DESCRIPTION

METHOD FOR DETERMINATION OF PROGRESSION 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 progression of glaucoma, or a single nucleotide polymorphism with a high progressive 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] In addition, glaucoma is a disease that progresses gradually over a long period of time; however, some of the patients with fast progression are known empirically. The reasons of the existence of the patients with fast progression of glaucoma are unknown, and the involvement of hereditary factors is suspected. By finding polymorphisms involved in the progression of glaucoma, a person having a polymorphism which is found in a high frequency in patients with the fast progression of glaucoma is predicted to have a high progressive risk of glaucoma, whereby the prediction can be used in designing of the treatment plan, in a manner that a more carefully handled treatment and a follow-up in a high frequency are carried out, the progression of glaucoma is controlled, and the like. Further, a clinical trial for studying whether or not a candidate substance for a glaucoma therapeutic drug is actually usable for the glaucoma therapeutic drug requires a long period of time for trials; however, the period of a clinical trial of a candidate substance for a glaucoma therapeutic drug can be shortened by performing a clinical trial on gathered patients having polymorphisms involved in the progression of glaucoma in the present invention. In addition, a glaucoma therapeutic drug selected according to a clinical trial as described above has a possibility of being especially effective in the treatment of glaucoma of which progression is fast.

[0010] An object of the present invention is to provide a method of detecting a single nucleotide polymorphism involved in the progression of glaucoma, thereby predicting a progressive 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 progression of glaucoma by a comprehensive analysis of known polymorphic sites existing on the genome of patients with fast progression and patients with slow progression in the glaucoma patients, and further found an allele identified in a high frequency in patients with fast progression of glaucoma and an opposite allele thereof, and a genotype identified in a high frequency in patients with fast progression of glaucoma, 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 progression 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 progression 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 752 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 752 (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 752 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: 753 to 1061 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 752 (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 752 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: 753 to 1061 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 752 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 752 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 752 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 752 (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 a progressive risk of glaucoma, including the following steps of:

step (I): determining the presence or the absence of the progressive

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 progressive 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 progressive 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 progressive 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, the method is useful because the period of a clinical trial for a glaucoma therapeutic drug can be shortened by selecting patients with a high progressive risk of glaucoma using a single nucleotide polymorphism associated with the progression of glaucoma in the present invention, and performing a clinical trial for a glaucoma therapeutic drug.

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 progression of glaucoma is found, further that in the single nucleotide polymorphism, an allele identified in a high frequency in progressive glaucoma cases and an opposite allele thereof, and a genotype, which is a combination of each of the alleles identified in a

high frequency in progressive glaucoma cases 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 progressive glaucoma group than that of a nonprogressive glaucoma 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 progressive glaucoma group and the nonprogressive glaucoma 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 progressive risk, and the latter means an embodiment where a homozygote of a high-risk allele is involved with the progressive risk.

[0021] In the present invention, the glaucoma risk refers to a risk concerning glaucoma. The progressive risk of glaucoma refers to a possibility of fast progression of glaucoma determined by susceptibility to a disease in a case where a patient suffers from glaucoma (or will suffer from the glaucoma in future). 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 patients with fast progression of glaucoma, i.e. progressive glaucoma cases, and patients with slow progression of glaucoma, i.e. nonprogressive glaucoma cases, and comparing allele or genotype frequencies of individual single nucleotide polymorphisms in the progressive glaucoma cases and the nonprogressive glaucoma cases 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 progressive glaucoma cases and nonprogressive glaucoma cases 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, although the details will be explained in the section of Examples, the progressive glaucoma cases refer to patients who are found to show progression in visual field within a certain period of time, even though a treatment by an intraocular pressure-lowering drug or surgical operation is given, and the nonprogressive glaucoma cases refer to patients of which progression in the visual field is inhibited by these treatments. Here, a group composed of the progressive glaucoma cases is referred to as a progressive glaucoma group, and a group composed of the nonprogressive glaucoma cases is referred to as a nonprogressive glaucoma group. By using the alleles or genotypes having a single nucleotide polymorphism associated with the progression of glaucoma found according to these analyses, the determination of the presence or the absence of the progressive risk of glaucoma, and the prediction of the level of a progressive 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 progressive glaucoma cases and nonprogressive glaucoma cases. 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 progressive glaucoma cases and nonprogressive glaucoma cases according to the method as mentioned above, statistically comparing each of the allele frequencies and the genotype frequencies in a progressive glaucoma group against a nonprogressive glaucoma 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 progressive glaucoma group and the nonprogressive glaucoma group are compared to determine whether any of the alleles or genotypes are identified in a high frequency in the progressive glaucoma 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 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 progressive glaucoma group than that of a nonprogressive glaucoma 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 a progressive 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 progressive 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 progressive 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 progressive glaucoma group as compared to that of a nonprogressive glaucoma group, it is said that these genotypes comply with a dominant genetic model. The presence of a progressive 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 progressive glaucoma group as compared to that of a nonprogressive glaucoma group, it is said that these genotypes comply with a recessive genetic model. The presence of a progressive 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 a progressive 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 nonprogressive glaucoma group. In a case where the determination is carried out according to an allele, the presence of a progressive 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, the presence of a progressive 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 nonprogressive glaucoma group as compared to that of a progressive glaucoma group, it is said that these genotypes comply with a dominant genetic model. The presence of the progressive 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 nonprogressive glaucoma group as compared to that of a progressive glaucoma group, it is said that these genotypes comply with a recessive

genetic model. The presence of the progressive 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 progression 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 progressive glaucoma group, over a ratio of frequencies obtained in the same manner in a nonprogressive glaucoma group. In the present invention, an extent to which a progressive 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 progressive glaucoma group, in which the larger the odds ratio, the higher the progressive 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 progressive 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

progressive glaucoma group, over a ratio of the high-risk allele frequency to the low-risk allele frequency in a nonprogressive glaucoma 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 progressive glaucoma 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 nonprogressive glaucoma 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 progressive glaucoma 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 nonprogressive glaucoma 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 a progressive 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 progressive glaucoma group;

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

$RA3_{comb}$: an allele frequency corresponding to $RA1_{comb}$ in a nonprogressive glaucoma group; and

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

[0050] For example, in a case where two single nucleotide polymorphisms associated with the progressive risk of glaucoma are combined, an odds is determined by dividing the frequencies in a progressive glaucoma group all having high-risk alleles of a single nucleotide polymorphism, or having any

one of high-risk alleles, by the frequency in the progressive glaucoma 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 nonprogressive glaucoma 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 progressive glaucoma group;

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

$RGd3_{comb}$: a frequency of the genotype corresponding to $RGd1_{comb}$ in a nonprogressive glaucoma group; and

$RGd4_{comb}$: a frequency at which all the genotypes are homozygotes of a low-risk allele in the nonprogressive glaucoma 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 progressive glaucoma group to the frequency at which both the two single nucleotide polymorphisms are a homozygote of a low-risk allele in the progressive glaucoma group, over a ratio of frequencies of those obtained in the same manner in a nonprogressive glaucoma 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 progressive glaucoma group;

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

$RGr3_{comb}$: a frequency of the genotype corresponding to $RGr1_{comb}$ in a nonprogressive glaucoma group; and

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

[0055] 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 progressive glaucoma group to the frequency at which both the two single nucleotide polymorphisms are a homozygote of a

low-risk allele in the progressive glaucoma group, over a ratio of frequencies of those obtained in the same manner in a nonprogressive glaucoma 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 progressive 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 a progressive 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 a progressive 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 progression of glaucoma, the extent to which the precision of the prediction of a progressive 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 progressive glaucoma case. The determination results are collated with the matter of whether the sample donor having a single nucleotide polymorphism was actually a progressive glaucoma case. 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 a progressive 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 having a single nucleotide polymorphism associated with glaucoma, and a nucleic acid molecule comprising 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 progressive 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 progressive glaucoma cases, 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 70 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 70 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 progression 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 Progressive 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 progressive glaucoma cases 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 comprising 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 progression 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 26 to 28 or Tables 52 to 70 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 progressive glaucoma cases is determined, a high-risk allele in a sample is detected, whereby the existence of the allele that exists in a high frequency in progressive glaucoma cases can be determined.

[0097] In addition, as to any single nucleotide polymorphisms associated with the progression 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 progressive glaucoma group than that of a nonprogressive glaucoma 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 progressive glaucoma group than that of a nonprogressive glaucoma 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 progressive glaucoma group than that of a nonprogressive glaucoma 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 progressive glaucoma group than that of a nonprogressive glaucoma group exists in the sample, there are some high probabilities that a glaucoma patient donating the sample is predicted to have a high progressive risk of glaucoma, and that an individual donating the sample who is suspected of having glaucoma should be diagnosed as a progressive glaucoma case, and an individual donating the sample not having glaucoma at the present point is predicted to have a fast progression of glaucoma in a case of an onset of glaucoma in future.

[0099] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting a progressive 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 752 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 240 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 **s**, 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,

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

s: SEQ ID NO: 239 and/or SEQ ID NO: 240.

[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: 205, SEQ ID NO: 207, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 236, SEQ ID NO: 238, and SEQ ID NO: 240,

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 progressive 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, a progressive 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 a progressive risk.

[0104] In the method of detecting a single nucleotide polymorphism associated with glaucoma and the method of predicting a progressive 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 752 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 240 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 **s**, 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,

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

s: SEQ ID NO: 239 and/or SEQ ID NO: 240, 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:

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, and

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

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:

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

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

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

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, and/or

any one of the single nucleotide polymorphisms in Group 2 in a case that the single nucleotide polymorphisms belonging to Group 2 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: 205, SEQ ID NO: 207, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 236, SEQ ID NO: 238, and SEQ ID NO: 240,

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 70 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 71 to 81 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 comprising 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 a progressive 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 752 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: 753 to 1061 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 240 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: 753 to 776 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 **s** 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 **ss** or pairs of the base sequences, or a complementary sequence thereto,

wherein in pairs of SEQ ID NOs: shown in **a** to **s**, 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 **ss** 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**, **r** and **rr**, and **s** and **ss** 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,

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

s: SEQ ID NO: 239 and/or SEQ ID NO: 240, and

Group B

aa: SEQ ID NO: 753,

bb: SEQ ID NO: 754 and/or SEQ ID NO: 772,

cc: SEQ ID NO: 755,

dd: SEQ ID NO: 756,

ee: SEQ ID NO: 757,

ff: SEQ ID NO: 758,

gg: SEQ ID NO: 759,

hh: SEQ ID NO: 760 and/or SEQ ID NO: 773,

ii: SEQ ID NO: 761 and/or SEQ ID NO: 774,

jj: SEQ ID NO: 762 and/or SEQ ID NO: 775,

kk: SEQ ID NO: 763,

ll: SEQ ID NO: 764,

mm: SEQ ID NO: 765,

nn: SEQ ID NO: 766 and/or SEQ ID NO: 776,

oo: SEQ ID NO: 767,

pp: SEQ ID NO: 768,

qq: SEQ ID NO: 769,

rr: SEQ ID NO: 770, and

ss: SEQ ID NO: 771.

[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: 205, SEQ ID NO: 207, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 236, SEQ ID NO: 238, and SEQ ID NO: 240,

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: 753, SEQ ID NO: 754, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 757, SEQ ID NO: 758, SEQ ID NO: 759, SEQ ID NO: 760, SEQ ID NO: 761, SEQ ID NO: 775, SEQ ID NO: 763, SEQ ID NO: 764, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 768, SEQ ID NO: 769, SEQ ID NO: 770, and SEQ ID NO: 771,

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 a progressive 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 752 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: 753 to 1061 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 240 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: 753 to 776 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 **s** 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 **ss** or pairs of the base sequences, or a complementary sequence thereto,

wherein in pairs of SEQ ID NOs: shown in **a** to **s**, 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 **ss** 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**, **r** and **rr**, and **s** and **ss** 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,

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

s: SEQ ID NO: 239 and/or SEQ ID NO: 240, and

Group B

aa: SEQ ID NO: 753,

bb: SEQ ID NO: 754 and/or SEQ ID NO: 772,

cc: SEQ ID NO: 755,

dd: SEQ ID NO: 756,

ee: SEQ ID NO: 757,

ff: SEQ ID NO: 758,

gg: SEQ ID NO: 759,

hh: SEQ ID NO: 760 and/or SEQ ID NO: 773,

ii: SEQ ID NO: 761 and/or SEQ ID NO: 774,

jj: SEQ ID NO: 762 and/or SEQ ID NO: 775,

kk: SEQ ID NO: 763,

ll: SEQ ID NO: 764,

mm: SEQ ID NO: 765,

nn: SEQ ID NO: 766 and/or SEQ ID NO: 776,

oo: SEQ ID NO: 767,

pp: SEQ ID NO: 768,

qq: SEQ ID NO: 769,

rr: SEQ ID NO: 770, and

ss: SEQ ID NO: 771,

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:

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, and

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

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:

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

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

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

that in Group B,

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

cc: SEQ ID NO: 755,

dd: SEQ ID NO: 756,

ee: SEQ ID NO: 757,

ff: SEQ ID NO: 758,

gg: SEQ ID NO: 759, and

hh: SEQ ID NO: 760 and/or SEQ ID NO: 773,

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

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

ii: SEQ ID NO: 761 and/or SEQ ID NO: 774, and

jj: SEQ ID NO: 762 and/or SEQ ID NO: 775,

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

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, and/or

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.

[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: 205, SEQ ID NO: 207, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 236, SEQ ID NO: 238, and SEQ ID NO: 240,

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: 753, SEQ ID NO: 754, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 757, SEQ ID NO: 758, SEQ ID NO: 759, SEQ ID NO: 760, SEQ ID NO: 761, SEQ ID NO: 775, SEQ ID NO: 763, SEQ ID NO: 764, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 768, SEQ ID NO: 769, SEQ ID NO: 770, and SEQ ID NO: 771,

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 26 to 28 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 70 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 progressive glaucoma 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 the progressive glaucoma group in the sample using the kit of the present invention, a progressive risk of a glaucoma patient can be predicted, and a progressive risk upon future onset of glaucoma of an

individual not having glaucoma at the present stage can be predicted, 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 progressive 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 a progressive 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 progression of glaucoma or a kit of predicting a progressive 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 752 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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: 753 to 1061 or a complementary sequence thereto,

more preferably a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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 240 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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: 753 to 776 or a complementary sequence thereto,

even more preferably a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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 **s** 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 progression of glaucoma or a kit of predicting a progressive 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 **ss** or pairs of the base sequences, or a complementary sequence thereto,

wherein in pairs of SEQ ID NOs: shown in **a** to **s**, 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 **ss** 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**, **r** and **rr**, and **s** and **ss**, 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,

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

s: SEQ ID NO: 239 and/or SEQ ID NO: 240, and

Group B

aa: SEQ ID NO: 753,

bb: SEQ ID NO: 754 and/or SEQ ID NO: 772,

cc: SEQ ID NO: 755,

dd: SEQ ID NO: 756,

ee: SEQ ID NO: 757,

ff: SEQ ID NO: 758,

gg: SEQ ID NO: 759,

hh: SEQ ID NO: 760 and/or SEQ ID NO: 773,

ii: SEQ ID NO: 761 and/or SEQ ID NO: 774,

jj: SEQ ID NO: 762 and/or SEQ ID NO: 775,

kk: SEQ ID NO: 763,

ll: SEQ ID NO: 764,

mm: SEQ ID NO: 765,

nn: SEQ ID NO: 766 and/or SEQ ID NO: 776,

oo: SEQ ID NO: 767,

pp: SEQ ID NO: 768,

qq: SEQ ID NO: 769,

rr: SEQ ID NO: 770, and

ss: SEQ ID NO: 771.

[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 progression of glaucoma or predicting a progressive 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: 205, SEQ ID NO: 207, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 226,

SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 236, SEQ ID NO: 238, and SEQ ID NO: 240,
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 progression of glaucoma or predicting a progressive 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: 753, SEQ ID NO: 754, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 757, SEQ ID NO: 758, SEQ ID NO: 759, SEQ ID NO: 760, SEQ ID NO: 761, SEQ ID NO: 775, SEQ ID NO: 763, SEQ ID NO: 764, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 768, SEQ ID NO: 769, SEQ ID NO: 770, and SEQ ID NO: 771,
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 a progressive 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 progression of glaucoma or a kit of predicting a progressive 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 752 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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: 753 to 1061 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 progression of glaucoma or a kit of predicting a progressive 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 a base sequence containing a single nucleotide polymorphism, selected from the group consisting of base sequences shown in SEQ ID NOs: 203 to 240 or a complementary sequence thereto, or a partial sequence thereof, and/or

a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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: 753 to 776 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 progression of glaucoma or a kit of predicting a progressive 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 following Group A consisting of the following pairs of base sequences **a** to **s** 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 progression of glaucoma or a kit of predicting a progressive 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 **ss** 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 **s**, 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 **ss** 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**, **r** and **rr**, and **s** and **ss** 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,

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

s: SEQ ID NO: 239 and/or SEQ ID NO: 240, and

Group B

aa: SEQ ID NO: 753,

bb: SEQ ID NO: 754 and/or SEQ ID NO: 772,

cc: SEQ ID NO: 755,

dd: SEQ ID NO: 756,

ee: SEQ ID NO: 757,

ff: SEQ ID NO: 758,

gg: SEQ ID NO: 759,

hh: SEQ ID NO: 760 and/or SEQ ID NO: 773,

ii: SEQ ID NO: 761 and/or SEQ ID NO: 774,

jj: SEQ ID NO: 762 and/or SEQ ID NO: 775,

kk: SEQ ID NO: 763,

ll: SEQ ID NO: 764,

mm: SEQ ID NO: 765,

nn: SEQ ID NO: 766 and/or SEQ ID NO: 776,

oo: SEQ ID NO: 767,

pp: SEQ ID NO: 768,

qq: SEQ ID NO: 769,

rr: SEQ ID NO: 770, and

ss: SEQ ID NO: 771,

even more preferably a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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 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 progression of glaucoma or a kit of predicting a progressive 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 progression of glaucoma or a kit of predicting a progressive 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 progression of glaucoma or a kit of predicting a progressive 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:

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, and

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

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:

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

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

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

that in Group B,

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

SEQ ID NO: 755,

SEQ ID NO: 756,

SEQ ID NO: 757,

SEQ ID NO: 758,

SEQ ID NO: 759, and

SEQ ID NO: 760 and/or SEQ ID NO: 773,

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:

SEQ ID NO: 761 and/or SEQ ID NO: 774, and

SEQ ID NO: 762 and/or SEQ ID NO: 775,

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

it is preferable to use

a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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, and/or

a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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.

[0139] In all the embodiments of the combinations mentioned above, in Group A, preferred is a kit of detecting a single nucleotide polymorphism associated with the progression of glaucoma or a kit of predicting a progressive 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: 205, SEQ ID NO: 207, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 236, SEQ ID NO: 238, and SEQ ID NO: 240,
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 progression of glaucoma or a kit of predicting a progressive 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: 753, SEQ ID NO: 754, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 757, SEQ ID NO: 758, SEQ ID NO: 759, SEQ ID NO: 760, SEQ ID NO: 761, SEQ ID NO: 775, SEQ ID NO: 763, SEQ ID NO: 764,

SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 768, SEQ ID NO: 769, SEQ ID NO: 770, and SEQ ID NO: 771,
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 Progressive Risk of Glaucoma, Including Performing the Predicting Risk in Two-Steps or Multi-Steps)

When a prediction of a progressive 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 a progressive 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 a progressive 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 progression 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] In addition, an individual who has an allele or genotype on the genome that is identified in a high frequency in progressive glaucoma cases disclosed in the present invention has a high risk of the fast progression of glaucoma, and an individual who does not have an allele or genotype that is identified in a high frequency in the progressive glaucoma cases has a low risk of the fast progression of glaucoma. The period of the clinical trial for a candidate substance for a glaucoma therapeutic drug can be shortened by selecting patients having a high risk of the fast progression of glaucoma according to the present invention, and performing a clinical trial of a candidate substance of the glaucoma therapeutic drug.

EXAMPLES

[0146] 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.

[0147] 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.

[0148] 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.

[0149] 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.

[0150] 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.

[0151] 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.

[0152] 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).

[0153] 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)

[0154] [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 (Homozygote) (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 +697708p (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 -112539p (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 -178946p (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

[0155] [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 -117088bp (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) LOC402300 Intron2 (XM_377974), CALD1 Intron1 (NM_004342.5),	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	CALD1 Intron1 (NM_033138.2), CALD1 Intron1 (NM_033157.2), CALD1 -95572bp (NM_033139.2), CALD1 -95572bp (NM_033140.2) LOC402300 Intron1 (XM_377974), CALD1 Intron1 (NM_004342.5),	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	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

[0156] 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.

[0157] 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.

[0158] 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.

[0159] 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.

[0160] 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.

[0161] 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.

[0162] 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.

[0163] 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.

[0164] [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

[0165] [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

[0166] 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.

[0167] 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.

[0168] [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 -509600bp (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 -57048bp (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 +220772bp (XM_371250)	1	47,934,070	3.10	0.64	0.55	1.45	2.54	2.08	1.33

[0169] [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 +120346bp (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 +41877bp (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 +129689bp (NM_012413.2)	2	37,641,805	2.56	0.44	0.37	1.39	3.26	2.40	1.03
rs7571760	CDC42EP3 +127985bp (NM_006449.3)	2	37,654,409	3.06	0.40	0.31	1.46	3.13	2.69	1.17
rs6724538	QPCT +127553bp (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)	2	74,473,795	3.27	0.48	0.39	1.46	3.10	2.29	1.15
rs7601299	SP110 Intron3 (NM_004509.2), 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

[0170] [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 -39508p (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

[0171] [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 +122766bp (XM_371581)	2	171,412,281	3.19	0.73	0.65	1.49	2.41	1.92	1.23
rs7608898	SP5 +237119bp (XM_371581)	2	171,423,724	3.19	0.73	0.65	1.48	2.41	1.92	1.23
rs10184230	LOC389059 -250588p (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 -1350bp (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

[0172] [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) GRM7 Intron7 (NM_181875.1),	3	23,719,090	3.18	0.69	0.61	1.47	2.48	2.18	1.51
rs779701	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 +1686779bp (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

[0173] [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

[0174] [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

[0175] [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 -32056p (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 +2175048p (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

[0176] [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
rs1115357	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

[0177] [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)
rs12898	CTSB +629bp (NM_001908.2), CTSB +629bp (NM_147780.1), 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

[0178] [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 +182746bp (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 +480766bp (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 -478888bp (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 +1849bp (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

[0179] [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 +1706686bp (NM_003201.1), TFAM +1811711bp (NM_012251.1)	10	59,996,589	3.56	0.60	0.51	1.48	3.43	2.35	1.92
rs1649039	TFAM +1741444bp (NM_003201.1), TFAM +1846296bp (NM_012251.1)	10	60,000,047	3.59	0.60	0.50	1.48	3.43	2.34	1.91
rs1658456	TFAM +1484296bp (NM_003201.1), TFAM +1589146bp (NM_012251.1)	10	59,974,332	3.54	0.60	0.51	1.48	3.40	2.33	1.91
rs1649060	TFAM +1545836bp (NM_003201.1), TFAM +1650686bp (NM_012251.1)	10	59,980,486	3.54	0.60	0.51	1.48	3.40	2.33	1.91
rs17130394	HABP2 -1032636bp (NM_004132.2)	10	115,199,512	3.18	0.84	0.77	1.59	3.40	1.38	0.71
rs10763558	TFAM +1860376p (NM_003201.1), TFAM +1965226p (NM_012251.1)	10	60,011,940	3.62	0.60	0.50	1.49	3.36	2.33	1.87
rs10763556	TFAM +1855016p (NM_003201.1), TFAM +1959866p (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

[0180] [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 +772866bp (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) CNNM2 Intron1 (NM_017649.3),	10	58,583,444	3.22	0.18	0.11	1.72	2.46	4.17	1.49
rs7894588	CNNM2 Intron1 (NM_199076.1), CNNM2 +686555bp (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

[0181] [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 -37564bp (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

[0182] [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 +3710554bp (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 +341443bp (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 +4189915bp (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 +3735598bp (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 +4111113bp (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 +111128bp (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

[0183] [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)
rs1859336	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 +269026bp (XM_498445)	13	104,640,379	0.25	0.51	0.50	1.06	3.58	1.12	0.57
rs9558509	G30 +271368bp (XM_498445)	13	104,638,037	0.27	0.51	0.50	1.07	3.47	1.13	0.58
rs9300981	G30 +469126bp (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

[0184] [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)	14	87,879,410	0.64	0.77	0.75	1.16	3.00	0.64	0.38
rs2816632	BRF1 Intron2 (NM_001519.2), 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

[0185] [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 -312819bp (XM_378606)	16	64,480,523	3.63	0.24	0.16	1.65	2.84	3.03	1.56
rs173840	LOC283867 -313113bp (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 -9409bp (NM_003835.1)	17	60,605,875	1.17	0.75	0.71	1.25	3.80	3.21	3.78
rs9896245	RGS9 -11066bp (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 -63556bp (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

[0186] [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)
rs8065080	TRPV1 Exon11 (NM_080706.1), 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 Intron2 (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
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

[0187] [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) MATN4 Intron5 (NM_003833.2),	20	8,470,921	3.17	0.80	0.72	1.54	2.52	2.65	1.89
rs2743246	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

[0188] [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

[0189] 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.

[0190] 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.

[0191] 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.

[0192] 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.

[0193] 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 Genotype 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)

[0194] [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 +14847bp (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 +1758096p (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 +1758736p (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 -19056bp (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

[0195] [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 -37765bp (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 -38871bp (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 -53535bp (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 -56045bp (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 -68743bp (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 -84106bp (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 -112934bp (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 +1722099bp (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) NRG1 -233743bp (NM_013958.1), NRG1 -233775bp (NM_013957.1), NRG1 -233799bp (NM_004495.1), NRG1 -233842bp (NM_013961.1),	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 -234103bp (NM_013964.1), NRG1 -234127bp (NM_013960.1), NRG1 -234143bp (NM_013956.1), NRG1 -281336bp (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

[0196] [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 -473768bp (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/#	LOC442430 -505188bp (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/#	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_498340)	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/#	LOC440070 +380336bp (XM_498340)	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 +332395bp (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 +13577bp (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 -1820838bp (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/#	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/#	C20orf65 -265390bp (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

[0197] 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.

[0198] 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.

[0199] 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.

[0200] 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.

[0201] 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.

[0202] [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 +3647bp (NM_020365.1)	1	44,981,960	0.01	0.75	0.75	1.01	3.05	4.99	7.80
rs479714	GRIK3 +265768p (NM_000831.2)	1	36,909,131	2.84	0.39	0.28	1.64	3.01	1.86	2.26
rs7528341	GRIK3 +1254408p (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 -11088bp (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 +4031748p (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 -175335p (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

[0203] [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 +18093bp (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

[0204] [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 -413298p (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

[0205] [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

[0206] [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

[0207] [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

[0208] [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

[0209] [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

[0210] [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 +1817799bp (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 +73296bp (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 -529468p (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 +147488p (NM_207496.1)	6	30,873,874	3.08	0.13	0.06	2.44	2.57 ND		2.47

[0211] [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 -795050bp (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

[0212] [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

[0213] [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 +1391988p (XM_294592)	9	100,567,644	1.93	0.36	0.27	1.49	3.17	1.33	2.29
rs10815959	PTPRD -82533bp (NM_002839.1), PTPRD -82533bp (NM_130391.1), PTPRD -82533bp (NM_130392.1), PTPRD -82533bp (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 +1419993bp (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 +2264491bp (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 +2267888bp (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 +2351388p (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

[0214] [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 +621065bp (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 +15499bp (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 +2731128bp (NM_007057.2),	10	57,514,084	3.32	0.82	0.71	1.85	2.78	3.55	1.81
rs7903897	ZWINT +2731128bp (NM_032997.1) LOC285444 +40505bp (XM_497256)	10	135,321,566	3.05	0.61	0.49	1.63	2.72	2.68	2.21

[0215] [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 +341188p (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 +39468p (NM_182603.1)	11	82,641,607	3.17	0.57	0.45	1.64	3.05	2.97	1.30
rs524441	FLJ37874 +10458p (NM_182603.1)	11	82,638,706	3.11	0.56	0.44	1.63	2.93	2.90	1.29
rs681367	FLJ37874 +11118p (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

[0216] [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 +1990bp (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 +338146bp (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

[0217] [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 +1995585bp (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 +1060086bp (NM_182767.2), SLC6A15 +1278222bp (NM_018057.3)	12	83,650,812	3.08	0.73	0.62	1.68	2.48	2.41	1.27
rs908440	TRHDE +3742366bp (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 +1131194bp (NM_182767.2), SLC6A15 +1349306bp (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 -215185bp (NM_000621.1)	13	46,583,361	2.21	0.30	0.21	1.59	3.39	1.16	2.38
rs17640758	DNAJD1 +112976bp (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 -2371bp (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

[0218] [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 -1000176p (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 -7119bp (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 +259066bp (NM_001797.2), CDH11 +259066bp (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

[0219] [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 +154454bp (NM_001797.2), CDH11 +154454bp (NM_033664.1)	16	63,522,732	2.15	0.86	0.79	1.68	3.28	0.76	0.32
rs429065	CDH11 +220043bp (NM_001797.2), CDH11 +220043bp (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

[0220] [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
rs10790008	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 +54848p (NM_001797.2), CDH11 +54848p (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

[0221] [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

[0222] [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), CDH7 +60323bp (NM_004361.2)	18	61,759,477	3.15	0.50	0.38	1.64	2.60	2.56	1.91
rs6565975	LOC441825 +102358bp (XM_497596)	18	73,316,910	3.19	0.75	0.63	1.71	2.57	3.30	2.24
rs10451358	ANKRD12 Intron7 (NM_015208.2)	18	9,207,471	3.05	0.43	0.31	1.65	2.54	3.05	1.32
rs1942583	LOC441825 +112581bp (XM_497596)	18	73,327,133	3.02	0.72	0.61	1.66	2.42	3.03	2.17
rs12051936	LOC441825 +96235bp (XM_497596)	18	73,310,787	3.11	0.60	0.47	1.63	2.33	2.56	1.70
rs4482359	LOC440479 +52521bp (XM_498693)	18	10,180,764	3.16	0.64	0.51	1.66	2.30	2.51	1.46
rs12462868	FLJ36445 +22374bp (NM_153233.1)	19	41,163,676	2.44	0.30	0.21	1.64	3.69	11.93	1.05
rs7260296	NTE +9039bp (NM_006702.2)	19	7,541,689	0.57	0.62	0.58	1.18	3.37	1.89	3.13
rs1102152	KCTD15 +36141bp (NM_024076.1)	19	39,033,129	3.59	0.66	0.53	1.73	3.18	2.64	2.56
rs4802905	PPP2R1A Intron11 (NM_014225.3)	19	57,415,907	2.59	0.66	0.55	1.58	3.13	2.04	0.85
rs734380	RPS5 Intron1 (NM_001009.2)	19	63,590,775	2.85	0.52	0.41	1.59	3.11	2.72	2.35
rs10726778	ZNF600 +14950bp (NM_198457.1)	19	57,944,329	3.53	0.14	0.06	2.59	2.92 ND		2.53
rs734379	RPS5 Intron1 (NM_001009.2)	19	63,590,994	3.11	0.61	0.49	1.63	2.86	3.24	1.95
rs6132862	LOC400840 +29346bp (XM_375912)	20	25,669,248	3.95	0.37	0.24	1.86	3.67	2.58	2.31
rs4572656	PTPRT +222230bp (NM_007050.3), PTPRT +222230bp (NM_133170.1)	20	40,112,577	3.60	0.89	0.79	2.08	3.41	1.95	0.77
rs119416	KCNB1 Intron1 (NM_004975.2)	20	47,469,004	3.98	0.70	0.56	1.79	3.40	3.04	1.48
rs6019825	KCNB1 Intron1 (NM_004975.2)	20	47,472,824	3.55	0.56	0.43	1.70	3.29	3.06	1.30
rs6045666	PDYN +188999bp (NM_024411.2)	20	1,888,504	3.67	0.34	0.22	1.85	3.28	2.73	2.16
rs6138601	KIAA0980 -32244bp (NM_025176.3)	20	25,487,486	3.69	0.39	0.26	1.80	3.23	2.64	2.11
rs6035140	PTPNS1 +157555bp (NM_080792.1)	20	1,884,292	3.67	0.35	0.23	1.83	3.14	2.65	2.09
rs12480036	CHD6 Intron1 (NM_032221.3)	20	39,629,243	3.84	0.80	0.69	1.89	3.13	4.18	2.36
rs6138598	KIAA0980 -6294bp (NM_025176.3)	20	25,461,536	3.44	0.38	0.26	1.76	3.11	2.45	2.13
rs517578	SIRPB2 -508668bp (NM_018556.2), SIRPB2 -508668bp (NM_080816.1)	20	1,637,270	3.30	0.42	0.30	1.70	3.11	2.38	2.16

[0223] [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

[0224] [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 +131764bp (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
rs11139056	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

[0225] 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.

[0226] 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.

[0227] 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.

[0228] 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.

[0229] 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.

[0230] Example 7

The presence or the absence of the progression 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 progressive risk of glaucoma increases is evaluated. In a case where a value exceeds a threshold, it is determined that the progression of glaucoma takes place.

[0231] 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.

[0232] 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 progression of glaucoma identified in the primary analysis of Example 4 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).

[0233] For the custom array, a kit for analyzing a single nucleotide polymorphism commercially available from Illumina [Illumina, iSelect™ Genotyping BeadChip] was used. For 531 single nucleotide polymorphisms associated with the progression of glaucoma showing a p-value of 1×10^{-3} or less in Example 4, 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 477 single nucleotide polymorphisms out of 531 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.

[0234] 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.

[0235] 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.

[0236] 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.

[0237] Example 10 Determination of Genotypes in Progressive Glaucoma Cases and Nonprogressive Cases

Of primary open-angle glaucoma patients and normal tension glaucoma patients diagnosed on the basis of Guidelines offered by Japan Glaucoma Society, patients whose visual loss is progressed despite the treatment of lowering an intraocular pressure, such as an agent for lowering an intraocular pressure or surgical treatment within a certain period of time were assigned to a progressive glaucoma group, and patients without the progression were assigned to a nonprogressive glaucoma group. The determination of the progression of the visual loss was made, with reference to the standards used in The Advanced Glaucoma Intervention Study (the AIGS investigators, *Ophthalmology 1994* **101**: 1445-1455).

[0238] For the present analysis, the same samples used in Example 4 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 110 cases of the progressive glaucoma group and 113 cases of the nonprogressive glaucoma group, each group being different from those of Example 4 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 samples 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 progressive glaucoma group and the nonprogressive glaucoma 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, 464 single nucleotide polymorphisms considered to have a high experimental reliability in both of the methods described in Example 4 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 glaucoma at a p-value of 1.1×10^{-4} or less (the level of Bonferroni correction corresponding to $p < 0.05$ when 464 times of multiple comparisons were performed), that is, -log P of 3.96 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 progressive glaucoma group,

nA_i: a total number of detection of alleles in the nonprogressive glaucoma group,

NA_i: a total number of detection of alleles, and

hA_i: the number of detection of a high-risk allele in the progressive glaucoma 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 progressive glaucoma group,

nD_i: a total number of detection of genotypes in the nonprogressive glaucoma 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 progressive glaucoma 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,

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

nR_i: a total number of detection of genotypes in the nonprogressive glaucoma 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 progressive glaucoma 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 progressive glaucoma group,

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

Ca_i: the number of detection of a high-risk allele in the nonprogressive glaucoma group,

Da_i: the number of detection of a low-risk allele in the nonprogressive glaucoma 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 progressive glaucoma group and the number of detection of a heterozygote in the progressive glaucoma group,

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

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

Dd_i: the number of detection of a homozygote of a low-risk allele in the nonprogressive glaucoma 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 progressive glaucoma group,

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

Cr_i: the number of detection of a homozygote of a high-risk allele in the nonprogressive glaucoma group,

Dr_i: the sum of the number of detection of a heterozygote in the nonprogressive glaucoma group and the number of detection of a homozygote of a low-risk allele in the nonprogressive glaucoma 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 progressive glaucoma group,

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

cA_i: the number of detection of a high-risk allele in the nonprogressive glaucoma group,

dA_i: the number of detection of a low-risk allele in the nonprogressive glaucoma 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 progressive glaucoma group and the number of detection of a heterozygote in the progressive glaucoma group,

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

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

dD_i: the number of detection of a homozygote of a low-risk allele in the nonprogressive glaucoma 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 progressive glaucoma group,

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

cR_i: the number of detection of a homozygote of a high-risk allele in the nonprogressive glaucoma group,

dR_i: the sum of the number of detection of a heterozygote in the nonprogressive glaucoma group and the number of detection of a homozygote of a low-risk allele in the nonprogressive glaucoma 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 Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs1048416	14	32,145,585	AKAP6 intron7 (NM_004274.3)		A	G	A	0.80	0.70	0.000037	Recessive	2.01	1.4-2.8	SEQ ID No:203	SEQ ID No:204	SEQ ID No:753	
rs4076919	2	216,546,324	FLJ10116 +86710bp (NM_018000.1)		A	T	A	0.84	0.75	0.000017	Recessive	2.12	1.5-3	SEQ ID No:205	SEQ ID No:206	SEQ ID No:754	SEQ ID No:772
rs1358105	2	150,431,710	FLJ32955 +17818bp (NM_153041.1)	LD1	A	C	A	0.41	0.28	0.000005	Allele	1.76	1.4-2.3	SEQ ID No:207	SEQ ID No:208	SEQ ID No:755	
rs1641385	2	150,429,442	FLJ32955 +20886bp (NM_153041.1)	LD1	A	G	G	0.46	0.34	0.000044	Allele	1.64	1.3-2.1	SEQ ID No:209	SEQ ID No:210	SEQ ID No:756	
rs968871	2	150,428,575	FLJ32955 +20953bp (NM_153041.1)	LD1	A	G	G	0.46	0.34	0.000036	Allele	1.64	1.3-2.1	SEQ ID No:211	SEQ ID No:212	SEQ ID No:757	
rs848241	2	150,460,159	FLJ32955 intron3 (NM_153041.1)	LD1	A	G	G	0.45	0.33	0.000061	Allele	1.62	1.3-2.1	SEQ ID No:213	SEQ ID No:214	SEQ ID No:758	
rs4667333	2	150,461,734	FLJ32955 intron3 (NM_153041.1)	LD1	A	G	A	0.45	0.34	0.000075	Allele	1.62	1.3-2	SEQ ID No:215	SEQ ID No:216	SEQ ID No:759	
rs1724855	2	150,455,469	FLJ32955 intron3 (NM_153041.1)	LD1	A	T	T	0.44	0.33	0.000093	Allele	1.61	1.3-2	SEQ ID No:217	SEQ ID No:218	SEQ ID No:760	SEQ ID No:773
rs2395453	10	78,411,565	KCNMA1 intron18 (NM_002247.2)	LD2	C	G	G	0.60	0.52	0.000021	Recessive	2.19	1.5-3.1	SEQ ID No:219	SEQ ID No:220	SEQ ID No:761	SEQ ID No:774
rs2131216	10	78,426,609	KCNMA1 intron18 (NM_002247.2)	LD2	A	T	T	0.59	0.52	0.000107	Recessive	2.04	1.4-2.9	SEQ ID No:221	SEQ ID No:222	SEQ ID No:762	SEQ ID No:775
rs4316157	8	12,677,322	LOC340357 intron3 (XM_499106)		A	G	A	0.48	0.33	0.000000	Allele	1.84	1.5-2.3	SEQ ID No:223	SEQ ID No:224	SEQ ID No:763	
rs10781440	9	68,992,320	LOC392347 intron1 (XM_373298)		A	G	G	0.37	0.27	0.000051	Dominant	1.98	1.4-2.8	SEQ ID No:225	SEQ ID No:226	SEQ ID No:764	
rs6132862	20	25,669,248	LOC400840 +293468bp (XM_375912)		A	G	G	0.36	0.25	0.000028	Dominant	2.02	1.5-2.8	SEQ ID No:227	SEQ ID No:228	SEQ ID No:765	
rs787433	2	145,697,590	LOC401014 +295628bp (XM_379141)		C	G	G	0.42	0.31	0.000072	Allele	1.62	1.3-2.1	SEQ ID No:229	SEQ ID No:230	SEQ ID No:766	SEQ ID No:776
rs10172264	2	53,313,788	LOC402072 +152420bp (XM_377741)		A	C	C	0.19	0.11	0.000075	Dominant	2.13	1.5-3.1	SEQ ID No:231	SEQ ID No:232	SEQ ID No:767	
rs4802905	19	57,415,907	PPP2R1A intron11 (NM_014225.3)		A	G	A	0.67	0.59	0.000073	Recessive	2.01	1.4-2.8	SEQ ID No:233	SEQ ID No:234	SEQ ID No:768	
rs12554461	9	4,855,256	RCL1 +41936bp (NM_005772.2)		A	G	G	0.41	0.31	0.000096	Dominant	1.94	1.4-2.7	SEQ ID No:235	SEQ ID No:236	SEQ ID No:769	
rs166296	5	115,861,466	SEMA6A intron3 (NM_020796.2)		A	G	G	0.38	0.26	0.000020	Allele	1.72	1.3-2.2	SEQ ID No:237	SEQ ID No:238	SEQ ID No:770	
rs4927088	1	54,487,224	SSBP3 intron4 (NM_145716.1), SSBP3 intron4 (NM_018070.2)		A	G	G	0.58	0.54	0.000096	Dominant	2.29	1.5-3.5	SEQ ID No:239	SEQ ID No:240	SEQ ID No:771	

[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 and LD2 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 progressive glaucoma group and the nonprogressive glaucoma 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: or SEQ ID NOs: 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 nonprogressive glaucoma group and the progressive glaucoma group, 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 4, 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.

[0265] According to the above studies, 19 single nucleotide polymorphisms of which alleles or genotypes were associated with glaucoma at a p-value of 1.1×10^{-4} or less existing in clusters in relatively adjacent regions on the genome were found in 13 regions.

[0266] An allele identified in a high frequency in the progressive glaucoma 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 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.

[**0267**] Similarly, a single nucleotide polymorphism of which allele or genotype shows association with the progression 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 70.

[0268] [Table 53]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs6500718	16	5,751,661	A2BP1 -257472bp (NM_018723.2), A2BP1 -15710910bp (NM_145891.1), A2BP1 -15710910bp (NM_145892.1), A2BP1 -15710910bp (NM_145893.1)	A	C	A	0.94	0.90	0.005469	Allele	1.85	1.2-2.9	SEQ ID No:241	SEQ ID No:242	SEQ ID No:777	
rs7148801	14	32,206,647	AKAP6 Intron7 (NM_004274.3)	A	G	A	0.94	0.89	0.000405	Recessive	2.30	1.4-3.6	SEQ ID No:243	SEQ ID No:244	SEQ ID No:778	
rs1104870	2	29,366,069	ALK Intron15 (NM_004304.3)	A	G	A	0.16	0.11	0.006447	Allele	1.63	1.1-2.3	SEQ ID No:245	SEQ ID No:246	SEQ ID No:779	
rs13159932	6	130,008,475	ARHGAP18 Intron1 (NM_033515.2)	C	G	C	0.81	0.78	0.001225	Dominant	3.82	1.7-8.6	SEQ ID No:247	SEQ ID No:248	SEQ ID No:780	SEQ ID No:1033
rs1621819	7	7,087,571	C1GALT1 +30350bp (NM_020156.1)	A	G	G	0.58	0.48	0.000735	Allele	1.50	1.2-1.9	SEQ ID No:249	SEQ ID No:250	SEQ ID No:781	
rs1638213	7	7,090,455	C1GALT1 +33234bp (NM_020156.1)	C	G	G	0.57	0.47	0.001155	Allele	1.46	1.2-1.8	SEQ ID No:251	SEQ ID No:252	SEQ ID No:782	SEQ ID No:1034
rs1796121	7	7,090,845	C1GALT1 +33624bp (NM_020156.1)	C	G	G	0.57	0.47	0.001418	Allele	1.45	1.2-1.8	SEQ ID No:253	SEQ ID No:254	SEQ ID No:783	SEQ ID No:1035
rs2050223	20	15,649,814	C20orf23 +55099bp (NM_024704.3)	A	G	A	0.64	0.59	0.002597	Recessive	1.69	1.2-2.4	SEQ ID No:255	SEQ ID No:256	SEQ ID No:784	
rs6017164	20	41,815,520	C20orf65 -26539bp (NM_176791.2)	A	G	A	0.51	0.42	0.003116	Allele	1.42	1.1-1.8	SEQ ID No:257	SEQ ID No:258	SEQ ID No:785	
rs11691031	2	101,237,876	C2orf29 -90028bp (NM_017546.3)	A	G	G	0.49	0.44	0.000418	Dominant	1.93	1.3-2.8	SEQ ID No:259	SEQ ID No:260	SEQ ID No:786	
rs7338030	2	101,236,837	C2orf29 -91059bp (NM_017546.3)	A	G	A	0.49	0.44	0.000865	Dominant	1.85	1.3-2.7	SEQ ID No:261	SEQ ID No:262	SEQ ID No:787	
rs17171658	7	39,931,767	C7orf11 +138166bp (NM_138701.1)	A	C	C	0.77	0.68	0.002217	Allele	1.51	1.2-2	SEQ ID No:263	SEQ ID No:264	SEQ ID No:788	
rs6601569	8	11,110,988	C8orf7 -14730bp (XM_088376)	A	G	G	0.92	0.85	0.000375	Allele	1.96	1.4-2.8	SEQ ID No:265	SEQ ID No:266	SEQ ID No:789	
rs2773395	9	126,049,019	C9orf28 -119663bp (XM_088525)	A	C	A	0.33	0.26	0.002485	Dominant	1.66	1.2-2.3	SEQ ID No:267	SEQ ID No:268	SEQ ID No:790	
rs7038186	9	17,388,616	C9orf39 Intron10 (NM_017738.1)	A	C	A	0.70	0.62	0.006790	Allele	1.41	1.1-1.8	SEQ ID No:269	SEQ ID No:270	SEQ ID No:791	

[0269] [Table 54]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs2780197	9	17,416,186	C9orf39 intron13 (NM_017738.1)	A	G	G	0.80	0.72	0.001857	Allele	1.53	1.2-2	SEQ ID No:271	SEQ ID No:272	SEQ ID No:792	
rs2584554	9	17,416,808	C9orf39 intron13 (NM_017738.1)	C	G	C	0.79	0.72	0.006618	Allele	1.45	1.1-1.9	SEQ ID No:273	SEQ ID No:274	SEQ ID No:793	SEQ ID No:1036
rs6577539	1	8,923,501	CA6 -16705bp (NM_001215.1)	A	G	A	0.94	0.90	0.009973	Recessive	1.81	1.2-2.9	SEQ ID No:275	SEQ ID No:276	SEQ ID No:794	
rs1816581	16	47,812,497	CBLN1 +576996p (NM_004352.1)	A	G	A	0.40	0.31	0.002274	Allele	1.46	1.1-1.9	SEQ ID No:277	SEQ ID No:278	SEQ ID No:795	
rs2293325	1	164,157,804	CD3Z Intron1 (NM_000734.2), CD3Z Intron1 (NM_198853.1)	A	G	G	0.77	0.70	0.003712	Allele	1.47	1.1-1.9	SEQ ID No:279	SEQ ID No:280	SEQ ID No:796	
rs6779050	3	120,606,504	CDGAP Intron10 (XM_291085)	A	G	A	0.61	0.54	0.002115	Dominant	1.98	1.3-3.1	SEQ ID No:281	SEQ ID No:282	SEQ ID No:797	
rs1554401	16	63,588,839	CDH11 Intron4 (NM_001797.2), CDH11 Intron4 (NM_033664.1)	A	G	A	0.46	0.41	0.002996	Recessive	1.91	1.2-2.9	SEQ ID No:283	SEQ ID No:284	SEQ ID No:798	
rs1321001	20	44,250,143	CDH22 Intron7 (NM_021248.1)	A	C	A	0.62	0.54	0.006422	Allele	1.39	1.1-1.8	SEQ ID No:285	SEQ ID No:286	SEQ ID No:799	
rs4810317	20	39,456,460	CHD6 +81240p (NM_032221.3)	A	G	G	0.80	0.74	0.005706	Allele	1.47	1.1-1.9	SEQ ID No:287	SEQ ID No:288	SEQ ID No:800	
rs12480036	20	39,629,243	CHD6 Intron1 (NM_032221.3)	A	G	A	0.80	0.73	0.006334	Allele	1.46	1.1-1.9	SEQ ID No:289	SEQ ID No:290	SEQ ID No:801	
rs6072407	20	39,596,216	CHD6 Intron2 (NM_032221.3)	A	G	G	0.82	0.75	0.003421	Allele	1.52	1.1-2	SEQ ID No:291	SEQ ID No:292	SEQ ID No:802	
rs909882	20	39,509,923	CHD6 Intron24 (NM_032221.3)	A	G	A	0.80	0.72	0.002054	Allele	1.54	1.2-2	SEQ ID No:293	SEQ ID No:294	SEQ ID No:803	
rs7198530	16	51,641,067	CHD9 -179353bp (NM_025134.2)	A	C	A	0.17	0.13	0.009306	Dominant	1.64	1.1-2.4	SEQ ID No:295	SEQ ID No:296	SEQ ID No:804	
rs453570	3	50,612,473	CISH +6457bp (NM_013324.4), CISH +6457bp (NM_145071.1)	C	G	C	0.65	0.56	0.001906	Allele	1.46	1.1-1.8	SEQ ID No:297	SEQ ID No:298	SEQ ID No:805	SEQ ID No:1037
rs2282273	14	94,730,437	CLMN Intron11 (NM_024734.2)	A	G	A	0.65	0.57	0.005907	Allele	1.40	1.1-1.8	SEQ ID No:299	SEQ ID No:300	SEQ ID No:806	

[0270] [Table 55]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs3180753	14	94,729,500	CLMN Intron12 (NM_024734.2)	A	G	G	0.67	0.59	0.002886	Allele	1.43	1.1-1.8	SEQ ID No:301	SEQ ID No:302	SEQ ID No:807	
rs2282267	14	94,729,648	CLMN Intron12 (NM_024734.2)	A	G	A	0.67	0.59	0.003047	Allele	1.43	1.1-1.8	SEQ ID No:303	SEQ ID No:304	SEQ ID No:808	
rs1187627	14	94,734,482	CLMN Intron9 (NM_024734.2)	A	G	G	0.59	0.49	0.000667	Allele	1.49	1.2-1.9	SEQ ID No:305	SEQ ID No:306	SEQ ID No:809	
rs1187626	14	94,735,610	CLMN Intron9 (NM_024734.2)	A	G	G	0.59	0.50	0.001214	Recessive	1.83	1.3-2.6	SEQ ID No:307	SEQ ID No:308	SEQ ID No:810	
rs17156435	7	28,168,969	CREB5 Intron1 (NM_182899.2), CREB5 -56415bp (NM_182898.1), CREB5 -79503bp (NM_004904.1)	A	G	A	0.21	0.16	0.002094	Recessive	6.31	2-20.4	SEQ ID No:309	SEQ ID No:310	SEQ ID No:811	
rs6083320	20	23,839,641	CST5 -31324bp (NM_001900.2)	A	G	A	0.40	0.33	0.006655	Recessive	2.13	1.2-3.7	SEQ ID No:311	SEQ ID No:312	SEQ ID No:812	
rs10498642	14	94,658,292	DICER1 Intron9 (NM_030621.2), DICER1 Intron8 (NM_177438.1)	C	G	C	0.61	0.52	0.002984	Allele	1.42	1.1-1.8	SEQ ID No:313	SEQ ID No:314	SEQ ID No:813	SEQ ID No:1038
rs11059862	12	127,750,629	DKFZp761O2018 +32295bp (XM_044062)	A	G	A	0.91	0.85	0.004946	Allele	1.68	1.2-2.4	SEQ ID No:315	SEQ ID No:316	SEQ ID No:814	
rs11059865	12	127,752,135	DKFZp761O2018 +34801bp (XM_044062)	A	G	G	0.91	0.86	0.009337	Recessive	1.72	1.1-2.6	SEQ ID No:317	SEQ ID No:318	SEQ ID No:815	
rs7302136	12	127,752,520	DKFZp761O2018 +35186bp (XM_044062)	A	G	G	0.91	0.86	0.006401	Allele	1.65	1.2-2.4	SEQ ID No:319	SEQ ID No:320	SEQ ID No:816	
rs12227382	12	127,753,754	DKFZp761O2018 +36420bp (XM_044063)	A	G	A	0.91	0.86	0.008366	Allele	1.63	1.1-2.3	SEQ ID No:321	SEQ ID No:322	SEQ ID No:817	
rs16929359	9	1,440,010	DMRT2 +3924388bp (NM_006557.3), DMRT2 +3924588bp (NM_181872.1)	A	G	A	0.10	0.06	0.008247	Allele	1.84	1.2-2.9	SEQ ID No:323	SEQ ID No:324	SEQ ID No:818	
rs4142436	9	1,444,200	DMRT2 +3966488bp (NM_006557.3), DMRT2 +3966688bp (NM_181872.1)	A	G	A	0.12	0.07	0.002699	Dominant	1.99	1.3-3.1	SEQ ID No:325	SEQ ID No:326	SEQ ID No:819	
rs1801041	10	69,844,713	DNA2L Exon21 (XM_166103)	A	T	A	0.79	0.74	0.004254	Recessive	1.64	1.2-2.3	SEQ ID No:327	SEQ ID No:328	SEQ ID No:820	SEQ ID No:1039
rs17640758	13	42,590,879	DNAJD1 +11297bp (NM_013238.1)	A	C	A	0.14	0.09	0.005083	Dominant	1.80	1.2-2.7	SEQ ID No:329	SEQ ID No:330	SEQ ID No:821	

[0271] [Table 56]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs6446245	3	51,012,298	DOCK3 Intron5 (NM_004947.2)	A	C	C	0.63	0.55	0.003599	Dominant	1.93	1.2-3	SEQ ID No:331	SEQ ID No:332	SEQ ID No:822	
rs7428299	3	5,705,884	EDEM1 +469242bp (XM_376201)	A	G	A	0.68	0.59	0.000777	Allele	1.51	1.2-1.9	SEQ ID No:333	SEQ ID No:334	SEQ ID No:823	
rs10898459	11	85,650,587	EED Intron6 (NM_003797.2), EED Intron6 (NM_152991.1)	A	G	A	0.61	0.52	0.000836	Dominant	2.12	1.4-3.3	SEQ ID No:335	SEQ ID No:336	SEQ ID No:824	
rs6138532	20	25,118,787	ENTPD6 -5585bp (NM_001247.1)	A	G	A	0.41	0.35	0.008530	Dominant	1.59	1.1-2.2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:825	
rs7420360	2	221,739,147	EPHA4 +3691070bp (NM_004438.3)	A	G	G	0.42	0.38	0.001408	Dominant	1.76	1.2-2.5	SEQ ID No:339	SEQ ID No:340	SEQ ID No:826	
rs531970	6	94,221,384	EPHA7 -35391bp (NM_004440.2)	A	G	A	0.46	0.41	0.002310	Recessive	1.98	1.3-3.1	SEQ ID No:341	SEQ ID No:342	SEQ ID No:827	
rs1520855	2	190,107,426	FLJ12519 -242398bp (NM_032168.1)	A	G	G	0.64	0.63	0.001652	Dominant	2.10	1.3-3.3	SEQ ID No:343	SEQ ID No:344	SEQ ID No:828	
rs10931418	2	190,090,541	FLJ12519 -411240bp (NM_032168.1)	A	G	A	0.64	0.63	0.006060	Dominant	1.90	1.2-3	SEQ ID No:345	SEQ ID No:346	SEQ ID No:829	
rs13032853	2	190,134,918	FLJ12519 Intron1 (NM_032168.1)	A	G	G	0.64	0.63	0.005897	Dominant	1.90	1.2-3	SEQ ID No:347	SEQ ID No:348	SEQ ID No:830	
rs6739369	2	229,738,357	FLJ20701 Intron3 (NM_017933.3)	A	C	C	0.16	0.11	0.009245	Dominant	1.68	1.1-2.5	SEQ ID No:349	SEQ ID No:350	SEQ ID No:831	
rs1608976	2	150,460,868	FLJ32955 Intron3 (NM_153041.1)	A	G	G	0.45	0.34	0.000125	Allele	1.60	1.3-2	SEQ ID No:351	SEQ ID No:352	SEQ ID No:832	
rs12462868	19	41,163,676	FLJ36445 +223740bp (NM_153233.1)	A	G	A	0.28	0.22	0.004086	Recessive	3.00	1.4-6.3	SEQ ID No:353	SEQ ID No:354	SEQ ID No:833	
rs524441	11	82,638,706	FLJ37874 +1045bp (NM_182603.1)	A	G	A	0.57	0.47	0.000377	Allele	1.52	1.2-1.9	SEQ ID No:355	SEQ ID No:356	SEQ ID No:834	
rs681367	11	82,638,772	FLJ37874 +1111bp (NM_182603.1)	A	G	A	0.57	0.47	0.000382	Allele	1.52	1.2-1.9	SEQ ID No:357	SEQ ID No:358	SEQ ID No:835	
rs504105	11	82,641,607	FLJ37874 +3946bp (NM_182603.1)	C	G	G	0.58	0.48	0.000338	Allele	1.52	1.2-1.9	SEQ ID No:359	SEQ ID No:360	SEQ ID No:836	SEQ ID No:1040

[0272] [Table 57]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs7569506	2	165,535,617	FLJ39822 +44702bp (NM_173512.1)	A	G	A	0.85	0.79	0.006402	Allele	1.51	1.1-2	SEQ ID No:361	SEQ ID No:362	SEQ ID No:837	
rs4350423	12	38,515,235	FLJ40126 Intron18 (NM_173599.1), SLC2A13 Intron6 (NM_052885.1)	A	G	G	0.20	0.13	0.003164	Allele	1.61	1.2-2.2	SEQ ID No:363	SEQ ID No:364	SEQ ID No:838	
rs7962260	12	38,510,570	FLJ40126 Intron18 (NM_173599.1), SLC2A13 Intron6 (NM_052885.1)	A	G	A	0.20	0.14	0.006443	Allele	1.55	1.1-2.1	SEQ ID No:365	SEQ ID No:366	SEQ ID No:839	
rs7968509	12	38,541,115	FLJ40126 Intron18 (NM_173599.1), SLC2A13 Intron6 (NM_052885.1)	A	G	A	0.20	0.14	0.008215	Allele	1.53	1.1-2.1	SEQ ID No:367	SEQ ID No:368	SEQ ID No:840	
rs2322728	11	126,640,100	FLJ40224 +258937bp (NM_173579.1)	A	G	G	0.29	0.27	0.008947	Recessive	2.44	1.2-4.8	SEQ ID No:369	SEQ ID No:370	SEQ ID No:841	
rs687328	1	67,822,816	GADD45A -400688bp (NM_001924.2)	A	G	G	0.73	0.66	0.000202	Dominant	2.91	1.7-5.1	SEQ ID No:371	SEQ ID No:372	SEQ ID No:842	
rs479779	1	36,925,156	GRIK3 +10551bp (NM_000831.2)	A	G	A	0.38	0.28	0.000387	Allele	1.56	1.2-2	SEQ ID No:373	SEQ ID No:374	SEQ ID No:843	
rs34305923	1	36,813,233	GRIK3 +1224740bp (NM_000831.2)	A	G	G	0.72	0.64	0.001496	Recessive	1.71	1.2-2.4	SEQ ID No:375	SEQ ID No:376	SEQ ID No:844	
rs7520341	1	36,810,267	GRIK3 +1254400bp (NM_000831.2)	A	G	G	0.74	0.64	0.000317	Recessive	1.83	1.3-2.6	SEQ ID No:377	SEQ ID No:378	SEQ ID No:845	
rs4906447	1	36,911,856	GRIK3 +23871bp (NM_000831.2)	A	G	G	0.38	0.28	0.000256	Dominant	1.85	1.3-2.6	SEQ ID No:379	SEQ ID No:380	SEQ ID No:846	
rs525798	1	36,909,979	GRIK3 +25728bp (NM_000831.2)	A	C	C	0.39	0.29	0.000319	Dominant	1.83	1.3-2.5	SEQ ID No:381	SEQ ID No:382	SEQ ID No:847	
rs479714	1	36,909,131	GRIK3 +26576bp (NM_000831.2)	A	G	A	0.38	0.28	0.000543	Dominant	1.79	1.3-2.5	SEQ ID No:383	SEQ ID No:384	SEQ ID No:848	
rs4652921	1	36,843,866	GRIK3 +91841bp (NM_000831.2)	A	G	G	0.65	0.55	0.000539	Allele	1.51	1.2-1.9	SEQ ID No:385	SEQ ID No:386	SEQ ID No:849	
rs10230371	7	18,668,137	HDAC9 Intron21 (NM_058176.1), HDAC9 Intron21 (NM_178423.1), HDAC9 Intron19 (NM_178425.1), HDAC9 +186432bp (NM_014707.1), HDAC9 +196235bp (NM_058177.1)	A	G	A	0.41	0.37	0.000412	Dominant	1.84	1.3-2.6	SEQ ID No:387	SEQ ID No:388	SEQ ID No:850	
rs2232248	3	50,584,628	HEMK1 Exon3 (NM_016173.1)	A	C	C	0.65	0.56	0.001927	Allele	1.45	1.1-1.8	SEQ ID No:389	SEQ ID No:390	SEQ ID No:851	

[0273] [Table 58]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs4589168	10	70,800,223	HK1 intron10 (NM_033497.1), HK1 intron10 (NM_033498.1), HK1 intron11 (NM_033500.1), HK1 intron7 (NM_033496.1), HK1 intron7 (NM_000188.1)	A	C	A	0.88	0.83	0.004345	Recessive	1.72	1.2-2.5	SEQ ID No:391	SEQ ID No:392	SEQ ID No:852	
rs10823349	10	70,779,704	HK1 intron5 (NM_033497.1), HK1 intron5 (NM_033498.1), HK1 intron6 (NM_033500.1), HK1 intron2 (NM_033496.1), HK1 intron2 (NM_000188.1)	A	C	C	0.88	0.83	0.002179	Recessive	1.78	1.2-2.6	SEQ ID No:393	SEQ ID No:394	SEQ ID No:853	
rs1339411	1	211,859,142	KCNK2 +615898p (NM_014217.1)	A	G	A	0.31	0.24	0.003451	Dominant	1.63	1.2-2.3	SEQ ID No:395	SEQ ID No:396	SEQ ID No:854	
rs1416658	1	211,804,166	KCNK2 +66139p (NM_014217.1)	A	C	C	0.30	0.22	0.002224	Allele	1.51	1.2-2	SEQ ID No:397	SEQ ID No:398	SEQ ID No:855	
rs1416659	1	211,804,200	KCNK2 +66478p (NM_014217.1)	A	G	G	0.30	0.22	0.002680	Allele	1.50	1.2-2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:856	
rs11120527	1	211,796,452	KCNK2 Intron6 (NM_014217.1)	A	C	A	0.30	0.22	0.002240	Allele	1.51	1.2-2	SEQ ID No:401	SEQ ID No:402	SEQ ID No:857	
rs17588160	10	78,415,943	KCNMA1 Intron18 (NM_002247.2)	A	G	G	0.65	0.59	0.000142	Recessive	1.93	1.4-2.7	SEQ ID No:403	SEQ ID No:404	SEQ ID No:858	
rs3781158	10	78,426,444	KCNMA1 Intron18 (NM_002247.2)	A	G	A	0.59	0.53	0.000145	Recessive	2.00	1.4-2.9	SEQ ID No:405	SEQ ID No:406	SEQ ID No:859	
rs11712746	3	179,474,597	KCNMB2 -263239p (NM_181361.1), KCNMB2 -284723bp (NM_005832.3)	A	G	A	0.24	0.16	0.001381	Allele	1.62	1.2-2.2	SEQ ID No:407	SEQ ID No:408	SEQ ID No:860	
rs10494300	1	151,539,619	KCNN3 Intron3 (NM_170782.1), KCNN3 Intron3 (NM_002249.3)	C	G	G	0.60	0.51	0.001030	Allele	1.47	1.2-1.9	SEQ ID No:409	SEQ ID No:410	SEQ ID No:861	SEQ ID No:1041
rs6089908	20	61,519,098	KCNQ2 Intron10 (NM_004518.2), KCNQ2 Intron11 (NM_172106.1), KCNQ2 Intron12 (NM_172107.1), KCNQ2 Intron11 (NM_172108.1), KCNQ2 +163788p (NM_172109.1)	A	G	G	0.91	0.85	0.001266	Recessive	1.93	1.3-2.9	SEQ ID No:411	SEQ ID No:412	SEQ ID No:862	
rs6138601	20	25,487,486	KIAA0980 -322446p (NM_023176.3)	A	G	A	0.37	0.27	0.000204	Dominant	1.87	1.3-2.6	SEQ ID No:413	SEQ ID No:414	SEQ ID No:863	

[0274] [Table 59]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs6138598	20	25,461,536	KIAA0580 -62594bp (NM_025176.3)	A	G	A	0.36	0.27	0.000168	Dominant	1.88	1.4-2.6	SEQ ID No:415	SEQ ID No:416	SEQ ID No:864	
rs7692155	4	123,386,649	KIAA1109 -449068bp (XM_371706)	A	G	A	0.70	0.62	0.004467	Allele	1.42	1.1-1.8	SEQ ID No:417	SEQ ID No:418	SEQ ID No:865	
rs7112492	11	18,362,086	LDHA -10601bp (NM_005566.1)	A	C	C	0.37	0.29	0.000534	Dominant	1.78	1.3-2.5	SEQ ID No:419	SEQ ID No:420	SEQ ID No:866	
rs4274186	11	18,375,295	LDHA intron2 (NM_005566.1)	A	G	G	0.37	0.29	0.001542	Dominant	1.71	1.2-2.4	SEQ ID No:421	SEQ ID No:422	SEQ ID No:867	
rs1881716	11	18,381,594	LDHA intron5 (NM_005566.1)	A	G	A	0.37	0.29	0.000737	Dominant	1.76	1.3-2.4	SEQ ID No:423	SEQ ID No:424	SEQ ID No:868	
rs11590929	1	87,926,458	LMO4 +403174bp (NM_006769.2)	A	G	G	0.96	0.91	0.000640	Allele	2.30	1.4-3.7	SEQ ID No:425	SEQ ID No:426	SEQ ID No:869	
rs4643164	13	106,724,352	LOC122335 -355849bp (XM_063084)	A	C	A	0.36	0.32	0.006498	Recessive	2.17	1.2-3.8	SEQ ID No:427	SEQ ID No:428	SEQ ID No:870	
rs11117962	1	214,438,658	LOC128153 +97790bp (NM_138796.2)	A	G	G	0.60	0.52	0.000571	Recessive	1.88	1.3-2.7	SEQ ID No:429	SEQ ID No:430	SEQ ID No:871	
rs94967	21	40,117,177	LOC150084 +212990bp (XM_086761)	A	G	A	0.75	0.66	0.000624	Allele	1.56	1.2-2	SEQ ID No:431	SEQ ID No:432	SEQ ID No:872	
rs4816657	21	40,068,705	LOC150084 Intron4 (XM_086761)	A	C	C	0.75	0.66	0.001021	Allele	1.52	1.2-2	SEQ ID No:433	SEQ ID No:434	SEQ ID No:873	
rs1018350	21	40,070,715	LOC150084 Intron4 (XM_086761)	A	C	A	0.75	0.66	0.001261	Allele	1.51	1.2-1.9	SEQ ID No:435	SEQ ID No:436	SEQ ID No:874	
rs2837211	21	40,070,264	LOC150084 Intron4 (XM_086761)	A	C	C	0.75	0.66	0.001261	Allele	1.51	1.2-1.9	SEQ ID No:437	SEQ ID No:438	SEQ ID No:875	
rs1571713	21	40,075,065	LOC150084 Intron5 (XM_086761)	A	G	A	0.75	0.66	0.002192	Allele	1.49	1.2-1.9	SEQ ID No:439	SEQ ID No:440	SEQ ID No:876	
rs2837220	21	40,082,808	LOC150084 Intron6 (XM_086761)	A	G	G	0.70	0.61	0.001120	Allele	1.50	1.2-1.9	SEQ ID No:441	SEQ ID No:442	SEQ ID No:877	
rs463903	21	40,087,547	LOC150084 Intron8 (XM_086761)	A	G	A	0.75	0.66	0.001553	Allele	1.50	1.2-1.9	SEQ ID No:443	SEQ ID No:444	SEQ ID No:878	

[0275] [Table 60]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs465258	21	40,093,614	LOC150084 Intron6 (XM_086761)	A	G	A	0.74	0.66	0.002055	Allele	1.49	1.2-1.9	SEQ ID No:445	SEQ ID No:446	SEQ ID No:879	
rs6440874	3	154,583,971	LOC152118 -101011bp (XM_098163)	A	G	G	0.90	0.85	0.008965	Allele	1.61	1.1-2.3	SEQ ID No:447	SEQ ID No:448	SEQ ID No:880	
rs2174746	3	154,581,141	LOC152118 -103841bp (XM_098163)	A	G	A	0.90	0.85	0.006770	Allele	1.63	1.1-2.3	SEQ ID No:449	SEQ ID No:450	SEQ ID No:881	
rs12490570	3	154,577,350	LOC152118 -107632bp (XM_098163)	A	C	A	0.90	0.84	0.004737	Allele	1.65	1.2-2.3	SEQ ID No:451	SEQ ID No:452	SEQ ID No:882	
rs6440881	3	154,628,080	LOC152118 -569026bp (XM_098163)	A	C	A	0.88	0.82	0.005426	Allele	1.58	1.1-2.2	SEQ ID No:453	SEQ ID No:454	SEQ ID No:883	
rs10113600	8	96,514,178	LOC157657 -163565bp (NM_177965.2)	A	G	A	0.22	0.15	0.001831	Allele	1.62	1.2-2.2	SEQ ID No:455	SEQ ID No:456	SEQ ID No:884	
rs4394361	8	96,522,738	LOC157657 -172125bp (NM_177965.2)	A	C	A	0.23	0.15	0.000936	Allele	1.67	1.2-2.3	SEQ ID No:457	SEQ ID No:458	SEQ ID No:885	
rs1622029	14	83,697,804	LOC283583 -136685bp (XM_211092)	A	T	A	0.70	0.60	0.000203	Allele	1.58	1.2-2	SEQ ID No:459	SEQ ID No:460	SEQ ID No:886	SEQ ID No:1042
rs1828132	18	72,388,920	LOC284276 Intron2 (XM_378757)	A	G	A	0.50	0.41	0.001879	Recessive	1.93	1.3-2.9	SEQ ID No:461	SEQ ID No:462	SEQ ID No:887	
rs4812180	20	58,704,985	LOC284757 +3719938p (XM_496478)	A	G	G	0.08	0.04	0.004895	Allele	2.07	1.2-3.4	SEQ ID No:463	SEQ ID No:464	SEQ ID No:888	
rs9399445	6	143,900,997	LOC285740 +161638p (XM_379438)	A	G	A	0.53	0.45	0.004216	Allele	1.40	1.1-1.8	SEQ ID No:465	SEQ ID No:466	SEQ ID No:889	
rs4570564	6	143,896,965	LOC285740 +201950p (XM_379438)	A	G	G	0.51	0.42	0.003855	Allele	1.41	1.1-1.8	SEQ ID No:467	SEQ ID No:468	SEQ ID No:890	
rs9650336	8	38,625,315	LOC286140 -47378bp (XM_209913)	A	G	G	0.66	0.56	0.000158	Recessive	1.91	1.4-2.7	SEQ ID No:469	SEQ ID No:470	SEQ ID No:891	
rs12669138	7	9,564,997	LOC340268 Intron1 (XM_294634)	C	G	C	0.63	0.56	0.000574	Dominant	2.22	1.4-3.5	SEQ ID No:471	SEQ ID No:472	SEQ ID No:892	SEQ ID No:1043
rs1913603	7	9,664,816	LOC340268 Intron1 (XM_294634)	A	C	C	0.61	0.52	0.001215	Dominant	2.09	1.3-3.3	SEQ ID No:473	SEQ ID No:474	SEQ ID No:893	

[0276] [Table 61]

dBSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs1514880	7	9,664,527	LOC340268 Intron1 (XM_294634)	A	G	G	0.58	0.51	0.001614	Dominant	2.00	1.3-3.1	SEQ ID No:475	SEQ ID No:476	SEQ ID No:894	
rs1877885	7	9,625,295	LOC340268 Intron1 (XM_294634)	C	G	C	0.58	0.49	0.001965	Dominant	1.90	1.3-2.9	SEQ ID No:477	SEQ ID No:478	SEQ ID No:895	SEQ ID No:1044
rs7458284	7	9,670,774	LOC340268 Intron1 (XM_294634)	A	G	G	0.37	0.29	0.002537	Recessive	2.38	1.4-4.2	SEQ ID No:479	SEQ ID No:480	SEQ ID No:896	
rs10512277	9	100,567,355	LOC347273 +1389696p (XM_294592)	A	G	G	0.35	0.28	0.001943	Dominant	1.68	1.2-2.3	SEQ ID No:481	SEQ ID No:482	SEQ ID No:897	
rs4743420	9	100,567,644	LOC347273 +1391985p (XM_294592)	A	C	A	0.34	0.28	0.002543	Dominant	1.66	1.2-2.3	SEQ ID No:483	SEQ ID No:484	SEQ ID No:898	
rs7022939	9	100,568,349	LOC347273 +1399031p (XM_294592)	C	G	G	0.35	0.28	0.001943	Dominant	1.68	1.2-2.3	SEQ ID No:485	SEQ ID No:486	SEQ ID No:899	SEQ ID No:1045
rs9299341	9	100,570,439	LOC347273 +1419930p (XM_294592)	A	G	G	0.35	0.28	0.001943	Dominant	1.68	1.2-2.3	SEQ ID No:487	SEQ ID No:488	SEQ ID No:900	
rs161130	11	112,160,184	LOC387810 -1726778p (XM_373513)	A	G	G	0.81	0.73	0.000992	Allele	1.59	1.2-2.1	SEQ ID No:489	SEQ ID No:490	SEQ ID No:901	
rs2955869	17	32,221,458	LOC388375 +715919p (XM_373726)	A	G	G	0.42	0.36	0.001370	Dominant	1.73	1.2-2.4	SEQ ID No:491	SEQ ID No:492	SEQ ID No:902	
rs369977	21	15,532,948	LOC388814 +1317644p (XM_373926)	A	G	G	0.69	0.61	0.003698	Allele	1.43	1.1-1.8	SEQ ID No:493	SEQ ID No:494	SEQ ID No:903	
rs17605639	4	27,290,099	LOC389204 -2976259p (XM_374079)	A	G	G	0.79	0.69	0.000220	Allele	1.65	1.3-2.1	SEQ ID No:495	SEQ ID No:496	SEQ ID No:904	
rs10478702	5	125,550,583	LOC389319 -1730659p (XM_374134)	A	G	G	0.75	0.71	0.005653	Recessive	1.59	1.1-2.2	SEQ ID No:497	SEQ ID No:498	SEQ ID No:905	
rs7712363	5	125,542,548	LOC389319 -1811004p (XM_374134)	A	C	C	0.75	0.71	0.005438	Recessive	1.60	1.1-2.2	SEQ ID No:499	SEQ ID No:500	SEQ ID No:906	
rs10076364	5	125,510,888	LOC389319 -2127649p (XM_374134)	C	G	C	0.74	0.70	0.002399	Recessive	1.67	1.2-2.3	SEQ ID No:501	SEQ ID No:502	SEQ ID No:907	SEQ ID No:1046
rs1560026	5	125,497,684	LOC389319 -2259488p (XM_374134)	A	C	A	0.73	0.69	0.002114	Recessive	1.68	1.2-2.3	SEQ ID No:503	SEQ ID No:504	SEQ ID No:908	

[0277] [Table 62]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs271351	1	29,821,213	LOC391025 -1738699bp (XM_372775)	A	G	A	0.15	0.09	0.004629	Allele	1.71	1.2-2.5	SEQ ID No:505	SEQ ID No:506	SEQ ID No:909	
rs947130	1	119,728,774	LOC391075 -110888bp (XM_497702)	A	G	G	0.82	0.76	0.008087	Allele	1.46	1.1-1.9	SEQ ID No:507	SEQ ID No:508	SEQ ID No:910	
rs1154988	3	137,407,889	LOC391581 -434bp (XM_497940)	A	T	A	0.20	0.13	0.002265	Allele	1.66	1.2-2.3	SEQ ID No:509	SEQ ID No:510	SEQ ID No:911	SEQ ID No:1047
rs6560584	9	68,976,726	LOC392347 Intron2 (XM_373298)	A	G	A	0.39	0.28	0.000148	Allele	1.61	1.3-2.1	SEQ ID No:511	SEQ ID No:512	SEQ ID No:912	
rs7034303	9	68,976,425	LOC392347 Intron2 (XM_373298)	A	G	G	0.39	0.28	0.000161	Allele	1.60	1.3-2	SEQ ID No:513	SEQ ID No:514	SEQ ID No:913	
rs7048937	9	68,975,807	LOC392347 Intron2 (XM_373298)	A	G	G	0.39	0.28	0.000161	Allele	1.60	1.3-2	SEQ ID No:515	SEQ ID No:516	SEQ ID No:914	
rs7850573	9	68,976,814	LOC392347 Intron2 (XM_373298)	A	G	G	0.39	0.28	0.000161	Allele	1.60	1.3-2	SEQ ID No:517	SEQ ID No:518	SEQ ID No:915	
rs11175622	12	63,686,548	LOC400046 +289836bp (XM_378362)	A	G	A	0.28	0.20	0.001063	Allele	1.58	1.2-2.1	SEQ ID No:519	SEQ ID No:520	SEQ ID No:916	
rs11175627	12	63,691,379	LOC400046 +338148bp (XM_378362)	A	G	G	0.28	0.19	0.000923	Allele	1.60	1.2-2.1	SEQ ID No:521	SEQ ID No:522	SEQ ID No:917	
rs7136577	12	63,692,809	LOC400046 +352448bp (XM_378362)	A	C	C	0.28	0.20	0.001063	Allele	1.58	1.2-2.1	SEQ ID No:523	SEQ ID No:524	SEQ ID No:918	
rs7212115	17	10,832,202	LOC400573 -182083bp (XM_378649)	A	C	A	0.87	0.81	0.004979	Allele	1.59	1.1-2.2	SEQ ID No:525	SEQ ID No:526	SEQ ID No:919	
rs8098925	18	69,257,838	LOC400655 -175143bp (XM_378753)	A	G	G	0.63	0.56	0.009580	Allele	1.37	1.1-1.7	SEQ ID No:527	SEQ ID No:528	SEQ ID No:920	
rs17152703	7	78,929,412	LOC401384 +195612bp (XM_379506)	C	G	C	0.83	0.77	0.005507	Allele	1.51	1.1-2	SEQ ID No:529	SEQ ID No:530	SEQ ID No:921	SEQ ID No:1048
rs17152739	7	78,935,541	LOC401384 +201741bp (XM_379506)	A	G	G	0.75	0.67	0.002274	Allele	1.48	1.2-1.9	SEQ ID No:531	SEQ ID No:532	SEQ ID No:922	
rs7959848	12	82,248,474	LOC401725 +200037bp (XM_377278)	A	G	G	0.43	0.36	0.008743	Allele	1.37	1.1-1.7	SEQ ID No:533	SEQ ID No:534	SEQ ID No:923	

[0278] [Table 63]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma Group	Mantel-Haenszel Test p-value	Mantel-Haenszel Test Model	Odds Ratio	95% Confidence Interval	Sequence Catalog Allele 1	Sequence Catalog Allele 2	Sequence 1 for Secondary Analysis Probe	Sequence 2 for Secondary Analysis Probe
rs5750009	22	33,679,879	LOC402059 Intron8 (XM_497817)	A	G	G	0.79	0.75	0.007709	Dominant	2.86	1.3-6.2	SEQ ID No:535	SEQ ID No:536	SEQ ID No:924	
rs10892454	11	119,148,037	LOC440070 +324940bp (XM_498530)	A	C	A	0.48	0.46	0.005874	Recessive	1.83	1.2-2.8	SEQ ID No:537	SEQ ID No:538	SEQ ID No:925	
rs4269533	11	119,153,578	LOC440070 +380535bp (XM_498530)	A	G	A	0.48	0.46	0.005488	Recessive	1.83	1.2-2.8	SEQ ID No:539	SEQ ID No:540	SEQ ID No:926	
rs7296095	12	114,337,597	LOC440112 -115932bp (XM_498548)	A	G	G	0.28	0.20	0.003482	Allele	1.50	1.1-2	SEQ ID No:541	SEQ ID No:542	SEQ ID No:927	
rs9302502	16	13,517,321	LOC440339 +2513099bp (XM_498634)	A	G	G	0.32	0.22	0.000258	Allele	1.63	1.3-2.1	SEQ ID No:543	SEQ ID No:544	SEQ ID No:928	
rs13333495	16	13,503,539	LOC440339 +2650991bp (XM_498634)	A	G	G	0.31	0.22	0.000327	Allele	1.62	1.2-2.1	SEQ ID No:545	SEQ ID No:546	SEQ ID No:929	
rs16962155	16	13,495,836	LOC440339 +2727940bp (XM_498634)	A	G	G	0.31	0.22	0.000367	Allele	1.61	1.2-2.1	SEQ ID No:547	SEQ ID No:548	SEQ ID No:930	
rs17070891	6	141,790,772	LOC441173 +153727bp (XM_496827)	A	G	A	0.53	0.46	0.001173	Recessive	1.91	1.3-2.8	SEQ ID No:549	SEQ ID No:550	SEQ ID No:931	
rs17070863	6	141,772,290	LOC441173 +1723099bp (XM_496827)	A	G	G	0.53	0.45	0.000396	Recessive	2.05	1.4-3.1	SEQ ID No:551	SEQ ID No:552	SEQ ID No:932	
rs9484507	6	141,764,651	LOC441173 +1790648bp (XM_496827)	A	G	A	0.52	0.44	0.000890	Recessive	1.98	1.3-3	SEQ ID No:553	SEQ ID No:554	SEQ ID No:933	
rs9496008	6	141,762,720	LOC441173 +1817799bp (XM_496827)	A	G	G	0.52	0.45	0.000882	Recessive	1.97	1.3-2.9	SEQ ID No:555	SEQ ID No:556	SEQ ID No:934	
rs1336272	6	142,286,367	LOC441173 -231260bp (XM_496827)	A	T	T	0.30	0.22	0.001778	Dominant	1.69	1.2-2.4	SEQ ID No:557	SEQ ID No:558	SEQ ID No:935	SEQ ID No:1049
rs7767107	6	142,237,572	LOC441173 Intron1 (XM_496827)	A	C	A	0.29	0.22	0.001274	Dominant	1.72	1.2-2.4	SEQ ID No:559	SEQ ID No:560	SEQ ID No:936	
rs2152589	6	142,250,761	LOC441173 Intron1 (XM_496827)	A	G	A	0.30	0.23	0.003172	Dominant	1.64	1.2-2.3	SEQ ID No:561	SEQ ID No:562	SEQ ID No:937	
rs13213414	6	142,262,919	LOC441173 Intron1 (XM_496827)	A	G	G	0.30	0.23	0.003185	Dominant	1.64	1.2-2.3	SEQ ID No:563	SEQ ID No:564	SEQ ID No:938	

[0279] [Table 64]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs775-4052	6	142,254,496	LOC441173 Intron1 (XM_496827)	A	G	A	0.31	0.24	0.003495	Dominant	1.63	1.2-2.3	SEQ ID No:565	SEQ ID No:566	SEQ ID No:939	
rs9496179	6	142,254,945	LOC441173 Intron1 (XM_496827)	A	G	G	0.31	0.24	0.003920	Dominant	1.62	1.2-2.3	SEQ ID No:567	SEQ ID No:568	SEQ ID No:940	
rs2169856	12	53,858,919	LOC441639 +48992bp (XM_497345)	C	G	G	0.73	0.68	0.005853	Recessive	1.59	1.1-2.2	SEQ ID No:569	SEQ ID No:570	SEQ ID No:941	SEQ ID No:1050
rs4979255	9	107,542,392	LOC442430 -505188bp (XM_498339)	A	G	G	0.66	0.62	0.008140	Recessive	1.57	1.1-2.2	SEQ ID No:571	SEQ ID No:572	SEQ ID No:942	
rs16860887	2	197,723,413	LOC91526 Intron15 (NM_153697.1)	A	C	A	0.90	0.83	0.000450	Recessive	1.98	1.4-2.9	SEQ ID No:573	SEQ ID No:574	SEQ ID No:943	
rs13426748	2	197,723,066	LOC91526 Intron15 (NM_153697.1)	A	G	A	0.90	0.84	0.000601	Recessive	1.95	1.3-2.9	SEQ ID No:575	SEQ ID No:576	SEQ ID No:944	
rs4850410	2	197,745,675	LOC91526 Intron15 (NM_153697.1)	A	G	A	0.92	0.86	0.000623	Recessive	2.04	1.4-3.1	SEQ ID No:577	SEQ ID No:578	SEQ ID No:945	
rs7582411	2	197,738,392	LOC91526 Intron15 (NM_153697.1)	A	G	G	0.91	0.85	0.001709	Recessive	1.90	1.3-2.8	SEQ ID No:579	SEQ ID No:580	SEQ ID No:946	
rs12595990	16	12,378,613	LOC92017 Intron9 (XM_042234)	A	G	G	0.49	0.39	0.000870	Recessive	2.07	1.3-3.2	SEQ ID No:581	SEQ ID No:582	SEQ ID No:947	
rs16852789	3	170,106,556	LOC93556 +754678p (XM_376284)	A	G	A	0.33	0.30	0.008064	Dominant	1.57	1.1-2.2	SEQ ID No:583	SEQ ID No:584	SEQ ID No:948	
rs12800710	11	58,071,116	LPXN Intron7 (NM_004811.1)	A	G	G	0.83	0.77	0.009214	Allele	1.47	1.1-2	SEQ ID No:585	SEQ ID No:586	SEQ ID No:949	
rs2328883	6	25,510,510	LRRC16 -1084386p (NM_017640.2)	A	G	A	0.32	0.28	0.000622	Recessive	3.40	1.7-6.8	SEQ ID No:587	SEQ ID No:588	SEQ ID No:950	
rs880226	6	25,510,282	LRRC16 -1086668p (NM_017640.2)	A	G	G	0.32	0.27	0.000709	Recessive	3.37	1.7-6.8	SEQ ID No:589	SEQ ID No:590	SEQ ID No:951	
rs9461154	6	25,506,014	LRRC16 -1129340p (NM_017640.2)	A	G	A	0.32	0.28	0.000622	Recessive	3.40	1.7-6.8	SEQ ID No:591	SEQ ID No:592	SEQ ID No:952	
rs3863401	15	97,698,743	LRRC28 Intron6 (NM_144598.2)	C	G	G	0.59	0.50	0.001713	Allele	1.45	1.1-1.8	SEQ ID No:593	SEQ ID No:594	SEQ ID No:953	SEQ ID No:1051

[0280] [Table 65]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs7173844	15	97,694,416	LRRC28 Intron6 (NM_144598.2)	A	G	G	0.59	0.50	0.001964	Allele	1.44	1.1-1.8	SEQ ID No:595	SEQ ID No:596	SEQ ID No:954	
rs926663	20	38,679,189	MAFB +68744bp (NM_005461.3)	A	G	G	0.45	0.37	0.000663	Dominant	1.82	1.3-2.6	SEQ ID No:597	SEQ ID No:598	SEQ ID No:955	
rs11734419	4	141,040,368	MAML3 Intron2 (NM_018717.2)	A	G	G	0.44	0.37	0.007706	Dominant	1.60	1.1-2.3	SEQ ID No:599	SEQ ID No:600	SEQ ID No:956	
rs628223	11	82,645,812	MDS025 +4340bp (NM_021823.5)	A	G	A	0.57	0.47	0.000386	Allele	1.52	1.2-1.9	SEQ ID No:601	SEQ ID No:602	SEQ ID No:957	
rs784288	3	170,453,933	MDS1 Intron2 (NM_004991.1)	A	G	G	0.78	0.69	0.000432	Allele	1.60	1.2-2.1	SEQ ID No:603	SEQ ID No:604	SEQ ID No:958	
rs194229	5	158,600,287	MGC10067 -22589bp (NM_145049.1)	C	G	G	0.51	0.45	0.000255	Dominant	1.98	1.4-2.9	SEQ ID No:605	SEQ ID No:606	SEQ ID No:959	SEQ ID No:1052
rs7927545	11	11,403,040	MGC71806 Intron3 (NM_198516.1)	A	T	A	0.57	0.48	0.003494	Allele	1.41	1.1-1.8	SEQ ID No:607	SEQ ID No:608	SEQ ID No:960	SEQ ID No:1053
rs10967964	9	27,485,920	MOBKL2B Intron1 (NM_024761.3)	A	C	A	0.24	0.16	0.000249	Dominant	1.93	1.4-2.7	SEQ ID No:609	SEQ ID No:610	SEQ ID No:961	
rs1529404	2	16,137,052	MYCN +993288bp (NM_005378.3)	A	G	A	0.87	0.81	0.004076	Allele	1.59	1.2-2.2	SEQ ID No:611	SEQ ID No:612	SEQ ID No:962	
rs4261668	2	210,987,818	MYL1 Intron3 (NM_079422.1), MYL1 Intron3 (NM_079420.1)	A	G	G	0.36	0.26	0.000108	Allele	1.64	1.3-2.1	SEQ ID No:613	SEQ ID No:614	SEQ ID No:963	
rs16941388	15	57,459,340	MYO1E -6977bp (NM_004998.1)	A	G	G	0.92	0.88	0.008343	Recessive	1.77	1.2-2.7	SEQ ID No:615	SEQ ID No:616	SEQ ID No:964	
rs3798425	6	76,664,270	MYO6 Intron29 (XM_376516)	C	G	G	0.82	0.74	0.000829	Recessive	1.77	1.3-2.5	SEQ ID No:617	SEQ ID No:618	SEQ ID No:965	SEQ ID No:1054
rs6763643	3	40,072,995	MYRIP Intron3 (NM_015460.1)	A	G	G	0.38	0.34	0.005066	Recessive	2.07	1.2-3.4	SEQ ID No:619	SEQ ID No:620	SEQ ID No:966	
rs7275647	21	21,586,912	NCAM2 Intron5 (NM_004540.2)	A	G	A	0.65	0.57	0.004628	Allele	1.40	1.1-1.8	SEQ ID No:621	SEQ ID No:622	SEQ ID No:967	
rs12900219	15	21,583,560	NDN -1000179bp (NM_002487.2)	A	G	G	0.92	0.85	0.000310	Recessive	2.09	1.4-3.1	SEQ ID No:623	SEQ ID No:624	SEQ ID No:968	

[0281] [Table 66]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs1717831	15	21,578,625	NDN -95085bp (NM_002487.2)	A	C	C	0.89	0.83	0.003212	Recessive	1.75	1.2-2.5	SEQ ID No:625	SEQ ID No:626	SEQ ID No:969	
rs10503907	8	32,291,552	NRG1 -2337432bp (NM_013958.1), NRG1 -2337758bp (NM_013957.1), NRG1 -2337998bp (NM_004495.1), NRG1 -2338422bp (NM_013961.1), NRG1 -2341035bp (NM_013964.1), NRG1 -2341270bp (NM_013960.1), NRG1 -2341438bp (NM_013956.1), NRG1 -2811360bp (NM_013962.1), NRG1 -3327310bp (NM_013959.1)	A	G	A	0.93	0.86	0.000276	Allele	2.02	1.4-3	SEQ ID No:627	SEQ ID No:628	SEQ ID No:970	
rs595805	6	5,987,127	NRN1 -344958bp (NM_016388.2)	A	G	G	0.64	0.59	0.002840	Recessive	1.68	1.2-2.4	SEQ ID No:629	SEQ ID No:630	SEQ ID No:971	
rs943509	9	75,218,105	OSTF1 +2267888bp (NM_012383.3)	A	G	G	0.35	0.27	0.003765	Allele	1.45	1.1-1.9	SEQ ID No:631	SEQ ID No:632	SEQ ID No:972	
rs3803347	4	108,959,666	PAPSS1 Intron5 (NM_005443.4)	A	G	A	0.62	0.56	0.009262	Recessive	1.59	1.1-2.3	SEQ ID No:633	SEQ ID No:634	SEQ ID No:973	
rs684773	3	137,439,003	PCCB -128433bp (NM_000532.2)	A	C	A	0.20	0.13	0.001687	Allele	1.67	1.2-2.3	SEQ ID No:635	SEQ ID No:636	SEQ ID No:974	
rs3957816	3	137,438,550	PCCB -132968bp (NM_000532.2)	A	G	G	0.22	0.15	0.001412	Allele	1.64	1.2-2.2	SEQ ID No:637	SEQ ID No:638	SEQ ID No:975	
rs548288	3	137,452,453	PCCB Intron1 (NM_000532.2)	A	G	A	0.21	0.14	0.003173	Allele	1.60	1.2-2.2	SEQ ID No:639	SEQ ID No:640	SEQ ID No:976	
rs6956081	3	137,529,887	PCCB Intron13 (NM_000532.2)	A	G	A	0.23	0.16	0.004050	Allele	1.54	1.1-2.1	SEQ ID No:641	SEQ ID No:642	SEQ ID No:977	
rs2151078	10	55,864,965	PCDH15 Intron3 (NM_033056.2)	A	G	A	0.95	0.89	0.000379	Allele	2.25	1.4-3.5	SEQ ID No:643	SEQ ID No:644	SEQ ID No:978	
rs2537255	21	40,143,991	PCP4 -172598bp (NM_006198.1)	A	C	A	0.68	0.58	0.000724	Allele	1.51	1.2-1.9	SEQ ID No:645	SEQ ID No:646	SEQ ID No:979	
rs2837248	21	40,141,638	PCP4 -196126bp (NM_006198.1)	A	G	G	0.66	0.58	0.002496	Allele	1.44	1.1-1.8	SEQ ID No:647	SEQ ID No:648	SEQ ID No:980	

[0282] [Table 67]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs10869589	9	75,420,603	PCSK5 -314572bp (NM_006200.2)	A	C	C	0.71	0.65	0.000721	Dominant	2.89	1.6-5.3	SEQ ID No:649	SEQ ID No:650	SEQ ID No:981	
rs6045666	20	1,888,504	PDYN +18899bp (NM_024411.2)	A	G	A	0.32	0.24	0.001071	Allele	1.54	1.2-2	SEQ ID No:651	SEQ ID No:652	SEQ ID No:982	
rs12260432	6	12,624,571	PHACTR1 -291248bp (XM_166420)	A	G	G	0.56	0.54	0.009685	Recessive	1.62	1.1-2.3	SEQ ID No:653	SEQ ID No:654	SEQ ID No:983	
rs9349248	6	12,621,612	PHACTR1 -204207bp (XM_166420)	A	G	G	0.55	0.51	0.002906	Recessive	1.77	1.2-2.6	SEQ ID No:655	SEQ ID No:656	SEQ ID No:984	
rs1828632	3	147,397,711	PLSCR4 intron6 (NM_020353.1)	A	G	A	0.44	0.39	0.003839	Dominant	1.65	1.2-2.3	SEQ ID No:657	SEQ ID No:658	SEQ ID No:985	
rs1196185	2	182,710,465	PPP1R1C Intron2 (XM_067137)	A	T	T	0.65	0.56	0.002825	Allele	1.43	1.1-1.8	SEQ ID No:659	SEQ ID No:660	SEQ ID No:986	SEQ ID No:1055
rs1196155	2	182,746,778	PPP1R1C Intron2 (XM_067137)	C	G	G	0.66	0.57	0.003038	Allele	1.43	1.1-1.8	SEQ ID No:661	SEQ ID No:662	SEQ ID No:987	SEQ ID No:1056
rs2701664	2	182,734,170	PPP1R1C Intron2 (XM_067137)	A	G	A	0.65	0.56	0.003373	Allele	1.42	1.1-1.8	SEQ ID No:663	SEQ ID No:664	SEQ ID No:988	
rs1196160	2	182,733,518	PPP1R1C Intron3 (XM_067137)	A	G	A	0.65	0.56	0.004951	Allele	1.40	1.1-1.8	SEQ ID No:665	SEQ ID No:666	SEQ ID No:989	
rs7802749	7	94,432,292	PPP1R9A Intron4 (XM_371933)	A	G	A	0.54	0.44	0.000155	Recessive	2.16	1.4-3.2	SEQ ID No:667	SEQ ID No:668	SEQ ID No:990	
rs10485223	6	100,300,726	PRDM13 +130551bp (NM_021620.2)	A	G	G	0.77	0.70	0.003464	Dominant	2.95	1.4-6.1	SEQ ID No:669	SEQ ID No:670	SEQ ID No:991	
rs17826560	6	100,302,299	PRDM13 +132124bp (NM_021620.2)	A	G	A	0.77	0.70	0.003472	Dominant	2.85	1.4-5.8	SEQ ID No:671	SEQ ID No:672	SEQ ID No:992	
rs4240580	6	100,308,187	PRDM13 +138012bp (NM_021620.2)	A	G	A	0.77	0.70	0.004890	Dominant	2.60	1.3-5.1	SEQ ID No:673	SEQ ID No:674	SEQ ID No:993	
rs6991277	8	97,469,327	FTDSS1 +53377bp (NM_014754.1)	A	G	A	0.92	0.87	0.002092	Recessive	1.93	1.3-2.9	SEQ ID No:675	SEQ ID No:676	SEQ ID No:994	
rs6035140	20	1,884,292	FTTNS1 +157550bp (NM_080792.1)	A	G	G	0.33	0.24	0.000560	Allele	1.57	1.2-2	SEQ ID No:677	SEQ ID No:678	SEQ ID No:995	

[0283] [Table 68]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs10815959	9	8,806,479	PTPRD -82533bp (NM_002839.1), PTPRD -82533bp (NM_130391.1), PTPRD -82533bp (NM_130392.1), PTPRD -82533bp (NM_130393.1)	A	G	G	0.58	0.49	0.001073	Allele	1.47	1.2-1.9	SEQ ID No:679	SEQ ID No:680	SEQ ID No:996	
rs4572656	20	40,112,577	PTPRT +222308p (NM_007050.3), PTPRT +222308p (NM_133170.1)	A	G	G	0.87	0.81	0.001522	Recessive	1.80	1.3-2.6	SEQ ID No:681	SEQ ID No:682	SEQ ID No:997	
rs8003168	14	71,433,141	RGS6 -364458p (NM_004296.3)	A	G	G	0.46	0.38	0.002336	Dominant	1.70	1.2-2.4	SEQ ID No:683	SEQ ID No:684	SEQ ID No:998	
rs734380	19	63,590,775	RPS5 Intron1 (NM_001009.2)	A	C	C	0.50	0.42	0.000556	Dominant	1.91	1.3-2.8	SEQ ID No:685	SEQ ID No:686	SEQ ID No:999	
rs734379	19	63,590,994	RPS5 Intron1 (NM_001009.2)	A	G	A	0.58	0.50	0.004407	Allele	1.40	1.1-1.8	SEQ ID No:687	SEQ ID No:688	SEQ ID No:1000	
rs16833786	3	124,236,120	SEMA5B -59788p (NM_018987.1)	A	G	G	0.09	0.05	0.006753	Dominant	1.99	1.2-3.3	SEQ ID No:689	SEQ ID No:690	SEQ ID No:1001	
rs16833788	3	124,236,700	SEMA5B -65586p (NM_018987.1)	A	T	A	0.09	0.05	0.005712	Dominant	2.01	1.2-3.3	SEQ ID No:691	SEQ ID No:692	SEQ ID No:1002	SEQ ID No:1057
rs7624272	3	124,178,241	SEMA5B Intron1 (NM_018987.1)	A	G	G	0.10	0.06	0.005254	Dominant	1.99	1.2-3.2	SEQ ID No:693	SEQ ID No:694	SEQ ID No:1003	
rs6995270	8	134,582,401	SLAT4A Intron2 (NM_003033.2), SLAT4A Intron2 (NM_173344.1)	A	G	G	0.51	0.42	0.001415	Allele	1.46	1.2-1.8	SEQ ID No:695	SEQ ID No:696	SEQ ID No:1004	
rs517578	20	1,637,270	SIRPB2 -508668p (NM_018556.2), SIRPB2 -508668p (NM_080816.1)	A	G	A	0.40	0.32	0.000543	Dominant	1.80	1.3-2.5	SEQ ID No:697	SEQ ID No:698	SEQ ID No:1005	
rs10877835	12	38,637,759	SLC2A13 Intron3 (NM_052885.1)	A	C	A	0.14	0.08	0.001628	Allele	1.86	1.3-2.7	SEQ ID No:699	SEQ ID No:700	SEQ ID No:1006	
rs11116586	12	83,650,812	SLC6A15 +1060869p (NM_182767.2), SLC6A15 +1278229p (NM_018057.3)	A	G	A	0.71	0.63	0.002119	Allele	1.47	1.1-1.9	SEQ ID No:701	SEQ ID No:702	SEQ ID No:1007	
rs10862927	12	83,643,704	SLC6A15 +1131949p (NM_182767.2), SLC6A15 +1349309p (NM_018057.3)	C	G	G	0.71	0.63	0.002381	Allele	1.46	1.1-1.9	SEQ ID No:703	SEQ ID No:704	SEQ ID No:1008	SEQ ID No:1058
rs7736074	5	1,242,456	SLC6A19 -123108p (XM_291120)	C	G	G	0.63	0.54	0.002001	Allele	1.45	1.1-1.8	SEQ ID No:705	SEQ ID No:706	SEQ ID No:1009	SEQ ID No:1059
rs7757759	7	127,288,765	SND1 Intron16 (NM_014390.1)	A	C	C	0.33	0.25	0.001359	Allele	1.52	1.2-2	SEQ ID No:707	SEQ ID No:708	SEQ ID No:1010	

[0284] [Table 69]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency in Progressive Glaucoma Group	High-Risk Allele Frequency in Nonprogressive Glaucoma 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
rs3757760	7	127,252,147	SND1 Intron16 (NM_014390.1)	A	G	G	0.30	0.23	0.002990	Dominant	1.65	1.2-2.3	SEQ ID No:709	SEQ ID No:710	SEQ ID No:1011	
rs2241291	7	127,232,825	SND1 Intron16 (NM_014390.1), NAG8 Exon1 (NM_014411.1)	A	G	A	0.30	0.23	0.003295	Dominant	1.64	1.2-2.3	SEQ ID No:711	SEQ ID No:712	SEQ ID No:1012	
rs698408	7	126,939,887	SND1 Intron8 (NM_014390.1)	A	G	G	0.30	0.24	0.007498	Dominant	1.57	1.1-2.2	SEQ ID No:713	SEQ ID No:714	SEQ ID No:1013	
rs696518	3	137,602,998	STAG1 Intron21 (NM_005862.1)	A	C	A	0.24	0.17	0.003186	Allele	1.55	1.2-2.1	SEQ ID No:715	SEQ ID No:716	SEQ ID No:1014	
rs959983	3	137,547,245	STAG1 Intron29 (NM_005862.1)	A	G	G	0.21	0.14	0.002581	Allele	1.61	1.2-2.2	SEQ ID No:717	SEQ ID No:718	SEQ ID No:1015	
rs2547455	5	75,381,858	SV2C -331378bp (XM_043493)	A	G	G	0.78	0.71	0.004139	Allele	1.47	1.1-1.9	SEQ ID No:719	SEQ ID No:720	SEQ ID No:1016	
rs4308461	5	75,339,908	SV2C -750878bp (XM_043493)	A	C	A	0.78	0.70	0.002704	Allele	1.49	1.1-1.9	SEQ ID No:721	SEQ ID No:722	SEQ ID No:1017	
rs7703461	5	75,529,168	SV2C Intron3 (XM_043493)	A	G	A	0.38	0.28	0.000109	Recessive	3.09	1.7-5.5	SEQ ID No:723	SEQ ID No:724	SEQ ID No:1018	
rs7534078	1	199,346,710	SYT2 Intron1 (NM_177402.3)	A	G	A	0.36	0.27	0.000752	Allele	1.54	1.2-2	SEQ ID No:725	SEQ ID No:726	SEQ ID No:1019	
rs2247154	15	68,024,022	TLE3 +105451bp (NM_005078.1)	A	G	A	0.80	0.75	0.002275	Recessive	1.68	1.2-2.4	SEQ ID No:727	SEQ ID No:728	SEQ ID No:1020	
rs12591327	15	60,990,221	TLN2 +694888bp (NM_015059.1)	A	T	T	0.62	0.53	0.001432	Recessive	1.78	1.2-2.5	SEQ ID No:729	SEQ ID No:730	SEQ ID No:1021	SEQ ID No:1060
rs16886390	6	76,038,298	TMEM30A Intron1 (NM_018247.1)	A	G	A	0.88	0.82	0.000151	Recessive	2.15	1.4-3.2	SEQ ID No:731	SEQ ID No:732	SEQ ID No:1022	
rs9679229	2	181,320,188	UBE2E3 -350430bp (NM_182678.1), UBE2E3 -350660bp (NM_006357.2)	C	G	G	0.79	0.73	0.001212	Recessive	1.73	1.2-2.4	SEQ ID No:733	SEQ ID No:734	SEQ ID No:1023	SEQ ID No:1061
rs4667078	2	181,302,702	UBE2E3 -367916bp (NM_182678.1), UBE2E3 -368146bp (NM_006357.2)	A	G	G	0.79	0.73	0.001875	Recessive	1.69	1.2-2.4	SEQ ID No:735	SEQ ID No:736	SEQ ID No:1024	
rs10460373	2	181,298,487	UBE2E3 -372131bp (NM_182678.1), UBE2E3 -372361bp (NM_006357.2)	A	C	C	0.80	0.73	0.001107	Recessive	1.73	1.2-2.4	SEQ ID No:737	SEQ ID No:738	SEQ ID No:1025	

[0285] [Table 70]

dbSNP ID	Chromosome	Physical Location	Exon, Intron	Allele 1	Allele 2	High-Risk Allele	High-Risk Allele Frequency In Progressive Glaucoma Group	High-Risk Allele Frequency In Nonprogressive Glaucoma 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
rs11691504	2	181,292,695	UBE2E3 -377923bp (NM_182678.1), UBE2E3 -378153bp (NM_006357.2)	A	C	A	0.79	0.73	0.001937	Recessive	1.69	1.2-2.3	SEQ ID No:739	SEQ ID No:740	SEQ ID No:1026	
rs1840111	2	181,185,671	UBE2E3 -484947bp (NM_182678.1), UBE2E3 -485177bp (NM_006357.2)	A	G	G	0.74	0.68	0.006435	Recessive	1.58	1.1-2.2	SEQ ID No:741	SEQ ID No:742	SEQ ID No:1027	
rs1453054	2	181,185,413	UBE2E3 -485205bp (NM_182678.1), UBE2E3 -485435bp (NM_006357.2)	A	C	C	0.75	0.69	0.006785	Recessive	1.57	1.1-2.2	SEQ ID No:743	SEQ ID No:744	SEQ ID No:1028	
rs2756463	4	70,508,724	UGT2B4 +179208p (NM_021139.1)	A	G	G	0.55	0.44	0.000142	Allele	1.56	1.2-2	SEQ ID No:745	SEQ ID No:746	SEQ ID No:1029	
rs7093891	10	111,593,021	XPNPEP1 +214938p (NM_020383.2)	A	G	G	0.68	0.61	0.001935	Recessive	1.70	1.2-2.4	SEQ ID No:747	SEQ ID No:748	SEQ ID No:1030	
rs2076147	20	39,246,420	ZHX3 Exon4 (NM_015035.2)	A	G	A	0.48	0.41	0.008262	Dominant	1.62	1.1-2.3	SEQ ID No:749	SEQ ID No:750	SEQ ID No:1031	
rs9416465	10	57,514,084	ZWINT +2731288p (NM_007057.2), ZWINT +2731288p (NM_032997.1)	A	G	G	0.81	0.74	0.009354	Allele	1.45	1.1-1.9	SEQ ID No:751	SEQ ID No:752	SEQ ID No:1032	

[0286] The single nucleotide polymorphisms listed in Tables 53 to 70 can be also used as a marker for predicting a progressive risk of glaucoma in the same manner.

[0287] 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.

[0288] 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.

[0289] 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 71 to 81 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.

[0290] [Table 71]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs6577539	1	8,919,302	8,937,444	-
rs271351	1	29,730,945	29,826,068	-
rs490647	1	36,746,869	37,168,937	GRIK3
rs4927088	1	54,404,217	54,584,113	SSBP3
rs687328	1	67,652,235	67,824,796	-
rs11590929	1	87,841,409	87,950,062	-
rs947130	1	119,723,364	119,807,964	HSD3B1
rs10494300	1	151,492,990	151,655,827	KCNN3
rs2293325	1	164,125,293	164,219,505	CD3Z
rs7534078	1	199,296,545	199,563,030	SYT2 JARID1B AK125746
rs1416658	1	211,567,280	211,867,016	KCNK2
rs11117962	1	214,193,090	214,568,804	SPATA17
rs1529404	2	16,119,969	16,137,052	-
rs1104870	2	29,196,209	30,056,083	FLJ34931 ALK RSNL2
rs10172264	2	53,257,353	53,405,293	-
rs11691031	2	100,895,131	101,274,767	NPAS2 RPL31 TBC1D8
rs787433	2	145,590,348	145,799,392	-
rs1358105	2	150,299,586	150,541,213	FLJ32955
rs7569506	2	165,366,767	165,555,753	COBLL1

[0291] [Table 72]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs10460373	2	181,134,445	181,453,645	-
rs1196185	2	182,676,057	182,807,925	PPP1R1C
rs1520855	2	189,708,226	190,181,703	WDR75 COL5A2
rs16860887	2	197,523,235	197,888,268	PGAP1 ANKRD44
rs4261668	2	210,923,619	211,070,689	MYL1
rs4076919	2	216,497,213	216,578,828	-
rs7420360	2	221,677,221	221,753,564	-
rs6739369	2	229,714,194	229,961,562	PID1
rs7428299	3	5,570,819	5,773,991	-
rs6763643	3	39,826,307	40,276,808	MYRIP

[0292] [Table 73]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs453570	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

[**0293**] [Table 74]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs6773050	3	120,495,910	120,761,171	CDGAP CD80 BC003192 TMEM39A AK126736 MDS010 C3orf1
rs7624272	3	124,110,731	124,251,512	SEMA5B
rs3957816	3	137,167,265	137,992,964	PPP2R3A RNF184 PCCB STAG1
rs1828652	3	147,390,338	147,696,420	PLSCR2 PLSCR4
rs12490570	3	154,551,245	154,737,123	LOC152118
rs784288	3	170,068,388	170,864,176	MDS1 EV11
rs11712746	3	179,224,760	179,591,920	-
rs17605639	4	27,256,221	27,298,338	-
rs2736463	4	70,403,494	70,521,560	-
rs3805347	4	108,823,267	108,999,023	PAPSS1
rs7692155	4	123,377,225	123,922,063	KIAA1109 CR936613 IL2 Tenr IL21
rs11734419	4	140,995,151	141,432,838	MAML3
rs7736074	5	1,212,749	1,276,385	AK096054 SLC6A19

[0294] [Table 75]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs7703461	5	75,337,998	75,657,172	SV2C
rs166296	5	115,752,543	115,938,450	SEMA6A
rs1560026	5	125,151,015	125,717,338	-
rs194229	5	158,058,265	158,756,752	EBF FLJ31951 MGC10067 IL12B
rs595805	6	5,940,860	6,265,923	F13A1 NRN1
rs9349248	6	12,554,461	12,626,674	-
rs9461154	6	25,387,627	25,728,737	LRRC16A
rs16886390	6	75,850,763	76,260,216	COL12A1 FILIP1 COX7A2 TMEM30A
rs3798425	6	76,074,522	76,686,994	FILIP1 SENP6 MYO6
rs531970	6	94,007,862	94,384,201	EPHA7
rs10485223	6	100,160,966	100,372,844	PRDM13
rs13193932	6	129,939,934	130,073,063	ARHGAP18
rs17070863	6	141,512,817	141,829,487	-

[0295] [Table 76]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs7767107	6	141,944,499	142,393,247	AK097143
rs6570564	6	143,882,061	144,194,015	PHACTR2
rs1621819	7	6,940,080	7,128,749	C1GALT1 AJ132443
rs12669138	7	9,422,364	9,677,953	-
rs10230371	7	18,308,609	18,810,233	HDAC9
rs17156635	7	28,112,180	28,638,749	CREB5
rs17171658	7	39,637,423	40,673,597	C7orf10 CDC2L5
rs17152739	7	78,803,891	78,947,358	-
rs7802749	7	94,162,046	94,722,947	PPP1R9A PON1 PON2 PON3
rs3757759	7	126,534,572	127,377,349	ZNF800 GCC1 ARF5 FSCN3 PAX4 NAG8 LRRC4 SND1
rs6601569	8	10,791,891	11,126,489	C8orf21 C8orf5 C8orf6 C8orf15 C8orf16 XKR6

[0296] [Table 77]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs4316157	8	12,664,980	12,698,048	-
rs10503907	8	31,616,810	32,720,310	NRG1 AK127911
rs9650336	8	38,606,462	38,689,512	-
rs4394361	8	96,504,810	96,604,166	-
rs4394361	8	97,343,317	97,558,505	BC002376 AK126443 PTDSS1
rs6995270	8	134,533,189	134,653,344	ST3GAL1
rs4142436	9	1,377,505	1,450,365	-
rs12554461	9	4,777,149	4,866,435	RCL1
rs10815959	9	8,304,247	10,602,509	PTPRD
rs2780197	9	16,976,415	17,493,915	CNTLN C9orf39
rs10967964	9	27,315,208	27,589,202	MOBKL2B IFNK C9orf72
rs10781440	9	68,550,170	69,099,672	PIP5K1B TJP2 PRKACG FXN FAM122A
rs943509	9	75,083,939	75,297,469	-
rs10869589	9	75,394,767	75,450,986	-
rs10512277	9	100,256,889	100,625,025	MURC MGC17337 BC090888 AL831919 TMEFF1 Corf30
rs4979255	9	107,506,524	107,557,442	-
rs2773395	9	125,999,689	126,067,452	-
rs2151078	10	55,250,866	56,231,057	PCDH15
rs9416465	10	57,227,132	57,996,501	ZWINT

[0297] [Table 78]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs1801041	10	69,539,256	70,125,600	MYPN ATOH7 PBLD HNRPH3 MAWBP HNRPH3 RUFY2 SLC25A16 DNA2 CXXC6
rs10823349	10	70,699,762	70,831,641	HK1
rs2395453	10	78,299,370	79,067,583	KCNMA1
rs7093891	10	111,370,433	111,673,192	XPNPEP1
rs7927545	11	11,249,002	11,600,128	GALNTL4
rs7112492	11	18,349,559	18,457,723	LDHAL6A LDHA LDHC
rs12800710	11	57,713,408	58,200,377	LPXN OR9Q2 OR1S2 OR1S1 OR10Q1 UNQ6469 LOC399898 OR5B17 OR5B3 OR5B2 OR5B12 ZFF91
rs504105	11	82,583,199	84,312,113	ANKRD42 DLG2 CCDC90B
rs10898459	11	85,583,115	85,745,023	EED HSPC138
rs161130	11	112,150,907	112,255,730	-

[0298] [Table 79]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs4269933	11	119,110,064	119,202,392	-
rs2322728	11	126,615,901	126,702,818	-
rs10877835	12	38,306,287	39,318,456	LOC283461 SLC2A13 BC047507 LRRK2 AK127729 AK093065
rs2169856	12	53,730,141	53,972,700	OR9K2 OR10A7 OR6C74
rs11175627	12	63,667,042	63,801,383	WIF1
rs7959848	12	82,043,793	82,360,242	-
rs11116586	12	83,546,501	83,667,628	-
rs7296095	12	114,297,666	114,443,627	-
rs11059862	12	127,746,927	127,761,568	-
rs17640758	13	42,473,098	42,596,252	DNAJD1
rs4643164	13	106,618,880	107,317,084	LOC728215
rs10483416	14	31,868,274	32,372,018	AKAP6
rs8003168	14	71,294,225	72,102,991	RGS6 AF130114 C14orf57
rs1622029	14	83,422,711	84,117,961	-
rs1187627	14	94,607,134	94,855,955	CLMN DICER1 FLJ45244
rs12900219	15	21,568,517	21,589,571	-

[0299] [Table 80]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs16941388	15	57,215,856	57,465,385	MYO1E
rs12591327	15	60,926,419	61,002,704	-
rs2247154	15	67,997,515	68,083,355	-
rs3863401	15	97,440,341	97,748,455	AK127177 LRRC28 HCC-8 DMN AK125000
rs6500718	16	5,725,135	5,792,957	-
rs12595990	16	12,053,556	12,575,647	SNX29
rs9302502	16	13,340,184	13,545,371	-
rs1816581	16	47,722,996	47,860,850	-
rs7198530	16	51,635,508	51,918,914	CHD9
rs1554401	16	63,494,458	63,713,420	CDH11
rs7212115	17	10,832,202	10,865,630	-
rs295869	17	32,165,628	32,234,457	-
rs8098925	18	69,240,762	69,384,770	-
rs1828132	18	72,356,779	72,410,800	-
rs12462868	19	41,159,572	41,215,615	CLIP3 LOC644096 FLJ36445 BC052573 C19orf46 ALKBH6
rs4802905	19	57,349,937	57,487,778	FLJ16287 ZNF766 PPP2R1A
rs734380	19	63,548,356	63,597,982	A1BG RPS5 ZNF497
rs517578	20	1,557,798	1,674,903	SIRPB2
rs6035140	20	1,822,813	1,926,301	SIRPA PTPNS1 PDYN
rs2050223	20	13,924,146	15,981,839	MACROD2

[0300] [Table 81]

Representative Single Nucleotide Polymorphism in the Region (Single Nucleotide Polymorphism with Lowest p-value)	Chromosome	Start Location	End Location	Genes in the Region
rs6083320	20	23,811,795	23,841,840	-
rs6132862	20	24,988,884	25,706,656	VSX1 ENTPD6 PYGB ABHD12 GINS1 NLP ZNF337 HDHD4
rs926663	20	38,563,539	38,754,165	MAFB
rs2076147	20	39,011,156	39,443,459	TOP1 PLCG1 ZHX3 LPIN3 EMILIN3 AF090938
rs909882	20	39,456,460	39,703,552	CHD6 AK124874
rs4572656	20	40,018,906	41,251,971	PTPRT
rs6017164	20	41,815,520	41,816,915	-
rs1321001	20	44,235,783	44,313,741	CDH22
rs4812180	20	58,608,933	58,748,410	-
rs6089908	20	61,470,599	61,628,090	KCNQ2 AK127527 Ak127768 AY358189 EEF1A2 C20orf149
rs369977	21	15,496,913	15,621,381	-
rs7275647	21	21,292,504	21,833,085	NCAM2
rs94967	21	40,026,415	40,223,190	PCP4 IGSF5
rs5750009	22	33,671,179	33,694,293	-

[0301] The region listed in Tables 71 to 81 is a region or gene considered to be linked with a single nucleotide polymorphism associated with the progression of glaucoma in the present invention listed in Tables 53 to 70, 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 70, and any of these single nucleotide polymorphisms can be used in the prediction of a progressive risk of glaucoma in the same manner.

[0302] Example 11 Logistic Regression Analysis

In the present invention, by combining any two or more single nucleotide polymorphisms determined to be involved in the progression 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 progression of glaucoma by statistically comparing allele or genotype frequencies can be used. In one example, 19 single nucleotide polymorphisms that showed a significant difference under the Bonferroni correction were subjected to the logistic regression analysis.

[0303] Out of 19 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 a criterion 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 a 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 a progressive 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 progressive glaucoma case. 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 82 shows the number of single nucleotide polymorphisms, alone or in a combination of arbitrary number, the number of combinations when arbitrary number of single nucleotide polymorphisms are 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.

[0304] As listed in Table 82, according to a stepwise method, the 19 single nucleotide polymorphisms (13 single nucleotide polymorphisms, if those belonging to the same LD block were each counted as one) were narrowed down to 10 single nucleotide polymorphisms (rs4316157, rs1358105, rs4076919, rs2395453, rs6132862, rs10483416, rs787433, rs4802905, rs12554461, and rs4927088). Therefore, it shows that similar results are obtained with the combination of 10 single nucleotide polymorphisms even when the remaining 3 single nucleotide polymorphisms are added. 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 57.6 ± 2.4% 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 67.8% in a case that all the ten were combined.

[0305] [Table 82]

The Number of SNP	The Number of Combination	Concordance Rate (Mean Value)	Standard Deviation
1	10	57.6	2.4
2	45	59.0	1.7
3	120	60.6	1.8
4	210	62.1	1.9
5	252	63.1	1.8
6	210	64.1	1.5
7	120	64.9	1.7
8	45	65.7	1.5
9	10	66.6	1.4
10	1	67.8	-

[0306] As described above, it was evident that, in the determination of a progressive 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.

[0307] As described above, an individual who has an allele or a genotype that is identified in a high frequency in the progressive glaucoma group disclosed in the present invention on the genome has a high progressive 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 progressive glaucoma group has a low progressive risk of glaucoma in future.

INDUSTRIAL APPLICABILITY

[**0308**] According to the method of the present invention, the level of a progressive 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, the method is useful because the period of a clinical trial for a glaucoma therapeutic drug can be shortened by selecting patients with a high progressive risk of glaucoma using a single nucleotide polymorphism associated with the progression of glaucoma in the present invention, and performing a clinical trial for a glaucoma therapeutic drug.

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 752 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 752 (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 a progressive 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 240.

[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 240,

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 240,

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 progressive 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 752 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: 753 to 1061 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 752 (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 a progressive 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 240, or wherein the base sequence in said step C2 is selected from the group consisting of base sequences shown in SEQ ID NOs: 753 to 771.

[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 240, 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 240,

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 progressive 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 752 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: 753 to 1061 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 a progressive 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 240 and/or the group consisting of SEQ ID NOs: 753 to 771.

[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 240 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: 753 to 771 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 240 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: 753 to 771 or a complementary sequence thereto.

[23] The kit according to claim 19, for use in further predicting the level of the progressive 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 752 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 752 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 752 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 752 (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 a progressive risk of glaucoma, comprising

the following steps of:

step (I): determining the presence or the absence of the progressive 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 progressive 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 progressive 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

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Santen Pharmaceutical Co.,Ltd.

<120> Determination method of risik for proceeding glaucoma

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