.1)	10	59,968,483	3.11	0.59	0.50	1.44	2.69	2.13	1.69
rs3829154	ECHDC3 -1630bp (NM_024693.2)	10	11,822,759	3.17	0.49	0.40	1.44	2.61	2.16	1.29
rs1926029	NT5C2 Intron11 (NM_012229.2)	10	104,845,660	3.20	0.91	0.85	1.75	2.57	3.18	1.80
rs2802493	LOC283034 +233953bp (XM_210860)	10	43,873,589	3.15	0.39	0.31	1.47	2.50	2.27	1.38
rs718641	ECHDC3 -4475bp (NM_024693.2)	10	11,819,914	3.08	0.49	0.40	1.44	2.49	2.12	1.30
rs7913781	ZWINT -792415bp (NM_007057.2), ZWINT -792415bp (NM_032997.1)	10	58,583,444	3.22	0.18	0.11	1.72	2.46	4.17	1.49
rs7894588	CNNM2 Intron1 (NM_017649.3), CNNM2 Intron1 (NM_199076.1), CNNM2 +68655bp (NM_199077.1)	10	104,746,020	3.08	0.91	0.85	1.72	2.46	2.41	1.35
rs1569868	SH2D4B +852561bp (NM_207372.1)	10	83,248,857	3.13	0.93	0.88	1.88	2.45	3.12	1.65
rs10883843	NT5C2 -6408bp (NM_012229.2)	10	104,937,483	3.03	0.91	0.85	1.71	2.41	2.39	1.35
rs7074395	NT5C2 +2984bp (NM_012229.2)	10	104,834,918	3.00	0.91	0.85	1.71	2.39	2.39	1.35

[0182] [Table 18]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)		Odds Ratio (Homozygote) (Formula 4)		Odds Ratio (Heterozygote) (Formula 5)	
rs10829630	MGMT +6919bp (NM_002412.1)	10	131,462,275	3.02	0.58	0.49	1.43	2.21		1.96		1.40	
rs923811	BARX2 +93402bp (NM_003658.3)	11	128,920,427	0.82	0.67	0.63	1.17	3.76		0.91		0.49	
rs4937431	BARX2 +124127bp (NM_003658.3)	11	128,951,152	1.56	0.44	0.38	1.27	3.24		2.05		0.85	
rs11021202	MGC33371 +224211bp (NM_144664.3)	11	94,917,555	3.28	0.14	0.08	1.85	3.18		1.33		2.17	
rs497776	MAML2 Intron1 (NM_032427.1)	11	95,597,312	2.23	0.80	0.74	1.42	3.06		3.58		3.31	
rs11602121	LOC399921 Intron4 (XM_374904)	11	70,237,526	1.45	0.29	0.24	1.30	3.00		5.91		1.01	
rs11220171	CNTN5 Intron2 (NM_014361.2), CNTN5 Intron2 (NM_175566.1)	11	98,866,995	3.46	0.36	0.28	1.51	2.95		2.04		1.67	
rs4307718	LOC440033 +175532bp (XM_498512)	11	23,320,437	3.48	0.96	0.92	2.27	2.90	ND		ND		
rs1384483	LOC440033 +63001bp (XM_498512)	11	23,207,906	3.23	0.13	0.07	1.90	2.78	ND			1.79	
rs500629	ZBTB16 Intron3 (NM_006006.3)	11	113,550,770	3.13	0.29	0.22	1.52	2.72		1.88		1.69	
rs1507527	LOC387754 -33940bp (XM_373490)	11	13,882,655	3.25	0.77	0.69	1.51	2.72		2.23		1.39	
rs2007052	SPON1 -375664bp (NM_006108.1)	11	13,903,250	3.21	0.77	0.68	1.51	2.69		2.24		1.40	
rs7935243	PHACS Intron3 (NM_032592.1)	11	44,050,992	3.13	0.80	0.72	1.53	2.67		2.95		2.11	
rs562160	CHORDC1 -291532bp (NM_012124.1)	11	89,887,386	3.12	0.82	0.75	1.55	2.57		2.91		2.02	
rs474530	DLG2 Intron1 (NM_001364.1)	11	83,930,298	3.02	0.95	0.91	2.00	2.56	ND		ND		
rs493622	CHORDC1 -286443bp (NM_012124.1)	11	89,882,297	3.04	0.82	0.75	1.54	2.45		2.76		1.89	
rs610160	GRIA4 Intron3 (NM_000829.1)	11	105,202,105	3.06	0.20	0.14	1.64	2.25		3.19		1.42	
rs10844107	BICD1 -37784bp (NM_001714.1)	12	32,113,668	0.28	0.24	0.23	1.08	3.48		5.00		0.75	
rs10862853	LOC387871 +436103bp (XM_373539)	12	83,274,707	1.19	0.82	0.78	1.28	3.34		3.97		4.53	
rs979879	SLC6A15 +353475bp (NM_182767.2), SLC6A15 +375211bp (NM_018057.3)	12	83,403,423	1.63	0.83	0.78	1.36	3.33		4.41		4.61	
rs11116400	SLC6A15 +425437bp (NM_182767.2), SLC6A15 +447173bp (NM_018057.3)	12	83,331,461	1.53	0.83	0.78	1.34	3.33		4.38		4.65	
rs2611284	SLC6A15 +335334bp (NM_182767.2), SLC6A15 +357070bp (NM_018057.3)	12	83,421,564	1.66	0.83	0.78	1.36	3.31		4.41		4.57	

[0183] [Table 19]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs10746324	SLC6A15 +349318bp (NM_182767.2), SLC6A15 +371054bp (NM_018057.3)	12	83,407,580	1.61	0.83	0.78	1.36	3.29	4.38	4.57
rs11056970	LMO3 +34143bp (NM_018640.3), LMO3 +34143bp (NM_001001395.1)	12	16,558,431	3.21	0.86	0.79	1.63	3.27	3.21	3.17
rs4766663	OAS1 +7223bp (NM_002534.1), OAS1 +5266bp (NM_016816.1)	12	111,825,694	3.28	0.20	0.13	1.68	3.12	12.40	1.52
rs7134411	FLJ25056 +34943bp (NM_182530.1)	12	68,673,713	0.33	0.51	0.49	1.08	3.12	1.17	0.61
rs1382851	FLJ36004 -92384bp (NM_152590.1)	12	25,689,829	2.11	0.58	0.51	1.33	3.10	1.86	2.07
rs7295295	LOC387871 +418915bp (XM_373539)	12	83,257,519	1.84	0.82	0.76	1.38	3.09	4.09	4.00
rs1380405	SLC6A15 +351862bp (NM_182767.2), SLC6A15 +373598bp (NM_018057.3)	12	83,405,036	1.56	0.83	0.79	1.35	3.08	4.25	4.38
rs11116414	SLC6A15 +389377bp (NM_182767.2), SLC6A15 +411113bp (NM_018057.3)	12	83,367,521	1.46	0.83	0.79	1.33	3.07	4.21	4.42
rs2468302	SLC6A15 +354456bp (NM_182767.2), SLC6A15 +376192bp (NM_018057.3)	12	83,402,442	1.46	0.83	0.79	1.33	3.07	4.21	4.42
rs2555255	LOC144742 +11128bp (XM_378388)	12	118,173,222	0.08	0.25	0.24	1.03	3.04	3.04	0.72
rs2072133	OAS3 Exon16 (NM_006187.2)	12	111,871,980	3.71	0.68	0.59	1.51	3.03	2.27	1.46
rs1647106	THRAP2 +168009bp (NM_015335.2)	12	114,691,094	3.67	0.33	0.24	1.56	3.02	2.29	1.63
rs10779090	LOC387871 +423693bp (XM_373539)	12	83,262,297	1.14	0.82	0.78	1.27	3.01	3.58	4.04
rs2125093	KLRA1 +10392bp (NM_006611.1)	12	10,622,647	3.52	0.77	0.68	1.54	2.92	2.11	1.27
rs900610	MGC50559 Intron2 (NM_173802.2)	12	31,707,890	3.14	0.16	0.10	1.75	2.91	1.47	1.98
rs10772350	STYK1 -7029bp (NM_018423.1)	12	10,724,935	3.08	0.71	0.62	1.47	2.83	1.91	1.11
rs4767030	OAS1 +3826bp (NM_002534.1), OAS1 +1869bp (NM_016816.1)	12	111,822,297	3.40	0.21	0.14	1.68	2.81	3.49	1.66
rs1647110	THRAP2 +163373bp (NM_015335.2)	12	114,695,730	3.37	0.29	0.21	1.56	2.76	2.29	1.62

[0184] [Table 20]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs18559336	OAS3 -8940bp (NM_006187.2)	12	111,830,029	3.06	0.21	0.14	1.63	2.58	4.24	1.57
rs1700369	LOC441646 Intron8 (XM_497358)	12	126,367,113	3.00	0.95	0.90	1.97	2.55	1.54	0.71
rs7134391	OAS1 +10940bp (NM_002534.1), OAS1 +8983bp (NM_016816.1)	12	111,829,411	3.09	0.20	0.14	1.63	2.50	3.57	1.57
rs2270152	VWF Intron49 (NM_000552.2)	12	5,931,330	3.16	0.86	0.80	1.62	2.48	2.47	1.50
rs4767040	OAS3 -2232bp (NM_006187.2)	12	111,836,737	3.07	0.20	0.14	1.63	2.48	3.56	1.56
rs10774679	OAS3 -1501bp (NM_006187.2)	12	111,837,468	3.06	0.20	0.14	1.63	2.47	3.58	1.56
rs11104300	HGNT-IV-H -287319bp (NM_013244.2)	12	86,022,432	3.05	0.21	0.15	1.61	2.44	3.37	1.52
rs10735079	OAS3 Intron2 (NM_006187.2)	12	111,842,728	3.03	0.20	0.14	1.62	2.44	3.56	1.55
rs7961953	DKFZp762A217 Intron1 (NM_152588.1)	12	81,594,304	3.02	0.34	0.26	1.48	2.43	2.28	1.48
rs261912	ETNK1 Intron6 (NM_018638.3)	12	22,728,208	3.01	0.85	0.78	1.58	2.43	3.04	2.02
rs4145280	G30 +266246bp (XM_498445)	13	104,643,159	0.25	0.51	0.50	1.06	3.95	1.12	0.55
rs4772238	CLYBL -20285bp (NM_206808.1), CLYBL -20285bp (NM_138280.3)	13	99,202,794	0.14	0.12	0.11	1.06	3.78	0.00	1.53
rs9519091	SLC10A2 -518655bp (NM_000452.1)	13	103,035,852	1.56	0.49	0.43	1.27	3.58	1.48	2.06
rs3916959	G30 +2690226bp (XM_498445)	13	104,640,379	0.25	0.51	0.50	1.06	3.58	1.12	0.57
rs9558509	G30 +2713688bp (XM_498445)	13	104,638,037	0.27	0.51	0.50	1.07	3.47	1.13	0.58
rs9300981	G30 +4691268bp (XM_498445)	13	104,440,279	3.79	0.63	0.53	1.52	3.14	2.32	1.75
rs1606405	SLITRK1 +664827bp (NM_052910.1)	13	82,684,518	1.37	0.55	0.50	1.24	3.10	1.47	0.74
rs10492680	LOC400123 -23647bp (XM_378411)	13	39,702,836	3.01	0.93	0.88	1.83	2.46	6.22	3.50
rs7150435	ALKBH +19861bp (NM_006020.1)	14	77,189,287	0.00	0.53	0.53	1.00	3.42	1.09	1.92
rs759363	CHES1 Intron3 (NM_005197.1)	14	88,828,894	3.89	0.32	0.23	1.59	3.29	2.36	1.69
rs11159897	CHES1 Intron3 (NM_005197.1)	14	88,829,194	3.89	0.32	0.23	1.59	3.29	2.36	1.69
rs4902116	LOC401778 +110022bp (XM_377343)	14	61,774,890	2.61	0.57	0.49	1.38	3.12	1.93	1.98
rs2241127	CHES1 Intron2 (NM_005197.1)	14	88,892,969	1.47	0.31	0.26	1.29	3.11	0.99	1.80

[0185] [Table 21]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)		Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs10148022	LOC283584 -265499bp (XM_211108)	14	85,864,556	0.85	0.32	0.29	1.19	3.07		0.84	1.72
rs1571379	SEL1L -289804bp (NM_005065.3)	14	81,359,690	3.60	0.73	0.63	1.53	3.03		2.22	1.36
rs11622536	KCNK10 -72402bp (NM_138318.1), KCNK10 -20310bp (NM_138317.1), KCNK10 -16406bp (NM_021161.3) BRF1 Intron2 (NM_001519.2),	14	87,879,410	0.64	0.77	0.75	1.16	3.00		0.64	0.38
rs2816632	BRF1 -27133bp (NM_145685.1), BRF1 -26587bp (NM_145696.1)	14	104,812,400	3.27	0.21	0.14	1.64	2.78		4.49	1.36
rs1106845	STELLAR +19768bp (XM_375075)	14	35,931,107	3.26	0.11	0.06	2.06	2.71	ND		1.98
rs17115925	SEL1L -271331bp (NM_005065.3)	14	81,341,217	3.00	0.72	0.64	1.46	2.39		2.22	1.56
rs7176242	ATP10A +44699bp (NM_024490.2)	15	23,428,814	0.19	0.85	0.85	1.07	3.26		0.09	0.06
rs16969520	CIB2 Intron1 (NM_006383.2)	15	76,204,239	2.36	0.35	0.28	1.39	3.19		1.38	1.86
rs10902569	ADAMTS17 Intron3 (NM_139057.1)	15	98,663,829	0.08	0.67	0.67	1.03	3.10		0.64	0.41
rs11071129	UNC13C +173927bp (XM_496070)	15	52,882,022	0.20	0.59	0.58	1.05	3.08		1.37	2.11
rs1441354	FLJ13710 -290691bp (NM_024817.1)	15	69,517,251	0.22	0.25	0.24	1.07	3.07		5.71	0.78
rs11631211	ATP10A +61309bp (NM_024490.2)	15	23,412,204	0.22	0.86	0.85	1.08	3.06		0.10	0.07
rs12592527	UNC13C +174082bp (XM_496070)	15	52,882,177	0.27	0.60	0.58	1.07	3.05		1.42	2.13
rs4144951	FLJ38736 Intron17 (NM_182758.1)	15	51,643,802	3.40	0.16	0.09	1.82	2.73		2.80	1.87
rs2654216	EFTUD1 +28186bp (NM_024580.3)	15	80,181,440	3.18	0.60	0.51	1.44	2.57		2.14	1.54
rs8026133	SLCO3A1 -26936bp (NM_013272.2)	15	90,171,014	3.10	0.16	0.10	1.74	2.48		4.60	1.66
rs4780091	LOC440268 +506bp (XM_496063)	15	31,271,629	3.26	0.63	0.54	1.46	2.46		2.02	1.37
rs17191316	ANXA2 +144537bp (NM_004039.1)	15	58,282,291	3.23	0.07	0.03	2.61	2.37	ND		2.22
rs12597526	USP10 +4263bp (NM_005153.1)	16	83,374,937	1.28	0.38	0.33	1.24	3.91		2.51	0.81
rs2133803	LOC149329 -13263bp (XM_086494)	16	59,665,671	1.32	0.81	0.76	1.30	3.52		4.13	4.60
rs288601	CDH8 -492870bp (NM_001796.2)	16	61,120,407	1.81	0.53	0.47	1.30	3.35		1.61	0.77
rs1819829	FLJ31547 Intron9 (NM_145024.1)	16	54,444,785	2.53	0.79	0.73	1.46	3.32		4.58	3.80

[0186] [Table 22]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs2541639	HBZ +531bp (NM_005332.2)	16	145,035	2.77	0.22	0.16	1.55	3.13	1.23	1.90
rs372657	LOC283867 -3128119bp (XM_378606)	16	64,480,523	3.63	0.24	0.16	1.65	2.84	3.03	1.56
rs173840	LOC283867 -3131113bp (XM_378606)	16	64,480,817	3.63	0.24	0.16	1.65	2.84	3.03	1.56
rs4843428	FOXL1 +137429bp (NM_005250.1)	16	85,308,297	3.20	0.88	0.81	1.66	2.75	1.89	1.05
rs254353	LOC283867 -301507bp (XM_378606)	16	64,469,211	3.33	0.19	0.12	1.71	2.71	4.73	1.57
rs4077853	PLCG2 Intron27 (NM_002661.1)	16	80,528,471	3.16	0.35	0.27	1.49	2.62	2.17	1.57
rs3859079	CDH13 -112144bp (NM_001257.2)	16	81,105,935	3.17	0.66	0.58	1.46	2.51	2.17	1.60
rs8062968	LOC283867 -298359bp (XM_378606)	16	64,466,063	3.05	0.24	0.17	1.57	2.49	1.99	1.68
rs11074523	HS3ST2 Intron1 (NM_006043.1)	16	22,734,434	3.11	0.80	0.73	1.53	2.48	2.40	1.56
rs8045067	WWOX --1063753bp (NM_130844.1), WWOX --1063753bp (NM_130791.1), WWOX --1063753bp (NM_016373.1), WWOX --1063753bp (NM_018560.4), WWOX -48197bp (NM_130792.1)	16	77,754,805	3.35	0.75	0.67	1.52	2.43	2.17	1.49
rs12443833	WWOX --1063238bp (NM_130844.1), WWOX --1063238bp (NM_130791.1), WWOX --1063238bp (NM_016373.1), WWOX --1063238bp (NM_018560.4), WWOX -48712bp (NM_130792.1)	16	77,754,290	3.17	0.72	0.63	1.48	2.38	2.11	1.45
rs1877821	RGS9 -94096bp (NM_003835.1)	17	60,605,875	1.17	0.75	0.71	1.25	3.80	3.21	3.78
rs9896245	RGS9 -110666bp (NM_003835.1)	17	60,604,218	1.45	0.75	0.70	1.29	3.65	3.30	3.62
rs1029754	LOC401887 +487202bp (XM_497555)	17	66,236,699	2.11	0.89	0.84	1.51	3.62	0.23	0.12
rs17808998	NTN1 Intron2 (NM_004822.1)	17	8,919,071	2.23	0.63	0.56	1.35	3.30	1.57	0.81
rs9895463	SPACA3 -6355bp (NM_173847.2)	17	28,336,640	0.01	0.58	0.58	1.00	3.23	1.23	2.04
rs11868422	RPH3AL Intron1 (NM_006987.2)	17	198,072	3.62	0.21	0.14	1.71	3.05	2.06	1.85
rs1877823	RGS9 +3136bp (NM_003835.1)	17	60,657,405	1.20	0.77	0.73	1.26	3.03	3.22	3.52

[0187] [Table 23]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
	TRPV1 Exon11 (NM_080706.1),									
rs8065080	TRPV1 Exon12 (NM_080705.1), TRPV1 Exon12 (NM_018727.3), TRPV1 Exon13 (NM_080704.1)	17	3,427,196	3.67	0.69	0.60	1.51	2.88	2.25	1.51
rs8082149	LOC342600 Introu2 (XM_292624)	17	51,927,894	3.52	0.92	0.86	1.85	2.66	3.49	1.99
rs2269459	POLR2A Intron22 (NM_000937.2)	17	7,353,762	3.11	0.79	0.72	1.52	2.51	2.46	1.63
rs2072255	KIAA0672 Intron10 (XM_375408)	17	12,793,117	3.09	0.21	0.14	1.63	2.43	3.35	1.53
rs9788983	RPH3AL Intron6 (NM_006987.2)	17	129,457	3.05	0.89	0.82	1.65	2.40	3.21	2.00
rs1879610	LOC441825 +255198bp (XM_497596)	18	73,469,750	1.98	0.95	0.91	1.72	3.48	0.26	0.11
rs11876045	LOC441816 -222690bp (XM_497584)	18	20,564,102	3.73	0.28	0.20	1.61	3.41	1.79	1.88
rs17070861	BCL2 Intron1 (NM_000633.1), BCL2 +78655bp (NM_000657.1)	18	59,057,460	0.72	0.94	0.93	1.33	3.34 ND	ND	ND
rs1790870	CYB5 +163bp (NM_001914.1), CYB5 +163bp (NM_148923.1)	18	70,071,349	3.86	0.86	0.78	1.70	3.30	1.99	1.06
rs1790858	CYB5 Intron3 (NM_001914.1), CYB5 Intron3 (NM_148923.1)	18	70,075,799	3.74	0.86	0.78	1.68	3.18	1.99	1.08
rs17187933	LOC441816 -214621bp (XM_497584)	18	20,556,033	3.55	0.26	0.18	1.62	3.11	1.86	1.81
rs17088997	CYB5 +3361bp (NM_001914.1), CYB5 +3361bp (NM_148923.1)	18	70,068,151	3.62	0.86	0.78	1.67	3.07	1.95	1.06
rs1372481	LOC390856 Intron1 (XM_497590)	18	49,466,756	3.51	0.96	0.92	2.35	3.07	1.52	0.58
rs10468763	CLUL1 Intron5 (NM_014410.4), CLUL1 Intron5 (NM_199167.1)	18	622,239	0.40	0.22	0.21	1.12	3.06	0.50	1.61
rs3862680	DCC Intron1 (NM_005215.1)	18	48,184,338	3.65	0.60	0.50	1.49	2.97	2.24	1.56
rs3910695	LOC390856 Intron1 (XM_497590)	18	49,464,638	3.35	0.96	0.92	2.28	2.90	1.53	0.60
rs3862681	DCC Intron1 (NM_005215.1)	18	48,184,688	3.53	0.60	0.50	1.48	2.84	2.19	1.54
rs7238490	METTL4 +571947bp (NM_022840.2)	18	1,955,583	3.40	0.71	0.62	1.49	2.72	2.04	1.27
rs9951036	LOC390856 Intron1 (XM_497590)	18	49,515,735	3.18	0.96	0.92	2.23	2.72	1.52	0.62

[0188] [Table 24]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs339858	LOC441816 -124776bp (XM_497584)	18	20,466,188	3.14	0.16	0.10	1.75	2.70	1.95	1.90
rs11151937	CYB5 +4859bp (NM_001914.1), CYB5 +4859bp (NM_148923.1)	18	70,066,653	3.06	0.53	0.44	1.43	2.68	2.01	1.68
rs8094863	LOC390855 Intron3 (XM_497589)	18	47,458,218	3.17	0.50	0.41	1.44	2.55	2.12	1.32
rs17260163	LOC441816 -250775bp (XM_497584)	18	20,592,187	3.13	0.29	0.21	1.53	2.54	2.21	1.59
rs8086430	LOC147468 +250079bp (XM_091809)	18	20,600,317	3.10	0.29	0.21	1.52	2.51	2.20	1.58
rs16940484	C18orf17 Intron6 (NM_153211.1)	18	19,936,298	3.09	0.34	0.26	1.49	2.51	2.02	1.58
rs7229080	LOC390856 Intron1 (XM_497590)	18	49,503,583	3.19	0.97	0.93	2.28	2.49	3.03	1.30
rs10502927	LOC390855 Intron3 (XM_497589)	18	47,502,071	3.01	0.49	0.41	1.43	2.45	2.09	1.27
rs17660384	ZNF175 -10715bp (NM_007147.2)	19	56,755,628	3.53	0.21	0.14	1.69	3.02	5.12	1.57
rs2864107	ZNF175 -5504bp (NM_007147.2)	19	56,760,839	3.40	0.21	0.14	1.68	2.90	4.82	1.58
rs1433083	FLJ12644 Exon5 (NM_023074.2)	19	57,085,796	3.14	0.95	0.91	2.07	2.66	ND	ND
rs6097745	BCAS1 Intron3 (NM_003657.1)	20	52,101,533	1.67	0.29	0.24	1.33	3.56	1.00	1.92
rs2870304	BCAS1 Intron3 (NM_003657.1)	20	52,106,624	1.74	0.30	0.25	1.33	3.49	1.06	1.91
rs8123014	C20orf23 +571310bp (NM_024704.3)	20	15,629,440	2.16	0.75	0.68	1.38	3.20	1.23	0.66
rs6115865	C20orf194 -37687bp (XM_045421)	20	3,307,303	3.63	0.38	0.29	1.52	2.87	2.29	1.52
rs7268851	C20orf17 Intron2 (NM_173485.2)	20	51,501,200	3.45	0.73	0.65	1.51	2.86	2.08	1.27
rs6134494	LOC440753 +240718bp (XM_498845)	20	12,196,345	3.12	0.22	0.15	1.61	2.86	1.59	1.86
rs3817879	PLCB1 Intron3 (NM_015192.2), PLCB1 Intron3 (NM_182734.1)	20	8,470,921	3.17	0.80	0.72	1.54	2.52	2.65	1.89
rs2743246	MATN4 Intron5 (NM_003833.2), MATN4 Intron4 (NM_030590.1), MATN4 Intron3 (NM_030592.1)	20	43,362,112	3.10	0.88	0.81	1.64	2.43	2.97	1.85
rs6014430	KIAA1755 Intron2 (XM_028810)	20	36,305,948	3.05	0.11	0.06	1.94	2.03	3.66	1.69
rs2154450	RUNX1 Intron5 (NM_001754.2)	21	35,141,436	0.85	0.44	0.40	1.18	3.94	1.14	2.01
rs4817695	RUNX1 Intron5 (NM_001754.2)	21	35,141,187	0.66	0.44	0.41	1.14	3.69	1.10	1.94
rs2825423	LOC388817 +373452bp (XM_371409)	21	19,526,124	3.31	0.26	0.19	1.58	2.64	3.09	1.38

[0189] [Table 25]

dbSNP ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Odds Ratio (Formula 3)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 4)	Odds Ratio (Heterozygote) (Formula 5)
rs4823324	E46L Intron10 (NM_013236.1)	22	44,558,660	3.69	0.51	0.41	1.49	3.04	2.26	1.32
	NF2 Intron10 (NM_181825.1),									
	NF2 Intron8 (NM_181831.1),									
	NF2 Intron10 (NM_000268.2),									
	NF2 Intron10 (NM_016418.4),									
	NF2 Intron11 (NM_181826.1),									
	NF2 Intron10 (NM_181827.1),									
rs2857648	NF2 Intron9 (NM_181828.1),	22	28,391,122	3.02	0.73	0.65	1.46	2.79	1.67	0.95
	NF2 Intron9 (NM_181829.1),									
	NF2 Intron8 (NM_181830.1),									
	NF2 Intron10 (NM_181832.1),									
	NF2 Intron4 (NM_181833.1),									
	NF2 Intron5 (NM_181834.1),									
	NF2 Intron8 (NM_181835.1)									
	FBLN1 +65094bp (NM_006487.2),									
rs6006787	FBLN1 +60443bp (NM_001996.2),	22	44,340,222	3.31	0.50	0.40	1.46	2.72	2.22	1.38
	FBLN1 +58104bp (NM_006485.2),									
	FBLN1 +22671bp (NM_006486.2)									
rs572159	LOC284898 -273642bp (XM_379044)	22	26,054,663	3.11	0.94	0.89	1.92	2.48	4.67	2.44
rs467812	C22orf19 Intron2 (NM_003678.3)	22	28,265,503	3.22	0.27	0.19	1.56	2.48	2.23	1.57
rs5765558	E46L -24767bp (NM_013236.1)	22	44,363,516	3.05	0.58	0.49	1.43	2.34	2.01	1.37
rs6006179	C22orf19 Intron19 (NM_003678.3)	22	28,231,255	3.03	0.27	0.20	1.53	2.33	2.19	1.55

[0190] Tables 5 to 25 list dbSNP ID number or Affimetrix Array ID number for specifying known single nucleotide polymorphisms obtained, the exon, intron information (in a case where a single nucleotide polymorphism exists on a gene, the gene name and the exon or intron in which SNP exists are shown, and in a case where a single nucleotide polymorphism does not exist on a gene, neighboring genes and a distance between the gene and the single nucleotide polymorphism are shown), the chromosome number at which the single nucleotide polymorphism exists, the physical location of the single nucleotide polymorphism, the p-value for an allele according to a chi-square test (-log P), the high-risk allele frequencies in the glaucoma patient group and the non-patient group, the odds ratio for an allele, the p-value for a genotype according to a chi-square test (-log P), the odds ratio for a genotype of a homozygote, and the odds ratio for a genotype of a heterozygote. Here, in the tables, a portion of which odds ratio is indicated as ND shows a case where any one of the number of detection in the denominator is 0, so that the odds ratio could not be calculated.

[0191] According to the above studies, 413 single nucleotide polymorphisms of which alleles or genotypes were associated with glaucoma at a p-value of 1×10^{-3} or less were found.

[0192] When the allele or genotype frequencies listed in Tables 5 to 25 were compared between the non-patients without having family history and the glaucoma patients, a statistical difference was found. By determining an allele of any one of these single nucleotide polymorphisms, whether or not an allele that is identified in a higher frequency in the glaucoma patient

group than that of the non-patient group exists in the sample can be determined.

[0193] Example 4 Comparison of Single Nucleotide Polymorphisms Between Progressive Glaucoma Cases and Nonprogressive Glaucoma Cases

The comparison on single nucleotide polymorphisms was made for progressive glaucoma cases and nonprogressive glaucoma cases in the same manner as in Example 3.

[0194] Concretely, blood donated under the consent on free will of the participants after having sufficiently explained the contents of studies from 210 cases of patients with progressive visual loss within a given time period, despite the treatments for lowering an intraocular pressure such as a drug for lowering an intraocular pressure or a surgical operation (progressive glaucoma cases), and 175 cases of patients without the progression (nonprogressive glaucoma cases), among the primary open-angle glaucoma patients and the normal tension glaucoma patients diagnosed on the basis of Guidelines offered by Japan Glaucoma Society, was used as a specimen, and alleles frequencies and genotypes frequencies between the groups were also compared by performing the analysis in the same manner as in Example 3. Alleles frequencies and genotype frequencies were statistically compared according to the chi-square test in the same manner. Single nucleotide polymorphisms of which alleles or genotypes show association with the progression of glaucoma at a p-value of 1×10^{-4} or less, i.e. -log P of 4 or more are listed in Tables 26 to 28. Here, the odds ratio for association of an allele with the progression of glaucoma, and the odds ratio

for association of a genotype with the progression of glaucoma in each of the tables, respectively were calculated on the basis of the following formulas (6) to (8).

Odds Ratio for Allele

= [(Number of Detection of an Allele Identified in High Frequency in Progressive Glaucoma Group, in Progressive Glaucoma Group)/(Number of Detection of an Allele Opposite to the Allele Identified in High Frequency in Progressive Glaucoma Group, in Progressive Glaucoma Group)]/

[(Number of Detection of the Allele Identified in High Frequency in Progressive Glaucoma Group, in Nonprogressive Glaucoma Group)/(Number of Detection of the Allele Opposite to the Allele Identified in High Frequency in Progressive Glaucoma Group, in Nonprogressive Glaucoma Group)] formula (6)

Odds Ratio for Genotype of Homozygote

= [(Number of Detection of a Genotype Having Homozygote of an Allele Identified in High Frequency in Progressive Glaucoma Group, in Progressive Glaucoma Group)/(Number of Detection of a Genotypes Having Homozygote of an Allele Identified in High Frequency in Nonprogressive Glaucoma Group, in Progressive Glaucoma Group)]/

[(Number of Detection of the Genotype Having Homozygote of the Allele Identified in High Frequency in Progressive Glaucoma Group, in Nonprogressive Glaucoma Group)/(Number of Detection of the Genotype Having Homozygote of the Allele Identified in High Frequency in Nonprogressive Glaucoma Group, in Nonprogressive Glaucoma Group)]

formula (7)

Odds Ratio for Genotype of Heterozygote

= [(Number of Detection of a Genotype of Heterozygote in Progressive Glaucoma Group)/(Number of Detection of a Genotype Having Homozygote of an Allele Identified in High Frequency in Nonprogressive Glaucoma Group, in Progressive Glaucoma Group)]/

[(Number of Detection of the Genotype of Heterozygote in Nonprogressive Glaucoma Group)/(Number of Detection of the Genotype Having Homozygote of the Allele Identified in High Frequency in Nonprogressive Glaucoma Group, in Nonprogressive Glaucoma Group)]

formula (8)

[0195] [Table 26]

dbSNP ID	Allele1 / Allele2	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	High Risk Allele	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote1) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)	Sequence Containing Allele 1	Sequence Containing Allele 2
rs11211059	A/G	EIF2B3 Intron4 (NM_020365.1)	1	45,099,311	0.28	0.77	0.75	Allele 2	1.12	4.51	9.28	15.68	SEQ ID No:81	SEQ ID No:82
rs4927088	C/T	SSBP3 Intron4 (NM_145716.1), SSBP3 Intron4 (NM_018070.2)	1	54,487,224	1.10	0.60	0.54	Allele 1	1.29	4.56	2.12	3.61	SEQ ID No:83	SEQ ID No:84
rs10172264	G/T	LOC402072 +152420bp (XM_377741)	2	53,313,788	4.32	0.20	0.09	Allele 1	2.43	3.91	2.54	2.85	SEQ ID No:85	SEQ ID No:86
rs10460373	G/T	UBE2E3 -372131bp (NM_182678.1), UBE2E3 -372361bp (NM_006357.2)	2	181,298,487	3.24	0.82	0.72	Allele 1	1.81	4.16	1.42	0.54	SEQ ID No:87	SEQ ID No:88
rs1520855	C/T	FLJ12519 -24239bp (NM_032168.1)	2	190,107,426	1.13	0.65	0.59	Allele 1	1.31	4.67	2.51	4.22	SEQ ID No:89	SEQ ID No:90
rs1827101	C/T	ITPR1 +23268p (NM_002222.1)	3	4,866,407	1.36	0.75	0.69	Allele 2	1.39	4.66	0.73	0.29	SEQ ID No:91	SEQ ID No:92
rs4635691	C/G	ITPR1 +2783bp (NM_002222.1)	3	4,866,864	1.24	0.75	0.69	Allele 1	1.36	4.25	0.76	0.31	SEQ ID No:93	SEQ ID No:94
rs9819062	A/C	ITPR1 +148475p (NM_002222.1)	3	4,878,928	1.41	0.75	0.68	Allele 1	1.39	4.23	0.81	0.33	SEQ ID No:95	SEQ ID No:96
rs12638937	G/T	ITPR1 +15316bp (NM_002222.1)	3	4,879,397	1.32	0.75	0.69	Allele 1	1.38	4.03	0.80	0.33	SEQ ID No:97	SEQ ID No:98
rs3805345	A/G	PAPSS1 Intron5 (NM_005443.4)	4	108,943,706	3.56	0.65	0.52	Allele 2	1.73	4.10	2.57	0.94	SEQ ID No:99	SEQ ID No:100
rs3805347	C/T	PAPSS1 Intron5 (NM_005443.4)	4	108,959,666	3.70	0.67	0.53	Allele 2	1.77	4.07	2.92	1.09	SEQ ID No:101	SEQ ID No:102
rs17066530	A/G	LOC285501 +636489bp (XM_209640)	4	179,923,545	4.60	0.92	0.81	Allele 1	2.62	4.15	4.56	1.55	SEQ ID No:103	SEQ ID No:104
rs405806	A/C	LOC441062 +175809bp (XM_498994)	5	18,167,512	4.03	0.55	0.41	Allele 2	1.77	3.38	2.95	2.11	SEQ ID No:105	SEQ ID No:106
rs401889	A/G	LOC441062 +175873bp (XM_498994)	5	18,167,576	4.60	0.53	0.38	Allele 2	1.86	4.14	3.23	2.37	SEQ ID No:107	SEQ ID No:108
rs4308461	A/C	SV2C -75087bp (XM_043493)	5	75,339,908	4.03	0.79	0.66	Allele 1	1.89	3.12	3.36	1.81	SEQ ID No:109	SEQ ID No:110
rs2547455	C/T	SV2C -33137bp (XM_043493)	5	75,381,858	4.40	0.80	0.67	Allele 1	1.97	3.63	3.03	1.39	SEQ ID No:111	SEQ ID No:112
rs2042974	C/G	LHFPL2 -11058bp (NM_005779.1)	5	77,852,925	1.24	0.86	0.81	Allele 2	1.47	4.37	ND	ND	SEQ ID No:113	SEQ ID No:114
rs7719483	A/C	LHFPL2 -190566p (NM_005779.1)	5	77,860,923	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:115	SEQ ID No:116
rs17215893	C/T	LHFPL2 -20235bp (NM_005779.1)	5	77,862,102	0.85	0.86	0.82	Allele 1	1.34	5.14	ND	ND	SEQ ID No:117	SEQ ID No:118
rs10045987	C/T	LHFPL2 -31149bp (NM_005779.1)	5	77,873,016	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:119	SEQ ID No:120
rs11949567	A/G	LHFPL2 -35281bp (NM_005779.1)	5	77,877,148	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:121	SEQ ID No:122
rs11950379	A/G	LHFPL2 -35775bp (NM_005779.1)	5	77,877,642	0.79	0.85	0.82	Allele 2	1.31	4.97	ND	ND	SEQ ID No:123	SEQ ID No:124
rs6860516	A/G	LHFPL2 -35961bp (NM_005779.1)	5	77,877,828	0.88	0.86	0.82	Allele 1	1.34	5.18	ND	ND	SEQ ID No:125	SEQ ID No:126
rs6881598	A/G	LHFPL2 -37710bp (NM_005779.1)	5	77,879,577	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:127	SEQ ID No:128

[0196] [Table 27]

dbSNP ID	Allele1 / Allele2	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	High Risk Allele	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote1) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)	Sequence Containing Allele 1	Sequence Containing Allele 2
rs6886783	C/T	LHFPL2 -377635bp (NM_005779.1)	5	77,879,632	0.88	0.86	0.82	Allele 1	1.34	5.18	ND	ND	SEQ ID No:129	SEQ ID No:130
rs6877525	C/T	LHFPL2 -388711bp (NM_005779.1)	5	77,880,738	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:131	SEQ ID No:132
rs12697888	C/T	LHFPL2 -535336bp (NM_005779.1)	5	77,895,402	0.88	0.86	0.82	Allele 1	1.34	5.18	ND	ND	SEQ ID No:133	SEQ ID No:134
rs1978629	C/T	LHFPL2 -560459bp (NM_005779.1)	5	77,897,912	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:135	SEQ ID No:136
rs10076149	C/G	LHFPL2 -687439bp (NM_005779.1)	5	77,910,610	0.88	0.86	0.82	Allele 2	1.34	5.18	ND	ND	SEQ ID No:137	SEQ ID No:138
rs730781	C/T	LHFPL2 -841066bp (NM_005779.1)	5	77,925,973	0.85	0.86	0.82	Allele 1	1.34	5.09	ND	ND	SEQ ID No:139	SEQ ID No:140
rs9461154	C/T	LRRC16 -1129344bp (NM_017640.2)	6	25,506,014	1.41	0.32	0.25	Allele 2	1.39	4.01	11.34	0.85	SEQ ID No:141	SEQ ID No:142
rs13193932	C/G	ARHGAP18 Intron1 (NM_033515.2)	6	130,008,475	1.70	0.83	0.76	Allele 2	1.52	4.30	22.83	26.08	SEQ ID No:143	SEQ ID No:144
rs17070863	A/G	LOC441173 +172209bp (XM_496827)	6	141,772,290	4.46	0.55	0.40	Allele 2	1.86	3.61	3.42	1.72	SEQ ID No:145	SEQ ID No:146
rs1877885	C/G	LOC340268 Intron1 (XM_294634)	7	9,625,295	4.29	0.60	0.45	Allele 2	1.80	3.67	3.45	2.04	SEQ ID No:147	SEQ ID No:148
rs1913603	A/C	LOC340268 Intron1 (XM_294634) HDAC9 Intron21 (NM_058176.1), HDAC9 Intron21 (NM_178423.1),	7	9,664,816	4.03	0.64	0.49	Allele 2	1.79	3.75	3.85	2.37	SEQ ID No:149	SEQ ID No:150
rs10230371	A/G	HDAC9 Intron19 (NM_178425.1), HDAC9 +186432bp (NM_014707.1), HDAC9 +196258p (NM_058177.1)	7	18,668,137	1.05	0.41	0.35	Allele 1	1.29	4.38	1.11	2.63	SEQ ID No:151	SEQ ID No:152
rs17152739	A/G	LOC401384 +201741bp (XM_379506)	7	78,935,541	4.66	0.78	0.64	Allele 2	1.98	3.78	3.43	1.65	SEQ ID No:153	SEQ ID No:154
rs4316157	C/T	LOC340357 Intron3 (XM_499106)	8	12,677,322	4.65	0.48	0.33	Allele 2	1.89	3.65	3.29	1.88	SEQ ID No:155	SEQ ID No:156
rs10503907	A/G	NRG1 -233743bp (NM_013958.1), NRG1 -233775bp (NM_013957.1), NRG1 -233799bp (NM_004495.1), NRG1 -233842bp (NM_013961.1), NRG1 -234103bp (NM_013964.1), NRG1 -234127bp (NM_013960.1), NRG1 -234143bp (NM_013956.1), NRG1 -2813366bp (NM_013962.1), NRG1 -332731bp (NM_013959.1)	8	32,291,552	4.11	0.92	0.83	Allele 1	2.46	3.27	8.80	3.83	SEQ ID No:157	SEQ ID No:158

[0197] [Table 28]

dbSNP ID	Allele1 / Allele2	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	High Risk Allele	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote1) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)	Sequence Containing Allele 1	Sequence Containing Allele 2
rs9650336	C/T	LOC286140 -47376bp (XM_209913)	8	38,625,315	4.11	0.67	0.53	Allele 1	1.80	4.06	2.58	1.02	SEQ ID No:159	SEQ ID No:160
rs1541082	A/C	PIP5K1B Intron15 (NM_003558.1)	9	68,851,654	4.05	0.37	0.24	Allele 1	1.87	3.54	4.89	1.65	SEQ ID No:161	SEQ ID No:162
rs4979255	C/T	LOC442430 -50518bp (XM_498339)	9	107,542,392	1.50	0.69	0.61	Allele 1	1.39	4.03	1.16	0.46	SEQ ID No:163	SEQ ID No:164
rs2395453	C/G	KCNMA1 Intron18 (NM_002247.2)	10	78,411,565	1.77	0.60	0.51	Allele 1	1.42	4.73	1.68	0.55	SEQ ID No:165	SEQ ID No:166
rs2131216	A/T	KCNMA1 Intron18 (NM_002247.2)	10	78,426,609	1.67	0.59	0.51	Allele 2	1.40	4.14	1.72	0.59	SEQ ID No:167	SEQ ID No:168
rs7112492	A/C	LDHA -10601bp (NM_005566.1)	11	18,362,086	3.70	0.38	0.26	Allele 2	1.80	4.03	2.25	2.50	SEQ ID No:169	SEQ ID No:170
rs4755605	C/T	LOC387761 -170163bp (XM_373495)	11	42,404,449	3.08	0.57	0.45	Allele 1	1.63	4.13	3.34	3.05	SEQ ID No:171	SEQ ID No:172
rs10892454	A/C	LOC440070 +32494bp (XM_498530)	11	119,148,037	0.09	0.47	0.47	Allele 1	1.03	4.12	1.29	0.45	SEQ ID No:173	SEQ ID No:174
rs4269933	C/T	LOC440070 +38035bp (XM_498530)	11	119,153,578	0.08	0.47	0.47	Allele 2	1.03	4.20	1.29	0.44	SEQ ID No:175	SEQ ID No:176
rs2322728	A/G	FLJ40224 +258937bp (NM_173579.1)	11	126,640,100	0.04	0.28	0.28	Allele 2	1.02	4.00	3.53	0.55	SEQ ID No:177	SEQ ID No:178
rs4350423	A/G	FLJ40126 Intron18 (NM_173599.1), SLC2A13 Intron6 (NM_052885.1)	12	38,515,235	4.28	0.24	0.13	Allele 2	2.20	3.41	8.59	1.82	SEQ ID No:179	SEQ ID No:180
rs10784314	C/T	PPM1H Intron4 (XM_350880)	12	61,442,746	1.93	0.85	0.78	Allele 1	1.62	5.56	ND	ND	SEQ ID No:181	SEQ ID No:182
rs4408378	A/G	LOC401725 +252078bp (XM_377278)	12	82,300,515	4.01	0.82	0.70	Allele 1	1.97	3.22	3.63	1.81	SEQ ID No:183	SEQ ID No:184
rs11059862	A/G	DKFZp761O2018 +33295bp (XM_044062)	12	127,750,629	4.11	0.94	0.85	Allele 1	2.61	3.33	5.98	2.27	SEQ ID No:185	SEQ ID No:186
rs17184839	A/G	LOC440142 +135778bp (XM_495960)	13	59,763,528	4.07	0.14	0.05	Allele 1	2.98	3.54	ND	3.09	SEQ ID No:187	SEQ ID No:188
rs7212115	G/T	LOC400573 -182083bp (XM_378649)	17	10,832,202	4.05	0.88	0.78	Allele 2	2.17	2.12	2.65	1.55	SEQ ID No:189	SEQ ID No:190
rs295869	C/T	LOC388375 +71591bp (XM_373726)	17	32,221,458	2.76	0.44	0.33	Allele 1	1.60	4.93	1.80	3.00	SEQ ID No:191	SEQ ID No:192
rs6045676	C/G	PDYN +18232bp (NM_024411.2)	20	1,889,171	4.11	0.35	0.22	Allele 2	1.91	3.66	2.90	2.23	SEQ ID No:193	SEQ ID No:194
rs909882	A/G	CHD6 Intron24 (NM_032221.3)	20	39,509,923	4.37	0.81	0.68	Allele 1	2.01	3.58	4.37	2.25	SEQ ID No:195	SEQ ID No:196
rs6017164	C/T	C20orf65 -265396p (NM_176791.2)	20	41,815,520	4.15	0.55	0.40	Allele 2	1.80	3.44	3.33	1.62	SEQ ID No:197	SEQ ID No:198
rs7275647	A/G	NCAM2 Intron5 (NM_004540.2)	21	21,586,912	4.62	0.69	0.55	Allele 1	1.89	3.98	3.18	1.43	SEQ ID No:199	SEQ ID No:200
rs2837255	A/C	PCP4 -17259bp (NM_006198.1)	21	40,143,991	4.33	0.70	0.56	Allele 1	1.86	3.37	3.28	1.82	SEQ ID No:201	SEQ ID No:202

[0198] Tables 26 to 28 list dbSNP ID number or Affimetrix Array ID number specifying known single nucleotide polymorphisms obtained, each of bases constituting Allele 1 and Allele 2, the exon, intron information (in a case where a single nucleotide polymorphism exists on a gene, the gene name and the exon or intron in which SNP exists are shown, and in a case where a single nucleotide polymorphism does not exist on a gene, neighboring genes and a distance between the gene and the single nucleotide polymorphism are shown), the chromosome number at which the single nucleotide polymorphism exists, the physical location of the single nucleotide polymorphism, the p-value for an allele according to a chi-square test (-log P), the high-risk allele frequencies in the progressive glaucoma group and the nonprogressive glaucoma group, the type of the high-risk allele (indicating whether the high-risk allele is Allele 1 or Allele 2), the odds ratio for an allele, the p-value for genotype according to a chi-square test (-log P), the odds ratio for a genotype of a homozygote, the odds ratio for a genotype of a heterozygote, and SEQ ID NO of the sequence containing Allele 1 and SEQ ID NO of the sequence containing Allele 2 in each of the polymorphic sites. Here, in the tables, a portion of which odds ratio is indicated as ND shows a case where any one of the number of detection in the denominator is 0, so that the odds ratio could not be calculated.

[0199] According to the above studies, 61 single nucleotide polymorphisms of which alleles or genotypes were associated with the progression of glaucoma at a p-value of 1×10^{-4} or less were found.

[0200] When the allele or genotype frequencies listed in Tables 26 to 28 were compared between the progressive glaucoma cases and the

nonprogressive glaucoma cases, a statistical difference was found. By determining an allele of any one of these single nucleotide polymorphisms, whether or not an allele that is identified in a higher frequency in the progressive glaucoma group than that of the nonprogressive glaucoma group exists in the sample can be determined.

[0201] The allele or genotype identified in a high frequency in the progressive glaucoma group for a single nucleotide polymorphism listed in Tables 26 to 28 can be used as a marker showing that a progressive risk of glaucoma is high. On the other hand, an allele that is opposite to the allele or a genotype other than the genotype can be used as a marker showing that a progressive risk of glaucoma is low.

[0202] Also, a single nucleotide polymorphism of which allele or genotype shows association with the progression of glaucoma at a p-value of 1×10^{-3} or less, i.e. -log P of 3 or more, is listed in Tables 29 to 51.

[0203] [Table 29]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs1920146	FMO3 -14117bp (NM_006894.3)	1	167,777,607	3.00	0.16	0.08	2.14	3.79	0.78	3.05
rs594105	C8A Intron4 (NM_000562.1)	1	57,055,277	0.82	0.65	0.60	1.24	3.74	0.95	0.41
rs490647	GRIK3 +23871bp (NM_000831.2)	1	36,911,836	3.13	0.39	0.28	1.69	3.43	1.92	2.39
rs10489624	C8A Intron6 (NM_000562.1)	1	57,061,635	0.83	0.65	0.60	1.24	3.39	1.00	0.44
rs11117962	LOC128153 +9779bp (NM_138796.2)	1	214,438,658	1.33	0.60	0.53	1.34	3.32	1.49	0.60
rs868162	NPHP4 Intron22 (NM_015102.2)	1	5,868,502	0.74	0.76	0.72	1.25	3.32	0.41	0.21
rs525798	GRIK3 +25728bp (NM_000831.2)	1	36,909,979	3.12	0.40	0.28	1.68	3.28	1.97	2.33
rs11120300	SMYD2 Intron11 (NM_020197.1)	1	210,897,894	1.38	0.08	0.04	1.90	3.14	0.23	4.08
rs10494300	KCNN3 Intron3 (NM_170782.1), KCNN3 Intron3 (NM_002249.3)	1	151,539,619	3.13	0.61	0.49	1.64	3.14	2.56	1.09
rs17401966	KIF1B Intron24 (NM_015074.2), KIF1B +18633bp (NM_183416.2)	1	10,319,737	2.53	0.28	0.19	1.68	3.09	17.83	1.28
rs687328	GADD45A -40088bp (NM_001924.2)	1	67,822,816	3.19	0.75	0.63	1.71	3.07	3.66	3.07
rs7517439	EIF2B3 +36447bp (NM_020365.1)	1	44,981,960	0.01	0.75	0.75	1.01	3.05	4.99	7.80
rs479714	GRIK3 +26576bp (NM_000831.2)	1	36,909,131	2.84	0.39	0.28	1.64	3.01	1.86	2.26
rs7528341	GRIK3 +125440bp (NM_000831.2)	1	36,810,267	3.27	0.75	0.63	1.73	2.97	2.40	1.14
rs1339411	KCNK2 +61589bp (NM_014217.1)	1	211,859,142	3.20	0.33	0.22	1.76	2.91	2.53	2.08
rs947130	LOC391075 -110888bp (XM_497702)	1	119,728,774	3.47	0.82	0.71	1.86	2.89	4.69	2.75
rs7534078	SYT2 Intron1 (NM_177402.3)	1	199,346,710	3.84	0.37	0.25	1.84	2.89	2.83	1.87
rs479779	GRIK3 +10551bp (NM_000831.2)	1	36,925,156	3.03	0.39	0.28	1.67	2.86	2.00	2.16
rs2993076	GRIK3 +5529bp (NM_000831.2)	1	36,930,178	3.00	0.36	0.25	1.69	2.84	2.00	2.15
rs11590929	LMO4 +403174bp (NM_006769.2)	1	87,926,458	3.65	0.96	0.89	2.98	2.83	4.15	1.35
rs1416658	KCNK2 +6613bp (NM_014217.1)	1	211,804,166	3.28	0.32	0.21	1.79	2.82	2.63	2.02
rs4652921	GRIK3 +91841bp (NM_000831.2)	1	36,843,866	3.22	0.66	0.54	1.67	2.81	2.56	1.25
rs10157596	SLC35F3 -17535bp (NM_173508.1)	1	230,329,879	3.29	0.71	0.59	1.71	2.80	3.48	2.28
rs1416659	KCNK2 +6647bp (NM_014217.1)	1	211,804,200	3.17	0.31	0.21	1.77	2.79	2.48	2.04

[0204] [Table 30]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs11120527	KCNK2 Intron6 (NM_014217.1)	1	211,796,452	3.16	0.32	0.21	1.77	2.79	2.49	2.05
rs10494994	KCNK2 Intron5 (NM_014217.1)	1	211,750,602	3.50	0.26	0.16	1.93	2.76	3.29	1.97
rs6665581	VAMP4 -9932bp (NM_201994.1), VAMP4 -9932bp (NM_003762.2)	1	168,452,803	3.09	0.39	0.27	1.69	2.72	3.73	1.38
rs12120152	VAMP4 -12595bp (NM_201994.1), VAMP4 -12595bp (NM_003762.2)	1	168,455,466	3.09	0.39	0.27	1.69	2.72	3.73	1.38
rs2293325	CD3Z Intron1 (NM_000734.2), CD3Z Intron1 (NM_198053.1)	1	164,157,804	3.18	0.78	0.67	1.74	2.69	2.74	1.41
rs6577539	CA6 -16705bp (NM_001215.1)	1	8,923,501	3.16	0.94	0.87	2.40	2.69 ND	ND	
rs34305923	GRIK3 +122474bp (NM_000831.2)	1	36,813,233	3.10	0.74	0.62	1.69	2.66	2.43	1.23
rs1315219	FLJ23129 Intron7 (NM_024763.3), FLJ23129 Intron7 (NM_207014.1)	1	67,031,546	3.32	0.58	0.45	1.67	2.63	2.78	1.54
rs10798603	VAMP4 Intron4 (NM_201994.1), VAMP4 Intron4 (NM_003762.2)	1	168,412,039	3.37	0.36	0.24	1.77	2.60	3.30	1.65
rs1317252	TDE2L Intron2 (NM_178865.2)	1	31,566,351	3.25	0.91	0.82	2.10	2.51	4.36	2.10
rs12024194	VAMP4 -12277bp (NM_201994.1), VAMP4 -12277bp (NM_003762.2)	1	168,455,148	3.21	0.22	0.13	1.95	2.44	4.16	1.86
rs10489250	VAMP4 -4860bp (NM_201994.1), VAMP4 -4860bp (NM_003762.2)	1	168,447,731	3.03	0.22	0.13	1.91	2.28	3.12	1.91
rs271351	LOC391025 -173869bp (XM_372775)	1	29,821,213	3.21	0.16	0.08	2.22	2.23	4.90	1.96
rs6689380	LOC339535 -409013bp (XM_378941)	1	235,384,371	3.08	0.97	0.92	3.08	2.17 ND	ND	
rs9943293	VAMP4 +14337bp (NM_201994.1), VAMP4 +180935bp (NM_003762.2)	1	168,386,625	3.03	0.34	0.23	1.71	2.16	2.67	1.65
rs4342884	VAMP4 Intron4 (NM_201994.1), VAMP4 Intron4 (NM_003762.2)	1	168,416,489	3.03	0.36	0.25	1.72	2.11	2.81	1.52
rs11691504	UBE2E3 -377923bp (NM_182678.1), UBE2E3 -378153bp (NM_006357.2)	2	181,292,695	3.11	0.82	0.72	1.79	3.96	1.41	0.55

[0205] [Table 31]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs9679229	UBE2E3 -350430bp (NM_182678.1), UBE2E3 -350660bp (NM_006357.2)	2	181,320,188	3.05	0.82	0.72	1.77	3.90	1.41	0.55
rs11691031	C2orf29 -90020bp (NM_017546.3)	2	101,237,876	1.36	0.49	0.42	1.34	3.85	1.62	2.75
rs714545	UBE2E3 -463121bp (NM_182678.1), UBE2E3 -463351bp (NM_006357.2)	2	181,207,497	3.54	0.81	0.70	1.85	3.76	1.88	0.76
rs10931418	FLJ12519 -41124bp (NM_032168.1)	2	190,090,541	0.90	0.65	0.59	1.26	3.61	2.14	3.40
rs4667078	UBE2E3 -367916bp (NM_182678.1), UBE2E3 -368146bp (NM_006357.2)	2	181,302,702	2.87	0.81	0.72	1.74	3.57	1.42	0.58
rs1355216	SCN7A -183021bp (NM_002976.1)	2	167,352,006	3.14	0.86	0.77	1.91	3.55	1.25	0.50
rs11695159	FLJ12519 -22944bp (NM_032168.1)	2	190,108,721	0.79	0.64	0.59	1.23	3.47	2.07	3.32
rs13032853	FLJ12519 Intron1 (NM_032168.1)	2	190,134,918	1.05	0.65	0.59	1.29	3.45	2.20	3.33
rs733830	C2orf29 -91059bp (NM_017546.3)	2	101,236,837	1.54	0.49	0.41	1.38	3.31	1.73	2.57
rs16833004	GLS -41329bp (NM_014905.2)	2	191,529,780	2.52	0.97	0.92	2.77	3.29	1.02	0.15
rs11563200	TRPM8 Intron25 (NM_024080.3)	2	234,706,809	0.01	0.58	0.57	1.01	3.27	0.70	0.35
rs10930240	SCN7A -162624bp (NM_002976.1)	2	167,331,609	2.96	0.87	0.78	1.86	3.25	1.26	0.53
rs9287871	SCN7A -162839bp (NM_002976.1)	2	167,331,824	2.96	0.87	0.78	1.86	3.25	1.26	0.53
rs16860887	LOC91526 Intron15 (NM_153697.1)	2	197,723,413	3.53	0.90	0.81	2.15	3.23	2.07	0.82
rs1840111	UBE2E3 -484947bp (NM_182678.1), UBE2E3 -485177bp (NM_006357.2)	2	181,185,671	3.05	0.77	0.66	1.71	3.22	1.84	0.79
rs934706	NXPH2 -373561bp (XM_371573)	2	139,745,104	1.84	0.21	0.15	1.60	3.22	ND	0.99
rs7420360	EPHA4 +369107bp (NM_004438.3)	2	221,739,147	0.50	0.41	0.38	1.16	3.21	0.93	2.18
rs6739369	FLJ20701 Intron3 (NM_017933.3)	2	229,738,357	3.71	0.18	0.08	2.39	3.20	4.06	2.60
rs4850410	LOC91526 Intron15 (NM_153697.1)	2	197,745,675	3.81	0.93	0.84	2.40	3.20	2.97	1.13
rs1453054	UBE2E3 -485205bp (NM_182678.1), UBE2E3 -485435bp (NM_006357.2)	2	181,185,413	3.18	0.78	0.67	1.75	3.13	2.03	0.90

[0206] [Table 32]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs10186570	UBE2E3 -482951bp (NM_182678.1), UBE2E3 -483181bp (NM_006357.2)	2	181,187,667	2.67	0.78	0.68	1.65	3.08	1.62	0.71
rs4076919	FLJ10116 +86710bp (NM_018000.1)	2	216,546,324	3.09	0.83	0.73	1.80	3.07	1.92	0.86
rs968871	FLJ32955 +20953bp (NM_153041.1)	2	150,428,575	3.81	0.45	0.31	1.77	3.06	3.17	1.75
rs968873	FLJ32955 +20796bp (NM_153041.1)	2	150,428,732	3.81	0.45	0.31	1.77	3.06	3.17	1.75
rs13426748	LOC91526 Intron15 (NM_153697.1)	2	197,723,066	3.39	0.90	0.81	2.11	3.06	2.01	0.82
rs2564118	FLJ32312 Intron4 (NM_144709.1)	2	61,144,940	1.22	0.52	0.45	1.32	3.06	1.97	0.70
rs1468981	KLF7 +36314bp (NM_003709.1)	2	207,734,721	0.36	0.59	0.56	1.12	3.04	0.99	0.46
rs1641385	FLJ32955 +20086bp (NM_153041.1)	2	150,429,442	3.71	0.45	0.32	1.75	2.97	3.13	1.73
rs16825626	FLJ20701 Intron3 (NM_017933.3)	2	229,744,146	3.38	0.17	0.08	2.27	2.94	3.11	2.51
rs4261668	MYL1 Intron3 (NM_079422.1), MYL1 Intron3 (NM_079420.1)	2	210,987,818	3.62	0.35	0.23	1.81	2.91	3.39	1.81
rs848241	FLJ32955 Intron3 (NM_153041.1)	2	150,460,159	3.55	0.43	0.31	1.73	2.87	3.02	1.78
rs1196155	PPP1R1C Intron2 (XM_087137)	2	182,746,778	3.43	0.68	0.55	1.71	2.87	3.23	2.15
rs1104870	ALK Intron15 (NM_004304.3)	2	29,366,069	3.60	0.17	0.08	2.36	2.85	6.13	2.33
rs12692654	KCNH7 Intron2 (NM_033272.2), KCNH7 Intron2 (NM_173162.1)	2	163,309,182	3.36	0.77	0.65	1.76	2.83	2.82	1.44
rs4667333	FLJ32955 Intron3 (NM_153041.1)	2	150,461,734	3.44	0.44	0.31	1.72	2.78	3.00	1.77
rs787433	LOC401014 +29562bp (XM_379141)	2	145,697,590	3.44	0.42	0.30	1.72	2.78	3.29	1.54
rs1196185	PPP1R1C Intron2 (XM_087137)	2	182,710,465	3.33	0.67	0.55	1.68	2.78	3.08	2.11
rs10496018	LOC402072 +151618bp (XM_377741)	2	53,312,986	3.28	0.16	0.07	2.29	2.72	2.53	2.53
rs7582411	LOC91526 Intron15 (NM_153697.1)	2	197,738,392	3.10	0.91	0.83	2.13	2.71	2.16	0.89
rs1529404	MYCN +99328bp (NM_005378.3)	2	16,137,052	3.29	0.88	0.79	1.98	2.67	6.63	3.70
rs1608976	FLJ32955 Intron3 (NM_153041.1)	2	150,460,868	3.20	0.44	0.31	1.70	2.67	3.00	1.81
rs2701664	PPP1R1C Intron2 (XM_087137)	2	182,734,170	3.22	0.67	0.55	1.66	2.61	2.94	2.00
rs1196160	PPP1R1C Intron3 (XM_087137)	2	182,753,518	3.22	0.67	0.55	1.66	2.61	2.94	2.00

[0207] [Table 33]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs1358105	FLJ32955 +17818bp (NM_153041.1)	2	150,431,710	3.30	0.39	0.27	1.72	2.59	3.20	1.60
rs1724855	FLJ32955 Intron3 (NM_153041.1)	2	150,455,469	3.22	0.43	0.31	1.68	2.56	2.86	1.72
rs17589066	DNAH7 Intron48 (NM_018897.1)	2	196,522,530	3.05	0.83	0.72	1.82	2.53	4.89	2.95
rs31276	FLJ20701 Intron3 (NM_017933.3)	2	229,746,025	3.08	0.19	0.11	2.02	2.53	6.18	2.03
rs7569506	FLJ39822 +44702bp (NM_173512.1)	2	165,535,617	3.15	0.85	0.76	1.87	2.53	3.48	1.81
rs16838454	KIAA1679 Intron9 (XM_046570)	2	137,843,162	3.08	0.16	0.08	2.23	1.70	2.79	1.93
rs17041614	ITPR1 +16975bp (NM_002222.1)	3	4,881,056	1.28	0.75	0.69	1.37	3.98	0.79	0.33
rs784288	MDS1 Intron2 (NM_004991.1)	3	170,453,933	3.72	0.79	0.67	1.85	3.79	7.54	4.94
rs6773050	CDGAP Intron10 (XM_291085)	3	120,606,504	2.34	0.64	0.53	1.53	3.56	2.99	3.29
rs6792308	ITPR1 +11521bp (NM_002222.1)	3	4,875,602	1.14	0.73	0.67	1.33	3.52	0.83	0.37
rs1828652	PLSCR4 Intron6 (NM_020353.1)	3	147,397,711	3.96	0.47	0.34	1.78	3.49	2.66	2.23
rs1877268	LOC93556 +73662bp (XM_376284)	3	170,104,751	2.31	0.37	0.27	1.55	3.41	1.49	2.45
rs16852789	LOC93556 +75467bp (XM_376284)	3	170,106,556	2.31	0.37	0.27	1.55	3.41	1.49	2.45
rs11920980	LOC440985 -77863bp (XM_498948)	3	154,176,162	1.13	0.57	0.50	1.30	3.36	1.54	0.59
rs7429749	FTHFD Intron1 (NM_012190.2), FTHFD Intron1 (NM_144776.1)	3	127,371,520	2.65	0.21	0.13	1.85	3.23	ND	2.16
rs7624272	SEMA5B Intron1 (NM_018987.1)	3	124,178,241	3.01	0.10	0.04	2.83	3.22	ND	3.06
rs6763643	MYRIP Intron3 (NM_015460.1)	3	40,072,995	0.70	0.38	0.34	1.22	3.17	2.51	0.67
rs4685335	RAFTLIN Intron4 (NM_015150.1)	3	16,423,640	0.62	0.47	0.43	1.19	3.15	1.22	2.39
rs12490570	LOC152118 -107632bp (XM_098163)	3	154,577,350	3.96	0.92	0.82	2.35	3.05	5.13	2.26
rs7371987	CCR3 +10346bp (NM_001837.2), CCR3 +10346bp (NM_178329.1)	3	46,293,512	3.21	0.31	0.20	1.78	3.02	6.91	1.56
rs3957816	PCCB -13296bp (NM_000532.2)	3	137,438,550	3.71	0.25	0.14	2.01	2.97	5.03	1.91
rs9839623	CCR3 +15697bp (NM_001837.2), CCR3 +15697bp (NM_178329.1)	3	46,298,863	3.07	0.31	0.21	1.76	2.91	6.79	1.53
rs17016781	RARB Intron3 (NM_000965.2), RARB Intron3 (NM_016152.2)	3	25,580,890	3.62	0.65	0.51	1.72	2.88	2.77	1.46

[0208] [Table 34]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs453570	CISH +6457bp (NM_013324.4), CISH +6457bp (NM_145071.1)	3	50,612,473	3.25	0.67	0.55	1.68	2.88	3.30	1.85
rs13096142	CCR3 -1944bp (NM_001837.2), CCR3 -1944bp (NM_178329.1)	3	46,256,748	3.04	0.35	0.24	1.71	2.87	4.85	1.39
rs696518	STAG1 Intron21 (NM_005862.1)	3	137,602,998	3.63	0.28	0.16	1.94	2.87	4.86	1.74
rs6446245	DOCK3 Intron5 (NM_004947.2)	3	51,012,298	3.15	0.66	0.54	1.65	2.80	3.11	2.26
rs16833788	SEMA5B -6558bp (NM_018987.1)	3	124,236,700	3.37	0.10	0.03	3.22	2.78	ND	3.29
rs6440881	LOC152118 -56902bp (XM_098163)	3	154,628,080	3.51	0.90	0.80	2.10	2.74	6.57	3.53
rs10510568	RARB Intron3 (NM_000965.2), RARB Intron3 (NM_016152.2)	3	25,577,736	3.24	0.64	0.52	1.67	2.70	2.90	1.58
rs16833786	SEMA5B -5978bp (NM_018987.1)	3	124,236,120	3.26	0.10	0.03	3.16	2.68	ND	3.23
rs1545105	LOC389100 +81379bp (XM_374035)	3	29,199,691	3.01	0.37	0.26	1.68	2.67	2.20	2.04
rs9883170	LOC389100 +82213bp (XM_374035)	3	29,198,857	3.04	0.37	0.26	1.69	2.64	2.26	2.00
rs17016778	RARB Intron3 (NM_000965.2), RARB Intron3 (NM_016152.2)	3	25,580,286	3.28	0.64	0.52	1.67	2.61	2.73	1.53
rs2174746	LOC152118 -103841bp (XM_098163)	3	154,581,141	3.52	0.92	0.83	2.26	2.61	5.02	2.39
rs11712746	KCNMB2 -262329bp (NM_181361.1), KCNMB2 -284723bp (NM_005832.3)	3	179,474,597	3.12	0.25	0.15	1.87	2.60	6.36	1.74
rs684773	PCCB -12843bp (NM_000532.2)	3	137,439,003	3.26	0.22	0.13	1.98	2.58	5.71	1.84
rs695983	STAG1 Intron29 (NM_005862.1)	3	137,547,245	3.33	0.24	0.14	1.94	2.58	5.20	1.72
rs1154988	LOC391581 -434bp (XM_497940)	3	137,407,889	3.23	0.23	0.13	1.98	2.55	5.68	1.85
rs2232248	HEMK1 Exon3 (NM_016173.1)	3	50,584,628	3.11	0.66	0.55	1.65	2.55	2.94	1.85
rs696081	PCCB Intron13 (NM_000532.2)	3	137,529,887	3.21	0.26	0.16	1.86	2.49	4.24	1.72
rs2140450	PPP2R3A Intron5 (NM_002718.3), PPP2R3A Intron4 (NM_181897.1)	3	137,252,444	3.01	0.33	0.23	1.72	2.47	3.87	1.50

[0209] [Table 35]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs6440874	LOC152118 -101011bp (XM_098163)	3	154,583,971	3.33	0.92	0.83	2.21	2.45	4.99	2.44
rs9852831	LOC152118 -133737bp (XM_098163)	3	154,551,245	3.19	0.90	0.82	2.08	2.43	5.05	2.57
rs9822326	LOC339894 Intron2 (XM_379230)	3	158,286,267	3.17	0.54	0.42	1.64	2.41	2.56	1.39
rs548288	PCCB Intron1 (NM_000532.2)	3	137,452,453	3.09	0.23	0.13	1.91	2.34	4.47	1.76
rs7428299	EDEM1 +469242bp (XM_376201)	3	5,705,884	3.02	0.68	0.56	1.64	2.27	2.67	1.81
rs12648912	PAPSS1 +17033bp (NM_005443.4)	4	108,875,394	3.91	0.64	0.51	1.76	3.67	2.92	1.24
rs1865328	LYAR +1510bp (NM_017816.1)	4	4,386,001	0.23	0.50	0.48	1.08	3.41	1.21	0.48
rs531823	QDPR +272295bp (NM_000320.1)	4	16,891,997	3.28	0.64	0.51	1.67	2.94	1.78	0.67
rs2642849	UGT2B4 +7559bp (NM_021139.1)	4	70,519,085	3.18	0.55	0.43	1.64	2.90	2.77	2.13
rs2736463	UGT2B4 +17920bp (NM_021139.1)	4	70,508,724	3.08	0.55	0.43	1.63	2.86	2.72	2.15
rs11734419	MAML3 Intron2 (NM_018717.2)	4	141,040,368	3.22	0.46	0.34	1.67	2.79	2.64	1.96
rs12502059	PAPSS1 Intron4 (NM_005443.4)	4	108,962,816	3.03	0.61	0.49	1.64	2.75	2.62	1.22
rs4697446	DHX15 +259479bp (NM_001358.1)	4	23,945,891	3.30	0.38	0.26	1.73	2.67	3.40	1.64
rs7692155	KIAA1109 -44906bp (XM_371706)	4	123,386,649	3.06	0.72	0.61	1.67	2.60	3.39	2.28
rs17605639	LOC389204 -297625bp (XM_374079)	4	27,290,099	3.09	0.80	0.70	1.76	2.50	3.93	2.53
rs584374	PPARGC1A -165848bp (NM_013261.2)	4	23,733,817	3.55	0.11	0.04	3.20	1.90	5.93	1.94
rs17134333	EPB41L4A Intron2 (NM_022140.2)	5	111,670,626	2.67	0.71	0.60	1.63	3.71	1.80	0.69
rs7718321	EPB41L4A Intron1 (NM_022140.2)	5	111,697,251	0.93	0.69	0.64	1.27	3.38	0.94	0.42
rs7712363	LOC389319 -181104bp (XM_374134)	5	125,542,548	1.03	0.76	0.71	1.32	3.38	0.59	0.28
rs10076364	LOC389319 -212764bp (XM_374134)	5	125,510,888	0.93	0.75	0.70	1.29	3.27	0.67	0.32
rs7703461	SV2C Intron3 (XM_043493)	5	75,529,168	3.78	0.40	0.27	1.80	3.27	3.99	1.35
rs194229	MGC10067 -22589bp (NM_145049.1)	5	158,600,287	1.24	0.50	0.43	1.32	3.20	1.57	2.53
rs10478702	LOC389319 -173069bp (XM_374134)	5	125,550,583	1.04	0.76	0.70	1.32	3.19	0.71	0.33
rs17134365	EPB41L4A Intron1 (NM_022140.2)	5	111,694,455	1.04	0.72	0.66	1.30	3.12	0.92	0.42
rs11743891	FSTL4 Intron3 (XM_048786)	5	132,838,807	0.29	0.42	0.40	1.10	3.11	1.75	0.58
rs166296	SEMA6A Intron3 (NM_020796.2)	5	115,861,466	3.48	0.38	0.26	1.76	3.07	4.18	1.40
rs17731499	KIBRA Intron1 (NM_015238.1)	5	167,697,178	3.53	0.25	0.14	1.97	3.04	9.22	1.51

[0210] [Table 36]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs2055375	LOC441075 +72079bp (XM_499000)	5	60,566,977	3.56	0.26	0.15	1.97	3.03	7.10	1.84
rs1560026	LOC389319 -225968bp (XM_374134)	5	125,497,684	0.82	0.74	0.69	1.26	3.00	0.67	0.33
rs16869864	PTGER4 -300343bp (NM_000958.2)	5	40,415,446	3.36	0.21	0.12	2.04	2.96	5.54	2.19
rs7736074	SLC6A19 -12310bp (XM_291120)	5	1,242,456	3.35	0.65	0.52	1.69	2.76	3.00	2.07
rs581318	LOC441075 +56653bp (XM_499000)	5	60,551,551	3.24	0.25	0.15	1.89	2.75	6.89	1.73
rs30182	SV2C -30159bp (XM_043493)	5	75,384,836	3.46	0.84	0.73	1.89	2.74	4.40	2.54
rs7723981	PTGER4 -275120bp (NM_000958.2)	5	40,440,669	3.16	0.20	0.11	2.04	2.67	5.19	2.13
rs10473185	PTGER4 -304865bp (NM_000958.2)	5	40,410,924	3.06	0.20	0.11	2.00	2.58	5.23	2.09
rs10041973	ZSWIM6 -51723bp (XM_035299)	5	60,612,035	3.19	0.11	0.04	2.75	2.48	ND	2.55
rs4958734	GALNT10 Intron9 (NM_198321.2), GALNT10 Intron2 (NM_017540.3)	5	153,769,698	3.05	0.94	0.87	2.33	2.36	4.20	1.77
rs10079115	ZSWIM6 -71664bp (XM_035299)	5	60,592,094	3.04	0.11	0.04	2.68	2.34	ND	2.48
rs4379148	ZSWIM6 -72613bp (XM_035299)	5	60,591,145	3.03	0.11	0.04	2.75	2.32	ND	2.53
rs1501905	SV2C Intron1 (XM_043493)	5	75,433,640	3.04	0.79	0.68	1.73	2.29	3.12	1.94
rs30196	SV2C -1688bp (XM_043493)	5	75,413,307	3.06	0.78	0.67	1.72	2.25	2.77	1.65
rs158563	LOC91942 Intron1 (NM_174889.2)	5	60,290,761	3.44	0.20	0.10	2.19	2.19	4.28	1.69
rs10939888	ZSWIM6 -72737bp (XM_035299)	5	60,591,021	3.00	0.14	0.07	2.26	2.16	6.78	2.02
rs12696980	ZSWIM6 -71733bp (XM_035299)	5	60,592,025	3.00	0.14	0.07	2.26	2.16	6.78	2.02
rs2328883	LRRC16 -108438bp (NM_017640.2)	6	25,510,510	1.85	0.33	0.25	1.49	3.89	11.95	0.95
rs531970	EPHA7 -35391bp (NM_004440.2)	6	94,221,384	1.06	0.46	0.40	1.28	3.84	2.25	0.65
rs880226	LRRC16 -108666bp (NM_017640.2)	6	25,510,282	2.02	0.33	0.24	1.53	3.80	11.95	0.99
rs9469615	MLN -45140bp (NM_002418.1)	6	33,924,911	1.24	0.86	0.81	1.45	3.52	0.18	0.08
rs600709	NCOA7 Intron2 (NM_181782.2)	6	126,175,082	2.48	0.88	0.80	1.80	3.48	0.39	0.16
rs7767107	LOC441173 Intron1 (XM_496827)	6	142,237,572	3.49	0.30	0.19	1.86	3.35	2.24	2.29
rs1336272	LOC441173 -23126bp (XM_496827)	6	142,286,367	3.54	0.31	0.19	1.86	3.31	2.37	2.25
rs595805	NRN1 -34495bp (NM_016588.2)	6	5,987,127	1.27	0.65	0.58	1.33	3.31	1.29	0.54
rs763075	LOC442255 +235684bp (XM_498140)	6	122,253,219	0.20	0.71	0.69	1.08	3.23	0.41	0.22

[0211] [Table 37]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs13213414	LOC441173 Intron1 (XM_496827)	6	142,262,919	3.60	0.31	0.19	1.87	3.15	2.59	2.17
rs16886390	TMEM30A Intron1 (NM_018247.1)	6	76,038,298	1.18	0.87	0.82	1.47	3.14	0.78	0.27
rs1322867	TBX18 -222373bp (XM_496819)	6	85,752,991	1.35	0.35	0.28	1.38	3.14	1.00	2.24
rs2152589	LOC441173 Intron1 (XM_496827)	6	142,250,761	3.51	0.31	0.20	1.85	3.14	2.52	2.17
rs3798425	MYO6 Intron29 (XM_376516)	6	76,664,270	2.57	0.83	0.74	1.70	3.13	1.29	0.56
rs9496008	LOC441173 +181779bp (XM_496827)	6	141,762,720	3.74	0.54	0.40	1.73	3.04	3.06	1.62
rs9349248	PHACTR1 -204207bp (XM_166420)	6	12,621,612	0.77	0.57	0.52	1.22	3.03	1.32	0.55
rs12200432	PHACTR1 -201248bp (XM_166420)	6	12,624,571	0.44	0.58	0.55	1.14	3.01	1.09	0.49
rs6570564	LOC285740 +20195bp (XM_379438)	6	143,896,965	3.35	0.52	0.40	1.67	3.00	2.89	2.05
rs9399445	LOC285740 +16163bp (XM_379438)	6	143,900,997	3.41	0.55	0.42	1.68	2.97	2.98	2.01
rs4713376	C6orf214 +7329bp (NM_207496.1)	6	30,881,293	3.37	0.17	0.08	2.27	2.94	3.11	2.51
rs9484507	LOC441173 +179848bp (XM_496827)	6	141,764,651	3.93	0.53	0.39	1.80	2.93	2.98	1.58
rs9379712	C6orf32 -187336bp (NM_015864.2)	6	25,172,898	3.15	0.59	0.47	1.64	2.92	2.80	1.28
rs7754052	LOC441173 Intron1 (XM_496827)	6	142,254,496	3.20	0.32	0.21	1.77	2.88	2.37	2.09
rs9496179	LOC441173 Intron1 (XM_496827)	6	142,254,945	3.20	0.32	0.21	1.77	2.88	2.37	2.09
rs2039560	LOC441173 +145925bp (XM_496827)	6	141,798,574	3.40	0.67	0.54	1.70	2.84	3.04	1.71
rs10485223	PRDM13 +130551bp (NM_021620.2)	6	100,300,726	3.31	0.79	0.68	1.80	2.83	4.45	2.68
rs4240580	PRDM13 +138012bp (NM_021620.2)	6	100,308,187	3.51	0.79	0.68	1.82	2.81	3.79	2.25
rs9393611	C6orf32 -188810bp (NM_015864.2)	6	25,174,372	3.03	0.59	0.47	1.62	2.79	2.70	1.26
rs9356960	C6orf32 -188588bp (NM_015864.2)	6	25,174,150	3.07	0.59	0.47	1.63	2.78	2.81	1.33
rs9367520	ELOVL5 Intron1 (NM_021814.2)	6	53,271,883	3.41	0.35	0.23	1.82	2.76	4.12	1.62
rs12195469	C6orf214 Intron1 (NM_207496.1)	6	30,897,587	3.21	0.16	0.08	2.22	2.75	3.06	2.43
rs17826560	PRDM13 +132124bp (NM_021620.2)	6	100,302,299	3.29	0.79	0.68	1.79	2.73	4.08	2.50
rs1915463	VMP -52946bp (NM_080723.2)	6	24,181,383	3.24	0.53	0.41	1.66	2.61	2.72	1.84
rs17070891	LOC441173 +153727bp (XM_496827)	6	141,790,772	3.27	0.55	0.42	1.66	2.60	2.79	1.61
rs1402406	VMP -35757bp (NM_080723.2)	6	24,198,572	3.06	0.57	0.45	1.62	2.59	2.63	2.00
rs10947096	C6orf214 +147488bp (NM_207496.1)	6	30,873,874	3.08	0.13	0.06	2.44	2.57 ND		2.47

[0212] [Table 38]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs9403498	FUCA2 -18431bp (NM_032020.3)	6	143,892,987	3.04	0.63	0.51	1.63	2.56	2.89	2.01
rs1402405	VMP -35853bp (NM_080723.2)	6	24,198,476	3.13	0.58	0.45	1.63	2.53	2.63	1.91
rs7740547	SLC22A16 Intron1 (NM_033125.2)	6	110,897,601	3.13	0.49	0.37	1.64	2.43	2.66	1.33
rs221712	SLC22A16 Intron4 (NM_033125.2)	6	110,869,519	3.18	0.49	0.37	1.65	2.39	2.64	1.39
rs17577123	C6orf10 +2945bp (NM_006781.2)	6	32,365,525	3.07	0.11	0.04	2.71	1.95	3.88	2.47
rs7802749	PPP1R9A Intron4 (XM_371933)	7	94,432,292	1.20	0.53	0.46	1.32	3.58	1.78	0.61
rs6965857	DLD -36997bp (NM_000108.2)	7	107,088,565	0.76	0.65	0.60	1.23	3.13	1.00	0.45
rs11972734	CREB3L2 -6085bp (NM_194071.1)	7	137,150,143	3.19	0.26	0.16	1.86	3.12	15.95	1.54
rs1621819	C1GALT1 +30350bp (NM_020156.1)	7	7,087,571	3.80	0.61	0.47	1.76	3.11	3.14	2.03
rs1514880	LOC340268 Intron1 (XM_294634)	7	9,664,527	3.39	0.60	0.46	1.70	3.09	3.25	2.24
rs12669138	LOC340268 Intron1 (XM_294634)	7	9,564,997	2.83	0.65	0.54	1.60	3.08	3.15	2.74
rs698408	SND1 Intron8 (NM_014390.1)	7	126,939,887	2.61	0.30	0.21	1.66	3.03	1.55	2.28
rs7458284	LOC340268 Intron1 (XM_294634)	7	9,670,774	3.37	0.39	0.27	1.74	2.87	3.81	1.44
rs3757760	SND1 Intron16 (NM_014390.1)	7	127,252,147	3.23	0.30	0.19	1.81	2.85	2.51	2.08
rs2241291	SND1 Intron16 (NM_014390.1), NAG8 Exon1 (NM_014411.1)	7	127,232,825	3.27	0.30	0.19	1.81	2.81	2.63	2.04
rs17156635	CREB5 Intron1 (NM_182899.2), CREB5 -56415bp (NM_182898.1), CREB5 -79505bp (NM_004904.1)	7	28,168,969	3.16	0.23	0.13	1.99	2.80	14.75	1.50
rs1638213	C1GALT1 +33234bp (NM_020156.1)	7	7,090,455	3.36	0.60	0.47	1.67	2.72	2.82	1.90
rs320785	LOC340268 -6464bp (XM_294634)	7	9,532,629	3.41	0.59	0.46	1.68	2.71	2.84	1.73
rs1796121	C1GALT1 +33624bp (NM_020156.1)	7	7,090,845	3.24	0.59	0.47	1.65	2.58	2.74	1.84
rs3757759	SND1 Intron16 (NM_014390.1)	7	127,288,765	3.12	0.33	0.22	1.74	2.57	3.27	1.80
rs12530870	KIAA1706 -11363bp (NM_030636.1)	7	35,954,741	3.00	0.81	0.71	1.76	2.42	3.98	2.76
rs17152703	LOC401384 +195612bp (XM_379506)	7	78,929,412	3.33	0.85	0.75	1.89	2.37	3.41	2.01
rs10441198	LOC442363 -76453bp (XM_498255)	7	144,098,654	3.17	0.60	0.48	1.64	2.36	2.41	1.33

[0213] [Table 39]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs13225076	LOC285984 -162101bp (XM_208373)	7	84,095,361	3.16	0.86	0.76	1.93	2.31	3.53	1.92
rs17171658	C7orf11 +13816bp (NM_138701.1)	7	39,931,767	3.02	0.78	0.67	1.75	2.31	2.98	1.70
rs826824	CNTNAP2 Intron9 (NM_014141.3)	7	146,496,639	3.04	0.74	0.63	1.69	2.26	2.60	1.52
rs6993934	FBXO16 +12541bp (NM_172366.2)	8	28,329,307	0.01	0.27	0.27	1.00	3.56	0.37	1.81
rs1425735	EBF2 +148803bp (NM_022659.1)	8	25,608,687	1.50	0.66	0.58	1.38	3.28	1.37	0.57
rs6991277	PTDSS1 +53377bp (NM_014754.1)	8	97,469,327	3.10	0.93	0.85	2.28	3.26	0.74	0.26
rs6981589	LOC286186 Intron1 (XM_379586)	8	66,612,011	2.30	0.66	0.56	1.52	3.13	2.85	3.04
rs4394361	LOC157657 -172125bp (NM_177965.2)	8	96,522,738	3.55	0.24	0.13	2.04	3.09	10.03	1.97
rs3133744	LOC157657 -252889bp (NM_177965.2)	8	96,603,502	3.53	0.31	0.19	1.90	2.97	4.79	1.84
rs10113800	LOC157657 -163565bp (NM_177965.2)	8	96,514,178	3.12	0.23	0.14	1.92	2.70	10.58	1.76
rs6601569	C8orf7 -14730bp (XM_088376)	8	11,110,988	3.45	0.93	0.85	2.32	2.66	7.14	3.26
rs10105301	LOC286186 +84181bp (XM_379586)	8	66,517,616	3.04	0.27	0.17	1.81	2.63	2.22	2.10
rs6995270	SIAT4A Intron2 (NM_003033.2), SIAT4A Intron2 (NM_173344.1)	8	134,582,401	3.02	0.51	0.39	1.62	2.37	2.71	1.49
rs10811638	CDKN2A +44473bp (NM_000077.3), CDKN2A +44473bp (NM_058197.2), CDKN2A +44473bp (NM_058195.2)	9	21,913,279	0.15	0.42	0.41	1.06	3.80	0.84	2.27
rs10869589	PCSK5 -314572bp (NM_006200.2)	9	75,420,603	2.09	0.72	0.63	1.52	3.59	5.09	5.18
rs10967964	MOBKL2B Intron1 (NM_024761.3)	9	27,485,920	3.13	0.23	0.13	1.95	3.55	1.34	2.62
rs2518713	CDKN2A +38086bp (NM_000077.3), CDKN2A +38086bp (NM_058197.2), CDKN2A +38086bp (NM_058195.2)	9	21,919,666	0.38	0.44	0.41	1.13	3.39	1.01	2.32
rs10781440	LOC392347 Intron1 (XM_373298)	9	68,992,320	3.89	0.37	0.24	1.85	3.34	3.48	1.97
rs1412066	DBC1 -33786bp (NM_014618.1)	9	119,245,041	3.06	0.93	0.85	2.19	3.25	0.97	0.35
rs7022939	LOC347273 +139903bp (XM_294592)	9	100,568,349	1.91	0.36	0.28	1.48	3.21	1.32	2.30
rs4744780	PCSK5 Intron9 (NM_006200.2)	9	75,952,602	3.30	0.50	0.37	1.68	3.18	2.85	2.21

[0214] [Table 40]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs4743420	LOC347273 +139198bp (XM_294592)	9	100,567,644	1.93	0.36	0.27	1.49	3.17	1.33	2.29
rs10815959	PTPRD -825338bp (NM_002839.1), PTPRD -825338bp (NM_130391.1), PTPRD -825338bp (NM_130392.1), PTPRD -825338bp (NM_130393.1)	9	8,806,479	3.11	0.58	0.46	1.63	3.15	2.73	2.41
rs953924	FLJ31810 Intron3 (NM_152570.1)	9	28,313,673	2.54	0.85	0.77	1.74	3.10	18.06	14.20
rs4836767	DBC1 -34887bp (NM_014618.1)	9	119,246,142	3.24	0.93	0.85	2.24	3.09	1.46	0.53
rs4977749	CDKN2A +40425bp (NM_000077.3), CDKN2A +40425bp (NM_058197.2), CDKN2A +40425bp (NM_058195.2)	9	21,917,327	0.38	0.44	0.41	1.13	3.09	1.02	2.22
rs10512277	LOC347273 +1389099bp (XM_294592)	9	100,567,355	2.02	0.36	0.27	1.50	3.08	1.41	2.27
rs9299341	LOC347273 +1419938bp (XM_294592)	9	100,570,439	2.02	0.36	0.27	1.50	3.08	1.41	2.27
rs10491692	DOCK8 Intron13 (NM_203447.1)	9	336,887	0.35	0.16	0.14	1.17	3.08	0.00	1.80
rs2780197	C9orf39 Intron13 (NM_017738.1)	9	17,416,186	3.83	0.81	0.70	1.90	3.05	3.93	2.16
rs7038186	C9orf39 Intron10 (NM_017738.1)	9	17,388,616	3.69	0.81	0.69	1.87	2.96	3.91	2.20
rs2773395	C9orf28 -119663bp (XM_088525)	9	126,049,019	3.39	0.36	0.24	1.77	2.94	2.98	1.97
rs1412067	DBC1 -35540bp (NM_014618.1)	9	119,246,795	3.08	0.93	0.85	2.20	2.92	1.45	0.54
rs11144406	OSTF1 +226491bp (NM_012383.3)	9	75,217,808	3.39	0.20	0.11	2.10	2.91	5.39	2.22
rs10869690	PIP5K1B Intron15 (NM_003558.1)	9	68,851,241	3.37	0.38	0.26	1.74	2.85	3.90	1.51
rs10969339	LOC401497 +655774bp (XM_376822)	9	29,723,159	3.13	0.88	0.79	1.95	2.77	11.71	6.74
rs16929359	DMRT2 +392458bp (NM_006557.3), DMRT2 +392458bp (NM_181872.1)	9	1,440,010	3.62	0.11	0.04	3.02	2.70 ND		2.53
rs943509	OSTF1 +226788bp (NM_012383.3)	9	75,218,105	3.18	0.37	0.25	1.72	2.70	3.80	1.45
rs10869686	PIP5K1B Intron15 (NM_003558.1)	9	68,850,168	3.22	0.37	0.26	1.73	2.68	3.74	1.52
rs10869553	OSTF1 +235138bp (NM_012383.3)	9	75,226,455	3.09	0.20	0.11	2.01	2.62	5.19	2.10
rs12554461	RCL1 +4195bp (NM_005772.2)	9	4,855,256	3.19	0.41	0.29	1.69	2.60	2.49	1.90
rs4142436	DMRT2 +396648bp (NM_006557.3), DMRT2 +396648bp (NM_181872.1)	9	1,444,200	3.23	0.13	0.06	2.49	2.54	3.92	2.56

[0215] [Table 41]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs7048937	LOC392347 Intron2 (XM_373298)	9	68,975,807	3.16	0.38	0.27	1.70	2.52	2.57	1.85
rs7034303	LOC392347 Intron2 (XM_373298)	9	68,976,425	3.16	0.38	0.27	1.70	2.52	2.57	1.85
rs6560584	LOC392347 Intron2 (XM_373298)	9	68,976,726	3.16	0.38	0.27	1.70	2.52	2.57	1.85
rs7850573	LOC392347 Intron2 (XM_373298)	9	68,976,814	3.16	0.38	0.27	1.70	2.52	2.57	1.85
rs2584554	C9orf39 Intron13 (NM_017738.1)	9	17,416,808	3.13	0.80	0.70	1.78	2.50	3.38	1.91
rs1547335	LOC401497 +6210650bp (XM_376822)	9	29,757,868	3.11	0.77	0.66	1.73	2.25	2.90	1.82
rs3781158	KCNMA1 Intron18 (NM_002247.2) HK1 Intron5 (NM_033497.1), HK1 Intron5 (NM_033498.1),	10	78,426,444	1.61	0.60	0.51	1.39	3.96	1.65	0.59
rs10823349	HK1 Intron6 (NM_033500.1), HK1 Intron2 (NM_033496.1), HK1 Intron2 (NM_000188.1)	10	70,779,704	3.56	0.90	0.80	2.13	3.90	1.05	0.39
rs17388160	KCNMA1 Intron18 (NM_002247.2)	10	78,415,943	1.81	0.66	0.57	1.44	3.79	1.47	0.57
rs1801041	DNA2L Exon21 (XM_166103)	10	69,844,713	1.49	0.80	0.73	1.45	3.58	0.78	0.33
rs11001963	KCNMA1 Intron18 (NM_002247.2)	10	78,430,965	2.23	0.70	0.60	1.52	3.57	1.55	0.63
rs4454609	PHYH +154999bp (NM_006214.2) HK1 Intron10 (NM_033497.1), HK1 Intron10 (NM_033498.1),	10	13,344,307	2.46	0.66	0.55	1.55	3.56	3.42	3.45
rs4589168	HK1 Intron11 (NM_033500.1), HK1 Intron7 (NM_033496.1), HK1 Intron7 (NM_000188.1)	10	70,800,223	3.18	0.89	0.81	2.01	3.45	1.15	0.45
rs7093891	XPNPEP1 +21493bp (NM_020383.2)	10	111,593,021	3.00	0.69	0.57	1.64	3.31	2.15	0.92
rs10762840	LOC283050 Intron4 (XM_378238)	10	80,483,339	3.86	0.39	0.26	1.81	3.12	3.29	1.83
rs9416465	ZWINT +273128bp (NM_007057.2), ZWINT +273128bp (NM_032997.1)	10	57,514,084	3.32	0.82	0.71	1.85	2.78	3.55	1.81
rs7903897	LOC285444 +40505bp (XM_497256)	10	135,321,566	3.05	0.61	0.49	1.63	2.72	2.68	2.21

[0216] [Table 42]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs2496057	C10orf112 Intron20 (XM_295865)	10	19,623,674	3.05	0.56	0.44	1.62	2.57	2.75	1.90
rs1500763	ZWINT +308458bp (NM_007057.2), ZWINT +308458bp (NM_032997.1)	10	57,478,754	3.03	0.86	0.77	1.88	2.54	5.27	2.80
rs2151078	PCDH15 Intron3 (NM_033056.2)	10	55,864,965	3.11	0.95	0.88	2.49	2.21	3.40	1.37
rs1881716	LDHA Intron5 (NM_005566.1)	11	18,381,594	3.40	0.38	0.26	1.74	3.86	2.09	2.48
rs7107489	LOC119710 +809442bp (NM_138787.2)	11	37,446,835	1.46	0.65	0.58	1.37	3.69	2.69	3.66
rs6590698	SPAS1 +396277bp (NM_174927.1)	11	132,819,450	1.09	0.72	0.66	1.32	3.60	5.44	6.70
rs4274186	LDHA Intron2 (NM_005566.1)	11	18,375,295	3.41	0.38	0.26	1.76	3.58	2.15	2.41
rs7927545	MGC71806 Intron3 (NM_198516.1)	11	11,403,040	3.75	0.60	0.46	1.73	3.58	3.11	1.30
rs10792820	PICALM Intron12 (NM_007166.1)	11	85,381,622	0.44	0.49	0.46	1.15	3.46	1.48	0.53
rs9326253	LOC440070 +34118bp (XM_498530)	11	119,149,661	0.13	0.60	0.59	1.05	3.27	0.73	0.36
rs12576681	MGC71806 Intron3 (NM_198516.1)	11	11,402,663	3.67	0.31	0.19	1.88	3.23	6.26	1.53
rs10837846	LOC387761 -159308bp (XM_373495)	11	42,393,594	2.69	0.59	0.47	1.57	3.09	3.22	2.55
rs1462674	LOC387761 -160223bp (XM_373495)	11	42,394,509	2.71	0.59	0.47	1.57	3.07	3.22	2.53
rs1386239	LOC338645 Intron5 (XM_370616)	11	24,774,285	2.73	0.11	0.05	2.48	3.06	0.00	3.10
rs10837854	LOC387761 -227349bp (XM_373495)	11	42,461,635	2.09	0.56	0.47	1.47	3.05	2.58	2.69
rs504105	FLJ37874 +39466bp (NM_182603.1)	11	82,641,607	3.17	0.57	0.45	1.64	3.05	2.97	1.30
rs524441	FLJ37874 +1045bp (NM_182603.1)	11	82,638,706	3.11	0.56	0.44	1.63	2.93	2.90	1.29
rs681367	FLJ37874 +1111bp (NM_182603.1)	11	82,638,772	3.10	0.56	0.44	1.63	2.91	2.90	1.31
rs628223	MDS025 +4340bp (NM_021825.3)	11	82,645,812	3.10	0.56	0.44	1.63	2.91	2.90	1.31
rs6484897	MGC71806 Intron3 (NM_198516.1)	11	11,401,879	3.15	0.31	0.20	1.78	2.90	5.97	1.41
rs4937173	KIRREL3 Intron1 (NM_032531.1)	11	126,034,466	3.37	0.43	0.31	1.71	2.90	2.75	1.96
rs11220587	KIRREL3 Intron1 (NM_032531.1)	11	126,082,725	3.35	0.50	0.37	1.68	2.88	2.99	1.31
rs2252070	MMP13 -77bp (NM_002427.2)	11	102,331,749	3.46	0.60	0.47	1.69	2.82	2.88	1.55
rs693253	KIRREL3 Intron1 (NM_032531.1)	11	126,032,975	3.40	0.44	0.31	1.71	2.77	2.85	1.82
rs4937174	KIRREL3 Intron1 (NM_032531.1)	11	126,034,593	3.21	0.43	0.31	1.68	2.74	2.66	1.92

[0217] [Table 43]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs12800710	LPXN Intron7 (NM_004811.1)	11	58,071,116	3.73	0.87	0.77	2.04	2.73	3.91	2.08
rs10898459	EED Intron6 (NM_003797.2), EED Intron6 (NM_152991.1)	11	85,650,587	3.14	0.60	0.48	1.64	2.72	2.89	2.06
rs3862632	KIRREL3 Intron1 (NM_032531.1)	11	126,054,713	3.21	0.43	0.31	1.68	2.66	2.70	1.86
rs11229555	CNTF +15485bp (NM_000614.2), ZFP91-CNTF +15485bp (NM_170768.1)	11	58,165,263	3.57	0.87	0.77	2.01	2.59	3.88	2.12
rs1451316	OR1S2 +19906p (XM 166916)	11	57,725,262	3.06	0.53	0.41	1.63	2.58	2.53	1.97
rs7108068	KIRREL3 Intron1 (NM_032531.1)	11	126,035,753	3.18	0.43	0.31	1.67	2.58	2.74	1.79
rs10896715	OR1S1 +5325bp (XM_166917)	11	57,745,095	3.38	0.84	0.74	1.88	2.51	3.08	1.65
rs2298608	CNTF +11265bp (NM_000614.2), ZFP91-CNTF +11265bp (NM_170768.1)	11	58,161,043	3.47	0.87	0.77	1.99	2.51	3.83	2.12
rs655316	MMP13 -5902bp (NM_002427.2)	11	102,337,574	3.07	0.58	0.46	1.62	2.49	2.74	1.57
rs161130	LOC387810 -172677bp (XM_373513)	11	112,160,184	3.15	0.83	0.73	1.83	2.35	3.18	1.78
rs7102784	LOC399898 +878bp (XM_374885)	11	57,813,314	3.08	0.88	0.79	1.94	2.25	3.65	1.98
rs11175627	LOC400046 +33814bp (XM_378362)	12	63,691,379	3.08	0.27	0.17	1.83	3.15	16.90	1.47
rs7302136	DKFZp761O2018 +35186bp (XM_044062)	12	127,752,520	3.91	0.94	0.85	2.54	3.13	5.80	2.27
rs11175622	LOC400046 +28983bp (XM_378362)	12	63,686,548	2.98	0.27	0.17	1.79	3.10	16.58	1.46
rs7136577	LOC400046 +35244bp (XM_378362)	12	63,692,809	2.98	0.27	0.17	1.79	3.10	16.58	1.46
rs2169856	LOC441639 +48092bp (XM_497345)	12	53,858,919	1.26	0.72	0.66	1.35	3.06	0.97	0.45
rs7962260	FLJ40126 Intron18 (NM_173599.1), SLC2A13 Intron6 (NM_052885.1)	12	38,510,570	3.77	0.24	0.13	2.07	3.05	8.32	1.68
rs7296095	LOC440112 -115952bp (XM_498548)	12	114,337,597	2.55	0.28	0.19	1.68	3.05	10.32	1.19
rs7959848	LOC401725 +200037bp (XM_377278)	12	82,248,474	3.88	0.45	0.32	1.79	3.02	3.10	1.75
rs12227382	DKFZp761O2018 +36420bp (XM_044062)	12	127,753,754	3.72	0.94	0.85	2.48	2.94	5.75	2.33
rs11059865	DKFZp761O2018 +34801bp (XM_044062)	12	127,752,135	3.58	0.94	0.86	2.48	2.92	4.34	1.67
rs4882448	LOC401725 +200630bp (XM_377278)	12	82,249,067	3.62	0.44	0.31	1.76	2.85	3.01	1.76
rs4473002	FLJ40126 Intron18 (NM_173599.1), SLC2A13 Intron6 (NM_052885.1)	12	38,541,898	3.40	0.24	0.14	1.97	2.82	8.19	1.58

[0218] [Table 44]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs7968509	FLJ40126 Intron18 (NM_173599.1),	12	38,541,115	3.46	0.24	0.13	1.99	2.82	7.74	1.66
rs7956512	SLC2A13 Intron6 (NM_052885.1) LOC401725 +199585bp (XM_377278)	12	82,248,022	3.71	0.46	0.32	1.75	2.79	2.82	1.72
rs4768188	FLJ40126 Intron18 (NM_173599.1),	12	38,507,445	3.46	0.25	0.15	2.01	2.69	6.02	1.63
rs10877835	SLC2A13 Intron7 (NM_052885.1) SLC2A13 Intron3 (NM_052885.1)	12	38,637,759	3.13	0.15	0.07	2.28	2.50	4.03	2.36
rs11116586	SLC6A15 +106086bp (NM_182767.2),	12	83,650,812	3.08	0.73	0.62	1.68	2.48	2.41	1.27
rs908440	SLC6A15 +127822bp (NM_018057.3) TRHDE +374236bp (NM_013381.1)	12	71,719,925	3.11	0.73	0.62	1.69	2.48	3.10	1.95
rs7485210	LOC116437 -10703bp (XM_378394)	12	130,163,733	3.19	0.57	0.45	1.64	2.46	2.66	1.59
rs10862927	SLC6A15 +113194bp (NM_182767.2), SLC6A15 +134930bp (NM_018057.3)	12	83,643,704	3.01	0.73	0.62	1.67	2.40	2.40	1.29
rs4765680	CACNA1C Intron3 (NM_000719.3)	12	2,427,360	3.03	0.96	0.90	2.66	2.38	ND	ND
rs4643164	LOC122335 -355849bp (XM_063084)	13	106,724,352	0.88	0.38	0.33	1.26	3.63	3.26	0.70
rs2802402	HTR2A -2151859bp (NM_000621.1)	13	46,583,361	2.21	0.30	0.21	1.59	3.39	1.16	2.38
rs17640758	DNAJD1 +112979bp (NM_013238.1)	13	42,590,879	2.16	0.14	0.08	1.91	3.07	0.00	2.48
rs2282267	CLMN Intron12 (NM_024734.2)	14	94,729,648	3.75	0.69	0.55	1.76	3.33	3.22	1.59
rs2208986	SLC35F4 -84786bp (XM_292260)	14	57,218,154	0.82	0.76	0.71	1.26	3.29	0.70	0.33
rs4304940	SLC35F4 -89221bp (XM_292260)	14	57,222,589	0.84	0.75	0.71	1.27	3.22	0.72	0.34
rs1028591	LOC283547 -65737bp (XM_378454)	14	38,495,490	0.43	0.64	0.61	1.14	3.20	0.82	0.39
rs7148801	AKAP6 Intron7 (NM_004274.3)	14	32,206,647	3.68	0.95	0.88	2.80	3.18	2.11	0.64
rs3180753	CLMN Intron12 (NM_024734.2)	14	94,729,500	3.64	0.68	0.55	1.74	3.11	3.01	1.53
rs2150324	OR4L1 -23711bp (XM_063310)	14	19,595,673	0.29	0.54	0.52	1.10	3.07	1.11	0.49
rs10483416	AKAP6 Intron7 (NM_004274.3)	14	32,145,585	3.27	0.81	0.70	1.79	2.95	2.07	0.95
rs6571593	NPAS3 Intron2 (NM_022123.1), NPAS3 Intron3 (NM_173159.1)	14	32,865,564	3.22	0.48	0.36	1.67	2.93	2.02	2.29
rs2282273	CLMN Intron11 (NM_024734.2)	14	94,730,437	3.41	0.66	0.54	1.70	2.91	3.07	1.66

[0219] [Table 45]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs1622029	LOC283583 -1366892bp (XM_211092)	14	83,697,804	3.52	0.71	0.58	1.74	2.83	3.23	2.07
rs8003168	RGS6 -36445bp (NM_004296.3)	14	71,433,141	3.09	0.47	0.35	1.64	2.81	2.21	2.13
rs10498642	DICER1 Intron9 (NM_030621.2), DICER1 Intron8 (NM_177438.1)	14	94,658,292	3.42	0.62	0.49	1.68	2.80	2.91	1.97
rs9646147	LRFN5 -190930bp (NM_152447.2)	14	40,956,160	3.19	0.92	0.84	2.19	2.76	ND	ND
rs1187627	CLMN Intron9 (NM_024734.2)	14	94,734,482	3.50	0.59	0.46	1.69	2.75	2.82	1.79
SNP_A-18219	MAMDC1 -1035952bp (NM_182830.2)	14	47,918,097	3.37	0.59	0.47	1.67	2.72	2.68	1.38
rs14042	FLJ45244 Exon2 (NM_207443.1)	14	94,715,773	3.38	0.56	0.43	1.67	2.72	2.86	1.70
rs1187626	CLMN Intron9 (NM_024734.2)	14	94,735,610	3.38	0.60	0.47	1.68	2.71	2.88	1.80
rs1211448	CLMN Intron9 (NM_024734.2)	14	94,734,970	3.28	0.59	0.46	1.66	2.60	2.74	1.82
rs848117	SLC25A21 Intron3 (NM_030631.1)	14	36,326,610	3.15	0.12	0.05	2.62	2.43	ND	2.34
rs12900219	NDN -100017bp (NM_002487.2)	15	21,583,560	3.84	0.93	0.85	2.46	3.79	1.48	0.48
rs2247154	TLE3 +105451bp (NM_005078.1)	15	68,024,022	2.86	0.82	0.72	1.74	3.05	1.62	0.71
rs12324063	ATP10A Intron3 (NM_024490.2)	15	23,540,049	3.60	0.43	0.30	1.74	2.82	2.80	1.82
rs16941388	MYO1E -6977bp (NM_004998.1)	15	57,459,340	3.32	0.94	0.86	2.42	2.79	2.83	1.07
rs3863401	LRRC28 Intron6 (NM_144598.2)	15	97,698,743	3.59	0.61	0.48	1.71	2.79	2.85	1.66
rs12591327	TLN2 +69488bp (NM_015059.1)	15	60,990,221	3.18	0.64	0.51	1.65	2.75	2.88	1.51
rs7173844	LRRC28 Intron6 (NM_144598.2)	15	97,694,416	3.49	0.61	0.48	1.69	2.70	2.79	1.73
rs1717831	NDN -95082bp (NM_002487.2)	15	21,578,625	3.06	0.90	0.82	2.03	2.51	2.45	1.10
rs4410020	MGC26690 -71198bp (NM_152450.1)	15	57,510,545	3.02	0.63	0.51	1.64	2.46	2.76	2.01
rs7198530	CHD9 -179353bp (NM_025134.2)	16	51,641,067	1.00	0.17	0.13	1.40	3.77	0.00	2.13
rs9937509	CHD9 -162783bp (NM_025134.2)	16	51,657,637	1.00	0.18	0.14	1.39	3.74	0.00	2.11
rs436962	CDH11 +25906bp (NM_001797.2), CDH11 +25906bp (NM_033664.1)	16	63,512,280	1.68	0.84	0.77	1.54	3.73	0.71	0.28
rs4309380	LOC440339 +245434bp (XM_498634)	16	13,523,196	3.83	0.32	0.20	1.89	3.47	2.73	2.23

[0220] [Table 46]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs35146	CDH11 Intron12 (NM_001797.2), CDH11 Intron12 (NM_033664.1)	16	63,541,382	2.24	0.86	0.79	1.70	3.43	0.76	0.31
rs35572	LOC390735 -442487bp (XM_497515)	16	62,385,041	1.02	0.85	0.81	1.38	3.42	ND	ND
rs35165	CDH11 +5537bp (NM_001797.2), CDH11 +5537bp (NM_033664.1)	16	63,532,649	1.89	0.85	0.78	1.61	3.37	0.67	0.28
rs9302502	LOC440339 +251309bp (XM_498634)	16	13,517,321	3.58	0.33	0.21	1.84	3.36	2.44	2.24
rs35192	CDH11 Intron4 (NM_001797.2), CDH11 Intron4 (NM_033664.1)	16	63,587,141	2.72	0.87	0.78	1.85	3.31	ND	ND
rs16968101	CDH11 +28144bp (NM_001797.2), CDH11 +28144bp (NM_033664.1)	16	63,510,042	1.89	0.86	0.79	1.61	3.30	0.67	0.28
rs412474	CDH11 +15454bp (NM_001797.2), CDH11 +15454bp (NM_033664.1)	16	63,522,732	2.15	0.86	0.79	1.68	3.28	0.76	0.32
rs429065	CDH11 +22043bp (NM_001797.2), CDH11 +22043bp (NM_033664.1)	16	63,516,143	2.11	0.86	0.79	1.67	3.23	0.76	0.32
rs1554401	CDH11 Intron4 (NM_001797.2), CDH11 Intron4 (NM_033664.1)	16	63,588,839	1.62	0.49	0.41	1.39	3.21	2.24	0.76
rs35162	CDH11 +5129bp (NM_001797.2), CDH11 +5129bp (NM_033664.1)	16	63,533,057	2.08	0.86	0.79	1.66	3.19	0.75	0.32
rs35216	CDH11 Intron8 (NM_001797.2), CDH11 Intron8 (NM_033664.1)	16	63,572,992	2.08	0.86	0.79	1.66	3.15	0.77	0.33
rs40116	CDH11 Intron8 (NM_001797.2), CDH11 Intron8 (NM_033664.1)	16	63,572,366	2.07	0.86	0.79	1.65	3.14	0.76	0.33
rs28216	CDH11 Exon7 (NM_001797.2), CDH11 Exon7 (NM_033664.1)	16	63,579,615	2.07	0.86	0.79	1.65	3.14	0.76	0.33

[0221] [Table 47]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs35140	CDH11 Intron11 (NM_001797.2), CDH11 Intron11 (NM_033664.1) A2BP1 Intron2 (NM_018723.2),	16	63,548,272	2.03	0.86	0.79	1.64	3.12	0.75	0.32
rs9925034	A2BP1 -804582bp (NM_145891.1), A2BP1 -804582bp (NM_145892.1), A2BP1 -804582bp (NM_145893.1)	16	6,518,170	1.07	0.48	0.41	1.29	3.10	1.40	2.42
rs460538	CDH11 +22417bp (NM_001797.2), CDH11 +22417bp (NM_033664.1)	16	63,515,769	2.03	0.86	0.79	1.65	3.09	0.76	0.32
rs1079008	CDH11 Intron2 (NM_001797.2), CDH11 Intron2 (NM_033664.1)	16	63,628,424	1.48	0.85	0.79	1.49	3.09	0.50	0.23
rs35164	CDH11 +5484bp (NM_001797.2), CDH11 +5484bp (NM_033664.1)	16	63,532,702	1.99	0.86	0.79	1.64	3.08	0.74	0.32
rs35214	CDH11 Intron8 (NM_001797.2), CDH11 Intron8 (NM_033664.1)	16	63,573,409	2.02	0.86	0.79	1.64	3.08	0.76	0.33
rs35200	CDH11 Intron7 (NM_001797.2), CDH11 Intron7 (NM_033664.1)	16	63,579,045	2.02	0.86	0.79	1.64	3.08	0.76	0.33
rs13333495	LOC440339 +265091bp (XM_498634)	16	13,503,539	3.31	0.32	0.21	1.79	3.03	2.39	2.14
rs16962155	LOC440339 +272794bp (XM_498634) A2BP1 -257472bp (NM_018723.2),	16	13,495,836	3.13	0.32	0.21	1.75	2.81	2.34	2.07
rs6500718	A2BP1 -1571091bp (NM_145891.1), A2BP1 -1571091bp (NM_145892.1), A2BP1 -1571091bp (NM_145893.1)	16	5,751,661	3.43	0.95	0.88	2.65	2.74 ND	ND	
rs12595990	LOC92017 Intron9 (XM_042234)	16	12,378,613	3.07	0.51	0.39	1.63	2.52	2.69	1.30

[0222] [Table 48]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs8062798	A2BP1 -253070bp (NM_018723.2), A2BP1 -1566689bp (NM_145891.1), A2BP1 -1566689bp (NM_145892.1), A2BP1 -1566689bp (NM_145893.1)	16	5,756,063	3.02	0.95	0.89	2.50	2.38	ND	ND
rs1816581	CBLN1 +57699bp (NM_004352.1)	16	47,812,497	3.26	0.41	0.29	1.70	2.35	2.66	1.60
rs1898359	CBLN1 +57192bp (NM_004352.1)	16	47,813,004	3.26	0.41	0.29	1.70	2.35	2.66	1.60
rs9898312	SOCS3 +39255bp (NM_003955.3)	17	73,825,204	0.49	0.54	0.50	1.15	3.67	1.43	2.74
rs231005	PMP22 +34074bp (NM_153322.1), PMP22 +34074bp (NM_153321.1), PMP22 +34074bp (NM_000304.2)	17	15,039,748	2.71	0.69	0.58	1.60	3.43	3.86	3.49
rs10438771	BRIP1 +31746bp (NM_032043.1)	17	57,083,021	0.02	0.26	0.25	1.01	3.27	0.44	1.86
rs2074159	LGP2 Intron11 (NM_024119.1)	17	37,510,024	1.71	0.86	0.80	1.57	3.25	ND	ND
rs4890199	RPH3AL +18823bp (NM_006987.2)	17	43,474	2.70	0.10	0.04	2.60	3.17	0.48	3.74
rs230923	PMP22 +16078bp (NM_153322.1), PMP22 +16078bp (NM_153321.1), PMP22 +16078bp (NM_000304.2)	17	15,057,744	2.05	0.68	0.59	1.50	3.06	3.63	3.58
rs1553072	FLJ35773 +12632bp (NM_152599.2)	17	8,628,576	3.20	0.24	0.14	1.93	2.60	6.76	1.70
rs917593	MGC45562 Intron2 (NM_152349.1)	17	36,070,052	3.08	0.30	0.19	1.78	2.35	3.73	1.60
rs17057804	LOC284274 -273821bp (XM_378756)	18	71,542,467	0.03	0.29	0.29	1.01	3.88	2.55	0.53
rs11872151	GTSCR1 -653277bp (XM_496277)	18	67,282,963	2.77	0.97	0.91	2.74	3.77	0.46	0.10
rs11150900	LOC284274 -284312bp (XM_378756)	18	71,552,958	0.37	0.67	0.64	1.13	3.50	0.73	0.35
rs1551434	GTSCR1 -637101bp (XM_496277)	18	67,266,787	3.59	0.95	0.87	2.71	3.13	2.07	0.65
rs8098925	LOC400655 -175143bp (XM_378753)	18	69,257,838	3.34	0.64	0.51	1.69	2.88	2.84	1.41
rs1828132	LOC284276 Intron2 (XM_378757)	18	72,388,920	3.23	0.52	0.40	1.67	2.81	2.89	1.28
rs8088082	PPP4R1 -42712bp (NM_005134.1)	18	9,647,279	3.49	0.21	0.11	2.08	2.68	6.23	1.85

[0223] [Table 49]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs2587428	CDH7 +60322bp (NM_033646.1),	18	61,759,477	3.15	0.50	0.38	1.64	2.60	2.56	1.91
rs6565975	CDH7 +60323bp (NM_004361.2)	18	73,316,910	3.19	0.75	0.63	1.71	2.57	3.30	2.24
rs10451358	LOC441825 +102358bp (XM_497596)	18	9,207,471	3.05	0.43	0.31	1.65	2.54	3.05	1.32
rs1942583	ANKRD12 Intron7 (NM_015208.2)	18	73,327,133	3.02	0.72	0.61	1.66	2.42	3.03	2.17
rs12051936	LOC441825 +112581bp (XM_497596)	18	73,310,787	3.11	0.60	0.47	1.63	2.33	2.56	1.70
rs4482359	LOC441825 +96235bp (XM_497596)	18	10,180,764	3.16	0.64	0.51	1.66	2.30	2.51	1.46
rs12462868	LOC440479 +52521bp (XM_498693)	19	41,163,676	2.44	0.30	0.21	1.64	3.69	11.93	1.05
rs7260296	FLJ36445 +223746bp (NM_153233.1)	19	7,541,689	0.57	0.62	0.58	1.18	3.37	1.89	3.13
rs1102152	NTE +90398bp (NM_006702.2)	19	39,033,129	3.59	0.66	0.53	1.73	3.18	2.64	2.56
rs4802905	KCTD15 +36141bp (NM_024076.1)	19	57,415,907	2.59	0.66	0.55	1.58	3.13	2.04	0.85
rs734380	PPP2R1A Intron11 (NM_014225.3)	19	63,590,775	2.85	0.52	0.41	1.59	3.11	2.72	2.35
rs1072678	RPS5 Intron1 (NM_001009.2)	19	57,944,329	3.53	0.14	0.06	2.59	2.92	ND	2.53
rs734379	ZNF600 +14950bp (NM_198457.1)	19	63,590,994	3.11	0.61	0.49	1.63	2.86	3.24	1.95
rs6132862	RPS5 Intron1 (NM_001009.2)	20	25,669,248	3.95	0.37	0.24	1.86	3.67	2.58	2.31
rs4572656	LOC400840 +29346bp (XM_375912)	20	40,112,577	3.60	0.89	0.79	2.08	3.41	1.95	0.77
rs119416	PTPRT +22230bp (NM_007050.3),	20	47,469,004	3.98	0.70	0.56	1.79	3.40	3.04	1.48
rs6019825	PTPRT +22230bp (NM_133170.1)	20	47,472,824	3.55	0.56	0.43	1.70	3.29	3.06	1.30
rs6045666	KCNB1 Intron1 (NM_004975.2)	20	1,888,504	3.67	0.34	0.22	1.85	3.28	2.73	2.16
rs6138601	KCNB1 Intron1 (NM_004975.2)	20	25,487,486	3.69	0.39	0.26	1.80	3.23	2.64	2.11
rs6035140	PDYN +18899bp (NM_024411.2)	20	1,884,292	3.67	0.35	0.23	1.83	3.14	2.65	2.09
rs12480036	KIAA0980 -32244bp (NM_025176.3)	20	39,629,243	3.84	0.80	0.69	1.89	3.13	4.18	2.36
rs6138598	PTPNS1 +15755bp (NM_080792.1)	20	25,461,536	3.44	0.38	0.26	1.76	3.11	2.45	2.13
rs517578	CHD6 Intron1 (NM_032221.3)	20	1,637,270	3.30	0.42	0.30	1.70	3.11	2.38	2.16
	KIAA0980 -6294bp (NM_025176.3)									
	SIRPB2 -50868bp (NM_018556.2),									
	SIRPB2 -50868bp (NM_080816.1)									

[0224] [Table 50]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs2050223	C20orf23 +550936bp (NM_024704.3)	20	15,649,814	1.97	0.65	0.56	1.46	3.08	1.66	0.70
rs926663	MAFB +68744bp (NM_005461.3)	20	38,679,189	2.89	0.47	0.35	1.61	3.08	2.29	2.27
rs6072407	CHD6 Intron2 (NM_032221.3)	20	39,596,216	3.83	0.82	0.71	1.92	3.07	4.47	2.58
rs6138532	ENTPD6 -5585bp (NM_001247.1)	20	25,118,787	3.00	0.45	0.33	1.66	3.04	2.44	2.24
rs6083320	CST5 -31324bp (NM_001900.2)	20	23,839,641	3.26	0.41	0.29	1.70	3.02	4.16	1.53
rs2076147	ZHX3 Exon4 (NM_015035.2)	20	39,246,420	3.68	0.50	0.37	1.72	3.01	2.99	1.82
rs1857051	CST5 -33523bp (NM_001900.2)	20	23,841,840	3.35	0.50	0.38	1.68	2.90	3.22	1.65
rs4810317	CHD6 +8124bp (NM_032221.3)	20	39,456,460	3.54	0.81	0.70	1.85	2.89	3.27	1.68
rs6089908	KCNQ2 Intron10 (NM_004518.2), KCNQ2 Intron11 (NM_172106.1), KCNQ2 Intron12 (NM_172107.1), KCNQ2 Intron11 (NM_172108.1), KCNQ2 +16378bp (NM_172109.1)	20	61,519,098	3.33	0.90	0.81	2.16	2.76	2.60	1.09
rs6095508	KCNB1 Intron1 (NM_004975.2)	20	47,461,578	3.30	0.58	0.45	1.67	2.74	2.94	1.83
rs4812180	LOC284757 +371993bp (XM_496478)	20	58,704,985	3.73	0.09	0.03	3.77	2.72	ND	3.14
rs6115458	FLJ38374 -66026bp (NM_182583.1)	20	25,917,265	3.19	0.38	0.26	1.71	2.51	2.56	1.84
rs1321001	CDH22 Intron7 (NM_021248.1)	20	44,250,143	3.08	0.64	0.51	1.65	2.47	2.84	1.74
rs3761258	C20orf45 -727bp (NM_016045.1)	20	57,051,991	3.08	0.97	0.92	3.07	2.44	ND	ND
rs94967	LOC150084 +21299bp (XM_086761)	21	40,117,177	3.96	0.78	0.65	1.88	3.72	5.80	3.59
rs4816657	LOC150084 Intron4 (XM_086761)	21	40,068,705	3.77	0.77	0.65	1.83	3.07	3.69	2.12
rs2837211	LOC150084 Intron4 (XM_086761)	21	40,070,264	3.64	0.77	0.65	1.80	2.96	3.66	2.14
rs1018350	LOC150084 Intron4 (XM_086761)	21	40,070,715	3.64	0.77	0.65	1.80	2.96	3.66	2.14
rs463903	LOC150084 Intron8 (XM_086761)	21	40,087,547	3.51	0.77	0.65	1.78	2.86	3.63	2.17
rs2837248	PCP4 -19612bp (NM_006198.1)	21	40,141,638	3.50	0.67	0.55	1.71	2.83	3.10	1.94
rs2178882	LOC150084 Intron5 (XM_086761)	21	40,075,682	3.44	0.77	0.65	1.80	2.73	3.61	2.20

[0225] [Table 51]

DBSNP_ID	Exon, Intron	Chromosome	Physical Location	Critical rate, Allele (-logP)	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Odds Ratio (Formula 6)	Critical rate, Genotype (-logP)	Odds Ratio (Homozygote) (Formula 7)	Odds Ratio (Heterozygote) (Formula 8)
rs4816658	LOC150084 Intron5 (XM_086761)	21	40,075,924	3.53	0.77	0.65	1.82	2.72	3.32	1.92
rs458406	LOC150084 Intron8 (XM_086761)	21	40,089,698	3.32	0.77	0.65	1.75	2.69	3.46	2.07
rs2837220	LOC150084 Intron6 (XM_086761)	21	40,082,808	3.39	0.73	0.61	1.73	2.65	2.91	1.67
rs12627261	LOC150084 Intron6 (XM_086761)	21	40,085,416	3.39	0.73	0.61	1.73	2.65	2.91	1.67
rs1571713	LOC150084 Intron5 (XM_086761)	21	40,075,065	3.32	0.77	0.65	1.76	2.65	3.38	1.99
rs2826774	NCAM2 Intron5 (NM_004540.2)	21	21,588,847	3.34	0.60	0.47	1.68	2.62	2.81	1.71
rs465258	LOC150084 Intron8 (XM_086761)	21	40,093,614	3.22	0.76	0.65	1.73	2.62	3.45	2.10
rs369977	LOC388814 +1317764bp (XM_373926)	21	15,532,948	3.02	0.68	0.57	1.64	2.37	2.50	1.39
rs5750009	LOC402059 Intron8 (XM_497817)	22	33,679,879	2.13	0.81	0.73	1.58	3.68	12.15	11.55
rs1013513	LOC402059 Intron8 (XM_497817)	22	33,678,294	2.12	0.81	0.73	1.58	3.43	11.57	10.59
rs5999654	LOC402059 Intron8 (XM_497817)	22	33,682,537	2.12	0.81	0.73	1.58	3.43	11.57	10.59
rs1139056	CECR1 Exon7 (NM_177405.1), CECR1 Exon9 (NM_017424.2)	22	16,035,732	3.28	0.26	0.15	1.90	2.50	3.23	1.91
rs5759839	LOC388882 Intron4 (XM_371455)	22	22,141,794	3.04	0.59	0.47	1.62	2.36	2.61	1.55

[0226] Tables 29 to 51 list dbSNP ID number or Affimetrix Array ID number specifying known single nucleotide polymorphisms obtained, the exon, intron information (in a case where a single nucleotide polymorphism exists on a gene, the gene name and the exon or intron in which SNP exists are shown, and in a case where a single nucleotide polymorphism does not exist on a gene, neighboring genes and a distance between the gene and the single nucleotide polymorphism are shown), the chromosome number at which the single nucleotide polymorphism exists, the physical location of the single nucleotide polymorphism, the p-value for an allele according to a chi-square test (-log P), the high-risk allele frequencies in the progressive glaucoma group and the nonprogressive glaucoma group, the odds ratio for an allele, the p-value for a genotype according to a chi-square test (-log P), the odds ratio for a genotype of a homozygote, and the odds ratio for a genotype of a heterozygote. Here, in the tables, a portion of which odds ratio is indicated as ND shows a case where any one of the number of detection in the denominator is 0, so that the odds ratio could not be calculated.

[0227] According to the above studies, 480 single nucleotide polymorphisms of which alleles or genotypes were associated with the progression of glaucoma at a p-value of 1×10^{-3} or less were found.

[0228] When the allele or genotype frequencies listed in Tables 29 to 51 were compared between the progressive glaucoma cases and the nonprogressive glaucoma cases, a statistical difference was found. By determining an allele of any one of these single nucleotide polymorphisms, whether or not an allele that is identified in a higher frequency in the

progressive glaucoma group than that of the nonprogressive glaucoma group exists in the sample can be determined.

[0229] Example 5 Confirmation of Novel Single Nucleotide Polymorphisms by Sequencing Method of Surrounding of Specified Single Nucleotide Polymorphisms

Surrounding sequences of single nucleotide polymorphisms described in Tables 1 to 2 or Tables 26 to 28 are subjected to re-sequencing, so that the detection of a single nucleotide polymorphism can be confirmed, and that an unknown single nucleotide polymorphism that possibly exists can be identified. The re-sequencing can be performed according to any known methods, and for example, the re-sequencing can be performed by a direct sequencing method.

[0230] Example 6

In order to determine the single nucleotide polymorphisms associated with glaucoma identified in Example 3 or 4, or the alleles and genotypes of known single nucleotide polymorphisms existing in the surrounding sequences of the single nucleotide polymorphisms listed in Tables 1 to 51, an immobilized probe can be prepared. A known single nucleotide polymorphism can be referred to, for example, the database of dbSNP or J SNP. In the immobilized probe, for example, an oligonucleotide probe designed so as to maximize its sensitivity, specificity or reproducibility for several probes to several hundred-thousand probes can be loaded. The immobilized probe can be produced according to a method such as a method of synthesizing an oligonucleotide on a solid carrier or a method including

the steps of previously synthesizing an oligonucleotide and immobilizing the oligonucleotide in a high density on a solid carrier.

[0231] Example 7

The presence or the absence of the onset of glaucoma can be determined at a more accurate level using the immobilized probe produced in Example 6. A probe for detecting a single nucleotide polymorphism associated with a disease is plurally combined, so that the level of which the onset risk of glaucoma increases is evaluated. In a case where a value exceeds a threshold, it is determined that the onset of glaucoma takes place.

[0232] In addition, using the immobilized probe produced in Example 6, the single nucleotide polymorphism existing on the genome of the glaucoma patients and that of the non-glaucoma patients can be compared. There is a possibility that single nucleotide polymorphisms existing in locations with an adjacent distance to each other are linked and inherited by linkage disequilibrium. There is a possibility that single nucleotide polymorphisms linked with the single nucleotide polymorphisms listed in Tables 1 and 2 or Tables 26 to 28 can be identified by the immobilized probe, so that it can be expected that a single nucleotide polymorphism having an even stronger association with glaucoma is found.

[0233] Example 8 Design of Custom Array

In order to maintain a statistical power while lowering type I error, candidate single nucleotide polymorphisms associated with the onset of glaucoma identified in the primary analysis of Example 3 were subjected to a secondary analysis of a single nucleotide polymorphism in separately collected samples using an array for analyzing a single nucleotide

polymorphism designed in an original style (hereinafter, referred to as a custom array).

[0234] For the custom array, a kit for analyzing a single nucleotide polymorphism commercially available from Illumina [Illumina, iSelect™ Genotyping BeadChip] was used. For 446 single nucleotide polymorphisms associated with the onset of glaucoma showing a p-value of 1×10^{-3} or less in Example 3, the designing of a probe for specifically detecting these single nucleotide polymorphisms was tried. Since these probes are randomly immobilized to the substrate via beads, the step of specifying a location of the beads (decoding) is needed. A probe for detecting a single nucleotide polymorphism of which location was unable to be specified in a process of decoding was excluded from the subject for analysis. As a result, the preparation of a custom array capable of typing 412 single nucleotide polymorphisms out of 446 single nucleotide polymorphisms is made possible, and the custom array was used in the analysis of a single nucleotide polymorphism described later. Here, as described in the section of Infinium (registered trademark) assay in a beads-array method, in these assay methods, there are two methods, i.e. a method using one kind of a probe and a method using two kinds of probes. Basically, in the detection of one single nucleotide polymorphism, one kind of the probe was used, and two probes were used for some single nucleotide polymorphisms.

[0235] Example 9 Analysis of Single Nucleotide Polymorphism Using Custom Array

The experiment was performed in accordance with the instruction

manuals of the custom array kit and the analyzing instrument of Illumina, using specialized reagents contained in the kit. Briefly, the experimental procedures will be explained as follows. A reagent specialized in the treatment of the genome and a sodium hydroxide solution were added to 150 to 300 ng of the total DNA extracted in Example 1. Next, an enzyme for amplifying a whole genome was added thereto, and the mixture was incubated at 37°C for 20 to 24 hours, and a whole genome was amplified. Further, an enzyme for fragmentation was added thereto, and the mixture was incubated at 37°C for one hour. After the DNA was precipitated with isopropanol, a reagent for solubilization was added to the precipitates, and the mixture was suspended at 48°C for one hour. A mixture was heat-denatured at 95°C for 20 minutes, and this solution was injected into the custom array, and hybridization was carried out at 48°C for 16 to 24 hours.

[0236] After the hybridization, an allele-specific extension reaction or a single base extension reaction was performed for each probe, and the fluorescent signals were amplified. The signals were read with a scanner (Illumina, BeadArray Reader) compatible to the kit. In addition, a specialized software (Illumina, BeadStudio 3.1) was used in the analysis of the single nucleotide polymorphisms. According to the present analytical method, the opposite alleles of a single nucleotide polymorphism can be determined simultaneously, and the genotypes were determined on the basis of the analytical results. The genotype was determined to be a heterozygote when both the signals of each of the alleles constituting a single nucleotide polymorphism were detected, and the genotype was determined to be a

homozygote of the detected allele when only one of the signals of the alleles was detected.

[0237] The precision of the determination of a genotype was confirmed for all the single nucleotide polymorphisms to be analyzed on the basis of a cluster image showing a distribution of fluorescent signals, in accordance with Infinium (registered trademark) Genotyping Data Analysis, an analyzing manual of Illumina. The genotypes of the single nucleotide polymorphisms that are determined accurately are indicated on the image as three clusters of fluorescent signals that are completely separated from each other (two kinds of homozygotes and a heterozygote).

On the other hand, boundary lines of the three clusters become unclear for the single nucleotide polymorphisms that are not determined accurately. In a case where a degree of separation of the clusters is determined not to be high according to analysis software, the cluster image of the single nucleotide polymorphism was reconfirmed. In a case where a genotype was determined regardless of unclearness of the clusters, the sample was excluded from the subsequent analytical operations. Here, the confirmation of the cluster image was carried out under masking, in other words, in a state that the names of single nucleotide polymorphisms and p-values could not be compared with the single nucleotide polymorphisms. Here, the single nucleotide polymorphisms overlapping between the custom array used in the secondary analysis and GeneChip Human Mapping 500K of Affimetrix used in the primary analysis showed a concordance rate of 99% or more, when the concordance rates of the determination of genotypes were compared using 104 samples.

[0238] Example 10 Determination of Genotypes in Glaucoma Patients and Non-Patients

Primary open-angle glaucoma patients and normal tension glaucoma patients diagnosed on the basis of Guidelines offered by Japan Glaucoma Society were assigned to a glaucoma patient group, and healthy individuals confirmed to have no family history of glaucoma according to a medical interview were assigned to a non-patient group. For the present analysis, the same samples used in Example 3 for performing the primary analysis were not used, and new samples were collected. Blood donated under the consent on free will of the participants after having sufficiently explained the contents of studies from 409 cases of the glaucoma patient group and 448 controls of the non-patient group, each group being different from those of Example 3 was used as a specimen, a total DNA was extracted according to the method described in Example 1, and the analysis of single nucleotide polymorphisms was performed according to the method described in Example 9. The analytical results of a single nucleotide polymorphism obtained in each of the patients were stored in the Laboratory Information Management System (World Fusion, LaboServer) adopting a relational database. A specialized analysis program for a single nucleotide polymorphism was created and loaded within the system, and the analysis described as follows was performed. In detail, a single nucleotide polymorphism considered to have a high experimental reliability was extracted by rejecting a single nucleotide polymorphism having a call rate of less than 90% in both the glaucoma patient group and the non-patient

group, and a single nucleotide polymorphism having a minor allele frequency of less than 5%.

[0239] Example 11 Meta-Analysis

In a meta-analysis, the Mantel-Haenszel method was used (*Wakariyasui Igaku Tokeigaku (Easy Medical Statistics)*, pp. 48-80, Toshio MORIZANE, Medical Tribune). In detail, 402 single nucleotide polymorphisms considered to have a high experimental reliability in both of the methods described in Example 3 and Example 10 were subjected to statistical comparisons of the allele frequency and two genotype frequencies (a dominant genetic model and a recessive genetic model) using Mantel-Haenszel chi-square test. Single nucleotide polymorphisms of which any one of an allele model, a dominant genetic model, and a recessive genetic model shows association with the onset of glaucoma at a p-value of 1.2×10^{-4} or less (the level of Bonferroni correction corresponding to $p < 5 \times 10^{-2}$ when 402 times of multiple comparisons were performed), that is, -log P of 3.91 or more, are listed in Table 52.

[0240] The calculations of the Mantel-Haenszel chi-square test, and the odds ratio in the Mantel-Haenszel method for these single nucleotide polymorphisms, and a 95% confidence interval were performed according to the following procedures.

[0241] A Mantel-Haenszel chi-square value was determined for the allele model, the dominant genetic model, and the recessive genetic model, and a p-value was calculated by comparing the value with the chi-square distribution of a degree of freedom of 1.

[0242] The Mantel-Haenszel chi-square value (χA_{MH}^2) of the allele model was calculated according to the following formulas.

[0243]

$$EA_i = xA_i mA_i / NA_i$$

$$VA_i = \frac{mA_i nA_i xA_i yA_i}{NA_i^2 (NA_i - 1)}$$

$$\chi A_{MH}^2 = \frac{\left[\left| \sum_{i=1}^{k} (hA_i - EA_i) \right| - 0.5 \right]^2}{\sum_{i=1}^{k} VA_i}$$

xA_i: a total number of detection of a high-risk allele,

yA_i: a total number of detection of a low-risk allele,

mA_i: a total number of detection of alleles in the glaucoma patient group,

nA_i: a total number of detection of alleles in the non-patient group,

NA_i: a total number of detection of alleles, and

hA_i: the number of detection of a high-risk allele in the glaucoma patient group.

[0244] The Mantel-Haenszel chi-square value (χD_{MH}^2) of the dominant genetic model was calculated according to the following formulas.

[0245]

$$ED_i = xD_i mD_i / ND_i$$

$$VD_i = \frac{mD_i nD_i xD_i yD_i}{ND_i^2 (ND_i - 1)}$$

$$\chi D_{MH}^2 = \frac{\left[\left| \sum_{i=1}^{k} (hD_i - ED_i) \right| - 0.5 \right]^2}{\sum_{i=1}^{k} VD_i}$$

xD_i: the sum of a total number of detection of a homozygote of a high-risk allele and a total number of detection of a heterozygote,

yD_i: a total number of detection of a homozygote of a low-risk allele,

mD_i: a total number of detection of genotypes in the glaucoma patient group,

nD_i: a total number of detection of genotypes in the non-patient group,

ND_i: a total number of detection of genotypes, and

hD_i: the sum of the number of detection of a homozygote of a high-risk allele and the number of detection of a heterozygote in the glaucoma patient group.

[0246] The Mantel-Haenszel chi-square value (χR_{MH}^2) of the recessive genetic model was calculated according to the following formulas.

[0247]

$$ER_i = xR_i mR_i / NR_i$$

$$VR_i = \frac{mR_i nR_i xR_i yR_i}{NR_i^2 (NR_i - 1)}$$

$$\chi R_{MH}^2 = \frac{\left[\left| \sum_{i=1}^{k} (hR_i - ER_i) \right| - 0.5 \right]^2}{\sum_{i=1}^{k} VR_i}$$

xR_i: a total number of detection of a homozygote of a high-risk allele,

yR_i: the sum of a total number of detection of a homozygote of a low-risk allele and a total number of detection of a heterozygote of a genotype,

mR_i: a total number of detection of genotypes in the glaucoma patient group,

nR_i: a total number of detection of genotypes in the non-patient group,

NR_i: a total number of detection of genotypes, and

hR_i: the number of detection of a homozygote of a high-risk allele in the glaucoma patient group.

[0248] The odds ratio in the Mantel-Haenszel test was calculated for the allele model, the dominant genetic model, and the recessive genetic model.

[0249] The odds ratio in the Mantel-Haenszel test (ORa_{MH}) for the allele model was calculated according to the following formula.

[0250]

$$ORa_{MH} = \frac{\sum_{i=1}^{k} Aa_i Da_i / Za_i}{\sum_{i=1}^{k} Ba_i Ca_i / Za_i}$$

Aa_i: the number of detection of a high-risk allele in the glaucoma patient group,

Ba_i: the number of detection of a low-risk allele in the glaucoma patient group,

Ca_i: the number of detection of a high-risk allele in the non-patient group,

Da_i: the number of detection of a low-risk allele in the non-patient group, and

Za_i: a total number of detection of alleles.

[0251] The odds ratio in the Mantel-Haenszel test (ORd_{MH}) for the dominant genetic model was calculated according to the following formula.

[0252]

$$ORd_{MH} = \frac{\sum_{i=1}^{k} Ad_i Dd_i / Zd_i}{\sum_{i=1}^{k} Bd_i Cd_i / Zd_i}$$

Ad_i: the sum of the number of detection of a homozygote of a high-risk allele in the glaucoma patient group and the number of detection of a heterozygote in the glaucoma patient group,

Bd_i: the number of detection of a homozygote of a low-risk allele in the glaucoma patient group,

Cd_i: the sum of the number of detection of a homozygote of a high-risk allele in the non-patient group and the number of detection of a heterozygote in the non-patient group,

Dd_i: the number of detection of a homozygote of a low-risk allele in the non-patient group, and

Zd_i: a total number of detection of genotypes.

[0253] The odds ratio in the Mantel-Haenszel test (ORr_{MH}) for the recessive genetic model was calculated according to the following formula.

[0254]

$$ORr_{MH} = \frac{\sum_{i=1}^{k} Ar_i Dr_i / Zr_i}{\sum_{i=1}^{k} Br_i Cr_i / Zr_i}$$

Ar_i: the number of detection of a homozygote of a high-risk allele in the glaucoma patient group,

Br_i: the sum of the number of detection of a heterozygote in the glaucoma patient group and the number of detection of a homozygote of a low-risk allele in the glaucoma patient group,

Cr_i: the number of detection of a homozygote of a high-risk allele in the non-patient group,

Dr_i: the sum of the number of detection of a heterozygote in the non-patient group and the number of detection of a homozygote of a low-risk allele in the non-patient group, and

Zr_i: a total number of detection of genotypes.

[0255] A 95% confidence interval of the odds ratio in the Mantel-Haenszel test was calculated for the allele model, the dominant genetic model, and the recessive genetic model.

[0256] The 95% confidence interval ($95\%\ CI_A$) for the allele model was calculated according to the following formulas.

[0257]

$$PA_i = \frac{aA_i + dA_i}{zA_i}, QAi = \frac{bA_i + cA_i}{zA_i}, RA_i = \frac{aA_i dA_i}{zA_i}, SA_i = \frac{bA_i cA_i}{zA_i}$$

$$VarA = \frac{\sum_{i=1}^{k} PA_i RA_i}{2\left(\sum_{i=1}^{k} RA_i\right)} + \frac{\sum_{i=1}^{k}\left(PA_i SA_i + QA_i RA_i\right)}{2\sum_{i=1}^{k} RA_i \sum_{i=1}^{k} SA_i} + \frac{\sum_{i=1}^{k} QA_i SA_i}{2\left(\sum_{i=1}^{k} SA_i\right)^2}$$

$$95\%CI_A = \exp\left(\log ORa_{MH} \pm 1.96\sqrt{VarA}\right)$$

aA_i: the number of detection of a high-risk allele in the glaucoma patient group,

bA_i: the number of detection of a low-risk allele in the glaucoma patient group,

cA_i: the number of detection of a high-risk allele in the non-patient group,

dA_i: the number of detection of a low-risk allele in the non-patient group,

zA_i: a total number of detection of alleles, and

ORa_{MH} : an odds ratio in Mantel-Haenszel test for an allele model.

[0258] A 95% confidence interval ($95\%\ CI_d$) for the dominant genetic model was calculated according to the following formulas.

[0259]

$$PD_i = \frac{aD_i + dD_i}{zD_i}, QDi = \frac{bD_i + cD_i}{zD_i}, RD_i = \frac{aD_i dD_i}{zD_i}, SD_i = \frac{bD_i cD_i}{zD_i}$$

$$VarD = \frac{\sum_{i=1}^{k} PD_i RD_i}{2\left(\sum_{i=1}^{k} RD_i\right)} + \frac{\sum_{i=1}^{k}\left(PD_i SD_i + QD_i RD_i\right)}{2\sum_{i=1}^{k} RD_i \sum_{i=1}^{k} SD_i} + \frac{\sum_{i=1}^{k} QD_i SD_i}{2\left(\sum_{i=1}^{k} SD_i\right)^2}$$

$$95\%CI_d = \exp\left(\log ORd_{MH} \pm 1.96\sqrt{VarD}\right)$$

aD_i: the sum of the number of detection of a homozygote of a high-risk allele in the glaucoma patient group and the number of detection of a heterozygote in the glaucoma patient group,

bD_i: the number of detection of a homozygote of a low-risk allele in the glaucoma patient group,

cD_i: the sum of the number of detection of a homozygote of a high-risk allele in the non-patient group and the number of detection of a heterozygote in the non-patient group,

dD_i: the number of detection of a homozygote of a low-risk allele in the non-patient group,

zD_i: a total number of detection of genotypes, and

ORd_{MH}: an odds ratio in Mantel-Haenszel test for a dominant genetic model.

[0260] A 95% confidence interval (*95% CI_r*) for the recessive genetic model was calculated according to the following formulas.

[0261]

$$PR_i = \frac{aR_i + dR_i}{zR_i}, QRi = \frac{bR_i + cR_i}{zR_i}, RR_i = \frac{aR_i dR_i}{zR_i}, SR_i = \frac{bR_i cR_i}{zR_i}$$

$$VarR = \frac{\sum_{i=1}^{k} PR_i RR_i}{2\left(\sum_{i=1}^{k} RR_i\right)} + \frac{\sum_{i=1}^{k}\left(PR_i SR_i + QR_i RR_i\right)}{2\sum_{i=1}^{k} RR_i \sum_{i=1}^{k} SR_i} + \frac{\sum_{i=1}^{k} QR_i SR_i}{2\left(\sum_{i=1}^{k} SR_i\right)^2}$$

$$95\%CI_r = \exp\left(\log ORr_{MH} \pm 1.96\sqrt{VarR}\right)$$

aR_i: the number of detection of a homozygote of a high-risk allele in the glaucoma patient group,

bR_i: the sum of the number of detection of a heterozygote in the glaucoma patient group and the number of detection of a homozygote of a low-risk allele in the glaucoma patient group,

cR_i: the number of detection of a homozygote of a high-risk allele in the non-patient group,

dR_i: the sum of the number of detection of a heterozygote in the non-patient group and the number of detection of a homozygote of a low-risk allele in the non-patient group,

zR_i: a total number of detection of genotypes, and

ORr_{MH}: an odds ratio in Mantel-Haenszel test for a recessive genetic model.

[0262] [Table 52]

dBSNP ID	Chromosome	Physical Location	Exon, Intron	Linkage Disequilibrium	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs4516662	4	140,178,445	CCRN4L -116103bp (NM_012118.2)	LD1	C	G	C	0.56	0.51	0.000021	Dominant	1.7	1.4-2.3	SEQ ID No:203	SEQ ID No:204	SEQ ID No:515	SEQ ID No:533
rs13110551	4	140,178,323	CCRN4L -116225bp (NM_012118.2)	LD1	A	G	G	0.58	0.52	0.000004	Dominant	1.9	1.4-2.4	SEQ ID No:205	SEQ ID No:206	SEQ ID No:516	
rs11129034	2	124,776,617	CNTNAP5 Intron3 (NM_130773.2), CNTNAP5 Intron3 (NM_138996.1)	LD2	A	G	G	0.59	0.54	0.000074	Recessive	1.6	1.2-1.9	SEQ ID No:207	SEQ ID No:208	SEQ ID No:517	
rs12611812	2	124,776,344	CNTNAP5 Intron3 (NM_130773.2), CNTNAP5 Intron3 (NM_138996.1)	LD2	A	T	A	0.59	0.54	0.000074	Recessive	1.6	1.2-1.9	SEQ ID No:209	SEQ ID No:210	SEQ ID No:518	SEQ ID No:534
rs7961953	12	81,594,304	DKFZp762A217 Intron1 (NM_152588.1)		A	G	A	0.33	0.26	0.000067	Allele	1.4	1.2-1.6	SEQ ID No:211	SEQ ID No:212	SEQ ID No:519	
rs6451268	5	36,291,121	FLJ25422 Intron11 (NM_145000.2)		A	G	G	0.62	0.58	0.000072	Dominant	1.8	1.3-2.3	SEQ ID No:213	SEQ ID No:214	SEQ ID No:520	
rs7559118	2	133,706,762	FLJ34870 Intron4 (NM_207481.1)		A	G	G	0.64	0.58	0.000005	Dominant	1.9	1.4-2.5	SEQ ID No:215	SEQ ID No:216	SEQ ID No:521	
rs7850541	9	133,080,108	GBGT1 -11253bp (NM_021996.3)		A	G	G	0.78	0.72	0.000109	Allele	1.4	1.2-1.6	SEQ ID No:217	SEQ ID No:218	SEQ ID No:522	
rs9358578	6	22,810,626	LOC389370 Intron1 (XM_374162)		A	G	A	0.45	0.38	0.000106	Allele	1.3	1.2-1.5	SEQ ID No:219	SEQ ID No:220	SEQ ID No:523	
rs16935718	8	70,265,525	LOC389667 +60391bp (XM_372046)	LD3	A	G	A	0.74	0.68	0.000017	Dominant	2.4	1.6-3.5	SEQ ID No:221	SEQ ID No:222	SEQ ID No:524	
rs16935744	8	70,280,548	LOC389667 +75414bp (XM_372046)	LD3	A	C	C	0.74	0.68	0.000024	Dominant	2.3	1.6-3.4	SEQ ID No:223	SEQ ID No:224	SEQ ID No:525	
rs705998	8	70,295,144	LOC389667 +90018bp (XM_372046)	LD3	A	G	G	0.71	0.65	0.000390	Dominant	2.1	1.5-2.9	SEQ ID No:225	SEQ ID No:226	SEQ ID No:526	
rs10517556	4	62,947,647	LOC391656 -135832bp (XM_373027)		A	G	G	0.51	0.46	0.000067	Dominant	1.6	1.3-2	SEQ ID No:227	SEQ ID No:228	SEQ ID No:527	
rs7081455	10	20,678,891	PLXDC2 +697708bp (NM_032812.7)		A	C	A	0.83	0.76	0.000010	Allele	1.5	1.2-1.8	SEQ ID No:229	SEQ ID No:230	SEQ ID No:528	
rs547984	1	234,422,927	ZP4 -42951bp (NM_021186.2)	LD4	A	C	A	0.54	0.46	0.000056	Allele	1.3	1.2-1.5	SEQ ID No:231	SEQ ID No:232	SEQ ID No:529	
rs540782	1	234,423,080	ZP4 -43104bp (NM_021186.2)	LD4	C	G	G	0.54	0.46	0.000054	Dominant	1.6	1.3-2	SEQ ID No:233	SEQ ID No:234	SEQ ID No:530	SEQ ID No:535
rs693421	1	234,425,131	ZP4 -45155bp (NM_021186.2)	LD4	A	C	A	0.53	0.46	0.000032	Dominant	1.6	1.3-2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:531	
rs2499601	1	234,430,936	ZP4 -50968bp (NM_021186.2)	LD4	A	G	G	0.53	0.46	0.000078	Dominant	1.6	1.3-2	SEQ ID No:237	SEQ ID No:238	SEQ ID No:532	

[0263] Table 52 lists dbSNP ID number specifying known single nucleotide polymorphisms obtained, the chromosome number at which a single nucleotide polymorphism exists, the physical location of a single nucleotide polymorphism, the exon, intron information (in a case where a single nucleotide polymorphism exists on a gene, the gene name and the exon or intron in which SNP exists are shown, and in a case where a single nucleotide polymorphism does not exist on a gene, neighboring genes and a distance between the gene and the single nucleotide polymorphism are shown), the information on the linkage disequilibrium state (the numbers of LD1 to LD4 were assigned to single nucleotide polymorphisms which exist in the same linkage disequilibrium region), each of bases constituting Allele 1 and Allele 2, the base of a high-risk allele, high-risk allele frequencies of the glaucoma patient group and the non-patient group, the p-value in a test method having the lowest p-value among three Mantel-Haenszel tests (allele frequency, dominant genetic model, and recessive genetic model), the kinds of the tests thereof , the odds ratio thereof, the 95% confidence interval thereof, SEQ ID NO: of the sequence containing Allele 1 and SEQ ID NO: of the sequence containing Allele 2 in each of the polymorphic sites, and SEQ ID NO: showing a base sequence of a probe used in a secondary analysis (basically, both the alleles are detected by the same probe, and in a case where the alleles are discriminated using two kinds of probes, both the sequences are listed together.). Here, one of ordinary skill in the art can obtain the information for sequences or alleles of the single nucleotide polymorphisms from dbSNP ID number listed above.

[0264] When the allele or genotype frequencies of the single nucleotide polymorphisms listed in Table 52 were compared between the non-patients and the glaucoma patients, a statistical difference was found according to Mantel-Haenszel chi-square test. By determining an allele of any one of these single nucleotide polymorphisms in the same manner as that in Example 3, whether or not an allele that is identified in a higher frequency in the glaucoma patient group than that of the non-patient group exists in the sample can be determined.

[0265] According to the above studies, 18 single nucleotide polymorphisms of which alleles or genotypes were associated with glaucoma at a p-value of 1.2×10^{-4} or less existing in clusters in relatively adjacent regions on the genome were found in 11 regions.

[0266] An allele identified in a high frequency in the glaucoma patient group for single nucleotide polymorphisms listed in Table 52 (in other words, a high-risk allele) or a genotype (in other words,
a homozygote of a high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or a homozygote of a high-risk allele when the high-risk allele complies with a recessive genetic model) can be used as a marker showing that an onset risk of glaucoma is high. On the other hand, an allele that is opposite to the allele or a genotype other than the genotype can be used as a marker showing that an onset risk of glaucoma is low.

[0267] Similarly, a single nucleotide polymorphism of which allele or genotype shows association with the onset of glaucoma at a p-value of 1×10^{-2} or less, i.e. -log P of 2 or more is listed in Tables 53 to 62.

[0268] [Table 53]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Chaconas Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs429419	5	33,624,092	ADAMTS12 Intron17 (NM_030955.1)	C	G	G	0.91	0.87	0.002845	Allele	1.41	1.1-1.8	SEQ ID No:239	SEQ ID No:240	SEQ ID No:536	SEQ ID No:674
rs818725	5	33,624,060	ADAMTS12 Intron17 (NM_030955.1)	C	G	G	0.91	0.87	0.003115	Allele	1.41	1.1-1.8	SEQ ID No:241	SEQ ID No:242	SEQ ID No:537	SEQ ID No:675
rs10902569	15	98,663,829	ADAMTS17 Intron3 (NM_139057.1)	A	G	A	0.33	0.33	0.004911	Recessive	1.60	1.2-2.2	SEQ ID No:243	SEQ ID No:244	SEQ ID No:538	
rs2387658	10	1,413,905	ADARB2 Intron1 (NM_018702.1)	A	C	C	0.78	0.75	0.001798	Recessive	1.39	1.1-1.7	SEQ ID No:245	SEQ ID No:246	SEQ ID No:539	
rs9881866	3	106,304,709	ALCAM -264171bp (NM_001627.1)	A	G	G	0.14	0.11	0.006808	Allele	1.35	1.1-1.7	SEQ ID No:247	SEQ ID No:248	SEQ ID No:540	
rs1342022	9	72,935,061	ANXA1 -61274bp (NM_000700.1)	A	G	G	0.59	0.54	0.000210	Recessive	1.51	1.2-1.9	SEQ ID No:249	SEQ ID No:250	SEQ ID No:541	
rs6097745	20	52,101,533	BCAS1 Intron3 (NM_003657.1)	A	G	A	0.30	0.27	0.006893	Dominant	1.32	1.1-1.6	SEQ ID No:251	SEQ ID No:252	SEQ ID No:542	
rs2816632	14	104,812,400	BRF1 Intron2 (NM_001519.2), BRF1 -27133bp (NM_145685.1), BRF1 -26587bp (NM_145696.1)	A	G	G	0.21	0.16	0.002470	Allele	1.33	1.1-1.6	SEQ ID No:253	SEQ ID No:254	SEQ ID No:543	
rs16940484	18	19,936,298	C18orf17 Intron6 (NM_153211.1)	A	G	A	0.33	0.29	0.005060	Allele	1.25	1.1-1.5	SEQ ID No:255	SEQ ID No:256	SEQ ID No:544	
rs6115865	20	3,307,303	C20orf194 -37687bp (XM_045421)	A	G	A	0.39	0.33	0.000217	Dominant	1.47	1.2-1.8	SEQ ID No:257	SEQ ID No:258	SEQ ID No:545	
rs1467913	3	50,500,021	CACNA2D2 Intron2 (NM_006030.1)	A	C	A	0.57	0.52	0.001774	Dominant	1.49	1.2-1.9	SEQ ID No:259	SEQ ID No:260	SEQ ID No:546	
rs6786523	3	50,499,225	CACNA2D2 Intron2 (NM_006030.1)	A	G	A	0.57	0.52	0.001906	Dominant	1.49	1.2-1.9	SEQ ID No:261	SEQ ID No:262	SEQ ID No:547	
rs12494849	3	50,499,562	CACNA2D2 Intron2 (NM_006030.1)	C	G	C	0.57	0.52	0.005312	Allele	1.23	1.1-1.4	SEQ ID No:263	SEQ ID No:264	SEQ ID No:548	SEQ ID No:676
rs7571760	2	37,654,409	CDC42EP3 +1279858p (NM_006449.3)	A	G	A	0.40	0.35	0.000490	Recessive	1.68	1.3-2.2	SEQ ID No:265	SEQ ID No:266	SEQ ID No:549	
rs10130333	14	88,929,499	CHES1 Intron2 (NM_005197.1)	A	C	A	0.66	0.64	0.005714	Dominant	1.53	1.1-2.1	SEQ ID No:267	SEQ ID No:268	SEQ ID No:550	

[0269] [Table 54]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs493622	11	89,882,297	CHORDC1 -286443bp (NM_012124.1)	A	C	A	0.81	0.76	0.000467	Allele	1.36	1.1-1.6	SEQ ID No:269	SEQ ID No:270	SEQ ID No:551	
rs562160	11	89,887,386	CHORDC1 -291532bp (NM_012124.1)	A	G	G	0.81	0.76	0.000696	Allele	1.35	1.1-1.6	SEQ ID No:271	SEQ ID No:272	SEQ ID No:552	
rs2139539	1	31,786,872	COL16A1 +698bp (NM_001856.2)	A	G	G	0.84	0.80	0.008566	Dominant	2.36	1.2-4.5	SEQ ID No:273	SEQ ID No:274	SEQ ID No:553	
rs909002	1	31,808,728	COL16A1 Intron44 (NM_001856.2)	A	G	G	0.81	0.77	0.002649	Dominant	2.26	1.3-3.9	SEQ ID No:275	SEQ ID No:276	SEQ ID No:554	
rs7902091	10	68,268,298	CTNNA3 Intron7 (NM_013266.1)	A	C	A	0.50	0.45	0.001835	Recessive	1.47	1.2-1.9	SEQ ID No:277	SEQ ID No:278	SEQ ID No:555	
rs2233476	3	50,363,387	CYB561D2 Exon1 (NM_007022.3)	A	C	A	0.52	0.46	0.000169	Dominant	1.55	1.2-1.9	SEQ ID No:279	SEQ ID No:280	SEQ ID No:556	
rs7676755	4	187,490,196	CYP4V2 Intron2 (NM_207352.1)	C	G	C	0.81	0.80	0.006756	Dominant	1.96	1.2-3.2	SEQ ID No:281	SEQ ID No:282	SEQ ID No:557	SEQ ID No:677
rs3862680	18	48,184,338	DCC Intron1 (NM_005215.1)	A	C	A	0.58	0.53	0.002299	Allele	1.25	1.1-1.4	SEQ ID No:283	SEQ ID No:284	SEQ ID No:558	
rs3862681	18	48,184,688	DCC Intron1 (NM_005215.1)	A	G	A	0.58	0.53	0.002675	Allele	1.25	1.1-1.4	SEQ ID No:285	SEQ ID No:286	SEQ ID No:559	
rs11737784	4	84,300,869	DKFZp686L1814 -117088bp (NM_194282.1)	A	C	C	0.79	0.76	0.007584	Recessive	1.32	1.1-1.6	SEQ ID No:287	SEQ ID No:288	SEQ ID No:560	
rs13137759	4	84,262,335	DKFZp686L1814 Intron2 (NM_194282.1)	A	G	A	0.79	0.76	0.008987	Recessive	1.32	1.1-1.6	SEQ ID No:289	SEQ ID No:290	SEQ ID No:561	
rs12700287	7	21,385,860	DNAH11 Intron8 (NM_003777.1)	C	G	C	0.95	0.93	0.005463	Allele	1.54	1.1-2.1	SEQ ID No:291	SEQ ID No:292	SEQ ID No:562	SEQ ID No:678
rs5765558	22	44,363,516	E46L -24767bp (NM_013236.1)	A	G	A	0.58	0.53	0.003829	Allele	1.24	1.1-1.4	SEQ ID No:293	SEQ ID No:294	SEQ ID No:563	
rs4823324	22	44,558,660	E46L Intron10 (NM_013236.1)	A	G	A	0.50	0.45	0.003204	Allele	1.24	1.1-1.4	SEQ ID No:295	SEQ ID No:296	SEQ ID No:564	
rs1892116	1	243,406,363	ELYS Intron2 (NM_175865.1), ELYS Intron2 (NM_015446.1)	A	G	A	0.75	0.70	0.002178	Allele	1.28	1.1-1.5	SEQ ID No:297	SEQ ID No:298	SEQ ID No:565	

[0270] [Table 55]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs9398995	6	132,181,896	ENPP1 Intron1 (NM_006208.1)	A	G	A	0.56	0.52	0.008585	Recessive	1.35	1.1-1.7	SEQ ID No:299	SEQ ID No:300	SEQ ID No:566	
rs1441354	15	69,517,251	FLJ13710 -2906691bp (NM_024817.1)	A	T	T	0.27	0.27	0.003800	Recessive	1.92	1.2-3	SEQ ID No:301	SEQ ID No:302	SEQ ID No:567	SEQ ID No:679
rs1012728	3	21,519,300	FLJ22419 Intron4 (NM_024697.1)	A	C	C	0.48	0.43	0.001063	Dominant	1.44	1.2-1.8	SEQ ID No:303	SEQ ID No:304	SEQ ID No:568	
rs3922704	3	112,983,875	FLJ31579 Intron3 (NM_153268.1)	C	G	G	0.88	0.83	0.000294	Allele	1.46	1.2-1.8	SEQ ID No:305	SEQ ID No:306	SEQ ID No:569	SEQ ID No:680
rs1382851	12	25,689,829	FLJ36004 -92384bp (NM_152590.1)	A	C	C	0.57	0.53	0.003765	Dominant	1.45	1.1-1.9	SEQ ID No:307	SEQ ID No:308	SEQ ID No:570	
rs4144951	15	51,643,802	FLJ38736 Intron17 (NM_182758.1)	A	G	A	0.14	0.11	0.005496	Dominant	1.42	1.1-1.8	SEQ ID No:309	SEQ ID No:310	SEQ ID No:571	
rs11750584	5	41,129,616	FLJ40243 -22454bp (NM_173489.2)	C	G	C	0.20	0.16	0.005023	Allele	1.31	1.1-1.6	SEQ ID No:311	SEQ ID No:312	SEQ ID No:572	SEQ ID No:681
rs9300981	13	104,440,279	G30 +469126bp (XM_498445)	A	C	C	0.64	0.59	0.005027	Dominant	1.50	1.1-2	SEQ ID No:313	SEQ ID No:314	SEQ ID No:573	
rs9640055	7	7,802,756	GLCCI1 Intron1 (XM_166529)	A	G	A	0.82	0.79	0.003780	Allele	1.30	1.1-1.6	SEQ ID No:315	SEQ ID No:316	SEQ ID No:574	
rs9852677	3	50,266,621	GNAI2 Intron4 (NM_002070.1)	A	G	A	0.54	0.47	0.000278	Allele	1.30	1.1-1.5	SEQ ID No:317	SEQ ID No:318	SEQ ID No:575	
rs2236944	3	50,267,197	GNAI2 Intron4 (NM_002070.1)	A	C	A	0.52	0.46	0.000383	Dominant	1.51	1.2-1.9	SEQ ID No:319	SEQ ID No:320	SEQ ID No:576	
rs610160	11	105,202,105	GRIA4 Intron3 (NM_000829.1)	A	G	G	0.20	0.15	0.002530	Allele	1.34	1.1-1.6	SEQ ID No:321	SEQ ID No:322	SEQ ID No:577	
rs9498701	6	102,336,911	GRIK2 Intron6 (NM_021956.2), GRIK2 Intron6 (NM_175768.1)	A	G	A	0.59	0.54	0.000935	Recessive	1.45	1.2-1.8	SEQ ID No:323	SEQ ID No:324	SEQ ID No:578	
rs4840196	6	102,359,520	GRIK2 Intron8 (NM_021956.2), GRIK2 Intron8 (NM_175768.1)	A	T	A	0.59	0.54	0.001162	Recessive	1.44	1.2-1.8	SEQ ID No:325	SEQ ID No:326	SEQ ID No:579	SEQ ID No:682
rs4840195	6	102,359,490	GRIK2 Intron8 (NM_021956.2), GRIK2 Intron8 (NM_175768.1)	A	G	G	0.58	0.54	0.001597	Recessive	1.43	1.1-1.8	SEQ ID No:327	SEQ ID No:328	SEQ ID No:580	

[0271] [Table 56]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs9322609	6	102,357,540	GRIK2 Intron8 (NM_021956.2), GRIK2 Intron8 (NM_175768.1)	A	G	G	0.58	0.54	0.001827	Recessive	1.42	1.1-1.8	SEQ ID No:329	SEQ ID No:330	SEQ ID No:581	
rs2764236	6	102,389,150	GRIK2 Intron9 (NM_021956.2), GRIK2 Intron9 (NM_175768.1)	A	G	A	0.59	0.54	0.001904	Recessive	1.42	1.1-1.8	SEQ ID No:331	SEQ ID No:332	SEQ ID No:582	
rs779701	3	7,493,772	GRM7 Intron7 (NM_181875.1), GRM7 Intron7 (NM_000844.2), GRM7 Intron7 (NM_181874.1)	A	G	G	0.33	0.28	0.002130	Allele	1.28	1.1-1.5	SEQ ID No:333	SEQ ID No:334	SEQ ID No:583	
rs4430902	2	189,010,443	GULP1 Intron1 (NM_016315.1)	A	G	A	0.84	0.82	0.009243	Recessive	1.33	1.1-1.7	SEQ ID No:335	SEQ ID No:336	SEQ ID No:584	
rs10271531	7	80,758,592	HGF +2175048p (NM_000601.3)	A	G	A	0.41	0.36	0.004906	Allele	1.23	1.1-1.4	SEQ ID No:337	SEQ ID No:338	SEQ ID No:585	
rs4430896	2	23,246,431	KBTBD9 -239670bp (XM_496546)	A	G	A	0.74	0.69	0.008598	Allele	1.24	1.1-1.4	SEQ ID No:339	SEQ ID No:340	SEQ ID No:586	
rs17279573	4	154,937,893	KIAA0922 +224425bp (NM_015196.2)	A	G	A	0.72	0.67	0.000685	Allele	1.31	1.1-1.5	SEQ ID No:341	SEQ ID No:342	SEQ ID No:587	
rs1206153	6	97,652,757	KIAA1900 Intron6 (NM_052904.1)	A	G	A	0.53	0.50	0.001009	Recessive	1.47	1.2-1.9	SEQ ID No:343	SEQ ID No:344	SEQ ID No:588	
rs4763559	12	10,622,909	KLRA1 +10130bp (NM_006611.1)	C	G	G	0.75	0.70	0.000624	Allele	1.32	1.1-1.5	SEQ ID No:345	SEQ ID No:346	SEQ ID No:589	SEQ ID No:683
rs2125094	12	10,622,012	KLRA1 +11027bp (NM_006611.1)	A	G	G	0.74	0.69	0.001004	Allele	1.30	1.1-1.5	SEQ ID No:347	SEQ ID No:348	SEQ ID No:590	
rs11056970	12	16,558,431	LMO3 +34143bp (NM_018640.3), LMO3 +34143bp (NM_001001395.1)	A	C	C	0.85	0.82	0.002381	Dominant	2.07	1.3-3.3	SEQ ID No:349	SEQ ID No:350	SEQ ID No:591	
rs8086430	18	20,600,317	LOC147468 +250079bp (XM_091809)	A	G	G	0.27	0.23	0.006316	Allele	1.26	1.1-1.5	SEQ ID No:351	SEQ ID No:352	SEQ ID No:592	
rs7910849	10	31,144,546	LOC220929 +290288bp (NM_182755.1)	A	G	A	0.73	0.68	0.000272	Recessive	1.46	1.2-1.8	SEQ ID No:353	SEQ ID No:354	SEQ ID No:593	
rs1462840	3	118,345,185	LOC285194 +426618bp (XM_379207)	A	G	G	0.62	0.56	0.000975	Dominant	1.57	1.2-2.1	SEQ ID No:355	SEQ ID No:356	SEQ ID No:594	
rs7612549	3	34,789,105	LOC285307 +209732bp (XM_211837)	A	C	C	0.42	0.39	0.005641	Recessive	1.49	1.1-2	SEQ ID No:357	SEQ ID No:358	SEQ ID No:595	

[0272] [Table 57]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs6550308	3	34,911,573	LOC285307 +332200bp (XM_211837)	A	G	G	0.46	0.40	0.000835	Dominant	1.44	1.2-1.8	SEQ ID No:359	SEQ ID No:360	SEQ ID No:596	
rs10517578	4	155,005,757	LOC285533 Intron4 (NM_173662.1)	A	G	G	0.74	0.69	0.002228	Allele	1.28	1.1-1.5	SEQ ID No:361	SEQ ID No:362	SEQ ID No:597	
rs6468360	8	29,863,536	LOC286135 -350349bp (XM_379573)	C	G	C	0.55	0.52	0.003998	Recessive	1.39	1.1-1.7	SEQ ID No:363	SEQ ID No:364	SEQ ID No:598	SEQ ID No:684
rs2040073	1	38,498,317	LOC339442 -148785bp (XM_378855)	A	G	A	0.35	0.30	0.001364	Dominant	1.39	1.1-1.7	SEQ ID No:365	SEQ ID No:366	SEQ ID No:599	
rs6431929	2	8,255,994	LOC339789 +41877bp (NM_207358.1)	A	G	G	0.69	0.66	0.004709	Dominant	1.59	1.2-2.2	SEQ ID No:367	SEQ ID No:368	SEQ ID No:600	
rs10488110	7	9,827,710	LOC340268 Intron1 (XM_294634)	A	G	G	0.11	0.07	0.000465	Allele	1.59	1.2-2.1	SEQ ID No:369	SEQ ID No:370	SEQ ID No:601	
rs411102	9	99,196,524	LOC347265 +480768bp (XM_294590)	A	G	A	0.14	0.10	0.000158	Dominant	1.60	1.3-2.1	SEQ ID No:371	SEQ ID No:372	SEQ ID No:602	
rs782394	10	130,349,442	LOC387721 -251645bp (XM_370585)	A	T	A	0.53	0.49	0.001769	Recessive	1.46	1.2-1.8	SEQ ID No:373	SEQ ID No:374	SEQ ID No:603	SEQ ID No:685
rs10430126	1	47,934,070	LOC388630 +220728bp (XM_371250)	A	C	C	0.63	0.58	0.001484	Recessive	1.41	1.1-1.7	SEQ ID No:375	SEQ ID No:376	SEQ ID No:604	
rs4668312	2	171,432,334	LOC389059 -203659bp (XM_374017)	A	G	A	0.73	0.68	0.001698	Allele	1.28	1.1-1.5	SEQ ID No:377	SEQ ID No:378	SEQ ID No:605	
rs6433243	2	171,431,002	LOC389059 -216978p (XM_374017)	A	G	G	0.73	0.68	0.001306	Allele	1.29	1.1-1.5	SEQ ID No:379	SEQ ID No:380	SEQ ID No:606	
rs10184230	2	171,427,641	LOC389059 -250586p (XM_374017)	A	G	A	0.73	0.68	0.001306	Allele	1.29	1.1-1.5	SEQ ID No:381	SEQ ID No:382	SEQ ID No:607	
rs6746374	2	171,445,013	LOC389059 -7686bp (XM_374017)	A	G	A	0.73	0.68	0.001303	Allele	1.29	1.1-1.5	SEQ ID No:383	SEQ ID No:384	SEQ ID No:608	
rs10492680	13	39,702,836	LOC400123 -236477bp (XM_378411)	A	G	A	0.93	0.89	0.000655	Allele	1.55	1.2-2	SEQ ID No:385	SEQ ID No:386	SEQ ID No:609	
rs10228514	7	35,237,035	LOC401324 +477098p (XM_379484)	A	C	A	0.82	0.79	0.009024	Recessive	1.33	1.1-1.6	SEQ ID No:387	SEQ ID No:388	SEQ ID No:610	

[0273] [Table 58]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs17157033	10	44,613,470	LOC439960 -305453bp (XM_498478)	A	C	A	0.96	0.93	0.004744	Recessive	1.61	1.2-2.2	SEQ ID No:389	SEQ ID No:390	SEQ ID No:611	
rs4307718	11	23,320,437	LOC440033 +175532bp (XM_498512)	A	C	C	0.95	0.93	0.009971	Allele	1.51	1.1-2.1	SEQ ID No:391	SEQ ID No:392	SEQ ID No:612	
rs6550783	3	23,719,090	LOC440947 -8191bp (XM_496633)	A	G	A	0.68	0.63	0.003108	Allele	1.25	1.1-1.5	SEQ ID No:393	SEQ ID No:394	SEQ ID No:613	
rs16891164	4	14,590,288	LOC441009 +887670bp (XM_498965)	A	T	T	0.95	0.93	0.003660	Allele	1.56	1.2-2.1	SEQ ID No:395	SEQ ID No:396	SEQ ID No:614	SEQ ID No:686
rs339858	18	20,466,188	LOC441816 -124776bp (XM_497584)	A	G	A	0.15	0.11	0.007997	Allele	1.34	1.1-1.7	SEQ ID No:397	SEQ ID No:398	SEQ ID No:615	
rs17187933	18	20,556,033	LOC441816 -214621bp (XM_497584)	A	G	G	0.25	0.20	0.002141	Dominant	1.39	1.1-1.7	SEQ ID No:399	SEQ ID No:400	SEQ ID No:616	
rs11876045	18	20,564,102	LOC441816 -222690bp (XM_497584)	C	G	C	0.26	0.22	0.003407	Dominant	1.36	1.1-1.7	SEQ ID No:401	SEQ ID No:402	SEQ ID No:617	SEQ ID No:687
rs17260163	18	20,592,187	LOC441816 -250773bp (XM_497584)	A	G	G	0.27	0.23	0.006099	Allele	1.26	1.1-1.5	SEQ ID No:403	SEQ ID No:404	SEQ ID No:618	
rs2004243	8	143,815,988	LOC51337 +641bp (NM_016647.1)	A	G	A	0.43	0.37	0.001099	Allele	1.27	1.1-1.5	SEQ ID No:405	SEQ ID No:406	SEQ ID No:619	
rs1990702	2	169,802,022	LRP2 +83468bp (NM_004525.1)	A	G	A	0.69	0.64	0.004527	Allele	1.24	1.1-1.4	SEQ ID No:407	SEQ ID No:408	SEQ ID No:620	
rs16883860	6	36,110,440	MAPK14 Intron1 (NM_139013.1), MAPK14 Intron1 (NM_001315.1), MAPK14 Intron1 (NM_139012.1), MAPK14 Intron1 (NM_139014.1)	A	G	A	0.92	0.89	0.002150	Allele	1.46	1.1-1.9	SEQ ID No:409	SEQ ID No:410	SEQ ID No:621	
rs7761118	6	36,176,281	MAPK14 Intron9 (NM_139013.1), MAPK14 Intron9 (NM_001315.1), MAPK14 Intron9 (NM_139012.1), MAPK14 Intron9 (NM_139014.1)	A	G	G	0.92	0.89	0.004398	Allele	1.42	1.1-1.8	SEQ ID No:411	SEQ ID No:412	SEQ ID No:622	
rs2359112	1	34,548,776	MGC15882 +194951bp (NM_032884.2)	A	G	A	0.33	0.31	0.004022	Recessive	1.74	1.2-2.5	SEQ ID No:413	SEQ ID No:414	SEQ ID No:623	
rs16904092	8	130,571,112	MGC27434 Intron1 (NM_145050.2)	A	G	A	0.90	0.88	0.007732	Recessive	1.41	1.1-1.8	SEQ ID No:415	SEQ ID No:416	SEQ ID No:624	
rs10764881	10	131,153,821	MGMT -70674bp (NM_002412.1)	A	G	G	0.69	0.64	0.001557	Dominant	1.78	1.2-2.5	SEQ ID No:417	SEQ ID No:418	SEQ ID No:625	

[0274] [Table 59]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs11016249	10	130,138,328	MKI67 -323870bp (NM_002417.2)	A	G	G	0.68	0.64	0.008687	Allele	1.22	1.1-1.4	SEQ ID No:419	SEQ ID No:420	SEQ ID No:626	
rs2857648	22	28,391,122	NF2 Intron10 (NM_181825.1), NF2 Intron8 (NM_181831.1), NF2 Intron10 (NM_000268.2), NF2 Intron10 (NM_016418.4), NF2 Intron11 (NM_181826.1), NF2 Intron10 (NM_181827.1), NF2 Intron9 (NM_181828.1), NF2 Intron9 (NM_181829.1), NF2 Intron8 (NM_181830.1), NF2 Intron10 (NM_181832.1), NF2 Intron4 (NM_181833.1), NF2 Intron5 (NM_181834.1), NF2 Intron8 (NM_181835.1)	C	G	G	0.71	0.67	0.006985	Recessive	1.32	1.1-1.6	SEQ ID No:421	SEQ ID No:422	SEQ ID No:627	SEQ ID No:688
rs17808998	17	8,919,071	NTN1 Intron2 (NM_004822.1)	A	G	G	0.62	0.58	0.008779	Recessive	1.33	1.1-1.6	SEQ ID No:423	SEQ ID No:424	SEQ ID No:628	
rs2072133	12	111,871,980	OAS3 Exon16 (NM_006187.2)	A	G	A	0.66	0.61	0.003090	Allele	1.25	1.1-1.4	SEQ ID No:425	SEQ ID No:426	SEQ ID No:629	
rs4666488	2	19,608,777	ODD -128777bp (NM_145260.1)	A	G	A	0.38	0.33	0.000309	Dominant	1.46	1.2-1.8	SEQ ID No:427	SEQ ID No:428	SEQ ID No:630	
rs10798882	1	31,777,640	PEF Intron1 (NM_012392.1)	C	G	G	0.85	0.81	0.001679	Allele	1.36	1.1-1.6	SEQ ID No:429	SEQ ID No:430	SEQ ID No:631	SEQ ID No:689
rs17754672	2	64,312,259	PELI1 -61125bp (NM_020651.2)	A	G	A	0.22	0.18	0.006631	Recessive	2.36	1.3-4.4	SEQ ID No:431	SEQ ID No:432	SEQ ID No:632	
rs10116231	9	78,151,153	PSAT1 Intron5 (NM_021154.3), PSAT1 Intron5 (NM_058179.2)	A	G	G	0.76	0.71	0.003816	Allele	1.27	1.1-1.5	SEQ ID No:433	SEQ ID No:434	SEQ ID No:633	
rs2236913	1	223,380,860	PSEN2 Intron5 (NM_000447.1), PSEN2 Intron5 (NM_012486.1)	A	G	G	0.37	0.34	0.009042	Dominant	1.32	1.1-1.6	SEQ ID No:435	SEQ ID No:436	SEQ ID No:634	
rs7574012	2	37,638,881	QPCT +1267658p (NM_012413.2)	A	G	G	0.41	0.36	0.001545	Recessive	1.59	1.2-2.1	SEQ ID No:437	SEQ ID No:438	SEQ ID No:635	

[0275] [Table 60]

dBSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs6724538	2	37,639,669	QPCT +127553bp (NM_012413.2)	A	C	A	0.41	0.35	0.000321	Recessive	1.69	1.3-2.2	SEQ ID No:439	SEQ ID No:440	SEQ ID No:636	
rs7584987	2	37,641,805	QPCT +129689bp (NM_012413.2)	A	G	G	0.44	0.39	0.000572	Recessive	1.60	1.2-2.1	SEQ ID No:441	SEQ ID No:442	SEQ ID No:637	
rs1877823	17	60,657,405	RGS9 +31360bp (NM_003835.1)	A	G	A	0.77	0.74	0.001810	Dominant	1.98	1.3-3	SEQ ID No:443	SEQ ID No:444	SEQ ID No:638	
rs9896245	17	60,604,218	RGS9 -110660bp (NM_003835.1)	A	G	A	0.74	0.71	0.000141	Dominant	2.19	1.5-3.3	SEQ ID No:445	SEQ ID No:446	SEQ ID No:639	
rs1877821	17	60,605,875	RGS9 -94090bp (NM_003835.1)	A	G	G	0.74	0.72	0.000419	Dominant	2.10	1.4-3.2	SEQ ID No:447	SEQ ID No:448	SEQ ID No:640	
rs16865980	2	7,255,254	RNF144 +1203468bp (NM_014746.2)	A	G	A	0.25	0.21	0.000687	Dominant	1.43	1.2-1.8	SEQ ID No:449	SEQ ID No:450	SEQ ID No:641	
rs9788983	17	129,457	RPH3AL Intron6 (NM_006987.2)	A	G	A	0.88	0.84	0.000891	Allele	1.42	1.2-1.7	SEQ ID No:451	SEQ ID No:452	SEQ ID No:642	
rs17115925	14	81,341,217	SEL1L -271331bp (NM_005065.3)	A	T	T	0.73	0.70	0.009837	Allele	1.23	1.1-1.4	SEQ ID No:453	SEQ ID No:454	SEQ ID No:643	SEQ ID No:690
rs1571379	14	81,359,690	SEL1L -289804bp (NM_005065.3)	A	G	A	0.73	0.67	0.000529	Allele	1.32	1.1-1.5	SEQ ID No:455	SEQ ID No:456	SEQ ID No:644	
rs12632110	3	50,199,229	SEMA3F Intron18 (NM_004186.2)	A	G	A	0.52	0.47	0.000586	Dominant	1.50	1.2-1.9	SEQ ID No:457	SEQ ID No:458	SEQ ID No:645	
rs1951626	1	170,623,758	SERPINC1 -5704bp (NM_000488.1)	A	G	A	0.36	0.31	0.009171	Allele	1.22	1.1-1.4	SEQ ID No:459	SEQ ID No:460	SEQ ID No:646	
rs2044757	3	155,352,950	SGEF Intron5 (NM_015593.2)	A	G	G	0.64	0.61	0.001153	Dominant	1.61	1.2-2.1	SEQ ID No:461	SEQ ID No:462	SEQ ID No:647	
rs33954719	3	155,359,077	SGEF Intron6 (NM_015593.2)	A	G	A	0.64	0.61	0.001078	Dominant	1.61	1.2-2.2	SEQ ID No:463	SEQ ID No:464	SEQ ID No:648	
rs3761980	6	36,101,884	SLC26A8 -15298bp (NM_052961.2), SLC26A8 -16368bp (NM_138718.1)	A	G	A	0.92	0.89	0.002750	Allele	1.44	1.1-1.8	SEQ ID No:465	SEQ ID No:466	SEQ ID No:649	
rs1606405	13	82,684,518	SLITRK1 +6648276bp (NM_052910.1)	A	G	A	0.54	0.50	0.002823	Recessive	1.42	1.1-1.8	SEQ ID No:467	SEQ ID No:468	SEQ ID No:650	

[0276] [Table 61]

dBSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs2356232	2	171,412,281	SP5 +122760bp (XM_371581)	A	G	A	0.73	0.68	0.001522	Allele	1.29	1.1-1.5	SEQ ID No:469	SEQ ID No:470	SEQ ID No:651	
rs7608898	2	171,423,724	SP5 +237198bp (XM_371581)	A	G	A	0.73	0.68	0.001306	Allele	1.29	1.1-1.5	SEQ ID No:471	SEQ ID No:472	SEQ ID No:652	
rs10930437	2	171,406,848	SP5 +6843bp (XM_371581)	A	G	A	0.73	0.68	0.001587	Allele	1.29	1.1-1.5	SEQ ID No:473	SEQ ID No:474	SEQ ID No:653	
rs4667649	2	171,408,395	SP5 +8390bp (XM_371581)	A	G	A	0.73	0.68	0.001662	Allele	1.28	1.1-1.5	SEQ ID No:475	SEQ ID No:476	SEQ ID No:654	
rs2049723	11	13,922,920	SPON1 -178941bp (NM_006108.1)	A	G	A	0.74	0.69	0.002649	Allele	1.27	1.1-1.5	SEQ ID No:477	SEQ ID No:478	SEQ ID No:655	
rs2268794	2	31,691,055	SRD5A2 intron1 (NM_000348.2)	A	T	A	0.19	0.15	0.006152	Allele	1.31	1.1-1.6	SEQ ID No:479	SEQ ID No:480	SEQ ID No:656	SEQ ID No:691
rs1106845	14	35,931,107	STELLAR +197688bp (XM_375075)	A	T	T	0.10	0.07	0.006141	Allele	1.45	1.1-1.9	SEQ ID No:481	SEQ ID No:482	SEQ ID No:657	SEQ ID No:692
rs2966712	7	142,683,960	TAS2R41 -7843bp (NM_176883.1)	A	G	A	0.11	0.07	0.000304	Dominant	1.66	1.3-2.2	SEQ ID No:483	SEQ ID No:484	SEQ ID No:658	
rs1658456	10	59,974,332	TFAM +148429bp (NM_003201.1), TFAM +158914bp (NM_012251.1)	A	G	G	0.58	0.53	0.006414	Allele	1.22	1.1-1.4	SEQ ID No:485	SEQ ID No:486	SEQ ID No:659	
rs1649060	10	59,980,486	TFAM +154583bp (NM_003201.1), TFAM +165068bp (NM_012251.1)	C	G	C	0.58	0.53	0.006414	Allele	1.22	1.1-1.4	SEQ ID No:487	SEQ ID No:488	SEQ ID No:660	SEQ ID No:693
rs1649048	10	59,994,288	TFAM +168385bp (NM_003201.1), TFAM +178870bp (NM_012251.1)	A	G	G	0.58	0.53	0.006480	Allele	1.22	1.1-1.4	SEQ ID No:489	SEQ ID No:490	SEQ ID No:661	
rs1658438	10	59,996,389	TFAM +170686bp (NM_003201.1), TFAM +181171bp (NM_012251.1)	A	G	G	0.58	0.52	0.006270	Allele	1.22	1.1-1.4	SEQ ID No:491	SEQ ID No:492	SEQ ID No:662	
rs1649039	10	60,000,047	TFAM +174144bp (NM_003201.1), TFAM +184629bp (NM_012251.1)	A	G	G	0.57	0.52	0.007438	Allele	1.22	1.1-1.4	SEQ ID No:493	SEQ ID No:494	SEQ ID No:663	
rs10763558	10	60,011,940	TFAM +186037bp (NM_003201.1), TFAM +196522bp (NM_012251.1)	A	C	C	0.57	0.52	0.008997	Allele	1.21	1-1.4	SEQ ID No:495	SEQ ID No:496	SEQ ID No:664	
rs11727442	4	154,943,527	TLR2 -23144bp (NM_003264.2)	A	G	G	0.69	0.64	0.000624	Recessive	1.43	1.2-1.8	SEQ ID No:497	SEQ ID No:498	SEQ ID No:665	

[0277] [Table 62]

dBSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Glaucoma Patient Group	High-Risk Allele Frequency in Non-Patient Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Containing Allele 1	Sequence Containing Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs3804100	4	154,983,014	TLR2 Exon2 (NM_003264.2)	A	G	A	0.73	0.68	0.003499	Allele	1.26	1.1-1.5	SEQ ID No:499	SEQ ID No:500	SEQ ID No:666	
rs1028534	10	51,898,627	TMEM23 Intron3 (NM_147156.3)	A	C	C	0.63	0.60	0.005678	Dominant	1.48	1.1-2	SEQ ID No:501	SEQ ID No:502	SEQ ID No:667	
rs1210065	10	51,882,795	TMEM23 Intron5 (NM_147156.3)	A	G	A	0.40	0.35	0.001850	Dominant	1.39	1.1-1.7	SEQ ID No:503	SEQ ID No:504	SEQ ID No:668	
rs17473451	8	15,368,500	TUSC3 -73601bp (NM_006765.2), TUSC3 -73601bp (NM_178234.1)	C	G	C	0.76	0.72	0.003504	Recessive	1.35	1.1-1.7	SEQ ID No:505	SEQ ID No:506	SEQ ID No:669	SEQ ID No:694
rs6829490	4	47,908,795	TXK +894bp (NM_003328.1)	A	G	G	0.54	0.49	0.009776	Dominant	1.37	1.1-1.7	SEQ ID No:507	SEQ ID No:508	SEQ ID No:670	
rs500629	11	113,550,770	ZBTB16 Intron3 (NM_006006.3)	A	C	C	0.28	0.23	0.001621	Dominant	1.39	1.1-1.7	SEQ ID No:509	SEQ ID No:510	SEQ ID No:671	
rs2864107	19	56,760,839	ZNF175 -5504bp (NM_007147.2)	A	G	A	0.21	0.17	0.000428	Dominant	1.47	1.2-1.8	SEQ ID No:511	SEQ ID No:512	SEQ ID No:672	
rs3755827	3	62,335,411	ZNF312 -1350bp (NM_018008.2)	A	G	A	0.79	0.74	0.004467	Allele	1.28	1.1-1.5	SEQ ID No:513	SEQ ID No:514	SEQ ID No:673	

[0278] The single nucleotide polymorphisms listed in Tables 53 to 62 can be also used as a marker for predicting an onset risk of glaucoma in the same manner.

[0279] Next, regions and/or genes of the surrounding of single nucleotide polymorphism listed in Table 52 were determined by making reference to the database provided by the HapMap project. In detail, regions in which the single nucleotide polymorphism considered to be in a linkage disequilibrium with the single nucleotide polymorphisms listed in Table 52 exists were determined, on the basis of the linkage disequilibrium data in combination of the Japanese and the Chinese in the HapMap project.

[0280] Also, in a case where the single nucleotide polymorphism listed in Table 52 exists in the linkage disequilibrium region containing genes, the physical location of the region and the gene name were determined. On the other hand, in a case where the single nucleotide polymorphism listed in Table 52 exists in the linkage disequilibrium region without containing the genes, only the physical location of the region was determined. In addition, in a case where the single nucleotide polymorphism listed in Table 52 exists on one gene beyond the linkage disequilibrium region, the gene name and the physical location of the gene were determined.

[0281] A single nucleotide polymorphism of which p-value is the lowest for each region is considered to be a single nucleotide polymorphism representing the region, and Tables 63 to 70 list a single nucleotide polymorphism representing the region, the chromosome number at which the region exists, the physical location of the region (start point and end point) and the gene name contained in the region.

[0282] [Table 63]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs10798882	1	31,707,055	31,838,861	COL16A1 LCN7 HCRTR1 PEF1
rs2359112	1	34,477,408	34,552,678	-
rs2040073	1	38,408,125	38,527,689	-
rs10430126	1	47,930,338	48,198,192	-
rs1951626	1	170,033,793	171,848,859	TNN MRPS14 CACYBP RABGAP1L RC3H1 SERPINC1 ZBTB37 DARS2 CENPL KLHL20 ANKRD45 SLC9A11 PRDX6
rs2236913	1	223,126,127	223,405,511	ITPKB PSEN2
rs693421	1	234,339,548	234,432,433	ZP4
rs1892116	1	243,319,348	243,497,348	ZNF695 ELYS AHCTF1
rs16865980	2	7,200,812	7,280,358	-
rs6431929	2	8,187,182	8,419,147	LOC339789
rs4666488	2	19,472,875	19,608,452	OSR1
rs4430896	2	23,145,684	23,366,310	-

[0283] [Table 64]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs2268794	2	31,468,839	33,038,731	XDH SRD5A2 MEMO1 DPY30 SPAST SLC30A6 NLRC4 YIPF4 BIRC6 TTC27
rs6724538	2	37,588,322	37,740,529	-
rs17754672	2	62,704,890	64,419,622	EHBP1 OTX1 LOC51057 MDH1 UGP2 VPS54 PELI1
rs12611812	2	124,499,094	125,389,091	CNTNAP5
rs7559118	2	133,263,104	134,159,763	NAP5 FLJ34870
rs1990702	2	169,796,465	170,044,629	LRP2
rs6746374	2	171,322,396	171,550,925	AK127400 GAD1 SP5 LOC440925
rs4430902	2	188,685,976	189,579,329	GULP1 DIRC1
rs779701	3	6,877,927	7,758,217	GRM7
rs1012728	3	21,437,673	21,767,820	ZNF385D
rs6550783	3	23,654,468	23,750,569	-

[0284] [Table 65]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs6550308	3	34,785,788	35,165,798	-
rs2233476	3	49,686,439	51,799,207	APEH
				MST1
				RNF123
				AMIGO3
				GMPPB
				IHPK1
				LOC389118
				C3orf54
				UBA7
				TRAIP
				CAMKV
				MST1R
				MON1A
				RBM6
				RBM5
				SEMA3F
				GNAT1
				SLC38A3
				GNAI2
				SEMA3B
				IFRD2
				NAT6
				C3orf45
				HYAL3
				HYAL1
				HYAL2
				TUSC2
				RASSF1
				ZMYND10
				TUSC4
				CYB561D2
				TMEM115
				CACNA2D2
				C3orf18
				HEMK1
				CISH
				MAPKAPK3
				DOCK3
				ARMET
				RBM15B
				VPRBP
				RAD54L2
				TEX264
				GRM2

[0285] [Table 66]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs3755827	3	62,280,436	62,836,094	C3orf14 CADPS ZNF312
rs9881866	3	106,122,067	106,319,409	-
rs3922704	3	112,876,213	113,177,795	PLCXD2 CR749654 AY358772
rs1462840	3	118,332,596	118,498,089	-
rs33954719	3	155,198,039	155,457,039	SGEF
rs16891164	4	14,149,949	14,598,571	BC036758
rs6829490	4	47,436,948	48,813,871	CORIN NFXL1 CNGA1 NPAL1 TXK TEC SLAIN2 ZAR1 FRYL OCIAD1 OCIAD2
rs10517556	4	62,191,605	63,083,785	LPHN3
rs11737784	4	83,907,869	84,368,310	SCD5 SEC31A THAP9 LIN54 COPS4
rs13110551	4	140,152,121	140,188,487	-
rs11727442	4	154,745,157	155,130,602	KIAA0922 TLR2 RNF175 SFRP2
rs7676755	4	187,346,286	187,611,026	TLR3 DKFZP564J102 CYP4V2 KLKB1 F11

[0286] [Table 67]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs429419	5	33,563,046	33,927,881	ADAMTS12
rs6451268	5	36,139,171	36,337,761	DKFZp434H2226 SKP2 FLJ30596 FLJ25422
rs11750584	5	41,033,879	41,298,707	FLJ40243 C6
rs9358578	6	22,707,365	22,854,322	LOC389370
rs16883860	6	36,015,011	36,252,339	SLC26A8 MAPK14 MAPK13
rs1206153	6	97,479,326	97,864,503	KIAA1900 C6orf167
rs9498701	6	101,953,626	102,624,651	GRIK2
rs9398995	6	132,000,135	132,286,336	ENPP3 ENPP1
rs9640055	7	7,772,656	8,075,425	ICA1 GLCCI1
rs10488110	7	9,768,215	9,875,870	-
rs12700287	7	21,338,075	21,714,695	DNAH11
rs10228514	7	35,169,289	35,359,069	-
rs10271531	7	80,612,379	80,941,240	-
rs2966712	7	142,596,643	142,732,627	ZYX EPHA1 TAS2R60 TAS2R41
rs17473451	8	15,324,913	15,422,271	-
rs6468360	8	29,800,821	29,866,436	-
rs16935718	8	69,986,592	70,338,390	ratara. bAug05 swakoy.aAug05 LOC389667
rs16904092	8	130,556,102	130,700,866	-

[0287] [Table 68]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs2004243	8	143,716,339	143,900,127	JRK PSCA LY6K C8orf55 SLURP1 LYNX1 LYPD2 LY6D
rs1342022	9	72,743,457	72,939,880	ALDH1A1
rs10116231	9	78,136,500	78,174,561	PSAT1
rs411102	9	99,100,781	99,364,219	-
rs7850541	9	132,883,652	133,218,347	GFI1B CR615294 GTF3C5 CEL CELP RALGDS GBGT1 OBP2B ABO
rs2387658	10	1,218,073	1,769,718	ADARB2
rs7081455	10	20,662,930	20,719,326	-
rs7910849	10	31,072,503	31,165,996	-
rs17157033	10	44,456,300	44,698,295	-
rs1210065	10	51,696,167	52,116,588	TMEM23 AK056520
rs1658438	10	59,803,487	60,258,851	BICC1 TFAM
rs7902091	10	67,349,937	69,125,933	CTNNA3
rs11016249	10	129,959,024	130,173,385	-
rs782394	10	130,233,084	130,350,260	-
rs10764881	10	131,138,138	131,455,356	MGMT
rs2049723	11	13,850,243	14,246,222	SPON1
rs4307718	11	23,202,964	23,481,112	-

[0288] [Table 69]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs493622	11	89,679,112	90,004,712	-
rs610160	11	104,896,113	105,358,029	GRIA4
rs500629	11	113,435,641	113,626,604	ZBTB16
rs4763559	12	10,539,469	10,726,280	KLRA1 FLJ10292 STYK1
rs11056970	12	16,468,226	16,587,335	-
rs1382851	12	25,669,680	25,892,423	-
rs7961953	12	81,537,331	82,030,531	TMTC2
rs2072133	12	111,807,459	111,912,247	OAS1 OAS2 OAS3
rs10492680	13	39,608,046	39,760,155	-
rs1606405	13	82,325,708	82,739,954	BC016673
rs9300981	13	104,391,167	104,481,207	-
rs1106845	14	35,808,124	35,947,704	MBIP
rs1571379	14	81,213,431	81,378,859	-
rs10130333	14	88,692,269	89,155,247	CHES1
rs2816632	14	104,746,671	104,838,374	BRF1 BTBD6
rs4144951	15	51,558,394	51,892,014	WDR72
rs1441354	15	69,220,842	69,862,776	THSD4
rs10902569	15	98,329,166	98,699,706	ADAMTS17
rs9788983	17	62,294	271,176	RPH3AL LOC400566
rs17808998	17	8,845,288	9,088,042	NTN1
rs9896245	17	60,532,473	60,654,283	RGS9
rs1877823	17	60,564,011	60,680,796	RGS9
rs16940484	18	19,826,735	20,231,788	C18orf17 OSBPL1A CABYR
rs17187933	18	20,389,931	20,699,770	-

[0289] [Table 70]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs3862680	18	48,050,184	49,311,780	DCC
rs2864107	19	56,686,425	56,784,802	SIGLEC12 ZNF175 SIGLEC6
rs6115865	20	3,156,064	3,351,824	SLC4A11 C20orf194
rs6097745	20	51,935,413	52,170,007	BCAS1
rs2857648	22	28,153,305	28,436,178	RFPL1 NEFH THOC5 NIPSNAP1 NF2
rs4823324	22	44,219,256	44,580,747	FBLN1 ATXN10

[0290] The region listed in Tables 63 to 70 is a region or gene considered to be linked with a single nucleotide polymorphism associated with the onset of glaucoma in the present invention listed in Tables 53 to 62, and a single nucleotide polymorphism which exists in these regions or genes is considered to be linked with a single nucleotide polymorphism in the present invention. In other words, any single nucleotide polymorphisms which exist in these regions are linked with the single nucleotide polymorphism which exists in the region listed in Tables 53 to 62, and any of these single nucleotide polymorphisms can be used in the prediction of an onset risk of glaucoma in the same manner.

[0291] Example 11 Logistic Regression Analysis

In the present invention, by combining any two or more single nucleotide polymorphisms determined to be involved in the onset of

glaucoma, an extent to which the precision of the prediction of a risk of a disease improves is examined with logistic regression analysis, as compared to that where each of the single nucleotide polymorphisms is used alone. In the present analysis, any combinations of the single nucleotide polymorphisms determined to be significantly associated with the onset of glaucoma by statistically comparing allele or genotype frequencies can be used. In one example, 17 single nucleotide polymorphisms that showed a significant difference under the Bonferroni correction were subjected to the logistic regression analysis.

[0292] Out of 17 single nucleotide polymorphisms that had a significance under the Bonferroni correction, single nucleotide polymorphisms for use in the logistic regression analysis were further narrowed down according to a stepwise method. The value of 0.01 was adopted as criteria of variable incorporation and variable exclusion in the stepwise method. Upon the application of a stepwise method, a single nucleotide polymorphism belonging to the same LD block (ones having the same description in the column of linkage disequilibrium in Table 52) is represented by any one of single nucleotide polymorphisms belonging to each of the LD blocks, and it is set so that any one of the single nucleotide polymorphisms is to be a subject to be incorporated. Each of the narrowed-down single nucleotide polymorphisms is defined as an independent variable(Π) (homozygote of one allele = 0, heterozygote = 1, homozygote of opposite allele = 2), and each regression coefficient (λ) can be determined according to the logistic regression analysis, and the following formula (18) was obtained.

formula (18)

$$\Phi = 1/\{1 + \exp[-(\lambda 0 + \lambda 1\Pi 1 + \lambda 2\Pi 2 + \lambda 3\Pi 3 + \cdot\cdot\cdot)]\}$$

Next, in each sample, a value for risk prediction (Φ) was calculated by substituting a variable for each single nucleotide polymorphisms into this formula. When Φ is greater than 0.5, this sample donor was determined to be with an onset risk. A concordance rate was calculated by comparing the determination results with the matter of whether the sample donor having a single nucleotide polymorphism was actually a glaucoma patient. Further, the concordance rate was determined as mentioned above for each of the incorporated single nucleotide polymorphisms alone, and all the combinations of any two or more single nucleotide polymorphisms, and means and standard deviations of the concordance rate were obtained for each of the number of single nucleotide polymorphisms used in combination. Table 71 lists the number of single nucleotide polymorphisms, alone or in a combination of arbitrary number, the number of combinations when arbitrary number of single nucleotide polymorphism is combined, and the relationship between the mean and the standard deviation of the concordance rate. Here, all the calculations were performed using SAS 9.1.3, Windows (registered trademark) Edition, SAS Institute Japan Corporation.

[0293] As listed in Table 71, according to a stepwise method, out of the 17 single nucleotide polymorphisms, assuming that a pair of single nucleotide polymorphisms belonging to the same LD block were each counted as one, all ten single nucleotide polymorphisms were selected (rs7081455, rs693421, rs9358578, rs7961953, rs16935718, rs11123034, rs13110551, rs7559118, rs10517556, and rs6451268). A value for risk prediction (Φ) of

individual cases was calculated using a logistic regression formula, alone or in a combination of any two or more of these 10 single nucleotide polymorphisms. When a cut-off value for a value for risk prediction is defined as 0.5, mean ± standard deviation of the concordance rate was 54.7 ± 1.4% in a case that each of the single nucleotide polymorphisms was used alone. This concordance rate was elevated as an increase in the number of single nucleotide polymorphisms used in combination, and reached the maximum of 59.9% in a case that all the ten were combined.

[0294] [Table 71]

The Number of SNP	The Number of Combination	Concordance Rate (Mean Value)	Standard Deviation
1	10	54.7	1.4
2	45	55.7	1.1
3	120	56.3	1.0
4	210	57.0	1.0
5	252	57.5	1.0
6	210	58.0	1.0
7	120	58.4	1.0
8	45	58.8	1.0
9	10	59.1	0.9
10	1	59.9	-

[0295] As described above, it was evident that in the determination of an onset risk of glaucoma by a single nucleotide polymorphism, an excellent concordance rate can be obtained even in a case that each of the single nucleotide polymorphisms are used alone, and the diagnostic precision can be further enhanced by combining these single nucleotide polymorphisms.

[0296] As described above, an individual who has an allele or a genotype that is identified in a high frequency in the glaucoma patients disclosed in the present invention on the genome has a high onset risk of glaucoma in future, and an individual who does not have an allele or a genotype that is

identified in a high frequency in the glaucoma patients has a low onset risk of glaucoma in future.

INDUSTRIAL APPLICABILITY

[0297] According to the method of the present invention, the level of an onset risk of glaucoma of a sample donor can be determined by analyzing an allele or a genotype of a single nucleotide polymorphism in the present invention in a sample. A sample donor can take a preventive measure of glaucoma, or can receive appropriate treatments, on the basis of this risk. In addition, it is useful because, a sample donor who has an allele or a genotype that is identified in a high frequency in the glaucoma patients of a single nucleotide polymorphism in the present invention on the genome can be given a precision examination in whether or not the donor is with an early glaucoma which is difficult to be determined sufficiently by an intraocular pressure or an ocular fundus photograph, and can be started with a treatment at an early stage in a case where the donor is diagnosed as glaucoma.

CLAIMS

[1] A method of determining the presence or the absence of a glaucoma risk, comprising the steps of:

detecting *in vitro* an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence, in a sample from a subject, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto (step A), and

comparing the allele and/or the genotype detected in said step A with at least one of an allele and/or a genotype, comprising a high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 514 (step B),

wherein the presence of a glaucoma risk is determined in a case where the allele detected in said step A is the high-risk allele, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step A is a homozygote of the genotype comprising the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step A is a homozygote of the genotype comprising the high-risk allele when the high-risk allele complies with a recessive genetic model.

[2] The method according to claim 1, wherein the glaucoma risk is an onset risk of glaucoma.

[3] The method according to claim 2, wherein the base sequence is selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238.

[4] The method according to claim 3, wherein the comparison in said step B comprises selecting and combining any two or more alleles and/or genotypes, comprising the high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 238,

wherein the presence of a glaucoma risk is determined in a case where the allele detected in said step A is any one of the alleles selected for the comparison in said step B, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step A is a homozygote or a heterozygote of any one of the genotypes selected for the comparison in said step B when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step A is a homozygote of any one of the genotypes selected for the comparison in said step B when the high-risk allele complies with a recessive genetic model.

[5] The method according to claim 4, wherein the comparison in said step B comprises selecting and combining all the alleles and/or the genotypes, comprising the high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 238,

wherein the presence of a glaucoma risk is determined in a case where the allele detected in said step A is any one of the alleles selected for the comparison in said step B, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step A is a homozygote or a heterozygote of any one of the genotypes selected for the comparison in the said step B when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step A is a homozygote of any one of the genotypes selected for the comparison in said step B when the high-risk allele complies with a recessive genetic model.

[6] The method according to claim 2, further comprising the step of predicting the level of the onset risk.

[7] The method according to claim 1, wherein the glaucoma is primary open-angle glaucoma (POAG) or normal tension glaucoma (NTG).

[8] A method of determining the presence or the absence of a glaucoma risk, comprising the steps of:

detecting *in vitro*, in a sample from a subject, an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence in a nucleic acid molecule, wherein the nucleic acid molecule comprises at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto (step C1), or

detecting *in vitro*, in a sample from a subject, an allele and/or a genotype of a single nucleotide polymorphism, using a nucleic acid molecule comprising a base sequence comprising at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto (step C2),

and

comparing the allele and/or the genotype detected in said step C1 or C2 with at least one nucleic acid molecule comprising an allele and/or a genotype, comprising a high-risk allele, in the base sequences shown in the SEQ ID NOs: 203 to 514 (step D),

wherein the presence of a glaucoma risk is determined in a case where the allele detected in said step C1 or C2 is the high-risk allele, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step C1 or C2 is a homozygote of the genotype comprising the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step C1 or C2 is a homozygote of the genotype comprising the high-risk allele when the high-risk allele complies with a recessive genetic model.

[9] The method according to claim 8, wherein the glaucoma risk is an onset risk of glaucoma.

[10] The method according to claim 9, wherein the base sequence in said steps C1 and D is selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238, or wherein the base sequence in said step C2 is selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 535.

[11] The method according to claim 10, wherein the comparison in said step D comprises selecting and combining any two or more nucleic acid molecules comprising the allele and/or the genotype, comprising the

high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 238,

wherein the presence of a glaucoma risk is determined in a case where the allele detected in said step C1 or C2 is a high-risk allele in any one of the nucleic acid molecules selected for the comparison in said step D, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step C1 or C2 is a homozygote or a heterozygote of the genotype in any one of the nucleic acid molecules selected for the comparison in said step D when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step C1 or C2 is a homozygote of the genotype in any one of the nucleic acid molecules selected for the comparison in said step D when the high-risk allele complies with a recessive genetic model.

[12] The method according to claim 12, wherein the comparison in said step D comprises selecting and combining all the nucleic acid molecules comprising the alleles and/or the genotypes, comprising the high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 238,

wherein the presence of a glaucoma risk is determined in a case where the allele detected in said step C1 or C2 is a high-risk allele in any one of the nucleic acid molecules selected for the comparison in said step D, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step C1 or C2 is a homozygote or a heterozygote of the genotype in any one of the nucleic acid molecules selected for the comparison in said step D when the high-risk allele complies with a dominant genetic model, or

wherein the presence of a glaucoma risk is determined in a case where the genotype detected in said step C1 or C2 is a homozygote of the genotype in any one of the nucleic acid molecules selected for the comparison in said step D when the high-risk allele complies with a recessive genetic model.

[13] The method according to claim 9, further comprising the step of predicting the level of the onset risk.

[14] The method according to any one of claims 8 to 13, wherein the nucleic acid molecule is used as a probe.

[15] The method according to claim 14, wherein the nucleic acid molecule is in the length of from 23 to 55 bases.

[16] The method according to claim 14, wherein the probe is immobilized.

[17] The method according to claim 8, wherein the glaucoma is primary open-angle glaucoma (POAG) or normal tension glaucoma (NTG).

[18] A kit of determining the presence or the absence of a glaucoma risk, comprising

a nucleic acid molecule comprising at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, wherein the nucleic acid molecule comprises a single nucleotide polymorphism which is located on a 31st base of a base sequence, and/or

a nucleic acid molecule comprising a base sequence comprising at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 515 to 694 or a complementary sequence thereto,

wherein the kit is for use in detecting *in vitro* an allele and/or a genotype of a single nucleotide polymorphism in a sample from a subject.

[19] The kit according to claim 18, wherein the glaucoma risk is an onset risk of glaucoma.

[20] The kit according to claim 19, wherein the base sequence is selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 238 and/or the group consisting of SEQ ID NOs: 515 to 535.

[21] The kit according to claim 20, wherein the kit comprises any two or more nucleic acid molecules comprising a base sequence shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto, or a partial sequence thereof, and/or any two or more nucleic acid molecules comprising a base sequence shown in SEQ ID NOs: 515 to 535 or a complementary sequence thereto.

[22] The kit according to claim 21, wherein the kit comprises all the nucleic acid molecules comprising a base sequence shown in SEQ ID NOs: 203 to 238 or a complementary sequence thereto, or a partial sequence thereof, and/or all the nucleic acid molecules comprising a base sequence shown in SEQ ID NOs: 515 to 535 or a complementary sequence thereto.

[23] The kit according to claim 19, for use in further predicting the level of the onset risk.

[24] The kit according to any one of claims 18 to 23, wherein the nucleic acid molecule is used as a probe.

[25] The kit according to claim 24, wherein the nucleic acid molecule is in the length of from 23 to 55 bases.

[26] The kit according to claim 24, wherein the probe is immobilized.

[27] The kit according to claim 18, wherein the glaucoma is primary open-angle glaucoma (POAG) or normal tension glaucoma (NTG).

[28] A method of determining the presence or the absence of a glaucoma risk, comprising the following steps of:

step (i): extracting a nucleic acid molecule from a sample from a subject,

step (ii): detecting an allele of a single nucleotide polymorphism which is located on a 31st base of a base sequence, wherein the base sequence is at least one base sequence selected from base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, for the nucleic acid molecule extracted in said step (i), and

step (iii): determining the presence or the absence of a glaucoma risk, based on the allele detected in said step (ii).

[29] The method according to claim 28, wherein said step (iii) comprises the step of determining a genotype, based on the allele detected in said step (ii).

[30] The method according to claim 28 or 29, wherein said step (iii) comprises the step of determining whether or not the allele detected in said step (ii) is a high-risk allele.

[31] The method according to claim 30, wherein said step (iii) comprises the step of determining that the glaucoma risk is high in a case where the allele detected in said step (ii) is the high-risk allele.

[32] Use of a nucleic acid molecule for determining a glaucoma risk, wherein the nucleic acid molecule comprises at least one base sequence, the base sequence being a base sequence selected from the group consisting of

base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto, or a partial sequence thereof, wherein the nucleic acid molecule comprises an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence.

[33] A method of diagnosing glaucoma, comprising the steps of:

detecting *in vitro* an allele and/or a genotype of a single nucleotide polymorphism which is located on a 31st base of a base sequence, in a sample from a subject, wherein the base sequence is at least one base sequence selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 514 or a complementary sequence thereto (step E), and

comparing the allele and/or the genotype detected in said step E with at least one of an allele and/or a genotype, comprising a high-risk allele, in the base sequences shown in SEQ ID NOs: 203 to 514 (step F),

wherein the subject is diagnosed as glaucoma in a case where the allele detected in said step E is the high-risk allele, or

wherein the subject is diagnosed as glaucoma in a case where the genotype detected in said step E is a homozygote of the genotype comprising the high-risk allele or a heterozygote when the high-risk allele complies with a dominant genetic model, or

wherein the subject is diagnosed as glaucoma in a case where the genotype detected in said step E is a homozygote of the genotype comprising the high-risk allele when the high-risk allele complies with a recessive genetic model.

[34] A method of determining an onset risk of glaucoma, comprising the

following steps of:

step (I): determining the presence or the absence of the onset risk of glaucoma, with the method as defined in claim 3,

step (II): determining that a further risk determination is needed, in a case where the presence of the onset risk is determined in said step (I) for any one of single nucleotide polymorphisms, and

step (III): further determining the presence or the absence of the onset risk of glaucoma, with the method as defined in claim 5, in a case of being determined that a further risk determination is needed in said step (II).

SEQUENCE LISTING

<110> Kinoshita, Shigeru
Tashiro, Kei
Santen Pharmaceutical Co.,Ltd.

<120> Determination method of risik for developing glaucoma

<130> 08-017-PCTJP

<150> JP 2007-108688
<151> 2007-04-17

<160> 694

<170> PatentIn version Ver. 3.3

<210> 1
<211> 61
<212> DNA
<213> Homo sapiens

<400> 1
cggtgctgca ccgtggatgt gagtccttgc acagtggtga aatgtagtag aggagtgatc 60

t 61

<210> 2
<211> 61
<212> DNA
<213> Homo sapiens

<400> 2
cggtgctgca ccgtggatgt gagtccttgc gcagtggtga aatgtagtag aggagtgatc 60

t 61

<210> 3
<211> 61
<212> DNA
<213> Homo sapiens

<400> 3
ccggagtatc ccgctttctt tggaggaaac aaccgcatca gatctgcgct gcggcagagg 60

c 61

<210> 4
<211> 61
<212> DNA
<213> Homo sapiens

<400> 4
ccggagtatc ccgctttctt tggaggaaac caccgcatca gatctgcgct gcggcagagg 60

c 61

<210> 5
<211> 61
<212> DNA
<213> Homo sapiens

<400> 5
tcagcaccct gcaccagtcc aagtacatga cagataccac agggaaggag ttcagaactg 60

t 61

<210> 6
<211> 61
<212> DNA
<213> Homo sapiens

<400> 6
tcagcaccct gcaccagtcc aagtacatga tagataccac agggaaggag ttcagaactg 60

t 61

<210> 7
<211> 61
<212> DNA
<213> Homo sapiens

<400> 7
ttctccatca tcctctttct ctattctcca gacattaggc acccactgtg tgcccagcac 60

a 61

<210> 8
<211> 61
<212> DNA
<213> Homo sapiens

<400> 8
ttctccatca tcctctttct ctattctcca tacattaggc acccactgtg tgcccagcac 60

a 61

<210> 9
<211> 61
<212> DNA

<213> Homo sapiens

<400> 9
gtttccagaa ctctttttgg ccaggctcca agctaagctc tgtaggaagc ttgatgatgg 60

g 61

<210> 10
<211> 61
<212> DNA
<213> Homo sapiens

<400> 10
gtttccagaa ctctttttgg ccaggctcca ggctaagctc tgtaggaagc ttgatgatgg 60

g 61

<210> 11
<211> 61
<212> DNA
<213> Homo sapiens

<400> 11
cctgcagagg ggatttgctt tgctaaagga gtcaccacag agcacccgag agtaacaggt 60

t 61

<210> 12
<211> 61
<212> DNA
<213> Homo sapiens

<400> 12

cctgcagagg ggatttgctt tgctaaagga ttcaccacag agcacccgag agtaacaggt 60

t 61

<210> 13
<211> 61
<212> DNA
<213> Homo sapiens

<400> 13
gagtgggcag ttggaaacag ctatgaaacc agcatttagt gatggggcag tagggctggg 60

g 61

<210> 14
<211> 61
<212> DNA
<213> Homo sapiens

<400> 14
gagtgggcag ttggaaacag ctatgaaacc ggcatttagt gatggggcag tagggctggg 60

g 61

<210> 15
<211> 61
<212> DNA
<213> Homo sapiens

<400> 15
aaccccatgc ctacatccat tatcaaccta cgcctatgct aaagcttgtt acaatgagca 60

g 61

<210> 16
<211> 61
<212> DNA
<213> Homo sapiens

<400> 16
aaccccatgc ctacatccat tatcaaccta tgcctatgct aaagcttgtt acaatgagca 60

g 61

<210> 17
<211> 61
<212> DNA
<213> Homo sapiens

<400> 17
ttccctgact cttgaagagg acagtggaca atgctgttta atggtggaca cagaaggatc 60

a 61

<210> 18
<211> 61
<212> DNA
<213> Homo sapiens

<400> 18
ttccctgact cttgaagagg acagtggaca gtgctgttta atggtggaca cagaaggatc 60

a 61

<210> 19

<211> 61
<212> DNA
<213> Homo sapiens

<400> 19
tatggaagca ctgtgaaaga caaactactc cgaatactga aagtttcttt tacaaaaaca 60

t 61

<210> 20
<211> 61
<212> DNA
<213> Homo sapiens

<400> 20
tatggaagca ctgtgaaaga caaactactc tgaatactga aagtttcttt tacaaaaaca 60

t 61

<210> 21
<211> 61
<212> DNA
<213> Homo sapiens

<400> 21
ataacacctg ccactgacct tccatgagca gtgactatgt ggtttcaaca ttggtcccac 60

c 61

<210> 22
<211> 61
<212> DNA
<213> Homo sapiens

<400> 22
ataacacctg ccactgacct tccatgagca ttgactatgt ggtttcaaca ttggtcccac 60

c 61

<210> 23
<211> 61
<212> DNA
<213> Homo sapiens

<400> 23
gccactgcca ccactcctgc agattgttcc agctgtgtta ctaaatacag gttgcttttc 60

t 61

<210> 24
<211> 61
<212> DNA
<213> Homo sapiens

<400> 24
gccactgcca ccactcctgc agattgttcc cgctgtgtta ctaaatacag gttgcttttc 60

t 61

<210> 25
<211> 61
<212> DNA
<213> Homo sapiens

<400> 25
gtgagccacc atgcccagcc ctgtcatcta cctttctgag agcagcttct acccatctga 60

a 61

<210> 26
<211> 61
<212> DNA
<213> Homo sapiens

<400> 26
gtgagccacc atgcccagcc ctgtcatcta tctttctgag agcagcttct acccatctga 60

a 61

<210> 27
<211> 61
<212> DNA
<213> Homo sapiens

<400> 27
cttgtcttca agagcagatg cagattatcc cgagcccagg ggacctatgt gagggagctt 60

c 61

<210> 28
<211> 61
<212> DNA
<213> Homo sapiens

<400> 28
cttgtcttca agagcagatg cagattatcc tgagcccagg ggacctatgt gagggagctt 60

c 61

<210> 29
<211> 61
<212> DNA
<213> Homo sapiens

<400> 29
agtgggaccc tgtgaggcaa acatcaccac aaggctggga acagcaggac tcaggcactg 60

c 61

<210> 30
<211> 61
<212> DNA
<213> Homo sapiens

<400> 30
agtgggaccc tgtgaggcaa acatcaccac gaggctggga acagcaggac tcaggcactg 60

c 61

<210> 31
<211> 61
<212> DNA
<213> Homo sapiens

<400> 31
tatataataa agacatctga taacatgaca gctaaggctc cttctaggta taaaacgtta 60

t 61

<210> 32
<211> 61

<212> DNA
<213> Homo sapiens

<400> 32
tatataataa agacatctga taacatgaca tctaaggctc cttctaggta taaaacgtta 60

t 61

<210> 33
<211> 61
<212> DNA
<213> Homo sapiens

<400> 33
atggcagggg ccagggtgag tggagaatac cgcttgatga gagaacccca aggcggagag 60

g 61

<210> 34
<211> 61
<212> DNA
<213> Homo sapiens

<400> 34
atggcagggg ccagggtgag tggagaatac tgcttgatga gagaacccca aggcggagag 60

g 61

<210> 35
<211> 61
<212> DNA
<213> Homo sapiens

<400> 35
ccctttttctt tcttgttctt tttaagactc aatctcaaat ctgcaaccta cctaccataa 60

g 61

<210> 36
<211> 61
<212> DNA
<213> Homo sapiens

<400> 36
ccctttttctt tcttgttctt tttaagactc gatctcaaat ctgcaaccta cctaccataa 60

g 61

<210> 37
<211> 61
<212> DNA
<213> Homo sapiens

<400> 37
tttctggctt agaattattc ataggtacaa cgctgatggc tcttctgaaa ttgcccctgc 60

a 61

<210> 38
<211> 61
<212> DNA
<213> Homo sapiens

<400> 38
tttctggctt agaattattc ataggtacaa ggctgatggc tcttctgaaa ttgcccctgc 60

a 61

<210> 39
<211> 61
<212> DNA
<213> Homo sapiens

<400> 39
acaaagcagc tatgatcata ggcacatgaa agcaaaatgt actggtgatt tcatgttcct 60

c 61

<210> 40
<211> 61
<212> DNA
<213> Homo sapiens

<400> 40
acaaagcagc tatgatcata ggcacatgaa cgcaaaatgt actggtgatt tcatgttcct 60

c 61

<210> 41
<211> 61
<212> DNA
<213> Homo sapiens

<400> 41
aagagatagg aaaagacaca gagacacaga cgggaatgcc gggtgaagac agaggaaaat 60

a 61

<210> 42
<211> 61
<212> DNA
<213> Homo sapiens

<400> 42
aagagatagg aaaagacaca gagacacaga ggggaatgcc gggtgaagac agaggaaaat 60

a 61

<210> 43
<211> 61
<212> DNA
<213> Homo sapiens

<400> 43
taatatactg caaccacatg agatttatct aagaagtgca agttttgttt aacatgcaga 60

a 61

<210> 44
<211> 61
<212> DNA
<213> Homo sapiens

<400> 44
taatatactg caaccacatg agatttatct gagaagtgca agttttgttt aacatgcaga 60

a 61

<210> 45
<211> 61
<212> DNA

<213> Homo sapiens

<400> 45
tgcaaagaaa atgaatcact catgggtata caaaatgtta cagcctcttt ggaaaacagt 60

t 61

<210> 46
<211> 61
<212> DNA
<213> Homo sapiens

<400> 46
tgcaaagaaa atgaatcact catgggtata taaaatgtta cagcctcttt ggaaaacagt 60

t 61

<210> 47
<211> 61
<212> DNA
<213> Homo sapiens

<400> 47
ccggagtatc ccgctttctt tggaggaaac aaccgcatca gatctgcgct gcggcagagg 60

c 61

<210> 48
<211> 61
<212> DNA
<213> Homo sapiens

<400> 48

ccggagtatc ccgctttctt tggaggaaac caccgcatca gatctgcgct gcggcagagg 60

c 61

<210> 49
<211> 61
<212> DNA
<213> Homo sapiens

<400> 49
tcagcaccct gcaccagtcc aagtacatga cagataccac agggaaggag ttcagaactg 60

t 61

<210> 50
<211> 61
<212> DNA
<213> Homo sapiens

<400> 50
tcagcaccct gcaccagtcc aagtacatga tagataccac agggaaggag ttcagaactg 60

t 61

<210> 51
<211> 61
<212> DNA
<213> Homo sapiens

<400> 51
ttctccatca tcctctttct ctattctcca gacattaggc acccactgtg tgcccagcac 60

a 61

<210> 52
<211> 61
<212> DNA
<213> Homo sapiens

<400> 52
ttctccatca tcctctttct ctattctcca tacattaggc acccactgtg tgcccagcac 60

a 61

<210> 53
<211> 61
<212> DNA
<213> Homo sapiens

<400> 53
tagggagcaa caccatggtg gtagagaacc aaagtttatt agcatctcta aactcatata 60

g 61

<210> 54
<211> 61
<212> DNA
<213> Homo sapiens

<400> 54
tagggagcaa caccatggtg gtagagaacc gaagtttatt agcatctcta aactcatata 60

g 61

<210> 55

<211> 61
<212> DNA
<213> Homo sapiens

<400> 55
aatgatatat caatgatata ttgaggagcc cagtaagatc ttaaatctag agggaaggta 60

g 61

<210> 56
<211> 61
<212> DNA
<213> Homo sapiens

<400> 56
aatgatatat caatgatata ttgaggagcc tagtaagatc ttaaatctag agggaaggta 60

g 61

<210> 57
<211> 61
<212> DNA
<213> Homo sapiens

<400> 57
aattgtgtgt gtgtgttttt aagtttgata cgtctaatgc ttatgaaaat ttttaccaga 60

t 61

<210> 58
<211> 61
<212> DNA
<213> Homo sapiens

<400> 58
aattgtgtgt gtgtgttttt aagtttgata tgtctaatgc ttatgaaaat ttttaccaga 60

t 61

<210> 59
<211> 61
<212> DNA
<213> Homo sapiens

<400> 59
catatacttg ttctcaaacc attcactagc aagaaaaagt ggcctagagc aggggtcagc 60

a 61

<210> 60
<211> 61
<212> DNA
<213> Homo sapiens

<400> 60
catatacttg ttctcaaacc attcactagc cagaaaaagt ggcctagagc aggggtcagc 60

a 61

<210> 61
<211> 61
<212> DNA
<213> Homo sapiens

<400> 61
ggaagggaac ctgagtatga gaaggacaga cgaggagaag ttggttaatg tttacaaact 60

t 61

<210> 62
<211> 61
<212> DNA
<213> Homo sapiens

<400> 62
ggaagggaac ctgagtatga gaaggacaga tgaggagaag ttggttaatg tttacaaact 60

t 61

<210> 63
<211> 61
<212> DNA
<213> Homo sapiens

<400> 63
cttgatttta ttgctaggga ttgtggtaaa acacccaaag aatgtgggta tgtgcctact 60

t 61

<210> 64
<211> 61
<212> DNA
<213> Homo sapiens

<400> 64
cttgatttta ttgctaggga ttgtggtaaa gcacccaaag aatgtgggta tgtgcctact 60

t 61

<210> 65
<211> 61
<212> DNA
<213> Homo sapiens

<400> 65
caacattatc tttctgaggg atacaactca accctgaaca cctgcttaca caggaaacgc 60

a 61

<210> 66
<211> 61
<212> DNA
<213> Homo sapiens

<400> 66
caacattatc tttctgaggg atacaactca cccctgaaca cctgcttaca caggaaacgc 60

a 61

<210> 67
<211> 61
<212> DNA
<213> Homo sapiens

<400> 67
ccatacagcc aaaagcccac atcctacatc cgagtaacag cccaggctga catgacccca 60

g 61

<210> 68
<211> 61

<212> DNA
<213> Homo sapiens

<400> 68
ccatacagcc aaaagcccac atcctacatc tgagtaacag cccaggctga catgacccca 60

g 61

<210> 69
<211> 61
<212> DNA
<213> Homo sapiens

<400> 69
gtttgtccct ttttaaagtt gttggtttaa aatttctctg atacaaaaat agtgacccag 60

g 61

<210> 70
<211> 61
<212> DNA
<213> Homo sapiens

<400> 70
gtttgtccct ttttaaagtt gttggtttaa catttctctg atacaaaaat agtgacccag 60

g 61

<210> 71
<211> 61
<212> DNA
<213> Homo sapiens

<400> 71
acaaagcagc tatgatcata ggcacatgaa agcaaaatgt actggtgatt tcatgttcct 60

c 61

<210> 72
<211> 61
<212> DNA
<213> Homo sapiens

<400> 72
acaaagcagc tatgatcata ggcacatgaa cgcaaaatgt actggtgatt tcatgttcct 60

c 61

<210> 73
<211> 61
<212> DNA
<213> Homo sapiens

<400> 73
gagctctctg gatagatatt tccattccac cgtcgcatct tcccagcaga gtgtgggtga 60

a 61

<210> 74
<211> 61
<212> DNA
<213> Homo sapiens

<400> 74
gagctctctg gatagatatt tccattccac tgtcgcatct tcccagcaga gtgtgggtga 60

a 61

<210> 75
<211> 61
<212> DNA
<213> Homo sapiens

<400> 75
cttaggaagt ggtatcctaa ggtgagatgt aaaggaagac taggagttag gtcagcaaga 60

g 61

<210> 76
<211> 61
<212> DNA
<213> Homo sapiens

<400> 76
cttaggaagt ggtatcctaa ggtgagatgt gaaggaagac taggagttag gtcagcaaga 60

g 61

<210> 77
<211> 61
<212> DNA
<213> Homo sapiens

<400> 77
gttgaacttt tatttctcaa ggagcagata ctagatatac ataccatgtt gactcaagcc 60

c 61

<210> 78
<211> 61
<212> DNA
<213> Homo sapiens

<400> 78
gttgaacttt tatttctcaa ggagcagata gtagatatac ataccatgtt gactcaagcc 60

c 61

<210> 79
<211> 61
<212> DNA
<213> Homo sapiens

<400> 79
ggtgctttga aagaacaatt gctcctacaa acatcaaatc aaacttttag aagctgataa 60

a 61

<210> 80
<211> 61
<212> DNA
<213> Homo sapiens

<400> 80
ggtgctttga aagaacaatt gctcctacaa ccatcaaatc aaacttttag aagctgataa 60

a 61

<210> 81
<211> 61
<212> DNA

<213> Homo sapiens

<400> 81
tatgccaatg aaatccccat gctggagaca acttattaga aagactgagc atatgtacta 60

t 61

<210> 82
<211> 61
<212> DNA
<213> Homo sapiens

<400> 82
tatgccaatg aaatccccat gctggagaca gcttattaga aagactgagc atatgtacta 60

t 61

<210> 83
<211> 61
<212> DNA
<213> Homo sapiens

<400> 83
attcccctta ggattcaagg cagactgcac cgtgagaaat catttgtcct ttgcacacag 60

t 61

<210> 84
<211> 61
<212> DNA
<213> Homo sapiens

<400> 84

attcccctta ggattcaagg cagactgcac tgtgagaaat catttgtcct ttgcacacag 60

t 61

<210> 85
<211> 61
<212> DNA
<213> Homo sapiens

<400> 85
gtcaatactt tagagtaatg ttatagacca gggctaaaat ttacatgaga atagaagagg 60

c 61

<210> 86
<211> 61
<212> DNA
<213> Homo sapiens

<400> 86
gtcaatactt tagagtaatg ttatagacca tggctaaaat ttacatgaga atagaagagg 60

c 61

<210> 87
<211> 61
<212> DNA
<213> Homo sapiens

<400> 87
tgtgagattt gtaacaaata aattagctct gaactcttca tgtaacaaga tgtctagttt 60

c 61

<210> 88
<211> 61
<212> DNA
<213> Homo sapiens

<400> 88
tgtgagattt gtaacaaata aattagctct taactcttca tgtaacaaga tgtctagttt 60

c 61

<210> 89
<211> 61
<212> DNA
<213> Homo sapiens

<400> 89
cgattactta attattccat ctggaattta cggactaaaa cagaagtcta tttttatttt 60

a 61

<210> 90
<211> 61
<212> DNA
<213> Homo sapiens

<400> 90
cgattactta attattccat ctggaattta tggactaaaa cagaagtcta tttttatttt 60

a 61

<210> 91

<211> 61
<212> DNA
<213> Homo sapiens

<400> 91
tttttttttt ttacagattt tgataacata cgtgcttgtt agaagacaaa ttatatgaca 60

g 61

<210> 92
<211> 61
<212> DNA
<213> Homo sapiens

<400> 92
tttttttttt ttacagattt tgataacata tgtgcttgtt agaagacaaa ttatatgaca 60

g 61

<210> 93
<211> 61
<212> DNA
<213> Homo sapiens

<400> 93
caagaccgaa aactttgtgg caaagataag cagtgagtga gctcctgaag tctttatctt 60

t 61

<210> 94
<211> 61
<212> DNA
<213> Homo sapiens

<400> 94
caagaccgaa aactttgtgg caaagataag gagtgagtga gctcctgaag tctttatctt 60

t 61

<210> 95
<211> 61
<212> DNA
<213> Homo sapiens

<400> 95
acctcttagg taagctttga gtgtctgtca agaaatgtgt ccatttgatt tatcaaattt 60

a 61

<210> 96
<211> 61
<212> DNA
<213> Homo sapiens

<400> 96
acctcttagg taagctttga gtgtctgtca cgaaatgtgt ccatttgatt tatcaaattt 60

a 61

<210> 97
<211> 61
<212> DNA
<213> Homo sapiens

<400> 97
aacatacttt taaataactt gtaagtcaaa gaggaaggca taaggaaatt aaaaactatt 60

t 61

<210> 98
<211> 61
<212> DNA
<213> Homo sapiens

<400> 98
aacatacttt taaataactt gtaagtcaaa taggaaggca taaggaaatt aaaaactatt 60

t 61

<210> 99
<211> 61
<212> DNA
<213> Homo sapiens

<400> 99
ttaaaaatat tgttgggtgt gaattttgaa aagggaagag ttttatgaaa tgcttctaat 60

g 61

<210> 100
<211> 61
<212> DNA
<213> Homo sapiens

<400> 100
ttaaaaatat tgttgggtgt gaattttgaa gagggaagag ttttatgaaa tgcttctaat 60

g 61

<210> 101
<211> 61
<212> DNA
<213> Homo sapiens

<400> 101
tagaaataat gtaaatcgat actgctctga cgtttttctt tgtatttact gatcagatat 60

c 61

<210> 102
<211> 61
<212> DNA
<213> Homo sapiens

<400> 102
tagaaataat gtaaatcgat actgctctga tgtttttctt tgtatttact gatcagatat 60

c 61

<210> 103
<211> 61
<212> DNA
<213> Homo sapiens

<400> 103
gtcaatagag gtcagaactt caaggacata agttgggaat gctacagccg agaaaggcag 60

t 61

<210> 104
<211> 61

<212> DNA
<213> Homo sapiens

<400> 104
gtcaatagag gtcagaactt caaggacata ggttgggaat gctacagccg agaaaggcag 60

t 61

<210> 105
<211> 61
<212> DNA
<213> Homo sapiens

<400> 105
tatttatgaa gtcaactata ttctagtaga acgatgctta atgaattatt acacatccag 60

a 61

<210> 106
<211> 61
<212> DNA
<213> Homo sapiens

<400> 106
tatttatgaa gtcaactata ttctagtaga ccgatgctta atgaattatt acacatccag 60

a 61

<210> 107
<211> 61
<212> DNA
<213> Homo sapiens

<400> 107
cacatttttt cttagatgaa tttttatgta aatcaaggca taatcaaaat aaatttttgt 60

c 61

<210> 108
<211> 61
<212> DNA
<213> Homo sapiens

<400> 108
cacatttttt cttagatgaa tttttatgta gatcaaggca taatcaaaat aaatttttgt 60

c 61

<210> 109
<211> 61
<212> DNA
<213> Homo sapiens

<400> 109
aactcctttt gaagagtctc tgagctaaca agtcaacatc agcataaagt aatgcagcct 60

g 61

<210> 110
<211> 61
<212> DNA
<213> Homo sapiens

<400> 110
aactcctttt gaagagtctc tgagctaaca cgtcaacatc agcataaagt aatgcagcct 60

g 61

<210> 111
<211> 61
<212> DNA
<213> Homo sapiens

<400> 111
agagatgcta taaattgtac ttggtttcaa cgtagggtga tcacctttc tttcatgact 60

a 61

<210> 112
<211> 61
<212> DNA
<213> Homo sapiens

<400> 112
agagatgcta taaattgtac ttggtttcaa tgtagggtga tcacctttc tttcatgact 60

a 61

<210> 113
<211> 61
<212> DNA
<213> Homo sapiens

<400> 113
ttacatctat ccaggggcaa tttctgatga ctatttttat taatgatcta ataaaatgtc 60

t 61

<210> 114
<211> 61
<212> DNA
<213> Homo sapiens

<400> 114
ttacatctat ccaggggcaa tttctgatga gtatttttat taatgatcta ataaaatgtc 60

t 61

<210> 115
<211> 61
<212> DNA
<213> Homo sapiens

<400> 115
cgcagaccaa cacctggaat cctgtagcaa atgccttcat aagaactgaa aaggactctt 60

a 61

<210> 116
<211> 61
<212> DNA
<213> Homo sapiens

<400> 116
cgcagaccaa cacctggaat cctgtagcaa ctgccttcat aagaactgaa aaggactctt 60

a 61

<210> 117
<211> 61
<212> DNA

<213> Homo sapiens

<400> 117
tcagggcaaa tgacctcact ccatgatgga cgctttgagg aagggaataa atgaataaat 60

a 61

<210> 118
<211> 61
<212> DNA
<213> Homo sapiens

<400> 118
tcagggcaaa tgacctcact ccatgatgga tgctttgagg aagggaataa atgaataaat 60

a 61

<210> 119
<211> 61
<212> DNA
<213> Homo sapiens

<400> 119
gctgtgcggt ttgaaatatg aactctgtaa cctcttcagt ggctcccaca tcccagggct 60

g 61

<210> 120
<211> 61
<212> DNA
<213> Homo sapiens

<400> 120

gctgtgcggt ttgaaatatg aactctgtaa tctcttcagt ggctcccaca tcccagggct 60

g 61

<210> 121
<211> 61
<212> DNA
<213> Homo sapiens

<400> 121
tccctgaggg cctcacttgc tccatgagac aaactcacta cagcgttcat cttgtttaaa 60

a 61

<210> 122
<211> 61
<212> DNA
<213> Homo sapiens

<400> 122
tccctgaggg cctcacttgc tccatgagac gaactcacta cagcgttcat cttgtttaaa 60

a 61

<210> 123
<211> 61
<212> DNA
<213> Homo sapiens

<400> 123
tcatgttact tactgagttc taatttctac agtaccacta aaaactctgg agtgaccgtc 60

t 61

<210> 124
<211> 61
<212> DNA
<213> Homo sapiens

<400> 124
tcatgttact tactgagttc taatttctac ggtaccacta aaaactctgg agtgaccgtc 60

t 61

<210> 125
<211> 61
<212> DNA
<213> Homo sapiens

<400> 125
atcaatccac tcaaaaattg ccccatataa agttgaaatt taatgttgca tgtaaatgat 60

c 61

<210> 126
<211> 61
<212> DNA
<213> Homo sapiens

<400> 126
atcaatccac tcaaaaattg ccccatataa ggttgaaatt taatgttgca tgtaaatgat 60

c 61

<210> 127

<211> 61
<212> DNA
<213> Homo sapiens

<400> 127
tggctggaag actcccagcc tgagtcattc agaaacagat ttacaaagca ctcgggagga 60

t 61

<210> 128
<211> 61
<212> DNA
<213> Homo sapiens

<400> 128
tggctggaag actcccagcc tgagtcattc ggaaacagat ttacaaagca ctcgggagga 60

t 61

<210> 129
<211> 61
<212> DNA
<213> Homo sapiens

<400> 129
gaggatcccg agggaatgat caggccgaga cggaggaaga gccttcatga ccaagtgggt 60

c 61

<210> 130
<211> 61
<212> DNA
<213> Homo sapiens

<400> 130
gaggatcccg agggaatgat caggccgaga tggaggaaga gccttcatga ccaagtgggt 60

c 61

<210> 131
<211> 61
<212> DNA
<213> Homo sapiens

<400> 131
ccacaaaggc ttccttcacg tgtctggtca cgaatgctgc ctgccaacag gggaaccttg 60

g 61

<210> 132
<211> 61
<212> DNA
<213> Homo sapiens

<400> 132
ccacaaaggc ttccttcacg tgtctggtca tgaatgctgc ctgccaacag gggaaccttg 60

g 61

<210> 133
<211> 61
<212> DNA
<213> Homo sapiens

<400> 133
taaacaggaa ttgtaaatac ttgtgtgtta cgaaattatt tgagcagaat tccttctcat 60

a 61

<210> 134
<211> 61
<212> DNA
<213> Homo sapiens

<400> 134
taaacaggaa ttgtaaatac ttgtgtgtta tgaaattatt tgagcagaat tccttctcat 60

a 61

<210> 135
<211> 61
<212> DNA
<213> Homo sapiens

<400> 135
gaaaagccaa cagtggcaca aaggccacta cctaaaaacg tcattttagt ttagtaataa 60

a 61

<210> 136
<211> 61
<212> DNA
<213> Homo sapiens

<400> 136
gaaaagccaa cagtggcaca aaggccacta tctaaaaacg tcattttagt ttagtaataa 60

a 61

<210> 137
<211> 61
<212> DNA
<213> Homo sapiens

<400> 137
ctgggttcaa gttaataatc cctgttagac cgaatgtacc tccccagaag ggcctacctc 60

a 61

<210> 138
<211> 61
<212> DNA
<213> Homo sapiens

<400> 138
ctgggttcaa gttaataatc cctgttagac ggaatgtacc tccccagaag ggcctacctc 60

a 61

<210> 139
<211> 61
<212> DNA
<213> Homo sapiens

<400> 139
ctattagcta ttcactgtat ctgtaatata cgctgtctaa tgtatctgta agggttaaat 60

c 61

<210> 140
<211> 61

<212> DNA
<213> Homo sapiens

<400> 140
ctattagcta ttcactgtat ctgtaatata tgctgtctaa tgtatctgta agggttaaat 60

c 61

<210> 141
<211> 61
<212> DNA
<213> Homo sapiens

<400> 141
taaaattaag atttcacgtt tcatgtattc cccgagaaaa ttaagctgag tgatggaata 60

c 61

<210> 142
<211> 61
<212> DNA
<213> Homo sapiens

<400> 142
taaaattaag atttcacgtt tcatgtattc tccgagaaaa ttaagctgag tgatggaata 60

c 61

<210> 143
<211> 61
<212> DNA
<213> Homo sapiens

<400> 143
agaagctccc gcatttctca ccttttacaa ctataatgac agaactagac gctgtcctct 60

a 61

<210> 144
<211> 61
<212> DNA
<213> Homo sapiens

<400> 144
agaagctccc gcatttctca ccttttacaa gtataatgac agaactagac gctgtcctct 60

a 61

<210> 145
<211> 61
<212> DNA
<213> Homo sapiens

<400> 145
accttaatca gaaatttcca gtttccaaaa attgtattat actcaggttg gccctaggtt 60

t 61

<210> 146
<211> 61
<212> DNA
<213> Homo sapiens

<400> 146
accttaatca gaaatttcca gtttccaaaa gttgtattat actcaggttg gccctaggtt 60

t 61

<210> 147
<211> 61
<212> DNA
<213> Homo sapiens

<400> 147
accaaagtgg gtaggatttg ttttcagtgg ccacatatca agcccatttt taaattattg 60

a 61

<210> 148
<211> 61
<212> DNA
<213> Homo sapiens

<400> 148
accaaagtgg gtaggatttg ttttcagtgg gcacatatca agcccatttt taaattattg 60

a 61

<210> 149
<211> 61
<212> DNA
<213> Homo sapiens

<400> 149
ctagctaaag gactaagaac ggggcagcct aacaaaatga aggcttttag acaataacca 60

c 61

<210> 150
<211> 61
<212> DNA
<213> Homo sapiens

<400> 150
ctagctaaag gactaagaac ggggcagcct cacaaaatga aggcttttag acaataacca 60

c 61

<210> 151
<211> 61
<212> DNA
<213> Homo sapiens

<400> 151
cccttctctg taataacact acgctaggtc acgatagatc tttaggggt gtatatttgg 60

a 61

<210> 152
<211> 61
<212> DNA
<213> Homo sapiens

<400> 152
cccttctctg taataacact acgctaggtc gcgatagatc tttaggggt gtatatttgg 60

a 61

<210> 153
<211> 61
<212> DNA

<213> Homo sapiens

<400> 153
ggaactagag tttctgagag caaggtgaga agattatgca tgaagacact gggctgtcat 60

c 61

<210> 154
<211> 61
<212> DNA
<213> Homo sapiens

<400> 154
ggaactagag tttctgagag caaggtgaga ggattatgca tgaagacact gggctgtcat 60

c 61

<210> 155
<211> 61
<212> DNA
<213> Homo sapiens

<400> 155
ttagaaaata actgagaagt aaagtgtaga cgaaggaaag tgtatattgg taaaagcata 60

t 61

<210> 156
<211> 61
<212> DNA
<213> Homo sapiens

<400> 156

ttagaaaata actgagaagt aaagtgtaga tgaaggaaag tgtatattgg taaaagcata 60

t 61

<210> 157
<211> 61
<212> DNA
<213> Homo sapiens

<400> 157
tgctattacc ctcctcggtt ggctccagca ataagcctaa tgacctctac aaagctgttc 60

t 61

<210> 158
<211> 61
<212> DNA
<213> Homo sapiens

<400> 158
tgctattacc ctcctcggtt ggctccagca gtaagcctaa tgacctctac aaagctgttc 60

t 61

<210> 159
<211> 61
<212> DNA
<213> Homo sapiens

<400> 159
attctcgttt gaggaagatt ttctaagtca ctaacctgta atcttcctat tacaaccaat 60

t 61

<210> 160
<211> 61
<212> DNA
<213> Homo sapiens

<400> 160
attctcgttt gaggaagatt ttctaagtca ttaacctgta atcttcctat tacaaccaat 60

t 61

<210> 161
<211> 61
<212> DNA
<213> Homo sapiens

<400> 161
ttctgtttaa caattaatat tttatctgag actattgtgc actgtaattt ttatgaactt 60

a 61

<210> 162
<211> 61
<212> DNA
<213> Homo sapiens

<400> 162
ttctgtttaa caattaatat tttatctgag cctattgtgc actgtaattt ttatgaactt 60

a 61

<210> 163

<211> 61
<212> DNA
<213> Homo sapiens

<400> 163
ctaagcagga gtctttcagg actgaaaaaa cgttatgagg ctgttggtga aacttgaatg 60

g 61

<210> 164
<211> 61
<212> DNA
<213> Homo sapiens

<400> 164
ctaagcagga gtctttcagg actgaaaaaa tgttatgagg ctgttggtga aacttgaatg 60

g 61

<210> 165
<211> 61
<212> DNA
<213> Homo sapiens

<400> 165
taagcctagc tgggggagta gaacacatta caattgaaca caaattataa taatgcaagg 60

c 61

<210> 166
<211> 61
<212> DNA
<213> Homo sapiens

<400> 166
taagcctagc tgggggagta gaacacatta gaattgaaca caaattataa taatgcaagg 60

c 61

<210> 167
<211> 61
<212> DNA
<213> Homo sapiens

<400> 167
agttttaggt gacttcctca aattccccaa acctaaattc tatttgctta ttttacttct 60

g 61

<210> 168
<211> 61
<212> DNA
<213> Homo sapiens

<400> 168
agttttaggt gacttcctca aattccccaa tcctaaattc tatttgctta ttttacttct 60

g 61

<210> 169
<211> 61
<212> DNA
<213> Homo sapiens

<400> 169
acagtggaga cttcgtgctc agagaagaga agggaagttt tcttggtccg ccctagtgtt 60

t 61

<210> 170
<211> 61
<212> DNA
<213> Homo sapiens

<400> 170
acagtggaga cttcgtgctc agagaagaga cgggaagttt tcttggtccg ccctagtgtt 60

t 61

<210> 171
<211> 61
<212> DNA
<213> Homo sapiens

<400> 171
agcaaaggag gtaaatggtg tccttgaaaa cacttgcctg tgagtttctg gatctccatg 60

c 61

<210> 172
<211> 61
<212> DNA
<213> Homo sapiens

<400> 172
agcaaaggag gtaaatggtg tccttgaaaa tacttgcctg tgagtttctg gatctccatg 60

c 61

<210> 173
<211> 61
<212> DNA
<213> Homo sapiens

<400> 173
agcagcacag aattgcaggt ggactcttta aagctattct gttctgctaa caaggagcaa 60

g 61

<210> 174
<211> 61
<212> DNA
<213> Homo sapiens

<400> 174
agcagcacag aattgcaggt ggactcttta cagctattct gttctgctaa caaggagcaa 60

g 61

<210> 175
<211> 61
<212> DNA
<213> Homo sapiens

<400> 175
gtccctcact ggaacaagat ctgtgagtga cgtaaagctt tctggtaaag gcaaaggaag 60

t 61

<210> 176
<211> 61

<212> DNA
<213> Homo sapiens

<400> 176
gtccctcact ggaacaagat ctgtgagtga tgtaaagctt tctggtaaag gcaaaggaag 60

t 61

<210> 177
<211> 61
<212> DNA
<213> Homo sapiens

<400> 177
cacatgtgta gaccctggtc tatgcaagca acatatattt tctcatttat ttcttaccac 60

a 61

<210> 178
<211> 61
<212> DNA
<213> Homo sapiens

<400> 178
cacatgtgta gaccctggtc tatgcaagca gcatatattt tctcatttat ttcttaccac 60

a 61

<210> 179
<211> 61
<212> DNA
<213> Homo sapiens

<400> 179
ttggtctatt ttggtgaaaa gcagatatta agcctatttg tccccttcca cagtgtgacc 60

t 61

<210> 180
<211> 61
<212> DNA
<213> Homo sapiens

<400> 180
ttggtctatt ttggtgaaaa gcagatatta ggcctatttg tccccttcca cagtgtgacc 60

t 61

<210> 181
<211> 61
<212> DNA
<213> Homo sapiens

<400> 181
ccactgggcc atttctgtgt gtaagttccc cataataaaa ccttgtgcct tgtttgttgg 60

c 61

<210> 182
<211> 61
<212> DNA
<213> Homo sapiens

<400> 182
ccactgggcc atttctgtgt gtaagttccc tataataaaa ccttgtgcct tgtttgttgg 60

c 61

<210> 183
<211> 61
<212> DNA
<213> Homo sapiens

<400> 183
tttgatgaca tattctgaga gatgttctga atattaaata cttggttttg aaaacaagtt 60

t 61

<210> 184
<211> 61
<212> DNA
<213> Homo sapiens

<400> 184
tttgatgaca tattctgaga gatgttctga gtattaaata cttggttttg aaaacaagtt 60

t 61

<210> 185
<211> 61
<212> DNA
<213> Homo sapiens

<400> 185
tagcaattag gaatgctact agtaatacca atatctgcac tgagtagttt caaagagctg 60

a 61

<210> 186
<211> 61
<212> DNA
<213> Homo sapiens

<400> 186
tagcaattag gaatgctact agtaatacca gtatctgcac tgagtagttt caaagagctg 60

a 61

<210> 187
<211> 61
<212> DNA
<213> Homo sapiens

<400> 187
gttatagaag aggtgaaagg tgaatcaata aaatcaataa agagtttata atgtcagtac 60

a 61

<210> 188
<211> 61
<212> DNA
<213> Homo sapiens

<400> 188
gttatagaag aggtgaaagg tgaatcaata gaatcaataa agagtttata atgtcagtac 60

a 61

<210> 189
<211> 61
<212> DNA

<213> Homo sapiens

<400> 189
ttccttattc ctcttctaca cagtcttcat gaaatcaatc actggagccc acattgctgc 60

c 61

<210> 190
<211> 61
<212> DNA
<213> Homo sapiens

<400> 190
ttccttattc ctcttctaca cagtcttcat taaatcaatc actggagccc acattgctgc 60

c 61

<210> 191
<211> 61
<212> DNA
<213> Homo sapiens

<400> 191
cgttctgatc aagggctgta agtactagaa cggaagaaca gtgtgctgtg ggaagaaatg 60

g 61

<210> 192
<211> 61
<212> DNA
<213> Homo sapiens

<400> 192

cgttctgatc aagggctgta agtactagaa tggaagaaca gtgtgctgtg ggaagaaatg 60

g 61

<210> 193
<211> 61
<212> DNA
<213> Homo sapiens

<400> 193
ggaagaattc atcaccagca tacctgtata caaaaaaagt gttgataagt cctttaggca 60

a 61

<210> 194
<211> 61
<212> DNA
<213> Homo sapiens

<400> 194
ggaagaattc atcaccagca tacctgtata gaaaaaaagt gttgataagt cctttaggca 60

a 61

<210> 195
<211> 61
<212> DNA
<213> Homo sapiens

<400> 195
tgaaggatct cctgccaggt aaagcaaatg aaacttaaca tatcaacgtt aaagaattga 60

c 61

<210> 196
<211> 61
<212> DNA
<213> Homo sapiens

<400> 196
tgaaggatct cctgccaggt aaagcaaatg gaacttaaca tatcaacgtt aaagaattga 60

c 61

<210> 197
<211> 61
<212> DNA
<213> Homo sapiens

<400> 197
ccctagaggg tatcaagggt tgagcaagaa cgtttacttg tgtcaagcca tttatattta 60

t 61

<210> 198
<211> 61
<212> DNA
<213> Homo sapiens

<400> 198
ccctagaggg tatcaagggt tgagcaagaa tgtttacttg tgtcaagcca tttatattta 60

t 61

<210> 199

<211> 61
<212> DNA
<213> Homo sapiens

<400> 199
atcatgttaa cacaggaagg aactatatag aagaagcaac tttggaggaa gagatttcat 60

c 61

<210> 200
<211> 61
<212> DNA
<213> Homo sapiens

<400> 200
atcatgttaa cacaggaagg aactatatag gagaagcaac tttggaggaa gagatttcat 60

c 61

<210> 201
<211> 61
<212> DNA
<213> Homo sapiens

<400> 201
tgtatttaaa aatggggcta attatgccca aatcatgatg ggatgaagtg ttgtaaggct 60

t 61

<210> 202
<211> 61
<212> DNA
<213> Homo sapiens

<400> 202
tgtatttaaa aatggggcta attatgccca catcatgatg ggatgaagtg ttgtaaggct 60

t 61

<210> 203
<211> 61
<212> DNA
<213> Homo sapiens

<400> 203
ttcagtacac aaatattcag cctctcacaa ctgctagata aacgctgtgc tgttaactgg 60

g 61

<210> 204
<211> 61
<212> DNA
<213> Homo sapiens

<400> 204
ttcagtacac aaatattcag cctctcacaa gtgctagata aacgctgtgc tgttaactgg 60

g 61

<210> 205
<211> 61
<212> DNA
<213> Homo sapiens

<400> 205
actgttctta actgtactga tagctcttct atagctttgt caaggataag agattcttcc 60

c 61

<210> 206
<211> 61
<212> DNA
<213> Homo sapiens

<400> 206
actgttctta actgtactga tagctcttct gtagctttgt caaggataag agattcttcc 60

c 61

<210> 207
<211> 61
<212> DNA
<213> Homo sapiens

<400> 207
caaagacttc tgggcttgag taagctgagt atgttgcaaa gagtacttag tttagaaagt 60

a 61

<210> 208
<211> 61
<212> DNA
<213> Homo sapiens

<400> 208
caaagacttc tgggcttgag taagctgagt gtgttgcaaa gagtacttag tttagaaagt 60

a 61

<210> 209
<211> 61
<212> DNA
<213> Homo sapiens

<400> 209
gtgggttcct ggtaaaatgg taggtttagt acttttcctc tctcactctc ttgccctcac 60

c 61

<210> 210
<211> 61
<212> DNA
<213> Homo sapiens

<400> 210
gtgggttcct ggtaaaatgg taggtttagt tcttttcctc tctcactctc ttgccctcac 60

c 61

<210> 211
<211> 61
<212> DNA
<213> Homo sapiens

<400> 211
atctaagtaa ggttagaaat gcttcggcct atatgacttt ttaacctggt acacttaaac 60

c 61

<210> 212
<211> 61

<212> DNA
<213> Homo sapiens

<400> 212
atctaagtaa ggttagaaat gcttcggcct gtatgacttt ttaacctggt acacttaaac 60

c 61

<210> 213
<211> 61
<212> DNA
<213> Homo sapiens

<400> 213
gatttaaaaa cttatcaagg tcactagtta atcactgctg gagccagaac tggagcccat 60

g 61

<210> 214
<211> 61
<212> DNA
<213> Homo sapiens

<400> 214
gatttaaaaa cttatcaagg tcactagtta gtcactgctg gagccagaac tggagcccat 60

g 61

<210> 215
<211> 61
<212> DNA
<213> Homo sapiens

<400> 215
gcaaaaccag taaatctaac tgcaattgtg attgatggca aatctacaga gtgaacaatc 60

a 61

<210> 216
<211> 61
<212> DNA
<213> Homo sapiens

<400> 216
gcaaaaccag taaatctaac tgcaattgtg gttgatggca aatctacaga gtgaacaatc 60

a 61

<210> 217
<211> 61
<212> DNA
<213> Homo sapiens

<400> 217
ttcagatggg tagaagctgc tctcagaaag atagatgaca gggctgggca tggtggctca 60

c 61

<210> 218
<211> 61
<212> DNA
<213> Homo sapiens

<400> 218
ttcagatggg tagaagctgc tctcagaaag gtagatgaca gggctgggca tggtggctca 60

c 61

<210> 219
<211> 61
<212> DNA
<213> Homo sapiens

<400> 219
gctgtatata atatttgaaa atgacactga acaagcgaag attacagtgg tttttcttct 60

t 61

<210> 220
<211> 61
<212> DNA
<213> Homo sapiens

<400> 220
gctgtatata atatttgaaa atgacactga gcaagcgaag attacagtgg tttttcttct 60

t 61

<210> 221
<211> 61
<212> DNA
<213> Homo sapiens

<400> 221
attagccatg aacactaaag aaatagcctg ataacacttt gtggattata aagttagcaa 60

g 61

<210> 222
<211> 61
<212> DNA
<213> Homo sapiens

<400> 222
attagccatg aacactaaag aaatagcctg gtaacacttt gtggattata aagttagcaa 60

g 61

<210> 223
<211> 61
<212> DNA
<213> Homo sapiens

<400> 223
tgattcctca taaaaggata agatttagct aggcaaagtt gaggaaagac attccaagag 60

a 61

<210> 224
<211> 61
<212> DNA
<213> Homo sapiens

<400> 224
tgattcctca taaaaggata agatttagct cggcaaagtt gaggaaagac attccaagag 60

a 61

<210> 225
<211> 61
<212> DNA

<213> Homo sapiens

<400> 225
acaaataaaa tttcttcttt caatcattcc ataattccct ggggctacag ccactttggt 60

a 61

<210> 226
<211> 61
<212> DNA
<213> Homo sapiens

<400> 226
acaaataaaa tttcttcttt caatcattcc gtaattccct ggggctacag ccactttggt 60

a 61

<210> 227
<211> 61
<212> DNA
<213> Homo sapiens

<400> 227
aagttcctat accgtgaagc tggccaaaac agtataatct caatatttac acttaaagtt 60

a 61

<210> 228
<211> 61
<212> DNA
<213> Homo sapiens

<400> 228

aagttcctat accgtgaagc tggccaaaac ggtataatct caatatttac acttaaagtt 60

a 61

<210> 229
<211> 61
<212> DNA
<213> Homo sapiens

<400> 229
gccactgcca ccactcctgc agattgttcc agctgtgtta ctaaatacag gttgcttttc 60

t 61

<210> 230
<211> 61
<212> DNA
<213> Homo sapiens

<400> 230
gccactgcca ccactcctgc agattgttcc cgctgtgtta ctaaatacag gttgcttttc 60

t 61

<210> 231
<211> 61
<212> DNA
<213> Homo sapiens

<400> 231
acttttctca taataaaacc tttattgctc aaggtgcctc aaattggttt cgcttaactt 60

g 61

<210> 232
<211> 61
<212> DNA
<213> Homo sapiens

<400> 232
actttctca taataaaacc tttattgctc caggtgcctc aaattggttt cgcttaactt 60

g 61

<210> 233
<211> 61
<212> DNA
<213> Homo sapiens

<400> 233
gtgacctgtc cttgtgactt ggaaaaaatg ccatcatgtt ctgtccgatg tgtttccgct 60

a 61

<210> 234
<211> 61
<212> DNA
<213> Homo sapiens

<400> 234
gtgacctgtc cttgtgactt ggaaaaaatg gcatcatgtt ctgtccgatg tgtttccgct 60

a 61

<210> 235

<211> 61
<212> DNA
<213> Homo sapiens

<400> 235
cccaaaataa aactctccta ttattgtgac acttggatgg ccccatccaa cagcaaaatc 60

a 61

<210> 236
<211> 61
<212> DNA
<213> Homo sapiens

<400> 236
cccaaaataa aactctccta ttattgtgac ccttggatgg ccccatccaa cagcaaaatc 60

a 61

<210> 237
<211> 61
<212> DNA
<213> Homo sapiens

<400> 237
ctgtactttt atatacgcct aatttgttcc atctcaatga caatattccc cacatctaat 60

a 61

<210> 238
<211> 61
<212> DNA
<213> Homo sapiens

<400> 238
ctgtactttt atatacgcct aatttgttcc gtctcaatga caatattccc cacatctaat 60

a 61

<210> 239
<211> 61
<212> DNA
<213> Homo sapiens

<400> 239
accccaaaag tggtttataa aacattgact ccacatcact gtagttaacc caaaccaaaa 60

g 61

<210> 240
<211> 61
<212> DNA
<213> Homo sapiens

<400> 240
accccaaaag tggtttataa aacattgact gcacatcact gtagttaacc caaaccaaaa 60

g 61

<210> 241
<211> 61
<212> DNA
<213> Homo sapiens

<400> 241
acatcactgt agttaaccca aaccaaaaga ctgtcgcttg acactgagaa aaatcccctc 60

a 61

<210> 242
<211> 61
<212> DNA
<213> Homo sapiens

<400> 242
acatcactgt agttaaccca aaccaaaaga gtgtcgcttg acactgagaa aaatcccctc 60

a 61

<210> 243
<211> 61
<212> DNA
<213> Homo sapiens

<400> 243
gcagagggat cagagacagc tcgaggagag agcatattcc atagttcaga gacagcatac 60

c 61

<210> 244
<211> 61
<212> DNA
<213> Homo sapiens

<400> 244
gcagagggat cagagacagc tcgaggagag ggcatattcc atagttcaga gacagcatac 60

c 61

<210> 245
<211> 61
<212> DNA
<213> Homo sapiens

<400> 245
tttgcaacca gtgtgcatga aactggagga actcatccta agtgaaatgt caggcataga 60

a 61

<210> 246
<211> 61
<212> DNA
<213> Homo sapiens

<400> 246
tttgcaacca gtgtgcatga aactggagga cctcatccta agtgaaatgt caggcataga 60

a 61

<210> 247
<211> 61
<212> DNA
<213> Homo sapiens

<400> 247
tttcaaaatt aattttcaaa tttctactgg acgataacta ataatcattt atttaaaact 60

t 61

<210> 248
<211> 61

<212> DNA
<213> Homo sapiens

<400> 248
tttcaaaatt aattttcaaa tttctactgg gcgataacta ataatcattt atttaaaact 60

t 61

<210> 249
<211> 61
<212> DNA
<213> Homo sapiens

<400> 249
gcaatagaga gaaatgagct tctgaaatgc aaaactatgg attaatttca gaaatattat 60

a 61

<210> 250
<211> 61
<212> DNA
<213> Homo sapiens

<400> 250
gcaatagaga gaaatgagct tctgaaatgc gaaactatgg attaatttca gaaatattat 60

a 61

<210> 251
<211> 61
<212> DNA
<213> Homo sapiens

<400> 251
tctgctcaac cagttctttt gcttcctctg aattcatcac tgggggcagg aggagtctgc 60

a 61

<210> 252
<211> 61
<212> DNA
<213> Homo sapiens

<400> 252
tctgctcaac cagttctttt gcttcctctg gattcatcac tgggggcagg aggagtctgc 60

a 61

<210> 253
<211> 61
<212> DNA
<213> Homo sapiens

<400> 253
ttgactttat atggggatgg aggccgcctc aggtagtctt tgcaggagga ctgtgggttt 60

g 61

<210> 254
<211> 61
<212> DNA
<213> Homo sapiens

<400> 254
ttgactttat atggggatgg aggccgcctc gggtagtctt tgcaggagga ctgtgggttt 60

g 61

<210> 255
<211> 61
<212> DNA
<213> Homo sapiens

<400> 255
atagagtagt tatgttttca gcatctccac atgaatgaat agcaatcacc ttgaaaagtg 60

a 61

<210> 256
<211> 61
<212> DNA
<213> Homo sapiens

<400> 256
atagagtagt tatgttttca gcatctccac gtgaatgaat agcaatcacc ttgaaaagtg 60

a 61

<210> 257
<211> 61
<212> DNA
<213> Homo sapiens

<400> 257
cctatgcgtg tgcctttctt acctctgaca acatctagtt ccatcttgtt aggaggccta 60

a 61

<210> 258
<211> 61
<212> DNA
<213> Homo sapiens

<400> 258
cctatgcgtg tgcctttctt acctctgaca gcatctagtt ccatcttgtt aggaggccta 60

a 61

<210> 259
<211> 61
<212> DNA
<213> Homo sapiens

<400> 259
aacctgttac tctcgggtgc tctgtggtga atcctttagc aaagcaaatc ccctctgcag 60

g 61

<210> 260
<211> 61
<212> DNA
<213> Homo sapiens

<400> 260
aacctgttac tctcgggtgc tctgtggtga ctcctttagc aaagcaaatc ccctctgcag 60

g 61

<210> 261
<211> 61
<212> DNA

<213> Homo sapiens

<400> 261
gtttccagaa ctctttttgg ccaggctcca agctaagctc tgtaggaagc ttgatgatgg 60

g 61

<210> 262
<211> 61
<212> DNA
<213> Homo sapiens

<400> 262
gtttccagaa ctctttttgg ccaggctcca ggctaagctc tgtaggaagc ttgatgatgg 60

g 61

<210> 263
<211> 61
<212> DNA
<213> Homo sapiens

<400> 263
ggccatggct gagttgactg ggttcagatt ctggttcagc agtgtggtct cgggcaagtt 60

g 61

<210> 264
<211> 61
<212> DNA
<213> Homo sapiens

<400> 264

ggccatggct gagttgactg ggttcagatt gtggttcagc agtgtggtct cgggcaagtt 60

g 61

<210> 265
<211> 61
<212> DNA
<213> Homo sapiens

<400> 265
acaagttgca gagaaacctt taataattac accagagctg ggcacagtgg ctcacacctg 60

t 61

<210> 266
<211> 61
<212> DNA
<213> Homo sapiens

<400> 266
acaagttgca gagaaacctt taataattac gccagagctg ggcacagtgg ctcacacctg 60

t 61

<210> 267
<211> 61
<212> DNA
<213> Homo sapiens

<400> 267
caacattatc tttctgaggg atacaactca accctgaaca cctgcttaca caggaaacgc 60

a 61

<210> 268
<211> 61
<212> DNA
<213> Homo sapiens

<400> 268
caacattatc tttctgaggg atacaactca cccctgaaca cctgcttaca caggaaacgc 60

a 61

<210> 269
<211> 61
<212> DNA
<213> Homo sapiens

<400> 269
ataaccacag atgttctatt tcaagcaatt aaaggcatta atctcatact aagtggatcg 60

c 61

<210> 270
<211> 61
<212> DNA
<213> Homo sapiens

<400> 270
ataaccacag atgttctatt tcaagcaatt caaggcatta atctcatact aagtggatcg 60

c 61

<210> 271

<211> 61
<212> DNA
<213> Homo sapiens

<400> 271
ttttcataag acattatact ctagccatga attggttttg actacttgca atcccctaaa 60

c 61

<210> 272
<211> 61
<212> DNA
<213> Homo sapiens

<400> 272
ttttcataag acattatact ctagccatga gttggttttg actacttgca atcccctaaa 60

c 61

<210> 273
<211> 61
<212> DNA
<213> Homo sapiens

<400> 273
atgggggcag ctgatgaccc tttgctcctc aggatcttgt gccctgttct tcatgcctac 60

g 61

<210> 274
<211> 61
<212> DNA
<213> Homo sapiens

<400> 274
atgggggcag ctgatgaccc tttgctcctc gggatcttgt gccctgttct tcatgcctac 60

g 61

<210> 275
<211> 61
<212> DNA
<213> Homo sapiens

<400> 275
cagttacatg ttggatcaca gtgaggttgt agcaacgaaa cccccagctc ttctcccctc 60

t 61

<210> 276
<211> 61
<212> DNA
<213> Homo sapiens

<400> 276
cagttacatg ttggatcaca gtgaggttgt ggcaacgaaa cccccagctc ttctcccctc 60

t 61

<210> 277
<211> 61
<212> DNA
<213> Homo sapiens

<400> 277
agagctatgt tggggaagat ggtgaagcca agtctaaatt cagcaaataa ataaataaat 60

a 61

<210> 278
<211> 61
<212> DNA
<213> Homo sapiens

<400> 278
agagctatgt tggggaagat ggtgaagcca cgtctaaatt cagcaaataa ataaataaat 60

a 61

<210> 279
<211> 61
<212> DNA
<213> Homo sapiens

<400> 279
ccggagtatc ccgctttctt tggaggaaac aaccgcatca gatctgcgct gcggcagagg 60

c 61

<210> 280
<211> 61
<212> DNA
<213> Homo sapiens

<400> 280
ccggagtatc ccgctttctt tggaggaaac caccgcatca gatctgcgct gcggcagagg 60

c 61

<210> 281
<211> 61
<212> DNA
<213> Homo sapiens

<400> 281
ttggcttcca actggcctct aaactctaat ctagcatttt ccagtccatt gtgacaaagt 60

c 61

<210> 282
<211> 61
<212> DNA
<213> Homo sapiens

<400> 282
ttggcttcca actggcctct aaactctaat gtagcatttt ccagtccatt gtgacaaagt 60

c 61

<210> 283
<211> 61
<212> DNA
<213> Homo sapiens

<400> 283
tttagtcatg ggcaattagt aagcattaac actcctggtg atttacactg tatttcttag 60

a 61

<210> 284
<211> 61

<212> DNA
<213> Homo sapiens

<400> 284
tttagtcatg ggcaattagt aagcattaac cctcctggtg atttacactg tatttcttag 60

a 61

<210> 285
<211> 61
<212> DNA
<213> Homo sapiens

<400> 285
gttctccatg gtactaaccc attctcttca ataaaagcat agtcagcctg acctatggaa 60

g 61

<210> 286
<211> 61
<212> DNA
<213> Homo sapiens

<400> 286
gttctccatg gtactaaccc attctcttca gtaaaagcat agtcagcctg acctatggaa 60

g 61

<210> 287
<211> 61
<212> DNA
<213> Homo sapiens

<400> 287
catatacttg ttctcaaacc attcactagc aagaaaaagt ggcctagagc aggggtcagc 60

a 61

<210> 288
<211> 61
<212> DNA
<213> Homo sapiens

<400> 288
catatacttg ttctcaaacc attcactagc cagaaaaagt ggcctagagc aggggtcagc 60

a 61

<210> 289
<211> 61
<212> DNA
<213> Homo sapiens

<400> 289
atctggtaaa aattttcata agcattagac atatcaaact taaaaacaca cacacacaat 60

t 61

<210> 290
<211> 61
<212> DNA
<213> Homo sapiens

<400> 290
atctggtaaa aattttcata agcattagac gtatcaaact taaaaacaca cacacacaat 60

t 61

<210> 291
<211> 61
<212> DNA
<213> Homo sapiens

<400> 291
taagagagcc tctaggttag cgccgctgaa cgagctagtg gaggaggagt gtgagactga 60

g 61

<210> 292
<211> 61
<212> DNA
<213> Homo sapiens

<400> 292
taagagagcc tctaggttag cgccgctgaa ggagctagtg gaggaggagt gtgagactga 60

g 61

<210> 293
<211> 61
<212> DNA
<213> Homo sapiens

<400> 293
tgtcctatgc cctctcgttg aatgctcaca atgacccaat gggatgaccc tgtcaccatc 60

g 61

<210> 294
<211> 61
<212> DNA
<213> Homo sapiens

<400> 294
tgtcctatgc cctctcgttg aatgctcaca gtgacccaat gggatgaccc tgtcaccatc 60

g 61

<210> 295
<211> 61
<212> DNA
<213> Homo sapiens

<400> 295
gtagggcatt tgatttaatc accaagagcc atgtaaacct catgcaaaca ttaagctatt 60

a 61

<210> 296
<211> 61
<212> DNA
<213> Homo sapiens

<400> 296
gtagggcatt tgatttaatc accaagagcc gtgtaaacct catgcaaaca ttaagctatt 60

a 61

<210> 297
<211> 61
<212> DNA

<213> Homo sapiens

<400> 297
acctctatga ctttacattg caggcagggt aaaatccaaa catgactaat aggcggagaa 60

g 61

<210> 298
<211> 61
<212> DNA
<213> Homo sapiens

<400> 298
acctctatga ctttacattg caggcagggt gaaatccaaa catgactaat aggcggagaa 60

g 61

<210> 299
<211> 61
<212> DNA
<213> Homo sapiens

<400> 299
aaaaaaccac attcctcgct atcttcatca attttgtgta aggatcagga agctgttaca 60

c 61

<210> 300
<211> 61
<212> DNA
<213> Homo sapiens

<400> 300

aaaaaaccac attcctcgct atcttcatca gttttgtgta aggatcagga agctgttaca 60

c 61

<210> 301
<211> 61
<212> DNA
<213> Homo sapiens

<400> 301
ttcccttat cagactggca aatagccaaa aagtggatag caaaccactc tcatacattg 60

c 61

<210> 302
<211> 61
<212> DNA
<213> Homo sapiens

<400> 302
ttcccttat cagactggca aatagccaaa tagtggatag caaaccactc tcatacattg 60

c 61

<210> 303
<211> 61
<212> DNA
<213> Homo sapiens

<400> 303
ctcatgacat gcttcagatt ggtcaaagaa agagatttta tcaagtgttc ccttctcaag 60

a 61

<210> 304
<211> 61
<212> DNA
<213> Homo sapiens

<400> 304
ctcatgacat gcttcagatt ggtcaaagaa cgagatttta tcaagtgttc ccttctcaag 60

a 61

<210> 305
<211> 61
<212> DNA
<213> Homo sapiens

<400> 305
ttcctggcaa ttaagtcaaa ccttaagcta ctctcatagt tcagtgctct cagttccaaa 60

a 61

<210> 306
<211> 61
<212> DNA
<213> Homo sapiens

<400> 306
ttcctggcaa ttaagtcaaa ccttaagcta gtctcatagt tcagtgctct cagttccaaa 60

a 61

<210> 307

<211> 61
<212> DNA
<213> Homo sapiens

<400> 307
gatgttgctg tatcgctcag atctaatgtt atgtggccca ttttaccatg gtatcactga 60

a 61

<210> 308
<211> 61
<212> DNA
<213> Homo sapiens

<400> 308
gatgttgctg tatcgctcag atctaatgtt ctgtggccca ttttaccatg gtatcactga 60

a 61

<210> 309
<211> 61
<212> DNA
<213> Homo sapiens

<400> 309
gtttaaatgt aaaaatttaa attatgagaa acagttgaca tttcaggttt atattcttaa 60

c 61

<210> 310
<211> 61
<212> DNA
<213> Homo sapiens

<400> 310
gtttaaatgt aaaaatttaa attatgagaa gcagttgaca tttcaggttt atattcttaa 60

c 61

<210> 311
<211> 61
<212> DNA
<213> Homo sapiens

<400> 311
aatatcttat gactactact cttacaaaat cccactctat acccccctgcc tcctggaata 60

g 61

<210> 312
<211> 61
<212> DNA
<213> Homo sapiens

<400> 312
aatatcttat gactactact cttacaaaat gccactctat acccccctgcc tcctggaata 60

g 61

<210> 313
<211> 61
<212> DNA
<213> Homo sapiens

<400> 313
atagagcata agaatctata gcataaaaga aaatgatgtg aattaacact gcagcatcgc 60

t 61

<210> 314
<211> 61
<212> DNA
<213> Homo sapiens

<400> 314
atagagcata agaatctata gcataaaaga caatgatgtg aattaacact gcagcatcgc 60

t 61

<210> 315
<211> 61
<212> DNA
<213> Homo sapiens

<400> 315
tctaaagtga aagtaaaata gctgagatat aggtgaaaag agagacagat acaagtgtgt 60

g 61

<210> 316
<211> 61
<212> DNA
<213> Homo sapiens

<400> 316
tctaaagtga aagtaaaata gctgagatat gggtgaaaag agagacagat acaagtgtgt 60

g 61

<210> 317
<211> 61
<212> DNA
<213> Homo sapiens

<400> 317
acagttctga actccttccc tgtggtatct atcatgtact tggactggtg cagggtgctg 60

a 61

<210> 318
<211> 61
<212> DNA
<213> Homo sapiens

<400> 318
acagttctga actccttccc tgtggtatct gtcatgtact tggactggtg cagggtgctg 60

a 61

<210> 319
<211> 61
<212> DNA
<213> Homo sapiens

<400> 319
tgtgctgggc acacagtggg tgcctaatgt atggagaata gagaaagagg atgatggaga 60

a 61

<210> 320
<211> 61

<212> DNA
<213> Homo sapiens

<400> 320
tgtgctgggc acacagtggg tgcctaatgt ctggagaata gagaaagagg atgatggaga 60

a 61

<210> 321
<211> 61
<212> DNA
<213> Homo sapiens

<400> 321
ctccatatcc cctccatccc atgctacccc aatttcagct gctttaagga aaaagatgtt 60

t 61

<210> 322
<211> 61
<212> DNA
<213> Homo sapiens

<400> 322
ctccatatcc cctccatccc atgctacccc gatttcagct gctttaagga aaaagatgtt 60

t 61

<210> 323
<211> 61
<212> DNA
<213> Homo sapiens

<400> 323
aagtttgtaa acattaacca acttctcctc atctgtcctt ctcatactca ggttcccttc 60

c 61

<210> 324
<211> 61
<212> DNA
<213> Homo sapiens

<400> 324
aagtttgtaa acattaacca acttctcctc gtctgtcctt ctcatactca ggttcccttc 60

c 61

<210> 325
<211> 61
<212> DNA
<213> Homo sapiens

<400> 325
agtcctcatt ttaaatttag tagaatagtt aacagctcaa ggtctagatt cagagatatt 60

t 61

<210> 326
<211> 61
<212> DNA
<213> Homo sapiens

<400> 326
agtcctcatt ttaaatttag tagaatagtt tacagctcaa ggtctagatt cagagatatt 60

t 61

<210> 327
<211> 61
<212> DNA
<213> Homo sapiens

<400> 327
gaaggaacaa aatgctgcta agtagcaaaa agtcctcatt ttaaatttag tagaatagtt 60

t 61

<210> 328
<211> 61
<212> DNA
<213> Homo sapiens

<400> 328
gaaggaacaa aatgctgcta agtagcaaaa ggtcctcatt ttaaatttag tagaatagtt 60

t 61

<210> 329
<211> 61
<212> DNA
<213> Homo sapiens

<400> 329
cttgatttta ttgctaggga ttgtggtaaa acacccaaag aatgtgggta tgtgcctact 60

t 61

<210> 330
<211> 61
<212> DNA
<213> Homo sapiens

<400> 330
cttgatttta ttgctaggga ttgtggtaaa gcacccaaag aatgtgggta tgtgcctact 60

t 61

<210> 331
<211> 61
<212> DNA
<213> Homo sapiens

<400> 331
agtgctttga aatcaagcag aacactcatc acttaaatca aaccagactt tggatttcag 60

a 61

<210> 332
<211> 61
<212> DNA
<213> Homo sapiens

<400> 332
agtgctttga aatcaagcag aacactcatc gcttaaatca aaccagactt tggatttcag 60

a 61

<210> 333
<211> 61
<212> DNA

<213> Homo sapiens

<400> 333
aagtgttaga catcaaactg atgcttgaaa atgaaaatgt aaagtggtaa aaacttgaat 60

c 61

<210> 334
<211> 61
<212> DNA
<213> Homo sapiens

<400> 334
aagtgttaga catcaaactg atgcttgaaa gtgaaaatgt aaagtggtaa aaacttgaat 60

c 61

<210> 335
<211> 61
<212> DNA
<213> Homo sapiens

<400> 335
tagggagcaa caccatggtg gtagagaacc aaagtttatt agcatctcta aactcatata 60

g 61

<210> 336
<211> 61
<212> DNA
<213> Homo sapiens

<400> 336

tagggagcaa caccatggtg gtagagaacc gaagtttatt agcatctcta aactcatata 60

g 61

<210> 337
<211> 61
<212> DNA
<213> Homo sapiens

<400> 337
aatcacaggc tagactatta gtgaaggtct attcctacaa tgaacacctg taaaggccaa 60

a 61

<210> 338
<211> 61
<212> DNA
<213> Homo sapiens

<400> 338
aatcacaggc tagactatta gtgaaggtct gttcctacaa tgaacacctg taaaggccaa 60

a 61

<210> 339
<211> 61
<212> DNA
<213> Homo sapiens

<400> 339
tacgcaccag gcagtgaggg aaaaggagca actgaacctc tccccacaca gcaagtgagc 60

c 61

<210> 340
<211> 61
<212> DNA
<213> Homo sapiens

<400> 340
tacgcaccag gcagtgaggg aaaaggagca gctgaacctc tccccacaca gcaagtgagc 60

c 61

<210> 341
<211> 61
<212> DNA
<213> Homo sapiens

<400> 341
ctggcaccat gtctgctcca ttcaccatca atgcacatca gagtgacata acctgtgtgt 60

c 61

<210> 342
<211> 61
<212> DNA
<213> Homo sapiens

<400> 342
ctggcaccat gtctgctcca ttcaccatca gtgcacatca gagtgacata acctgtgtgt 60

c 61

<210> 343

<211> 61
<212> DNA
<213> Homo sapiens

<400> 343
caatgtgagc tgcacattgt aaacaccagc attattagat gtctgtatcg tttttagcct 60

a 61

<210> 344
<211> 61
<212> DNA
<213> Homo sapiens

<400> 344
caatgtgagc tgcacattgt aaacaccagc gttattagat gtctgtatcg tttttagcct 60

a 61

<210> 345
<211> 61
<212> DNA
<213> Homo sapiens

<400> 345
aagagatagg aaaagacaca gagacacaga cgggaatgcc gggtgaagac agaggaaaat 60

a 61

<210> 346
<211> 61
<212> DNA
<213> Homo sapiens

<400> 346
aagagatagg aaaagacaca gagacacaga ggggaatgcc gggtgaagac agaggaaaat 60

a 61

<210> 347
<211> 61
<212> DNA
<213> Homo sapiens

<400> 347
aactgttttc caaagaggct gtaacatttt atatacccat gagtgattca ttttctttgc 60

a 61

<210> 348
<211> 61
<212> DNA
<213> Homo sapiens

<400> 348
aactgttttc caaagaggct gtaacatttt gtatacccat gagtgattca ttttctttgc 60

a 61

<210> 349
<211> 61
<212> DNA
<213> Homo sapiens

<400> 349
ccaatcatac accaagaaca tggtcttaca aagtgagggt gtggcaggct tcaccatggt 60

t 61

<210> 350
<211> 61
<212> DNA
<213> Homo sapiens

<400> 350
ccaatcatac accaagaaca tggtcttaca cagtgagggt gtggcaggct tcaccatggt 60

t 61

<210> 351
<211> 61
<212> DNA
<213> Homo sapiens

<400> 351
tggggcctga tgagttgtga ttggcctctg attagagcac agcatagccg aagaagagag 60

t 61

<210> 352
<211> 61
<212> DNA
<213> Homo sapiens

<400> 352
tggggcctga tgagttgtga ttggcctctg gttagagcac agcatagccg aagaagagag 60

t 61

<210> 353
<211> 61
<212> DNA
<213> Homo sapiens

<400> 353
ctgtgaaagc agaggctcga gggaccattc acttttgttt tcttataaat ggtaaaacaa 60

g 61

<210> 354
<211> 61
<212> DNA
<213> Homo sapiens

<400> 354
ctgtgaaagc agaggctcga gggaccattc gcttttgttt tcttataaat ggtaaaacaa 60

g 61

<210> 355
<211> 61
<212> DNA
<213> Homo sapiens

<400> 355
agaatcattc tttctccttc ctactccttc atatctgctc agtacaacat cagacaagca 60

t 61

<210> 356
<211> 61

<212> DNA
<213> Homo sapiens

<400> 356
agaatcattc tttctccttc ctactccttc gtatctgctc agtacaacat cagacaagca 60

t 61

<210> 357
<211> 61
<212> DNA
<213> Homo sapiens

<400> 357
caaaatgctg ataatgatat ggacaataaa attcaggata agacgttctc aggtggagat 60

g 61

<210> 358
<211> 61
<212> DNA
<213> Homo sapiens

<400> 358
caaaatgctg ataatgatat ggacaataaa cttcaggata agacgttctc aggtggagat 60

g 61

<210> 359
<211> 61
<212> DNA
<213> Homo sapiens

<400> 359
attaaaagta tttgcaagga gctggttaca attctggccc atgcattcta tagttctgtg 60

t 61

<210> 360
<211> 61
<212> DNA
<213> Homo sapiens

<400> 360
attaaaagta tttgcaagga gctggttaca gttctggccc atgcattcta tagttctgtg 60

t 61

<210> 361
<211> 61
<212> DNA
<213> Homo sapiens

<400> 361
taaaggcagt gtctttgtgc acatcagttc atgcaatgca gaggaacttt attacaagaa 60

a 61

<210> 362
<211> 61
<212> DNA
<213> Homo sapiens

<400> 362
taaaggcagt gtctttgtgc acatcagttc gtgcaatgca gaggaacttt attacaagaa 60

a 61

<210> 363
<211> 61
<212> DNA
<213> Homo sapiens

<400> 363
aaagctgacc tgtgagggct tctttagggt cctctctgat ttgtatccca tctcacctcc 60

c 61

<210> 364
<211> 61
<212> DNA
<213> Homo sapiens

<400> 364
aaagctgacc tgtgagggct tctttagggt gctctctgat ttgtatccca tctcacctcc 60

c 61

<210> 365
<211> 61
<212> DNA
<213> Homo sapiens

<400> 365
tggcagacat cagttccttg aagctgaagg actgaggctc tcaactccta caaaccacct 60

a 61

<210> 366
<211> 61
<212> DNA
<213> Homo sapiens

<400> 366
tggcagacat cagttccttg aagctgaagg gctgaggctc tcaactccta caaaccacct 60

a 61

<210> 367
<211> 61
<212> DNA
<213> Homo sapiens

<400> 367
cccttgtatt acacatgaat tattatttgg aaaaactgaa aggctaaaat atcttcagaa 60

t 61

<210> 368
<211> 61
<212> DNA
<213> Homo sapiens

<400> 368
cccttgtatt acacatgaat tattatttgg gaaaactgaa aggctaaaat atcttcagaa 60

t 61

<210> 369
<211> 61
<212> DNA

<213> Homo sapiens

<400> 369
tacttttta attagaataa tactgccagc ataggtaagt gggtaaagaa acattacttt 60

c 61

<210> 370
<211> 61
<212> DNA
<213> Homo sapiens

<400> 370
tacttttta attagaataa tactgccagc gtaggtaagt gggtaaagaa acattacttt 60

c 61

<210> 371
<211> 61
<212> DNA
<213> Homo sapiens

<400> 371
attggaatta taacaagcaa gacccctggc atacctcaga aactaatctc tgcaggaatt 60

a 61

<210> 372
<211> 61
<212> DNA
<213> Homo sapiens

<400> 372

attggaatta taacaagcaa gacccctggc gtacctcaga aactaatctc tgcaggaatt 60

a 61

<210> 373
<211> 61
<212> DNA
<213> Homo sapiens

<400> 373
gatggcaaaa taacagcaaa ttaacctgaa atgactacat agctttcctc attttaaatt 60

g 61

<210> 374
<211> 61
<212> DNA
<213> Homo sapiens

<400> 374
gatggcaaaa taacagcaaa ttaacctgaa ttgactacat agctttcctc attttaaatt 60

g 61

<210> 375
<211> 61
<212> DNA
<213> Homo sapiens

<400> 375
gggccttggt ttccaaagct ttcttacatc aaccatctca ttaaaacctc actgcagcct 60

g 61

<210> 376
<211> 61
<212> DNA
<213> Homo sapiens

<400> 376
gggccttggt ttccaaagct ttcttacatc caccatctca ttaaaacctc actgcagcct 60

g 61

<210> 377
<211> 61
<212> DNA
<213> Homo sapiens

<400> 377
tgtctaaaaa gggtccctgt tttgccttcc atttttcac agagattttg gctgggtaaa 60

g 61

<210> 378
<211> 61
<212> DNA
<213> Homo sapiens

<400> 378
tgtctaaaaa gggtccctgt tttgccttcc gtttttcac agagattttg gctgggtaaa 60

g 61

<210> 379

<211> 61
<212> DNA
<213> Homo sapiens

<400> 379
tatacactga attttgaaga tgtggtttca aaaagtaaag aatatgaaat atctaatgaa 60

t 61

<210> 380
<211> 61
<212> DNA
<213> Homo sapiens

<400> 380
tatacactga attttgaaga tgtggtttca gaaagtaaag aatatgaaat atctaatgaa 60

t 61

<210> 381
<211> 61
<212> DNA
<213> Homo sapiens

<400> 381
atatttctct gaactgcctg cagcttttac aacatccttc cttcctttta tgcagtggta 60

a 61

<210> 382
<211> 61
<212> DNA
<213> Homo sapiens

<400> 382
atatttctct gaactgcctg cagcttttac gacatccttc cttcctttta tgcagtggta 60

a 61

<210> 383
<211> 61
<212> DNA
<213> Homo sapiens

<400> 383
acccgtcgac atggtctccc tggtgatctc atttacactg acggttttat cgaccacctt 60

t 61

<210> 384
<211> 61
<212> DNA
<213> Homo sapiens

<400> 384
acccgtcgac atggtctccc tggtgatctc gtttacactg acggttttat cgaccacctt 60

t 61

<210> 385
<211> 61
<212> DNA
<213> Homo sapiens

<400> 385
tcccagcttc ccccttcaag gtatatgtcc atgcactaga atatccatca caacactccc 60

c 61

<210> 386
<211> 61
<212> DNA
<213> Homo sapiens

<400> 386
tcccagcttc ccccttcaag gtatatgtcc gtgcactaga atatccatca caacactccc 60

c 61

<210> 387
<211> 61
<212> DNA
<213> Homo sapiens

<400> 387
agaagggaag tataatttca gaggcctggc aataaagcac tggagaaagg atatttggaa 60

a 61

<210> 388
<211> 61
<212> DNA
<213> Homo sapiens

<400> 388
agaagggaag tataatttca gaggcctggc cataaagcac tggagaaagg atatttggaa 60

a 61

<210> 389
<211> 61
<212> DNA
<213> Homo sapiens

<400> 389
aggccactca aagtgcaatc aggaagcata atagatcatc caagttaaag gctttggggc 60

a 61

<210> 390
<211> 61
<212> DNA
<213> Homo sapiens

<400> 390
aggccactca aagtgcaatc aggaagcata ctagatcatc caagttaaag gctttggggc 60

a 61

<210> 391
<211> 61
<212> DNA
<213> Homo sapiens

<400> 391
aatacttgag agttttctaa tctgtcattt atggttgact ttgatgcctt ttgcaaggag 60

g 61

<210> 392
<211> 61

<212> DNA
<213> Homo sapiens

<400> 392
aatacttgag agttttctaa tctgtcattt ctggttgact ttgatgcctt ttgcaaggag 60

g 61

<210> 393
<211> 61
<212> DNA
<213> Homo sapiens

<400> 393
gaacctagaa actgtggctt acaggatgca acctatttga tggaactcat agtcacttct 60

a 61

<210> 394
<211> 61
<212> DNA
<213> Homo sapiens

<400> 394
gaacctagaa actgtggctt acaggatgca gcctatttga tggaactcat agtcacttct 60

a 61

<210> 395
<211> 61
<212> DNA
<213> Homo sapiens

<400> 395
ttcagcacgt tttcttgtga tttgctgatt acccttaaaa gtctagtagc ataagttttc 60

t 61

<210> 396
<211> 61
<212> DNA
<213> Homo sapiens

<400> 396
ttcagcacgt tttcttgtga tttgctgatt tcccttaaaa gtctagtagc ataagttttc 60

t 61

<210> 397
<211> 61
<212> DNA
<213> Homo sapiens

<400> 397
agtgagacag tatattttca ggaaacgtac acaggtccct cacatgaaaa taccggagag 60

c 61

<210> 398
<211> 61
<212> DNA
<213> Homo sapiens

<400> 398
agtgagacag tatattttca ggaaacgtac gcaggtccct cacatgaaaa taccggagag 60

c 61

<210> 399
<211> 61
<212> DNA
<213> Homo sapiens

<400> 399
acttctatta cattcacagc taaatatggc agctttggtt tggaatagac tgtaaaaacc 60

t 61

<210> 400
<211> 61
<212> DNA
<213> Homo sapiens

<400> 400
acttctatta cattcacagc taaatatggc ggctttggtt tggaatagac tgtaaaaacc 60

t 61

<210> 401
<211> 61
<212> DNA
<213> Homo sapiens

<400> 401
atgctctcgc cccgcatctg tgcactgact cggtcctctg catggatgct ctttccttgg 60

a 61

<210> 402
<211> 61
<212> DNA
<213> Homo sapiens

<400> 402
atgctctcgc cccgcatctg tgcactgact gggtcctctg catggatgct ctttccttgg 60

a 61

<210> 403
<211> 61
<212> DNA
<213> Homo sapiens

<400> 403
gctaaaatca atagccattg aagctccact aatgtgttca gttcgctttg aacaatgcaa 60

a 61

<210> 404
<211> 61
<212> DNA
<213> Homo sapiens

<400> 404
gctaaaatca atagccattg aagctccact gatgtgttca gttcgctttg aacaatgcaa 60

a 61

<210> 405
<211> 61
<212> DNA

<213> Homo sapiens

<400> 405
gagtgggcag ttggaaacag ctatgaaacc agcatttagt gatggggcag tagggctggg 60

g 61

<210> 406
<211> 61
<212> DNA
<213> Homo sapiens

<400> 406
gagtgggcag ttggaaacag ctatgaaacc ggcatttagt gatggggcag tagggctggg 60

g 61

<210> 407
<211> 61
<212> DNA
<213> Homo sapiens

<400> 407
ggtgccactg gattgcttaa gatcttcctg agagggaatt tgaacaatac ttagagggct 60

a 61

<210> 408
<211> 61
<212> DNA
<213> Homo sapiens

<400> 408

ggtgccactg gattgcttaa gatcttcctg ggagggaatt tgaacaatac ttagagggct 60

a 61

<210> 409
<211> 61
<212> DNA
<213> Homo sapiens

<400> 409
atgtttttgt aaaagaaact ttcagtattc agagtagttt gtctttcaca gtgcttccat 60

a 61

<210> 410
<211> 61
<212> DNA
<213> Homo sapiens

<400> 410
atgtttttgt aaaagaaact ttcagtattc ggagtagttt gtctttcaca gtgcttccat 60

a 61

<210> 411
<211> 61
<212> DNA
<213> Homo sapiens

<400> 411
ttggttgtgt gaatttagtg cttgtgaggc agtttctttc taggtgctct gcctgtagct 60

a 61

<210> 412
<211> 61
<212> DNA
<213> Homo sapiens

<400> 412
ttggttgtgt gaatttagtg cttgtgaggc ggtttctttc taggtgctct gcctgtagct 60

a 61

<210> 413
<211> 61
<212> DNA
<213> Homo sapiens

<400> 413
aaagacagag tgctgtttga acctagagaa agcaagacca ggcagcttgg gcaggaagtc 60

c 61

<210> 414
<211> 61
<212> DNA
<213> Homo sapiens

<400> 414
aaagacagag tgctgtttga acctagagaa ggcaagacca ggcagcttgg gcaggaagtc 60

c 61

<210> 415

<211> 61
<212> DNA
<213> Homo sapiens

<400> 415
attttataga tatatgaact gaggatcgga aaggcaaagg gactatctta aggtattgct 60

g 61

<210> 416
<211> 61
<212> DNA
<213> Homo sapiens

<400> 416
attttataga tatatgaact gaggatcgga gaggcaaagg gactatctta aggtattgct 60

g 61

<210> 417
<211> 61
<212> DNA
<213> Homo sapiens

<400> 417
tgtgaatggc tgcttggaac acagtgttga aaaggattcc gaggctgtgt ccaggttcag 60

t 61

<210> 418
<211> 61
<212> DNA
<213> Homo sapiens

<400> 418
tgtgaatggc tgcttggaac acagtgttga gaaggattcc gaggctgtgt ccaggttcag 60

t 61

<210> 419
<211> 61
<212> DNA
<213> Homo sapiens

<400> 419
atgtctcctc cccaggtcat cagaataatc aatacttgtc tccaacactg tagaaattgt 60

g 61

<210> 420
<211> 61
<212> DNA
<213> Homo sapiens

<400> 420
atgtctcctc cccaggtcat cagaataatc gatacttgtc tccaacactg tagaaattgt 60

g 61

<210> 421
<211> 61
<212> DNA
<213> Homo sapiens

<400> 421
tcaatcttat cccacactct ggtcatacaa cgtttctaag actgctgctt tttctaaatc 60

c 61

<210> 422
<211> 61
<212> DNA
<213> Homo sapiens

<400> 422
tcaatcttat cccacactct ggtcatacaa ggtttctaag actgctgctt tttctaaatc 60

c 61

<210> 423
<211> 61
<212> DNA
<213> Homo sapiens

<400> 423
agagacttgg taaacaaacc aactaggccc aaccacaaca tgttgaggct gactttctaa 60

c 61

<210> 424
<211> 61
<212> DNA
<213> Homo sapiens

<400> 424
agagacttgg taaacaaacc aactaggccc gaccacaaca tgttgaggct gactttctaa 60

c 61

<210> 425
<211> 61
<212> DNA
<213> Homo sapiens

<400> 425
ctccgccccc tggcacttgg cacccattca atcatacatg tctcagactc ctctgcagcc 60

a 61

<210> 426
<211> 61
<212> DNA
<213> Homo sapiens

<400> 426
ctccgccccc tggcacttgg cacccattca gtcatacatg tctcagactc ctctgcagcc 60

a 61

<210> 427
<211> 61
<212> DNA
<213> Homo sapiens

<400> 427
gcagatggaa gatgccgggc ttttcatttc aaggactgag taggaaggtt aatgatggaa 60

g 61

<210> 428
<211> 61

<212> DNA
<213> Homo sapiens

<400> 428
gcagatggaa gatgccgggc ttttcatttc gaggactgag taggaaggtt aatgatggaa 60

g 61

<210> 429
<211> 61
<212> DNA
<213> Homo sapiens

<400> 429
tgtgcatcct aaaagcagtg acaggttaga cagaactgtg ctagaattct agctgtatta 60

c 61

<210> 430
<211> 61
<212> DNA
<213> Homo sapiens

<400> 430
tgtgcatcct aaaagcagtg acaggttaga gagaactgtg ctagaattct agctgtatta 60

c 61

<210> 431
<211> 61
<212> DNA
<213> Homo sapiens

<400> 431
gacctcagta aatatgttga tggtccagac aaaaatgtgt agataatatc cattcgtgat 60

t 61

<210> 432
<211> 61
<212> DNA
<213> Homo sapiens

<400> 432
gacctcagta aatatgttga tggtccagac gaaaatgtgt agataatatc cattcgtgat 60

t 61

<210> 433
<211> 61
<212> DNA
<213> Homo sapiens

<400> 433
agtgggaccc tgtgaggcaa acatcaccac aaggctggga acagcaggac tcaggcactg 60

c 61

<210> 434
<211> 61
<212> DNA
<213> Homo sapiens

<400> 434
agtgggaccc tgtgaggcaa acatcaccac gaggctggga acagcaggac tcaggcactg 60

c 61

<210> 435
<211> 61
<212> DNA
<213> Homo sapiens

<400> 435
actttgggt tgtagctgcc tatagctgcc aagtagcccc agggagtagt ggaagggcag 60

a 61

<210> 436
<211> 61
<212> DNA
<213> Homo sapiens

<400> 436
actttgggt tgtagctgcc tatagctgcc gagtagcccc agggagtagt ggaagggcag 60

a 61

<210> 437
<211> 61
<212> DNA
<213> Homo sapiens

<400> 437
taccttctgt taaaacttct ttgtctggct aaacccaaaa actttagggg agattgaagt 60

a 61

<210> 438
<211> 61
<212> DNA
<213> Homo sapiens

<400> 438
taccttctgt taaaacttct ttgtctggct gaacccaaaa actttagggg agattgaagt 60

a 61

<210> 439
<211> 61
<212> DNA
<213> Homo sapiens

<400> 439
aagacttttt ttttttttt ggtagaatca acaacttaga tagattgctt acttttcag 60

g 61

<210> 440
<211> 61
<212> DNA
<213> Homo sapiens

<400> 440
aagacttttt ttttttttt ggtagaatca ccaacttaga tagattgctt acttttcag 60

g 61

<210> 441
<211> 61
<212> DNA

<213> Homo sapiens

<400> 441
ggtcagcagg cagagattct gtgacggact aaagctctca agaaaacatc ttaaaacatg 60

t 61

<210> 442
<211> 61
<212> DNA
<213> Homo sapiens

<400> 442
ggtcagcagg cagagattct gtgacggact gaagctctca agaaaacatc ttaaaacatg 60

t 61

<210> 443
<211> 61
<212> DNA
<213> Homo sapiens

<400> 443
caatttgacc ttcttcacag ggctgcttgg aaacctatag agtgatatgg atataactgt 60

g 61

<210> 444
<211> 61
<212> DNA
<213> Homo sapiens

<400> 444

caatttgacc ttcttcacag ggctgcttgg gaacctatag agtgatatgg atataactgt 60

g 61

<210> 445
<211> 61
<212> DNA
<213> Homo sapiens

<400> 445
atgggctagg ccacaagctc ttctcagctc aatctcacaa ttggcagatt aaccaagacc 60

c 61

<210> 446
<211> 61
<212> DNA
<213> Homo sapiens

<400> 446
atgggctagg ccacaagctc ttctcagctc gatctcacaa ttggcagatt aaccaagacc 60

c 61

<210> 447
<211> 61
<212> DNA
<213> Homo sapiens

<400> 447
aaaggaaggg tctctccagc ttgtggacaa aagacctaat ggttcccccg gtgaccctct 60

c 61

<210> 448
<211> 61
<212> DNA
<213> Homo sapiens

<400> 448
aaaggaaggg tctctccagc ttgtggacaa gagacctaat ggttcccccg gtgaccctct 60

c 61

<210> 449
<211> 61
<212> DNA
<213> Homo sapiens

<400> 449
tacttaagca gcacgtgctc ttcatttcaa attcagatgt gtcacctccc aactaacaat 60

a 61

<210> 450
<211> 61
<212> DNA
<213> Homo sapiens

<400> 450
tacttaagca gcacgtgctc ttcatttcaa gttcagatgt gtcacctccc aactaacaat 60

a 61

<210> 451

<211> 61
<212> DNA
<213> Homo sapiens

<400> 451
cacagctgag ctgtgggagg gcagaagtga aggatctttg aaggaaaaga aagtgaatgg 60

a 61

<210> 452
<211> 61
<212> DNA
<213> Homo sapiens

<400> 452
cacagctgag ctgtgggagg gcagaagtga gggatctttg aaggaaaaga aagtgaatgg 60

a 61

<210> 453
<211> 61
<212> DNA
<213> Homo sapiens

<400> 453
gacaggtggc tagataattc tgaggaaaaa atgggaatgt cagtttcatg gagtttcgaa 60

t 61

<210> 454
<211> 61
<212> DNA
<213> Homo sapiens

<400> 454
gacaggtggc tagataattc tgaggaaaaa ttgggaatgt cagtttcatg gagtttcgaa 60

t 61

<210> 455
<211> 61
<212> DNA
<213> Homo sapiens

<400> 455
ttcagatttt ggggtcacac tgcagacacc aggctttctt ttccctccac attttaacat 60

a 61

<210> 456
<211> 61
<212> DNA
<213> Homo sapiens

<400> 456
ttcagatttt ggggtcacac tgcagacacc gggctttctt ttccctccac attttaacat 60

a 61

<210> 457
<211> 61
<212> DNA
<213> Homo sapiens

<400> 457
cggtgctgca ccgtggatgt gagtccttgc acagtggtga aatgtagtag aggagtgatc 60

t 61

<210> 458
<211> 61
<212> DNA
<213> Homo sapiens

<400> 458
cggtgctgca ccgtggatgt gagtccttgc gcagtggtga aatgtagtag aggagtgatc 60

t 61

<210> 459
<211> 61
<212> DNA
<213> Homo sapiens

<400> 459
gagtgcctgg ctggtgacag gggagaaaag aagaacgggt ctgcaggtgg aaagaggtgt 60

t 61

<210> 460
<211> 61
<212> DNA
<213> Homo sapiens

<400> 460
gagtgcctgg ctggtgacag gggagaaaag gagaacgggt ctgcaggtgg aaagaggtgt 60

t 61

<210> 461
<211> 61
<212> DNA
<213> Homo sapiens

<400> 461
caaggggtag aatctatgga aggaagcgag agcatgtcat aaaatctcag tgagacatta 60

a 61

<210> 462
<211> 61
<212> DNA
<213> Homo sapiens

<400> 462
caaggggtag aatctatgga aggaagcgag ggcatgtcat aaaatctcag tgagacatta 60

a 61

<210> 463
<211> 61
<212> DNA
<213> Homo sapiens

<400> 463
actctacttc cttcctgttt aactgtacca acttcttccc tctgactcaa attcatgagc 60

t 61

<210> 464
<211> 61

<212> DNA
<213> Homo sapiens

<400> 464
actctacttc cttcctgttt aactgtacca gcttcttccc tctgactcaa attcatgagc 60

t 61

<210> 465
<211> 61
<212> DNA
<213> Homo sapiens

<400> 465
ctgctcattg taacaagctt tagcataggc ataggttgat aatggatgta ggcatggggt 60

t 61

<210> 466
<211> 61
<212> DNA
<213> Homo sapiens

<400> 466
ctgctcattg taacaagctt tagcataggc gtaggttgat aatggatgta ggcatggggt 60

t 61

<210> 467
<211> 61
<212> DNA
<213> Homo sapiens

<400> 467
ctctattcaa taaatggtgc tgggataatg agttagacgt atacagaagg gtgaacctgg 60

a 61

<210> 468
<211> 61
<212> DNA
<213> Homo sapiens

<400> 468
ctctattcaa taaatggtgc tgggataatg ggttagacgt atacagaagg gtgaacctgg 60

a 61

<210> 469
<211> 61
<212> DNA
<213> Homo sapiens

<400> 469
ctaattctca ccaatggaat gtgtgtggaa ataatgcgtc tccttcaggc tgaggcagtt 60

a 61

<210> 470
<211> 61
<212> DNA
<213> Homo sapiens

<400> 470
ctaattctca ccaatggaat gtgtgtggaa gtaatgcgtc tccttcaggc tgaggcagtt 60

a 61

<210> 471
<211> 61
<212> DNA
<213> Homo sapiens

<400> 471
aactcttaat aaacattcac tgttcaatgg atagtcatca tagtgattga cactgcatat 60

t 61

<210> 472
<211> 61
<212> DNA
<213> Homo sapiens

<400> 472
aactcttaat aaacattcac tgttcaatgg gtagtcatca tagtgattga cactgcatat 60

t 61

<210> 473
<211> 61
<212> DNA
<213> Homo sapiens

<400> 473
agaaatgcag attctcgggt ccaaccgcca aacttactaa atcagaaacc ctgagaacgg 60

c 61

<210> 474
<211> 61
<212> DNA
<213> Homo sapiens

<400> 474
agaaatgcag attctcgggt ccaaccgcca gacttactaa atcagaaacc ctgagaacgg 60

c 61

<210> 475
<211> 61
<212> DNA
<213> Homo sapiens

<400> 475
gcttgagcca ccgtgcccag cctcagagtc agtgattttt aagtctccaa ccccaacatg 60

c 61

<210> 476
<211> 61
<212> DNA
<213> Homo sapiens

<400> 476
gcttgagcca ccgtgcccag cctcagagtc ggtgattttt aagtctccaa ccccaacatg 60

c 61

<210> 477
<211> 61
<212> DNA

<213> Homo sapiens

<400> 477
ccctttttctt tcttgttctt tttaagactc aatctcaaat ctgcaaccta cctaccataa 60

g 61

<210> 478
<211> 61
<212> DNA
<213> Homo sapiens

<400> 478
ccctttttctt tcttgttctt tttaagactc gatctcaaat ctgcaaccta cctaccataa 60

g 61

<210> 479
<211> 61
<212> DNA
<213> Homo sapiens

<400> 479
acacatgctt aatatgaatg ctttaatcaa atcataatca gatggtactt gccctaccta 60

a 61

<210> 480
<211> 61
<212> DNA
<213> Homo sapiens

<400> 480

acacatgctt aatatgaatg ctttaatcaa ttcataatca gatggtactt gccctaccta 60

a 61

<210> 481
<211> 61
<212> DNA
<213> Homo sapiens

<400> 481
ttggattggt actttccatt accaactgat agcttttaga ccattgtcca aattacccat 60

a 61

<210> 482
<211> 61
<212> DNA
<213> Homo sapiens

<400> 482
ttggattggt actttccatt accaactgat tgcttttaga ccattgtcca aattacccat 60

a 61

<210> 483
<211> 61
<212> DNA
<213> Homo sapiens

<400> 483
tgaggctgtc ttgagacttg actgatagaa acgcccagtg aactgtgaaa gctccagcag 60

c 61

<210> 484
<211> 61
<212> DNA
<213> Homo sapiens

<400> 484
tgaggctgtc ttgagacttg actgatagaa gcgcccagtg aactgtgaaa gctccagcag 60

c 61

<210> 485
<211> 61
<212> DNA
<213> Homo sapiens

<400> 485
ctttttttcta tttctttcct ttctacatac ataacacaga tcacacatat atatccatac 60

t 61

<210> 486
<211> 61
<212> DNA
<213> Homo sapiens

<400> 486
ctttttttcta tttctttcct ttctacatac gtaacacaga tcacacatat atatccatac 60

t 61

<210> 487

<211> 61
<212> DNA
<213> Homo sapiens

<400> 487
agactatgct tttttcattg aatcgccttt ctgtgttttt cataaatcag ttgactacat 60

t 61

<210> 488
<211> 61
<212> DNA
<213> Homo sapiens

<400> 488
agactatgct tttttcattg aatcgccttt gtgtgttttt cataaatcag ttgactacat 60

t 61

<210> 489
<211> 61
<212> DNA
<213> Homo sapiens

<400> 489
gtcactcagt gagcaagagg ttgatttttt aaacttcatg acaactatga cattatgctg 60

t 61

<210> 490
<211> 61
<212> DNA
<213> Homo sapiens

<400> 490
gtcactcagt gagcaagagg ttgatttttt gaacttcatg acaactatga cattatgctg 60

t 61

<210> 491
<211> 61
<212> DNA
<213> Homo sapiens

<400> 491
gaataacaga agaatgcaca cacattccaa ataagggcct ttctcacaaa cacatcagaa 60

g 61

<210> 492
<211> 61
<212> DNA
<213> Homo sapiens

<400> 492
gaataacaga agaatgcaca cacattccaa gtaagggcct ttctcacaaa cacatcagaa 60

g 61

<210> 493
<211> 61
<212> DNA
<213> Homo sapiens

<400> 493
atagatgtag tatccagttc tgatgtcagg attagagaaa ttatctttgg ctaaggttat 60

c 61

<210> 494
<211> 61
<212> DNA
<213> Homo sapiens

<400> 494
atagatgtag tatccagttc tgatgtcagg gttagagaaa ttatctttgg ctaaggttat 60

c 61

<210> 495
<211> 61
<212> DNA
<213> Homo sapiens

<400> 495
aatatacaca taacctaaca tccactaaaa acaacagaaa tgtccactaa gagaatacta 60

g 61

<210> 496
<211> 61
<212> DNA
<213> Homo sapiens

<400> 496
aatatacaca taacctaaca tccactaaaa ccaacagaaa tgtccactaa gagaatacta 60

g 61

<210> 497
<211> 61
<212> DNA
<213> Homo sapiens

<400> 497
ggaggaggta gcttgaacta ggatgacggc agtgggaata aaaagagttg gatgaattca 60

a 61

<210> 498
<211> 61
<212> DNA
<213> Homo sapiens

<400> 498
ggaggaggta gcttgaacta ggatgacggc ggtgggaata aaaagagttg gatgaattca 60

a 61

<210> 499
<211> 61
<212> DNA
<213> Homo sapiens

<400> 499
ttccagtgtc ttgggaatgc agcctgttac actgtgtatt cgtgtgctgg ataagttcaa 60

a 61

<210> 500
<211> 61

<212> DNA
<213> Homo sapiens

<400> 500
ttccagtgtc ttgggaatgc agcctgttac gctgtgtatt cgtgtgctgg ataagttcaa 60

a 61

<210> 501
<211> 61
<212> DNA
<213> Homo sapiens

<400> 501
aatatatcaa agacatgtag ctaaaaagat attcctacat cctcactggt gaacacaaag 60

t 61

<210> 502
<211> 61
<212> DNA
<213> Homo sapiens

<400> 502
aatatatcaa agacatgtag ctaaaaagat cttcctacat cctcactggt gaacacaaag 60

t 61

<210> 503
<211> 61
<212> DNA
<213> Homo sapiens

<400> 503
ataaatactc tctggaaaaa tctaccttca atctaggcct tgaacagctc acacagataa 60

a 61

<210> 504
<211> 61
<212> DNA
<213> Homo sapiens

<400> 504
ataaatactc tctggaaaaa tctaccttca gtctaggcct tgaacagctc acacagataa 60

a 61

<210> 505
<211> 61
<212> DNA
<213> Homo sapiens

<400> 505
gagacattca gtcttgtctt aagtcatata ctagctatcc aacttagaga atgtctcaaa 60

t 61

<210> 506
<211> 61
<212> DNA
<213> Homo sapiens

<400> 506
gagacattca gtcttgtctt aagtcatata gtagctatcc aacttagaga atgtctcaaa 60

t 61

<210> 507
<211> 61
<212> DNA
<213> Homo sapiens

<400> 507
acagcaaaag cagatggaag ggaggttaat attatgacat aggaaataat gtagtatcaa 60

t 61

<210> 508
<211> 61
<212> DNA
<213> Homo sapiens

<400> 508
acagcaaaag cagatggaag ggaggttaat gttatgacat aggaaataat gtagtatcaa 60

t 61

<210> 509
<211> 61
<212> DNA
<213> Homo sapiens

<400> 509
tctcttttcc tggaaactcc accaggaagc agtgccatag accccaaaga catccaggtc 60

a 61

<210> 510
<211> 61
<212> DNA
<213> Homo sapiens

<400> 510
tctcttttcc tggaaactcc accaggaagc cgtgccatag accccaaaga catccaggtc 60

a 61

<210> 511
<211> 61
<212> DNA
<213> Homo sapiens

<400> 511
gcctatgggc tgccttcctg aaaactatct agcttgtggt tacatgaagc cagagtccac 60

t 61

<210> 512
<211> 61
<212> DNA
<213> Homo sapiens

<400> 512
gcctatgggc tgccttcctg aaaactatct ggcttgtggt tacatgaagc cagagtccac 60

t 61

<210> 513
<211> 61
<212> DNA

<213> Homo sapiens

<400> 513
gcaaacagat gaattcagcc cctccaaacc aagcgcggag cgcgctgctt ttgtgcgcca 60

g 61

<210> 514
<211> 61
<212> DNA
<213> Homo sapiens

<400> 514
gcaaacagat gaattcagcc cctccaaacc gagcgcggag cgcgctgctt ttgtgcgcca 60

g 61

<210> 515
<211> 50
<212> DNA
<213> Homo sapiens

<400> 515
cagacttctt gaatgtatcc ccagttaaca gcacagcgtt tatctagcag 50

<210> 516
<211> 50
<212> DNA
<213> Homo sapiens

<400> 516
aacctgaggc aggatttcat actgttctta actgtactga tagctcttct 50

<210> 517
<211> 50
<212> DNA
<213> Homo sapiens

<400> 517
atttggctct ttaccctgac caaagacttc tgggcttgag taagctgagt 50

<210> 518
<211> 50
<212> DNA
<213> Homo sapiens

<400> 518
tgagttagtt actccaggag tgggttcctg gtaaaatggt aggtttagta 50

<210> 519
<211> 50
<212> DNA
<213> Homo sapiens

<400> 519
tgatgctctt cagtgaaggt atctaagtaa ggttagaaat gcttcggcct 50

<210> 520
<211> 50
<212> DNA
<213> Homo sapiens

<400> 520
taggctctcc tgttagactg catgggctcc agttctggct ccagcagtga 50

<210> 521
<211> 50
<212> DNA
<213> Homo sapiens

<400> 521
aaaattcccc cagattgaaa gcaaaaccag taaatctaac tgcaattgtg 50

<210> 522
<211> 50
<212> DNA
<213> Homo sapiens

<400> 522
tcaatcagac ctcccagggt ttcagatggg tagaagctgc tctcagaaag 50

<210> 523
<211> 50
<212> DNA
<213> Homo sapiens

<400> 523
gaggatcatt ctcttgaaga aagaagaaaa accactgtaa tcttcgcttg 50

<210> 524
<211> 50
<212> DNA
<213> Homo sapiens

<400> 524
attcagtttg ctaaaggccc attagccatg aacactaaag aaatagcctg 50

<210> 525
<211> 50
<212> DNA
<213> Homo sapiens

<400> 525
gaggaggttc tctttttagc tgattcctca taaaaggata agatttagct 50

<210> 526
<211> 50
<212> DNA
<213> Homo sapiens

<400> 526
gtaggaacgt atctatacaa taccaaagtg gctgtagccc cagggaatta 50

<210> 527
<211> 50
<212> DNA
<213> Homo sapiens

<400> 527
aaagatctta tcaaagcttc aagttcctat accgtgaagc tggccaaaac 50

<210> 528
<211> 50
<212> DNA
<213> Homo sapiens

<400> 528
taaattagac cttttctctc gccactgcca ccactcctgc agattgttcc 50

<210> 529
<211> 50
<212> DNA
<213> Homo sapiens

<400> 529
gtggttccat ggaatttccc acttttctca taataaaacc tttattgctc 50

<210> 530
<211> 50
<212> DNA
<213> Homo sapiens

<400> 530
gtgagtcctg ggtgcacttg tgacctgtcc ttgtgacttg gaaaaaatgc 50

<210> 531
<211> 50
<212> DNA
<213> Homo sapiens

<400> 531
ttaaaaaata gtgtttggcc tgattttgct gttggatggg gccatccaag 50

<210> 532
<211> 50
<212> DNA
<213> Homo sapiens

<400> 532
ctattataat gctactcaac ctgtactttt atatacgcct aatttgttcc 50

<210> 533
<211> 50
<212> DNA
<213> Homo sapiens

<400> 533
cagacttctt gaatgtatcc ccagttaaca gcacagcgtt tatctagcac 50

<210> 534
<211> 50
<212> DNA
<213> Homo sapiens

<400> 534
tgagttagtt actccaggag tgggttcctg gtaaaatggt aggtttagtt 50

<210> 535
<211> 50
<212> DNA
<213> Homo sapiens

<400> 535
gtgagtcctg ggtgcacttg tgacctgtcc ttgtgacttg gaaaaaatgg 50

<210> 536
<211> 50
<212> DNA
<213> Homo sapiens

<400> 536
gataagggac ctcccacaca ccccaaaagt ggtttataaa acattgactc 50

<210> 537
<211> 50
<212> DNA
<213> Homo sapiens

<400> 537
tttataaaac attgactcca catcactgta gttaacccaa accaaaagac 50

<210> 538
<211> 50
<212> DNA
<213> Homo sapiens

<400> 538
ggctgaagag ccccataccc ggtatgctgt ctctgaacta tggaatatgc 50

<210> 539
<211> 50
<212> DNA
<213> Homo sapiens

<400> 539
aaaaaaggga aatcctgcca tttgcaacca gtgtgcatga aactggagga 50

<210> 540
<211> 50
<212> DNA
<213> Homo sapiens

<400> 540
agaatttggt gaatgaatct tttcaaaatt aattttcaaa tttctactgg 50

<210> 541
<211> 50
<212> DNA
<213> Homo sapiens

<400> 541
tcataggatg ggagtactca gcaatagaga gaaatgagct tctgaaatgc 50

<210> 542
<211> 50
<212> DNA
<213> Homo sapiens

<400> 542
gctatgttag aagggtgtct tctgctcaac cagttctttt gcttcctctg 50

<210> 543
<211> 50
<212> DNA
<213> Homo sapiens

<400> 543
taaatctggg aggtcagttt ttgactttat atggggatgg aggccgcctc 50

<210> 544
<211> 50
<212> DNA
<213> Homo sapiens

<400> 544
ggtggattca gttgcataac tcacttttca aggtgattgc tattcattca 50

<210> 545
<211> 50
<212> DNA
<213> Homo sapiens

<400> 545
ctcctcagaa acaagagcca ttaggcctcc taacaagatg gaactagatg 50

<210> 546
<211> 50
<212> DNA
<213> Homo sapiens

<400> 546
acctgccttg acacgccatg aacctgttac tctcgggtgc tctgtggtga 50

<210> 547
<211> 50
<212> DNA
<213> Homo sapiens

<400> 547
ggctggggct gcagcctagt cccatcatca agcttcctac agagcttagc 50

<210> 548
<211> 50
<212> DNA
<213> Homo sapiens

<400> 548
ctgacagcct aggggacagg gccatggctg agttgactgg gttcagattc 50

<210> 549
<211> 50
<212> DNA
<213> Homo sapiens

<400> 549
ctggagacac tgctaagagt acaagttgca gagaaacctt taataattac 50

<210> 550
<211> 50
<212> DNA
<213> Homo sapiens

<400> 550
ggtaccagag atgagaactt caacattatc tttctgaggg atacaactca 50

<210> 551
<211> 50
<212> DNA
<213> Homo sapiens

<400> 551
ttgtgtcagc atgtcttgga gcgatccact tagtatgaga ttaatgcctt 50

<210> 552
<211> 50
<212> DNA
<213> Homo sapiens

<400> 552
cagttattgc cccaggttct ttttcataag acattatact ctagccatga 50

<210> 553
<211> 50
<212> DNA
<213> Homo sapiens

<400> 553
gtgctgtgag attctgctgg atgggggcag ctgatgaccc tttgctcctc 50

<210> 554
<211> 50
<212> DNA
<213> Homo sapiens

<400> 554
tcggggtaac ctcttggcat cagttacatg ttggatcaca gtgaggttgt 50

<210> 555
<211> 50
<212> DNA
<213> Homo sapiens

<400> 555
gataaatagt ggatgcctga agagctatgt tggggaagat ggtgaagcca 50

<210> 556
<211> 50
<212> DNA
<213> Homo sapiens

<400> 556
tccacgctag ggacttgcct gcctctgccg cagcgcagat ctgatgcggt 50

<210> 557
<211> 50
<212> DNA
<213> Homo sapiens

<400> 557
ttcaccttga agattgcagt tggcttccaa ctggcctcta aactctaatc 50

<210> 558
<211> 50
<212> DNA
<213> Homo sapiens

<400> 558
cactagacat tatgtagagc tttagtcatg ggcaattagt aagcattaac 50

<210> 559
<211> 50
<212> DNA
<213> Homo sapiens

<400> 559
acatcattga gcaactcttc cttccatagg tcaggctgac tatgctttta 50

<210> 560
<211> 50
<212> DNA
<213> Homo sapiens

<400> 560
tgtgctggtc aaacctggac catatacttg ttctcaaacc attcactagc 50

<210> 561
<211> 50
<212> DNA
<213> Homo sapiens

<400> 561
ttaagtttgc tttctaagtt atctggtaaa aattttcata agcattagac 50

<210> 562
<211> 50
<212> DNA
<213> Homo sapiens

<400> 562
acgtacagaa tgggattctt aagagagcct ctaggttagc gccgctgaac 50

<210> 563
<211> 50
<212> DNA
<213> Homo sapiens

<400> 563
tatgagcact taccagccac tgtcctatgc cctctcgttg aatgctcaca 50

<210> 564
<211> 50
<212> DNA
<213> Homo sapiens

<400> 564
tagcatcgcc acatcactga gtagggcatt tgatttaatc accaagagcc 50

<210> 565
<211> 50
<212> DNA
<213> Homo sapiens

<400> 565
gataggaagt ctcagaacct cttctccgcc tattagtcat gtttggattt 50

<210> 566
<211> 50
<212> DNA
<213> Homo sapiens

<400> 566
aacttgtatt tgccatttga gtgtaacagc ttcctgatcc ttacacaaaa 50

<210> 567
<211> 50
<212> DNA
<213> Homo sapiens

<400> 567
tactacagga gataccactt tccccttatc agactggcaa atagccaaaa 50

<210> 568
<211> 50
<212> DNA
<213> Homo sapiens

<400> 568
ctgctagcac ttatcacaca tcttgagaag ggaacacttg ataaaatctc 50

<210> 569
<211> 50
<212> DNA
<213> Homo sapiens

<400> 569
tcttgaaaag gacattacgt tcctggcaat taagtcaaac cttaagctac 50

<210> 570
<211> 50
<212> DNA
<213> Homo sapiens

<400> 570
agctcttttc cttgtgctgt gatgttgctg tatcgctcag atctaatgtt 50

<210> 571
<211> 50
<212> DNA
<213> Homo sapiens

<400> 571
atgaggaata gttatatact gttaagaata taaacctgaa atgtcaactg 50

<210> 572
<211> 50
<212> DNA
<213> Homo sapiens

<400> 572
acagtgcgga aagaggcaac tattccagga ggcaggggt atagagtggg 50

<210> 573
<211> 50
<212> DNA
<213> Homo sapiens

<400> 573
taacactctt aaatattttg agcgatgctg cagtgttaat tcacatcatt 50

<210> 574
<211> 50
<212> DNA
<213> Homo sapiens

<400> 574
cacttatttc tcatggagat cacacacttg tatctgtctc tcttttcacc 50

<210> 575
<211> 50
<212> DNA
<213> Homo sapiens

<400> 575
gacaagcctg cacccttcc acagttctga actccttccc tgtggtatct 50

<210> 576
<211> 50
<212> DNA
<213> Homo sapiens

<400> 576
cctgtattca ctcccaaaac tgtgctgggc acacagtggg tgcctaatgt 50

<210> 577
<211> 50
<212> DNA
<213> Homo sapiens

<400> 577
ctggcctcag ccctgcccct aaacatcttt ttccttaaag cagctgaaat 50

<210> 578
<211> 50
<212> DNA
<213> Homo sapiens

<400> 578
atgatagcta ctgaaaactt ggaagggaac ctgagtatga gaaggacaga 50

<210> 579
<211> 50
<212> DNA
<213> Homo sapiens

<400> 579
agagtgagaa tttgagccaa aatatctctg aatctagacc ttgagctgtt 50

<210> 580
<211> 50
<212> DNA
<213> Homo sapiens

<400> 580
gaatctagac cttgagctgt aaactattct actaaattta aaatgaggac 50

<210> 581
<211> 50
<212> DNA
<213> Homo sapiens

<400> 581
ctcacactaa aatattcatt aagtaggcac atacccacat tctttgggtg 50

<210> 582
<211> 50
<212> DNA
<213> Homo sapiens

<400> 582
gtatagctag tgattaccag agtgctttga aatcaagcag aacactcatc 50

<210> 583
<211> 50
<212> DNA
<213> Homo sapiens

<400> 583
gtctcttcca gggcctagca aagtgttaga catcaaactg atgcttgaaa 50

<210> 584
<211> 50
<212> DNA
<213> Homo sapiens

<400> 584
agctgatgcc aaatgtcccc tagggagcaa caccatggtg gtagagaacc 50

<210> 585
<211> 50
<212> DNA
<213> Homo sapiens

<400> 585
ggagttgtca gccctttcag aatcacaggc tagactatta gtgaaggtct 50

<210> 586
<211> 50
<212> DNA
<213> Homo sapiens

<400> 586
ccaacttttg ccaccatggg tacgcaccag gcagtgaggg aaaaggagca 50

<210> 587
<211> 50
<212> DNA
<213> Homo sapiens

<400> 587
cagtgcctgg ctggtttaga gacacacagg ttatgtcact ctgatgtgca 50

<210> 588
<211> 50
<212> DNA
<213> Homo sapiens

<400> 588
gtacaaagct cattataaca caatgtgagc tgcacattgt aaacaccagc 50

<210> 589
<211> 50
<212> DNA
<213> Homo sapiens

<400> 589
tatagatgca taactacaat attttcctct gtcttcaccc ggcattcccg 50

<210> 590
<211> 50
<212> DNA
<213> Homo sapiens

<400> 590
acaccaaatg atggccagta tgcaaagaaa atgaatcact catgggtata 50

<210> 591
<211> 50
<212> DNA
<213> Homo sapiens

<400> 591
attatacgcc attgtcgctg ccaatcatac accaagaaca tggtcttaca 50

<210> 592
<211> 50
<212> DNA
<213> Homo sapiens

<400> 592
acttcttttc ttttgtgtac actctcttct tcggctatgc tgtgctctaa 50

<210> 593
<211> 50
<212> DNA
<213> Homo sapiens

<400> 593
ctccctcaaa gcacaaacat ctgtgaaagc agaggctcga gggaccattc 50

<210> 594
<211> 50
<212> DNA
<213> Homo sapiens

<400> 594
aggaatttta agacagtgcg agaatcattc tttctccttc ctactccttc 50

<210> 595
<211> 50
<212> DNA
<213> Homo sapiens

<400> 595
ccagttccca acaagttcct catctccacc tgagaacgtc ttatcctgaa 50

<210> 596
<211> 50
<212> DNA
<213> Homo sapiens

<400> 596
atgttatgtc ctctttacta acacagaact atagaatgca tgggccagaa 50

<210> 597
<211> 50
<212> DNA
<213> Homo sapiens

<400> 597
aatgaggcag catttgggta tttcttgtaa taaagttcct ctgcattgca 50

<210> 598
<211> 50
<212> DNA
<213> Homo sapiens

<400> 598
tctctgtcta tcttaacaga aagctgacct gtgagggctt ctttagggtc 50

<210> 599
<211> 50
<212> DNA
<213> Homo sapiens

<400> 599
acccacgtgg caaagaactg taggtggttt gtaggagttg agagcctcag 50

<210> 600
<211> 50
<212> DNA
<213> Homo sapiens

<400> 600
acctgttggg aaatatctct cccttgtatt acacatgaat tattatttgg 50

<210> 601
<211> 50
<212> DNA
<213> Homo sapiens

<400> 601
gctaaataat agcatgtaat tacttttttа attagaataa tactgccagc 50

<210> 602
<211> 50
<212> DNA
<213> Homo sapiens

<400> 602
taactttctc tcttggtcca attggaatta taacaagcaa gacccctggc 50

<210> 603
<211> 50
<212> DNA
<213> Homo sapiens

<400> 603
cctctgtttt gtattattac aatttaaaat gaggaaagct atgtagtcat 50

<210> 604
<211> 50
<212> DNA
<213> Homo sapiens

<400> 604
taacagctaa cacgtgctct gggccttggt ttccaaagct ttcttacatc 50

<210> 605
<211> 50
<212> DNA
<213> Homo sapiens

<400> 605
aaattctttt ggcttttgta tgtctaaaaa gggtccctgt tttgccttcc 50

<210> 606
<211> 50
<212> DNA
<213> Homo sapiens

<400> 606
agatgtaccc aagtgtaaaa tatacactga attttgaaga tgtggtttca 50

<210> 607
<211> 50
<212> DNA
<213> Homo sapiens

<400> 607
cccggccgcc tttttcaata atatttctct gaactgcctg cagcttttac 50

<210> 608
<211> 50
<212> DNA
<213> Homo sapiens

<400> 608
agtttagggc cagtcagcat aaaggtggtc gataaaaccg tcagtgtaaa 50

<210> 609
<211> 50
<212> DNA
<213> Homo sapiens

<400> 609
ttctttaggc aggtcaatgt ggggagtgtt gtgatggata ttctagtgca 50

<210> 610
<211> 50
<212> DNA
<213> Homo sapiens

<400> 610
gggccccttt ccaatgttat tttccaaata tcctttctcc agtgctttat 50

<210> 611
<211> 50
<212> DNA
<213> Homo sapiens

<400> 611
aattttatct ttcttccctg tgccccaaag cctttaactt ggatgatcta 50

<210> 612
<211> 50
<212> DNA
<213> Homo sapiens

<400> 612
gggctatcca caggccaagg aatacttgag agttttctaa tctgtcattt 50

<210> 613
<211> 50
<212> DNA
<213> Homo sapiens

<400> 613
gtaggtgcca tctttttcta tagaagtgac tatgagttcc atcaaatagg 50

<210> 614
<211> 50
<212> DNA
<213> Homo sapiens

<400> 614
gtctaaaaaa ctgttaatga gaaaacttat gctactagac ttttaagggt 50

<210> 615
<211> 50
<212> DNA
<213> Homo sapiens

<400> 615
ctctttcttg ctggaccctg agtgagacag tatattttca ggaaacgtac 50

<210> 616
<211> 50
<212> DNA
<213> Homo sapiens

<400> 616
gggtataggg gaaggaacaa acttctatta cattcacagc taaatatggc 50

<210> 617
<211> 50
<212> DNA
<213> Homo sapiens

<400> 617
gcttttcttt atgctaggca tgctctcgcc ccgcatctgt gcactgactc 50

<210> 618
<211> 50
<212> DNA
<213> Homo sapiens

<400> 618
gtatccttaa atatccattg gctaaaatca atagccattg aagctccact 50

<210> 619
<211> 50
<212> DNA
<213> Homo sapiens

<400> 619
tgagcaagtt tgcttcccct ccccagccct actgccccat cactaaatgc 50

<210> 620
<211> 50
<212> DNA
<213> Homo sapiens

<400> 620
tgaagacact ctattgagag tagccctcta agtattgttc aaattccctc 50

<210> 621
<211> 50
<212> DNA
<213> Homo sapiens

<400> 621
aaacttcttt aaacttggaa atgtttttgt aaaagaaact ttcagtattc 50

<210> 622
<211> 50
<212> DNA
<213> Homo sapiens

<400> 622
gtcacgatag tagcacaccc tagctacagg cagagcacct agaaagaaac 50

<210> 623
<211> 50
<212> DNA
<213> Homo sapiens

<400> 623
cagcacgctg agatgggatg aaagacagag tgctgtttga acctagagaa 50

<210> 624
<211> 50
<212> DNA
<213> Homo sapiens

<400> 624
aatatctgcc ccagtatctg cagcaatacc ttaagatagt ccctttgcct 50

<210> 625
<211> 50
<212> DNA
<213> Homo sapiens

<400> 625
tccttccaca ttagtttaaa tgtgaatggc tgcttggaac acagtgttga 50

<210> 626
<211> 50
<212> DNA
<213> Homo sapiens

<400> 626
caaatgactc ttttaagttg atgtctcctc cccaggtcat cagaataatc 50

<210> 627
<211> 50
<212> DNA
<213> Homo sapiens

<400> 627
catttaatta cttcttgctt caatcttatc ccacactctg gtcatacaac 50

<210> 628
<211> 50
<212> DNA
<213> Homo sapiens

<400> 628
gatgtggaat atgctagctt gttagaaagt cagcctcaac atgttgtggt 50

<210> 629
<211> 50
<212> DNA
<213> Homo sapiens

<400> 629
ctaaattaca gccagacctc tggctgcaga ggagtctgag acatgtatga 50

<210> 630
<211> 50
<212> DNA
<213> Homo sapiens

<400> 630
atcatcataa ataacgtgga gcagatggaa gatgccgggc ttttcatttc 50

<210> 631
<211> 50
<212> DNA
<213> Homo sapiens

<400> 631
aagcattagg gacaattggt gtgcatccta aaagcagtga caggttagac 50

<210> 632
<211> 50
<212> DNA
<213> Homo sapiens

<400> 632
gaggaggagg taaaggagag gacctcagta aatatgttga tggtccagac 50

<210> 633
<211> 50
<212> DNA
<213> Homo sapiens

<400> 633
ggtagttccc caaggactcg agtgggaccc tgtgaggcaa acatcaccac 50

<210> 634
<211> 50
<212> DNA
<213> Homo sapiens

<400> 634
aggtcttgca gccctgggag acttttgggt tgtagctgcc tatagctgcc 50

<210> 635
<211> 50
<212> DNA
<213> Homo sapiens

<400> 635
aaaagagtga ccattgggct taccttctgt taaaacttct ttgtctggct 50

<210> 636
<211> 50
<212> DNA
<213> Homo sapiens

<400> 636
aaaggaaatt tatttttct cctgaaaaag taagcaatct atctaagttg 50

<210> 637
<211> 50
<212> DNA
<213> Homo sapiens

<400> 637
gtaatagcat tctccattcc acatgtttta agatgttttc ttgagagctt 50

<210> 638
<211> 50
<212> DNA
<213> Homo sapiens

<400> 638
catctgtgaa ctgggagtaa caatttgacc ttcttcacag ggctgcttgg 50

<210> 639
<211> 50
<212> DNA
<213> Homo sapiens

<400> 639
tccagtttct ggttaactgt gggtcttggt taatctgcca attgtgagat 50

<210> 640
<211> 50
<212> DNA
<213> Homo sapiens

<400> 640
gactgtgccc tgtgtgtatc aaaggaaggg tctctccagc ttgtggacaa 50

<210> 641
<211> 50
<212> DNA
<213> Homo sapiens

<400> 641
atgctgaaga accttaagca tacttaagca gcacgtgctc ttcatttcaa 50

<210> 642
<211> 50
<212> DNA
<213> Homo sapiens

<400> 642
ttgtgggatg aaaagatggt cacagctgag ctgtgggagg gcagaagtga 50

<210> 643
<211> 50
<212> DNA
<213> Homo sapiens

<400> 643
ggggaaagag aaaagaaaga ttcgaaactc catgaaactg acattcccat 50

<210> 644
<211> 50
<212> DNA
<213> Homo sapiens

<400> 644
atctgtagag acttgccaga tatgttaaaa tgtggaggga aaagaaagcc 50

<210> 645
<211> 50
<212> DNA
<213> Homo sapiens

<400> 645
cacagcatga gagttgctcc agatcactcc tctactacat ttcaccactg 50

<210> 646
<211> 50
<212> DNA
<213> Homo sapiens

<400> 646
tcacaggcag ggcacaccta aacacctctt tccacctgca gacccgttct 50

<210> 647
<211> 50
<212> DNA
<213> Homo sapiens

<400> 647
gagatgaccc caaaggttaa ttaatgtctc actgagattt tatgacatgc 50

<210> 648
<211> 50
<212> DNA
<213> Homo sapiens

<400> 648
gaaaaaggct ttgacttcca actctacttc cttcctgttt aactgtacca 50

<210> 649
<211> 50
<212> DNA
<213> Homo sapiens

<400> 649
gtgaatgggc aaggcattct aaccccatgc ctacatccat tatcaaccta 50

<210> 650
<211> 50
<212> DNA
<213> Homo sapiens

<400> 650
tatattgtaa aaagaagaag tccaggttca cccttctgta tacgtctaac 50

<210> 651
<211> 50
<212> DNA
<213> Homo sapiens

<400> 651
ccccaatagt ccttgtctct taactgcctc agcctgaagg agacgcatta 50

<210> 652
<211> 50
<212> DNA
<213> Homo sapiens

<400> 652
actgtgccca aaacatagca aactcttaat aaacattcac tgttcaatgg 50

<210> 653
<211> 50
<212> DNA
<213> Homo sapiens

<400> 653
gttaaaacac agattgccag gccgttctca gggtttctga tttagtaagt 50

<210> 654
<211> 50
<212> DNA
<213> Homo sapiens

<400> 654
gccacaactt acagaattta gcatgttggg gttggagact taaaaatcac 50

<210> 655
<211> 50
<212> DNA
<213> Homo sapiens

<400> 655
ttttttgaga gaagaagggg cttatggtag gtaggttgca gatttgagat 50

<210> 656
<211> 50
<212> DNA
<213> Homo sapiens

<400> 656
tttcacagtg gagttgctat taggtagggc aagtaccatc tgattatgat 50

<210> 657
<211> 50
<212> DNA
<213> Homo sapiens

<400> 657
aatccaaaac acccagcatt atgggtaatt tggacaatgg tctaaaagct 50

<210> 658
<211> 50
<212> DNA
<213> Homo sapiens

<400> 658
gcagggagac agcatgtgtg tgaggctgtc ttgagacttg actgatagaa 50

<210> 659
<211> 50
<212> DNA
<213> Homo sapiens

<400> 659
acacctctgt ttagcagtga agtatggata tatatgtgtg atctgtgtta 50

<210> 660
<211> 50
<212> DNA
<213> Homo sapiens

<400> 660
cccagaaatc aacccataca atgtagtcaa ctgatttatg aaaaacacag 50

<210> 661
<211> 50
<212> DNA
<213> Homo sapiens

<400> 661
atcactgtaa gctgctcctt gtcactcagt gagcaagagg ttgatttttt 50

<210> 662
<211> 50
<212> DNA
<213> Homo sapiens

<400> 662
agcaagcttg ctgaaatcgt gaataacaga agaatgcaca cacattccaa 50

<210> 663
<211> 50
<212> DNA
<213> Homo sapiens

<400> 663
gggaaattta tttaaagaca atagatgtag tatccagttc tgatgtcagg 50

<210> 664
<211> 50
<212> DNA
<213> Homo sapiens

<400> 664
gatgtactaa tattatttgg ctagtattct cttagtggac atttctgttg 50

<210> 665
<211> 50
<212> DNA
<213> Homo sapiens

<400> 665
tttgtactcc aggaaagaga ggaggaggta gcttgaacta ggatgacggc 50

<210> 666
<211> 50
<212> DNA
<213> Homo sapiens

<400> 666
tggccagaaa agatgaaata tttgaactta tccagcacac gaatacacag 50

<210> 667
<211> 50
<212> DNA
<213> Homo sapiens

<400> 667
tttattgtca ctgagatact actttgtgtt caccagtgag gatgtaggaa 50

<210> 668
<211> 50
<212> DNA
<213> Homo sapiens

<400> 668
ggcacctggg agaagcaaat ataaatactc tctggaaaaa tctaccttca 50

<210> 669
<211> 50
<212> DNA
<213> Homo sapiens

<400> 669
cagacaaatg caaaagatta tttgagacat tctctaagtt ggatagctag 50

<210> 670
<211> 50
<212> DNA
<213> Homo sapiens

<400> 670
agaagacatg agactactaa acagcaaaag cagatggaag ggaggttaat 50

<210> 671
<211> 50
<212> DNA
<213> Homo sapiens

<400> 671
aagccctgta gatgagagct tctcttttcc tggaaactcc accaggaagc 50

<210> 672
<211> 50
<212> DNA
<213> Homo sapiens

<400> 672
atcgtgtgct cataaccaca agtggactct ggcttcatgt aaccacaagc 50

<210> 673
<211> 50
<212> DNA
<213> Homo sapiens

<400> 673
atacgcaggt ggaatggtct gcaaacagat gaattcagcc cctccaaacc 50

<210> 674
<211> 50
<212> DNA
<213> Homo sapiens

<400> 674
gataagggac ctcccacaca ccccaaaagt ggtttataaa acattgactg 50

<210> 675
<211> 50
<212> DNA
<213> Homo sapiens

<400> 675
tttataaaac attgactcca catcactgta gttaacccaa accaaaagag 50

<210> 676
<211> 50
<212> DNA
<213> Homo sapiens

<400> 676
ctgacagcct aggggacagg gccatggctg agttgactgg gttcagattg 50

<210> 677
<211> 50
<212> DNA
<213> Homo sapiens

<400> 677
ttcaccttga agattgcagt tggcttccaa ctggcctcta aactctaatg 50

<210> 678
<211> 50
<212> DNA
<213> Homo sapiens

<400> 678
acgtacagaa tgggattctt aagagagcct ctaggttagc gccgctgaag 50

<210> 679
<211> 50
<212> DNA
<213> Homo sapiens

<400> 679
tactacagga gataccactt tcccctttatc agactggcaa atagccaaat 50

<210> 680
<211> 50
<212> DNA
<213> Homo sapiens

<400> 680
tcttgaaaag gacattacgt tcctggcaat taagtcaaac cttaagctag 50

<210> 681
<211> 50
<212> DNA
<213> Homo sapiens

<400> 681
acagtgcgga aagaggcaac tattccagga ggcaggggt atagagtggc 50

<210> 682
<211> 50
<212> DNA
<213> Homo sapiens

<400> 682
agagtgagaa tttgagccaa aatatctctg aatctagacc ttgagctgta 50

<210> 683
<211> 50
<212> DNA
<213> Homo sapiens

<400> 683
tatagatgca taactacaat attttcctct gtcttcaccc ggcattcccc 50

<210> 684
<211> 50
<212> DNA
<213> Homo sapiens

<400> 684
tctctgtcta tcttaacaga aagctgacct gtgagggctt ctttagggtg 50

<210> 685
<211> 50
<212> DNA
<213> Homo sapiens

<400> 685
cctctgtttt gtattattac aatttaaaat gaggaaagct atgtagtcaa 50

<210> 686
<211> 50
<212> DNA
<213> Homo sapiens

<400> 686
gtctaaaaaa ctgttaatga gaaaacttat gctactagac ttttaaggga 50

<210> 687
<211> 50
<212> DNA
<213> Homo sapiens

<400> 687
gcttttcttt atgctaggca tgctctcgcc ccgcatctgt gcactgactg 50

<210> 688
<211> 50
<212> DNA
<213> Homo sapiens

<400> 688
catttaatta cttcttgctt caatcttatc ccacactctg gtcatacaag 50

<210> 689
<211> 50
<212> DNA
<213> Homo sapiens

<400> 689
aagcattagg gacaattggt gtgcatccta aaagcagtga caggttagag 50

<210> 690
<211> 50
<212> DNA
<213> Homo sapiens

<400> 690
ggggaaagag aaaagaaaga ttcgaaactc catgaaactg acattcccaa 50

<210> 691
<211> 50
<212> DNA
<213> Homo sapiens

<400> 691
tttcacagtg gagttgctat taggtagggc aagtaccatc tgattatgaa 50

<210> 692
<211> 50
<212> DNA
<213> Homo sapiens

<400> 692
aatccaaaac acccagcatt atgggtaatt tggacaatgg tctaaaagca 50

<210> 693
<211> 50
<212> DNA
<213> Homo sapiens

<400> 693
cccagaaatc aacccataca atgtagtcaa ctgatttatg aaaaacacac 50

<210> 694
<211> 50
<212> DNA
<213> Homo sapiens

<400> 694
cagacaaatg caaaagatta tttgagacat tctctaagtt ggatagctac 50