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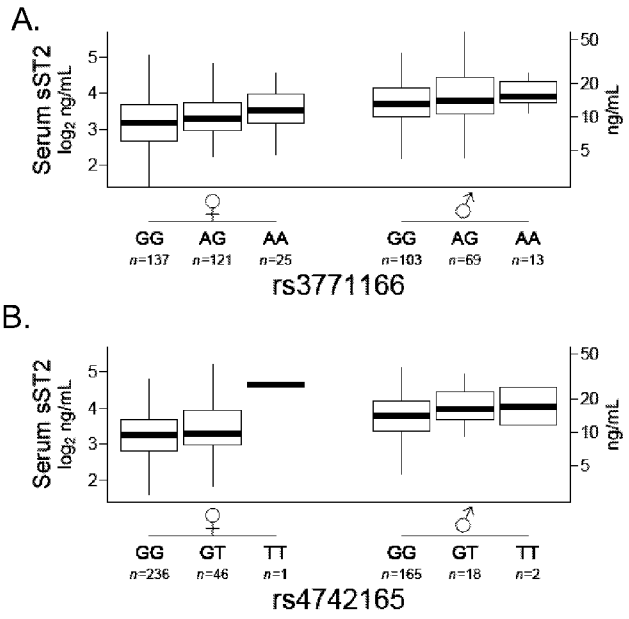
Figures 7A-7B



(57) Abstract: The invention relates to methods of treating a patient suffering from an IL-33-mediated disorder, such as asthma, comprising administering to the patient an IL-33 axis binding antagonist based on the genotype of the /L1RL1gene, the genotype of a polymorphism in genomic vicinity to the IL-33 gene, the expression level of periostin or the expression level of soluble ST2. The invention further relates to methods of determining whether a patient is at increased risk of an IL-33-mediated disorder, as well as methods of determining whether a patient suffering from such a disorder is likely to respond to a treatment comprising an IL-33 axis binding antagonist, based on the genotype of the/L1RL1gene the genotype of a polymorphism in genomic vicinity to the IL-33 gene, the expression level of periostin or the expression level of soluble ST2.

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THERAPEUTIC AND DIAGNOSTIC METHODS FOR IL-33-MEDIATED DISORDERS

FIELD OF THE INVENTION

The present invention is directed to methods of treating patients suffering from interleukin-33 (IL-33)-mediated disorders and methods of determining whether a patient is at increased risk for an IL-33-mediated disorder.

BACKGROUND

Interleukin-33 (IL-33) is a member of the interleukin-1 (IL-1) cytokine family that is encoded by the *IL33* gene, and is constitutively expressed in structural cells, such as smooth muscle, epithelial, and endothelial cells. IL-33 can be induced by inflammatory factors in macrophages and dendritic cells. Cellular stress caused by environmental triggers, such as allergens, toxins, and pathogens, can lead to IL-33 release. Bioavailable IL-33 associates with a heterodimeric IL-33 receptor complex composed of suppression of tumorigenicity 2 (ST2) protein and interleukin-1 receptor accessory protein (IL-1RAcP) to activate the AP-1 and NF-κB pathways through the adaptor protein myeloid differentiation primary response 88 (MyD88) and possibly MyD88-adapter-like (Mal) protein. IL-33 stimulates a number of cell types, including innate type II (ILC2) cells, mast cells, basophils, eosinophils, and dendritic cells, to promote Type 2 immunity.

The IL-33 pathway has been suggested to be involved in various diseases, including allergy-related diseases, for which there remains a need to develop improved methods for identifying patient populations best suited to therapy options.

SUMMARY

The present invention is directed to methods of treating patients suffering from interleukin-33 (IL-33)-mediated disorders and methods of determining whether a patient is at increased risk for an IL-33-mediated disorder.

In one aspect, the invention features a method of treating a patient suffering from an interleukin-33 (IL-33)-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs4988956 (SEQ ID NO: 1) or at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs4988956 (SEQ ID NO: 1) or at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each G allele at polymorphism rs4988956 (SEQ ID NO: 1) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist. In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) has a D' value greater than or equal to 0.6 to polymorphism rs4988956 (SEQ ID NO: 1). In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) is a polymorphism in Table 3. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1). In some embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10204137 (SEQ ID NO: 2) or at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding

antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10204137 (SEQ ID NO: 2) or at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each A allele at polymorphism rs10204137 (SEQ ID NO: 2) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist. In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) has a D' value greater than or equal to 0.6 to polymorphism rs10204137 (SEQ ID NO: 2). In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) is a polymorphism in Table 3. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2). In other embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10192036 (SEQ ID NO: 3) or at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10192036 (SEQ ID NO: 3) or at a polymorphism

in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each C allele at polymorphism rs10192036 (SEQ ID NO: 3) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist. In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) has a D' value greater than or equal to 0.6 to polymorphism rs10192036 (SEQ ID NO: 3). In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) is a polymorphism in Table 3. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3). In other embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10192157 (SEQ ID NO: 4) or at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10192157 (SEQ ID NO: 4) or at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype,

wherein the presence of each C allele at polymorphism rs10192157 (SEQ ID NO: 4) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist. In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) has a D' value greater than or equal to 0.6 to polymorphism rs10192157 (SEQ ID NO: 4). In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) is a polymorphism in Table 3. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4). In other embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10206753 (SEQ ID NO: 5) or at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10206753 (SEQ ID NO: 5) or at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each T allele at polymorphism rs10206753 (SEQ ID NO: 5) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5)

indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist. In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) has a D' value greater than or equal to 0.6 to polymorphism rs10206753 (SEQ ID NO: 5). In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) is a polymorphism in Table 3. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5). In other embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs4742165 (SEQ ID NO: 6) or at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs4742165 (SEQ ID NO: 6) or at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each T allele at polymorphism rs4742165 (SEQ ID NO: 6) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-

33 axis binding antagonist. In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) has a D' value greater than or equal to 0.6 to polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) is a polymorphism in Table 4. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6). In other embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise two or more of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at two or more polymorphisms selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), rs4742165 (SEQ ID NO: 6), and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if: (a) the genotype of the patient comprises a G allele at polymorphism rs4988956 (SEQ ID NO: 1); (b) the genotype of the patient comprises an A allele at polymorphism rs10204137 (SEQ ID NO: 2); (c) the genotype of the patient comprises a C allele at polymorphism rs10192036 (SEQ ID NO: 3); (d) the genotype of the patient comprises a C allele at polymorphism rs10192157 (SEQ ID NO: 4); (e) the genotype of the patient comprises a T allele at polymorphism rs10206753 (SEQ ID NO: 5) (f) the genotype of the patient comprises a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or (g) the genotype of the patient comprises an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at two or more polymorphisms selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), rs4742165 (SEQ ID NO: 6), and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); and (b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of: (i) each G allele at polymorphism rs4988956 (SEQ ID NO: 1); (ii) each A allele at polymorphism rs10204137 (SEQ ID NO: 2); (iii) each C allele at polymorphism rs10192036 (SEQ ID NO: 3); (iv) each C allele at polymorphism rs10192157 (SEQ ID NO: 4); (v) each T allele at polymorphism rs10206753 (SEQ ID NO: 5); (vi) each T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or (vii) each equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist. In some embodiments of this aspect, the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and an A allele at polymorphism rs10204137 (SEQ ID NO: 2). In some embodiments of this aspect, the genotype of the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a C allele at polymorphism rs10192036 (SEQ ID NO: 3). In some embodiments of this aspect, the genotype of the patient has been determined to further comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or a T allele at polymorphism rs10206753 (SEQ ID NO: 5). In some embodiments of this aspect, the genotype of the patient has been determined to further comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5). In some embodiments of this aspect, the genotype of the patient has been determined to comprise: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); and a T allele at polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the method further comprises administering an IL-33 axis binding antagonist to the patient.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the polymorphism in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1),

rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) has a D' value greater than or equal to 0.6 to the selected polymorphism. In some embodiments, the D' value is greater than or equal to 0.8. In some embodiments, the polymorphism in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) is a polymorphism in Table 3 or Table 4. In some embodiments, the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6). In other embodiments, the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

In another aspect, the invention features a method of selecting a therapy for a patient having an IL-33-mediated disorder, the method comprising: (a) determining the level of periostin in a sample derived from the patient; (b) comparing the level of periostin in the sample derived from the patient to a reference level of periostin; and (c) selecting a therapy comprising an IL-33 axis binding antagonist if the level of periostin in the sample is at or below the reference level. In some embodiments, the method further comprises administering a therapy comprising an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the level of soluble ST2 (sST2) in a sample derived from the patient has been determined to be at or above a reference level of sST2.

In another aspect, the invention features a method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising: (a) determining the level of sST2 in a sample derived from the patient; and (b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2, wherein the patient is at an increased risk of an IL-33-mediated disorder if the level of sST2 in the sample derived from the patient is at or above the reference level. In some embodiments, the method further comprises administering a therapy comprising an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of selecting a therapy for a patient having an IL-33-mediated disorder, the method comprising: (a) determining the level of sST2 in a sample derived from the patient; (b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2; and (c) selecting a therapy comprising an IL-33 axis binding antagonist if the level of sST2 in the sample is at or above the reference level. In some embodiments, the method further comprises administering a therapy comprising an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising: (a) determining the level of sST2 in a sample derived from the patient; (b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2; and (c) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the level of sST2 in the sample derived from the patient, wherein the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist if the level of sST2

in the sample is at or above the reference level. In some embodiments, the method further comprises administering a therapy comprising an IL-33 axis binding antagonist to the patient.

In another aspect, the invention features a method for assessing a treatment response of a patient treated with an IL-33 axis binding antagonist, the method comprising: (a) determining the level of sST2 in a sample derived from the patient at a time point during or after administration of the IL-33 axis binding antagonist; and (b) maintaining, adjusting, or stopping the treatment of the patient based on a comparison of the level of sST2 in the sample derived from the patient with a reference level of sST2, wherein a change in the level of sST2 in the sample derived from the patient compared to the reference level is indicative of a response to treatment with the IL-33 axis binding antagonist. In some embodiments of this aspect, the change is an increase in the level of sST2 and treatment is maintained. In other embodiments of this aspect, the change is a decrease in the level of sST2 and treatment is stopped.

In another aspect, the invention features a method for monitoring the response of a patient treated with a IL-33 axis binding antagonist, the method comprising: (a) determining the level of sST2 in a sample derived from the patient at a time point during or after administration of the IL-33 axis binding antagonist; and (b) comparing the level of sST2 in the sample derived from the patient with a reference level of sST2, thereby monitoring the response in the patient undergoing treatment with the IL-33 axis binding antagonist.

In some embodiments of any one of the above aspects, the method further comprises determining the level of periostin in a sample derived from the patient. In some embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin. In other embodiments, the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

In some embodiments of any one of the above aspects, the level of sST2 is a level of sST2 protein. In some embodiments, the sample derived from the patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof. In some embodiments, the sample derived from the patient is a serum sample. In some embodiments, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8). In some embodiments, the group of individuals is suffering from asthma. In some embodiments, the reference level of sST2 is a median level. In some embodiments, the group of individuals is a group of female individuals and the patient is female. In some embodiments, the group of individuals is a group of male individuals and the patient is male. In some embodiments, the reference level is determined in an individual at an earlier timepoint, e.g., before treatment with an an IL-33 axis binding antagonist or at an earlier timepoint during treatment with an an IL-33 axis binding antagonist.

In some embodiments of any one of the above aspects, the IL-33 axis binding antagonist is administered in combination with a tryptase-beta binding antagonist, a chemoattractant receptor-

homologous molecule expressed on Th2 cells (CRTH2) binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a JAK1 antagonist, and/or an interleukin-5 (IL-5) binding antagonist. In some embodiments, the IL-33 axis binding antagonist is an IL-33 binding antagonist, an ST2 binding antagonist, or an IL-1RAcP binding antagonist. In some embodiments, (a) the IL-33 binding antagonist is an anti-IL33 antibody or antigen-binding fragment thereof; (b) the ST2 binding antagonist is an ST2-Fc protein, an anti-ST2 antibody, or antigen-binding fragment thereof; or (c) the IL-1RAcP binding antagonist is an anti-IL-1RAcP antibody.

In some embodiments of any one of the above aspects, the IL-33-mediated disorder is selected from the group consisting of an inflammatory condition, an immune disorder, a fibrotic disorder, an eosinophilic disorder, an infection, pain, a central nervous system disorder, a solid tumor, and an ophthalmologic disorder. In some embodiments, the inflammatory condition is selected from the group consisting of asthma, sepsis, septic shock, atopic dermatitis, allergic rhinitis, rheumatoid arthritis, and chronic obstructive pulmonary disease (COPD). In some embodiments, the immune disorder is selected from the group consisting of asthma, rheumatoid arthritis, allergy, anaphylaxis, anaphylactic shock, allergic rhinitis, psoriasis, inflammatory bowel disease (IBD), Crohn's disease, diabetes, and liver disease. In some embodiments, the fibrotic disease is idiopathic pulmonary fibrosis (IPF). In some embodiments, the eosinophilic disorder is an eosinophil-associated gastrointestinal disorder (EGID). In some embodiments, the EGID is eosinophilic esophagitis. In some embodiments, the infection is a helminth infection, a protozoan infection, or a viral infection. In some embodiments, the protozoan infection is a *Leishmania major* infection. In some embodiments, the viral infection is a respiratory syncytial virus (RSV) infection or an influenza infection. In some embodiments, the pain is inflammatory pain. In some embodiments, the central nervous system disorder is Alzheimer's disease. In some embodiments, the solid tumor is selected from the group consisting of breast tumor, colon tumor, prostate tumor, lung tumor, kidney tumor, liver tumor, pancreas tumor, stomach tumor, intestinal tumor, brain tumor, bone tumor, and skin tumor. In some embodiments, the ophthalmologic disorder is age-related macular degeneration (AMD) or retinopathy of the eye.

In some embodiments of any one of the above aspects, the reference level of periostin is between about 23 ng/ml and about 50 ng/ml.

In some embodiments of any one of the above aspects, the sample derived from the patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof.

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise two or more of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise two or more of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise two or more of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In another aspect, the invention features an IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level.

In another aspect, the invention features a use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level.

In another aspect, the invention features a composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated

disorder, wherein the patient has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level.

Brief Description of the Drawings

FIGURE 1A shows a schematic representation of the interleukin-33 (IL-33) receptor complex. Red lines indicate the location of the indicated protective ST2 variants. MAPKK, Mitogen activated protein kinase kinase.

FIGURE 1B is a rendering of the crystal structure of the TLR10 Toll/Interleukin-1 receptor (TIR) domain showing the mapped locations of the A433T and Q501R variants of ST2.

FIGURES 1C and 1D are graphs showing the results of reporter assay experiments to determine the IL-33 response of the common ST2 variant or protective ST2 variant (A433T Q501R T549I L551S). HEK-BLUE™ cells expressing the indicated variant were stimulated with increasing concentrations of recombinant human IL-33 (Figure 1C) or IL-1β (Figure 1D) for 20 h. Cytokine activity was measured by induction of the NF-κB/AP-1 secreted alkaline phosphatase (SEAP) reporter gene. Graphs show mean ± SEM of 3 single clone cell lines. * indicates $p < 0.05$. Data are representative of three independent experiments. The half-maximal effective concentration (EC50) of IL-33 (Figure 1C) or IL-1β (Figure 1D) for the indicated variant is shown in the table.

FIGURES 2A and 2B are graphs showing the results of reporter assay experiments to determine the IL-33 response of the common variant or protective ST2 variants. Batch clones of HEK-BLUE™ cells expressing the indicated ST2 variant were stimulated with increasing concentrations of human recombinant IL-33 (Figure 2A) or IL-1β (Figure 2B) for 20 h. Cytokine activity was measured by induction of the NF-κB/AP-1 SEAP reporter gene. Graphs show mean ± SD of triplicates. Data are representative of three independent experiments. The table shows the EC50 of IL-33 (Figure 2A) or IL-1β (Figure 2B) for the indicated variant.

FIGURE 3A are histograms showing the results of flow cytometry experiments comparing the surface expression levels of the indicated *IL1RL1* variants in HEK-BLUE™ cells.

FIGURE 3B is a histogram showing the results of flow cytometry experiments comparing IL-1RAcP surface expression levels in HEK-BLUE™ cells expressing the indicated *IL1RL1* variants.

FIGURE 3C is a graph showing the mean fluorescence intensity (MFI) of ST2 surface expression from the graphs shown in Figure 3A.

FIGURE 3D are graphs showing the results of quantitative reverse transcription polymerase chain reaction (RT-PCR) measurements of *IL1RL1* (left panel) and *IL1RAcP* (right panel) expression. mRNA levels are presented relative to expression of the housekeeping gene *RPL19* (encoding the ribosomal protein L19).

FIGURE 4 is a graph showing interleukin-8 (IL-8) secretion levels of purified blood eosinophils obtained from human donors carrying either the protective or common *IL1RL1* variants treated with the indicated concentration of purified IL-33, as assessed by an enzyme-linked immunosorbent assay (ELISA).

FIGURE 5A is a graph showing quantitative RT-PCR of sST2 mRNA levels from purified blood eosinophils and basophils from human donors carrying either the protective or common *IL1RL1* variants, as assessed by ELISA.

FIGURE 5B is a graph showing plasma sST2 levels from human donors carrying either the protective or common *IL1RL1* variants, as assessed by ELISA. Plots display mean ± SEM of 3 single clones or 4 individual donors per group. * indicates $p < 0.05$ as determined by paired *t* test.

FIGURE 6 is a table showing the association of protective *IL1RL1* variants with periostin levels. CHR, chromosome; P, *p* value; OR, odds ratio; and MAF, minor allele frequency.

FIGURE 7A is a box plot graph showing observed distributions of log2-transformed asthmatic serum soluble ST2 (sST2) by genotype at rs3771166 and sex (female ♀, male ♂).

FIGURE 7B is a box plot graph showing observed distributions of log2-transformed asthmatic serum soluble ST2 (sST2) by genotype at rs4742165 and sex (female ♀, male ♂).

FIGURE 7C is a graph showing the least squares mean (lsmean) and standard error of log2-transformed asthmatic sST2 levels with rs4742165 (x-axis) and rs3771166 genotypes (series). Right axes correspond to untransformed values of sST2 levels (ng/mL).

FIGURE 8 is a series of graphs showing pairwise correlation of baseline biomarker levels. Pairwise analyses are represented for baseline biomarker levels. Lower panels are scatterplots and upper panels are Spearman's ρ estimates and counts of paired data. The x and y axes are defined by the row and column intersection with the diagonal (biomarker and units) and plot margins (scales). A line represents a LOWESS fit of the data.

Detailed Description of Embodiments of the Invention

I. Definitions

The term "administering" means the administration of a pharmaceutical composition (e.g., comprising an interleukin-33 (IL-33) axis binding antagonist) to a patient (e.g., a patient suffering from asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)).

"Antagonists" as used herein refer to compounds or agents which inhibit or reduce the biological activity of the molecule to which they bind. Antagonists include antibodies, synthetic or native-sequence peptides, immunoadhesins, and small-molecule antagonists that bind to, for example, an IL-33 axis protein, optionally conjugated with or fused to another molecule. A "blocking" antibody or an "antagonist" antibody is one which inhibits or reduces biological activity of the antigen it binds.

The term "asthma" refers herein to a disorder characterized by variable and recurring symptoms, reversible airflow obstruction (e.g., by bronchodilator), and bronchial hyper-responsiveness, which may or may not be associated with underlying inflammation. Asthma may therefore be inflammatory/inflamed asthma or non-inflammatory/non-inflamed asthma. Examples of asthma include allergic asthma, exercise-induced asthma, aspirin sensitive/exacerbated asthma, atopic asthma, severe asthma, mild asthma, moderate to severe asthma, corticosteroid naïve asthma, chronic asthma, corticosteroid resistant asthma, corticosteroid refractory asthma, newly diagnosed and untreated asthma, asthma due to smoking, asthma uncontrolled on corticosteroids, and other asthmas as mentioned in Bousquet et al. (*J. Allergy Clin. Immunol.* 126(5): 926-938, 2010).

The terms "biomarker" and "marker" are used interchangeably herein to refer to a DNA, RNA, protein, carbohydrate, or glycolipid-based molecular marker, the expression or presence of which in a subject's or patient's sample can be detected by standard methods (or methods disclosed herein) and is useful, for example, for identifying the risk profile of a subject for a disease or disorder and/or the likelihood of responsiveness or sensitivity of a mammalian subject to a treatment (e.g., a treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)). Expression of such a biomarker may be determined to be higher or lower in a sample obtained from a patient that has an increased or decreased likelihood of being responsive to an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) than a reference level (including, e.g., the median expression level of the biomarker in samples from a group/population of patients (e.g., asthma patients); the level of the biomarker in samples from a group/population of control individuals (e.g., healthy individuals); or the level in a sample previously obtained from the individual at a prior time). In some embodiments, individuals having an expression level that is greater than or less than the reference expression level of at least one gene, such as periostin or ST2 (e.g., sST2), can also be identified as likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist).

A "disorder" or "disease" is any condition that would benefit from treatment or diagnosis (e.g., determination of risk for an IL-33-mediated disorder) with a method of the invention. This includes chronic and acute disorders or diseases including those pathological conditions which predispose the mammal to the disorder in question. Examples of disorders to be treated herein include IL-33-mediated disorders (e.g., asthma, allergic rhinitis, atopic dermatitis, and fibrosis (e.g., pulmonary fibrosis, e.g., idiopathic pulmonary fibrosis)).

The term "effective amount" refers to an amount of a drug effective to treat a disease or disorder in a subject or patient, such as a mammal, e.g., a human.

The term "genotype" refers to a description of the alleles of a gene contained in an individual or a sample. In the context of this invention, no distinction is made between the genotype of an individual and the genotype of a sample originating from the individual. Although typically a genotype is determined from samples of diploid cells, a genotype can be determined from a sample of haploid cells, such as a sperm cell.

The terms "interleukin 1 receptor-like 1 (IL1RL1)" and "ST2," used interchangeably herein, refer to any native ST2 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. ST2 is also referred to in the art as DER4, T1, and FIT-1. The term encompasses "full-length," unprocessed ST2, as well as any form of ST2 that results from processing in the cell. At least four isoforms of ST2 are known in the art, including soluble (sST2, also known as IL1RL1-a) and transmembrane (ST2L, also known as IL1RL1-b), which arise from differential mRNA expression from a dual promoter system, and ST2V and ST2LV, which arise from alternative splicing, as described below. The domain structure of ST2L includes three extracellular immunoglobulin-like C2 domains, a transmembrane domain, and a cytoplasmic Toll/Interleukin-1 receptor (TIR) domain. sST2 lacks the transmembrane and cytoplasmic domains contained within ST2L and includes a unique 9 amino acid (a.a.) C-terminal sequence (see, e.g., Kakkar et al. *Nat. Rev. Drug Disc.* 7: 827-840, 2008). sST2 can function as a decoy receptor to inhibit soluble IL-33. The term also

encompasses naturally occurring variants of ST2, e.g., splice variants (e.g., ST2V, which lacks the third immunoglobulin motif and has a unique hydrophobic tail, and ST2LV, which lacks the transmembrane domain of ST2L) or allelic variants (e.g., variants that are protective against asthma risk or that confer asthma risk as described herein). The amino acid sequence of an exemplary human ST2 can be found, for example, under UniProtKB accession number Q01638. ST2 is a part of the IL-33 receptor along with the co-receptor protein IL-1RAcP. Binding of IL-33 to ST2 and the co-receptor interleukin-1 receptor accessory protein (IL-1RAcP) forms a 1:1:1 ternary signaling complex to promote downstream signal transduction, as depicted in Figure 1A (see, e.g., Lingel et al. *Structure* 17(10): 1398-1410, 2009, and Liu et al. *Proc. Natl. Acad. Sci.* 110(37): 14918-14924, 2013).

The term "interleukin-33 (IL-33)," as used herein, refers to any native IL-33 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. IL-33 is also referred to in the art as nuclear factor of high endothelial venules (NF-HEV; see, e.g., Baekkevold et al. *Am. J. Pathol.* 163(1): 69-79, 2003), DVS27, C9orf26, and interleukin-1 family member 11 (IL-1F11). The term encompasses "full-length," unprocessed IL-33, as well as any form of IL-33 that results from processing in the cell. Human full-length, unprocessed IL-33 contains 270 a.a. and may also be referred to as IL-$33_{1\text{-}270}$. Processed forms of human IL-33 include, for example, IL-$33_{95\text{-}270}$, IL-$33_{99\text{-}270}$, IL-$33_{109\text{-}270}$, IL-$33_{112\text{-}270}$, IL-$33_{1\text{-}178}$, and IL-$33_{179\text{-}270}$ (Lefrançais et al. *Proc. Natl. Acad. Sci.* 109(5): 1673-1678, 2012 and Martin, *Semin. Immunol.* 25: 449-457, 2013). In some embodiments, processed forms of human IL-33, e.g., IL-$33_{95\text{-}270}$, IL-$33_{99\text{-}270}$, IL-$33_{109\text{-}270}$, or other forms processed by proteases such as calpain, proteinase 3, neutrophil elastase, and cathepsin G may have increased biological activity compared to full-length IL-33. The term also encompasses naturally occurring variants of IL-33, for example, splice variants (e.g., the constitutively active splice variant *spIL-33* which lacks exon 3, Hong et al. *J. Biol. Chem.* 286(22): 20078-20086, 2011) or allelic variants. IL-33 may be present within a cell (e.g., within the nucleus) or as a secreted cytokine form. Full-length IL-33 protein contains a helix-turn-helix DNA-binding motif including nuclear localization sequence (a.a.1-75 of human IL-33), which includes a chromatin binding motif (a.a. 40-58 of human IL-33). Forms of IL-33 that are processed and secreted lack these N-terminal motifs. The amino acid sequence of an exemplary human IL-33 can be found, for example, under UniProtKB accession number O95760.

By "IL-33 axis" is meant a nucleic acid (e.g., a gene or mRNA transcribed from the gene) or polypeptide that is involved in IL-33 signal transduction. For example, the IL-33 axis may include the ligand IL-33, a receptor (e.g., ST2 and/or IL-1RAcP), adaptor molecules (e.g., MyD88), or proteins that associate with receptor molecules and/or adaptor molecules (e.g., kinases, such as interleukin-1 receptor-associated kinase 1 (IRAK1) and interleukin-1 receptor-associated kinase 4 (IRAK4), or E3 ubiquitin ligases, such as TNF receptor associated factor 6 (TRAF6)).

An "IL-33 axis binding antagonist" refers to a molecule that inhibits the interaction of an IL-33 axis binding partner with one or more of its binding partners. As used herein, an IL-33 axis binding antagonist includes IL-33 binding antagonists, ST2 binding antagonists, and IL1RAcP binding antagonists. Exemplary IL-33 axis binding antagonists include anti-IL-33 antibodies and antigen-binding fragments thereof (e.g., anti-IL-33 antibodies such as ANB-020 (AnaptysBio Inc.) or any of the antibodies described in EP1725261, US8187596, WO2011031600, WO2014164959, WO2015099175 or WO2015106080,

which are each incorporated herein by reference in their entirety); polypeptides that bind IL-33 and/or its receptor (ST2 and/or IL-1RAcP) and block ligand-receptor interaction (e.g., ST2-Fc proteins; immunoadhesins, peptibodies, and soluble ST2, or derivatives thereof); anti-IL-33 receptor antibodies (e.g., anti-ST2 antibodies, for example, AMG-282 (Amgen) or STLM15 (Janssen) or any of the anti-ST2 antibodies described in WO 2013/173761 or WO 2013/165894, which are each incorporated herein by reference in their entirety; or ST2-Fc proteins, such as those described in WO 2013/173761; WO 2013/165894; or WO 2014/152195, which are each incorporated herein by reference in their entirety); and IL-33 receptor antagonists, such as small molecule inhibitors, aptamers that bind IL-33, and nucleic acids that hybridize under stringent conditions to IL-33 axis nucleic acid sequences (e.g., short interfering RNAs (siRNA) or clustered regularly interspaced short palindromic repeat RNAs (CRISPR-RNA or crRNA)).

The term "ST2 binding antagonist" refers to a molecule that inhibits the interaction of an ST2 with IL-33, IL1RAcP, and/or a second ST2 molecule. The ST2 binding antagonist may be a protein, such as an "ST2-Fc protein" that includes an IL-33-binding domain (e.g., all or a portion of an ST2 or IL1RAcP protein) and a multimerizing domain (e.g., an Fc portion of an immunoglobulin, e.g., an Fc domain of an IgG selected from the isotypes IgG1, IgG2, IgG3, and IgG4, as well as any allotype within each isotype group), which are attached to one another either directly or indirectly through a linker (e.g., a serine-glycine (SG) linker, glycine-glycine (GG) linker, or variant thereof (e.g., a SGG, a GGS, an SGS, or a GSG linker)), and includes, but is not limited to, ST2-Fc proteins and variants thereof described in WO 2013/173761, WO 2013/165894, and WO 2014/152195, which are each incorporated herein by reference in their entirety.

The term "IL-33-mediated disorder," as used herein, refers to any disorder or condition mediated by, or associated with, the IL-33 axis. In some embodiments, IL-33-mediated disorders are associated with excess IL-33 levels or activity in which atypical symptoms may manifest due to the levels or activity of IL-33 locally and/or systemically in the body. Exemplary IL-33-mediated disorders include inflammatory conditions, immune disorders, fibrotic disorders, eosinophilic disorders, infections, pain, central nervous system disorders, solid tumors, and ophthalmologic disorders. IL-33-mediated disorders are described, for example, in Liew et al. *Nature Reviews Immunology* 10: 103-110, 2010, which is incorporated herein by reference in its entirety.

Exemplary inflammatory conditions include asthma (e.g., allergic asthma, exercise-induced asthma, aspirin sensitive/exacerbated asthma, atopic asthma, severe asthma, mild asthma, moderate to severe asthma, corticosteroid naïve asthma, chronic asthma, corticosteroid resistant asthma, corticosteroid refractory asthma, newly diagnosed and untreated asthma, asthma due to smoking, asthma uncontrolled on corticosteroids, etc.), airway inflammation, airway hyperreactivity, airway hyperresponsiveness, rhinosinusitis, rhinosinusitis with polyps, nasal polyposis, arthritis (e.g., osteoarthritis, rheumatoid arthritis, collagen-induced arthritis, arthritic joints as a result of injury, etc.), eosinophilic inflammation, mast cell-mediated inflammatory diseases, sepsis, septic shock, seronegative enthesopathy and arthropathy (SEA) syndrome, osteoporosis, eosinophilic esophagitis, scleroderma, dermatitis, atopic dermatitis, allergic rhinitis, bullous pemphigoid, chronic urticaria, cartilage inflammation, polymyalgia rheumatic, polyarteritis nodossa, Wegener's granulomatosis, Behcet's disease, myolitis,

polymyolitis, dermatomyolitis, dermatomyositis, vasculitis, arteritis, diabetic nephropathy, interstitial cystitis, graft versus host disease (GVHD), gastrointestinal inflammatory conditions (e.g., inflammatory bowel disease (IBD), ulcerative colitis (UC), Crohn's disease (CD), colitis (e.g., colitis caused by environmental insults (e.g., caused by or associated with a therapeutic regimen, such as chemotherapy, radiation therapy, etc.), infectious colitis, ischemic colitis, collagenous or lymphocytic colitis, necrotizing enterocolitis, colitis in conditions such as chronic granulomatous disease or celiac disease, food allergies, gastritis, infectious gastritis or enterocolitis (e.g., *Helicobacter pylori*-infected chronic active gastritis), and other forms of gastrointestinal inflammation caused by an infectious agent), and inflammatory pulmonary conditions (e.g., chronic obstructive pulmonary disease (COPD), eosinophilic pulmonary inflammation, infection-induced pulmonary conditions (including those associated with viral (e.g., influenza, parainfluenza, rotavirus, human metapneumovirus, and respiratory syncytial virus), bacterial, fungal (e.g., Aspergillus), parasitic, or prion infection, allergen-induced pulmonary conditions, pollutant-induced pulmonary conditions (e.g., asbestosis, silicosis, or berylliosis), gastric aspiration-induced pulmonary conditions, immune dysregulation, inflammatory conditions with genetic predisposition such as cystic fibrosis, physical trauma-induced pulmonary conditions (e.g., ventilator injury), emphysema, bronchitis, sarcoidosis, histiocytosis, lymphangiomyomatosis, acute lung injury, acute respiratory distress syndrome, chronic lung disease, bronchopulmonary dysplasia, pneumonia (e.g., community-acquired pneumonia, nosocomial pneumonia, ventilator-associated pneumonia, viral pneumonia, bacterial pneumonia, and severe pneumonia), airway exacerbations, and acute respiratory distress syndrome (ARDS)).

Exemplary immune disorders include those mediated at least in part by mast cells, such as asthma (e.g., allergic asthma), eczema, itch, allergy, atopic allergy, anaphylaxis, anaphylactic shock, allergic bronchopulmonary aspergillosis, allergic rhinitis, allergic conjunctivitis, as well as autoimmune disorders including rheumatoid arthritis, juvenile rheumatoid arthritis, psoriatic arthritis, pancreatitis, psoriasis, plaque psoriasis, guttate psoriasis, inverse psoriasis, pustular psoriasis, erythrodermic psoriasis, paraneoplastic autoimmune diseases, autoimmune hepatitis, bullous pemphigoid, myasthenia gravis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, celiac disease, thyroiditis (e.g., Graves' disease), Sjogren's syndrome, Guillain-Barre disease, Raynaud's phenomenon, Addison's disease, liver diseases (e.g., primary biliary cirrhosis, primary sclerosing cholangitis, non-alcoholic fatty liver disease, and non-alcoholic steatohepatitis), and diabetes (e.g., type I diabetes).

As used herein, the terms "fibrotic disorder" or "fibrosis" refer to conditions involving formation of excess fibrous connective tissue in an organ or tissue. Exemplary fibrotic disorders include lung fibrosis, liver fibrosis (e.g., fibrosis associated with cirrhosis (e.g., alcohol-induced cirrhosis, viral-induced cirrhosis, post-hepatitis C cirrhosis, and primary biliary cirrhosis), schistosomiasis, cholangitis (e.g., sclerosing cholangitis), and autoimmune-induced hepatitis), kidney fibrosis (e.g., tubulointerstitial fibrosis, scleroderma, diabetic nephritis, and glomerular nephritis), dermal fibrosis (e.g., scleroderma, hypertrophic and keloid scarring, nephrogenic fibrosing dermatopathy, and burns), myelofibrosis, neurofibromatosis, fibroma, intestinal fibrosis, and fibrotic adhesions resulting from surgical procedures), heart fibrosis (e.g., fibrosis associated with myocardial infarction), vascular fibrosis (e.g., fibrosis associated with postangioplasty arterial restenosis and atherosclerosis), eye fibrosis (e.g., fibrosis associated with post-cataract surgery, proliferative vitreoretinopathy, and retro-orbital fibrosis), and bone marrow fibrosis (e.g.,

idiopathic myelofibrosis and drug-induced myelofibrosis). The fibrosis can be organ-specific or systemic (e.g., systemic sclerosis and fibrosis associated with GVHD).

Examples of lung fibrosis include, for example, lung or pulmonary fibrosis associated with idiopathic pulmonary fibrosis, fibrosis with collagen vascular disease, Hermansky-Pudlak syndrome, adult respiratory distress syndrome, nonspecific interstitial pneumonia, respiratory bronciolitis, sarcoidosis, histiocytosis X, bronchiolitis obliterans, and cryptogenic organizing pneumonia. In one embodiment, the lung fibrosis is idiopathic pulmonary fibrosis.

As used herein, an "eosinophilic disorder" is a disorder associated with excess eosinophil numbers in which atypical symptoms may manifest due to the levels or activity of eosinophils locally or systemically in the body. Eosinophilic disorders include but are not limited to, asthma (including aspirin sensitive asthma, atopic asthma, and severe asthma), eosinophilic inflammation, atopic dermatitis, allergic rhinitis (including seasonal allergic rhinitis), non-allergic rhinitis, chronic eosinophilic pneumonia, allergic bronchopulmonary aspergillosis, celiac disease, Churg-Strauss syndrome (periarteritis nodosa plus atopy), eosinophilic myalgia syndrome, hypereosinophilic syndrome, edematous reactions including episodic angiodema, helminth infections, where eosinophils may have a protective role, onchocercal dermatitis, eosinophil-associated gastrointestinal disorders (EGIDs), including but not limited to, eosinophilic esophagitis, eosinophilic gastritis, eosinophilic gastroenteritis, eosinophilic enteritis and eosinophilic colitis, nasal micropolyposis and polyposis, aspirin intolerance, and obstructive sleep apnea. Eosinophil-derived secretory products have also been associated with the promotion of angiogenesis and connective tissue formation in tumors and the fibrotic responses seen in conditions such as chronic asthma, Crohn's disease, scleroderma and endomyocardial fibrosis (Munitz et al. *Allergy* 59: 268-275, 2004; Adamko et al. *Allergy* 60: 13-22, 2005; Oldhoff et al. *Allergy* 60: 693-696, 2005). Other examples include cancer (e.g., glioblastoma (such as glioblastoma multiforme) and non-Hodgkin's lymphoma (NHL)), atopic dermatitis, allergic rhinitis, inflammatory bowel disease, fibrosis (e.g., pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis (IPF) and pulmonary fibrosis secondary to sclerosis) and hepatic fibrosis), and COPD.

Examples of infection include helminth infection (e.g., nematode infection, such as *Trichuris muris* infection of mice, which is a model for infection by the human parasite *Trichuris trichiura*), protozoan infection (e.g., *Leishmania major* infection), and viral infection (e.g., respiratory syncytial virus infection and influenza virus infection).

Examples of pain include inflammatory pain, hyperalgesia (e.g., mechanical hyperalgesia), allodynia, and hypernociception (e.g., cutaneous and articular hypernociception, which may or may not be antigen-induced).

Examples of central nervous system disorders include subarachnoid hemorrhage, inflammatory diseases of the central nervous system, neurodegenerative diseases (e.g., Alzheimer's disease, multiple sclerosis, Parkinson's disease, Huntington's disease), bipolar disorder, and infection of the central nervous system (e.g., viral infection).

Examples of solid tumors include tumors of the colon, breast, prostate, lung, kidney, liver, pancreas, ovary, head and neck, oral cavity, stomach, duodenum, small intestine, large intestine, gastrointestinal tract, anus, gall bladder, labium, nasopharynx, skin, uterus, male genital organ, urinary

organs, bladder, and skin. Solid tumors of non-epithelial origin include sarcomas, brain tumors, and bone tumors.

Examples of ophthalmologic disorders include age-related macular degeneration (AMD), including wet or dry AMD, geographic atrophy (GA), retinopathy (e.g., diabetic retinopathy (DR) and retinopathy of prematurity (ROP)), polypoidal choroidal vasculopathy (PCV), diabetic macular edema, dry eye disease, Bechet's disease, and retina detachment.

The above list is not all-inclusive, and it will be understood by the skilled artisan that a disease or disorder may fall within various categories. For example, asthma can be categorized in some instances as both an inflammatory disorder and immune disorder and considered by some clinicians to be an autoimmune disorder.

As used herein, "chemoattractant receptor-homologous molecule expressed on Th2 cells (CRTH2)" refers to any native CRTH2 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. CRTH2 is also referred to as G protein coupled receptor 44 (GPR44), cluster of differentiation 294 (CD294), DL1R, and DP2. The term encompasses "full-length," unprocessed CRTH2, as well as any form of CRTH2 that results from processing in the cell. The amino acid sequence of an exemplary human CRTH2 can be found, for example, under UniProtKB accession number Q9Y5Y4.

The term "CRTH2 binding antagonist" refers to a molecule that decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of CRTH2 with one or more of its binding partners, such as prostaglandin D_2. Exemplary CRTH2 binding antagonists known in the art include AMG-853, AP768, AP-761, MLN6095, and ACT129968.

The term "interleukin-5 (IL-5)," as used herein, refers to any native IL-5 from any vertebrate source, including mammals such as primates (e.g. humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed IL-5, as well as any form of IL-5 that results from processing in the cell. The term also encompasses naturally occurring variants of IL-5, such as splice variants or allelic variants. The amino acid sequence of an exemplary IL-5 can be found, for example, under UniProtKB accession number P05113.

The term "IL-5 binding antagonist" refers to a molecule that decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of IL-5 with one or more of its binding partners, such as IL-5 receptor, alpha (*IL5RA*). Exemplary IL-5 binding antagonists that can be used in the methods of the invention include, for example, anti-IL-5 antibodies (e.g., mepolizumab and reslizumab) and anti-IL-5R antibodies.

As used herein, "interleukin-13 (IL-13)" refers to any native IL-13 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. IL-13 is a cytokine secreted by many cell types, including T helper type 2 (Th2) cells. The term encompasses "full-length," unprocessed IL-13, as well as any form of IL-13 that results from processing in the cell. The amino acid sequence of an exemplary human IL-13 can be found, for example, under UniProtKB accession number P35225.

The term "IL-13 binding antagonist" refers to a molecule that decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of IL-13 with one or more of

its binding partners, such as IL-4 receptor alpha (IL4Rα), IL-13 receptor alpha1 (IL13RA1) and IL-13 receptor alpha2 (IL13RA2). IL-13 binding antagonists include anti-IL-13 antibodies, for example, lebrikizumab, 228B/C-1, 228A-4, 227-26, and 227-43 (see, for example, U.S. Pat. Nos. 7,674,459; 8,067,199; 8,088,618; 8,318,160; and 8,734,797).

As used herein, "interleukin-17 (IL-17)" refers to any native IL-17 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated, and includes family members IL-17A, IL-17B, IL-17C, IL-17D, IL-17E, and IL-17F. The term encompasses "full-length," unprocessed IL-17, as well as any form of IL-17 that results from processing in the cell. The amino acid sequence of an exemplary human IL-17A can be found, for example, under UniProtKB accession number Q16552. The amino acid sequence of an exemplary human IL-17B can be found, for example, under UniProtKB accession number Q9UHF5. The amino acid sequence of an exemplary human IL-17C can be found, for example, under UniProtKB accession number Q9P0M4. The amino acid sequence of an exemplary human IL-17D can be found, for example, under UniProtKB accession number Q8TAD2. The amino acid sequence of an exemplary human IL-17E can be found, for example, under UniProtKB accession number Q9H293. The amino acid sequence of an exemplary human IL-17F can be found, for example, under UniProtKB accession number Q96PD4.

The term "IL-17 binding antagonist" refers to a molecule that decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of IL-17 with one or more of its binding partners, such as interleukin-17 receptor (IL-17R) family member proteins interleukin 17 receptor A (IL17RA), interleukin 17 receptor B (IL17RB), interleukin 17 receptor C (IL17RC), interleukin 17 receptor D (IL17RD), interleukin 17 receptor E (IL17RE), and interleukin 17 receptor E-like (IL17REL). Exemplary IL-17 binding antagonists include, for example, anti-IL-17 antibodies (e.g., ixekizumab (LY2439821) and anti-IL-17R antibodies (e.g., brodalumab (AMG-827)).

The term "Janus kinase 1 (JAK1)," as used herein, refers to any native JAK1 from any vertebrate source, including mammals such as primates (e.g. humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed JAK1 as well as any form of JAK1 that results from processing in the cell. The term also encompasses naturally occurring variants of JAK1, e.g., splice variants or allelic variants. The amino acid sequence of an exemplary JAK1 can be found, for example, under UniProtKB accession number P23458.

The term "JAK1 antagonist," as used herein, refers to compounds or agents which inhibit or reduce the biological activity of JAK1. Exemplary JAK1 antagonists include small molecule inhibitors (e.g., ruxolitinib, GLPG0634, and GSK2586184).

As used herein, "tryptase-beta" refers to any native tryptase-beta from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. As used herein, the term encompasses tryptase beta-1 (encoded by the *TPSAB1* gene, which also encodes tryptase alpha-1) and tryptase beta-2 (encoded by the *TPSB2* gene). The term encompasses "full-length," unprocessed tryptase-beta as well as any form of tryptase-beta that results from processing in the cell. The amino acid sequence of an exemplary human tryptase beta-2 can be found, for example, under UniProtKB accession number P20231.

The term "tryptase-beta antagonist," as used herein, refers to compounds or agents which inhibit or reduce the biological activity of tryptase beta.

The phrase "informing the patient" with respect to a treatment, as used herein, refers to using the information or data generated relating to the genotype of a polymorphism as described herein and/or the level or presence of at least one marker, for example, periostin, in a sample of a patient to identify the patient as suitably treated or not suitably treated with a therapy (e.g., a therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)). In some embodiments the recommendation may include the identification of a patient who requires adaptation of an effective amount of a therapy (e.g., an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)) being administered. In some embodiments, recommending a treatment includes recommending that the amount of a therapy (e.g., an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)) being administered is adapted. The phrase "informing the patient" or "providing a recommendation," with respect to a treatment, as used herein also may refer to using the information or data generated for proposing or selecting a therapy (e.g., therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)) for a patient identified or selected as more or less likely to respond to the therapy. The information or data used or generated may be in any form, written, oral or electronic. In some embodiments, using the information or data generated includes communicating, presenting, reporting, storing, sending, transferring, supplying, transmitting, dispensing, or combinations thereof. In some embodiments, communicating, presenting, reporting, storing, sending, transferring, supplying, transmitting, dispensing, or combinations thereof are performed by a computing device, analyzer unit or combination thereof. In some further embodiments, communicating, presenting, reporting, storing, sending, transferring, supplying, transmitting, dispensing, or combinations thereof are performed by a laboratory or medical professional. In some embodiments, the information or data includes a comparison of the level of a marker, for example, periostin, to a reference level. In some embodiments, the information or data includes an indication that a marker, for example, periostin, is present or absent in the sample. In some embodiments, the information or data includes an indication that the patient is suitably treated or not suitably treated with a therapy (e.g., therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)).

A "kit" is any manufacture (e.g., a package or container) comprising at least one reagent, for example, a probe for determining the genotype of a polymorphism as described herein and/or a medicament for treatment of an IL-33-mediated disorder (e.g., an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist)). The manufacture is preferably promoted, distributed, or sold as a unit for performing the methods of the present invention.

The terms "level," "level of expression," or "expression level" are used interchangeably and generally refer to the amount of a polynucleotide or an amino acid product or protein in a biological sample. "Expression" generally refers to the process by which gene-encoded information is converted into the structures present and operating in the cell. Therefore, according to the invention, "expression" of a gene may refer to transcription into a polynucleotide, translation into a protein, or even posttranslational modification of the protein. Fragments of the transcribed polynucleotide, the translated protein, or the post-translationally modified protein shall also be regarded as expressed whether they originate from a transcript generated by alternative splicing or a degraded transcript, or from a post-translational

processing of the protein, e.g., by proteolysis. "Expressed genes" include those that are transcribed into a polynucleotide as mRNA and then translated into a protein, and also those that are transcribed into RNA but not translated into a protein (e.g., transfer and ribosomal RNAs).

The terms "oligonucleotide" and "polynucleotide" are used interchangeably and refer to a molecule comprised of two or more deoxyribonucleotides or ribonucleotides, preferably more than three. Its exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide. An oligonucleotide can be derived synthetically or by cloning. Chimeras of deoxyribonucleotides and ribonucleotides may also be in the scope of the present invention.

The term "patient" refers to any single animal, more specifically a mammal (including such non-human animals as, for example, dogs, cats, horses, rabbits, zoo animals, cows, pigs, sheep, and non-human primates) for which diagnosis or treatment is desired. Even more specifically, the patient herein is a human. In the context of the present invention, the patient may be a subject of any suitable population group, for example, any population group described in Example 4. In some embodiments, the patient may belong to a population group of African ancestry, Asian ancestry, and/or European ancestry, for example, a patient of Northern European ancestry. The patient may be a clinical patient, a clinical trial volunteer, an experimental animal, etc. The patient may be suspected of having, at risk for having, or diagnosed with an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)).

The term "a patient suffering from" refers to a patient showing clinical signs in respect to a certain disease, such as, for example, an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)).

The term "periostin," as used herein, refers to a protein that, in humans, is encoded by the *POSTN* gene, including any known isoform or variant thereof. Periostin is also referred to in the art as osteoblast specific factor or OSF-2. Human periostin isoforms 1, 2, 3 and 4 are known in the art as comprising the following amino acid sequences: NP_006466.2; NP_001129406.1, NP_001129407.1, and NP_001129408.1, respectively, according to the NCBI database. An additional form of periostin is described in U.S. Patent Publication 2012/0156194. This isoform is referred to herein as "isoform 5" and has been partially sequenced. Isoform 5 comprises the amino acid sequence of SEQ ID NO: 23 of U.S. Patent Publication 2012/0156194, the entirety of which is incorporated herein by reference. In some embodiments, periostin is serum periostin or plasma periostin (i.e., periostin from a serum sample obtained from whole blood or a plasma sample obtained from whole blood, respectively, the whole blood obtained from a patient).

The term "pharmaceutical composition" refers to a sterile preparation that is in such form as to permit the biological activity of the medicament to be effective, and which contains no additional components that are unacceptably toxic to a subject to which the formulation would be administered.

A nucleotide position in a genome at which more than one sequence is possible in a population is referred to herein as a "polymorphism" or "polymorphic site." A polymorphic site may be a nucleotide sequence of two or more nucleotides, an inserted nucleotide or nucleotide sequence, a deleted nucleotide or nucleotide sequence, or a microsatellite, for example. A polymorphic site that is two or

more nucleotides in length may be 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more, 20 or more, 30 or more, 50 or more, 75 or more, 100 or more, 500 or more, or about 1000 nucleotides in length, where all or some of the nucleotide sequences differ within the region. A polymorphic site which is a single nucleotide in length is referred to herein as a single nucleotide polymorphism (SNP), as described below. When there are two, three or four alternative nucleotide sequences at a polymorphic site, each nucleotide sequence is referred to as a "polymorphic variant" or "nucleic acid variant." Each possible variant in the DNA sequence is referred to as an "allele." Typically, the first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. A "common" allele is an allele that is prevalent in a given population, e.g., the allele is present in multiple members of a population at a generally accepted frequency of greater than about 2%. Where two polymorphic variants exist, the polymorphic variant represented in a majority of samples from a population is referred to as a "prevalent allele," or "major allele," and the polymorphic variant that is less prevalent in the population is referred to as an "uncommon allele" or "minor allele." An individual who carries two prevalent alleles or two uncommon alleles is "homozygous" with respect to the polymorphism. An individual who carries one prevalent allele and one uncommon allele is "heterozygous" with respect to the polymorphism. With C/G or A/T SNPs, the alleles are ambiguous and dependent on the strand used to extract the data from the genotyping platform. With these C/G or A/T SNPs, the C or G nucleotide or the A or T nucleotide, respectively, may be the risk allele and is determined by correlation of allele frequencies.

The allele that correlates with an increased risk for a disease or disorder (e.g., an IL-33-mediated disorder, such an asthma) or is associated with an odds ratio or relative risk of >1 is referred to as the "risk allele" or "effect allele." The "risk allele" or "effect allele" may be the minor allele or major allele.

"Equivalent allele" or "surrogate allele," as used herein, refers to an allele that is expected to behave similarly to a risk allele and is selected based on allele frequencies and/or high r^2 value (greater than or equal to (≥) 0.6) and/or high D' value (≥0.6) with the risk alleles and/or selected SNP as defined herein. In one embodiment, the high r^2 value is ≥ 0.6, ≥ 0.7, ≥0.8, ≥0.9, or 1.0. In one embodiment, the high D' value is ≥ 0.6, ≥ 0.7, ≥ 0.8, ≥ 0.9, or 1.0.

"Linkage disequilibrium" or "LD" when used herein refers to alleles at different loci that are not associated at random, i.e., not associated in proportion to their frequencies. If the alleles are in positive linkage disequilibrium, then the alleles occur together more often than expected assuming statistical independence. Conversely, if the alleles are in negative linkage disequilibrium, then the alleles occur together less often than expected assuming statistical independence.

"Odds ratio" or "OR" when used herein refers to the ratio of the odds of the disease for individuals with the marker (allele or polymorphism) relative to the odds of the disease in individuals without the marker (allele or polymorphism).

"Haplotype" when used herein refers to a group of alleles on a single chromosome that are closely enough linked to be inherited usually as a unit.

In certain embodiments, the term "reference level" herein refers to a predetermined value. As the skilled artisan will appreciate, the reference level is predetermined and set to meet the requirements in terms of, for example, specificity and/or sensitivity. These requirements can vary, e.g., from regulatory

body to regulatory body. It may be, for example, that assay sensitivity or specificity, respectively, has to be set to certain limits, e.g., 80%, 90% or 95%. These requirements may also be defined in terms of positive or negative predictive values. Nonetheless, based on the teaching given in the present invention it will always be possible to arrive at the reference level meeting those requirements. In one embodiment, the reference level is determined in healthy individuals. The reference value in one embodiment has been predetermined in the disease entity to which the patient belongs (e.g., an IL-33-mediated disorder, such as asthma). In certain embodiments, the reference level can be set to any percentage between, e.g., 25% and 75% of the overall distribution of the values in a disease entity investigated. In other embodiments, the reference level can be set to, for example, the median, tertiles, quartiles, or quintiles as determined from the overall distribution of the values in a disease entity investigated or in a given population. In one embodiment, the reference level is set to the median value as determined from the overall distribution of the values in a disease entity investigated. In one embodiments, the reference level may depend on the gender of the patient, e.g., males may have a different reference level than females.

In certain embodiments, the term "increase" or "above" refers to a level at the reference level or to an overall increase of 5%, 10%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 100% or greater, in the level of a marker (e.g., periostin or sST2) detected by the methods described herein, as compared to the level from a reference sample.

In certain embodiments, the term "decrease" or "below" herein refers to a level below the reference level or to an overall reduction of 5%, 10%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater, in the level of a marker (e.g., periostin or sST2) detected by the methods described herein, as compared to the level from a reference sample.

In certain embodiments, the term "at a reference level" refers to a level of a marker (e.g., periostin or sST2) that is the same as the level, detected by the methods described herein, from a reference sample.

A "response" of a patient or a patient's "responsiveness" to treatment or therapy, for example treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), refers to the clinical or therapeutic benefit imparted to a patient at risk for or having an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis, e.g., idiopathic pulmonary fibrosis) from or as a result of the treatment. Such benefit may include cellular or biological responses, a complete response, a partial response, a stable disease (without progression or relapse), or a response with a later relapse of the patient from or as a result of the treatment with the antagonist. A skilled person will readily be in position to determine whether a patient is responsive. For example, a patient suffering from asthma who is responsive to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) may show observable and/or measurable reduction in or absence of one or more of the following exemplary symptoms: recurrent wheezing, coughing, trouble breathing, chest tightness, symptoms that occur or worsen at night, symptoms that are triggered by cold air, exercise or exposure to allergens.

The term "single nucleotide polymorphism" or "SNP" refers to a single base substitution within a DNA sequence that leads to genetic variability. Single nucleotide polymorphisms may occur at any region of a gene. In some instances the polymorphism can result in a change in protein sequence. The change in protein sequence may affect protein function or not.

The term "selected SNP" when used herein refers to a SNP selected from the group consisting of polymorphism rs4988956 (SEQ ID NO: 1); polymorphism rs10204137 (SEQ ID NO: 2); polymorphism rs10192036 (SEQ ID NO: 3); polymorphism rs10192157 (SEQ ID NO: 4); polymorphism rs10206753 (SEQ ID NO: 5); and polymorphism rs4742165 (SEQ ID NO: 6).

The term "alternate SNP" when used herein refers to a SNP that is expected to behave similarly to a selected SNP and is selected based on similar allele frequencies and/or has linkage disequilibrium with a selected SNP as measured by an $r^2 \geq 0.6$ and/or $D' \geq 0.6$. Alternate SNPs include SNPs listed in Tables 3 and 4 that are in linkage disequilibrium with the SNPs described herein including polymorphism rs4988956 (SEQ ID NO: 1); polymorphism rs10204137 (SEQ ID NO: 2); polymorphism rs10192036 (SEQ ID NO: 3); polymorphism rs10192157 (SEQ ID NO: 4); polymorphism rs10206753 (SEQ ID NO: 5); and polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the alternate SNP is in Table 3. In other embodiments, the alternate SNP is in Table 4.

The terms "sample" and "biological sample" are used interchangeably to refer to any biological sample obtained from an individual including body fluids, body tissue (e.g., lung samples), nasal samples (including nasal swabs or nasal polyps), sputum, cells, or other sources. Body fluids include, e.g., lymph, sera, whole fresh blood, frozen whole blood, plasma (including fresh or frozen), peripheral blood mononuclear cells, urine, saliva, semen, synovial fluid and spinal fluid. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art.

As used herein, "therapy" or "treatment" refers to clinical intervention in an attempt to alter the natural course of the individual or cell being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. Those in need of treatment include can include those already with the disorder as well as those at risk to have the disorder or those in whom the disorder is to be prevented. A patient may be successfully "treated" for asthma if, for example, after receiving an asthma therapy, the patient shows observable and/or measurable reduction in or absence of one or more of the following: recurrent wheezing, coughing, trouble breathing, chest tightness, symptoms that occur or worsen at night, symptoms that are triggered by cold air, exercise or exposure to allergens.

"Tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms "cancer," "cancerous," "cell proliferative disorder," "proliferative disorder," and "tumor" are not mutually exclusive as referred to herein.

II. Therapeutic Methods

The present invention provides methods of treating a patient suffering from an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis, e.g., idiopathic pulmonary fibrosis). In some embodiments, the methods of the invention include administering a therapy to a patient based on the presence and/or expression level of a biomarker of the invention, for example, a polymorphism (e.g., a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); rs10206753 (SEQ ID NO: 5); rs4742165 (SEQ

ID NO: 6); and a SNP that is in linkage disequilibrium to rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and/or rs4742165 (SEQ ID NO: 6)), periostin, and/or sST2. In some instances, the polymorphism that is in linkage disequilibrium to rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), and/or rs10206753 (SEQ ID NO: 5) is listed in Table 3. In some instances, the polymorphism that is in linkage disequilibrium to rs4742165 (SEQ ID NO: 6) is listed in Table 4.

In some embodiments, the methods of the invention include administering to the patient a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a Janus kinase 1 (JAK1) antagonist, and/or an interleukin-5 (IL-5) binding antagonist, wherein the genotype of the patient has been determined to comprise at least one (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7) allele(s) selected from the group consisting of a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6). In some embodiments, the SNP that is in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1), polymorphism rs10204137 (SEQ ID NO: 2), polymorphism rs10192036 (SEQ ID NO: 3), polymorphism rs10192157 (SEQ ID NO: 4), and/or polymorphism rs10206753 (SEQ ID NO: 5) is listed in Table 3. In some embodiments, the SNP that is in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) is listed in Table 4.

In some embodiments, the methods of the invention include administering to the patient a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a Janus kinase 1 (JAK1) antagonist, and/or an interleukin-5 (IL-5) binding antagonist, wherein the genotype of the patient has been determined to comprise at least one allele (e.g., 1, 2, 3, 4, or 5 alleles) listed in Table 2 (e.g., the genotype of the patient may comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); and/or a T allele at polymorphism rs10206753 (SEQ ID NO: 5)).

In some embodiments, the methods of the invention include administering to the patient a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a Janus kinase 1 (JAK1) antagonist, and/or an interleukin-5 (IL-5) binding antagonist, wherein the genotype of the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6).

In any of the preceding methods, the equivalent allele may be at an alternate SNP that is in linkage disequilibrium with one or more of the selected SNPs described herein. In some embodiments, the linkage disequilibrium is a D' value or an r^2 value. In some embodiments, the D' measure between the selected SNP and the alternate SNP is ≥ 0.60 (e.g., ≥ 0.60, ≥ 0.65, ≥ 0.7, ≥ 0.75, ≥ 0.8, ≥ 0.85, ≥ 0.9, ≥ 0.95, or higher). In some embodiments, the D' value between the selected SNP and the alternate SNP is ≥0.70, ≥ 0.80, or ≥ 0.90. In some embodiments, the D' value between the selected SNP and the alternate SNP is 1.0. In some embodiments, the r^2 value between the selected SNP and the alternate SNP is ≥ 0.60 (e.g., ≥ 0.60, ≥ 0.65, ≥ 0.7, ≥ 0.75, ≥ 0.8, ≥ 0.85, ≥ 0.9, ≥ 0.95, or higher). In some embodiments the r^2 value between the selected SNP and the alternate SNP is ≥ 0.70, ≥ 0.80, or ≥ 0.90. In some embodiments, the r^2 value between the selected SNP and the alternate SNP is 1.0. In some embodiments, the alternate SNP is a SNP designated in Table 3 or 4. In any of the preceding methods, the equivalent allele may be the minor allele or the major allele. In some instances, the equivalent allele is the minor allele. In other instances, the equivalent allele is the major allele.

The genotype of a patient can be determined using any of the methods or assays described herein (e.g., in Section IV of the Detailed Description of the Invention or in Example 1) or that are known in the art. In some embodiments, the methods are directed to, or further include, determining the level of a biomarker (e.g., periostin or sST2) in a sample derived from the patient. The level of a biomarker (e.g., periostin or sST2) can be determined using any of the assays or methods described herein or known in the art. For example, the level of periostin can be determined, for example, using the periostin assays described in WO 2012/083132, the entirety of which is incorporated herein by reference. In another example, the level of sST2 can be determined using any of the assays or methods described herein or known in the art, for example, in Example 3.

In other embodiments, the methods of the invention include administering to the patient a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a Janus kinase 1 (JAK1) antagonist, and/or an interleukin-5 (IL-5) binding antagonist, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level. In some instances, the level of sST2 is a level of sST2 protein. In some instances, the sample derived from a patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof. In some instances, the sample derived from a patient a serum sample. In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6). In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8). In some instances, the group of individuals is suffering from asthma. In some instances, the reference level of sST2 is a median level. In some instances, the group of individuals is a group of female individuals and the patient is female. In some instances, the group of individuals is a group of male individuals and the patient is male.

In some embodiments, the IL-33 mediated disorder may be an inflammatory condition, an immune disorder, a fibrotic disorder, an eosinophilic disorder, an infection, pain, a central nervous system disorder, a solid tumor, or an ophthalmologic disorder. For example, in some instances, an inflammatory condition may be asthma, airway hyperresponsiveness, airway inflammation, sepsis, septic shock, atopic dermatitis, allergic rhinitis, rheumatoid arthritis, or chronic obstructive pulmonary disease (COPD). In some instances, an immune disorder may be asthma, rheumatoid arthritis, allergy, atopic allergy, anaphylaxis, anaphylactic shock, allergic rhinitis, psoriasis, inflammatory bowel disease (IBD), Crohn's disease, diabetes, or liver disease. In some instances, the fibrotic disease may be idiopathic pulmonary fibrosis (IPF). In some instances, the eosinophilic disorder may be an eosinophil-associated gastrointestinal disorder (EGID). In some instances, the EGID may be eosinophilic esophagitis. In some instances, the infection may be a helminth infection, a protozoan infection, or a viral infection. In some instances, the protozoan infection may be *Leishmania major* infection. In some instances, the viral infection may be respiratory syncytial virus (RSV) infection or influenza infection. In some instances, the pain may be inflammatory pain. In some instances, the central nervous system disorder may be Alzheimer's disease. In some instances, the solid tumor may be a breast tumor, colon tumor, prostate tumor, lung tumor, kidney tumor, liver tumor, pancreas tumor, stomach tumor, intestinal tumor, brain tumor, bone tumor, or skin tumor. In some embodiments, the ophthalmologic disorder may be age-related macular degeneration (AMD) or retinopathy of the eye. In particular instances, the IL-33-mediated disorder may be asthma, allergic rhinitis, atopic dermatitis, COPD, eosinophilic esophagitis, or pulmonary fibrosis (e.g., IPF). For example, in some instances, the IL-33-mediated disorder is asthma. In other instances, the IL-33-mediated disorder is pulmonary fibrosis (e.g., IPF).

In some instances, the methods of the invention include administering to the patient a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. For example, the method may include administering a therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, or an IL-5 binding antagonist. In other instances, the method may include administering a therapy comprising at least two agents, for example, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and a tryptase-beta binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and a CRTH2 binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and an IL-13 binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and an IL-17 binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and a JAK1 antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and an IL-5 binding antagonist, a tryptase-beta binding antagonist and a CRTH2 binding antagonist, a tryptase-beta binding antagonist and an IL-13 binding antagonist, a tryptase-beta binding antagonist and an IL-17 binding antagonist, a tryptase-beta binding antagonist and a JAK1 antagonist, a tryptase-beta binding antagonist and an IL-5 binding antagonist, a CRTH2 binding antagonist and an IL-13 binding antagonist, a CRTH2 binding antagonist and an IL-17 binding antagonist, a CRTH2 binding antagonist and a JAK1 antagonist, a CRTH2 binding

antagonist and an IL-5 binding antagonist, an IL-13 binding antagonist and an IL-17 binding antagonist, an IL-13 binding antagonist and a JAK1 antagonist, an IL-13 binding antagonist and an IL-5 binding antagonist, an IL-17 binding antagonist and a JAK1 antagonist, an IL-17 binding antagonist and an IL-5 binding antagonist, or a JAK1 antagonist and an IL-5 binding antagonist. In other instances, the method may include administering a therapy comprising at least three agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In other instances, the method may include administering a therapy comprising at least four agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In other instances, the method may include administering a therapy comprising at least five agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In yet other instances, the method may include administering a therapy comprising at least six agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In yet other instances, the method may include administering a therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist.

In some instances, the invention includes an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), has been determined to comprise one, two, three, four, five, six, seven, or more than seven of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In some instances, the invention includes the use of an effective amount of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise one, two, three, four, five, six, seven, or more than seven of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a

polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In some instances, the invention includes a composition including an effective amount of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise one, two, three, four, five, six, or seven, or more than seven of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6). The composition may be a pharmaceutical composition.

In some instances, the invention includes an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level. In some instances, the level of sST2 is a level of sST2 protein. In some instances, the sample derived from a patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof. In some instances, the sample derived from a patient a serum sample. In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6). In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8). In some instances, the group of individuals is suffering from asthma. In some instances, the reference level of sST2 is a median level. In some instances, the group of individuals is a group of female individuals and the patient is female. In some instances, the group of individuals is a group of male individuals and the patient is male.

In other instances, the invention includes the use of an effective amount of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level. In some instances, the level of sST2 is a level of sST2 protein. In some instances, the sample derived from a patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof. In some instances, the sample derived from a patient a serum sample. In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6). In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8). In some

instances, the group of individuals is suffering from asthma. In some instances, the reference level of sST2 is a median level. In some instances, the group of individuals is a group of female individuals and the patient is female. In some instances, the group of individuals is a group of male individuals and the patient is male.

In some instances, the invention includes a composition including an effective amount of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level. In some instances, the level of sST2 is a level of sST2 protein. In some instances, the sample derived from a patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof. In some instances, the sample derived from a patient a serum sample. In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6). In some instances, the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8). In some instances, the group of individuals is suffering from asthma. In some instances, the reference level of sST2 is a median level. In some instances, the group of individuals is a group of female individuals and the patient is female. In some instances, the group of individuals is a group of male individuals and the patient is male.

Exemplary IL-33 axis binding antagonists include anti-IL-33 antibodies such as ANB-020 (AnaptyxBio Inc.) or any of the antibodies described in WO2014164959, EP1725261, US8187569, WO2011031600, WO2015099175 or WO2015106080, which are each incorporated herein by reference in their entirety; or anti-ST2 antibodies such as AMG-282 (Amgen) or STLM15 (Janssen), or any of the antibodies described in WO2013173761 or WO2013165894, which are each incorporated herein by reference in their entirety.

Exemplary ST2 binding antagonists include ST2-Fc proteins and variants thereof described in WO 2013/173761, WO 2013/165894, and WO 2014/152195, which are each incorporated herein by reference in their entirety.

Exemplary CRTH2 binding antagonists that can be used in the methods of the invention include, for example, AMG-853, AP768, AP-761, MLN6095, and ACT129968.

Exemplary IL-13 binding antagonists that can be used in the methods of the invention include, for example, anti-IL-13 antibodies, including lebrikizumab, 228B/C-1, 228A-4, 227-26, and 227-43. Additional anti-IL-13 antibodies are described, for example, in U.S. Pat. Nos. 7,674,459; 8,067,199; 8,088,618; 8,318,160; and 8,734,797.

Exemplary IL-17 binding antagonists that can be used in the methods of the invention include, for example, anti-IL-17 antibodies (e.g., ixekizumab (LY2439821) and anti-IL-17R antibodies (e.g., brodalumab (AMG-827)).

Exemplary JAK1 antagonists that can be used in the methods of the invention include, for example, small molecule inhibitors (e.g., ruxolitinib, GLPG0634, and GSK2586184).

Exemplary IL-5 binding antagonists that can be used in the methods of the invention include, for example, anti-IL-5 antibodies (e.g., mepolizumab and reslizumab) and anti-IL-5R antibodies.

In some embodiments, the genotype of the patient includes one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7) of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6)

. In other embodiments, the genotype of the patient includes at least two of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

For example, in some instances the genotype of the patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a C allele at polymorphism rs10192036 (SEQ ID NO: 3); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a C allele at polymorphism rs10192157 (SEQ ID NO: 4); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2),

rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); a T allele at polymorphism rs10206753 (SEQ ID NO: 5) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a T allele at polymorphism rs10206753 (SEQ ID NO: 5) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); or a T allele at polymorphism rs4742165 (SEQ ID NO: 6) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In other embodiments, the genotype of the patient includes at least three of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In other embodiments, the genotype of the patient includes at least four of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In some embodiments, the genotype of the patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); and a T allele at polymorphism rs10206753 (SEQ ID NO: 5). In some embodiments, the genotype of the patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); and a T allele at polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the genotype of the

patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In any of the preceding embodiments, the equivalent allele may be in an alternate SNP that is in linkage disequilibrium with one or more of the selected SNPs described herein. In some embodiments, the linkage disequilibrium is a D' value or an r^2 value. In some embodiments, the D' measure between the selected SNP and the alternate SNP is ≥ 0.60 (e.g., ≥ 0.60, ≥ 0.65, ≥ 0.7, ≥ 0.75, ≥ 0.8, ≥ 0.85, ≥ 0.9, ≥ 0.95, or higher). In some embodiments, the D' value between the selected SNP and the alternate SNP is ≥ 0.70, ≥ 0.80, or ≥ 0.90. In some embodiments, the D' value between the selected SNP and the alternate SNP is 1.0. In some embodiments, the r^2 value between the selected SNP and the alternate SNP is ≥ 0.60 (e.g., ≥ 0.60, ≥ 0.65, ≥ 0.7, ≥ 0.75, ≥ 0.8, ≥ 0.85, ≥ 0.9, ≥ 0.95, or higher). In some embodiments the r^2 value between the selected SNP and the alternate SNP is ≥ 0.70, ≥ 0.80, or ≥ 0.90. In some embodiments, the r^2 value between the selected SNP and the alternate SNP is 1.0. In some embodiments, the alternate SNP is a SNP designated in Table 3 or 4. In any of the preceding methods, the equivalent allele may be the minor allele or the major allele. In some instances, the equivalent allele is the minor allele. In other instances, the equivalent allele is the major allele.

The therapy (e.g., a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a Janus kinase 1 (JAK1) antagonist, and/or an interleukin-5 (IL-5) binding antagonist) is administered by any suitable means, including parenteral, topical, subcutaneous, intraperitoneal, intrapulmonary, intranasal, and/or intralesional administration. Parenteral infusions include intramuscular, intravenous, intraarterial, intraperitoneal, or subcutaneous administration. Intrathecal administration is also contemplated. In addition, the antagonist may suitably be administered by pulse infusion, e.g., with declining doses of the antagonist.

As a general proposition, the effective amount of the antagonist administered parenterally per dose will be in the range of about 20 mg to about 5000 mg, by one or more dosages. Exemplary dosage regimens for antibodies such as anti-IL-33 antibodies include 100 or 400 mg every 1, 2, 3, or 4 weeks or is administered a dose of about 1, 3, 5, 10, 15, or 20 mg/kg every 1, 2, 3, or 4 weeks. The dose may be administered as a single dose or as multiple doses (e.g., 2 or 3 doses), such as infusions.

As noted above, however, these suggested amounts of antagonist are subject to a great deal of therapeutic discretion. The key factor in selecting an appropriate dose and scheduling is the result obtained, as indicated above. In some embodiments, the antagonist is administered as close to the first sign, diagnosis, appearance, or occurrence of the IL-33-mediated disorder as possible. The pharmaceutical composition comprising an antagonist will be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the

particular type of IL-33-mediated disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the IL-33-mediated disorder, the site of delivery of the agent, possible side-effects, the type of antagonist, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The effective amount of the antagonist to be administered will be governed by such considerations.

An antagonist, for example, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a JAK1 antagonist, or an interleukin-5 (IL-5) binding antagonist, may be combined in a pharmaceutical combination formulation, or dosing regimen as combination therapy, with at least one additional compound having anti-asthma, anti-inflammatory, anti-autoimmune, anti-fibrotic, and/or anti-cancer properties. The at least one additional compound of the pharmaceutical combination formulation or dosing regimen preferably has complementary activities to the antagonist composition such that they do not adversely affect each other.

Suitable dosages for any of the above co-administered agents are those presently used and may be lowered due to the combined action (synergy) of the newly identified agent and other chemotherapeutic agents or treatments.

The combination therapy may provide "synergy" and prove "synergistic", i.e., the effect achieved when the active ingredients used together is greater than the sum of the effects that results from using the compounds separately. A synergistic effect may be attained when the active ingredients are: (1) co-formulated and administered or delivered simultaneously in a combined, unit dosage formulation; (2) delivered by alternation or in parallel as separate formulations; or (3) by some other regimen. The combined administration includes co-administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. When delivered in alternation therapy, a synergistic effect may be attained when the compounds are administered or delivered sequentially, e.g., by different injections in separate syringes. In general, during alternation therapy, an effective dosage of each active ingredient is administered sequentially, *i.e.* serially, whereas in combination therapy, effective dosages of two or more active ingredients are administered together. When administered sequentially, the combination may be administered in two or more administrations.

In the context of the invention, a therapy (e.g., a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist) may be administered in addition to or as a co-therapy or a co-treatment with a further asthma therapy, as described below or known in the art. Moderate asthma is currently treated with a daily inhaled anti-inflammatory-corticosteroid or mast cell inhibitor such as cromolyn sodium or nedocromil plus an inhaled beta2-agonist as needed (3-4 times per day) to relieve breakthrough symptoms or allergen- or exercise-induced asthma. Exemplary inhaled corticosteroids include QVAR®, PULMICORT®, SYMBICORT®, AEROBID®, FLOVENT®, FLONASE®, ADVAIR®, and AZMACORT®. Additional asthma therapies include long acting bronchial dilators (LABD). In certain

embodiments, the LABD is a long-acting beta-2 agonist (LABA), leukotriene receptor antagonist (LTRA), long-acting muscarinic antagonist (LAMA), theophylline, or oral corticosteroids (OCS). Exemplary LABDs include SYMBICORT®, ADVAIR®, BROVANA®, FORADIL®, PERFOROMIST™ and SEREVENT®.

In the context of the present invention, the therapy (e.g., a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist, e.g., an ST2-Fc protein), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist) may be administered in addition to or as a co-therapy or a co-treatment with one or more chemotherapeutic agents administered as part of standard chemotherapy regimen for a solid tumor as known in the art. Examples of agents included in such standard chemotherapy regimens include 5-fluorouracil, leucovorin, irinotecan, gemcitabine, erlotinib, capecitabine, taxanes, such as docetaxel and paclitaxel, interferon alpha, vinorelbine, and platinum-based chemotherapeutic agents, such as paclitaxel, carboplatin, cisplatin and oxaliplatin. Examples of co-treatments for metastatic pancreatic cancer include gemcitabine-erlotinib plus bevacizumab at a dosage of 5 mg/kg or 10 mg/kg of body weight given once every two weeks or 7.5 mg/kg or 15 mg/kg of body weight given once every three weeks. Examples of co-treatments for renal cell cancer include interferon alpha plus bevacizumab at a dosage of or 10 mg/kg of body weight given once every two weeks. Further, a patient may be co-treated with a combination of irinotecan, 5-fluorouracil, leucovorin, also referred to as IFL, as, for example, a bolus-IFL, with a combination of oxaliplatin, leucovorin, and 5-fluorouracil, also referred to a FOLFOX4 regimen, or with a combination of capecitabine and oxaliplatin, also referred to as XELOX. Accordingly, in a further embodiment of the invention, the patient suffering from an IL-33-mediated disorder is being treated with one or more chemotherapeutic agents such as 5-fluorouracil, leucovorin, irinotecan, gemcitabine-erlotinib, capecitabine and/or platinum-based chemotherapeutic agents, such as paclitaxel, carboplatin and oxaliplatin. Further, the therapy to be administered may be administered as a co-therapy or a co-treatment with radiotherapy.

The at least one additional compound may be a chemotherapeutic agent, a cytotoxic agent, a cytokine, a growth inhibitory agent, an anti-hormonal agent, and combinations thereof. Such molecules are suitably present in combination in amounts that are effective for the purpose intended. A pharmaceutical composition containing an IL-33 axis binding antagonist (e.g., an anti-IL-33 antibody or an ST2 binding antagonist, e.g., an ST2-Fc protein) may also comprise a therapeutically effective amount of an anti-neoplastic agent, a chemotherapeutic agent a growth inhibitory agent, a cytotoxic agent, or combinations thereof.

III. Diagnostic Methods

The present invention provides methods for identifying and/or monitoring patients at increased risk (i.e., increased susceptibility) of having or developing one or more IL-33-mediated disorders (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)). The methods are useful, *inter alia*, for increasing the likelihood that administration of a therapy (e.g., a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1

antagonist, and/or an IL-5 binding antagonist) to a patient having an IL-33-mediated disorder will be efficacious. In several embodiments, the methods include determining the genotype at one or more polymorphisms (e.g., *IL1RL1* and/or *IL33* polymorphisms) in a biological sample from a patient (e.g., the polymorphisms listed in Table 1, Table 2, Table 3, and Table 4). In some embodiments, the invention provides methods for identifying and/or monitoring patients at increased risk (i.e., increased susceptibility) of having or developing one or more IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)) based on the presence and/or expression level of a biomarker of the invention, for example, a polymorphism (e.g., a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); rs10206753 (SEQ ID NO: 5); rs4742165 (SEQ ID NO: 6); a polymorphism that is in linkage disequilibrium to rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and/or rs4742165 (SEQ ID NO: 6)); periostin; and/or sST2. In some instances, the polymorphism that is in linkage disequilibrium to rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); and/or rs10206753 (SEQ ID NO: 5) is listed in Table 3. In some instances, the polymorphism that is in linkage disequilibrium to rs4742165 (SEQ ID NO: 6) is listed in Table 4. In some embodiments, the methods include determining the level of one or more biomarkers (e.g., periostin and/or sST2) in a sample derived from the patient.

The methods and assays of the invention provide for convenient, efficient, and potentially cost-effective means to obtain data and information useful in assessing appropriate or effective therapies for treating patients (e.g., patients suffering from an IL-33-mediated disorder). For example, a patient could provide a biological sample (e.g., a blood sample, nasal samples, lung samples, sputum, etc.) before treatment (e.g., administration of a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist) and the sample could be examined by way of various *in vitro* assays to determine whether the patient's cells are likely to be responsive to the treatment.

The methods may be conducted in a variety of assay formats, including assays detecting genetic information (e.g., DNA or RNA sequencing), genetic or protein expression (such as polymerase chain reaction (PCR) and enzyme immunoassays), and biochemical assays detecting appropriate activity, for example, as described below. The presence of one or more of the alleles for the polymorphisms listed in Table 2 in a sample from a patient correlates with the likelihood that the patient is at risk for an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)). Example 1 shows that the presence of one or more of the alleles for the polymorphisms listed in Table 2 indicates such risk, and thus in various embodiments determination of the genotype at one or more of these polymorphisms in the methods described herein are included in the invention.

In one instance, this invention provides a method of determining whether a patient is at increased risk of an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)), the method including determining the genotype of at least one allele (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7 alleles) listed in Table 1, Table 2, Table 3, or Table 4 in a sample derived from the patient,

wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises an allele listed in Table 2; a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele in a SNP that is in linkage disequilibrium to rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and/or rs4742165 (SEQ ID NO: 6).

For example, in some embodiments, the method includes determining the genotype at one or more polymorphisms (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7 polymorphisms) selected from the group consisting of rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); rs10206753 (SEQ ID NO: 5); rs4742165 (SEQ ID NO: 6); and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) in a sample derived from the patient, wherein the patient is at increased risk of asthma if the genotype of the patient comprises (a) a G allele at polymorphism rs4988956 (SEQ ID NO: 1); (b) an A allele at polymorphism rs10204137 (SEQ ID NO: 2); (c) a C allele at polymorphism rs10192036 (SEQ ID NO: 3); (d) a C allele at polymorphism rs10192157 (SEQ ID NO: 4); (e) a T allele at polymorphism rs10206753 (SEQ ID NO: 5); (f) a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or (g) an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In some instances, the patient is at an increased risk of an IL-33-mediated disorder if the genotype of the patient includes one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7) of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6). In some instances, the genotype of the patient at increased risk of an IL-33-mediated disorder includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5) a T allele at polymorphism rs4742165 (SEQ ID NO: 6); or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In other embodiments, the genotype of a patient at increased risk for an IL-33-mediated disorder includes at least two of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID

NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

For example, in some instances the genotype of the patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a C allele at polymorphism rs10192036 (SEQ ID NO: 3); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a C allele at polymorphism rs10192157 (SEQ ID NO: 4); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); an A allele at polymorphism rs10204137 (SEQ ID NO: 2) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192036 (SEQ ID NO: 3) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); a T allele at polymorphism rs10206753 (SEQ ID NO: 5) and a T allele at polymorphism rs4742165 (SEQ ID NO: 6); a T allele at polymorphism rs10206753 (SEQ ID NO: 5) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); or a T allele at polymorphism

rs4742165 (SEQ ID NO: 6) and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In other embodiments, the genotype of a patient at risk for an IL-33-mediated disorder includes at least three of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In other embodiments, the genotype of the patient includes at least four of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In other embodiments, the genotype of the patient at risk for an IL-33-mediated disorder includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); and a T allele at polymorphism rs10206753 (SEQ ID NO: 5). In some embodiments, the genotype of the patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); and a T allele at polymorphism rs4742165 (SEQ ID NO: 6). In some embodiments, the genotype of the patient includes a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

In another embodiment, the present invention provides a method of determining whether a patient suffering from an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)) is likely to respond to treatment comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1

antagonist, and/or an IL-5 binding antagonist, the method comprising: (a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at one or more polymorphisms (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7 polymorphisms) selected from the group consisting of rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); rs10206753 (SEQ ID NO: 5); rs4742165 (SEQ ID NO: 6); and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); and (b) identifying the patient as likely to respond to the treatment based on the genotype, wherein the presence of: (i) each G allele at polymorphism rs4988956 (SEQ ID NO: 1); (ii) each A allele at polymorphism rs10204137 (SEQ ID NO: 2); (iii) each C allele at polymorphism rs10192036 (SEQ ID NO: 3); (iv) each C allele at polymorphism rs10192157 (SEQ ID NO: 4); (v) each T allele at polymorphism rs10206753 (SEQ ID NO: 5); (vi) each T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or (vii) each equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) indicates that the patient has an increased likelihood of being responsive to the treatment. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In another embodiment, the present invention provides a method of improving the therapeutic efficacy of an IL-33-mediated disorder therapy for a patient suffering from an IL-33-mediated disorder, the method including: (a) determining in a sample derived from a patient suffering from asthma the genotype at one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or more than 7) polymorphisms selected from the group consisting of rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); rs10206753 (SEQ ID NO: 5); rs4742165 (SEQ ID NO: 6); and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); and (b) identifying the patient as more suitably treated by the addition of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist to the IL-33-mediated disorder therapy based on the genotype, wherein the presence of: (i) each G allele at polymorphism rs4988956 (SEQ ID NO: 1); (ii) each A allele at polymorphism rs10204137 (SEQ ID NO: 2); (iii) each C allele at polymorphism rs10192036 (SEQ ID NO: 3); (iv) each C allele at polymorphism rs10192157 (SEQ ID NO: 4); (v) each T allele at polymorphism rs10206753 (SEQ ID NO: 5); (vi) each T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or (vii) each equivalent allele at a polymorphism that is in

linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) indicates an increased likelihood of improving the therapeutic efficacy of an IL-33-mediated disorder therapy by the addition of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In any of the preceding embodiments, the equivalent allele may be in an alternate SNP that is in linkage disequilibrium with one or more of the selected SNPs described herein. In some embodiments, the linkage disequilibrium is a D' value or an r^2 value. In some embodiments, the D' measure between the selected SNP and the alternate SNP is ≥ 0.60 (e.g., ≥ 0.60, ≥ 0.65, ≥ 0.7, ≥ 0.75, ≥ 0.8, ≥ 0.85, ≥ 0.9, ≥ 0.95, or higher). In some embodiments, the D' value between the selected SNP and the alternate SNP is ≥ 0.70, ≥ 0.80, or ≥ 0.90. In some embodiments, the D' value between the selected SNP and the alternate SNP is 1.0. In some embodiments, the r^2 value between the selected SNP and the alternate SNP is ≥ 0.60 (e.g., ≥ 0.60, ≥ 0.65, ≥ 0.7, ≥ 0.75, ≥ 0.8, ≥ 0.85, ≥ 0.9, ≥ 0.95, or higher). In some embodiments the r^2 value between the selected SNP and the alternate SNP is ≥ 0.70, ≥ 0.80, or ≥ 0.90. In some embodiments, the r^2 value between the selected SNP and the alternate SNP is 1.0. In some embodiments, the alternate SNP is a SNP designated in Table 3 or 4. In any of the preceding methods, the equivalent allele may be the minor allele or the major allele. In some instances, the equivalent allele is the minor allele. In other instances, the equivalent allele is the major allele.

In any of the above diagnostic methods, the method may further include administering to the patient a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. For example, the method may further include administering a therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, or an IL-5 binding antagonist. In other instances, the method may further include administering a therapy comprising at least two agents, for example, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and a tryptase-beta binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and a CRTH2 binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and an IL-13 binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and an IL-17 binding antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and a JAK1 antagonist, an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and an IL-5 binding antagonist, a tryptase-beta binding antagonist and a CRTH2 binding antagonist, a

tryptase-beta binding antagonist and an IL-13 binding antagonist, a tryptase-beta binding antagonist and an IL-17 binding antagonist, a tryptase-beta binding antagonist and a JAK1 antagonist, a tryptase-beta binding antagonist and an IL-5 binding antagonist, a CRTH2 binding antagonist and an IL-13 binding antagonist, a CRTH2 binding antagonist and an IL-17 binding antagonist, a CRTH2 binding antagonist and a JAK1 antagonist, a CRTH2 binding antagonist and an IL-5 binding antagonist, an IL-13 binding antagonist and an IL-17 binding antagonist, an IL-13 binding antagonist and a JAK1 antagonist, an IL-13 binding antagonist and an IL-5 binding antagonist, an IL-17 binding antagonist and a JAK1 antagonist, an IL-17 binding antagonist and an IL-5 binding antagonist, or a JAK1 antagonist and an IL-5 binding antagonist. In other instances, the method may further include administering a therapy comprising at least three agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In other instances, the method may further include administering a therapy comprising at least four agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In other instances, the method may further include administering a therapy comprising at least five agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In yet other instances, the method may further include administering a therapy comprising at least six agents selected from an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist. In yet other instances, the method may include administering a therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 binding antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and an IL-5 binding antagonist.

In yet other instances, the present invention provides a method of selecting a therapy for a patient having an IL-33-mediated disorder, the method comprising: (a) determining the level of periostin in a sample derived from the patient; (b) comparing the level of periostin in the sample derived from the patient to a reference level of periostin, wherein a level of periostin in the sample at or below the reference level of periostin identifies a patient who is likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist); and (c) selecting a therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) if the patient is identified as likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) and recommending to the patient the selected therapy comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist). In some embodiments, the method further includes administering an asthma therapy including an antagonist selected from one or more of an IL-33 binding antagonist (e.g., an anti-IL-33 antibody or antigen-binding fragment thereof), a ST2 binding antagonist (e.g., an ST2-Fc protein, an anti-ST2 antibody, or antigen-binding fragment thereof), and/or an IL-1RAcP binding antagonist (e.g., an anti-IL1RAcP antibody). For example, in some embodiments, the method further includes administering

an IL-33 binding antagonist, a ST2 binding antagonist, or an IL1RAcP binding antagonist. In some embodiments, the method further includes administering at least two of the following: an IL-33 binding antagonist, a ST2 binding antagonist, and an IL1RAcP binding antagonist (e.g., an IL-33 binding antagonist and an ST2 binding antagonist (e.g., an ST2-Fc protein); an IL-33 binding antagonist and an IL1RAcP binding antagonist; or an ST2 binding antagonist (e.g., an ST2-Fc protein) and an IL1RAcP binding antagonist). In some embodiments, the method further includes administering an IL-33 binding antagonist, a ST2 binding antagonist (e.g., an ST2-Fc protein), and an IL1RAcP binding antagonist.

In other instances, the present invention provides a method of determining whether a patient is at increased risk of an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)), the method comprising: (a) determining the level of sST2 in a sample derived from the patient; and (b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2, wherein the patient is at an increased risk of an IL-33-mediated disorder if the level of sST2 in the sample derived from the patient is at or above the reference level. In some instances, the method further includes administering a therapy comprising a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In yet another instance, the present invention provides a method of selecting a therapy for a patient having an IL-33 mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)), the method comprising: (a) determining the level of sST2 in a sample derived from the patient; (b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2; and (c) selecting a therapy comprising an IL-33 axis binding antagonist if the level of sST2 in the sample is at or above the reference level. In some instances, the method further includes administering a therapy comprising a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In another instance, the present invention provides a method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis

binding antagonist, the method comprising: (a) determining the level of sST2 in a sample derived from the patient; (b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2; and (c) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the level of sST2 in the sample derived from the patient, wherein the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist if the level of sST2 in the sample is at or above the reference level. In some instances, the method further includes administering a therapy comprising a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In another instance, the present invention provides a method for assessing a treatment response of a patient treated with an IL-33 axis binding antagonist, the method comprising: (a) determining the level of sST2 in a sample derived from the patient at a time point during or after administration of the IL-33 axis binding antagonist; and (b) maintaining, adjusting, or stopping the treatment of the patient based on a comparison of the level of sST2 in the sample derived from the patient with a reference level of sST2, wherein a change in the level of sST2 in the sample derived from the patient compared to the reference level is indicative of a response to treatment with the IL-33 axis binding antagonist. In some embodiments, the change is an increase in the level of sST2 and treatment is maintained. In some embodiments, the change is an increase in the level of sST2 and treatment is changed to a different therapeutic agent (e.g., a different IL-33 axis binding antagonist). In some embodiments, the change is an increase in the level of sST2 and treatment is changed by increasing the dose of the IL-33 binding antagonist or increasing the frequency of dosing the IL-33 binding antagonist. In other embodiments, the change is a decrease in the level of sST2 and treatment is maintained. In other embodiments, the change is a decrease in the level of sST2 and treatment is decreased. In other embodiments, the change is a decrease in the level of sST2 and treatment is changed by decreasing the dose of the IL-33 binding antagonist or descreasing the frequency of dosing the IL-33 binding antagonist. In other embodiments, the change is a decrease in the level of sST2 and treatment is stopped. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In yet another instance, the present invention provides a method for monitoring the response of a patient treated with an IL-33 axis binding antagonist, the method comprising: (a) determining the level of sST2 in a sample derived from the patient at a time point during or after administration of the IL-33 axis binding antagonist; and (b) comparing the level of sST2 in the sample derived from the patient with a reference level of sST2, thereby monitoring the response in the patient undergoing treatment with the IL-33 axis binding antagonist. In some instances, the method further includes determining the level of periostin in a sample derived from the patient. In these instances, the method may further include informing the patient that they have an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist if the level of periostin in the sample is at, below, or above a reference level of periostin.

In any of the preceding methods, the level of sST2 may be, for example, a level of sST2 protein or a level of sST2 nucleic acid (e.g., mRNA). In some embodiments, the level is a level of sST2 protein.

In any of the preceding methods, the sample derived from the patient may be a whole blood sample, a serum sample, a plasma sample, or a combination thereof. In some embodiments, the sample derived from the patient may be a serum sample.

In any of the preceding methods, in some embodiments, the level of sST2 in the sample derived from the patient may be at least 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 2.2-fold, 2.4-fold, 2.6-fold, 2.8-fold, 3-fold, 3.5-fold, 4-fold, 4.5-fold, 5-fold, 5.5-fold, 6-fold, 6.5-fold, 7-fold, 7.5-fold, 8-fold, 9-fold, 10-fold, 15-fold, or 20-fold above the reference level. In any of the preceding methods, in some embodiments, the level of sST2 in the sample derived from the patient may be at least 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 2.2-fold, 2.4-fold, 2.6-fold, 2.8-fold, 3-fold, 3.5-fold, 4-fold, 4.5-fold, 5-fold, 5.5-fold, 6-fold, 6.5-fold, 7-fold, 7.5-fold, 8-fold, 9-fold, 10-fold, 15-fold, or 20-fold below the reference level.

Any suitable reference level of sST2 may be used in any of the preceding methods. In any of the preceding methods, the reference level may be is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6). In any of the preceding methods, the reference level of sST2 may be a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8). In some instances, the group of individuals is suffering from asthma. In some embodiments, the reference level of sST2 may be an average, a median, or any suitable value. In some instances, reference level is a median level. In some instances, the group of individuals is a group of female individuals and the patient is female. In other instances, the group of individuals is a group of male individuals and the patient is male. In any of the preceding methods, the reference level of sST2 may be determined in an individual at an earlier timepoint, e.g., before administration of an IL-33 binding antagonist or at an earlier timepoint during treatment with an IL-33 binding antagonist.

In some instances, any of the preceding methods further includes administering a therapy comprising a therapy comprising one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following: an IL-33 axis

binding antagonist (e.g., an ST2 binding antagonist), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a JAK1 antagonist, and/or an IL-5 binding antagonist. In some embodiments, the IL-33 axis binding antagonist is an IL-33 binding antagonist, an ST2 binding antagonist, or an IL-1RAcP binding antagonist.

In some instances, any of the preceding methods further includes administering an antagonist selected from one or more of an IL-33 binding antagonist (e.g., an anti-IL-33 antibody or antigen-binding fragment thereof), a ST2 binding antagonist (e.g., an ST2-Fc protein, an anti-ST2 antibody, or antigen-binding fragment thereof), and/or an IL-1RAcP binding antagonist (e.g., an anti-IL1RAcP antibody) based on the level of sST2 in a sample derived from the patient being at or above a reference level. For example, in some embodiments, the method further includes administering an IL-33 binding antagonist, a ST2 binding antagonist, or an IL1RAcP binding antagonist. In some embodiments, the method further includes administering at least two of the following: an IL-33 binding antagonist, a ST2 binding antagonist, and an IL1RAcP binding antagonist (e.g., an IL-33 binding antagonist and an ST2 binding antagonist (e.g., an ST2-Fc protein); an IL-33 binding antagonist and an IL1RAcP binding antagonist; or an ST2 binding antagonist (e.g., an ST2-Fc protein) and an IL1RAcP binding antagonist). In some embodiments, the method further includes administering an IL-33 binding antagonist, a ST2 binding antagonist (e.g., an ST2-Fc protein), and an IL1RAcP binding antagonist.

One of skill in the medical arts, particularly pertaining to the application of diagnostic tests and treatment with therapeutics, will recognize that biological systems are somewhat variable and not always entirely predictable, and thus many good diagnostic tests or therapeutics are occasionally ineffective. Thus, it is ultimately up to the judgment of the attending physician to determine the most appropriate course of treatment for an individual patient, based upon test results, patient condition and history, and his or her own experience. There may even be occasions, for example, when a physician will choose to treat a patient with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) even when a patient is not determined to be at increased risk of an IL-33-mediated disorder (e.g., asthma and/or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)), based on data from diagnostic tests or from other criteria, particularly if all or most of the other obvious treatment options have failed, or if some synergy is anticipated when given with another treatment.

The present invention also provides a method of identifying a biomarker that is useful for monitoring sensitivity or responsiveness to an IL-33 axis binding antagonist, such as an anti-IL-33 antibody or an ST2 binding antagonist, the method comprising: (a) measuring the level of a candidate biomarker in samples from patients with IL-33-mediated disorders obtained before any dose of an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) is administered to the patients, wherein an change (i.e., an increase or decrease) in the expression of the candidate biomarker relative to a control indicates that the biomarker is diagnostic for more effective treatment of the IL-33-mediated disorder with an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist). In some embodiments, the biomarker is genetic and its expression is analyzed.

IV. Detection of Nucleic Acid Polymorphisms

In several embodiments, the methods of treatment and diagnosis provided by the invention involve determination of the genotype of a patient at one or more polymorphisms (e.g., polymorphisms in *IL1RL1* described in Tables 1 and 2). Detection techniques for evaluating nucleic acids for the presence of a SNP involve procedures well known in the field of molecular genetics. Many, but not all, of the methods involve amplification of nucleic acids. Ample guidance for performing amplification is provided in the art. Exemplary references include manuals such as Erlich, ed., *PCR Technology: Principles and Applications for DNA Amplification,* Freeman Press, 1992; Innis et al. eds., *PCR Protocols: A Guide to Methods and Applications,* Academic Press, 1990; Ausubel, ed., *Current Protocols in Molecular Biology,* 1994-1999, including supplemental updates through April 2004; and Sambrook et al. eds., *Molecular Cloning, A Laboratory Manual*, 2001. General methods for detection of single nucleotide polymorphisms are disclosed in Kwok, ed., *Single Nucleotide Polymorphisms: Methods and Protocols*, Humana Press, 2003.

Although the methods typically employ PCR steps, other amplification protocols may also be used. Suitable amplification methods include ligase chain reaction (see, e.g., Wu et al. *Genomics* 4:560-569, 1988); strand displacement assay (see, e.g., Walker et al. *Proc. Natl. Acad. Sci.* USA 89:392-396, 1992; U.S. Pat. No. 5,455,166); and several transcription-based amplification systems, including the methods described in U.S. Pat. Nos. 5,437,990; 5,409,818; and 5,399,491; the transcription amplification system (TAS) (Kwoh et al. *Proc. Natl. Acad. Sci.* USA 86:1173-1177, 1989); and self-sustained sequence replication (3SR) (Guatelli et al. *Proc. Natl. Acad. Sci.* USA 87:1874-1878, 1990; WO 1992/08800). Alternatively, methods that amplify the probe to detectable levels can be used, such as Qβ-replicase amplification (Kramer et al. *Nature* 339:401-402, 1989; Lomeli et al. *Clin. Chem.* 35:1826-1831,1989). A review of known amplification methods is provided, for example, by Abramson et al. *Curr. Opin. Biotech.* 4:41-47, 1993.

Detection of the genotype, haplotype, SNP, microsatellite, or other polymorphism of an individual can be performed using oligonucleotide primers and/or probes. Oligonucleotides can be prepared by any suitable method, usually chemical synthesis. Oligonucleotides can be synthesized using commercially available reagents and instruments. Alternatively, they can be purchased through commercial sources. Methods of synthesizing oligonucleotides are well known in the art (see, e.g., Narang et al. *Meth. Enzymol.* 68:90-99, 1979; Brown et al. *Meth. Enzymol.* 68:109-151, 1979; Beaucage et al. *Tetra. Lett.* 22:1859-1862, 1981; and the solid support method of U.S. Pat. No. 4,458,066). In addition, modifications to the above-described methods of synthesis may be used to desirably impact enzyme behavior with respect to the synthesized oligonucleotides. For example, incorporation of modified phosphodiester linkages (e.g., phosphorothioate, methylphosphonates, phosphoamidate, or boranophosphate) or linkages other than a phosphorous acid derivative into an oligonucleotide may be used to prevent cleavage at a selected site. In addition, the use of 2'-amino modified sugars tends to favor displacement over digestion of the oligonucleotide when hybridized to a nucleic acid that is also the template for synthesis of a new nucleic acid strand.

The genotype of an individual (e.g., a patient suffering from or at risk for an IL-33-mediated disorder, for example, asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)) can be

determined using many detection methods that are well known in the art. Most assays entail one of several general protocols: hybridization using allele-specific oligonucleotides, primer extension, allele-specific ligation, sequencing, or electrophoretic separation techniques, e.g., single-stranded conformational polymorphism (SSCP) and heteroduplex analysis. Exemplary assays include 5'-nuclease assays, template-directed dye-terminator incorporation, molecular beacon allele-specific oligonucleotide assays, single-base extension assays, and SNP scoring by real-time pyrophosphate sequences. Analysis of amplified sequences can be performed using various technologies such as microchips, fluorescence polarization assays, and MALDI-TOF (matrix assisted laser desorption ionization-time of flight) mass spectrometry. Two methods that can also be used are assays based on invasive cleavage with Flap nucleases and methodologies employing padlock probes.

Determination of the presence or absence of a particular allele is generally performed by analyzing a nucleic acid sample that is obtained from the individual to be analyzed. Often, the nucleic acid sample comprises genomic DNA. The genomic DNA is typically obtained from blood samples, but may also be obtained from other cells or tissues.

It is also possible to analyze RNA samples for the presence of polymorphic alleles. For example, mRNA can be used to determine the genotype of an individual at one or more polymorphic sites. In this case, the nucleic acid sample is obtained from cells in which the target nucleic acid is expressed, e.g., T helper-2 (Th2) cells and mast cells. Such an analysis can be performed by first reverse-transcribing the target RNA using, for example, a viral reverse transcriptase, and then amplifying the resulting cDNA; or using a combined high-temperature reverse-transcription-polymerase chain reaction (RT-PCR), as described in U.S. Pat. Nos. 5,310,652; 5,322,770; 5,561,058; 5,641,864; and 5,693,517.

The sample may be taken from a patient who is suspected of having, or is diagnosed as having an IL-33-mediated disorder, and hence is likely in need of treatment, or from a normal individual who is not suspected of having any disorder. For determination of genotypes, patient samples, such as those containing cells, or nucleic acids produced by these cells, may be used in the methods of the present invention. Bodily fluids or secretions useful as samples in the present invention include, e.g., blood, urine, saliva, stool, pleural fluid, lymphatic fluid, sputum, ascites, prostatic fluid, cerebrospinal fluid (CSF), or any other bodily secretion or derivative thereof. The word blood is meant to include whole blood, plasma, serum, or any derivative of blood. Sample nucleic acid for use in the methods described herein can be obtained from any cell type or tissue of a subject. For example, a subject's bodily fluid (e.g. blood) can be obtained by known techniques. Alternatively, nucleic acid tests can be performed on dry samples (e.g., hair or skin).

The sample may be frozen, fresh, fixed (e.g., formalin fixed), centrifuged, and/or embedded (e.g., paraffin embedded), etc. The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (e.g., nucleic acid and/or protein extraction, fixation, storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the genotype in the sample. Likewise, biopsies may also be subjected to post-collection preparative and storage techniques, e.g., fixation.

Frequently used methodologies for analysis of nucleic acid samples to detect SNPs which are useful in the present invention are briefly described below. However, any method known in the art can be

used in the invention to detect the presence of single nucleotide substitutions.

a. Allele-Specific Hybridization

This technique, also commonly referred to as allele-specific oligonucleotide hybridization (ASO) (e.g., Stoneking et al. *Am. J. Hum. Genet.* 48:70-382, 1991; Saiki et al. *Nature* 324, 163-166, 1986; EP 235,726; and WO 1989/11548), relies on distinguishing between two DNA molecules differing by one base by hybridizing an oligonucleotide probe that is specific for one of the variants to an amplified product obtained from amplifying the nucleic acid sample. This method typically employs short oligonucleotides, e.g., 15-20 bases in length. The probes are designed to differentially hybridize to one variant versus another. Principles and guidance for designing such probe is available in the art, for example, in the references cited herein. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and producing an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-base oligonucleotide at the 7 position; in a 16-based oligonucleotide at either the 8 or 9 position) of the probe, but this design is not required.

The amount and/or presence of an allele can be determined by measuring the amount of allele-specific oligonucleotide that is hybridized to the sample. Typically, the oligonucleotide is labeled with a label such as a fluorescent label. For example, an allele-specific oligonucleotide is applied to immobilized oligonucleotides representing SNP sequences. After stringent hybridization and washing conditions, fluorescence intensity is measured for each SNP oligonucleotide.

In one embodiment, the nucleotide present at the polymorphic site is identified by hybridization under sequence-specific hybridization conditions with an oligonucleotide probe or primer exactly complementary to one of the polymorphic alleles in a region encompassing the polymorphic site. The probe or primer hybridizing sequence and sequence-specific hybridization conditions are selected such that a single mismatch at the polymorphic site destabilizes the hybridization duplex sufficiently so that it is effectively not formed. Thus, under sequence-specific hybridization conditions, stable duplexes will form only between the probe or primer and the exactly complementary allelic sequence. Thus, oligonucleotides from about 10 to about 35 nucleotides in length, usually from about 15 to about 35 nucleotides in length, which are exactly complementary to an allele sequence in a region which encompasses the polymorphic site are within the scope of the invention.

In an alternative embodiment, the nucleotide present at the polymorphic site is identified by hybridization under sufficiently stringent hybridization conditions with an oligonucleotide substantially complementary to one of the SNP alleles in a region encompassing the polymorphic site, and exactly complementary to the allele at the polymorphic site. Because mismatches which occur at non-polymorphic sites are mismatches with both allele sequences, the difference in the number of mismatches in a duplex formed with the target allele sequence and in a duplex formed with the corresponding non-target allele sequence is the same as when an oligonucleotide exactly complementary to the target allele sequence is used. In this embodiment, the hybridization conditions are relaxed sufficiently to allow the formation of stable duplexes with the target sequence, while maintaining sufficient

stringency to preclude the formation of stable duplexes with non-target sequences. Under such sufficiently stringent hybridization conditions, stable duplexes will form only between the probe or primer and the target allele. Thus, oligonucleotides from about 10 to about 35 nucleotides in length, usually from about 15 to about 35 nucleotides in length, which are substantially complementary to an allele sequence in a region which encompasses the polymorphic site, and are exactly complementary to the allele sequence at the polymorphic site, are within the scope of the invention.

The use of substantially, rather than exactly, complementary oligonucleotides may be desirable in assay formats in which optimization of hybridization conditions is limited. For example, in a typical multi-target immobilized-oligonucleotide assay format, probes or primers for each target are immobilized on a single solid support. Hybridizations are carried out simultaneously by contacting the solid support with a solution containing target DNA. As all hybridizations are carried out under identical conditions, the hybridization conditions cannot be separately optimized for each probe or primer. The incorporation of mismatches into a probe or primer can be used to adjust duplex stability when the assay format precludes adjusting the hybridization conditions. The effect of a particular introduced mismatch on duplex stability is well known, and the duplex stability can be routinely both estimated and empirically determined, as described above. Suitable hybridization conditions, which depend on the exact size and sequence of the probe or primer, can be selected empirically using the guidance provided herein and well known in the art. The use of oligonucleotide probes or primers to detect single base pair differences in sequence is described in, for example, Conner et al. *Proc. Natl. Acad. Sci.* USA 80:278-282, 1983, and U.S. Pat. Nos. 5,468,613 and 5,604,099.

The proportional change in stability between a perfectly matched and a single-base mismatched hybridization duplex depends on the length of the hybridized oligonucleotides. Duplexes formed with shorter probe sequences are destabilized proportionally more by the presence of a mismatch. Oligonucleotides between about 15 and about 35 nucleotides in length are often used for sequence-specific detection. Furthermore, because the ends of a hybridized oligonucleotide undergo continuous random dissociation and re-annealing due to thermal energy, a mismatch at either end destabilizes the hybridization duplex less than a mismatch occurring internally. For discrimination of a single base pair change in target sequence, the probe sequence is selected which hybridizes to the target sequence such that the polymorphic site occurs in the interior region of the probe.

The above criteria for selecting a probe sequence that hybridizes to a specific allele apply to the hybridizing region of the probe, i.e., that part of the probe which is involved in hybridization with the target sequence. A probe may be bound to an additional nucleic acid sequence, such as a poly-T tail used to immobilize the probe, without significantly altering the hybridization characteristics of the probe. One of skill in the art will recognize that for use in the present methods, a probe bound to an additional nucleic acid sequence which is not complementary to the target sequence and, thus, is not involved in the hybridization, is essentially equivalent to the unbound probe.

Suitable assay formats for detecting hybrids formed between probes and target nucleic acid sequences in a sample are known in the art and include the immobilized target (dot-blot) format and immobilized probe (reverse dot-blot or line-blot) assay formats. Dot blot and reverse dot blot assay formats are described in U.S. Pat. Nos. 5,310,893; 5,451,512; 5,468,613; and 5,604,099.

In a dot-blot format, amplified target DNA is immobilized on a solid support, such as a nylon membrane. The membrane-target complex is incubated with labeled probe under suitable hybridization conditions, unhybridized probe is removed by washing under suitably stringent conditions, and the membrane is monitored for the presence of bound probe.

In the reverse dot-blot (or line-blot) format, the probes are immobilized on a solid support, such as a nylon membrane or a microtiter plate. The target DNA is labeled, typically during amplification by the incorporation of labeled primers. One or both of the primers can be labeled. The membrane-probe complex is incubated with the labeled amplified target DNA under suitable hybridization conditions, unhybridized target DNA is removed by washing under suitably stringent conditions, and the membrane is monitored for the presence of bound target DNA. A reverse line-blot detection assay is described in the example.

An allele-specific probe that is specific for one of the polymorphism variants is often used in conjunction with the allele-specific probe for the other polymorphism variant. In some embodiments, the probes are immobilized on a solid support and the target sequence in an individual is analyzed using both probes simultaneously. Examples of nucleic acid arrays are described by WO 95/11995. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of variant forms of a pre-characterized polymorphism. Such a subarray can be used in detecting the presence of the polymorphisms described herein.

b. Allele-Specific Primers

Polymorphisms are also commonly detected using allele-specific amplification or primer extension methods. These reactions typically involve use of primers that are designed to specifically target a polymorphism *via* a mismatch at the 3'-end of a primer. The presence of a mismatch affects the ability of a polymerase to extend a primer when the polymerase lacks error-correcting activity. For example, to detect an allele sequence using an allele-specific amplification- or extension-based method, a primer complementary to one allele of a polymorphism is designed such that the 3'-terminal nucleotide hybridizes at the polymorphic position. The presence of the particular allele can be determined by the ability of the primer to initiate extension. If the 3'-terminus is mismatched, the extension is impeded.

In some embodiments, the primer is used in conjunction with a second primer in an amplification reaction. The second primer hybridizes at a site unrelated to the polymorphic position. Amplification proceeds from the two primers leading to a detectable product signifying the particular allelic form is present. Allele-specific amplification- or extension-based methods are described in, for example, WO 93/22456; U.S. Pat. Nos. 5,137,806; 5,595,890; 5,639,611; and U.S. Pat. No. 4,851,331.

Using allele-specific amplification-based genotyping, identification of the alleles requires only detection of the presence or absence of amplified target sequences. Methods for the detection of amplified target sequences are well known in the art. For example, gel electrophoresis and probe hybridization assays described are often used to detect the presence of nucleic acids.

In an alternative probe-less method, the amplified nucleic acid is detected by monitoring the increase in the total amount of double-stranded DNA in the reaction mixture, is described, e.g. in U.S.

Pat. No. 5,994,056; and European Patent Publication Nos. 487,218 and 512,334. The detection of double-stranded target DNA relies on the increased fluorescence various DNA-binding dyes, e.g., SYBR Green, exhibit when bound to double-stranded DNA.

As appreciated by one in the art, allele-specific amplification methods can be performed in reactions that employ multiple allele-specific primers to target particular alleles. Primers for such multiplex applications are generally labeled with distinguishable labels or are selected such that the amplification products produced from the alleles are distinguishable by size. Thus, for example, both alleles in a single sample can be identified using a single amplification by gel analysis of the amplification product.

As in the case of allele-specific probes, an allele-specific oligonucleotide primer may be exactly complementary to one of the polymorphic alleles in the hybridizing region or may have some mismatches at positions other than the 3'-terminus of the oligonucleotide, which mismatches occur at non-polymorphic sites in both allele sequences.

c. Detectable Probes

i) 5'-Nuclease Assay Probes

Genotyping can also be performed using a "TAQMAN®" or "5'-nuclease assay," as described in U.S. Pat. Nos. 5,210,015; 5,487,972; and 5,804,375; and Holland et al. *Proc. Natl. Acad. Sci. USA* 88:7276-7280, 1988. In the TAQMAN® assay, labeled detection probes that hybridize within the amplified region are added during the amplification reaction. The probes are modified so as to prevent the probes from acting as primers for DNA synthesis. The amplification is performed using a DNA polymerase having 5'- to 3'-exonuclease activity. During each synthesis step of the amplification, any probe which hybridizes to the target nucleic acid downstream from the primer being extended is degraded by the 5'- to 3'-exonuclease activity of the DNA polymerase. Thus, the synthesis of a new target strand also results in the degradation of a probe, and the accumulation of degradation product provides a measure of the synthesis of target sequences.

The hybridization probe can be an allele-specific probe that discriminates between the SNP alleles. Alternatively, the method can be performed using an allele-specific primer and a labeled probe that binds to amplified product.

Any method suitable for detecting degradation product can be used in a 5'-nuclease assay. Often, the detection probe is labeled with two fluorescent dyes, one of which is capable of quenching the fluorescence of the other dye. The dyes are attached to the probe, usually one attached to the 5'-terminus and the other is attached to an internal site, such that quenching occurs when the probe is in an unhybridized state and such that cleavage of the probe by the 5'- to 3'-exonuclease activity of the DNA polymerase occurs in between the two dyes. Amplification results in cleavage of the probe between the dyes with a concomitant elimination of quenching and an increase in the fluorescence observable from the initially quenched dye. The accumulation of degradation product is monitored by measuring the increase in reaction fluorescence. U.S. Pat. Nos. 5,491,063 and 5,571,673 describe alternative methods for detecting the degradation of probe which occurs concomitant with amplification.

ii) Secondary Structure Probes

Probes detectable upon a secondary structural change are also suitable for detection of a polymorphism, including SNPs. Exemplified secondary structure or stem-loop structure probes include molecular beacons or SCORPION® primer/probes. Molecular beacon probes are single-stranded oligonucleic acid probes that can form a hairpin structure in which a fluorophore and a quencher are usually placed on the opposite ends of the oligonucleotide. At either end of the probe short complementary sequences allow for the formation of an intramolecular stem, which enables the fluorophore and the quencher to come into close proximity. The loop portion of the molecular beacon is complementary to a target nucleic acid of interest. Binding of this probe to its target nucleic acid of interest forms a hybrid that forces the stem apart. This causes a conformation change that moves the fluorophore and the quencher away from each other and leads to a more intense fluorescent signal. Molecular beacon probes are, however, highly sensitive to small sequence variation in the probe target (see, e.g., Tyagi et al. *Nature Biotech.* 14:303-308, 1996; Tyagi et al. *Nature Biotech.* 16:49-53, 1998; Piatek et al. *Nature Biotech.* 16: 359-363, 1998; Marras et al. *Genetic Analysis: Biomolecular Engineering* 14:151-156,1999; Tapp et al, *BioTechniques* 28: 732-738, 2000). A SCORPION® primer/probe comprises a stem-loop structure probe covalently linked to a primer.

d. DNA Sequencing and Single Base Extensions

SNPs can also be detected by direct sequencing. Methods include e.g. dideoxy sequencing-based methods and other methods such as Maxam and Gilbert sequence (see, e.g. Sambrook and Russell, supra).

Other detection methods include PYROSEQUENCING™ of oligonucleotide-length products. Such methods often employ amplification techniques such as PCR. For example, in pyrosequencing, a sequencing primer is hybridized to a single stranded, PCR-amplified, DNA template and incubated with the enzymes DNA polymerase, ATP sulfurylase, luciferase, and apyrase, and the substrates adenosine 5' phosphosulfate (APS) and luciferin. The first of four deoxynucleotide triphosphates (dNTP) is added to the reaction. DNA polymerase catalyzes the incorporation of the deoxynucleotide triphosphate into the DNA strand if it is complementary to the base in the template strand. Each incorporation event is accompanied by release of pyrophosphate (PPi) in a quantity equimolar to the amount of incorporated nucleotide. ATP sulfurylase quantitatively converts PPi to ATP in the presence of APS. This ATP drives the luciferase-mediated conversion of luciferin to oxyluciferin that generates visible light in amounts that are proportional to the amount of ATP. The light produced in the luciferase-catalyzed reaction is detected by a charge coupled device (CCD) camera and seen as a peak in a PYROGRAM™. Each light signal is proportional to the number of nucleotides incorporated. Apyrase, a nucleotide degrading enzyme, continuously degrades unincorporated dNTPs and excess ATP. When degradation is complete, another dNTP is added.

Another similar method for characterizing SNPs does not require use of a complete PCR, but typically uses only the extension of a primer by a single, fluorescence-labeled dideoxyribonucleic acid molecule (ddNTP) that is complementary to the nucleotide to be investigated. The nucleotide at the

polymorphic site can be identified *via* detection of a primer that has been extended by one base and is fluorescently labeled (e.g., Kobayashi et al, *Mol. Cell. Probes*, 9:175-182, 1995).

e. Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution (see, e.g. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, W. H. Freeman and Co., 1992).

Distinguishing of microsatellite polymorphisms can be done using capillary electrophoresis. Capillary electrophoresis conveniently allows identification of the number of repeats in a particular microsatellite allele. The application of capillary electrophoresis to the analysis of DNA polymorphisms is well known to those in the art (see, for example, Szantai et al. *J Chromatogr A*. 1079(1-2):41-9, 2005; Bjorheim et al. *Electrophoresis* 26(13):2520-30, 2005 and Mitchelson, *Mol. Biotechnol.* 24(1):41-68, 2003).

The identity of the allelic variant may also be obtained by analyzing the movement of a nucleic acid comprising the polymorphic region in polyacrylamide gels containing a gradient of denaturant, which is assayed using denaturing gradient gel electrophoresis (DGGE) (see, e.g., Myers et al. *Nature* 313:495-498, 1985). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example, by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (see, e.g., Rosenbaum et al. *Biophys. Chem.* 265:1275, 1987).

f. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described, e.g, in Orita et al. *Proc. Nat. Acad. Sci.* 86, 2766-2770, 1989; Cotton *Mutat. Res.* 285:125-144, 1993; and Hayashi *Genet. Anal. Tech. Appl.* 9:73-79, 1992. Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence difference between alleles of target, and the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In another preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (see, e.g., Keen et al. *Trends Genet.* 7:5-10, 1991).

SNP detection methods often employ labeled oligonucleotides. Oligonucleotides can be labeled by incorporating a label detectable by spectroscopic, photochemical, biochemical, immunochemical, or

chemical means. Useful labels include fluorescent dyes, radioactive labels, e.g. ^{32}P, electron-dense reagents, enzyme, such as peroxidase or alkaline phosphatase, biotin, or haptens and proteins for which antisera or monoclonal antibodies are available. Labeling techniques are well known in the art (see, e.g. *Current Protocols in Molecular Biology*, supra; Sambrook et al., supra).

g. Additional Methods to Determine the Genotype of an Individual at Polymorphisms

DNA microarray technology, e.g., DNA chip devices, high-density microarrays for high-throughput screening applications, and lower-density microarrays may be used. Methods for microarray fabrication are known in the art and include various inkjet and microjet deposition or spotting technologies and processes, in situ or on-chip photolithographic oligonucleotide synthesis processes, and electronic DNA probe addressing processes. DNA microarray hybridization applications have been successfully applied in the areas of gene expression analysis and genotyping for point mutations, single nucleotide polymorphisms (SNPs), and short tandem repeats (STRs). Additional methods include interference RNA microarrays and combinations of microarrays and other methods such as laser capture microdissection (LCM), comparative genomic hybridization (CGH), array CGH, and chromatin immunoprecipitation (ChIP). See, e.g., He et al. *Adv. Exp. Med. Biol.* 593:117-133, 2007 and Heller *Annu. Rev. Biomed. Eng.* 4:129-153, 2002.

In some embodiments, protection from cleavage agents (such as a nuclease, hydroxylamine or osmium tetroxide and with piperidine) can be used to detect mismatched bases in RNA/RNA, DNA/DNA, or RNA/DNA heteroduplexes (see, e.g., Myers et al. *Science* 230:1242, 1985). In general, the technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing a control nucleic acid, which is optionally labeled, e.g., RNA or DNA, comprising a nucleotide sequence of the allelic variant of the gene with a sample nucleic acid, e.g., RNA or DNA, obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex, such as duplexes formed based on base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids can be treated with S1 nuclease to enzymatically digest the mismatched regions. Alternatively, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine whether the control and sample nucleic acids have an identical nucleotide sequence or in which nucleotides they are different. See, for example, U.S. Pat. No. 6,455,249, Cotton et al. *Proc. Natl. Acad. Sci. USA* 85:4397-4401, 1988; Saleeba et al. *Meth. Enzymol.* 217:286-295, 1992.

In some cases, the presence of the specific allele in DNA from a subject can be shown by restriction enzyme analysis. For example, the specific nucleotide polymorphism can result in a nucleotide sequence comprising a restriction site which is absent from the nucleotide sequence of another allelic variant.

In another embodiment, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, for example, in U.S. Pat. No. 4,998,617 and Laridegren et al. *Science* 241:1077-1080, 1988. The OLA protocol uses two oligonucleotides which are designed to be capable of

hybridizing to abutting sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g., by biotinylation, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin or another biotin ligand. Also known in the art is a nucleic acid detection assay that combines attributes of PCR and OLA (see, e.g., Nickerson et al. *Proc. Natl. Acad. Sci. USA* 87:8923-8927, 1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

A single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as described, for example, in U.S. Pat. No. 4,656,127. According to the method, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was complementary to that of the nucleotide derivative used in the reaction. This method has the advantage that it does not require the determination of large amounts of extraneous sequence data.

A solution-based method may also be used for determining the identity of the nucleotide of the polymorphic site (see, e.g., WO 1991/02087). As above, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

An alternative method that may be used is described in WO 92/15712. This method uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. The method is usually a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

Many other primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have been described (Komher et al. *Nucl. Acids. Res.* 17:7779-7784, 1989; Sokolov *Nucl. Acids Res.* 18:3671, 1990; Syvanen et al. *Genomics* 8:684-692, 1990; Kuppuswamy et al. *Proc. Natl. Acad. Sci. USA* 88:1143-1147, 1991; Prezant et al. *Hum. Mutat.* 1:159-164, 1992; Ugozzoli et al. *GATA* 9:107-112, 1992; Nyren et al. *Anal. Biochem.* 208:171-175, 1993). These methods all rely on the incorporation of labeled deoxynucleotides to discriminate between bases at a polymorphic site.

V. Biomarkers

The therapeutic and diagnostic methods of the invention can involve determination of the level of one or more biomarkers (e.g., periostin and/or sST2). The determination of the level of biomarkers can be performed by any of the methods known in the art or described below.

A. Detection of Gene Expression

The genetic biomarkers described herein (e.g., periostin) can be detected using any method known in the art. For example, tissue or cell samples from mammals can be conveniently assayed for, e.g., mRNAs or DNAs from a genetic biomarker of interest using Northern, dot-blot, or PCR analysis, array hybridization, RNase protection assay, or using DNA SNP chip microarrays, which are commercially available, including DNA microarray snapshots. For example, real-time PCR (RT-PCR) assays such as quantitative PCR assays are well known in the art. In an illustrative embodiment of the invention, a method for detecting mRNA from a genetic biomarker of interest (e.g., periostin and/or sST2) in a biological sample comprises producing cDNA from the sample by reverse transcription using at least one primer; amplifying the cDNA so produced; and detecting the presence of the amplified cDNA. In addition, such methods can include one or more steps that allow one to determine the levels of mRNA in a biological sample (*e.g.,* by simultaneously examining the levels a comparative control mRNA sequence of a "housekeeping" gene such as an actin family member). Optionally, the sequence of the amplified cDNA can be determined.

i. Detection of Nucleic Acids

In one specific embodiment, expression of a biomarker (e.g., periostin and/or sST2) can be performed by RT-PCR technology. Probes used for PCR may be labeled with a detectable marker, such as, for example, a radioisotope, fluorescent compound, bioluminescent compound, a chemiluminescent compound, metal chelator, or enzyme. Such probes and primers can be used to detect the presence of an expressed biomarker (e.g., periostin) in a sample. As will be understood by the skilled artisan, a great many different primers and probes may be prepared based on the sequences provided in herein and used effectively to amplify, clone and/or determine the presence and/or levels of a biomarker (e.g., periostin).

Other methods include protocols that examine or detect mRNAs from a biomarker (e.g., periostin and/or sST2 mRNAs), in a tissue or cell sample by microarray technologies. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes that have potential to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. Differential gene expression analysis of disease tissue can provide valuable information. Microarray technology utilizes nucleic acid hybridization techniques and computing technology to evaluate the mRNA expression profile of thousands of genes within a single experiment (see, e.g., WO 2001/75166). See, for example, U.S. Pat. Nos. 5,700,637, 5,445,934, and 5,807,522, Lockart, *Nat. Biotech.* 14:1675-1680, 1996; and Cheung *et al. Nat. Genet.* 21(Suppl):15-19, 1999 for a discussion of array fabrication.

In addition, the DNA profiling and detection method utilizing microarrays described in European Patent EP 1753878 may be employed. This method rapidly identifies and distinguishes between different

DNA sequences utilizing short tandem repeat (STR) analysis and DNA microarrays. In an embodiment, a labeled STR target sequence is hybridized to a DNA microarray carrying complementary probes. These probes vary in length to cover the range of possible STRs. The labeled single-stranded regions of the DNA hybrids are selectively removed from the microarray surface utilizing a post-hybridization enzymatic digestion. The number of repeats in the unknown target is deduced based on the pattern of target DNA that remains hybridized to the microarray.

One example of a microarray processor is the Affymetrix GENECHIP® system, which is commercially available and comprises arrays fabricated by direct synthesis of oligonucleotides on a glass surface. Other systems may be used as known to one skilled in the art.

The specialized microarrays herein, e.g., oligonucleotide microarrays or cDNA microarrays, may comprise one or more biomarkers having expression profiles that correlate with either sensitivity or resistance to one or more IL-33 axis binding antagonists (e.g., an ST2 binding antagonist, e.g., an ST2-Fc protein). Other methods that can be used to detect nucleic acids, for use in the invention, involve high-throughput RNA sequence expression analysis, including RNA-based genomic analysis, such as, for example, RNASeq.

Many references are available to provide guidance in applying the above techniques (Kohler et al. *Hybridoma Techniques*, Cold Spring Harbor Laboratory, 1980; Tijssen, *Practice and Theory of Enzyme Inimunoassays*, Elsevier, 1985; Campbell, *Monoclonal Antibody Technology*, Elsevier, 1984; Hurrell, *Monoclonal Hybridoma Antibodies: Techniques and Applications*, CRC Press, 1982; and Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp. 147-158, CRC Press, Inc., 1987). Northern blot analysis is a conventional technique well known in the art and is described, for example, in Sambrook et al, supra. Typical protocols for evaluating the status of genes and gene products are found, for example in Ausubel et al., supra.

ii. Detection of Proteins

As to detection of protein biomarkers, such as periostin and/or sST2, various protein assays are available including, for example, antibody-based methods as well as mass spectroscopy and other similar means known in the art. In the case of antibody-based methods, for example, the sample may be contacted with an antibody specific for the biomarker (e.g., periostin protein or sST2 protein) under conditions sufficient for an antibody-biomarker complex to form, and then detecting the complex. Detection of the presence of the protein biomarker may be accomplished in a number of ways, such as by Western blotting (with or without immunoprecipitation), 2-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), immunoprecipitation, fluorescence activated cell sorting (FACS™), flow cytometry, and enzyme-linked immunosorbent assay (ELISA) procedures for assaying a wide variety of tissues and samples, including plasma or serum. A wide range of immunoassay techniques using such an assay format are available, see, e.g., U.S. Patent Nos. 4,016,043; 4,424,279; and 4,018,653. These include both single-site and two-site or "sandwich" assays of the non-competitive types, as well as in the traditional competitive binding assays. These assays also include direct binding of a labeled antibody to a target biomarker.

Sandwich assays are among the most useful and commonly used assays. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, in a typical forward assay, an unlabelled antibody is immobilized on a solid substrate, and the sample to be tested is brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen complex, a second antibody specific to the antigen, labeled with a reporter molecule capable of producing a detectable signal is then added and incubated, allowing time sufficient for the formation of another complex of antibody-antigen-labeled antibody. Any unreacted material is washed away, and the presence of the antigen is determined by observation of a signal produced by the reporter molecule. The results may either be qualitative, by simple observation of the visible signal, or may be quantitated by comparing with a control sample containing known amounts of biomarker.

Variations on the forward assay include a simultaneous assay, in which both sample and labeled antibody are added simultaneously to the bound antibody. These techniques are well known to those skilled in the art, including any minor variations as will be readily apparent. In a typical forward sandwich assay, a first antibody having specificity for the biomarker is either covalently or passively bound to a solid surface. The solid surface is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride, or polypropylene. The solid supports may be in the form of tubes, beads, discs of microplates, or any other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically adsorbing, the polymer-antibody complex is washed in preparation for the test sample. An aliquot of the sample to be tested is then added to the solid phase complex and incubated for a period of time sufficient (e.g., 2-40 minutes or overnight if more convenient) and under suitable conditions (e.g., from room temperature to 40°C such as between 25°C and 32°C inclusive) to allow binding of any subunit present in the antibody. Following the incubation period, the antibody subunit solid phase is washed, dried, and incubated with a second antibody specific for a portion of the biomarker. The second antibody is linked to a reporter molecule which is used to indicate the binding of the second antibody to the molecular marker.

An alternative method involves immobilizing the target biomarkers in the sample and then exposing the immobilized target to specific antibody which may or may not be labeled with a reporter molecule. Depending on the amount of target and the strength of the reporter molecule signal, a bound target may be detectable by direct labeling with the antibody. Alternatively, a second labeled antibody specific to the first antibody is exposed to the target-first antibody complex to form a target-first antibody-second antibody tertiary complex. The complex is detected by the signal emitted by the reporter molecule. By “reporter molecule”, as used in the present specification, is meant a molecule which, by its chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules (i.e., radioisotopes) and chemiluminescent molecules.

In the case of an enzyme immunoassay (EIA), an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily available to the skilled artisan. Examples of

commonly used enzymes suitable for methods of the present invention include horseradish peroxidase, glucose oxidase, beta-galactosidase, and alkaline phosphatase. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable color change. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above. In all cases, the enzyme-labeled antibody is added to the first antibody-molecular marker complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the complex of antibody-antigen-antibody. The substrate will react with the enzyme linked to the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of biomarker (e.g., periostin and/or sST2) which was present in the sample. Alternately, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength, the fluorochrome-labeled antibody adsorbs the light energy, inducing a state to excitability in the molecule, followed by emission of the light at a characteristic color visually detectable with a light microscope. As in the EIA, the fluorescent labeled antibody is allowed to bind to the first antibody-molecular marker complex. After washing off the unbound reagent, the remaining tertiary complex is then exposed to the light of the appropriate wavelength, the fluorescence observed indicates the presence of the molecular marker of interest. Immunofluorescence and EIA techniques are both very well established in the art. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed.

In some embodiments of the present invention, a Total Periostin Assay, as described in WO 2012/083132, is used to determine the level of periostin in a sample derived from the patient.

For example, a periostin capture ELISA assay that is very sensitive (sensitivity of approximately 1.88 ng/ml) referred to as the E4 assay is described below. The antibodies recognize periostin isoforms 1-4 (SEQ ID NOs:5-8 of WO 2012/083132) at nanomolar affinity.

The steps of the method are as follows. Dilute 80 µL of purified monoclonal antibody, 25D4 (Coat Antibody, SEQ ID NOs: 1 and 2 of WO 2012/083132 expressed from a hybridoma or a CHO cell line) with phosphate buffered saline (PBS) to a final concentration of 2 µg/mL. Coat a microtiter plate overnight, covered, at 2-8°C with Coat Antibody, 100 µL per well. Wash the plate three times with 400 µL wash buffer (PBS/0.05% Tween (polysorbate 20) per well per cycle of wash buffer at room temperature. Add 200 µL per well of blocking buffer to the plate. Incubate covered plate at room temp with shaking for 1.5 hours.

Prepare a recombinant human periostin (rhuPeriostin) standard curve (Standard Stock of rhuPeriostin = rhuPeriostin isoform 1, R&D systems #3548-F2, 5.25 ng/ml, in Assay Diluent (PBS/0.5%bovine serum albumin (BSA)/0.05% polysorbate 20/0.05% ProClin300, pH7.4). Standard curve diluent = PBS/0.5%BSA/0.05% polysorbate 20, 0.05% ProClin300, pH 7.4.

Prepare controls and samples. Three controls: Spike Source Control (rhuPeriostin full length, isoform 1, R&D Systems #3548-F2), Normal Matrix Control (normal human serum pool, Bioreclamation, Inc.), High Matrix Control (normal human serum pool, plus 100ng/ml rhuPeriostin spike).

For example:

10 µL Control (or sample) serum + 1.99 mL sample/control diluent = 1:200

300 µL 1:200 dilution + 300 µL sample/control diluent = 1:400

300 µL 1:400 dilution + 300 µL sample/control diluent = 1:800

300 µL 1:800 dilution + 300 µL sample/control diluent = 1:1600

Each dilution is run in singlicate.

Construct Matrix Controls using a normal human serum pool. Use unspiked pooled human serum as the Normal Control. Generate the High Control by spiking 100 ng/mL rhuPeriostin into the pooled serum as described above. Compute mean, standard deviation (SD), and % coefficient of variance (CV, expressed in percent) for the four dilutions for each control on every plate. CV quantifies magnitude of variance in replicate measurements with respect to mean of replicates (e.g., %CV=100*(SD/mean)). Evaluate these mean concentrations across all plates to determine inter-plate precision. This control table is then used to define the Normal and High Control pass/fail criteria, setting allowable variance to ± 20% of the mean concentration for each control.

Wash the plate three times with 400 µL per well per cycle of wash buffer (PBS/0.05% polysorbate 20). Add diluted standards (duplicate wells), controls (all four dilutions), and samples (all four dilutions) to the plate, 100 µL per well. Incubate the plate covered, at room temperature with shaking for 2 hours at room temp. Dilute 80 µL detection MAb stock I (biotinylated murine anti-human periostin, MAb 23B9, 7.5ug/ml in Assay Diluent) to 12 mL with Assay Diluent = 50 ng/mL. Wash plate four times with 400 µL per well per cycle of wash buffer. Add diluted detection MAb to plate, 100 µL per well. Incubate covered plate at room temp for one hour with shaking. Dilute 80 uL streptavidin-HRP stock I (AMDEX streptavidin-HRP, GE Healthcare #RPN4401 ,approximately 1mg/ml) diluted 1:80 in Assay Diluent to 12 mL with Assay Diluent = 1:12k. Wash the plate four times with 400 µL per well per cycle of wash buffer. Add diluted streptavidin-HRP to the plate, 100 µL per well. Incubate covered plate at room temperature for 45 min with shaking. Bring Kirkegaard and Perry (KPL) two-step TMB reagents to room temperature; do not combine. Wash the plate four times with 400 µL per well per cycle of wash buffer. Mix equal volumes of KPL TMB substrate components and add to the plate, 100 µL per well. Incubate the plate for 20 minutes at room temperature with shaking. Add 1 M phosphoric acid to plate, 100 µL per well. Read the plate using 450 nm read wavelength and 650 nm reference wavelength.

In other embodiments, the ELECSYS® periostin assay described in WO 2012/083132 is used to determine the level of periostin in a sample derived from the patient, as described below.

The quantitative detection of periostin is assessed in an automated Roche cobas e601 ELECSYS® analyzer (Roche Diagnostics GmbH). The test is carried out in the sandwich format wherein the analyte periostin is sandwiched between two monoclonal antibodies binding to two different epitopes on periostin. One antibody is biotinylated and enables the capture of the immunocomplex to streptavidin-coated magnetic beads. The second antibody bears a complexed ruthenium cation as the signaling moiety that allows a voltage dependent electrochemi-luminescent detection of the bound immunocomplex.

In detail, the reagents used are as follows:

-Beads (M): Streptavidin-coated magnetic microparticles 0.72 mg/mL; preservative.

-Reagent 1 (R1): Anti-periostin-antibody~biotin:

This purified mouse monoclonal-antibody corresponds to the coating antibody 25D4 described above in relation to the E4 assay and is used in biotinylated form >1.0 mg/L; TRIS buffer >100 mmol/L, pH 7.0; preservative.

-Reagent 2 (R2): Anti-periostin-antibody~Ru(bpy):

This purified mouse monoclonal anti-periostin antibody corresponds to the detection antibody 23B9 described above in relation to the E4 assay and is used in labeled form (labeled with a (Tris(2,2'-bipyridyl)ruthenium(II)-complex (Ru(bpy)) complex) >1.0 mg/L; TRIS buffer >100 mmol/L, pH 7.0; preservative.

The immunoassay is carried out using two incubations. In the first incubation of about 9 minutes, periostin in 20 µL of sample and the biotinylated monoclonal anti-periostin antibody (R1) form a complex. In the second incubation step of an additional 9 minutes, ruthenylated monoclonal anti-periostin antibody (R2) and streptavidin-coated microparticles (M) are added to the vial of the first incubation so that a 3-membered sandwich complex is formed and becomes bound to the solid phase (microparticles) *via* the interaction of biotin and streptavidin.

The reaction mixture is aspirated into the measuring cell where the microparticles are magnetically captured onto the surface of a platinum electrode. Unbound substances are washed away and the cell flushed with ProCell, a reagent containing tripropylamine. Application of a voltage to the electrode then induces a chemi-luminescent emission which is measured by a photomultiplier. Results are determined *via* an instrument-specific calibration curve which is generated by 2-point calibration and a master curve provided *via* the reagent barcode. Calibrator 1 is analyte free, whereas calibrator 2 contains 50 ng/mL rhuPeriostin in a buffered matrix. To verify calibration, two controls with approximately 30 and 80 ng/mL periostin are employed.

In some embodiments, an exemplary reference level for periostin levels is 23 ng/ml, for example, when using the E4 assay described above. For instance, when using the E4 assay, a patient may have a periostin level at or greater than a reference level if the patient's periostin level is 23 ng/ml or higher, 24 ng/ml or higher, 25 ng/ml or higher, 26 ng/ml or higher, 27 ng/ml or higher, 28 ng/ml or higher, 29 ng/ml or higher, 30 ng/ml or higher, 31 ng/ml or higher, 32 ng/ml or higher, 33 ng/ml or higher, 34 ng/ml or higher, 35 ng/ml or higher, 36 ng/ml or higher, 37 ng/ml or higher, 38 ng/ml or higher, 39 ng/ml or higher, 40 ng/ml or higher, 41 ng/ml or higher, 42 ng/ml or higher, 43 ng/ml or higher, 44 ng/ml or higher, 45 ng/ml or higher, 46 ng/ml or higher, 47 ng/ml or higher, 48 ng/ml or higher, 49 ng/ml or higher, 50 ng/ml or higher, 51 ng/ml or higher, 52 ng/ml or higher, 53 ng/ml or higher, 54 ng/ml or higher, 55 ng/ml or higher, 56 ng/ml or higher, 57 ng/ml or higher, 58 ng/ml or higher, 59 ng/ml or higher, 60 ng/ml or higher, 61 ng/ml or higher, 62 ng/ml or higher, 63 ng/ml or higher, 64 ng/ml or higher, 65 ng/ml or higher, 66 ng/ml or higher, 67 ng/ml or higher, 68 ng/ml or higher, 69 ng/ml or higher or 70ng/ml or higher in the serum or plasma.

When using the E4 assay, a patient may have a periostin level at or below a reference level if the patient's periostin level is 23 ng/ml or lower, 22 ng/ml or lower, 21 ng/ml or lower, 20 ng/ml or lower, 19 ng/ml or lower, 18 ng/ml or lower, 17 ng/ml or lower, 16 ng/ml or lower, 15 ng/ml or lower, 14 ng/ml or lower, 13 ng/ml or lower, 12 ng/ml or lower, 11 ng/ml or lower, 10 ng/ml or lower, 9 ng/ml or lower, 8 ng/ml or lower, 7 ng/ml or lower, 6 ng/ml or lower, 5 ng/ml or lower, 4 ng/ml or lower, 3 ng/ml or lower, 2 ng/ml or lower, or 1 ng/ml or lower.

In other embodiments, an exemplary reference level for periostin levels is 50 ng/ml, for example, when using the ELECSYS® periostin assay described above. For instance, when using the ELECSYS® periostin assay, a patient may have a periostin level at or greater than a reference level if the patient's periostin level is 50 ng/ml or higher, 51 ng/ml or higher, 52 ng/ml or higher, 53 ng/ml or higher, 54 ng/ml or higher, 55 ng/ml or higher, 56 ng/ml or higher, 57 ng/ml or higher, 58 ng/ml or higher, 59 ng/ml or higher, 60 ng/ml or higher, 61 ng/ml or higher, 62 ng/ml or higher, 63 ng/ml or higher, 64 ng/ml or higher, 65 ng/ml or higher, 66 ng/ml or higher, 67 ng/ml or higher, 68 ng/ml or higher, 69 ng/ml or higher, 70 ng/ml or higher, 71 ng/ml or higher, 72 ng/ml or higher, 73 ng/ml or higher, 74 ng/ml or higher, 75 ng/ml or higher, 76 ng/ml or higher, 77 ng/ml or higher, 78 ng/ml or higher, 79 ng/ml or higher, 80 ng/ml or higher, 81 ng/ml or higher, 82 ng/ml or higher, 83 ng/ml or higher, 84 ng/ml or higher, 85 ng/ml or higher, 86 ng/ml or higher, 87 ng/ml or higher, 88 ng/ml or higher, 89 ng/ml or higher, 90 ng/ml or higher, 91 ng/ml or higher, 92 ng/ml or higher, 93 ng/ml or higher, 94 ng/ml or higher, 95 ng/ml or higher, 96 ng/ml or higher, 97 ng/ml or higher, 98 ng/ml or higher, or 99 ng/ml or higher.

When using the ELECSYS® periostin assay, a patient may have a periostin level at or below a reference level if the patient's periostin level is 50 ng/ml or lower, 49 ng/ml or lower, 48 ng/ml or lower, 47 ng/ml or lower, 46 ng/ml or lower, 45 ng/ml or lower, 44 ng/ml or lower, 43 ng/ml or lower, 42 ng/ml or lower, 41 ng/ml or lower, 40 ng/ml or lower, 39 ng/ml or lower, 38 ng/ml or lower, 37 ng/ml or lower, 36 ng/ml or lower, 35 ng/ml or lower, 34 ng/ml or lower, 33 ng/ml or lower, 32 ng/ml or lower, 31 ng/ml or lower, 30 ng/ml or lower, 29 ng/ml or lower, 28 ng/ml or lower, 27 ng/ml or lower, 26 ng/ml or lower, 25 ng/ml or lower, 24 ng/ml or lower, 23 ng/ml or lower, 22 ng/ml or lower, 21 ng/ml or lower, 20 ng/ml or lower, 19 ng/ml or lower, 18 ng/ml or lower, 17 ng/ml or lower, 16 ng/ml or lower, 15 ng/ml or lower, 14 ng/ml or lower, 13 ng/ml or lower, 12 ng/ml or lower, 11 ng/ml or lower, 10 ng/ml or lower, 9 ng/ml or lower, 8 ng/ml or lower, 7 ng/ml or lower, 6 ng/ml or lower, 5 ng/ml or lower, 4 ng/ml or lower, 3 ng/ml or lower, 2 ng/ml or lower, or 1 ng/ml or lower.

In some embodiments, the level of sST2 in a patient sample may be determined using any suitable method known in the art and/or described herein, for example, in Example 3. In some embodiments, a patient may have a sST2 level at or above a reference level if the patient's sST2 level is 0.1 ng/ml or higher, 0.5 ng/ml or higher, 1 ng/ml or higher, 2 ng/ml or higher, 3 ng/ml or higher, 4 ng/ml or higher, 5 ng/ml or higher, 6 ng/ml or higher, 7 ng/ml or higher, 8 ng/ml or higher, 9 ng/ml or higher, 10 ng/ml or higher, 11 ng/ml or higher, 12 ng/ml or higher, 13 ng/ml or higher, 14 ng/ml or higher, 15 ng/ml or higher, 16 ng/ml or higher, 17 ng/ml or higher, 18 ng/ml or higher, 19 ng/ml or higher, 20 ng/ml or higher, 21 ng/ml or higher, 22 ng/ml or higher, 23 ng/ml or higher, 24 ng/ml or higher, 25 ng/ml or higher, 26 ng/ml or higher, 27 ng/ml or higher, 28 ng/ml or higher, 29 ng/ml or higher, 30 ng/ml or higher, 31 ng/ml or higher, 32 ng/ml or higher, 33 ng/ml or higher, 34 ng/ml or higher, 35 ng/ml or higher, 36 ng/ml or higher, 37 ng/ml or higher, 38 ng/ml or higher, 39 ng/ml or higher, 40 ng/ml or higher, 41 ng/ml or higher, 42 ng/ml or higher, 43 ng/ml or higher, 44 ng/ml or higher, 45 ng/ml or higher, 46 ng/ml or higher, 47 ng/ml or higher, 48 ng/ml or higher, 49 ng/ml or higher, 50 ng/ml or higher, or higher than 50 ng/ml.

VI. Kits

In some embodiments, the invention provides a kit for carrying out the methods of the invention,

for example, for determining the genotype of a patient at a polymorphism as described herein. In some embodiments, the invention provides a kit for determining whether a patient is at risk of an IL-33-mediated disorder (e.g., asthma or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis)). Such kits typically contain one of more of the compositions described above and instructions for use. As an example only, the invention also provides kits for determining whether a patient is at risk of an IL-33-mediated disorder (e.g., asthma) containing a first and second oligonucleotide specific for a polymorphic region of *IL1RL1*, for example, specific for polymorphism rs4988956 (SEQ ID NO: 1); polymorphism rs10204137 (SEQ ID NO: 2); polymorphism rs10192036 (SEQ ID NO: 3); polymorphism rs10192157 (SEQ ID NO: 4); or polymorphism rs10206753 (SEQ ID NO: 5). In another example, the invention also provides kits for determining whether a patient is at risk of an IL-33-mediated disorder (e.g., asthma) containing a first and second oligonucleotide specific for a polymorphic region of *IL33*, for example, polymorphism rs4742165 (SEQ ID NO: 6). In yet another example, the invention provides kits for determining whether a patient is at risk of an IL-33-mediated disorder (e.g., asthma) containing a first and second oligonucleotide specific for a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6), for example, any polymorphism listed in Table 3 or Table 4. As another example, the invention also provides kits for determining whether a patient is likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) containing a first and second oligonucleotide specific for a polymorphic region of *IL1RL1*, for example, specific for polymorphism rs4988956 (SEQ ID NO: 1); polymorphism rs10204137 (SEQ ID NO: 2); polymorphism rs10192036 (SEQ ID NO: 3); polymorphism rs10192157 (SEQ ID NO: 4); or polymorphism rs10206753 (SEQ ID NO: 5). As yet another example, the invention also provides kits for determining whether a patient is likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) containing a first and second oligonucleotide specific for a polymorphic region of *IL33*, for example, polymorphism rs4742165 (SEQ ID NO: 6). In a further example, the invention provides kits for determining whether a patient is likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist) containing a first and second oligonucleotide specific for a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6), for example, any polymorphism listed in Table 3 or Table 4.

Oligonucleotides "specific for" a genetic locus bind either to the polymorphic region of the locus or bind adjacent to the polymorphic region of the locus. For oligonucleotides that are to be used as primers for amplification, primers are adjacent if they are sufficiently close to be used to produce a polynucleotide comprising the polymorphic region. In one embodiment, oligonucleotides are adjacent if they bind within about 1-2 kb, e.g., less than 1 kb from the polymorphism. Specific oligonucleotides are capable of hybridizing to a sequence, and under suitable conditions will not bind to a sequence differing by a single nucleotide.

Oligonucleotides, whether used as probes or primers, contained in a kit can be detectably labeled. Labels can be detected either directly, for example for fluorescent labels, or indirectly. Indirect

detection can include any detection method known to one of skill in the art, including biotin-avidin interactions, antibody binding and the like. Fluorescently labeled oligonucleotides also can contain a quenching molecule. Oligonucleotides can be bound to a surface. In some embodiments, the surface is silica or glass. In some embodiments, the surface is a metal electrode.

Yet other kits of the invention comprise at least one reagent necessary to perform the assay. For example, the kit can comprise an enzyme. Alternatively the kit can comprise a buffer or any other necessary reagent.

The kits can include all or some of the positive controls, negative controls, reagents, primers, sequencing markers, probes and antibodies described herein for determining the subject's genotype at one or more polymorphisms in the *IL1RL1* gene (e.g., polymorphism rs4988956 (SEQ ID NO: 1); polymorphism rs10204137 (SEQ ID NO: 2); polymorphism rs10192036 (SEQ ID NO: 3); polymorphism rs10192157 (SEQ ID NO: 4); or polymorphism rs10206753 (SEQ ID NO: 5), one or more polymorphisms in the *IL33* gene (e.g., polymorphism rs4742165 (SEQ ID NO: 6)), or one or more polymorphisms that is in linkage disequilibrium with a polymorphism in the *IL1RL1* gene or *IL33* gene (e.g., a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6), for example, any polymorphism listed in Table 3 or Table 4).

For use in detection of the biomarkers (e.g., periostin), kits or articles of manufacture are also provided by the invention. Such kits can be used to determine if a subject with an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist). These kits may comprise a carrier means being compartmentalized to receive in close confinement one or more container means such as vials, tubes, and the like, each of the container means comprising one of the separate elements to be used in the method. For example, one of the container means may comprise a probe that is or can be detectably labeled. Such probe may be an antibody or polynucleotide specific for a protein or message, respectively. Where the kit utilizes nucleic acid hybridization to detect the target nucleic acid, the kit may also have containers containing nucleotide(s) for amplification of the target nucleic acid sequence and/or a container comprising a reporter-means, such as a biotin-binding protein (e.g., avidin or streptavidin) bound to a reporter molecule, such as an enzymatic, florescent, or radioisotope label.

Such kits will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes, and package inserts with instructions for use. A label may be present on the container to indicate that the composition is used for a specific application, and may also indicate directions for either *in vivo* or *in vitro* use, such as those described above.

The kits of the invention have a number of embodiments. A typical embodiment is a kit comprising a container, a label on said container, and a composition contained within said container, wherein the composition includes a primary antibody that binds to a protein or autoantibody biomarker (e.g., periostin), and the label on said container indicates that the composition can be used to evaluate the presence of such proteins or antibodies in a sample, and wherein the kit includes instructions for

using the antibody for evaluating the presence of biomarker proteins in a particular sample type. The kit can further comprise a set of instructions and materials for preparing a sample and applying antibody to the sample. The kit may include both a primary and secondary antibody, wherein the secondary antibody is conjugated to a label, *e.g.*, an enzymatic label.

Another embodiment is a kit comprising a container, a label on said container, and a composition contained within said container, wherein the composition includes one or more polynucleotides that hybridize to a complement of a biomarker (e.g., periostin) under stringent conditions, and the label on said container indicates that the composition can be used to evaluate the presence of a biomarker (e.g., periostin) in a sample, and wherein the kit includes instructions for using the polynucleotide(s) for evaluating the presence of the biomarker RNA or DNA in a particular sample type.

Other optional components of the kit include one or more buffers (e.g., block buffer, wash buffer, substrate buffer, etc.), other reagents such as substrate (e.g., chromogen) that is chemically altered by an enzymatic label, epitope retrieval solution, control samples (positive and/or negative controls), control slide(s), etc. Kits can also include instructions for interpreting the results obtained using the kit.

In further specific embodiments, for antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) that binds to a biomarker protein (e.g., periostin); and, optionally, (2) a second, different antibody that binds to either the protein or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a polymorphic region of the *IL1RL1* gene (e.g., polymorphism rs4988956 (SEQ ID NO: 1); polymorphism rs10204137 (SEQ ID NO: 2); polymorphism rs10192036 (SEQ ID NO: 3); polymorphism rs10192157 (SEQ ID NO: 4); or polymorphism rs10206753 (SEQ ID NO: 5); a polymorphic region of the *IL33* gene (e.g., polymorphism rs4742165 (SEQ ID NO: 6)), or a polymorphism that is in linkage disequilibrium with a polymorphism in the *IL1RL1* gene or *IL33* gene (e.g., a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6), for example, any polymorphism listed in Table 3 or Table 4), as described above, and/or a nucleic acid sequence encoding a biomarker protein (e.g., periostin or sST2) or (2) a pair of primers useful for amplifying a biomarker nucleic acid molecule. The kit can also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components necessary for detecting the detectable label (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples that can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

VII. Pharmaceutical Formulations

Therapeutic formulations of the antagonists used in accordance with the present invention (e.g., an IL-33 axis binding antagonist (e.g., an ST2 binding antagonist, e.g., an ST2-Fc protein), a tryptase-beta binding antagonist, a CRTH2 antagonist, an IL-13 binding antagonist, an IL-17 binding antagonist, a

JAK1 antagonist, and/or an IL-5 binding antagonist) are prepared for storage by mixing the antagonist having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients, or stabilizers in the form of lyophilized formulations or aqueous solutions. For general information concerning formulations, see, e.g., Gilman et al. (eds.) *The Pharmacological Bases of Therapeutics*, 8th Ed., Pergamon Press, 1990; A. Gennaro (ed.), *Remington's Pharmaceutical Sciences,* 18th Edition, Mack Publishing Co., Pennsylvania, 1990; Avis et al. (eds.) *Pharmaceutical Dosage Forms: Parenteral Medications* Dekker, New York, 1993; Lieberman et al. (eds.) *Pharmaceutical Dosage Forms: Tablets* Dekker, New York, 1990; Lieberman et al. (eds.), *Pharmaceutical Dosage Forms: Disperse Systems* Dekker, New York, 1990; and Walters (ed.) *Dermatological and Transdermal Formulations* (Drugs and the Pharmaceutical Sciences), Vol 119, Marcel Dekker, 2002.

Acceptable carriers, excipients, or stabilizers are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.,* Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™, or polyethylene glycol (PEG).

The formulation herein may also contain more than one active compound, preferably those with complementary activities that do not adversely affect each other. The type and effective amounts of such medicaments depend, for example, on the amount and type of antagonist present in the formulation, and clinical parameters of the subjects.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antagonist, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

EXAMPLES

The following examples are provided to illustrate, but not to limit the presently claimed invention.

Example 1. Identification of causative SNPs that confer protection from asthma risk

In this analysis, we have identified amino acid changing variants in *IL1RL1* associated with asthma risk (see Table 1 and 2) that are tightly linked (r^2=1.0) to the intronic SNP rs3771166. These amino acid changing SNPs were identified in the 1000 Genomes European samples and tested for association with asthma risk in our case-control dataset. Asthma cases included 522 samples from patients of European ancestry from Genentech clinical trials BOBCAT, EXTRA, MILLY, and MOLLY, which were compared to control samples from 4465 individuals of European ancestry from the Cancer Genetic Markers of Susceptibility (CGEMS) genome-wide association study (GWAS) (Jia et al. *J. Allergy Clin. Immunol.* 130: 647-654, 2012; Hanania et al. *Am. J. Respir. Crit. Care Med.* 187: 804-811, 2013; Corren et al. *N. Engl. J. Med.* 365: 1088-1098, 2011; Noonen et al. *J. Allergy Clin. Immunol.* 132: 567-574, 2013). These same polymorphisms have also been reported to be associated with risk to cardiovascular disease and elevated soluble ST2 (sST2) and IL-33 levels (Ho et al. *J. Clin. Invest.* 123: 4208-4218, 2013).

This analysis revealed that these SNPs are each protective from asthma risk in the study population (see Table 1). Two SNPs, rs10192036 and rs10204137, are located in the same codon, resulting only in Q501R due to tight linkage disequilibrium (LD) between the two SNPS (r^2=1.0).

Table 1: Multiple amino acid changing SNPs within *IL1RL1* are protective for asthma risk

SNP	Amino acid change	Chr	Position	MAF Cases (n = 522)	MAF Controls (n = 4465)	*P* value	OR
rs4988956	A433T	2	102968007	0.32	0.38	5.38E-04	0.78
rs10192036	Q501K	2	102968211	0.32	0.38	5.32E-04	0.78
rs10204137	Q501R	2	102968212	0.32	0.38	5.32E-04	0.78
rs10192157	T549I	2	102968356	0.32	0.38	5.32E-04	0.78
rs10206753	L551S	2	102968362	0.32	0.38	5.32E-04	0.78
rs3771166	intronic	2	102986222	0.32	0.37	3.55E-04	0.77

Chr, chromosome; MAF, minor allele frequency; OR, odds ratio

The locus containing *IL1RL1* on chromosome 2 is complex, containing multiple linkage disequilibrium (LD) blocks, each of which contain SNPs predisposing to asthma susceptibility. Furthermore, the SNPs in *IL1RL1* are in LD with SNPs in *IL18R1*, making it difficult to assign causality to

either gene. To address this issue, a conditional analysis of rs3771166 on SNPs in the locus within 500 kb in either direction was performed. Conditioning on the rs3771166 genotype eliminated the majority of the signal in the region, with only one SNP retaining its unconditioned *p*-value (rs17766515; p=0.01). From this same window, we selected SNPs not in LD with rs3771166 (D'<0.6) and performed a conditional analysis of these SNPs on rs3771166. For these analyses, rs3771166 retained its statistical significance (max *p*=0.01). These conditional analyses and the functional analysis presented below indicate that the amino acid changing SNPs in *IL1RL1* captured by the tagSNP rs3771166 are the causal SNPs in this region. In view of these results, individuals whose genotype includes the common *IL1RL1* variants are at an increased risk of asthma compared to the individuals whose genotype includes the protective *IL1RL1* variants. The genotypes for each causative SNP of patients at an increased risk of asthma are shown in Table 2.

Table 2: SNP genotypes associated with increased risk of asthma

SNP	Genotype
rs4988956	G
rs10204137	A
rs10192036	C
rs10192157	C
rs10206753	T

The functional significance of these amino acid mutations *in vivo* was investigated to determine how these protective variants influence the IL-33 response. These variants result in coding changes to the intracellular region of ST2, which contains the signal-modulating Toll/IL-1R (TIR) domain of the receptor. The TIR domain is critical for downstream signal transduction by IL-1 cytokine family and Toll-like receptors (TLR), and mutations or deletions in this domain can result in diminished or abrogated responses to ligand. IL-33-induced dimerization of ST2 and IL-1RAcP is thought to promote TIR-TIR domain interaction, followed by recruitment of the adaptor molecule MyD88 and Myddosome assembly (see Figure 1A). Two of the variants in *IL1RL1*, A443T and Q501R, are located within the TIR domain, while the T549I and L551S variants map to a poorly-characterized region of the C-terminus that has not been implicated in signal propagation (see Figure 1A). To further define how the polymorphisms within the TIR domain may affect IL-33 signaling, the location of each variant was mapped to the known structure of the TLR10 TIR dimer (Figure 1B). The Q501R variant mapped to the αD helix of the TIR domain, which is partially disordered in the TLR10 TIR dimer, while the A433T variant mapped to the αB helix in close proximity to the B-B loop (Figure 1B). The conserved B-B loop of the TIR is thought to mediate dimerization of TLR10-linked TIR domains (Nyman et al. *J. Biol. Chem.* 283: 11861-11865, 2008).

To test the effects of these missense variants on IL-33-mediated signaling, cell lines expressing various permutations of the protective *IL1RL1* variants were generated. Single TIR mutants, double C-terminal mutants, or mutants containing all four polymorphisms were generated and incorporated into expression vectors. To avoid endogenous IL-33 activity, HEK-BLUE™ (Invivogen) IL-1β cells that are

responsive to IL-1β but are devoid of IL-33 activity were used. Stimulation of HEK- BLUE™ IL-1β cells with IL-1β results in robust NF-κB and AP-1 activation, which can be measured by NF-κB/AP-1-driven secreted alkaline phosphatase (SEAP) reporter activity. Stable transfection of ST2 expression vectors to HEK- BLUE™ IL-1β cells resulted in IL-33-dependent reporter activity, thus enabling the evaluation of both IL-1β and IL-33 responses using the same reporter system. While activation with IL-1β resulted in similar reporter gene induction between the different cell-lines, the response to IL-33 was diminished in cells expressing mutations in the TIR domains alone, or all 4 missense variants (see Figures 1C, 1D, 2A, and 2B). As a control, measurement of receptor expression revealed equivalent surface levels of all ST2 mutants (see Figures 3A-3C).

To further elucidate how the protective ST2 variants could affect IL-33 activity in the context of asthma, we compared IL-33 activity and ST2 expression between human donors carrying either the protective *IL1RL1* variants or the common *IL1RL1* variants. In agreement with the reporter cell lines, we observed reduced IL-33-mediated interleukin-8 (IL-8) secretion from purified blood eosinophils derived from individuals carrying the protective *IL1RL1* variants compared to individuals carrying the common *IL1RL1* variants (Figure 4). Further, we observed greater soluble ST2 expression in these individuals (Figures 5A and 5B).

These results provide a link between the genetic predisposition to asthma and IL-33 mediated responses. Given that IL-33 has a pro-inflammatory role in Th2-mediated immunity, perturbations to this pathway that diminish the IL-33 response can promote protection from asthma risk. The location of the variants within the TIR domain of ST2 predicts alterations to MyD88-mediated signaling. The subtle decrease in IL-33 responses conferred by these variants is consistent with the nature of the amino acid substitutions, the modest protective OR of the variants in *IL1RL1* in the asthma genetics studies, and the chemical properties of their side chains. The fact that individuals bearing the common *IL1RL1* variants are at increased risk of asthma compared to individuals bearing the protective *IL1RL1* variants indicates that the genotype at these amino acid changing SNPs can be used in diagnostic methods to determine whether a patient is at increased risk of asthma. Further, these patients are likely to be responsive to therapies including an IL-33 axis binding antagonist, for example, an anti-IL-33 antibody or an ST2 binding antagonist, e.g., an ST2-Fc protein.

Methods

Stable expression of ST2L and protective variants

ST2L cDNA was cloned into the pCMV Neo expression vector, and the protective variants were generated *via* PCR-based site-directed mutagenesis. Stable transfection of linearized plasmids into HEK-BLUE™ IL-1β reporter cells (Invivogen) was performed using LIPOFECTAMINE® (Life Technologies). HEK-BLUE™ IL-1β cells were maintained in DMEM, 2 mM L-glutamine, 10% heat-inactivated fetal bovine serum (FBS), NORMOCIN™ (100 µg/ml), hygromycin B (200 µg/ml), ZEOCIN™ (100 µg/ml), 50 U/ml penicillin and 50 µg/ml streptomycin. After 48h, the transfected cells were selected in HEK-BLUE™ IL-1β growth media supplemented with 2 mg/ml G418 for 2 weeks. Stable expression of ST2L was confirmed *via* flow cytometry and mRNA analysis. Single clonal cultures were generated through limiting dilution of the batch cultures.

Cell culture and stimulation

IL-33 pathway activity in stably-transfected HEK-BLUE™ IL-1β reporter cells was measured *via* a colorimetric assay performed according to the manufacturer's instructions. Briefly, stably-transfected HEK-BLUE™ IL-1β reporter cells (50,000 cells/well in 96-well plates) were stimulated with increasing concentrations of IL-33 or IL-1β for 20 h at 37°C in 5% CO_2. SEAP reporter activity was detected from supernatants with the QUANTI-BLUE™ assay (Invivogen) using a spectrophotometer at 620 nm.

RNA isolation and quantitative RT-PCR

RNA was isolated with an RNEASY® Mini Kit (Qiagen). An ABI 7500 Real-Time PCR system (Applied Biosystems) and TAQMAN® One-Step RT-PCR Master Mix (Applied Biosystems) were used for real-time RT-PCR (primers and probe sets from Applied Biosystems). Results were normalized to those of *RPL19* and relative expression was calculated by change in threshold (ΔΔCT method).

Recombinant proteins

Recombinant processed human IL-33 ($IL\text{-}33_{112\text{-}270}$) was prepared in-house. Recombinant IL-1β was purchased from R&D Systems.

Flow cytometry analysis

ST2L surface expression was detected using a biotinylated polyclonal antibody (BAF523, R&D Systems). Surface expression of IL-1RAcP was detected with an allophycocyanin (APC)-conjugated monoclonal antibody (FAB676A, R&D Systems). Mean fluorescence intensity (MFI) was calculated using FLOWJO™ software.

Human eosinophil and basophils isolation

Primary human eosinophils and basophils were enriched from whole blood via negative selection using Miltenyi Biotec kits. Purity (>92%) was confirmed by flow cytometry analysis. Eosinophils were plated at $1x10^6$ cells/ml in DMEM supplemented with 10% FBS, GLUTAMAX™, penicillin/streptomycin and containing 10 ng/ml recombinant human IL-3 (R&D Systems). Cell culture supernatants were collected after 24 h.

ELISA Analysis

IL-8 secretion from culture supernatants and plasma sST2 levels were measured using ELISA kits obtained from R&D Systems.

Genotyping

Asthma cases were genotyped on the ILLUMINA® 2.5M Omni array and variants were called using Illumina's GENOMESTUDIO™ software. Population controls were from the Cancer Genetic Markers of Susceptibility study (CGEMS) (cgems.cancer.gov). Population controls consisted of controls from the Cancer Genetic Markers of Susceptibility study (CGEMS) and were downloaded *via* database of

Genotypes and Phenotypes (dbGAP) authorized access.

Sample Quality Control

Various quality control measures were performed on the asthma cases and controls. Samples missing more than 10% of the genotypes were removed (n=29). Samples with heterozygosity ± 3 standard deviations (SD) from the mean were removed (n=47). Identity by descent (IBD) analysis was performed to identify and remove related samples with a proportion of alleles shared IBD > 0.4 (n=11). We assessed population substructure by filtering the GWAS data on minor allele frequency (MAF) and linkage disequilibrium. This subset of SNPs was merged with HapMap data and was then analyzed in EIGENSTRAT (Price et al. *Nat. Genet.* 38: 904-909, 2006) to use principle components to remove ancestry outliers that did not cluster near Caucasian samples (n=242). After applying quality control filters, we analyzed 4,987 Northern European Caucasian samples, including 522 asthma cases and 4465 controls.

SNP Quality Control

Quality control was performed to identify and remove low-quality SNPs. SNPs with a genotyping call rate < 95% were excluded from analysis. SNPs showing evidence of deviation from Hardy Weinberg Equilibrium (HWE) were also removed (Purcell et al. *Am. J. Hum. Genet.* 81(3): 559-575, 2007). In addition, any SNP that failed liftover to human genome assembly hg19 or had a 1000 Genomes Project (kgp) identifier that did not map to a Reference SNP ID (rsid) were also removed from the dataset. After these quality control measures, 297,157 SNPs remained for imputation.

Genotype imputation

Genotype imputation was performed for those samples using a workflow that included pre-phasing using Shapeit (Delaneau et al. *Nat. Methods* 9: 179-181, 2012) followed by imputation using IMPUTE2 (Marchini et al. *Nat. Genet.* 39: 906-913, 2007) and reference haplotypes from the 1000 Genomes Project (Durbin et al. *Nature* 467: 1061-1073, 2010).

Example 2. Periostin levels are predictive of asthma risk for individuals bearing the protective ST2 variants

To examine whether asthma biomarkers can be used to refine diagnostic and prognostic methods for determining whether asthma patients are likely to respond to IL-33 axis binding antagonists, we tested whether the level of periostin was predictive of asthma susceptibility in individuals bearing the protective SNPs shown in Figure 6. The individuals were classified as having high or low periostin levels, and the association of each group with asthma was determined. Individuals with low periostin levels compared to reference levels bearing the protective SNPs were less susceptible to asthma (i.e., lower odds ratio) compared to those with high periostin levels (Figure 6). However, both groups were less susceptible to asthma compared to individuals bearing the common variants.

Example 3. Association of serum sST2 levels with IL-33 axis genetic susceptibility factors

To examine whether peripheral blood sST2 levels were linked with IL-33 pathway activity via association of the IL-33 axis genetic susceptibility factors for asthma, we extended our previous findings of an association of serum sST2 levels with *IL1RL1* genetic variants in healthy donors (described in Example 1) and measured serum sST2 levels at baseline in 760 well-characterized, moderate-to-severe asthmatics from the BOBCAT (Jia et al. *J. Allergy Clin. Immunol.* 130:647-654, 2012), MILLY (Corren et al. *N. Engl. J. Med.* 365:1088-1098, 2011), and COSTA (Jeffrey et al. in: C101. Allergic airway inflammation and hyper-responsiveness: novel mechanisms and therapy American Thoracic Society; 2015. p. A5168-A) clinical studies.

Utilizing a previously described asthma discovery set (Ramirez-Carrozzi et al. *J. Allergy Clin. Immunol.* 135:1080-1083, 2015), we scanned the *IL33* locus, which was identified previously as an asthma risk locus (see, e.g., Moffatt et al. *N. Engl. J. Med.* 363:1211-1221, 2010), and identified rs4742165 (SEQ ID NO: 6) as the top SNP in that locus by *P*-value (OR = 1.71; P=5.26x10^{-4}). The SNP identified in Moffatt et al. *supra* (rs1342326; SEQ ID NO: 7) was not in our dataset, and the strongest proxy was not associated with risk of disease, however, the r^2 for this SNP with rs1342326 (r^2=0.66) was under a threshold that is commonly used to identify a strongly-linked SNP ($r^2 \geq 0.8$) (Moffatt et al. *supra*). Therefore, we performed an expression quantitative train linkage (eQTL) analysis of rs3771166 (SEQ ID NO: 8) and rs4742165 (SEQ ID NO: 6) with asthmatic serum sST2, to assess their combined genetic effect. *IL1RL1* and *IL33* are located on chromosomes 2 and 9, respectively, so they are completely independent of each other.

The observed distribution and summary statistics of serum sST2 by the genotypes of rs3771166 and rs4742165 and sex are represented in Figures 7A and 7B, respectively. Median levels of serum sST2 were greater in males as was previously reported (Ramirez-Carrozzi et al. *J. Allergy Clin. Immunol.* 135:1080-1083, 2015 and Ho et al. *J. Clin. Invest.* 123: 4208-4218, 2013). In addition, median levels of serum sST2 increased with genotype of increasing minor allele count. Multiple regression of $\log_2$-transformed serum sST2 levels with rs3771166 and rs4742165 genotypes, adjusted for sex, was employed to assess the strength and significance of these SNPs to simultaneously predict serum sST2 levels. All terms were statistically significant (P<0.05, ANOVA *F*-test), indicating that rs4742165 predicted serum sST2 levels, even after accounting for rs3771166. The magnitude and variability of the predictivity

of genotypes are represented by a plot of serum sST2 least squares means (lsmean) and standard errors (Figure 7C). The magnitude of the genetic effect of rs4742165 was approximately 1.6 times greater than that of rs3771166. Soluble ST2 levels increased 23% and 14% for each minor allele count of rs4742165 and rs3771166, respectively. Serum sST2 levels were 43% higher in male as compared to female subjects.

IL-33 is a potent stimulator of Type 2 cytokine production, e.g., IL-13, in mast cells and group 2 innate lymphoid cells (ILC2) (Nagarkar et al. *J. Allergy Clin. Immunol.* 136:202-205, 2015). Therefore, we assessed the pair-wise relationship of serum periostin, fractional exhaled nitric oxide (FeNO), and blood eosinophil counts, which are each Type 2 biomarkers which predict response to IL-13 blockade in asthmatics (Arron et al. *Ann. Am. Thorac. Soc.* 10(Suppl):S206-213, 2013), with serum sST2 levels (Figure 8). Interestingly, no correlation was observed between serum sST2 and each Type 2 biomarker (Spearman's ρ estimates -0.15 to -0.078). These data suggest that the biology associated with sST2 may play a role in both Type 2 high and Type 2 low asthma.

These data demonstrate a positive link between serum sST2 levels with *IL33*-associated risk of asthma, indicating that sST2 may be a biomarker of IL-33 axis activity in asthma and may have utility in predicting clinical response and measuring pharmacodynamic effects of IL-33 axis targeted therapies, including IL-33 axis binding antagonists, such as anti-IL-33 antibodies.

Methods

Biomarkers

sST2 was measured by ELISA (#DST200, R&D Systems, Quantikine). Serum periostin was measured by immunoassay using the ELECSYS® Periostin assay on the Cobas e601 analyzer (Roche Professional Diagnostics, Penzberg, Germany), as previously reported (Jia et al. *J. Allergy Clin. Immunol.* 130:647-654, 2012). FeNO was measured using the NIOX MINO® device (Aerocrine, Solna, Sweden). Blood eosinophil count was assessed as part of a Complete Blood Cell Count (CBC) on automated hematology analyzers at central laboratories.

Statistics

R software (RCoreteam. *R: A Language and Environment for Statistical Computing*) was used for plotting and analysis. Spearman's rank correlation was utilized to assess correlation of baseline biomarker levels. Expression Quantitative Trail Linkage (eQTL) was performed as described previously (Stranger et al. *Nat. Genet.* 39:1217-1224, 2007). Multiple linear regression was utilized to model $\log_2$-transformed serum sST2 levels with respect to rs4742165 (SEQ ID NO: 6) and rs3771166 genotypes, adjusted for sex. Significance of model terms was determined by *F*-test.

Genotyping

Asthma cases were genotyped as described above in Example 1.

Example 4. SNPs in high linkage disequilibrium with IL-33 axis genetic susceptibility factors

HapMap (International HapMap Consortium, *Nature* 437(7063):1299-1320, 2005) linkage disequilibrium (LD) data and the 1000 Genomes dataset (McVean et al. *Nature*. 491: 56-65, 2012) were used to identify SNPs in high LD with the IL-33 axis genetic susceptibility factors (selected SNPs) described in Examples 1 and 3. SNPs in high LD with the selected SNPs rs4988956 (SEQ ID NO: 1); rs10204137 (SEQ ID NO: 2); rs10192036 (SEQ ID NO: 3); rs10192157 (SEQ ID NO: 4); rs10206753 (SEQ ID NO: 5); and/or rs4742165 (SEQ ID NO: 6), such as those presented in Tables 3 and 4, function as alternate SNPs that may be used as biomarkers for IL-33-mediated disorders, e.g., asthma. The genotype at these selected or alternate SNPs can be used in diagnostic methods to determine whether a patient is at increased risk of an IL-33-mediated disorder, e.g., asthma. Further, patients having the equivalent allele of the alternate SNP are likely to be responsive to therapies including an IL-33 axis binding antagonist, for example, an anti-IL-33 antibody or an ST2 binding antagonist, e.g., an ST2-Fc protein. With respect to the SNPs described in Tables 3 and 4, typically the minor allele in a population is the equivalent allele, although it is possible in some cases that the major allele in a population is the equivalent allele. Routine methods in the art can be used to confirm whether a given allele of the SNPs listed in Table 3 and 4 is an equivalent allele.

HapMap samples were separated based on ancestry in order to identify ancestry-specific LD SNPs. These populations were grouped into several categories: (1) ASW (African ancestry in Southwest USA), LWK (Luhya in Webuye, Kenya), MKK (Maasai in Kinyawa, Kenya), and YRI (Yoruba in Ibadan, Nigeria; West Africa); (2) CEU (Utah residents with Northern and Western European ancestry from the CEPH collection) and TSI (Toscans in Italy); (3) CHB (Han Chinese in Beijing, China), CHD (Chinese in Metropolitan Denver, Colorado), and JPT (Japanese in Tokyo, Japan); and (4) GIH (Gujarati Indians in Houston, Texas) and MEX (Mexican ancestry in Los Angeles, California). Within the different ancestry groups, LD was assessed for SNPs in regions around rs4988956 (SEQ ID NO: 1) or rs4742165 (SEQ ID NO: 6), and were included if the D' values was greater than or equal to 0.6. There was a subset of SNPs where LD information was available in the HapMap data but allele frequency data were not available. For these SNPs, the information from the 1000 Genomes Project (1000GP) was used. These SNPs are indicated in the column "Freq Source" in Tables 3 and 4 with the label "1000GP."

For the SNPs in Tables 3 and 4 that were missing HapMap allele frequencies, the following tags were used:

For CEU ancestry, this is indicated as "EUR_MAF" and comes from the minor allele and frequency of the SNP in 1000 Genomes Phase 1 combined European population. For Asian populations, this is indicated as "ASN_MAF" and comes from the minor allele and frequency of the SNP in the 1000 Genomes Phase 1 combined Asian population. For YRI ancestry, this is indicated as "AFR_MAF" and comes from the minor allele and frequency of the SNP in the 1000 Genomes Phase 1 combined African population.

Table 3 shows SNPs in linkage disequilibrium with rs4988956 (SEQ ID NO: 1). Because rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), and rs10206753 (SEQ ID NO: 5) are all 100% linked, the SNPs in Table 3 are also in linkage disequilibrium with rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO:

4), and rs10206753 (SEQ ID NO: 5). Table 4 shows SNPs in linkage disequilibrium with rs4742165 (SEQ ID NO: 6).

Terms used in Tables 3 and 4 are defined as follows: (1) Ancestry or "ANC" refers to the ancestry of the population used to determine r^2 and D' values; (2) "LD_SNP" refers to the SNP in LD with the IL-33 axis genetic susceptibility SNPs rs4988956 (SEQ ID NO: 1) with respect to Table 3 and rs4742165 (SEQ ID NO: 6) with respect to Table 4 (rsID designation comes from NCBI dbSNP build 137 (Jun. 6, 2012)); (3) CHR refers to the chromosome location of the LD_SNP (genome build hg19; UCSC HG19 Genome Assembly; February 2009); (4) BP refers to the DNA base pair location of the LD_SNP (genome build hg19; UCSC HG19 Genome Assembly; February 2009); (5) "RSQ" refers to the r-squared (r^2) value of the IL-33 axis genetic susceptibility SNP and the LD_SNP; "DPRIME" refers to the D′ value of the IL-33 axis genetic susceptibility SNP and the LD_SNP; (6) "LD SOURCE" refers to the database from which the LD data for a given LD_SNP was obtained; (7) "FREQ SOURCE" refers to the database (i.e., HapMap or 1000gp) from which the allele frequency data for a given LD_SNP was obtained; (8) "A1" refers to allele 1 of the LD_SNP; (9) A1_FREQ refers to the allele frequency of allele 1 of the LD_SNP; (10) A2 refers to allele 2 of the LD_SNP; (11) "A2 FREQ" refers to the allele frequency of allele 2 of the LD_SNP; and (12) ALLELES refers to the alleles of the LD_SNP.

Table 3: SNPs in high LD with rs4988956

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
JPT	rs1005043	2	102511858	0.05	0.62	HapMap	HapMap	A	0.436	G	0.564	A/G
CHB	rs1005043	2	102511858	0.17	1	HapMap	HapMap	A	0.53	G	0.47	A/G
CHD	rs1005043	2	102511858	0.098	0.814	HapMap	HapMap	A	0.541	G	0.459	A/G
CHB	rs1014286	2	102515532	0.162	1	HapMap	HapMap	G	0.524	A	0.476	G/A
CHD	rs1014286	2	102515532	0.096	0.808	HapMap	HapMap	G	0.536	A	0.464	G/A
JPT	rs1014286	2	102515532	0.047	0.623	HapMap	HapMap	G	0.429	A	0.571	G/A
YRI	rs10168308	2	102430350	0.019	1	HapMap	HapMap	G	0.956	A	0.044	G/A
MKK	rs10168308	2	102430350	0.018	1	HapMap	HapMap	G	0.975	A	0.025	G/A
LWK	rs10172153	2	102313878	0.004	0.919	HapMap	HapMap	T	0.983	C	0.017	T/C
MKK	rs10172153	2	102313878	0.018	1	HapMap	HapMap	T	0.976	C	0.024	T/C
YRI	rs10172153	2	102313878	0.019	1	HapMap	HapMap	T	0.965	C	0.035	T/C
CHB	rs10175045	2	102469664	0.132	0.677	HapMap	HapMap	T	0.643	C	0.357	T/C
MKK	rs10175045	2	102469664	0.063	0.761	HapMap	HapMap	T	0.073	C	0.927	T/C
YRI	rs10175045	2	102469664	0.071	1	HapMap	HapMap	T	0.027	C	0.973	T/C
CEU	rs10175045	2	102469664	0.273	1	HapMap	HapMap	T	0.265	C	0.735	T/C
LWK	rs10175045	2	102469664	0.129	1	HapMap	HapMap	T	0.039	C	0.961	T/C
ASW	rs10175045	2	102469664	0.063	1	HapMap	HapMap	T	0.019	C	0.981	T/C
CHD	rs10175045	2	102469664	0.133	0.768	HapMap	HapMap	T	0.641	C	0.359	T/C
GIH	rs10175045	2	102469664	0.059	0.713	HapMap	HapMap	T	0.295	C	0.705	T/C
JPT	rs10175045	2	102469664	0.102	0.604	HapMap	HapMap	T	0.605	C	0.395	T/C
CHB	rs10176820	2	102420852	0.64	1	HapMap	HapMap	T	0.915	C	0.085	T/C
CEU	rs10176820	2	102420852	0.193	1	HapMap	HapMap	T	0.851	C	0.149	T/C
ASW	rs10176820	2	102420852	0.166	0.738	HapMap	HapMap	T	0.644	C	0.356	T/C
CHD	rs10176820	2	102420852	0.713	1	HapMap	HapMap	T	0.918	C	0.082	T/C
GIH	rs10176820	2	102420852	0.22	0.74	HapMap	HapMap	T	0.903	C	0.097	T/C
JPT	rs10176820	2	102420852	0.654	1	HapMap	HapMap	T	0.882	C	0.118	T/C
LWK	rs10176820	2	102420852	0.115	0.825	HapMap	HapMap	T	0.646	C	0.354	T/C
ASW	rs10177815	2	102400747	0.055	1	HapMap	HapMap	C	0.906	T	0.094	C/T
LWK	rs10177815	2	102400747	0.06	1	HapMap	HapMap	C	0.839	T	0.161	C/T
MKK	rs10177815	2	102400747	0.051	1	HapMap	HapMap	C	0.934	T	0.066	C/T
YRI	rs10177815	2	102400747	0.038	0.729	HapMap	HapMap	C	0.819	T	0.181	C/T

ASW	rs10178191	2	102279524	0.03	1	HapMap	HapMap	G	0.953	T	0.047	G/T
LWK	rs10178191	2	102279524	0.005	1	HapMap	HapMap	G	0.983	T	0.017	G/T
MEX	rs10178191	2	102279524	0.031	1	HapMap	HapMap	G	0.99	T	0.01	G/T
MKK	rs10178191	2	102279524	0.04	1	HapMap	HapMap	G	0.948	T	0.052	G/T
YRI	rs10178191	2	102279524	0.015	1	HapMap	HapMap	G	0.96	T	0.04	G/T
CEU	rs10178214	2	102225353	0.21	1	HapMap	HapMap	G	0.839	T	0.161	G/T
CHB	rs10178214	2	102225353	0.599	0.867	HapMap	HapMap	G	0.873	T	0.127	G/T
CHD	rs10178214	2	102225353	0.574	0.758	HapMap	HapMap	G	0.888	T	0.112	G/T
GIH	rs10178214	2	102225353	0.217	0.736	HapMap	HapMap	G	0.903	T	0.097	G/T
JPT	rs10178214	2	102225353	0.457	0.707	HapMap	HapMap	G	0.872	T	0.128	G/T
MEX	rs10178214	2	102225353	0.241	0.636	HapMap	HapMap	G	0.81	T	0.19	G/T
CHB	rs10178436	2	102292943	0.141	1	HapMap	HapMap	T	0.47	C	0.53	T/C
CHD	rs10178436	2	102292943	0.132	1	HapMap	HapMap	T	0.512	C	0.488	T/C
JPT	rs10178436	2	102292943	0.095	1	HapMap	HapMap	T	0.384	C	0.616	T/C
CEU	rs10183812	2	102518362	0.047	1	HapMap	HapMap	T	0.929	C	0.071	T/C
CHB	rs10183812	2	102518362	0.385	0.68	HapMap	HapMap	T	0.863	C	0.137	T/C
CHD	rs10183812	2	102518362	0.431	0.677	HapMap	HapMap	T	0.894	C	0.106	T/C
JPT	rs10183812	2	102518362	0.442	0.766	HapMap	HapMap	T	0.843	C	0.157	T/C
ASW	rs10189629	2	102245896	0.124	1	HapMap	HapMap	C	0.811	A	0.189	C/A
CEU	rs10189629	2	102245896	0.159	1	HapMap	HapMap	C	0.889	A	0.111	C/A
CHB	rs10189629	2	102245896	0.366	0.819	HapMap	HapMap	C	0.911	A	0.089	C/A
CHD	rs10189629	2	102245896	0.604	1	HapMap	HapMap	C	0.929	A	0.071	C/A
GIH	rs10189629	2	102245896	0.283	0.901	HapMap	HapMap	C	0.915	A	0.085	C/A
JPT	rs10189629	2	102245896	0.385	1	HapMap	HapMap	C	0.936	A	0.064	C/A
LWK	rs10189629	2	102245896	0.081	0.818	HapMap	HapMap	C	0.722	A	0.278	C/A
MEX	rs10189629	2	102245896	0.344	1	HapMap	HapMap	C	0.88	A	0.12	C/A
MKK	rs10189629	2	102245896	0.257	1	HapMap	HapMap	C	0.738	A	0.262	C/A
YRI	rs10189629	2	102245896	0.072	0.77	HapMap	HapMap	C	0.741	A	0.259	C/A
ASW	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.302	A	0.698	C/A
CEU	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.593	A	0.407	C/A
CHB	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.857	A	0.143	C/A
CHD	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.888	A	0.112	C/A
GIH	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.787	A	0.213	C/A
JPT	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.843	A	0.157	C/A

LWK	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.239	A	0.761	C/A
MEX	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.72	A	0.28	C/A
MKK	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.42	A	0.58	C/A
YRI	rs10192036	2	102334643	1	1	HapMap	HapMap	C	0.235	A	0.765	C/A
ASW	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.302	T	0.698	C/T
CEU	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.593	T	0.407	C/T
CHB	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.857	T	0.143	C/T
CHD	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.888	T	0.112	C/T
GIH	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.79	T	0.21	C/T
JPT	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.849	T	0.151	C/T
LWK	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.239	T	0.761	C/T
MEX	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.73	T	0.27	C/T
MKK	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.42	T	0.58	C/T
YRI	rs10192157	2	102334788	1	1	HapMap	HapMap	C	0.235	T	0.765	C/T
CHD	rs10194822	2	102531936	0.039	0.752	HapMap	HapMap	T	0.647	G	0.353	T/G
ASW	rs10197310	2	102386462	0.119	0.699	HapMap	HapMap	T	0.689	A	0.311	T/A
CEU	rs10197310	2	102386462	0.156	0.863	HapMap	HapMap	T	0.832	A	0.168	T/A
CHB	rs10197310	2	102386462	0.632	1	HapMap	HapMap	T	0.905	A	0.095	T/A
CHD	rs10197310	2	102386462	0.713	1	HapMap	HapMap	T	0.917	A	0.083	T/A
GIH	rs10197310	2	102386462	0.22	0.74	HapMap	HapMap	T	0.903	A	0.097	T/A
JPT	rs10197310	2	102386462	0.753	1	HapMap	HapMap	T	0.863	A	0.137	T/A
LWK	rs10197310	2	102386462	0.068	0.649	HapMap	HapMap	T	0.661	A	0.339	T/A
MEX	rs10197310	2	102386462	0.364	0.813	HapMap	HapMap	T	0.82	A	0.18	T/A
ASW	rs10197862	2	102332981	0.214	1	HapMap	HapMap	A	0.726	G	0.274	A/G
CEU	rs10197862	2	102332981	0.176	1	HapMap	HapMap	A	0.872	G	0.128	A/G
CHB	rs10197862	2	102332981	0.632	1	HapMap	HapMap	A	0.905	G	0.095	A/G
CHD	rs10197862	2	102332981	0.713	1	HapMap	HapMap	A	0.918	G	0.082	A/G
GIH	rs10197862	2	102332981	0.375	1	HapMap	HapMap	A	0.909	G	0.091	A/G
JPT	rs10197862	2	102332981	0.753	1	HapMap	HapMap	A	0.872	G	0.128	A/G
LWK	rs10197862	2	102332981	0.093	1	HapMap	HapMap	A	0.772	G	0.228	A/G
MEX	rs10197862	2	102332981	0.464	1	HapMap	HapMap	A	0.85	G	0.15	A/G
MKK	rs10197862	2	102332981	0.296	1	HapMap	HapMap	A	0.71	G	0.29	A/G
YRI	rs10197862	2	102332981	0.216	1	HapMap	HapMap	A	0.668	G	0.332	A/G
CHD	rs10201184	2	102455510	0.079	0.706	HapMap	HapMap	G	0.559	C	0.441	G/C

JPT	rs10201184	2	102455510	0.058	0.65	HapMap	HapMap	G	0.453	C	0.547	G/C
ASW	rs10202813	2	102386172	0.119	0.699	HapMap	HapMap	G	0.689	T	0.311	G/T
CEU	rs10202813	2	102386172	0.193	1	HapMap	HapMap	G	0.842	T	0.158	G/T
CHB	rs10202813	2	102386172	0.632	1	HapMap	HapMap	G	0.905	T	0.095	G/T
CHD	rs10202813	2	102386172	0.713	1	HapMap	HapMap	G	0.917	T	0.083	G/T
GIH	rs10202813	2	102386172	0.22	0.74	HapMap	HapMap	G	0.903	T	0.097	G/T
JPT	rs10202813	2	102386172	0.753	1	HapMap	HapMap	G	0.872	T	0.128	G/T
LWK	rs10202813	2	102386172	0.099	0.805	HapMap	HapMap	G	0.663	T	0.337	G/T
MEX	rs10202813	2	102386172	0.364	0.813	HapMap	HapMap	G	0.82	T	0.18	G/T
ASW	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.302	G	0.698	A/G
CEU	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.593	G	0.407	A/G
CHB	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.857	G	0.143	A/G
CHD	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.888	G	0.112	A/G
GIH	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.79	G	0.21	A/G
JPT	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.849	G	0.151	A/G
LWK	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.239	G	0.761	A/G
MEX	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.73	G	0.27	A/G
MKK	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.42	G	0.58	A/G
YRI	rs10204137	2	102334644	1	1	HapMap	HapMap	A	0.235	G	0.765	A/G
ASW	rs10204837	2	102344162	0.877	1	HapMap	HapMap	C	0.349	A	0.651	C/A
CEU	rs10204837	2	102344162	1	1	HapMap	HapMap	C	0.593	A	0.407	C/A
CHB	rs10204837	2	102344162	1	1	HapMap	HapMap	C	0.857	A	0.143	C/A
CHD	rs10204837	2	102344162	1	1	HapMap	HapMap	C	0.888	A	0.112	C/A
GIH	rs10204837	2	102344162	1	1	HapMap	HapMap	C	0.79	A	0.21	C/A
JPT	rs10204837	2	102344162	1	1	HapMap	HapMap	C	0.849	A	0.151	C/A
LWK	rs10204837	2	102344162	0.555	1	HapMap	HapMap	C	0.361	A	0.639	C/A
MEX	rs10204837	2	102344162	1	1	HapMap	HapMap	C	0.73	A	0.27	C/A
MKK	rs10204837	2	102344162	0.855	1	HapMap	HapMap	C	0.458	A	0.542	C/A
YRI	rs10204837	2	102344162	0.916	1	HapMap	HapMap	C	0.265	A	0.735	C/A
ASW	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.302	C	0.698	T/C
CEU	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.589	C	0.411	T/C
CHB	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.857	C	0.143	T/C
CHD	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.888	C	0.112	T/C
GIH	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.79	C	0.21	T/C

JPT	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.849	C	0.151	T/C
LWK	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.239	C	0.761	T/C
MEX	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.73	C	0.27	T/C
MKK	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.42	C	0.58	T/C
YRI	rs10206753	2	102334794	1	1	HapMap	HapMap	T	0.235	C	0.765	T/C
CHD	rs10207579	2	102469721	0.125	0.626	HapMap	HapMap	C	0.714	T	0.286	C/T
ASW	rs10210176	2	102445948	0.119	0.699	HapMap	HapMap	C	0.689	A	0.311	C/A
CEU	rs10210176	2	102445948	0.193	1	HapMap	HapMap	C	0.835	A	0.165	C/A
CHB	rs10210176	2	102445948	0.632	1	HapMap	HapMap	C	0.905	A	0.095	C/A
CHD	rs10210176	2	102445948	0.713	1	HapMap	HapMap	C	0.918	A	0.082	C/A
GIH	rs10210176	2	102445948	0.22	0.74	HapMap	HapMap	C	0.903	A	0.097	C/A
JPT	rs10210176	2	102445948	0.753	1	HapMap	HapMap	C	0.872	A	0.128	C/A
LWK	rs10210176	2	102445948	0.074	0.67	HapMap	HapMap	C	0.656	A	0.344	C/A
MEX	rs10210176	2	102445948	0.405	0.826	HapMap	HapMap	C	0.81	A	0.19	C/A
ASW	rs1030021	2	102167910	0.119	0.699	HapMap	HapMap	A	0.651	C	0.349	A/C
LWK	rs1030021	2	102167910	0.098	1	HapMap	HapMap	A	0.758	C	0.242	A/C
MKK	rs1030021	2	102167910	0.157	0.734	HapMap	HapMap	A	0.713	C	0.287	A/C
CHB	rs1035127	2	102386351	0.141	1	HapMap	HapMap	A	0.476	G	0.524	A/G
CHD	rs1035127	2	102386351	0.128	1	HapMap	HapMap	A	0.5	G	0.5	A/G
GIH	rs1035127	2	102386351	0.155	0.821	HapMap	HapMap	A	0.455	G	0.545	A/G
ASW	rs1035127	2	102386351	0.022	1	HapMap	HapMap	A	0.057	G	0.943	A/G
CEU	rs1035127	2	102386351	0.209	1	HapMap	HapMap	A	0.204	G	0.796	A/G
JPT	rs1035127	2	102386351	0.105	1	HapMap	HapMap	A	0.413	G	0.587	A/G
LWK	rs1035127	2	102386351	0.032	0.764	HapMap	HapMap	A	0.15	G	0.85	A/G
MEX	rs1035127	2	102386351	0.333	1	HapMap	HapMap	A	0.46	G	0.54	A/G
MKK	rs1035127	2	102386351	0.125	0.653	HapMap	HapMap	A	0.175	G	0.825	A/G
ASW	rs1035130	2	102367834	0.448	1	HapMap	HapMap	C	0.83	T	0.17	C/T
CHB	rs1035130	2	102367834	0.038	0.636	HapMap	HapMap	C	0.639	T	0.361	C/T
CHD	rs1035130	2	102367834	0.043	0.766	HapMap	HapMap	C	0.637	T	0.363	C/T
CEU	rs1035130	2	102367834	0.301	1	HapMap	HapMap	C	0.723	T	0.277	C/T
GIH	rs1035130	2	102367834	0.112	1	HapMap	HapMap	C	0.699	T	0.301	C/T
JPT	rs1035130	2	102367834	0.167	1	HapMap	HapMap	C	0.583	T	0.417	C/T
LWK	rs1035130	2	102367834	0.248	1	HapMap	HapMap	C	0.928	T	0.072	C/T
MEX	rs1035130	2	102367834	0.059	0.78	HapMap	HapMap	C	0.78	T	0.22	C/T

MKK	rs1035130	2	102367834	0.122	0.902	HapMap	HapMap	C	0.902	T	0.098	C/T
CEU	rs1035131	2	102229073	0.345	0.774	HapMap	HapMap	T	0.588	G	0.412	T/G
CHB	rs1035131	2	102229073	0.211	0.836	HapMap	HapMap	T	0.315	G	0.685	T/G
CHD	rs1035131	2	102229073	0.302	0.915	HapMap	HapMap	T	0.259	G	0.741	T/G
GIH	rs1035131	2	102229073	0.429	0.95	HapMap	HapMap	T	0.358	G	0.642	T/G
JPT	rs1035131	2	102229073	0.144	0.665	HapMap	HapMap	T	0.36	G	0.64	T/G
MEX	rs1035131	2	102229073	0.091	0.628	HapMap	HapMap	T	0.62	G	0.38	T/G
GIH	rs10439410	2	102357220	0.703	0.924	HapMap	HapMap	G	0.756	T	0.244	G/T
JPT	rs10439410	2	102357220	0.85	1	HapMap	HapMap	G	0.831	T	0.169	G/T
ASW	rs10439410	2	102357220	0.408	0.796	HapMap	HapMap	G	0.236	T	0.764	G/T
CEU	rs10439410	2	102357220	0.759	1	HapMap	HapMap	G	0.482	T	0.518	G/T
CHB	rs10439410	2	102357220	0.564	0.892	HapMap	HapMap	G	0.833	T	0.167	G/T
CHD	rs10439410	2	102357220	0.615	0.874	HapMap	HapMap	G	0.865	T	0.135	G/T
MEX	rs10439410	2	102357220	0.709	0.939	HapMap	HapMap	G	0.68	T	0.32	G/T
MKK	rs10439410	2	102357220	0.278	0.732	HapMap	HapMap	G	0.273	T	0.727	G/T
CEU	rs10469856	2	102255261	0.245	0.637	HapMap	HapMap	A	0.336	T	0.664	A/T
JPT	rs10469856	2	102255261	0.01	1	HapMap	HapMap	A	0.035	T	0.965	A/T
ASW	rs10490204	2	102422966	0.254	1	HapMap	HapMap	A	0.904	C	0.096	A/C
LWK	rs10490204	2	102422966	0.056	1	HapMap	HapMap	A	0.983	C	0.017	A/C
MEX	rs10490204	2	102422966	0.071	0.804	HapMap	HapMap	A	0.76	C	0.24	A/C
MKK	rs10490204	2	102422966	0.023	0.718	HapMap	HapMap	A	0.969	C	0.031	A/C
CEU	rs10490204	2	102422966	0.301	1	HapMap	HapMap	A	0.721	C	0.279	A/C
CHD	rs10490204	2	102422966	0.041	0.76	HapMap	HapMap	A	0.641	C	0.359	A/C
GIH	rs10490204	2	102422966	0.115	1	HapMap	HapMap	A	0.693	C	0.307	A/C
JPT	rs10490204	2	102422966	0.173	1	HapMap	HapMap	A	0.581	C	0.419	A/C
YRI	rs10490204	2	102422966	0.143	0.711	HapMap	HapMap	A	0.92	C	0.08	A/C
ASW	rs10515921	2	102347450	0.022	1	HapMap	HapMap	T	0.953	G	0.047	T/G
CEU	rs10515921	2	102347450	0.302	1	HapMap	HapMap	T	0.845	G	0.155	T/G
CHB	rs10515921	2	102347450	0.073	1	HapMap	HapMap	T	0.994	G	0.006	T/G
GIH	rs10515921	2	102347450	0.481	1	HapMap	HapMap	T	0.886	G	0.114	T/G
LWK	rs10515921	2	102347450	0.007	1	HapMap	HapMap	T	0.978	G	0.022	T/G
MEX	rs10515921	2	102347450	0.162	1	HapMap	HapMap	T	0.94	G	0.06	T/G
MKK	rs10515921	2	102347450	0.043	1	HapMap	HapMap	T	0.944	G	0.056	T/G
YRI	rs10515921	2	102347450	0.035	1	HapMap	HapMap	T	0.938	G	0.062	T/G

ASW	rs10515922	2	102281086	0.031	1	HapMap	HapMap	A	0.991	G	0.009	A/G
CHB	rs10515922	2	102281086	0.029	1	HapMap	HapMap	A	0.881	G	0.119	A/G
CHD	rs10515922	2	102281086	0.015	1	HapMap	HapMap	A	0.894	G	0.106	A/G
JPT	rs10515922	2	102281086	0.058	1	HapMap	HapMap	A	0.762	G	0.238	A/G
LWK	rs10515922	2	102281086	0.018	1	HapMap	HapMap	A	0.994	G	0.006	A/G
MEX	rs10515922	2	102281086	0.013	1	HapMap	HapMap	A	0.96	G	0.04	A/G
YRI	rs11123914	2	102213164	0.007	1	HapMap	HapMap	T	0.032	C	0.968	T/C
CEU	rs11123915	2	102247255	0.245	0.637	HapMap	HapMap	G	0.336	T	0.664	G/T
JPT	rs11123915	2	102247255	0.01	1	HapMap	HapMap	G	0.041	T	0.959	G/T
ASW	rs11123923	2	102334276	0.643	1	HapMap	HapMap	C	0.774	A	0.226	C/A
CEU	rs11123923	2	102334276	0.414	1	HapMap	HapMap	C	0.611	A	0.389	C/A
CHB	rs11123923	2	102334276	0.111	1	HapMap	HapMap	C	0.613	A	0.387	C/A
CHD	rs11123923	2	102334276	0.074	1	HapMap	HapMap	C	0.619	A	0.381	C/A
GIH	rs11123923	2	102334276	0.135	1	HapMap	HapMap	C	0.659	A	0.341	C/A
JPT	rs11123923	2	102334276	0.21	1	HapMap	HapMap	C	0.541	A	0.459	C/A
LWK	rs11123923	2	102334276	0.562	1	HapMap	HapMap	C	0.85	A	0.15	C/A
MEX	rs11123923	2	102334276	0.125	1	HapMap	HapMap	C	0.73	A	0.27	C/A
MKK	rs11123923	2	102334276	0.615	1	HapMap	HapMap	C	0.692	A	0.308	C/A
YRI	rs11123923	2	102334276	0.466	1	HapMap	HapMap	C	0.872	A	0.128	C/A
JPT	rs11123936	2	102534189	0.442	0.766	HapMap	HapMap	C	0.843	T	0.157	C/T
CHB	rs11123936	2	102534189	0.385	0.68	HapMap	HapMap	C	0.863	T	0.137	C/T
CHD	rs11123936	2	102534189	0.431	0.677	HapMap	HapMap	C	0.894	T	0.106	C/T
CEU	rs11123936	2	102534189	0.047	1	HapMap	HapMap	C	0.929	T	0.071	C/T
ASW	rs1135354	2	102380734	0.448	1	HapMap	HapMap	T	0.83	G	0.17	T/G
CEU	rs1135354	2	102380734	0.301	1	HapMap	HapMap	T	0.721	G	0.279	T/G
CHB	rs1135354	2	102380734	0.038	0.642	HapMap	HapMap	T	0.637	G	0.363	T/G
CHD	rs1135354	2	102380734	0.041	0.76	HapMap	HapMap	T	0.641	G	0.359	T/G
GIH	rs1135354	2	102380734	0.112	1	HapMap	HapMap	T	0.699	G	0.301	T/G
JPT	rs1135354	2	102380734	0.173	1	HapMap	HapMap	T	0.581	G	0.419	T/G
LWK	rs1135354	2	102380734	0.248	1	HapMap	HapMap	T	0.928	G	0.072	T/G
MEX	rs1135354	2	102380734	0.059	0.78	HapMap	HapMap	T	0.78	G	0.22	T/G
MKK	rs1135354	2	102380734	0.116	0.898	HapMap	HapMap	T	0.906	G	0.094	T/G
MEX	rs11465597	2	102353645	0.021	1	HapMap	HapMap	A	0.94	G	0.06	A/G
MKK	rs11465597	2	102353645	0.391	1	HapMap	HapMap	A	0.78	G	0.22	A/G

LWK	rs11465597	2	102353645	0.376	1	HapMap	HapMap	A	0.894	G	0.106	A/G
ASW	rs11465597	2	102353645	0.24	1	HapMap	HapMap	A	0.877	G	0.123	A/G
CEU	rs11465597	2	102353645	0.056	1	HapMap	HapMap	A	0.889	G	0.111	A/G
CHD	rs11465597	2	102353645	0.002	0.614	HapMap	HapMap	A	0.965	G	0.035	A/G
GIH	rs11465597	2	102353645	0.018	1	HapMap	HapMap	A	0.938	G	0.062	A/G
YRI	rs11465597	2	102353645	0.2	1	HapMap	HapMap	A	0.934	G	0.066	A/G
ASW	rs11465598	2	102353696	0.055	1	HapMap	HapMap	A	0.906	G	0.094	A/G
LWK	rs11465598	2	102353696	0.022	1	HapMap	HapMap	A	0.933	G	0.067	A/G
MKK	rs11465598	2	102353696	0.084	1	HapMap	HapMap	A	0.897	G	0.103	A/G
YRI	rs11465598	2	102353696	0.035	1	HapMap	HapMap	A	0.938	G	0.062	A/G
MEX	rs11465635	2	102364515	0.004	1	HapMap	HapMap	G	0.99	A	0.01	G/A
MKK	rs11465635	2	102364515	0.005	1	HapMap	HapMap	G	0.997	A	0.003	G/A
YRI	rs11465635	2	102364515	0.023	1	HapMap	HapMap	G	0.996	A	0.004	G/A
CEU	rs11465644	2	102367777	0.013	1	HapMap	HapMap	C	0.991	A	0.009	C/A
CHB	rs11465644	2	102367777	0.002	1	HapMap	HapMap	C	0.994	A	0.006	C/A
CHD	rs11465644	2	102367777	0.001	1	HapMap	HapMap	C	0.994	A	0.006	C/A
GIH	rs11465644	2	102367777	0.021	1	HapMap	HapMap	C	0.994	A	0.006	C/A
LWK	rs11465644	2	102367777	0.002	1	HapMap	HapMap	C	0.994	A	0.006	C/A
MEX	rs11465644	2	102367777	0.004	1	HapMap	HapMap	C	0.98	A	0.02	C/A
YRI	rs11465644	2	102367777	0.023	1	HapMap	HapMap	C	0.996	A	0.004	C/A
ASW	rs11465648	2	102369872	0.031	1	HapMap	HapMap	G	0.99	A	0.01	G/A
CHD	rs11465648	2	102369872	0.002	1	HapMap	HapMap	G	0.988	A	0.012	G/A
GIH	rs11465648	2	102369872	0.023	1	HapMap	HapMap	G	0.994	A	0.006	G/A
MEX	rs11465648	2	102369872	0.009	1	HapMap	HapMap	G	0.969	A	0.031	G/A
MKK	rs11465657	2	102380153	0.005	1	HapMap	HapMap	C	0.997	T	0.003	C/T
LWK	rs11465658	2	102380449	0.018	1	HapMap	HapMap	G	0.994	A	0.006	G/A
YRI	rs11465658	2	102380449	0.023	1	HapMap	HapMap	G	0.996	A	0.004	G/A
CEU	rs11465670	2	102400872	0.264	1	HapMap	HapMap	T	0.845	C	0.155	T/C
CHB	rs11465670	2	102400872	0.223	1	HapMap	HapMap	T	0.976	C	0.024	T/C
LWK	rs11465670	2	102400872	0.057	1	HapMap	HapMap	T	0.848	C	0.152	T/C
MEX	rs11465670	2	102400872	0.128	1	HapMap	HapMap	T	0.95	C	0.05	T/C
MKK	rs11465670	2	102400872	0.132	0.882	HapMap	HapMap	T	0.81	C	0.19	T/C
CHD	rs11465670	2	102400872	0.093	0.697	HapMap	HapMap	T	0.976	C	0.024	T/C
GIH	rs11465670	2	102400872	0.481	1	HapMap	HapMap	T	0.886	C	0.114	T/C

JPT	rs11465670	2	102400872	0.185	1	HapMap	HapMap	T	0.983	C	0.017	T/C
ASW	rs11465676	2	102402097	0.03	1	HapMap	HapMap	T	0.953	C	0.047	T/C
LWK	rs11465676	2	102402097	0.046	1	HapMap	HapMap	T	0.872	C	0.128	T/C
MKK	rs11465676	2	102402097	0.023	1	HapMap	HapMap	T	0.969	C	0.031	T/C
ASW	rs11465684	2	102404056	0.038	1	HapMap	HapMap	C	0.943	T	0.057	C/T
LWK	rs11465684	2	102404056	0.046	1	HapMap	HapMap	C	0.872	T	0.128	C/T
MKK	rs11465684	2	102404056	0.023	1	HapMap	HapMap	C	0.969	T	0.031	C/T
ASW	rs11465687	2	102406175	0.055	1	HapMap	HapMap	C	0.906	T	0.094	C/T
LWK	rs11465687	2	102406175	0.06	1	HapMap	HapMap	C	0.839	T	0.161	C/T
YRI	rs11465687	2	102406175	0.036	0.713	HapMap	HapMap	C	0.817	T	0.183	C/T
CEU	rs11465699	2	102421199	0.047	1	HapMap	HapMap	G	0.96	A	0.04	G/A
GIH	rs11465699	2	102421199	0.002	1	HapMap	HapMap	G	0.994	A	0.006	G/A
ASW	rs11465707	2	102425454	0.066	1	HapMap	HapMap	G	0.972	A	0.028	G/A
CEU	rs11465707	2	102425454	0.014	1	HapMap	HapMap	G	0.991	A	0.009	G/A
MKK	rs11465707	2	102425454	0.013	1	HapMap	HapMap	G	0.982	A	0.018	G/A
MEX	rs11465716	2	102428208	0.008	1	HapMap	HapMap	G	0.98	A	0.02	G/A
ASW	rs11465716	2	102428208	0.007	1	HapMap	HapMap	G	0.991	A	0.009	G/A
CHB	rs11465716	2	102428208	0.002	1	HapMap	HapMap	G	0.994	A	0.006	G/A
GIH	rs11465716	2	102428208	0	1	HapMap	HapMap	G	0.994	A	0.006	G/A
LWK	rs11465716	2	102428208	0.002	1	HapMap	HapMap	G	0.994	A	0.006	G/A
YRI	rs11465716	2	102428208	0.004	1	HapMap	HapMap	G	0.987	A	0.013	G/A
ASW	rs11465722	2	102429921	0.063	1	HapMap	HapMap	C	0.953	T	0.047	C/T
CEU	rs11465722	2	102429921	0.21	1	HapMap	HapMap	C	0.881	T	0.119	C/T
LWK	rs11465722	2	102429921	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MEX	rs11465722	2	102429921	0.196	1	HapMap	HapMap	C	0.94	T	0.06	C/T
YRI	rs11465722	2	102429921	0.019	1	HapMap	HapMap	C	0.96	T	0.04	C/T
ASW	rs11465724	2	102430287	0.066	1	HapMap	HapMap	C	0.972	T	0.028	C/T
CEU	rs11465724	2	102430287	0.047	1	HapMap	HapMap	C	0.951	T	0.049	C/T
GIH	rs11465724	2	102430287	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MEX	rs11465724	2	102430287	0.004	1	HapMap	HapMap	C	0.99	T	0.01	C/T
MKK	rs11465724	2	102430287	0.071	1	HapMap	HapMap	C	0.951	T	0.049	C/T
CHD	rs11465730	2	102433290	0.081	0.707	HapMap	HapMap	A	0.56	G	0.44	A/G
JPT	rs11465730	2	102433290	0.058	0.65	HapMap	HapMap	A	0.453	G	0.547	A/G
CEU	rs11465732	2	102434255	0.039	1	HapMap	HapMap	C	0.938	T	0.062	C/T

CHB	rs11465732	2	102434255	0.034	1	HapMap	HapMap	C	0.857	T	0.143	C/T
CHD	rs11465732	2	102434255	0.02	1	HapMap	HapMap	C	0.865	T	0.135	C/T
GIH	rs11465732	2	102434255	0.013	1	HapMap	HapMap	C	0.955	T	0.045	C/T
JPT	rs11465732	2	102434255	0.058	1	HapMap	HapMap	C	0.779	T	0.221	C/T
LWK	rs11465732	2	102434255	0.036	1	HapMap	HapMap	C	0.989	T	0.011	C/T
MEX	rs11465732	2	102434255	0.004	1	HapMap	HapMap	C	0.98	T	0.02	C/T
MKK	rs11465732	2	102434255	0.005	1	HapMap	HapMap	C	0.997	T	0.003	C/T
YRI	rs11465732	2	102434255	0.023	1	HapMap	HapMap	C	0.982	T	0.018	C/T
ASW	rs11465732	2	102434255	0.063	1	HapMap	HapMap	C	0.981	T	0.019	C/T
LWK	rs11465739	2	102435269	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MKK	rs11465739	2	102435269	0.005	1	HapMap	HapMap	C	0.997	T	0.003	C/T
YRI	rs11465739	2	102435269	0.023	1	HapMap	HapMap	C	0.996	T	0.004	C/T
ASW	rs11674302	2	102253560	0.229	1	HapMap	HapMap	T	0.726	C	0.274	T/C
CEU	rs11674302	2	102253560	0.159	1	HapMap	HapMap	T	0.889	C	0.111	T/C
CHB	rs11674302	2	102253560	0.366	0.819	HapMap	HapMap	T	0.911	C	0.089	T/C
CHD	rs11674302	2	102253560	0.604	1	HapMap	HapMap	T	0.929	C	0.071	T/C
GIH	rs11674302	2	102253560	0.283	0.901	HapMap	HapMap	T	0.915	C	0.085	T/C
JPT	rs11674302	2	102253560	0.385	1	HapMap	HapMap	T	0.936	C	0.064	T/C
LWK	rs11674302	2	102253560	0.069	0.708	HapMap	HapMap	T	0.694	C	0.306	T/C
MEX	rs11674302	2	102253560	0.344	1	HapMap	HapMap	T	0.88	C	0.12	T/C
MKK	rs11674302	2	102253560	0.33	0.936	HapMap	HapMap	T	0.656	C	0.344	T/C
YRI	rs11674302	2	102253560	0.142	0.862	HapMap	HapMap	T	0.673	C	0.327	T/C
ASW	rs11687768	2	102392170	0.093	0.648	HapMap	HapMap	A	0.716	G	0.284	A/G
CEU	rs11687768	2	102392170	0.193	1	HapMap	HapMap	A	0.851	G	0.149	A/G
CHB	rs11687768	2	102392170	0.632	1	HapMap	HapMap	A	0.916	G	0.084	A/G
CHD	rs11687768	2	102392170	0.713	1	HapMap	HapMap	A	0.918	G	0.082	A/G
GIH	rs11687768	2	102392170	0.22	0.74	HapMap	HapMap	A	0.903	G	0.097	A/G
JPT	rs11687768	2	102392170	0.753	1	HapMap	HapMap	A	0.872	G	0.128	A/G
MEX	rs11687768	2	102392170	0.364	0.813	HapMap	HapMap	A	0.82	G	0.18	A/G
ASW	rs11688802	2	102492971	0.031	1	HapMap	HapMap	A	0.991	G	0.009	A/G
CEU	rs11688802	2	102492971	0.039	1	HapMap	HapMap	A	0.942	G	0.058	A/G
MEX	rs11688802	2	102492971	0.004	1	HapMap	HapMap	A	0.98	G	0.02	A/G
CEU	rs11690532	2	102442858	0.2	1	HapMap	HapMap	C	0.809	T	0.191	C/T
CHD	rs11690532	2	102442858	0.002	1	HapMap	HapMap	C	0.988	T	0.012	C/T

MEX	rs11690532	2	102442858	0.017	0.617	HapMap	HapMap	C	0.885	T	0.115	C/T
MKK	rs11690532	2	102442858	0.02	1	HapMap	HapMap	C	0.986	T	0.014	C/T
ASW	rs11692065	2	102250407	0.124	1	HapMap	HapMap	C	0.811	T	0.189	C/T
CEU	rs11692065	2	102250407	0.159	1	HapMap	HapMap	C	0.889	T	0.111	C/T
CHB	rs11692065	2	102250407	0.366	0.819	HapMap	HapMap	C	0.911	T	0.089	C/T
CHD	rs11692065	2	102250407	0.603	1	HapMap	HapMap	C	0.929	T	0.071	C/T
GIH	rs11692065	2	102250407	0.283	0.901	HapMap	HapMap	C	0.915	T	0.085	C/T
JPT	rs11692065	2	102250407	0.385	1	HapMap	HapMap	C	0.936	T	0.064	C/T
LWK	rs11692065	2	102250407	0.081	0.818	HapMap	HapMap	C	0.722	T	0.278	C/T
MEX	rs11692065	2	102250407	0.322	1	HapMap	HapMap	C	0.888	T	0.112	C/T
MKK	rs11692065	2	102250407	0.257	1	HapMap	HapMap	C	0.738	T	0.262	C/T
YRI	rs11692065	2	102250407	0.068	0.752	HapMap	HapMap	C	0.748	T	0.252	C/T
MKK	rs11692230	2	102221497	0.269	0.675	HapMap	HapMap	A	0.704	G	0.296	A/G
JPT	rs11692304	2	102461836	0.071	1	HapMap	HapMap	G	0.773	A	0.227	G/A
CHD	rs11692304	2	102461836	0.035	1	HapMap	HapMap	G	0.782	A	0.218	G/A
MKK	rs11693697	2	102282094	0.015	1	HapMap	HapMap	T	0.99	C	0.01	T/C
MEX	rs11695455	2	102407134	0	1	HapMap	HapMap	A	0.99	G	0.01	A/G
CEU	rs11886793	2	102438652	0.337	0.656	HapMap	HapMap	T	0.646	G	0.354	T/G
GIH	rs11886793	2	102438652	0.319	0.685	HapMap	HapMap	T	0.847	G	0.153	T/G
MEX	rs11886793	2	102438652	0.209	0.671	HapMap	HapMap	T	0.86	G	0.14	T/G
ASW	rs11888547	2	102249158	0.031	1	HapMap	HapMap	G	0.981	T	0.019	G/T
LWK	rs11888547	2	102249158	0.054	1	HapMap	HapMap	G	0.983	T	0.017	G/T
YRI	rs11888547	2	102249158	0.074	0.711	HapMap	HapMap	G	0.96	T	0.04	G/T
ASW	rs11891965	2	102386928	0.055	1	HapMap	HapMap	C	0.906	T	0.094	C/T
LWK	rs11891965	2	102386928	0.063	1	HapMap	HapMap	C	0.833	T	0.167	C/T
MKK	rs11891965	2	102386928	0.051	1	HapMap	HapMap	C	0.934	T	0.066	C/T
YRI	rs11891965	2	102386928	0.038	0.729	HapMap	HapMap	C	0.819	T	0.181	C/T
ASW	rs11900775	2	102169654	0.046	1	HapMap	HapMap	T	0.906	C	0.094	T/C
CHB	rs11900775	2	102169654	0.073	1	HapMap	HapMap	T	0.97	C	0.03	T/C
MKK	rs11900775	2	102169654	0.039	0.806	HapMap	HapMap	T	0.923	C	0.077	T/C
CEU	rs11903354	2	102176860	0.076	0.771	HapMap	HapMap	T	0.915	C	0.085	T/C
CHB	rs11903354	2	102176860	0.012	1	HapMap	HapMap	T	0.929	C	0.071	T/C
GIH	rs11903354	2	102176860	0.021	1	HapMap	HapMap	T	0.994	C	0.006	T/C
JPT	rs11903354	2	102176860	0.005	1	HapMap	HapMap	T	0.977	C	0.023	T/C

MEX	rs11903354	2	102176860	0.095	1	HapMap	HapMap	T	0.97	C	0.03	T/C
MKK	rs11903354	2	102176860	0.035	0.71	HapMap	HapMap	T	0.913	C	0.087	T/C
JPT	rs12053526	2	102481372	0.6	1	HapMap	HapMap	C	0.872	T	0.128	C/T
LWK	rs12053526	2	102481372	0.013	1	HapMap	HapMap	C	0.961	T	0.039	C/T
MEX	rs12053526	2	102481372	0.031	1	HapMap	HapMap	C	0.99	T	0.01	C/T
MKK	rs12053526	2	102481372	0.013	1	HapMap	HapMap	C	0.983	T	0.017	C/T
CHD	rs12053526	2	102481372	0.604	1	HapMap	HapMap	C	0.929	T	0.071	C/T
ASW	rs12053526	2	102481372	0.008	1	HapMap	HapMap	C	0.961	T	0.039	C/T
CHB	rs12053526	2	102481372	0.546	1	HapMap	HapMap	C	0.911	T	0.089	C/T
GIH	rs12053526	2	102481372	0.021	1	HapMap	HapMap	C	0.994	T	0.006	C/T
CEU	rs12469892	2	102262216	0.172	0.882	HapMap	HapMap	G	0.821	A	0.179	G/A
CHB	rs12469892	2	102262216	0.052	1	HapMap	HapMap	G	0.774	A	0.226	G/A
CHD	rs12469892	2	102262216	0.021	0.714	HapMap	HapMap	G	0.753	A	0.247	G/A
GIH	rs12469892	2	102262216	0.132	0.893	HapMap	HapMap	G	0.625	A	0.375	G/A
MEX	rs12475055	2	102245323	0.123	0.68	HapMap	HapMap	A	0.58	C	0.42	A/C
CEU	rs12475055	2	102245323	0.572	0.787	HapMap	HapMap	A	0.496	C	0.504	A/C
CHB	rs12475055	2	102245323	0.396	0.776	HapMap	HapMap	A	0.179	C	0.821	A/C
CHD	rs12475055	2	102245323	0.582	0.872	HapMap	HapMap	A	0.141	C	0.859	A/C
GIH	rs12475055	2	102245323	0.436	0.864	HapMap	HapMap	A	0.312	C	0.688	A/C
CHD	rs12712133	2	102232705	0.021	0.972	HapMap	HapMap	A	0.153	G	0.847	A/G
JPT	rs12712133	2	102232705	0.058	1	HapMap	HapMap	A	0.233	G	0.767	A/G
CHB	rs12712135	2	102297380	0.144	1	HapMap	HapMap	A	0.47	G	0.53	A/G
CHD	rs12712135	2	102297380	0.131	1	HapMap	HapMap	A	0.506	G	0.494	A/G
JPT	rs12712135	2	102297380	0.1	1	HapMap	HapMap	A	0.39	G	0.61	A/G
ASW	rs12712142	2	102327016	0.28	0.66	HapMap	HapMap	C	0.594	A	0.406	C/A
CEU	rs12712142	2	102327016	0.414	1	HapMap	HapMap	C	0.611	A	0.389	C/A
CHB	rs12712142	2	102327016	0.111	1	HapMap	HapMap	C	0.613	A	0.387	C/A
CHD	rs12712142	2	102327016	0.076	1	HapMap	HapMap	C	0.624	A	0.376	C/A
GIH	rs12712142	2	102327016	0.132	1	HapMap	HapMap	C	0.667	A	0.333	C/A
JPT	rs12712142	2	102327016	0.216	1	HapMap	HapMap	C	0.535	A	0.465	C/A
MEX	rs12712142	2	102327016	0.125	1	HapMap	HapMap	C	0.73	A	0.27	C/A
CEU	rs12712157	2	102531561	0.145	0.859	HapMap	HapMap	T	0.19	C	0.81	T/C
CHB	rs12712157	2	102531561	0.155	1	HapMap	HapMap	T	0.518	C	0.482	T/C
CHD	rs12712157	2	102531561	0.129	1	HapMap	HapMap	T	0.506	C	0.494	T/C

JPT	rs12712157	2	102531561	0.111	1	HapMap	HapMap	T	0.413	C	0.587	T/C
CHB	rs12905	2	102326439	0.083	1	HapMap	HapMap	G	0.649	A	0.351	G/A
CHD	rs12905	2	102326439	0.065	1	HapMap	HapMap	G	0.659	A	0.341	G/A
MKK	rs12905	2	102326439	0.093	1	HapMap	HapMap	G	0.937	A	0.063	G/A
ASW	rs12905	2	102326439	0.361	1	HapMap	HapMap	G	0.887	A	0.113	G/A
CEU	rs12905	2	102326439	0.301	1	HapMap	HapMap	G	0.721	A	0.279	G/A
GIH	rs12905	2	102326439	0.097	1	HapMap	HapMap	G	0.727	A	0.273	G/A
JPT	rs12905	2	102326439	0.182	1	HapMap	HapMap	G	0.57	A	0.43	G/A
LWK	rs12905	2	102326439	0.129	1	HapMap	HapMap	G	0.961	A	0.039	G/A
MEX	rs12905	2	102326439	0.085	1	HapMap	HapMap	G	0.796	A	0.204	G/A
YRI	rs12905	2	102326439	0.2	1	HapMap	HapMap	G	0.942	A	0.058	G/A
CEU	rs12987222	2	102180548	0.027	1	HapMap	HapMap	G	0.942	T	0.058	G/T
GIH	rs12987222	2	102180548	0.002	1	HapMap	HapMap	G	0.994	T	0.006	G/T
LWK	rs12987222	2	102180548	0.135	0.682	HapMap	HapMap	G	0.917	T	0.083	G/T
MKK	rs12987222	2	102180548	0.206	0.941	HapMap	HapMap	G	0.858	T	0.142	G/T
ASW	rs12987782	2	102304398	0.24	1	HapMap	HapMap	G	0.877	A	0.123	G/A
CEU	rs12987782	2	102304398	0.015	1	HapMap	HapMap	G	0.929	A	0.071	G/A
GIH	rs12987782	2	102304398	0.018	1	HapMap	HapMap	G	0.938	A	0.062	G/A
LWK	rs12987782	2	102304398	0.398	1	HapMap	HapMap	G	0.889	A	0.111	G/A
MEX	rs12987782	2	102304398	0.021	1	HapMap	HapMap	G	0.94	A	0.06	G/A
MKK	rs12987782	2	102304398	0.448	1	HapMap	HapMap	G	0.755	A	0.245	G/A
YRI	rs12987782	2	102304398	0.227	1	HapMap	HapMap	G	0.929	A	0.071	G/A
CEU	rs12987900	2	102215780	0.04	1	HapMap	HapMap	G	0.947	A	0.053	G/A
GIH	rs12987900	2	102215780	0.002	1	HapMap	HapMap	G	0.994	A	0.006	G/A
LWK	rs12987900	2	102215780	0.172	0.72	HapMap	HapMap	G	0.906	A	0.094	G/A
MKK	rs12987900	2	102215780	0.212	0.945	HapMap	HapMap	G	0.856	A	0.144	G/A
CEU	rs12992518	2	102204030	0.04	1	HapMap	HapMap	C	0.947	T	0.053	C/T
GIH	rs12992518	2	102204030	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
LWK	rs12992518	2	102204030	0.135	0.682	HapMap	HapMap	C	0.917	T	0.083	C/T
MKK	rs12992518	2	102204030	0.226	0.949	HapMap	HapMap	C	0.846	T	0.154	C/T
CEU	rs12995644	2	102246459	0.04	1	HapMap	HapMap	C	0.956	A	0.044	C/A
GIH	rs12995644	2	102246459	0.003	1	HapMap	HapMap	C	0.989	A	0.011	C/A
LWK	rs12995644	2	102246459	0.231	0.893	HapMap	HapMap	C	0.917	A	0.083	C/A
MKK	rs12995644	2	102246459	0.2	0.938	HapMap	HapMap	C	0.862	A	0.138	C/A

YRI	rs12995644	2	102246459	0.152	0.819	HapMap	HapMap	C	0.925	A	0.075	C/A
ASW	rs12998521	2	102340849	0.643	1	HapMap	HapMap	G	0.774	T	0.226	G/T
CEU	rs12998521	2	102340849	0.414	1	HapMap	HapMap	G	0.611	T	0.389	G/T
CHB	rs12998521	2	102340849	0.111	1	HapMap	HapMap	G	0.613	T	0.387	G/T
CHD	rs12998521	2	102340849	0.076	1	HapMap	HapMap	G	0.624	T	0.376	G/T
GIH	rs12998521	2	102340849	0.135	1	HapMap	HapMap	G	0.659	T	0.341	G/T
JPT	rs12998521	2	102340849	0.191	1	HapMap	HapMap	G	0.564	T	0.436	G/T
LWK	rs12998521	2	102340849	0.562	1	HapMap	HapMap	G	0.85	T	0.15	G/T
MEX	rs12998521	2	102340849	0.125	1	HapMap	HapMap	G	0.73	T	0.27	G/T
MKK	rs12998521	2	102340849	0.625	1	HapMap	HapMap	G	0.689	T	0.311	G/T
YRI	rs12998521	2	102340849	0.499	1	HapMap	HapMap	G	0.867	T	0.133	G/T
CEU	rs12999517	2	102325692	0.056	1	HapMap	HapMap	T	0.894	C	0.106	T/C
GIH	rs12999517	2	102325692	0.018	1	HapMap	HapMap	T	0.938	C	0.062	T/C
MEX	rs12999517	2	102325692	0.021	1	HapMap	HapMap	T	0.94	C	0.06	T/C
CEU	rs13002972	2	102218293	0.04	1	HapMap	HapMap	G	0.947	A	0.053	G/A
GIH	rs13002972	2	102218293	0.002	1	HapMap	HapMap	G	0.994	A	0.006	G/A
LWK	rs13002972	2	102218293	0.153	0.702	HapMap	HapMap	G	0.911	A	0.089	G/A
MKK	rs13002972	2	102218293	0.213	0.946	HapMap	HapMap	G	0.853	A	0.147	G/A
GIH	rs13014084	2	102221197	0.002	1	HapMap	HapMap	A	0.994	G	0.006	A/G
MKK	rs13014084	2	102221197	0.187	0.852	HapMap	HapMap	A	0.843	G	0.157	A/G
ASW	rs13015714	2	102338297	0.202	1	HapMap	HapMap	G	0.075	T	0.925	G/T
CEU	rs13015714	2	102338297	0.209	1	HapMap	HapMap	G	0.204	T	0.796	G/T
CHB	rs13015714	2	102338297	0.135	1	HapMap	HapMap	G	0.47	T	0.53	G/T
CHD	rs13015714	2	102338297	0.132	1	HapMap	HapMap	G	0.512	T	0.488	G/T
GIH	rs13015714	2	102338297	0.225	1	HapMap	HapMap	G	0.449	T	0.551	G/T
JPT	rs13015714	2	102338297	0.095	1	HapMap	HapMap	G	0.39	T	0.61	G/T
LWK	rs13015714	2	102338297	0.311	1	HapMap	HapMap	G	0.089	T	0.911	G/T
MEX	rs13015714	2	102338297	0.333	1	HapMap	HapMap	G	0.46	T	0.54	G/T
MKK	rs13015714	2	102338297	0.174	1	HapMap	HapMap	G	0.112	T	0.888	G/T
YRI	rs13015714	2	102338297	0.372	1	HapMap	HapMap	G	0.106	T	0.894	G/T
CHB	rs13018263	2	102458702	0.213	0.63	HapMap	HapMap	T	0.753	C	0.247	T/C
CHD	rs13018263	2	102458702	0.216	0.822	HapMap	HapMap	T	0.714	C	0.286	T/C
JPT	rs13018263	2	102458702	0.263	0.747	HapMap	HapMap	T	0.735	C	0.265	T/C
ASW	rs13018263	2	102458702	0.101	0.686	HapMap	HapMap	T	0.708	C	0.292	T/C

ASW	rs13019081	2	102317254	0.643	1	HapMap	HapMap	A	0.774	C	0.226	A/C
CEU	rs13019081	2	102317254	0.292	0.918	HapMap	HapMap	A	0.646	C	0.354	A/C
CHB	rs13019081	2	102317254	0.111	1	HapMap	HapMap	A	0.607	C	0.393	A/C
CHD	rs13019081	2	102317254	0.074	1	HapMap	HapMap	A	0.629	C	0.371	A/C
GIH	rs13019081	2	102317254	0.095	0.839	HapMap	HapMap	A	0.659	C	0.341	A/C
JPT	rs13019081	2	102317254	0.21	1	HapMap	HapMap	A	0.541	C	0.459	A/C
LWK	rs13019081	2	102317254	0.538	1	HapMap	HapMap	A	0.856	C	0.144	A/C
MEX	rs13019081	2	102317254	0.125	1	HapMap	HapMap	A	0.73	C	0.27	A/C
MKK	rs13019081	2	102317254	0.587	0.957	HapMap	HapMap	A	0.684	C	0.316	A/C
YRI	rs13019081	2	102317254	0.466	1	HapMap	HapMap	A	0.872	C	0.128	A/C
CHD	rs13019784	2	102489733	0.034	0.607	HapMap	HapMap	A	0.577	G	0.423	A/G
CEU	rs13019784	2	102489733	0.145	0.859	HapMap	HapMap	A	0.19	G	0.81	A/G
ASW	rs13019803	2	102142634	0.054	0.603	HapMap	HapMap	C	0.774	T	0.226	C/T
CHD	rs13019803	2	102142634	0.026	1	HapMap	HapMap	C	0.829	T	0.171	C/T
GIH	rs13019803	2	102142634	0.044	1	HapMap	HapMap	C	0.862	T	0.138	C/T
MEX	rs13019803	2	102142634	0.048	1	HapMap	HapMap	C	0.878	T	0.122	C/T
ASW	rs13383035	2	102421766	0.03	1	HapMap	HapMap	C	0.943	A	0.057	C/A
LWK	rs13383035	2	102421766	0.01	0.964	HapMap	HapMap	C	0.967	A	0.033	C/A
MKK	rs13383035	2	102421766	0.026	1	HapMap	HapMap	C	0.965	A	0.035	C/A
YRI	rs13383035	2	102421766	0.039	1	HapMap	HapMap	C	0.912	A	0.088	C/A
ASW	rs13386900	2	102247181	0.102	1	HapMap	HapMap	G	0.849	A	0.151	G/A
CHB	rs13386900	2	102247181	0.208	0.738	HapMap	HapMap	G	0.946	A	0.054	G/A
CHD	rs13386900	2	102247181	0.444	1	HapMap	HapMap	G	0.947	A	0.053	G/A
JPT	rs13386900	2	102247181	0.385	1	HapMap	HapMap	G	0.936	A	0.064	G/A
LWK	rs13386900	2	102247181	0.081	0.818	HapMap	HapMap	G	0.722	A	0.278	G/A
MEX	rs13386900	2	102247181	0.031	1	HapMap	HapMap	G	0.99	A	0.01	G/A
MKK	rs13386900	2	102247181	0.225	1	HapMap	HapMap	G	0.762	A	0.238	G/A
YRI	rs13386900	2	102247181	0.064	0.762	HapMap	HapMap	G	0.752	A	0.248	G/A
CEU	rs13413002	2	102216915	0.008	1	HapMap	HapMap	C	0.987	T	0.013	C/T
LWK	rs13413002	2	102216915	0.011	1	HapMap	HapMap	C	0.967	T	0.033	C/T
MKK	rs13413002	2	102216915	0.032	1	HapMap	HapMap	C	0.958	T	0.042	C/T
ASW	rs13416708	2	102265736	0.03	1	HapMap	HapMap	G	0.953	A	0.047	G/A
CEU	rs13416708	2	102265736	0.014	1	HapMap	HapMap	G	0.996	A	0.004	G/A
LWK	rs13416708	2	102265736	0.005	1	HapMap	HapMap	G	0.983	A	0.017	G/A

MEX	rs13416708	2	102265736	0.031	1	HapMap	HapMap	G	0.99	A	0.01	G/A
MKK	rs13416708	2	102265736	0.032	1	HapMap	HapMap	G	0.958	A	0.042	G/A
YRI	rs13416708	2	102265736	0.015	1	HapMap	HapMap	G	0.956	A	0.044	G/A
ASW	rs13431828	2	102321085	0.214	1	HapMap	HapMap	C	0.726	T	0.274	C/T
CEU	rs13431828	2	102321085	0.159	1	HapMap	HapMap	C	0.876	T	0.124	C/T
CHB	rs13431828	2	102321085	0.632	1	HapMap	HapMap	C	0.905	T	0.095	C/T
CHD	rs13431828	2	102321085	0.713	1	HapMap	HapMap	C	0.917	T	0.083	C/T
GIH	rs13431828	2	102321085	0.374	1	HapMap	HapMap	C	0.908	T	0.092	C/T
JPT	rs13431828	2	102321085	0.753	1	HapMap	HapMap	C	0.872	T	0.128	C/T
LWK	rs13431828	2	102321085	0.096	1	HapMap	HapMap	C	0.767	T	0.233	C/T
MEX	rs13431828	2	102321085	0.423	1	HapMap	HapMap	C	0.86	T	0.14	C/T
MKK	rs13431828	2	102321085	0.296	1	HapMap	HapMap	C	0.71	T	0.29	C/T
YRI	rs13431828	2	102321085	0.216	1	HapMap	HapMap	C	0.664	T	0.336	C/T
ASW	rs1362348	2	102351056	0.877	1	HapMap	HapMap	C	0.358	G	0.642	C/G
CEU	rs1362348	2	102351056	1	1	HapMap	HapMap	C	0.593	G	0.407	C/G
CHB	rs1362348	2	102351056	1	1	HapMap	HapMap	C	0.857	G	0.143	C/G
CHD	rs1362348	2	102351056	1	1	HapMap	HapMap	C	0.888	G	0.112	C/G
GIH	rs1362348	2	102351056	1	1	HapMap	HapMap	C	0.79	G	0.21	C/G
JPT	rs1362348	2	102351056	1	1	HapMap	HapMap	C	0.849	G	0.151	C/G
LWK	rs1362348	2	102351056	0.554	1	HapMap	HapMap	C	0.365	G	0.635	C/G
MEX	rs1362348	2	102351056	1	1	HapMap	HapMap	C	0.724	G	0.276	C/G
MKK	rs1362348	2	102351056	0.855	1	HapMap	HapMap	C	0.458	G	0.542	C/G
YRI	rs1362348	2	102351056	0.916	1	HapMap	HapMap	C	0.284	G	0.716	C/G
CEU	rs1403548	2	102476807	0.213	0.887	HapMap	HapMap	C	0.261	T	0.739	C/T
CHB	rs1403548	2	102476807	0.11	0.657	HapMap	HapMap	C	0.622	T	0.378	C/T
CHD	rs1403548	2	102476807	0.083	0.621	HapMap	HapMap	C	0.617	T	0.383	C/T
GIH	rs1403548	2	102476807	0.059	0.713	HapMap	HapMap	C	0.295	T	0.705	C/T
YRI	rs1403548	2	102476807	0.015	1	HapMap	HapMap	C	0.031	T	0.969	C/T
ASW	rs1403548	2	102476807	0.063	1	HapMap	HapMap	C	0.019	T	0.981	C/T
ASW	rs1403550	2	102502741	0.031	1	HapMap	HapMap	T	0.009	C	0.991	T/C
CEU	rs1403550	2	102502741	0.145	0.859	HapMap	HapMap	T	0.19	C	0.81	T/C
CHB	rs1403550	2	102502741	0.148	1	HapMap	HapMap	T	0.5	C	0.5	T/C
CHD	rs1403550	2	102502741	0.126	1	HapMap	HapMap	T	0.5	C	0.5	T/C
JPT	rs1403550	2	102502741	0.111	1	HapMap	HapMap	T	0.407	C	0.593	T/C

YRI	rs1403550	2	102502741	0.011	1	HapMap	HapMap	T	0.027	C	0.973	T/C
CEU	rs1403551	2	102502878	0.145	0.859	HapMap	HapMap	T	0.19	G	0.81	T/G
CHB	rs1403551	2	102502878	0.148	1	HapMap	HapMap	T	0.5	G	0.5	T/G
CHD	rs1403551	2	102502878	0.126	1	HapMap	HapMap	T	0.5	G	0.5	T/G
JPT	rs1403551	2	102502878	0.111	1	HapMap	HapMap	T	0.407	G	0.593	T/G
ASW	rs1403552	2	102455209	0.119	0.699	HapMap	HapMap	C	0.689	T	0.311	C/T
CEU	rs1403552	2	102455209	0.193	1	HapMap	HapMap	C	0.836	T	0.164	C/T
CHB	rs1403552	2	102455209	0.632	1	HapMap	HapMap	C	0.905	T	0.095	C/T
CHD	rs1403552	2	102455209	0.713	1	HapMap	HapMap	C	0.918	T	0.082	C/T
MEX	rs1403552	2	102455209	0.364	0.813	HapMap	HapMap	C	0.82	T	0.18	C/T
LWK	rs1403552	2	102455209	0.074	0.67	HapMap	HapMap	C	0.656	T	0.344	C/T
GIH	rs1403552	2	102455209	0.22	0.74	HapMap	HapMap	C	0.903	T	0.097	C/T
JPT	rs1403552	2	102455209	0.753	1	HapMap	HapMap	C	0.872	T	0.128	C/T
CEU	rs1420089	2	102304821	0.193	1	HapMap	HapMap	T	0.876	C	0.124	T/C
GIH	rs1420089	2	102304821	0.021	1	HapMap	HapMap	T	0.994	C	0.006	T/C
LWK	rs1420089	2	102304821	0.051	0.82	HapMap	HapMap	T	0.806	C	0.194	T/C
MEX	rs1420089	2	102304821	0.196	1	HapMap	HapMap	T	0.94	C	0.06	T/C
MKK	rs1420089	2	102304821	0.091	1	HapMap	HapMap	T	0.888	C	0.112	T/C
YRI	rs1420089	2	102304821	0.023	0.61	HapMap	HapMap	T	0.796	C	0.204	T/C
ASW	rs1420092	2	102240817	0.031	1	HapMap	HapMap	A	0.009	C	0.991	A/C
CEU	rs1420092	2	102240817	0.047	1	HapMap	HapMap	A	0.102	C	0.898	A/C
CHB	rs1420092	2	102240817	0.006	0.749	HapMap	HapMap	A	0.036	C	0.964	A/C
GIH	rs1420092	2	102240817	0.019	0.79	HapMap	HapMap	A	0.102	C	0.898	A/C
JPT	rs1420092	2	102240817	0.01	1	HapMap	HapMap	A	0.041	C	0.959	A/C
MEX	rs1420092	2	102240817	0.021	1	HapMap	HapMap	A	0.06	C	0.94	A/C
MKK	rs1420092	2	102240817	0.124	0.86	HapMap	HapMap	A	0.108	C	0.892	A/C
YRI	rs1420092	2	102240817	0.004	1	HapMap	HapMap	A	0.018	C	0.982	A/C
ASW	rs1420094	2	102382119	0.358	0.778	HapMap	HapMap	C	0.226	T	0.774	C/T
CEU	rs1420094	2	102382119	0.759	1	HapMap	HapMap	C	0.478	T	0.522	C/T
CHB	rs1420094	2	102382119	0.622	1	HapMap	HapMap	C	0.837	T	0.163	C/T
CHD	rs1420094	2	102382119	0.583	0.873	HapMap	HapMap	C	0.859	T	0.141	C/T
GIH	rs1420094	2	102382119	0.703	0.924	HapMap	HapMap	C	0.756	T	0.244	C/T
JPT	rs1420094	2	102382119	0.92	1	HapMap	HapMap	C	0.835	T	0.165	C/T
MEX	rs1420094	2	102382119	0.709	0.939	HapMap	HapMap	C	0.68	T	0.32	C/T

MKK	rs1420094	2	102382119	0.278	0.732	HapMap	HapMap	C	0.273	T	0.727	C/T
ASW	rs1420097	2	102375786	0.408	0.796	HapMap	HapMap	C	0.236	G	0.764	C/G
CEU	rs1420097	2	102375786	0.759	1	HapMap	HapMap	C	0.478	G	0.522	C/G
CHB	rs1420097	2	102375786	0.564	0.892	HapMap	HapMap	C	0.833	G	0.167	C/G
CHD	rs1420097	2	102375786	0.615	0.874	HapMap	HapMap	C	0.865	G	0.135	C/G
GIH	rs1420097	2	102375786	0.703	0.924	HapMap	HapMap	C	0.756	G	0.244	C/G
JPT	rs1420097	2	102375786	0.85	1	HapMap	HapMap	C	0.831	G	0.169	C/G
MEX	rs1420097	2	102375786	0.709	0.939	HapMap	HapMap	C	0.68	G	0.32	C/G
MKK	rs1420097	2	102375786	0.278	0.732	HapMap	HapMap	C	0.273	G	0.727	C/G
ASW	rs1420101	2	102324148	0.28	0.66	HapMap	HapMap	C	0.594	T	0.406	C/T
CEU	rs1420101	2	102324148	0.331	1	HapMap	HapMap	C	0.65	T	0.35	C/T
CHB	rs1420101	2	102324148	0.113	1	HapMap	HapMap	C	0.614	T	0.386	C/T
CHD	rs1420101	2	102324148	0.077	1	HapMap	HapMap	C	0.625	T	0.375	C/T
GIH	rs1420101	2	102324148	0.132	1	HapMap	HapMap	C	0.665	T	0.335	C/T
JPT	rs1420101	2	102324148	0.21	1	HapMap	HapMap	C	0.535	T	0.465	C/T
MEX	rs1420101	2	102324148	0.125	1	HapMap	HapMap	C	0.73	T	0.27	C/T
CHD	rs1420105	2	102401551	0.619	0.862	HapMap	HapMap	T	0.88	C	0.12	T/C
GIH	rs1420105	2	102401551	0.68	0.923	HapMap	HapMap	T	0.75	C	0.25	T/C
CHB	rs1420105	2	102401551	0.564	0.892	HapMap	HapMap	T	0.833	C	0.167	T/C
ASW	rs1420105	2	102401551	0.358	0.778	HapMap	HapMap	T	0.226	C	0.774	T/C
CEU	rs1420105	2	102401551	0.754	1	HapMap	HapMap	T	0.482	C	0.518	T/C
JPT	rs1420105	2	102401551	0.85	1	HapMap	HapMap	T	0.831	C	0.169	T/C
MEX	rs1420105	2	102401551	0.692	0.934	HapMap	HapMap	T	0.688	C	0.312	T/C
MKK	rs1420105	2	102401551	0.223	0.699	HapMap	HapMap	T	0.248	C	0.752	T/C
CEU	rs1420106	2	102401476	0.209	1	HapMap	HapMap	A	0.205	G	0.795	A/G
CHB	rs1420106	2	102401476	0.141	1	HapMap	HapMap	A	0.482	G	0.518	A/G
CHD	rs1420106	2	102401476	0.122	1	HapMap	HapMap	A	0.5	G	0.5	A/G
GIH	rs1420106	2	102401476	0.149	0.816	HapMap	HapMap	A	0.449	G	0.551	A/G
JPT	rs1420106	2	102401476	0.105	1	HapMap	HapMap	A	0.405	G	0.595	A/G
LWK	rs1420106	2	102401476	0.034	0.806	HapMap	HapMap	A	0.149	G	0.851	A/G
MEX	rs1420106	2	102401476	0.333	1	HapMap	HapMap	A	0.458	G	0.542	A/G
MKK	rs1420106	2	102401476	0.128	0.701	HapMap	HapMap	A	0.16	G	0.84	A/G
CEU	rs1523196	2	102530132	0.245	1	HapMap	HapMap	T	0.867	G	0.133	T/G
CHB	rs1523196	2	102530132	0.147	1	HapMap	HapMap	T	0.988	G	0.012	T/G

JPT	rs1523196	2	102530132	0.122	1	HapMap	HapMap	T	0.983	G	0.017	T/G
LWK	rs1523196	2	102530132	0.044	1	HapMap	HapMap	T	0.878	G	0.122	T/G
MKK	rs1523196	2	102530132	0.088	1	HapMap	HapMap	T	0.892	G	0.108	T/G
ASW	rs1523198	2	102464906	0.063	1	HapMap	HapMap	C	0.019	T	0.981	C/T
CEU	rs1523198	2	102464906	0.273	1	HapMap	HapMap	C	0.265	T	0.735	C/T
CHB	rs1523198	2	102464906	0.132	0.677	HapMap	HapMap	C	0.643	T	0.357	C/T
CHD	rs1523198	2	102464906	0.133	0.768	HapMap	HapMap	C	0.641	T	0.359	C/T
GIH	rs1523198	2	102464906	0.059	0.713	HapMap	HapMap	C	0.295	T	0.705	C/T
JPT	rs1523198	2	102464906	0.102	0.604	HapMap	HapMap	C	0.605	T	0.395	C/T
LWK	rs1523198	2	102464906	0.129	1	HapMap	HapMap	C	0.039	T	0.961	C/T
MKK	rs1523198	2	102464906	0.063	0.761	HapMap	HapMap	C	0.073	T	0.927	C/T
YRI	rs1523198	2	102464906	0.071	1	HapMap	HapMap	C	0.027	T	0.973	C/T
CHD	rs1558625	2	102228596	0.021	0.972	HapMap	HapMap	A	0.153	G	0.847	A/G
JPT	rs1558625	2	102228596	0.058	1	HapMap	HapMap	A	0.233	G	0.767	A/G
YRI	rs1558625	2	102228596	0.033	0.705	HapMap	HapMap	A	0.181	G	0.819	A/G
ASW	rs1558646	2	102179710	0.103	0.712	HapMap	HapMap	G	0.915	A	0.085	G/A
JPT	rs1558653	2	102507155	0.456	0.751	HapMap	HapMap	C	0.847	T	0.153	C/T
CHD	rs1558653	2	102507155	0.431	0.677	HapMap	HapMap	C	0.894	T	0.106	C/T
CHB	rs1558653	2	102507155	0.385	0.68	HapMap	HapMap	C	0.861	T	0.139	C/T
CEU	rs1558653	2	102507155	0.047	1	HapMap	HapMap	C	0.929	T	0.071	C/T
LWK	rs17026782	2	102183509	0.036	1	HapMap	HapMap	A	0.989	G	0.011	A/G
MKK	rs17026782	2	102183509	0.04	1	HapMap	HapMap	A	0.972	G	0.028	A/G
YRI	rs17026782	2	102183509	0.023	1	HapMap	HapMap	A	0.996	G	0.004	A/G
ASW	rs17026974	2	102318792	0.319	1	HapMap	HapMap	G	0.896	A	0.104	G/A
CEU	rs17026974	2	102318792	0.301	1	HapMap	HapMap	G	0.721	A	0.279	G/A
CHB	rs17026974	2	102318792	0.083	1	HapMap	HapMap	G	0.649	A	0.351	G/A
CHD	rs17026974	2	102318792	0.065	1	HapMap	HapMap	G	0.659	A	0.341	G/A
GIH	rs17026974	2	102318792	0.097	1	HapMap	HapMap	G	0.727	A	0.273	G/A
JPT	rs17026974	2	102318792	0.182	1	HapMap	HapMap	G	0.57	A	0.43	G/A
LWK	rs17026974	2	102318792	0.072	1	HapMap	HapMap	G	0.978	A	0.022	G/A
MEX	rs17026974	2	102318792	0.091	1	HapMap	HapMap	G	0.79	A	0.21	G/A
MKK	rs17026974	2	102318792	0.071	1	HapMap	HapMap	G	0.951	A	0.049	G/A
YRI	rs17026974	2	102318792	0.2	1	HapMap	HapMap	G	0.942	A	0.058	G/A
ASW	rs17027006	2	102331764	0.361	1	HapMap	HapMap	G	0.887	C	0.113	G/C

CEU	rs17027006	2	102331764	0.287	1	HapMap	HapMap	G	0.726	C	0.274	G/C
CHB	rs17027006	2	102331764	0.091	1	HapMap	HapMap	G	0.643	C	0.357	G/C
CHD	rs17027006	2	102331764	0.065	1	HapMap	HapMap	G	0.659	C	0.341	G/C
GIH	rs17027006	2	102331764	0.097	1	HapMap	HapMap	G	0.727	C	0.273	G/C
JPT	rs17027006	2	102331764	0.182	1	HapMap	HapMap	G	0.576	C	0.424	G/C
LWK	rs17027006	2	102331764	0.129	1	HapMap	HapMap	G	0.961	C	0.039	G/C
MEX	rs17027006	2	102331764	0.091	1	HapMap	HapMap	G	0.79	C	0.21	G/C
MKK	rs17027006	2	102331764	0.093	1	HapMap	HapMap	G	0.937	C	0.063	G/C
YRI	rs17027006	2	102331764	0.2	1	HapMap	HapMap	G	0.942	C	0.058	G/C
ASW	rs17027056	2	102373483	0.031	1	HapMap	HapMap	C	0.991	T	0.009	C/T
MEX	rs17027056	2	102373483	0.008	1	HapMap	HapMap	C	0.96	T	0.04	C/T
CEU	rs17027056	2	102373483	0.039	1	HapMap	HapMap	C	0.942	T	0.058	C/T
CHB	rs17027056	2	102373483	0.032	1	HapMap	HapMap	C	0.863	T	0.137	C/T
CHD	rs17027056	2	102373483	0.02	1	HapMap	HapMap	C	0.865	T	0.135	C/T
GIH	rs17027056	2	102373483	0.011	1	HapMap	HapMap	C	0.96	T	0.04	C/T
JPT	rs17027056	2	102373483	0.058	1	HapMap	HapMap	C	0.773	T	0.227	C/T
ASW	rs17027087	2	102382350	0.448	1	HapMap	HapMap	C	0.83	T	0.17	C/T
CEU	rs17027087	2	102382350	0.301	1	HapMap	HapMap	C	0.721	T	0.279	C/T
LWK	rs17027087	2	102382350	0.248	1	HapMap	HapMap	C	0.928	T	0.072	C/T
MEX	rs17027087	2	102382350	0.059	0.78	HapMap	HapMap	C	0.78	T	0.22	C/T
MKK	rs17027087	2	102382350	0.102	0.809	HapMap	HapMap	C	0.899	T	0.101	C/T
CHB	rs17027087	2	102382350	0.033	0.62	HapMap	HapMap	C	0.643	T	0.357	C/T
CHD	rs17027087	2	102382350	0.043	0.766	HapMap	HapMap	C	0.637	T	0.363	C/T
GIH	rs17027087	2	102382350	0.112	1	HapMap	HapMap	C	0.699	T	0.301	C/T
JPT	rs17027087	2	102382350	0.173	1	HapMap	HapMap	C	0.581	T	0.419	C/T
CEU	rs17027166	2	102421852	0.301	1	HapMap	HapMap	G	0.721	A	0.279	G/A
CHB	rs17027166	2	102421852	0.033	0.62	HapMap	HapMap	G	0.643	A	0.357	G/A
CHD	rs17027166	2	102421852	0.043	0.764	HapMap	HapMap	G	0.639	A	0.361	G/A
GIH	rs17027166	2	102421852	0.112	1	HapMap	HapMap	G	0.698	A	0.302	G/A
JPT	rs17027166	2	102421852	0.173	1	HapMap	HapMap	G	0.581	A	0.419	G/A
MEX	rs17027166	2	102421852	0.071	0.804	HapMap	HapMap	G	0.76	A	0.24	G/A
CHD	rs17027173	2	102423475	0.093	0.697	HapMap	HapMap	G	0.976	A	0.024	G/A
GIH	rs17027173	2	102423475	0.469	0.936	HapMap	HapMap	G	0.875	A	0.125	G/A
JPT	rs17027173	2	102423475	0.185	1	HapMap	HapMap	G	0.983	A	0.017	G/A

LWK	rs17027173	2	102423475	0.063	1	HapMap	HapMap	G	0.831	A	0.169	G/A
MEX	rs17027173	2	102423475	0.344	1	HapMap	HapMap	G	0.89	A	0.11	G/A
MKK	rs17027173	2	102423475	0.14	0.881	HapMap	HapMap	G	0.806	A	0.194	G/A
YRI	rs17027173	2	102423475	0.042	0.617	HapMap	HapMap	G	0.792	A	0.208	G/A
CEU	rs17027173	2	102423475	0.592	1	HapMap	HapMap	G	0.728	A	0.272	G/A
CHB	rs17027173	2	102423475	0.223	1	HapMap	HapMap	G	0.976	A	0.024	G/A
CHB	rs17027255	2	102456559	0.033	0.62	HapMap	HapMap	C	0.643	T	0.357	C/T
CHD	rs17027255	2	102456559	0.039	0.752	HapMap	HapMap	C	0.647	T	0.353	C/T
GIH	rs17027255	2	102456559	0.115	1	HapMap	HapMap	C	0.693	T	0.307	C/T
JPT	rs17027255	2	102456559	0.173	1	HapMap	HapMap	C	0.581	T	0.419	C/T
MEX	rs17027255	2	102456559	0.071	0.804	HapMap	HapMap	C	0.76	T	0.24	C/T
CEU	rs17027255	2	102456559	0.301	1	HapMap	HapMap	C	0.712	T	0.288	C/T
MKK	rs17027275	2	102461819	0.005	1	HapMap	HapMap	G	0.993	A	0.007	G/A
ASW	rs17027275	2	102461819	0.038	1	HapMap	HapMap	G	0.934	A	0.066	G/A
CHB	rs17027275	2	102461819	0.002	1	HapMap	HapMap	G	0.994	A	0.006	G/A
GIH	rs17027275	2	102461819	0	1	HapMap	HapMap	G	0.994	A	0.006	G/A
LWK	rs17027275	2	102461819	0.007	1	HapMap	HapMap	G	0.978	A	0.022	G/A
YRI	rs17027275	2	102461819	0.015	1	HapMap	HapMap	G	0.951	A	0.049	G/A
CEU	rs17027293	2	102465272	0.047	1	HapMap	HapMap	A	0.934	G	0.066	A/G
MEX	rs17027293	2	102465272	0.017	1	HapMap	HapMap	A	0.96	G	0.04	A/G
CHD	rs17027293	2	102465272	0.002	0.614	HapMap	HapMap	A	0.965	G	0.035	A/G
GIH	rs17027293	2	102465272	0.01	1	HapMap	HapMap	A	0.966	G	0.034	A/G
JPT	rs17027293	2	102465272	0.005	1	HapMap	HapMap	A	0.977	G	0.023	A/G
GIH	rs17027295	2	102465303	0.01	1	HapMap	HapMap	G	0.966	A	0.034	G/A
JPT	rs17027295	2	102465303	0.005	1	HapMap	HapMap	G	0.977	A	0.023	G/A
MEX	rs17027295	2	102465303	0.017	1	HapMap	HapMap	G	0.96	A	0.04	G/A
CEU	rs17027295	2	102465303	0.047	1	HapMap	HapMap	G	0.929	A	0.071	G/A
CHD	rs17027295	2	102465303	0.002	0.614	HapMap	HapMap	G	0.965	A	0.035	G/A
LWK	rs17027341	2	102502991	0.053	1	HapMap	HapMap	T	0.856	C	0.144	T/C
MKK	rs17027341	2	102502991	0.096	0.905	HapMap	HapMap	T	0.86	C	0.14	T/C
JPT	rs17027341	2	102502991	0.122	1	HapMap	HapMap	T	0.983	C	0.017	T/C
CEU	rs17027341	2	102502991	0.245	1	HapMap	HapMap	T	0.863	C	0.137	T/C
CHB	rs17027341	2	102502991	0.147	1	HapMap	HapMap	T	0.988	C	0.012	T/C
MKK	rs17027347	2	102504736	0.014	0.639	HapMap	HapMap	G	0.976	A	0.024	G/A

YRI	rs17027347	2	102504736	0.015	1	HapMap	HapMap	G	0.951	A	0.049	G/A
ASW	rs17027347	2	102504736	0.038	1	HapMap	HapMap	G	0.934	A	0.066	G/A
CEU	rs17027413	2	102520099	0.245	1	HapMap	HapMap	C	0.865	T	0.135	C/T
CHB	rs17027413	2	102520099	0.147	1	HapMap	HapMap	C	0.988	T	0.012	C/T
LWK	rs17027413	2	102520099	0.046	1	HapMap	HapMap	C	0.872	T	0.128	C/T
MKK	rs17027413	2	102520099	0.045	0.617	HapMap	HapMap	C	0.862	T	0.138	C/T
CEU	rs17027442	2	102531380	0.245	1	HapMap	HapMap	C	0.867	T	0.133	C/T
CHB	rs17027442	2	102531380	0.147	1	HapMap	HapMap	C	0.988	T	0.012	C/T
JPT	rs17027442	2	102531380	0.122	1	HapMap	HapMap	C	0.983	T	0.017	C/T
MKK	rs17027442	2	102531380	0.089	1	HapMap	HapMap	C	0.89	T	0.11	C/T
MEX	rs17637748	2	102208147	0.226	0.629	HapMap	HapMap	A	0.39	G	0.61	A/G
LWK	rs17651485	2	102368082	0.19	0.799	HapMap	HapMap	C	0.916	T	0.084	C/T
MKK	rs17651485	2	102368082	0.15	1	HapMap	HapMap	C	0.902	T	0.098	C/T
CEU	rs17651485	2	102368082	0.056	1	HapMap	HapMap	C	0.919	T	0.081	C/T
CHD	rs17651485	2	102368082	0.004	1	HapMap	HapMap	C	0.971	T	0.029	C/T
GIH	rs17651485	2	102368082	0.008	1	HapMap	HapMap	C	0.972	T	0.028	C/T
JPT	rs17651485	2	102368082	0.005	1	HapMap	HapMap	C	0.977	T	0.023	C/T
YRI	rs17651485	2	102368082	0.036	0.609	HapMap	HapMap	C	0.973	T	0.027	C/T
CHD	rs17772203	2	102482292	0.002	0.637	HapMap	HapMap	C	0.964	G	0.036	C/G
LWK	rs17772203	2	102482292	0.021	0.827	HapMap	HapMap	C	0.911	G	0.089	C/G
YRI	rs17772203	2	102482292	0.053	1	HapMap	HapMap	C	0.907	G	0.093	C/G
JPT	rs17772203	2	102482292	0.005	1	HapMap	HapMap	C	0.977	G	0.023	C/G
CEU	rs17772203	2	102482292	0.048	1	HapMap	HapMap	C	0.933	G	0.067	C/G
JPT	rs1829849	2	102516130	0.05	0.62	HapMap	HapMap	A	0.429	C	0.571	A/C
CHB	rs1829849	2	102516130	0.17	1	HapMap	HapMap	A	0.531	C	0.469	A/C
CHD	rs1829849	2	102516130	0.086	0.776	HapMap	HapMap	A	0.554	C	0.446	A/C
ASW	rs1921622	2	102332499	0.569	0.838	HapMap	HapMap	G	0.726	A	0.274	G/A
JPT	rs1921622	2	102332499	0.097	0.634	HapMap	HapMap	G	0.517	A	0.483	G/A
LWK	rs1921622	2	102332499	0.376	0.728	HapMap	HapMap	G	0.818	A	0.182	G/A
MKK	rs1921622	2	102332499	0.46	0.763	HapMap	HapMap	G	0.636	A	0.364	G/A
CEU	rs1946131	2	102328361	0.056	1	HapMap	HapMap	C	0.889	T	0.111	C/T
CHD	rs1946131	2	102328361	0.002	0.614	HapMap	HapMap	C	0.965	T	0.035	C/T
GIH	rs1946131	2	102328361	0.018	1	HapMap	HapMap	C	0.938	T	0.062	C/T
MEX	rs1946131	2	102328361	0.021	1	HapMap	HapMap	C	0.94	T	0.06	C/T

MKK	rs1946131	2	102328361	0.267	0.682	HapMap	HapMap	C	0.706	T	0.294	C/T
ASW	rs1997502	2	102210681	0.014	0.992	HapMap	HapMap	A	0.019	G	0.981	A/G
LWK	rs1997502	2	102210681	0.018	1	HapMap	HapMap	A	0.006	G	0.994	A/G
YRI	rs1997502	2	102210681	0.071	1	HapMap	HapMap	A	0.018	G	0.982	A/G
CEU	rs1997503	2	102175667	0.076	0.771	HapMap	HapMap	C	0.903	T	0.097	C/T
CHB	rs1997503	2	102175667	0.012	1	HapMap	HapMap	C	0.929	T	0.071	C/T
GIH	rs1997503	2	102175667	0.021	1	HapMap	HapMap	C	0.994	T	0.006	C/T
JPT	rs1997503	2	102175667	0.005	1	HapMap	HapMap	C	0.977	T	0.023	C/T
LWK	rs1997503	2	102175667	0.03	0.652	HapMap	HapMap	C	0.817	T	0.183	C/T
MKK	rs1997503	2	102175667	0.057	1	HapMap	HapMap	C	0.926	T	0.074	C/T
YRI	rs1997503	2	102175667	0.053	1	HapMap	HapMap	C	0.853	T	0.147	C/T
CHD	rs2008157	2	102515614	0.098	0.814	HapMap	HapMap	A	0.541	G	0.459	A/G
CHB	rs2008157	2	102515614	0.17	1	HapMap	HapMap	A	0.53	G	0.47	A/G
JPT	rs2008157	2	102515614	0.05	0.62	HapMap	HapMap	A	0.436	G	0.564	A/G
CHB	rs2008159	2	102515594	0.17	1	HapMap	HapMap	A	0.53	G	0.47	A/G
JPT	rs2008159	2	102515594	0.05	0.62	HapMap	HapMap	A	0.436	G	0.564	A/G
CHD	rs2008159	2	102515594	0.098	0.814	HapMap	HapMap	A	0.541	G	0.459	A/G
JPT	rs2015478	2	102507879	0.05	0.62	HapMap	HapMap	A	0.436	G	0.564	A/G
CHB	rs2015478	2	102507879	0.17	1	HapMap	HapMap	A	0.53	G	0.47	A/G
CHD	rs2015478	2	102507879	0.098	0.814	HapMap	HapMap	A	0.541	G	0.459	A/G
GIH	rs2041739	2	102360765	0.703	0.924	HapMap	HapMap	C	0.756	T	0.244	C/T
JPT	rs2041739	2	102360765	0.85	1	HapMap	HapMap	C	0.831	T	0.169	C/T
MEX	rs2041739	2	102360765	0.709	0.939	HapMap	HapMap	C	0.68	T	0.32	C/T
MKK	rs2041739	2	102360765	0.278	0.732	HapMap	HapMap	C	0.273	T	0.727	C/T
ASW	rs2041739	2	102360765	0.408	0.796	HapMap	HapMap	C	0.236	T	0.764	C/T
CEU	rs2041739	2	102360765	0.759	1	HapMap	HapMap	C	0.482	T	0.518	C/T
CHB	rs2041739	2	102360765	0.564	0.892	HapMap	HapMap	C	0.831	T	0.169	C/T
CHD	rs2041739	2	102360765	0.615	0.874	HapMap	HapMap	C	0.865	T	0.135	C/T
ASW	rs2041756	2	102416342	0.022	1	HapMap	HapMap	A	0.038	G	0.962	A/G
CEU	rs2041756	2	102416342	0.209	1	HapMap	HapMap	A	0.204	G	0.796	A/G
CHB	rs2041756	2	102416342	0.141	1	HapMap	HapMap	A	0.476	G	0.524	A/G
CHD	rs2041756	2	102416342	0.129	1	HapMap	HapMap	A	0.506	G	0.494	A/G
GIH	rs2041756	2	102416342	0.141	0.803	HapMap	HapMap	A	0.443	G	0.557	A/G
JPT	rs2041756	2	102416342	0.105	1	HapMap	HapMap	A	0.413	G	0.587	A/G

LWK	rs2041756	2	102416342	0.053	1	HapMap	HapMap	A	0.144	G	0.856	A/G
MEX	rs2041756	2	102416342	0.304	1	HapMap	HapMap	A	0.44	G	0.56	A/G
MKK	rs2041756	2	102416342	0.118	0.643	HapMap	HapMap	A	0.171	G	0.829	A/G
YRI	rs2041756	2	102416342	0.048	0.626	HapMap	HapMap	A	0.049	G	0.951	A/G
CEU	rs2058659	2	102420988	0.759	1	HapMap	HapMap	G	0.482	A	0.518	G/A
CHB	rs2058659	2	102420988	0.564	0.892	HapMap	HapMap	G	0.837	A	0.163	G/A
CHD	rs2058659	2	102420988	0.615	0.874	HapMap	HapMap	G	0.865	A	0.135	G/A
GIH	rs2058659	2	102420988	0.716	0.961	HapMap	HapMap	G	0.744	A	0.256	G/A
JPT	rs2058659	2	102420988	0.85	1	HapMap	HapMap	G	0.831	A	0.169	G/A
CEU	rs2058660	2	102420881	0.209	1	HapMap	HapMap	G	0.192	A	0.808	G/A
CHB	rs2058660	2	102420881	0.135	1	HapMap	HapMap	G	0.47	A	0.53	G/A
CHD	rs2058660	2	102420881	0.126	1	HapMap	HapMap	G	0.5	A	0.5	G/A
GIH	rs2058660	2	102420881	0.141	0.803	HapMap	HapMap	G	0.443	A	0.557	G/A
JPT	rs2058660	2	102420881	0.105	1	HapMap	HapMap	G	0.413	A	0.587	G/A
LWK	rs2058660	2	102420881	0.048	1	HapMap	HapMap	G	0.133	A	0.867	G/A
ASW	rs2058660	2	102420881	0.022	1	HapMap	HapMap	G	0.038	A	0.962	G/A
MEX	rs2058660	2	102420881	0.298	1	HapMap	HapMap	G	0.418	A	0.582	G/A
MKK	rs2058660	2	102420881	0.118	0.643	HapMap	HapMap	G	0.171	A	0.829	G/A
ASW	rs2075186	2	102423683	0.119	0.699	HapMap	HapMap	G	0.689	T	0.311	G/T
CEU	rs2075186	2	102423683	0.193	1	HapMap	HapMap	G	0.836	T	0.164	G/T
CHB	rs2075186	2	102423683	0.632	1	HapMap	HapMap	G	0.905	T	0.095	G/T
CHD	rs2075186	2	102423683	0.713	1	HapMap	HapMap	G	0.918	T	0.082	G/T
GIH	rs2075186	2	102423683	0.22	0.74	HapMap	HapMap	G	0.903	T	0.097	G/T
JPT	rs2075186	2	102423683	0.753	1	HapMap	HapMap	G	0.872	T	0.128	G/T
LWK	rs2075186	2	102423683	0.068	0.649	HapMap	HapMap	G	0.661	T	0.339	G/T
MEX	rs2075186	2	102423683	0.364	0.813	HapMap	HapMap	G	0.82	T	0.18	G/T
GIH	rs2075187	2	102486743	0.059	0.713	HapMap	HapMap	G	0.295	A	0.705	G/A
YRI	rs2075187	2	102486743	0.019	1	HapMap	HapMap	G	0.04	A	0.96	G/A
ASW	rs2075187	2	102486743	0.063	1	HapMap	HapMap	G	0.038	A	0.962	G/A
CEU	rs2075187	2	102486743	0.232	0.898	HapMap	HapMap	G	0.27	A	0.73	G/A
CHB	rs2075187	2	102486743	0.132	0.677	HapMap	HapMap	G	0.643	A	0.357	G/A
CHD	rs2075187	2	102486743	0.126	0.759	HapMap	HapMap	G	0.631	A	0.369	G/A
CEU	rs2075188	2	102486664	0.232	0.898	HapMap	HapMap	G	0.27	A	0.73	G/A
CHD	rs2075188	2	102486664	0.021	0.639	HapMap	HapMap	G	0.706	A	0.294	G/A

JPT	rs2075188	2	102486664	0.09	1	HapMap	HapMap	G	0.733	A	0.267	G/A
CHB	rs2075193	2	102484459	0.132	0.677	HapMap	HapMap	G	0.643	A	0.357	G/A
CHD	rs2075193	2	102484459	0.131	0.765	HapMap	HapMap	G	0.637	A	0.363	G/A
GIH	rs2075193	2	102484459	0.059	0.713	HapMap	HapMap	G	0.295	A	0.705	G/A
MKK	rs2075193	2	102484459	0.063	0.761	HapMap	HapMap	G	0.073	A	0.927	G/A
YRI	rs2075193	2	102484459	0.023	1	HapMap	HapMap	G	0.018	A	0.982	G/A
CEU	rs2075193	2	102484459	0.232	0.898	HapMap	HapMap	G	0.27	A	0.73	G/A
JPT	rs2075193	2	102484459	0.102	0.604	HapMap	HapMap	G	0.605	A	0.395	G/A
LWK	rs2075193	2	102484459	0.129	1	HapMap	HapMap	G	0.039	A	0.961	G/A
ASW	rs2075193	2	102484459	0.063	1	HapMap	HapMap	G	0.019	A	0.981	G/A
GIH	rs2080315	2	102470720	0.01	1	HapMap	HapMap	G	0.966	T	0.034	G/T
MEX	rs2080315	2	102470720	0.017	1	HapMap	HapMap	G	0.96	T	0.04	G/T
CHB	rs2080315	2	102470720	0.016	0.859	HapMap	HapMap	G	0.893	T	0.107	G/T
CHD	rs2080315	2	102470720	0.007	0.81	HapMap	HapMap	G	0.924	T	0.076	G/T
CEU	rs2080315	2	102470720	0.047	1	HapMap	HapMap	G	0.934	T	0.066	G/T
CEU	rs2110661	2	102229653	0.345	0.774	HapMap	HapMap	G	0.588	A	0.412	G/A
CHB	rs2110661	2	102229653	0.211	0.836	HapMap	HapMap	G	0.315	A	0.685	G/A
CHD	rs2110661	2	102229653	0.281	0.911	HapMap	HapMap	G	0.274	A	0.726	G/A
GIH	rs2110661	2	102229653	0.427	0.949	HapMap	HapMap	G	0.362	A	0.638	G/A
JPT	rs2110661	2	102229653	0.144	0.665	HapMap	HapMap	G	0.36	A	0.64	G/A
MEX	rs2110661	2	102229653	0.091	0.628	HapMap	HapMap	G	0.622	A	0.378	G/A
ASW	rs2110726	2	102160714	0.067	0.635	HapMap	HapMap	G	0.934	A	0.066	G/A
LWK	rs2110726	2	102160714	0.076	0.77	HapMap	HapMap	G	0.961	A	0.039	G/A
YRI	rs2110726	2	102160714	0.071	1	HapMap	HapMap	G	0.982	A	0.018	G/A
CEU	rs2141781	2	102449338	0.337	0.656	HapMap	HapMap	G	0.655	A	0.345	G/A
GIH	rs2141781	2	102449338	0.319	0.685	HapMap	HapMap	G	0.847	A	0.153	G/A
MEX	rs2141781	2	102449338	0.209	0.671	HapMap	HapMap	G	0.86	A	0.14	G/A
MKK	rs2160203	2	102327256	0.442	0.974	HapMap	HapMap	A	0.608	G	0.392	A/G
YRI	rs2160203	2	102327256	0.307	0.917	HapMap	HapMap	A	0.482	G	0.518	A/G
ASW	rs2160203	2	102327256	0.401	1	HapMap	HapMap	A	0.519	G	0.481	A/G
CEU	rs2160203	2	102327256	0.406	1	HapMap	HapMap	A	0.757	G	0.243	A/G
CHB	rs2160203	2	102327256	0.632	1	HapMap	HapMap	A	0.905	G	0.095	A/G
CHD	rs2160203	2	102327256	0.713	1	HapMap	HapMap	A	0.918	G	0.082	A/G
GIH	rs2160203	2	102327256	0.401	1	HapMap	HapMap	A	0.903	G	0.097	A/G

JPT	rs2160203	2	102327256	0.737	1	HapMap	HapMap	A	0.875	G	0.125	A/G
LWK	rs2160203	2	102327256	0.219	1	HapMap	HapMap	A	0.589	G	0.411	A/G
MEX	rs2160203	2	102327256	0.687	1	HapMap	HapMap	A	0.8	G	0.2	A/G
CEU	rs2192752	2	102135805	0.112	0.732	HapMap	HapMap	G	0.23	T	0.77	G/T
JPT	rs2192752	2	102135805	0.03	1	HapMap	HapMap	G	0.105	T	0.895	G/T
MKK	rs2192752	2	102135805	0.106	0.793	HapMap	HapMap	G	0.108	T	0.892	G/T
ASW	rs2241116	2	102369697	0.202	1	HapMap	HapMap	C	0.915	A	0.085	C/A
CEU	rs2241116	2	102369697	0.233	1	HapMap	HapMap	C	0.779	A	0.221	C/A
CHD	rs2241116	2	102369697	0.036	1	HapMap	HapMap	C	0.776	A	0.224	C/A
GIH	rs2241116	2	102369697	0.089	1	HapMap	HapMap	C	0.744	A	0.256	C/A
JPT	rs2241116	2	102369697	0.062	1	HapMap	HapMap	C	0.808	A	0.192	C/A
MEX	rs2241116	2	102369697	0.053	0.766	HapMap	HapMap	C	0.8	A	0.2	C/A
MKK	rs2241116	2	102369697	0.02	0.704	HapMap	HapMap	C	0.972	A	0.028	C/A
YRI	rs2241116	2	102369697	0.121	0.688	HapMap	HapMap	C	0.938	A	0.062	C/A
LWK	rs2241116	2	102369697	0.037	1	HapMap	HapMap	C	0.989	A	0.011	C/A
ASW	rs2241130	2	102202138	0.085	0.794	HapMap	HapMap	T	0.783	C	0.217	T/C
LWK	rs2241130	2	102202138	0.075	1	HapMap	HapMap	T	0.809	C	0.191	T/C
MEX	rs2241130	2	102202138	0.118	0.845	HapMap	HapMap	T	0.684	C	0.316	T/C
MKK	rs2241130	2	102202138	0.13	0.766	HapMap	HapMap	T	0.766	C	0.234	T/C
JPT	rs2272128	2	102406361	0.105	1	HapMap	HapMap	G	0.413	A	0.587	G/A
ASW	rs2272128	2	102406361	0.022	1	HapMap	HapMap	G	0.057	A	0.943	G/A
CEU	rs2272128	2	102406361	0.209	1	HapMap	HapMap	G	0.204	A	0.796	G/A
CHB	rs2272128	2	102406361	0.141	1	HapMap	HapMap	G	0.476	A	0.524	G/A
CHD	rs2272128	2	102406361	0.129	1	HapMap	HapMap	G	0.506	A	0.494	G/A
GIH	rs2272128	2	102406361	0.149	0.816	HapMap	HapMap	G	0.449	A	0.551	G/A
MEX	rs2272128	2	102406361	0.333	1	HapMap	HapMap	G	0.46	A	0.54	G/A
MKK	rs2272128	2	102406361	0.113	0.652	HapMap	HapMap	G	0.171	A	0.829	G/A
CEU	rs2287033	2	102377669	0.754	1	HapMap	HapMap	T	0.487	C	0.513	T/C
CHB	rs2287033	2	102377669	0.564	0.892	HapMap	HapMap	T	0.833	C	0.167	T/C
CHD	rs2287033	2	102377669	0.615	0.874	HapMap	HapMap	T	0.865	C	0.135	T/C
GIH	rs2287033	2	102377669	0.703	0.924	HapMap	HapMap	T	0.756	C	0.244	T/C
JPT	rs2287033	2	102377669	0.85	1	HapMap	HapMap	T	0.831	C	0.169	T/C
MEX	rs2287033	2	102377669	0.709	0.939	HapMap	HapMap	T	0.68	C	0.32	T/C
MKK	rs2287033	2	102377669	0.274	0.729	HapMap	HapMap	T	0.271	C	0.729	T/C

ASW	rs2287034	2	102377020	0.279	1	HapMap	HapMap	C	0.896	A	0.104	C/A
CEU	rs2287034	2	102377020	0.301	1	HapMap	HapMap	C	0.721	A	0.279	C/A
YRI	rs2287034	2	102377020	0.171	0.74	HapMap	HapMap	C	0.916	A	0.084	C/A
CHB	rs2287034	2	102377020	0.038	0.642	HapMap	HapMap	C	0.637	A	0.363	C/A
CHD	rs2287034	2	102377020	0.067	1	HapMap	HapMap	C	0.643	A	0.357	C/A
GIH	rs2287034	2	102377020	0.112	1	HapMap	HapMap	C	0.699	A	0.301	C/A
JPT	rs2287034	2	102377020	0.173	1	HapMap	HapMap	C	0.581	A	0.419	C/A
LWK	rs2287034	2	102377020	0.148	1	HapMap	HapMap	C	0.956	A	0.044	C/A
MEX	rs2287034	2	102377020	0.059	0.78	HapMap	HapMap	C	0.78	A	0.22	C/A
MKK	rs2287034	2	102377020	0.111	0.895	HapMap	HapMap	C	0.909	A	0.091	C/A
ASW	rs2287035	2	102376962	0.279	1	HapMap	HapMap	G	0.896	A	0.104	G/A
GIH	rs2287035	2	102376962	0.112	1	HapMap	HapMap	G	0.699	A	0.301	G/A
JPT	rs2287035	2	102376962	0.173	1	HapMap	HapMap	G	0.581	A	0.419	G/A
CEU	rs2287035	2	102376962	0.301	1	HapMap	HapMap	G	0.721	A	0.279	G/A
CHB	rs2287035	2	102376962	0.038	0.642	HapMap	HapMap	G	0.637	A	0.363	G/A
CHD	rs2287035	2	102376962	0.041	0.76	HapMap	HapMap	G	0.641	A	0.359	G/A
LWK	rs2287035	2	102376962	0.129	1	HapMap	HapMap	G	0.961	A	0.039	G/A
MEX	rs2287035	2	102376962	0.059	0.78	HapMap	HapMap	G	0.776	A	0.224	G/A
MKK	rs2287035	2	102376962	0.071	0.847	HapMap	HapMap	G	0.934	A	0.066	G/A
YRI	rs2287035	2	102376962	0.143	0.711	HapMap	HapMap	G	0.92	A	0.08	G/A
ASW	rs2287037	2	102345460	0.87	1	HapMap	HapMap	C	0.712	T	0.288	C/T
CEU	rs2287037	2	102345460	0.414	1	HapMap	HapMap	C	0.611	T	0.389	C/T
CHB	rs2287037	2	102345460	0.117	1	HapMap	HapMap	C	0.607	T	0.393	C/T
CHD	rs2287037	2	102345460	0.076	1	HapMap	HapMap	C	0.624	T	0.376	C/T
GIH	rs2287037	2	102345460	0.135	1	HapMap	HapMap	C	0.659	T	0.341	C/T
JPT	rs2287037	2	102345460	0.191	1	HapMap	HapMap	C	0.564	T	0.436	C/T
LWK	rs2287037	2	102345460	0.85	0.966	HapMap	HapMap	C	0.778	T	0.222	C/T
MKK	rs2287037	2	102345460	0.677	1	HapMap	HapMap	C	0.671	T	0.329	C/T
YRI	rs2287037	2	102345460	0.78	0.948	HapMap	HapMap	C	0.782	T	0.218	C/T
MEX	rs2287041	2	102219298	0.118	0.848	HapMap	HapMap	G	0.69	T	0.31	G/T
CEU	rs2287047	2	102140486	0.133	0.624	HapMap	HapMap	G	0.77	A	0.23	G/A
CHB	rs2287047	2	102140486	0.111	1	HapMap	HapMap	G	0.59	A	0.41	G/A
CHB	rs2287049	2	102137170	0.111	1	HapMap	HapMap	A	0.583	G	0.417	A/G
ASW	rs2293223	2	102401900	0.119	0.699	HapMap	HapMap	C	0.689	T	0.311	C/T

CEU	rs2293223	2	102401900	0.193	1	HapMap	HapMap	C	0.836	T	0.164	C/T
CHB	rs2293223	2	102401900	0.632	1	HapMap	HapMap	C	0.905	T	0.095	C/T
CHD	rs2293223	2	102401900	0.655	0.923	HapMap	HapMap	C	0.912	T	0.088	C/T
JPT	rs2293223	2	102401900	0.753	1	HapMap	HapMap	C	0.872	T	0.128	C/T
LWK	rs2293223	2	102401900	0.068	0.649	HapMap	HapMap	C	0.661	T	0.339	C/T
MEX	rs2293223	2	102401900	0.361	0.812	HapMap	HapMap	C	0.816	T	0.184	C/T
ASW	rs2293225	2	102402321	0.202	1	HapMap	HapMap	C	0.915	T	0.085	C/T
LWK	rs2293225	2	102402321	0.018	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MKK	rs2293225	2	102402321	0.02	0.704	HapMap	HapMap	C	0.972	T	0.028	C/T
YRI	rs2293225	2	102402321	0.121	0.688	HapMap	HapMap	C	0.938	T	0.062	C/T
CEU	rs2293225	2	102402321	0.233	1	HapMap	HapMap	C	0.779	T	0.221	C/T
CHD	rs2293225	2	102402321	0.036	1	HapMap	HapMap	C	0.776	T	0.224	C/T
GIH	rs2293225	2	102402321	0.089	1	HapMap	HapMap	C	0.744	T	0.256	C/T
JPT	rs2293225	2	102402321	0.062	1	HapMap	HapMap	C	0.808	T	0.192	C/T
MEX	rs2293225	2	102402321	0.053	0.766	HapMap	HapMap	C	0.8	T	0.2	C/T
GIH	rs2302612	2	102218140	0.015	0.606	HapMap	HapMap	T	0.869	C	0.131	T/C
MEX	rs2302612	2	102218140	0.085	0.607	HapMap	HapMap	T	0.61	C	0.39	T/C
ASW	rs2302620	2	102208899	0.085	0.794	HapMap	HapMap	T	0.783	C	0.217	T/C
LWK	rs2302620	2	102208899	0.055	1	HapMap	HapMap	T	0.85	C	0.15	T/C
MEX	rs2302620	2	102208899	0.118	0.848	HapMap	HapMap	T	0.69	C	0.31	T/C
MKK	rs2302620	2	102208899	0.148	0.87	HapMap	HapMap	T	0.787	C	0.213	T/C
ASW	rs2310300	2	102415506	0.358	0.778	HapMap	HapMap	A	0.208	G	0.792	A/G
GIH	rs2310300	2	102415506	0.674	0.921	HapMap	HapMap	A	0.753	G	0.247	A/G
JPT	rs2310300	2	102415506	0.85	1	HapMap	HapMap	A	0.831	G	0.169	A/G
MEX	rs2310300	2	102415506	0.709	0.939	HapMap	HapMap	A	0.68	G	0.32	A/G
MKK	rs2310300	2	102415506	0.223	0.699	HapMap	HapMap	A	0.248	G	0.752	A/G
CEU	rs2310300	2	102415506	0.759	1	HapMap	HapMap	A	0.482	G	0.518	A/G
CHB	rs2310300	2	102415506	0.564	0.892	HapMap	HapMap	A	0.833	G	0.167	A/G
CHD	rs2310300	2	102415506	0.615	0.874	HapMap	HapMap	A	0.865	G	0.135	A/G
CHB	rs2310303	2	102470311	0.142	0.667	HapMap	HapMap	A	0.655	G	0.345	A/G
CHD	rs2310303	2	102470311	0.123	0.683	HapMap	HapMap	A	0.676	G	0.324	A/G
CEU	rs28362304	2	102157518	0.017	1	HapMap	HapMap	C	0.991	T	0.009	C/T
GIH	rs28362304	2	102157518	0.03	1	HapMap	HapMap	C	0.901	T	0.099	C/T
MKK	rs28362304	2	102157518	0.015	1	HapMap	HapMap	C	0.99	T	0.01	C/T

YRI	rs28362304	2	102157518	0.077	1	HapMap	HapMap	C	0.981	T	0.019	C/T
YRI	rs28634469	2	102382598	0.038	0.729	HapMap	HapMap	C	0.819	T	0.181	C/T
MKK	rs28634469	2	102382598	0.041	1	HapMap	HapMap	C	0.947	T	0.053	C/T
ASW	rs28634469	2	102382598	0.055	1	HapMap	HapMap	C	0.906	T	0.094	C/T
LWK	rs28634469	2	102382598	0.063	1	HapMap	HapMap	C	0.833	T	0.167	C/T
GIH	rs3171845	2	102157813	0.021	1	HapMap	HapMap	G	0.994	A	0.006	G/A
LWK	rs3171845	2	102157813	0.099	1	HapMap	HapMap	G	0.761	A	0.239	G/A
MEX	rs3171845	2	102157813	0.128	1	HapMap	HapMap	G	0.96	A	0.04	G/A
MKK	rs3171845	2	102157813	0.061	0.665	HapMap	HapMap	G	0.839	A	0.161	G/A
CHB	rs3213733	2	102364316	0.632	1	HapMap	HapMap	C	0.905	A	0.095	C/A
CHD	rs3213733	2	102364316	0.713	1	HapMap	HapMap	C	0.918	A	0.082	C/A
CEU	rs3213733	2	102364316	0.193	1	HapMap	HapMap	C	0.841	A	0.159	C/A
ASW	rs3213733	2	102364316	0.086	0.636	HapMap	HapMap	C	0.708	A	0.292	C/A
GIH	rs3213733	2	102364316	0.25	0.816	HapMap	HapMap	C	0.908	A	0.092	C/A
JPT	rs3213733	2	102364316	0.753	1	HapMap	HapMap	C	0.872	A	0.128	C/A
LWK	rs3213733	2	102364316	0.074	0.666	HapMap	HapMap	C	0.657	A	0.343	C/A
MEX	rs3213733	2	102364316	0.364	0.813	HapMap	HapMap	C	0.82	A	0.18	C/A
ASW	rs3213734	2	102175115	0.085	0.794	HapMap	HapMap	G	0.783	A	0.217	G/A
LWK	rs3213734	2	102175115	0.052	1	HapMap	HapMap	G	0.858	A	0.142	G/A
MEX	rs3213734	2	102175115	0.132	0.851	HapMap	HapMap	G	0.67	A	0.33	G/A
MKK	rs3213734	2	102175115	0.131	0.808	HapMap	HapMap	G	0.783	A	0.217	G/A
CHB	rs3213736	2	102151574	0.056	1	HapMap	HapMap	G	0.78	C	0.22	G/C
CEU	rs3732123	2	102384509	0.301	1	HapMap	HapMap	C	0.721	G	0.279	C/G
CHD	rs3732123	2	102384509	0.043	0.766	HapMap	HapMap	C	0.637	G	0.363	C/G
MKK	rs3732123	2	102384509	0.087	0.87	HapMap	HapMap	C	0.923	G	0.077	C/G
ASW	rs3732123	2	102384509	0.448	1	HapMap	HapMap	C	0.83	G	0.17	C/G
CHB	rs3732123	2	102384509	0.033	0.62	HapMap	HapMap	C	0.643	G	0.357	C/G
GIH	rs3732123	2	102384509	0.112	1	HapMap	HapMap	C	0.699	G	0.301	C/G
JPT	rs3732123	2	102384509	0.173	1	HapMap	HapMap	C	0.581	G	0.419	C/G
LWK	rs3732123	2	102384509	0.228	1	HapMap	HapMap	C	0.933	G	0.067	C/G
MEX	rs3732123	2	102384509	0.059	0.78	HapMap	HapMap	C	0.78	G	0.22	C/G
ASW	rs3732124	2	102384484	0.358	0.778	HapMap	HapMap	C	0.226	T	0.774	C/T
CEU	rs3732124	2	102384484	0.759	1	HapMap	HapMap	C	0.482	T	0.518	C/T
CHB	rs3732124	2	102384484	0.564	0.892	HapMap	HapMap	C	0.825	T	0.175	C/T

CHD	rs3732124	2	102384484	0.614	0.874	HapMap	HapMap	C	0.863	T	0.137	C/T
GIH	rs3732124	2	102384484	0.703	0.924	HapMap	HapMap	C	0.756	T	0.244	C/T
JPT	rs3732124	2	102384484	0.85	1	HapMap	HapMap	C	0.831	T	0.169	C/T
MEX	rs3732124	2	102384484	0.709	0.939	HapMap	HapMap	C	0.68	T	0.32	C/T
MKK	rs3732124	2	102384484	0.231	0.705	HapMap	HapMap	C	0.252	T	0.748	C/T
ASW	rs3732126	2	102380394	0.279	1	HapMap	HapMap	A	0.896	C	0.104	A/C
CHB	rs3732126	2	102380394	0.038	0.642	HapMap	HapMap	A	0.637	C	0.363	A/C
CHD	rs3732126	2	102380394	0.041	0.76	HapMap	HapMap	A	0.641	C	0.359	A/C
GIH	rs3732126	2	102380394	0.112	1	HapMap	HapMap	A	0.699	C	0.301	A/C
MKK	rs3732126	2	102380394	0.052	0.821	HapMap	HapMap	A	0.948	C	0.052	A/C
YRI	rs3732126	2	102380394	0.143	0.711	HapMap	HapMap	A	0.92	C	0.08	A/C
MEX	rs3732126	2	102380394	0.059	0.78	HapMap	HapMap	A	0.78	C	0.22	A/C
CEU	rs3732126	2	102380394	0.301	1	HapMap	HapMap	A	0.721	C	0.279	A/C
JPT	rs3732126	2	102380394	0.173	1	HapMap	HapMap	A	0.581	C	0.419	A/C
LWK	rs3732126	2	102380394	0.072	1	HapMap	HapMap	A	0.978	C	0.022	A/C
CEU	rs3732131	2	102161035	0.023	1	HapMap	HapMap	A	0.951	G	0.049	A/G
LWK	rs3732131	2	102161035	0.06	1	HapMap	HapMap	A	0.839	G	0.161	A/G
MEX	rs3732131	2	102161035	0.123	0.844	HapMap	HapMap	A	0.68	G	0.32	A/G
MKK	rs3732131	2	102161035	0.101	0.767	HapMap	HapMap	A	0.808	G	0.192	A/G
CHD	rs3732134	2	102160649	0.026	1	HapMap	HapMap	C	0.833	G	0.167	C/G
GIH	rs3732134	2	102160649	0.031	1	HapMap	HapMap	C	0.898	G	0.102	C/G
JPT	rs3732134	2	102160649	0.051	1	HapMap	HapMap	C	0.797	G	0.203	C/G
MEX	rs3732134	2	102160649	0.032	1	HapMap	HapMap	C	0.918	G	0.082	C/G
MKK	rs3732134	2	102160649	0.005	1	HapMap	HapMap	C	0.993	G	0.007	C/G
CHD	rs3755266	2	102409144	0.615	0.874	HapMap	HapMap	G	0.865	A	0.135	G/A
GIH	rs3755266	2	102409144	0.68	0.923	HapMap	HapMap	G	0.75	A	0.25	G/A
MEX	rs3755266	2	102409144	0.709	0.939	HapMap	HapMap	G	0.68	A	0.32	G/A
MKK	rs3755266	2	102409144	0.223	0.696	HapMap	HapMap	G	0.246	A	0.754	G/A
ASW	rs3755266	2	102409144	0.358	0.778	HapMap	HapMap	G	0.208	A	0.792	G/A
CEU	rs3755266	2	102409144	0.759	1	HapMap	HapMap	G	0.482	A	0.518	G/A
CHB	rs3755266	2	102409144	0.564	0.892	HapMap	HapMap	G	0.833	A	0.167	G/A
JPT	rs3755266	2	102409144	0.85	1	HapMap	HapMap	G	0.831	A	0.169	G/A
CHB	rs3755267	2	102405019	0.141	1	HapMap	HapMap	T	0.476	G	0.524	T/G
CHD	rs3755267	2	102405019	0.131	1	HapMap	HapMap	T	0.518	G	0.482	T/G

GIH	rs3755267	2	102405019	0.149	0.816	HapMap	HapMap	T	0.449	G	0.551	T/G
JPT	rs3755267	2	102405019	0.105	1	HapMap	HapMap	T	0.411	G	0.589	T/G
CEU	rs3755267	2	102405019	0.209	1	HapMap	HapMap	T	0.218	G	0.782	T/G
MEX	rs3755267	2	102405019	0.342	1	HapMap	HapMap	T	0.458	G	0.542	T/G
ASW	rs3755267	2	102405019	0.022	1	HapMap	HapMap	T	0.057	G	0.943	T/G
CHB	rs3755276	2	102344891	1	1	HapMap	HapMap	C	0.857	T	0.143	C/T
ASW	rs3755276	2	102344891	0.877	1	HapMap	HapMap	C	0.349	T	0.651	C/T
CEU	rs3755276	2	102344891	1	1	HapMap	HapMap	C	0.593	T	0.407	C/T
CHD	rs3755276	2	102344891	1	1	HapMap	HapMap	C	0.887	T	0.113	C/T
GIH	rs3755276	2	102344891	1	1	HapMap	HapMap	C	0.79	T	0.21	C/T
JPT	rs3755276	2	102344891	1	1	HapMap	HapMap	C	0.849	T	0.151	C/T
LWK	rs3755276	2	102344891	0.555	1	HapMap	HapMap	C	0.361	T	0.639	C/T
MKK	rs3755276	2	102344891	0.855	1	HapMap	HapMap	C	0.458	T	0.542	C/T
YRI	rs3755276	2	102344891	0.916	1	HapMap	HapMap	C	0.265	T	0.735	C/T
ASW	rs3755287	2	102206288	0.085	0.794	HapMap	HapMap	G	0.783	A	0.217	G/A
LWK	rs3755287	2	102206288	0.075	1	HapMap	HapMap	G	0.812	A	0.188	G/A
MEX	rs3755287	2	102206288	0.118	0.845	HapMap	HapMap	G	0.684	A	0.316	G/A
MKK	rs3755287	2	102206288	0.135	0.773	HapMap	HapMap	G	0.762	A	0.238	G/A
CHD	rs3771150	2	102427283	0.041	0.76	HapMap	HapMap	G	0.641	A	0.359	G/A
GIH	rs3771150	2	102427283	0.115	1	HapMap	HapMap	G	0.693	A	0.307	G/A
JPT	rs3771150	2	102427283	0.173	1	HapMap	HapMap	G	0.581	A	0.419	G/A
LWK	rs3771150	2	102427283	0.11	1	HapMap	HapMap	G	0.966	A	0.034	G/A
MEX	rs3771150	2	102427283	0.071	0.804	HapMap	HapMap	G	0.76	A	0.24	G/A
ASW	rs3771150	2	102427283	0.279	1	HapMap	HapMap	G	0.896	A	0.104	G/A
CHB	rs3771150	2	102427283	0.033	0.62	HapMap	HapMap	G	0.643	A	0.357	G/A
MKK	rs3771150	2	102427283	0.039	0.769	HapMap	HapMap	G	0.955	A	0.045	G/A
CEU	rs3771150	2	102427283	0.301	1	HapMap	HapMap	G	0.721	A	0.279	G/A
YRI	rs3771150	2	102427283	0.143	0.711	HapMap	HapMap	G	0.92	A	0.08	G/A
GIH	rs3771157	2	102379864	0.013	1	HapMap	HapMap	C	0.955	A	0.045	C/A
LWK	rs3771157	2	102379864	0.018	1	HapMap	HapMap	C	0.994	A	0.006	C/A
MEX	rs3771157	2	102379864	0.04	1	HapMap	HapMap	C	0.9	A	0.1	C/A
MKK	rs3771157	2	102379864	0.008	0.896	HapMap	HapMap	C	0.986	A	0.014	C/A
ASW	rs3771157	2	102379864	0.066	1	HapMap	HapMap	C	0.972	A	0.028	C/A
CEU	rs3771157	2	102379864	0.031	1	HapMap	HapMap	C	0.965	A	0.035	C/A

CHD	rs3771157	2	102379864	0.031	1	HapMap	HapMap	C	0.8	A	0.2	C/A
JPT	rs3771157	2	102379864	0.04	1	HapMap	HapMap	C	0.86	A	0.14	C/A
ASW	rs3771158	2	102376326	0.119	0.699	HapMap	HapMap	A	0.689	G	0.311	A/G
CEU	rs3771158	2	102376326	0.193	1	HapMap	HapMap	A	0.841	G	0.159	A/G
CHB	rs3771158	2	102376326	0.632	1	HapMap	HapMap	A	0.905	G	0.095	A/G
LWK	rs3771158	2	102376326	0.068	0.649	HapMap	HapMap	A	0.661	G	0.339	A/G
MEX	rs3771158	2	102376326	0.343	0.801	HapMap	HapMap	A	0.827	G	0.173	A/G
CHD	rs3771158	2	102376326	0.713	1	HapMap	HapMap	A	0.917	G	0.083	A/G
GIH	rs3771158	2	102376326	0.234	0.805	HapMap	HapMap	A	0.914	G	0.086	A/G
JPT	rs3771158	2	102376326	0.753	1	HapMap	HapMap	A	0.872	G	0.128	A/G
CHD	rs3771161	2	102370393	0.713	1	HapMap	HapMap	C	0.918	A	0.082	C/A
GIH	rs3771161	2	102370393	0.25	0.816	HapMap	HapMap	C	0.909	A	0.091	C/A
JPT	rs3771161	2	102370393	0.753	1	HapMap	HapMap	C	0.866	A	0.134	C/A
ASW	rs3771161	2	102370393	0.107	0.67	HapMap	HapMap	C	0.679	A	0.321	C/A
CEU	rs3771161	2	102370393	0.198	1	HapMap	HapMap	C	0.839	A	0.161	C/A
CHB	rs3771161	2	102370393	0.632	1	HapMap	HapMap	C	0.904	A	0.096	C/A
LWK	rs3771161	2	102370393	0.067	0.644	HapMap	HapMap	C	0.663	A	0.337	C/A
MEX	rs3771161	2	102370393	0.364	0.813	HapMap	HapMap	C	0.816	A	0.184	C/A
ASW	rs3771166	2	102352654	0.877	1	HapMap	HapMap	G	0.349	A	0.651	G/A
CEU	rs3771166	2	102352654	1	1	HapMap	HapMap	G	0.593	A	0.407	G/A
CHB	rs3771166	2	102352654	1	1	HapMap	HapMap	G	0.857	A	0.143	G/A
CHD	rs3771166	2	102352654	1	1	HapMap	HapMap	G	0.888	A	0.112	G/A
GIH	rs3771166	2	102352654	1	1	HapMap	HapMap	G	0.79	A	0.21	G/A
JPT	rs3771166	2	102352654	1	1	HapMap	HapMap	G	0.849	A	0.151	G/A
LWK	rs3771166	2	102352654	0.55	1	HapMap	HapMap	G	0.36	A	0.64	G/A
MEX	rs3771166	2	102352654	1	1	HapMap	HapMap	G	0.73	A	0.27	G/A
MKK	rs3771166	2	102352654	0.855	1	HapMap	HapMap	G	0.458	A	0.542	G/A
YRI	rs3771166	2	102352654	0.916	1	HapMap	HapMap	G	0.265	A	0.735	G/A
LWK	rs3771175	2	102326642	0.093	1	HapMap	HapMap	T	0.772	A	0.228	T/A
MEX	rs3771175	2	102326642	0.423	1	HapMap	HapMap	T	0.86	A	0.14	T/A
MKK	rs3771175	2	102326642	0.296	1	HapMap	HapMap	T	0.71	A	0.29	T/A
YRI	rs3771175	2	102326642	0.216	1	HapMap	HapMap	T	0.664	A	0.336	T/A
ASW	rs3771175	2	102326642	0.214	1	HapMap	HapMap	T	0.726	A	0.274	T/A
CEU	rs3771175	2	102326642	0.159	1	HapMap	HapMap	T	0.876	A	0.124	T/A

CHB	rs3771175	2	102326642	0.462	1	HapMap	HapMap	T	0.917	A	0.083	T/A
CHD	rs3771175	2	102326642	0.658	1	HapMap	HapMap	T	0.924	A	0.076	T/A
GIH	rs3771175	2	102326642	0.375	1	HapMap	HapMap	T	0.909	A	0.091	T/A
JPT	rs3771175	2	102326642	0.753	1	HapMap	HapMap	T	0.866	A	0.134	T/A
ASW	rs3771179	2	102320324	0.24	1	HapMap	HapMap	T	0.877	G	0.123	T/G
CEU	rs3771179	2	102320324	0.015	1	HapMap	HapMap	T	0.929	G	0.071	T/G
CHD	rs3771179	2	102320324	0.002	0.614	HapMap	HapMap	T	0.965	G	0.035	T/G
GIH	rs3771179	2	102320324	0.018	1	HapMap	HapMap	T	0.938	G	0.062	T/G
LWK	rs3771179	2	102320324	0.398	1	HapMap	HapMap	T	0.889	G	0.111	T/G
MEX	rs3771179	2	102320324	0.021	1	HapMap	HapMap	T	0.94	G	0.06	T/G
MKK	rs3771179	2	102320324	0.393	1	HapMap	HapMap	T	0.782	G	0.218	T/G
YRI	rs3771179	2	102320324	0.227	1	HapMap	HapMap	T	0.933	G	0.067	T/G
ASW	rs3771180	2	102320049	0.214	1	HapMap	HapMap	G	0.726	T	0.274	G/T
CEU	rs3771180	2	102320049	0.176	1	HapMap	HapMap	G	0.872	T	0.128	G/T
CHB	rs3771180	2	102320049	0.538	0.864	HapMap	HapMap	G	0.899	T	0.101	G/T
CHD	rs3771180	2	102320049	0.655	0.923	HapMap	HapMap	G	0.912	T	0.088	G/T
GIH	rs3771180	2	102320049	0.401	1	HapMap	HapMap	G	0.903	T	0.097	G/T
JPT	rs3771180	2	102320049	0.753	1	HapMap	HapMap	G	0.867	T	0.133	G/T
LWK	rs3771180	2	102320049	0.093	1	HapMap	HapMap	G	0.772	T	0.228	G/T
MEX	rs3771180	2	102320049	0.369	0.892	HapMap	HapMap	G	0.84	T	0.16	G/T
MKK	rs3771180	2	102320049	0.296	1	HapMap	HapMap	G	0.71	T	0.29	G/T
YRI	rs3771180	2	102320049	0.216	1	HapMap	HapMap	G	0.664	T	0.336	G/T
LWK	rs3771184	2	102209384	0.076	1	HapMap	HapMap	G	0.806	A	0.194	G/A
MKK	rs3771184	2	102209384	0.132	0.769	HapMap	HapMap	G	0.766	A	0.234	G/A
ASW	rs3771188	2	102206780	0.085	0.794	HapMap	HapMap	T	0.783	C	0.217	T/C
LWK	rs3771188	2	102206780	0.073	1	HapMap	HapMap	T	0.811	C	0.189	T/C
MEX	rs3771188	2	102206780	0.118	0.848	HapMap	HapMap	T	0.69	C	0.31	T/C
MKK	rs3771188	2	102206780	0.132	0.772	HapMap	HapMap	T	0.766	C	0.234	T/C
CHB	rs3771200	2	102155206	0.047	0.603	HapMap	HapMap	G	0.542	A	0.458	G/A
CHD	rs3917225	2	102135734	0.045	0.861	HapMap	HapMap	A	0.676	G	0.324	A/G
YRI	rs3917225	2	102135734	0.047	1	HapMap	HapMap	A	0.969	G	0.031	A/G
ASW	rs3917232	2	102137838	0.014	1	HapMap	HapMap	C	0.981	T	0.019	C/T
LWK	rs3917232	2	102137838	0.013	1	HapMap	HapMap	C	0.961	T	0.039	C/T
MKK	rs3917232	2	102137838	0.005	1	HapMap	HapMap	C	0.993	T	0.007	C/T

YRI	rs3917232	2	102137838	0.023	1	HapMap	HapMap	C	0.973	T	0.027	C/T
ASW	rs3917234	2	102138227	0.031	1	HapMap	HapMap	G	0.981	A	0.019	G/A
YRI	rs3917235	2	102138283	0.004	1	HapMap	HapMap	A	0.996	G	0.004	A/G
LWK	rs3917249	2	102141882	0.058	1	HapMap	HapMap	G	0.844	A	0.156	G/A
MEX	rs3917249	2	102141882	0	1	HapMap	HapMap	G	0.99	A	0.01	G/A
GIH	rs3917254	2	102142950	0.031	0.618	HapMap	HapMap	G	0.773	A	0.227	G/A
ASW	rs3917285	2	102147598	0.007	1	HapMap	HapMap	T	0.991	A	0.009	T/A
CEU	rs3917285	2	102147598	0.112	1	HapMap	HapMap	T	0.92	A	0.08	T/A
GIH	rs3917285	2	102147598	0.046	1	HapMap	HapMap	T	0.989	A	0.011	T/A
LWK	rs3917285	2	102147598	0.002	1	HapMap	HapMap	T	0.994	A	0.006	T/A
MEX	rs3917285	2	102147598	0.267	1	HapMap	HapMap	T	0.908	A	0.092	T/A
CEU	rs3917286	2	102148061	0.008	1	HapMap	HapMap	G	0.991	A	0.009	G/A
GIH	rs3917286	2	102148061	0.029	1	HapMap	HapMap	G	0.902	A	0.098	G/A
LWK	rs3917286	2	102148061	0.018	1	HapMap	HapMap	G	0.994	A	0.006	G/A
MEX	rs3917286	2	102148061	0.004	1	HapMap	HapMap	G	0.99	A	0.01	G/A
MKK	rs3917286	2	102148061	0.015	1	HapMap	HapMap	G	0.989	A	0.011	G/A
YRI	rs3917286	2	102148061	0.047	1	HapMap	HapMap	G	0.987	A	0.013	G/A
CHB	rs3917288	2	102148288	0.073	1	HapMap	HapMap	T	0.97	G	0.03	T/G
CHD	rs3917289	2	102148343	0.001	1	HapMap	HapMap	G	0.994	T	0.006	G/T
GIH	rs3917289	2	102148343	0.022	1	HapMap	HapMap	G	0.994	T	0.006	G/T
JPT	rs3917289	2	102148343	0.003	1	HapMap	HapMap	G	0.994	T	0.006	G/T
LWK	rs3917289	2	102148343	0.098	1	HapMap	HapMap	G	0.756	T	0.244	G/T
MEX	rs3917289	2	102148343	0.081	0.706	HapMap	HapMap	G	0.95	T	0.05	G/T
MKK	rs3917289	2	102148343	0.062	0.655	HapMap	HapMap	G	0.83	T	0.17	G/T
ASW	rs3917292	2	102149484	0.031	1	HapMap	HapMap	G	0.991	A	0.009	G/A
GIH	rs3917292	2	102149484	0.008	1	HapMap	HapMap	G	0.971	A	0.029	G/A
MEX	rs3917292	2	102149484	0.013	1	HapMap	HapMap	G	0.969	A	0.031	G/A
MKK	rs3917292	2	102149484	0.05	1	HapMap	HapMap	G	0.965	A	0.035	G/A
CEU	rs3917296	2	102151265	0.123	0.8	HapMap	HapMap	A	0.898	G	0.102	A/G
CHB	rs3917296	2	102151265	0.015	0.609	HapMap	HapMap	A	0.833	G	0.167	A/G
CHD	rs3917296	2	102151265	0.021	1	HapMap	HapMap	A	0.857	G	0.143	A/G
GIH	rs3917296	2	102151265	0.025	1	HapMap	HapMap	A	0.915	G	0.085	A/G
JPT	rs3917296	2	102151265	0.04	1	HapMap	HapMap	A	0.865	G	0.135	A/G
CEU	rs3917301	2	102153396	0.008	1	HapMap	HapMap	C	0.991	T	0.009	C/T

GIH	rs3917301	2	102153396	0.029	1	HapMap	HapMap	C	0.903	T	0.097	C/T
MEX	rs3917301	2	102153396	0.004	1	HapMap	HapMap	C	0.99	T	0.01	C/T
MKK	rs3917301	2	102153396	0.02	1	HapMap	HapMap	C	0.986	T	0.014	C/T
YRI	rs3917301	2	102153396	0.046	1	HapMap	HapMap	C	0.982	T	0.018	C/T
ASW	rs3917304	2	102154557	0.119	0.699	HapMap	HapMap	G	0.651	T	0.349	G/T
LWK	rs3917304	2	102154557	0.102	1	HapMap	HapMap	G	0.756	T	0.244	G/T
MKK	rs3917304	2	102154557	0.158	0.741	HapMap	HapMap	G	0.715	T	0.285	G/T
ASW	rs3917318	2	102159192	0.119	0.699	HapMap	HapMap	A	0.651	G	0.349	A/G
LWK	rs3917318	2	102159192	0.093	1	HapMap	HapMap	A	0.772	G	0.228	A/G
MKK	rs3917318	2	102159192	0.146	0.728	HapMap	HapMap	A	0.724	G	0.276	A/G
ASW	rs3917323	2	102159873	0.014	1	HapMap	HapMap	G	0.953	A	0.047	G/A
CHB	rs3917323	2	102159873	0.008	1	HapMap	HapMap	G	0.964	A	0.036	G/A
MKK	rs3917323	2	102159873	0.015	1	HapMap	HapMap	G	0.979	A	0.021	G/A
CEU	rs3917325	2	102160339	0.04	1	HapMap	HapMap	T	0.947	G	0.053	T/G
GIH	rs3917325	2	102160339	0.002	1	HapMap	HapMap	T	0.994	G	0.006	T/G
MKK	rs3917325	2	102160339	0.227	0.904	HapMap	HapMap	T	0.833	G	0.167	T/G
CEU	rs3917328	2	102160973	0.04	1	HapMap	HapMap	C	0.947	T	0.053	C/T
GIH	rs3917328	2	102160973	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MKK	rs3917328	2	102160973	0.209	0.899	HapMap	HapMap	C	0.843	T	0.157	C/T
CEU	rs3917329	2	102162295	0.045	0.684	HapMap	HapMap	G	0.929	T	0.071	G/T
GIH	rs3917329	2	102162295	0.021	1	HapMap	HapMap	G	0.994	T	0.006	G/T
LWK	rs3917329	2	102162295	0.076	1	HapMap	HapMap	G	0.806	T	0.194	G/T
MEX	rs3917329	2	102162295	0.128	1	HapMap	HapMap	G	0.96	T	0.04	G/T
MKK	rs3917329	2	102162295	0.033	0.763	HapMap	HapMap	G	0.927	T	0.073	G/T
YRI	rs3917329	2	102162295	0.016	0.645	HapMap	HapMap	G	0.934	T	0.066	G/T
CHB	rs3917332	2	102162956	0.01	1	HapMap	HapMap	A	0.043	T	0.957	A/T
GIH	rs3917332	2	102162956	0.045	1	HapMap	HapMap	A	0.142	T	0.858	A/T
ASW	rs3917335	2	102137725	0.007	1	HapMap	HapMap	C	0.991	T	0.009	C/T
GIH	rs3917335	2	102137725	0.021	1	HapMap	HapMap	C	0.994	T	0.006	C/T
LWK	rs41319148	2	102488718	0.012	0.698	HapMap	HapMap	C	0.928	G	0.072	C/G
MKK	rs41319148	2	102488718	0.018	1	HapMap	HapMap	C	0.976	G	0.024	C/G
MEX	rs41319148	2	102488718	0.008	1	HapMap	HapMap	C	0.98	G	0.02	C/G
GIH	rs41348650	2	102470631	0.01	1	HapMap	HapMap	G	0.966	A	0.034	G/A
JPT	rs41348650	2	102470631	0.005	1	HapMap	HapMap	G	0.977	A	0.023	G/A

CHD	rs41348650	2	102470631	0.002	0.614	HapMap	HapMap	G	0.965	A	0.035	G/A
MEX	rs41348650	2	102470631	0.021	1	HapMap	HapMap	G	0.95	A	0.05	G/A
CEU	rs41348650	2	102470631	0.056	1	HapMap	HapMap	G	0.925	A	0.075	G/A
ASW	rs41484147	2	102490927	0.038	1	HapMap	HapMap	C	0.915	T	0.085	C/T
LWK	rs41484147	2	102490927	0.004	0.919	HapMap	HapMap	C	0.983	T	0.017	C/T
MKK	rs41484147	2	102490927	0.014	0.639	HapMap	HapMap	C	0.976	T	0.024	C/T
YRI	rs41484147	2	102490927	0.015	1	HapMap	HapMap	C	0.951	T	0.049	C/T
CEU	rs4851003	2	102275709	0.483	0.937	HapMap	HapMap	T	0.726	C	0.274	T/C
CHB	rs4851003	2	102275709	0.073	1	HapMap	HapMap	T	0.994	C	0.006	T/C
CHD	rs4851003	2	102275709	0.047	1	HapMap	HapMap	T	0.994	C	0.006	T/C
GIH	rs4851003	2	102275709	0.405	0.87	HapMap	HapMap	T	0.875	C	0.125	T/C
MEX	rs4851003	2	102275709	0.28	0.661	HapMap	HapMap	T	0.82	C	0.18	T/C
CEU	rs4851004	2	102375969	0.755	1	HapMap	HapMap	C	0.478	T	0.522	C/T
CHB	rs4851004	2	102375969	0.562	0.891	HapMap	HapMap	C	0.831	T	0.169	C/T
ASW	rs4851004	2	102375969	0.408	0.796	HapMap	HapMap	C	0.236	T	0.764	C/T
CHD	rs4851004	2	102375969	0.614	0.874	HapMap	HapMap	C	0.863	T	0.137	C/T
GIH	rs4851004	2	102375969	0.703	0.924	HapMap	HapMap	C	0.756	T	0.244	C/T
JPT	rs4851004	2	102375969	0.85	1	HapMap	HapMap	C	0.831	T	0.169	C/T
MEX	rs4851004	2	102375969	0.709	0.939	HapMap	HapMap	C	0.68	T	0.32	C/T
MKK	rs4851004	2	102375969	0.278	0.732	HapMap	HapMap	C	0.273	T	0.727	C/T
ASW	rs4851005	2	102377984	0.219	0.829	HapMap	HapMap	C	0.858	T	0.142	C/T
CHB	rs4851005	2	102377984	0.038	0.642	HapMap	HapMap	C	0.637	T	0.363	C/T
CHD	rs4851005	2	102377984	0.041	0.76	HapMap	HapMap	C	0.641	T	0.359	C/T
GIH	rs4851005	2	102377984	0.078	0.803	HapMap	HapMap	C	0.682	T	0.318	C/T
JPT	rs4851005	2	102377984	0.173	1	HapMap	HapMap	C	0.582	T	0.418	C/T
LWK	rs4851005	2	102377984	0.04	0.667	HapMap	HapMap	C	0.972	T	0.028	C/T
MKK	rs4851005	2	102377984	0.047	0.709	HapMap	HapMap	C	0.937	T	0.063	C/T
CEU	rs4851010	2	102422559	0.337	0.656	HapMap	HapMap	A	0.646	T	0.354	A/T
GIH	rs4851010	2	102422559	0.319	0.685	HapMap	HapMap	A	0.847	T	0.153	A/T
MEX	rs4851010	2	102422559	0.209	0.671	HapMap	HapMap	A	0.86	T	0.14	A/T
ASW	rs4851011	2	102456110	0.279	1	HapMap	HapMap	C	0.896	T	0.104	C/T
CEU	rs4851011	2	102456110	0.301	1	HapMap	HapMap	C	0.712	T	0.288	C/T
CHB	rs4851011	2	102456110	0.033	0.62	HapMap	HapMap	C	0.643	T	0.357	C/T
CHD	rs4851011	2	102456110	0.041	0.76	HapMap	HapMap	C	0.641	T	0.359	C/T

LWK	rs4851011	2	102456110	0.054	1	HapMap	HapMap	C	0.983	T	0.017	C/T
MKK	rs4851011	2	102456110	0.035	1	HapMap	HapMap	C	0.976	T	0.024	C/T
GIH	rs4851011	2	102456110	0.115	1	HapMap	HapMap	C	0.693	T	0.307	C/T
JPT	rs4851011	2	102456110	0.173	1	HapMap	HapMap	C	0.581	T	0.419	C/T
MEX	rs4851011	2	102456110	0.071	0.804	HapMap	HapMap	C	0.76	T	0.24	C/T
YRI	rs4851011	2	102456110	0.113	0.603	HapMap	HapMap	C	0.916	T	0.084	C/T
CEU	rs4851012	2	102482347	0.237	0.898	HapMap	HapMap	C	0.272	T	0.728	C/T
CHD	rs4851012	2	102482347	0.021	0.633	HapMap	HapMap	C	0.708	T	0.292	C/T
JPT	rs4851012	2	102482347	0.09	1	HapMap	HapMap	C	0.733	T	0.267	C/T
CEU	rs4851014	2	102482708	0.232	0.898	HapMap	HapMap	C	0.27	T	0.73	C/T
CHD	rs4851014	2	102482708	0.021	0.633	HapMap	HapMap	C	0.708	T	0.292	C/T
JPT	rs4851014	2	102482708	0.09	1	HapMap	HapMap	C	0.733	T	0.267	C/T
JPT	rs4851016	2	102486832	0.09	1	HapMap	HapMap	C	0.733	T	0.267	C/T
CEU	rs4851016	2	102486832	0.232	0.898	HapMap	HapMap	C	0.27	T	0.73	C/T
CHD	rs4851016	2	102486832	0.023	0.649	HapMap	HapMap	C	0.702	T	0.298	C/T
CHD	rs4851017	2	102487201	0.023	0.655	HapMap	HapMap	C	0.7	A	0.3	C/A
JPT	rs4851017	2	102487201	0.09	1	HapMap	HapMap	C	0.733	A	0.267	C/A
CEU	rs4851017	2	102487201	0.232	0.898	HapMap	HapMap	C	0.268	A	0.732	C/A
CEU	rs4851561	2	102218269	0.112	1	HapMap	HapMap	G	0.925	A	0.075	G/A
GIH	rs4851561	2	102218269	0.021	1	HapMap	HapMap	G	0.994	A	0.006	G/A
LWK	rs4851561	2	102218269	0.007	1	HapMap	HapMap	G	0.978	A	0.022	G/A
MEX	rs4851561	2	102218269	0.095	1	HapMap	HapMap	G	0.97	A	0.03	G/A
MKK	rs4851561	2	102218269	0.008	0.896	HapMap	HapMap	G	0.986	A	0.014	G/A
ASW	rs4851563	2	102251967	0.026	1	HapMap	HapMap	A	0.934	T	0.066	A/T
CEU	rs4851563	2	102251967	0.159	1	HapMap	HapMap	A	0.898	T	0.102	A/T
GIH	rs4851563	2	102251967	0.021	1	HapMap	HapMap	A	0.994	T	0.006	A/T
MEX	rs4851563	2	102251967	0.128	1	HapMap	HapMap	A	0.96	T	0.04	A/T
MEX	rs4851574	2	102391142	0.04	1	HapMap	HapMap	A	0.9	T	0.1	A/T
MKK	rs4851574	2	102391142	0.008	0.896	HapMap	HapMap	A	0.986	T	0.014	A/T
GIH	rs4851574	2	102391142	0.013	1	HapMap	HapMap	A	0.955	T	0.045	A/T
JPT	rs4851574	2	102391142	0.04	1	HapMap	HapMap	A	0.86	T	0.14	A/T
LWK	rs4851574	2	102391142	0.018	1	HapMap	HapMap	A	0.994	T	0.006	A/T
ASW	rs4851574	2	102391142	0.066	1	HapMap	HapMap	A	0.972	T	0.028	A/T
CEU	rs4851574	2	102391142	0.031	1	HapMap	HapMap	A	0.965	T	0.035	A/T

CHD	rs4851574	2	102391142	0.031	1	HapMap	HapMap	A	0.8	T	0.2	A/T
CEU	rs4851581	2	102401181	0.216	1	HapMap	HapMap	A	0.878	G	0.122	A/G
MEX	rs4851581	2	102401181	0.195	1	HapMap	HapMap	A	0.939	G	0.061	A/G
GIH	rs4851589	2	102443577	0.319	0.685	HapMap	HapMap	A	0.847	G	0.153	A/G
MEX	rs4851589	2	102443577	0.185	0.645	HapMap	HapMap	A	0.867	G	0.133	A/G
CEU	rs4851589	2	102443577	0.337	0.656	HapMap	HapMap	A	0.646	G	0.354	A/G
CEU	rs4851593	2	102455659	0.337	0.656	HapMap	HapMap	A	0.655	G	0.345	A/G
GIH	rs4851593	2	102455659	0.319	0.685	HapMap	HapMap	A	0.847	G	0.153	A/G
MEX	rs4851593	2	102455659	0.209	0.671	HapMap	HapMap	A	0.86	G	0.14	A/G
CHD	rs4851600	2	102482655	0.021	0.633	HapMap	HapMap	C	0.708	G	0.292	C/G
JPT	rs4851600	2	102482655	0.09	1	HapMap	HapMap	C	0.733	G	0.267	C/G
CEU	rs4851600	2	102482655	0.232	0.898	HapMap	HapMap	C	0.27	G	0.73	C/G
CHD	rs4851601	2	102482693	0.004	1	HapMap	HapMap	G	0.971	A	0.029	G/A
MKK	rs4851601	2	102482693	0.04	1	HapMap	HapMap	G	0.972	A	0.028	G/A
CHB	rs4851601	2	102482693	0.008	1	HapMap	HapMap	G	0.94	A	0.06	G/A
CHD	rs4851602	2	102482737	0.044	1	HapMap	HapMap	G	0.744	A	0.256	G/A
JPT	rs4851602	2	102482737	0.08	1	HapMap	HapMap	G	0.75	A	0.25	G/A
JPT	rs4851604	2	102485313	0.071	1	HapMap	HapMap	G	0.773	A	0.227	G/A
CHD	rs4851604	2	102485313	0.035	1	HapMap	HapMap	G	0.782	A	0.218	G/A
CHD	rs4851615	2	102513431	0.039	0.752	HapMap	HapMap	G	0.647	T	0.353	G/T
CEU	rs4851616	2	102518294	0.145	0.859	HapMap	HapMap	C	0.19	T	0.81	C/T
CHB	rs4851616	2	102518294	0.155	1	HapMap	HapMap	C	0.518	T	0.482	C/T
CHD	rs4851616	2	102518294	0.129	1	HapMap	HapMap	C	0.506	T	0.494	C/T
JPT	rs4851616	2	102518294	0.111	1	HapMap	HapMap	C	0.413	T	0.587	C/T
ASW	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.314	G	0.686	A/G
CEU	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.59	G	0.41	A/G
CHB	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.857	G	0.143	A/G
CHD	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.887	G	0.113	A/G
GIH	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.791	G	0.209	A/G
JPT	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.845	G	0.155	A/G
LWK	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.242	G	0.758	A/G
MEX	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.724	G	0.276	A/G
MKK	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.421	G	0.579	A/G
YRI	rs4988955	2	102334360	1	1	HapMap	HapMap	A	0.235	G	0.765	A/G

CHB	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.857	C	0.143	T/C
ASW	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.302	C	0.698	T/C
CEU	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.593	C	0.407	T/C
CHD	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.888	C	0.112	T/C
GIH	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.79	C	0.21	T/C
JPT	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.849	C	0.151	T/C
LWK	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.239	C	0.761	T/C
MEX	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.73	C	0.27	T/C
MKK	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.42	C	0.58	T/C
YRI	rs4988957	2	102334507	1	1	HapMap	HapMap	T	0.235	C	0.765	T/C
ASW	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.302	C	0.698	T/C
CEU	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.593	C	0.407	T/C
CHB	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.857	C	0.143	T/C
CHD	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.888	C	0.112	T/C
GIH	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.79	C	0.21	T/C
JPT	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.849	C	0.151	T/C
LWK	rs4988958	2	102334717	0.97	1	HapMap	HapMap	T	0.244	C	0.756	T/C
MEX	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.735	C	0.265	T/C
MKK	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.42	C	0.58	T/C
YRI	rs4988958	2	102334717	1	1	HapMap	HapMap	T	0.237	C	0.763	T/C
CEU	rs6543113	2	102277489	0.535	0.942	HapMap	HapMap	C	0.699	T	0.301	C/T
CHB	rs6543113	2	102277489	0.073	1	HapMap	HapMap	C	0.994	T	0.006	C/T
CHD	rs6543113	2	102277489	0.047	1	HapMap	HapMap	C	0.994	T	0.006	C/T
GIH	rs6543113	2	102277489	0.405	0.87	HapMap	HapMap	C	0.875	T	0.125	C/T
MEX	rs6543113	2	102277489	0.307	0.628	HapMap	HapMap	C	0.796	T	0.204	C/T
CHB	rs6543146	2	102463127	0.142	0.667	HapMap	HapMap	T	0.655	G	0.345	T/G
CHD	rs6543146	2	102463127	0.121	0.679	HapMap	HapMap	T	0.673	G	0.327	T/G
CEU	rs6543148	2	102466651	0.047	1	HapMap	HapMap	A	0.934	G	0.066	A/G
CHD	rs6543148	2	102466651	0.002	0.614	HapMap	HapMap	A	0.965	G	0.035	A/G
GIH	rs6543148	2	102466651	0.01	1	HapMap	HapMap	A	0.966	G	0.034	A/G
JPT	rs6543148	2	102466651	0.005	1	HapMap	HapMap	A	0.977	G	0.023	A/G
MEX	rs6543148	2	102466651	0.017	1	HapMap	HapMap	A	0.96	G	0.04	A/G
CEU	rs6543150	2	102480415	0.232	0.898	HapMap	HapMap	C	0.275	T	0.725	C/T
CHB	rs6543150	2	102480415	0.132	0.677	HapMap	HapMap	C	0.649	T	0.351	C/T

CHD	rs6543150	2	102480415	0.147	0.776	HapMap	HapMap	C	0.648	T	0.352	C/T
JPT	rs6543150	2	102480415	0.102	0.604	HapMap	HapMap	C	0.61	T	0.39	C/T
YRI	rs6543150	2	102480415	0.015	1	HapMap	HapMap	C	0.031	T	0.969	C/T
JPT	rs6543156	2	102482582	0.6	1	HapMap	HapMap	C	0.872	T	0.128	C/T
MEX	rs6543156	2	102482582	0.031	1	HapMap	HapMap	C	0.99	T	0.01	C/T
GIH	rs6543156	2	102482582	0.021	1	HapMap	HapMap	C	0.994	T	0.006	C/T
CHB	rs6543156	2	102482582	0.546	1	HapMap	HapMap	C	0.909	T	0.091	C/T
CHD	rs6543156	2	102482582	0.603	1	HapMap	HapMap	C	0.929	T	0.071	C/T
ASW	rs6708413	2	102429801	0.022	1	HapMap	HapMap	G	0.038	A	0.962	G/A
CHB	rs6708413	2	102429801	0.141	1	HapMap	HapMap	G	0.476	A	0.524	G/A
CHD	rs6708413	2	102429801	0.129	1	HapMap	HapMap	G	0.506	A	0.494	G/A
GIH	rs6708413	2	102429801	0.141	0.803	HapMap	HapMap	G	0.443	A	0.557	G/A
JPT	rs6708413	2	102429801	0.105	1	HapMap	HapMap	G	0.413	A	0.587	G/A
CEU	rs6708413	2	102429801	0.209	1	HapMap	HapMap	G	0.204	A	0.796	G/A
MEX	rs6708413	2	102429801	0.304	1	HapMap	HapMap	G	0.44	A	0.56	G/A
MKK	rs6708413	2	102429801	0.118	0.643	HapMap	HapMap	G	0.171	A	0.829	G/A
LWK	rs6708413	2	102429801	0.051	1	HapMap	HapMap	G	0.139	A	0.861	G/A
YRI	rs6708949	2	102490397	0.023	1	HapMap	HapMap	G	0.018	C	0.982	G/C
MKK	rs6708949	2	102490397	0.072	0.774	HapMap	HapMap	G	0.08	C	0.92	G/C
CEU	rs6708949	2	102490397	0.145	0.859	HapMap	HapMap	G	0.186	C	0.814	G/C
GIH	rs6708949	2	102490397	0.045	0.658	HapMap	HapMap	G	0.273	C	0.727	G/C
JPT	rs6708949	2	102490397	0.111	1	HapMap	HapMap	G	0.407	C	0.593	G/C
ASW	rs6708949	2	102490397	0.031	1	HapMap	HapMap	G	0.009	C	0.991	G/C
CHB	rs6708949	2	102490397	0.148	1	HapMap	HapMap	G	0.5	C	0.5	G/C
CHD	rs6708949	2	102490397	0.125	1	HapMap	HapMap	G	0.494	C	0.506	G/C
LWK	rs6708949	2	102490397	0.129	1	HapMap	HapMap	G	0.039	C	0.961	G/C
GIH	rs6710528	2	102382574	0.703	0.924	HapMap	HapMap	C	0.756	T	0.244	C/T
JPT	rs6710528	2	102382574	0.85	1	HapMap	HapMap	C	0.831	T	0.169	C/T
MEX	rs6710528	2	102382574	0.709	0.939	HapMap	HapMap	C	0.68	T	0.32	C/T
MKK	rs6710528	2	102382574	0.278	0.732	HapMap	HapMap	C	0.273	T	0.727	C/T
ASW	rs6710528	2	102382574	0.353	0.712	HapMap	HapMap	C	0.245	T	0.755	C/T
CEU	rs6710528	2	102382574	0.759	1	HapMap	HapMap	C	0.482	T	0.518	C/T
CHB	rs6710528	2	102382574	0.564	0.892	HapMap	HapMap	C	0.833	T	0.167	C/T
CHD	rs6710528	2	102382574	0.614	0.874	HapMap	HapMap	C	0.863	T	0.137	C/T

ASW	rs6710885	2	102343969	0.871	1	HapMap	HapMap	A	0.717	G	0.283	A/G
CEU	rs6710885	2	102343969	0.414	1	HapMap	HapMap	A	0.622	G	0.378	A/G
CHB	rs6710885	2	102343969	0.111	1	HapMap	HapMap	A	0.613	G	0.387	A/G
CHD	rs6710885	2	102343969	0.074	1	HapMap	HapMap	A	0.629	G	0.371	A/G
GIH	rs6710885	2	102343969	0.132	1	HapMap	HapMap	A	0.665	G	0.335	A/G
JPT	rs6710885	2	102343969	0.187	1	HapMap	HapMap	A	0.577	G	0.423	A/G
LWK	rs6710885	2	102343969	0.818	0.965	HapMap	HapMap	A	0.787	G	0.213	A/G
MKK	rs6710885	2	102343969	0.666	1	HapMap	HapMap	A	0.675	G	0.325	A/G
YRI	rs6710885	2	102343969	0.829	1	HapMap	HapMap	A	0.792	G	0.208	A/G
CEU	rs6724109	2	102491450	0.145	0.859	HapMap	HapMap	C	0.19	G	0.81	C/G
CHD	rs6724109	2	102491450	0.039	0.627	HapMap	HapMap	C	0.565	G	0.435	C/G
ASW	rs6731042	2	102214688	0.074	0.657	HapMap	HapMap	C	0.736	A	0.264	C/A
MEX	rs6731042	2	102214688	0.118	0.848	HapMap	HapMap	C	0.69	A	0.31	C/A
MKK	rs6731042	2	102214688	0.096	0.635	HapMap	HapMap	C	0.752	A	0.248	C/A
CEU	rs6737325	2	102465225	0.047	1	HapMap	HapMap	C	0.929	T	0.071	C/T
CHD	rs6737325	2	102465225	0.002	0.637	HapMap	HapMap	C	0.964	T	0.036	C/T
GIH	rs6737325	2	102465225	0.01	1	HapMap	HapMap	C	0.966	T	0.034	C/T
JPT	rs6737325	2	102465225	0.005	1	HapMap	HapMap	C	0.977	T	0.023	C/T
MEX	rs6737325	2	102465225	0.017	1	HapMap	HapMap	C	0.96	T	0.04	C/T
ASW	rs6741230	2	102436063	0.043	0.65	HapMap	HapMap	C	0.802	T	0.198	C/T
CEU	rs6741230	2	102436063	0.264	1	HapMap	HapMap	C	0.845	T	0.155	C/T
CHB	rs6741230	2	102436063	0.223	1	HapMap	HapMap	C	0.976	T	0.024	C/T
CHD	rs6741230	2	102436063	0.093	0.697	HapMap	HapMap	C	0.976	T	0.024	C/T
GIH	rs6741230	2	102436063	0.481	1	HapMap	HapMap	C	0.886	T	0.114	C/T
JPT	rs6741230	2	102436063	0.185	1	HapMap	HapMap	C	0.983	T	0.017	C/T
LWK	rs6741230	2	102436063	0.058	1	HapMap	HapMap	C	0.844	T	0.156	C/T
MEX	rs6741230	2	102436063	0.128	1	HapMap	HapMap	C	0.95	T	0.05	C/T
MKK	rs6741230	2	102436063	0.111	0.863	HapMap	HapMap	C	0.829	T	0.171	C/T
CEU	rs6741235	2	102483715	0.232	0.898	HapMap	HapMap	G	0.265	A	0.735	G/A
CHD	rs6741235	2	102483715	0.021	0.639	HapMap	HapMap	G	0.706	A	0.294	G/A
JPT	rs6741235	2	102483715	0.09	1	HapMap	HapMap	G	0.733	A	0.267	G/A
ASW	rs6742280	2	102502769	0.038	1	HapMap	HapMap	A	0.915	G	0.085	A/G
LWK	rs6742280	2	102502769	0.01	0.964	HapMap	HapMap	A	0.967	G	0.033	A/G
YRI	rs6742280	2	102502769	0.035	1	HapMap	HapMap	A	0.912	G	0.088	A/G

ASW	rs6743516	2	102402767	0.358	0.778	HapMap	HapMap	A	0.226	G	0.774	A/G
CEU	rs6743516	2	102402767	0.759	1	HapMap	HapMap	A	0.473	G	0.527	A/G
CHB	rs6743516	2	102402767	0.564	0.892	HapMap	HapMap	A	0.833	G	0.167	A/G
CHD	rs6743516	2	102402767	0.615	0.874	HapMap	HapMap	A	0.865	G	0.135	A/G
MEX	rs6743516	2	102402767	0.707	0.938	HapMap	HapMap	A	0.673	G	0.327	A/G
MKK	rs6743516	2	102402767	0.223	0.699	HapMap	HapMap	A	0.248	G	0.752	A/G
GIH	rs6743516	2	102402767	0.678	0.923	HapMap	HapMap	A	0.744	G	0.256	A/G
JPT	rs6743516	2	102402767	0.85	1	HapMap	HapMap	A	0.829	G	0.171	A/G
ASW	rs6744454	2	102165584	0.063	1	HapMap	HapMap	G	0.019	A	0.981	G/A
CHB	rs6744454	2	102165584	0.002	1	HapMap	HapMap	G	0.006	A	0.994	G/A
CHD	rs6744454	2	102165584	0.001	1	HapMap	HapMap	G	0.006	A	0.994	G/A
GIH	rs6744454	2	102165584	0.045	1	HapMap	HapMap	G	0.142	A	0.858	G/A
MKK	rs6744454	2	102165584	0.076	0.701	HapMap	HapMap	G	0.102	A	0.898	G/A
CEU	rs6747153	2	102270259	0.148	0.622	HapMap	HapMap	A	0.246	G	0.754	A/G
YRI	rs6747153	2	102270259	0.035	1	HapMap	HapMap	A	0.071	G	0.929	A/G
CHD	rs6749014	2	102372880	0.649	0.876	HapMap	HapMap	C	0.869	T	0.131	C/T
MKK	rs6749014	2	102372880	0.278	0.732	HapMap	HapMap	C	0.273	T	0.727	C/T
CHB	rs6749014	2	102372880	0.564	0.892	HapMap	HapMap	C	0.833	T	0.167	C/T
ASW	rs6749014	2	102372880	0.408	0.796	HapMap	HapMap	C	0.236	T	0.764	C/T
CEU	rs6749014	2	102372880	0.759	1	HapMap	HapMap	C	0.482	T	0.518	C/T
GIH	rs6749014	2	102372880	0.703	0.924	HapMap	HapMap	C	0.756	T	0.244	C/T
JPT	rs6749014	2	102372880	0.85	1	HapMap	HapMap	C	0.831	T	0.169	C/T
MEX	rs6749014	2	102372880	0.709	0.939	HapMap	HapMap	C	0.68	T	0.32	C/T
CEU	rs6750851	2	102505193	0.145	0.859	HapMap	HapMap	A	0.192	G	0.808	A/G
CHB	rs6750851	2	102505193	0.148	1	HapMap	HapMap	A	0.5	G	0.5	A/G
CHD	rs6750851	2	102505193	0.119	1	HapMap	HapMap	A	0.494	G	0.506	A/G
JPT	rs6750851	2	102505193	0.111	1	HapMap	HapMap	A	0.407	G	0.593	A/G
GIH	rs6750851	2	102505193	0.04	0.625	HapMap	HapMap	A	0.273	G	0.727	A/G
CEU	rs6751666	2	102465003	0.047	1	HapMap	HapMap	A	0.934	G	0.066	A/G
CHD	rs6751666	2	102465003	0.002	0.614	HapMap	HapMap	A	0.965	G	0.035	A/G
GIH	rs6751666	2	102465003	0.01	1	HapMap	HapMap	A	0.966	G	0.034	A/G
JPT	rs6751666	2	102465003	0.005	1	HapMap	HapMap	A	0.977	G	0.023	A/G
MEX	rs6751666	2	102465003	0.017	1	HapMap	HapMap	A	0.96	G	0.04	A/G
CHD	rs6752589	2	102221730	0.02	1	HapMap	HapMap	A	0.135	G	0.865	A/G

JPT	rs6752589	2	102221730	0.062	1	HapMap	HapMap	A	0.227	G	0.773	A/G
LWK	rs6752589	2	102221730	0.018	0.676	HapMap	HapMap	A	0.111	G	0.889	A/G
MEX	rs6752589	2	102221730	0.161	0.779	HapMap	HapMap	A	0.42	G	0.58	A/G
MEX	rs6756407	2	102402533	0.013	1	HapMap	HapMap	G	0.97	T	0.03	G/T
MKK	rs6756407	2	102402533	0.093	0.625	HapMap	HapMap	G	0.853	T	0.147	G/T
CEU	rs6756407	2	102402533	0.056	1	HapMap	HapMap	G	0.92	T	0.08	G/T
CHD	rs6756407	2	102402533	0.004	1	HapMap	HapMap	G	0.971	T	0.029	G/T
GIH	rs6756407	2	102402533	0.008	1	HapMap	HapMap	G	0.972	T	0.028	G/T
JPT	rs6756407	2	102402533	0.005	1	HapMap	HapMap	G	0.976	T	0.024	G/T
LWK	rs6756407	2	102402533	0.177	0.731	HapMap	HapMap	G	0.906	T	0.094	G/T
GIH	rs6758443	2	102214494	0.015	0.606	HapMap	HapMap	G	0.869	T	0.131	G/T
MEX	rs6758443	2	102214494	0.085	0.607	HapMap	HapMap	G	0.61	T	0.39	G/T
CHD	rs6758936	2	102357801	0.615	0.874	HapMap	HapMap	G	0.865	A	0.135	G/A
GIH	rs6758936	2	102357801	0.703	0.924	HapMap	HapMap	G	0.756	A	0.244	G/A
JPT	rs6758936	2	102357801	0.85	1	HapMap	HapMap	G	0.829	A	0.171	G/A
MEX	rs6758936	2	102357801	0.709	0.939	HapMap	HapMap	G	0.68	A	0.32	G/A
MKK	rs6758936	2	102357801	0.274	0.729	HapMap	HapMap	G	0.271	A	0.729	G/A
CHB	rs6758936	2	102357801	0.562	0.891	HapMap	HapMap	G	0.831	A	0.169	G/A
ASW	rs6758936	2	102357801	0.408	0.796	HapMap	HapMap	G	0.236	A	0.764	G/A
CEU	rs6758936	2	102357801	0.759	1	HapMap	HapMap	G	0.482	A	0.518	G/A
CHD	rs6761291	2	102521501	0.039	0.752	HapMap	HapMap	C	0.647	T	0.353	C/T
JPT	rs741285	2	102514601	0.05	0.62	HapMap	HapMap	C	0.436	T	0.564	C/T
CHB	rs741285	2	102514601	0.17	1	HapMap	HapMap	C	0.53	T	0.47	C/T
CHD	rs741285	2	102514601	0.098	0.814	HapMap	HapMap	C	0.541	T	0.459	C/T
LWK	rs7559479	2	102435219	0.032	0.764	HapMap	HapMap	G	0.15	A	0.85	G/A
MEX	rs7559479	2	102435219	0.304	1	HapMap	HapMap	G	0.429	A	0.571	G/A
MKK	rs7559479	2	102435219	0.117	0.64	HapMap	HapMap	G	0.173	A	0.827	G/A
YRI	rs7559479	2	102435219	0.054	0.666	HapMap	HapMap	G	0.049	A	0.951	G/A
ASW	rs7559479	2	102435219	0.022	1	HapMap	HapMap	G	0.038	A	0.962	G/A
CEU	rs7559479	2	102435219	0.209	1	HapMap	HapMap	G	0.204	A	0.796	G/A
CHB	rs7559479	2	102435219	0.141	1	HapMap	HapMap	G	0.476	A	0.524	G/A
CHD	rs7559479	2	102435219	0.129	1	HapMap	HapMap	G	0.506	A	0.494	G/A
GIH	rs7559479	2	102435219	0.141	0.803	HapMap	HapMap	G	0.443	A	0.557	G/A
JPT	rs7559479	2	102435219	0.105	1	HapMap	HapMap	G	0.412	A	0.588	G/A

ASW	rs7560478	2	102178958	0.085	0.794	HapMap	HapMap	T	0.783	C	0.217	T/C
LWK	rs7560478	2	102178958	0.051	1	HapMap	HapMap	T	0.861	C	0.139	T/C
MEX	rs7560478	2	102178958	0.118	0.848	HapMap	HapMap	T	0.69	C	0.31	T/C
MKK	rs7560478	2	102178958	0.131	0.808	HapMap	HapMap	T	0.783	C	0.217	T/C
JPT	rs7566613	2	102466927	0.005	1	HapMap	HapMap	G	0.977	A	0.023	G/A
MEX	rs7566613	2	102466927	0.017	1	HapMap	HapMap	G	0.96	A	0.04	G/A
CEU	rs7566613	2	102466927	0.047	1	HapMap	HapMap	G	0.934	A	0.066	G/A
GIH	rs7566613	2	102466927	0.011	1	HapMap	HapMap	G	0.96	A	0.04	G/A
CEU	rs7567885	2	102475284	0.222	0.893	HapMap	HapMap	T	0.268	G	0.732	T/G
JPT	rs7567885	2	102475284	0.09	1	HapMap	HapMap	T	0.738	G	0.262	T/G
CHB	rs7568913	2	102286469	0.141	1	HapMap	HapMap	T	0.47	C	0.53	T/C
CHD	rs7568913	2	102286469	0.134	1	HapMap	HapMap	T	0.512	C	0.488	T/C
JPT	rs7568913	2	102286469	0.095	1	HapMap	HapMap	T	0.384	C	0.616	T/C
CEU	rs7570468	2	102206539	0.008	1	HapMap	HapMap	C	0.982	A	0.018	C/A
MKK	rs7570468	2	102206539	0.017	0.655	HapMap	HapMap	C	0.972	A	0.028	C/A
ASW	rs7571371	2	102320159	0.046	1	HapMap	HapMap	C	0.925	T	0.075	C/T
JPT	rs7571371	2	102320159	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
LWK	rs7571371	2	102320159	0.02	1	HapMap	HapMap	C	0.939	T	0.061	C/T
MKK	rs7571371	2	102320159	0.037	1	HapMap	HapMap	C	0.951	T	0.049	C/T
YRI	rs7571371	2	102320159	0.024	1	HapMap	HapMap	C	0.96	T	0.04	C/T
CEU	rs7575867	2	102486611	0.245	1	HapMap	HapMap	C	0.863	T	0.137	C/T
MKK	rs7575867	2	102486611	0.1	0.909	HapMap	HapMap	C	0.857	T	0.143	C/T
LWK	rs7575867	2	102486611	0.055	1	HapMap	HapMap	C	0.85	T	0.15	C/T
JPT	rs7575867	2	102486611	0.122	1	HapMap	HapMap	C	0.983	T	0.017	C/T
CHB	rs7575867	2	102486611	0.147	1	HapMap	HapMap	C	0.988	T	0.012	C/T
CEU	rs7579737	2	102353793	0.26	0.614	HapMap	HapMap	A	0.646	G	0.354	A/G
GIH	rs7579737	2	102353793	0.291	0.669	HapMap	HapMap	A	0.852	G	0.148	A/G
YRI	rs7582710	2	102353917	0.027	1	HapMap	HapMap	T	0.92	G	0.08	T/G
ASW	rs7582710	2	102353917	0.046	1	HapMap	HapMap	T	0.925	G	0.075	T/G
LWK	rs7582710	2	102353917	0.013	1	HapMap	HapMap	T	0.961	G	0.039	T/G
MKK	rs7582710	2	102353917	0.032	1	HapMap	HapMap	T	0.958	G	0.042	T/G
MEX	rs7583215	2	102220486	0.132	0.851	HapMap	HapMap	C	0.67	T	0.33	C/T
MKK	rs7583215	2	102220486	0.112	0.619	HapMap	HapMap	C	0.708	T	0.292	C/T
CEU	rs7583683	2	102480195	0.245	1	HapMap	HapMap	A	0.863	G	0.137	A/G

CHB	rs7583683	2	102480195	0.073	1	HapMap	HapMap	A	0.994	G	0.006	A/G
LWK	rs7583683	2	102480195	0.053	1	HapMap	HapMap	A	0.856	G	0.144	A/G
MKK	rs7583683	2	102480195	0.101	1	HapMap	HapMap	A	0.878	G	0.122	A/G
CHD	rs7591872	2	102479073	0.133	0.768	HapMap	HapMap	G	0.641	C	0.359	G/C
GIH	rs7591872	2	102479073	0.059	0.713	HapMap	HapMap	G	0.295	C	0.705	G/C
JPT	rs7591872	2	102479073	0.102	0.604	HapMap	HapMap	G	0.605	C	0.395	G/C
YRI	rs7591872	2	102479073	0.015	1	HapMap	HapMap	G	0.031	C	0.969	G/C
ASW	rs7591872	2	102479073	0.063	1	HapMap	HapMap	G	0.038	C	0.962	G/C
CEU	rs7591872	2	102479073	0.232	0.898	HapMap	HapMap	G	0.27	C	0.73	G/C
CHB	rs7591872	2	102479073	0.132	0.677	HapMap	HapMap	G	0.643	C	0.357	G/C
CEU	rs759382	2	102460645	0.209	1	HapMap	HapMap	G	0.221	T	0.779	G/T
CHB	rs759382	2	102460645	0.148	1	HapMap	HapMap	G	0.5	T	0.5	G/T
CHD	rs759382	2	102460645	0.138	1	HapMap	HapMap	G	0.524	T	0.476	G/T
JPT	rs759382	2	102460645	0.111	1	HapMap	HapMap	G	0.424	T	0.576	G/T
MKK	rs759382	2	102460645	0.109	0.625	HapMap	HapMap	G	0.168	T	0.832	G/T
GIH	rs759382	2	102460645	0.108	0.71	HapMap	HapMap	G	0.438	T	0.562	G/T
MEX	rs759382	2	102460645	0.304	1	HapMap	HapMap	G	0.44	T	0.56	G/T
LWK	rs7600961	2	102401887	0.055	1	HapMap	HapMap	G	0.85	A	0.15	G/A
MEX	rs7600961	2	102401887	0.128	1	HapMap	HapMap	G	0.95	A	0.05	G/A
MKK	rs7600961	2	102401887	0.134	0.882	HapMap	HapMap	G	0.808	A	0.192	G/A
CEU	rs7600961	2	102401887	0.264	1	HapMap	HapMap	G	0.845	A	0.155	G/A
CHB	rs7600961	2	102401887	0.223	1	HapMap	HapMap	G	0.976	A	0.024	G/A
CHD	rs7600961	2	102401887	0.093	0.697	HapMap	HapMap	G	0.976	A	0.024	G/A
GIH	rs7600961	2	102401887	0.481	1	HapMap	HapMap	G	0.886	A	0.114	G/A
JPT	rs7600961	2	102401887	0.185	1	HapMap	HapMap	G	0.983	A	0.017	G/A
CEU	rs7601773	2	102486915	0.245	1	HapMap	HapMap	G	0.863	T	0.137	G/T
CHB	rs7601773	2	102486915	0.147	1	HapMap	HapMap	G	0.988	T	0.012	G/T
JPT	rs7601773	2	102486915	0.122	1	HapMap	HapMap	G	0.983	T	0.017	G/T
MKK	rs7601773	2	102486915	0.1	0.909	HapMap	HapMap	G	0.857	T	0.143	G/T
LWK	rs7601773	2	102486915	0.055	1	HapMap	HapMap	G	0.85	T	0.15	G/T
ASW	rs7603730	2	102340803	0.877	1	HapMap	HapMap	A	0.33	C	0.67	A/C
CEU	rs7603730	2	102340803	1	1	HapMap	HapMap	A	0.593	C	0.407	A/C
CHB	rs7603730	2	102340803	1	1	HapMap	HapMap	A	0.857	C	0.143	A/C
CHD	rs7603730	2	102340803	1	1	HapMap	HapMap	A	0.888	C	0.112	A/C

GIH	rs7603730	2	102340803	1	1	HapMap	HapMap	A	0.79	C	0.21	A/C
JPT	rs7603730	2	102340803	1	1	HapMap	HapMap	A	0.849	C	0.151	A/C
LWK	rs7603730	2	102340803	0.569	1	HapMap	HapMap	A	0.356	C	0.644	A/C
MEX	rs7603730	2	102340803	1	1	HapMap	HapMap	A	0.73	C	0.27	A/C
MKK	rs7603730	2	102340803	0.855	1	HapMap	HapMap	A	0.458	C	0.542	A/C
YRI	rs7603730	2	102340803	0.956	1	HapMap	HapMap	A	0.257	C	0.743	A/C
CEU	rs871657	2	102137773	0.189	0.878	HapMap	HapMap	C	0.836	T	0.164	C/T
CHB	rs871657	2	102137773	0.063	1	HapMap	HapMap	C	0.732	T	0.268	C/T
MEX	rs871657	2	102137773	0.369	0.892	HapMap	HapMap	C	0.85	T	0.15	C/T
CEU	rs871659	2	102138287	0.112	0.732	HapMap	HapMap	G	0.23	A	0.77	G/A
JPT	rs871659	2	102138287	0.03	1	HapMap	HapMap	G	0.105	A	0.895	G/A
YRI	rs871659	2	102138287	0.054	0.666	HapMap	HapMap	G	0.062	A	0.938	G/A
CHB	rs885088	2	102405476	0.564	0.892	HapMap	HapMap	A	0.833	G	0.167	A/G
CHD	rs885088	2	102405476	0.615	0.874	HapMap	HapMap	A	0.865	G	0.135	A/G
GIH	rs885088	2	102405476	0.68	0.923	HapMap	HapMap	A	0.75	G	0.25	A/G
JPT	rs885088	2	102405476	0.85	1	HapMap	HapMap	A	0.831	G	0.169	A/G
MEX	rs885088	2	102405476	0.672	0.937	HapMap	HapMap	A	0.67	G	0.33	A/G
MKK	rs885088	2	102405476	0.214	0.692	HapMap	HapMap	A	0.245	G	0.755	A/G
ASW	rs885088	2	102405476	0.358	0.778	HapMap	HapMap	A	0.226	G	0.774	A/G
CEU	rs885088	2	102405476	0.759	1	HapMap	HapMap	A	0.482	G	0.518	A/G
JPT	rs917997	2	102437000	0.105	1	HapMap	HapMap	T	0.413	C	0.587	T/C
LWK	rs917997	2	102437000	0.032	0.764	HapMap	HapMap	T	0.15	C	0.85	T/C
MEX	rs917997	2	102437000	0.304	1	HapMap	HapMap	T	0.44	C	0.56	T/C
CHB	rs917997	2	102437000	0.141	1	HapMap	HapMap	T	0.476	C	0.524	T/C
CHD	rs917997	2	102437000	0.129	1	HapMap	HapMap	T	0.506	C	0.494	T/C
GIH	rs917997	2	102437000	0.141	0.803	HapMap	HapMap	T	0.443	C	0.557	T/C
ASW	rs917997	2	102437000	0.022	1	HapMap	HapMap	T	0.038	C	0.962	T/C
CEU	rs917997	2	102437000	0.209	1	HapMap	HapMap	T	0.204	C	0.796	T/C
MKK	rs917997	2	102437000	0.118	0.643	HapMap	HapMap	T	0.171	C	0.829	T/C
YRI	rs917997	2	102437000	0.054	0.666	HapMap	HapMap	T	0.049	C	0.951	T/C
ASW	rs917998	2	102434588	0.031	1	HapMap	HapMap	C	0.962	T	0.038	C/T
CEU	rs917998	2	102434588	0.21	1	HapMap	HapMap	C	0.881	T	0.119	C/T
LWK	rs917998	2	102434588	0.002	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MEX	rs917998	2	102434588	0.196	1	HapMap	HapMap	C	0.94	T	0.06	C/T

YRI	rs917998	2	102434588	0.019	1	HapMap	HapMap	C	0.96	T	0.04	C/T
ASW	rs9308856	2	102261874	0.038	1	HapMap	HapMap	A	0.943	G	0.057	A/G
LWK	rs9308856	2	102261874	0.017	1	HapMap	HapMap	A	0.95	G	0.05	A/G
MEX	rs9308856	2	102261874	0.031	1	HapMap	HapMap	A	0.99	G	0.01	A/G
MKK	rs9308856	2	102261874	0.078	1	HapMap	HapMap	A	0.902	G	0.098	A/G
YRI	rs9308856	2	102261874	0.023	1	HapMap	HapMap	A	0.947	G	0.053	A/G
CEU	rs949963	2	102136218	0.189	0.878	HapMap	HapMap	C	0.836	T	0.164	C/T
CHB	rs949963	2	102136218	0.063	1	HapMap	HapMap	C	0.732	T	0.268	C/T
MEX	rs949963	2	102136218	0.369	0.892	HapMap	HapMap	C	0.85	T	0.15	C/T
GIH	rs951193	2	102152231	0.003	1	HapMap	HapMap	C	0.989	T	0.011	C/T
ASW	rs951774	2	102279096	0.063	1	HapMap	HapMap	C	0.953	A	0.047	C/A
CEU	rs951774	2	102279096	0.209	1	HapMap	HapMap	C	0.823	A	0.177	C/A
CHB	rs951774	2	102279096	0.049	1	HapMap	HapMap	C	0.78	A	0.22	C/A
CHD	rs951774	2	102279096	0.018	0.681	HapMap	HapMap	C	0.759	A	0.241	C/A
GIH	rs951774	2	102279096	0.149	0.9	HapMap	HapMap	C	0.603	A	0.397	C/A
LWK	rs951774	2	102279096	0.112	0.646	HapMap	HapMap	C	0.921	A	0.079	C/A
MEX	rs951774	2	102279096	0.242	1	HapMap	HapMap	C	0.61	A	0.39	C/A
MKK	rs951774	2	102279096	0.115	1	HapMap	HapMap	C	0.923	A	0.077	C/A
YRI	rs951774	2	102279096	0.131	0.81	HapMap	HapMap	C	0.947	A	0.053	C/A
GIH	rs955754	2	102215513	0.015	0.606	HapMap	HapMap	T	0.869	C	0.131	T/C
MEX	rs955754	2	102215513	0.085	0.607	HapMap	HapMap	T	0.61	C	0.39	T/C
ASW	rs995515	2	102205814	0.103	0.712	HapMap	HapMap	T	0.915	C	0.085	T/C
LWK	rs995515	2	102205814	0.077	0.771	HapMap	HapMap	T	0.961	C	0.039	T/C
YRI	rs995515	2	102205814	0.047	1	HapMap	HapMap	T	0.987	C	0.013	T/C
LWK	rs17026901	2	102256818	0.018	1	HapMap	HapMap	T	0.994	C	0.006	T/C
CHB	rs17026901	2	102256818	0.028	1	HapMap	HapMap	T	0.869	C	0.131	T/C
CHB	rs11904409	2	102169616	0.073	1	HapMap	HapMap	G	0.97	A	0.03	G/A
LWK	rs2310239	2	102190633	0.072	0.657	HapMap	HapMap	G	0.95	A	0.05	G/A
ASW	rs2310239	2	102190633	0.072	0.64	HapMap	HapMap	G	0.923	A	0.077	G/A
MKK	rs887972	2	102407377	0.023	0.714	HapMap	HapMap	G	0.968	A	0.032	G/A
GIH	rs887972	2	102407377	0.119	0.86	HapMap	HapMap	G	0.625	A	0.375	G/A
MEX	rs1041973	2	102321900	0.284	0.666	HapMap	HapMap	C	0.796	A	0.204	C/A
CHD	rs1041973	2	102321900	0.537	0.783	HapMap	HapMap	C	0.89	A	0.11	C/A
JPT	rs1041973	2	102321900	0.531	0.729	HapMap	HapMap	C	0.823	A	0.177	C/A

CEU	rs1041973	2	102321900	0.148	0.852	HapMap	HapMap	C	0.802	A	0.198	C/A
MKK	rs1362347	2	102286017	0.412	1	HapMap	HapMap	C	0.77	T	0.23	C/T
YRI	rs1362347	2	102286017	0.227	1	HapMap	HapMap	C	0.928	T	0.072	C/T
CHB	rs1861245	2	102966906	1	1	HapMap	1000GP	A	NA	G	NA	A/G
JPT	rs1861245	2	102966906	1	1	HapMap	1000GP	A	NA	G	NA	A/G
JPT	rs7559566	2	103028041	0.831	1	HapMap	1000GP	G	NA	T	NA	G/T
CHB	rs7559566	2	103028041	0.562	0.891	HapMap	1000GP	G	NA	T	NA	G/T
JPT	rs6705385	2	103076569	0.058	0.65	HapMap	1000GP	A	0.53	C	0.47	A/C
JPT	rs6705498	2	103076670	0.058	0.65	HapMap	1000GP	A	0.53	G	0.47	A/G
JPT	rs6719196	2	103076888	0.058	0.65	HapMap	1000GP	G	0.53	T	0.47	G/T
JPT	rs12463588	2	103085257	0.058	0.65	HapMap	1000GP	C	0.53	G	0.47	C/G
JPT	rs2310302	2	103086049	0.058	0.65	HapMap	1000GP	G	0.53	C	0.47	G/C
JPT	rs12469887	2	103086758	0.058	0.65	HapMap	1000GP	T	0.53	C	0.47	T/C
JPT	rs4140786	2	103088176	0.058	0.65	HapMap	1000GP	G	0.53	T	0.47	G/T
JPT	rs4851614	2	103140398	0.05	0.62	HapMap	1000GP	C	0.53	T	0.47	C/T
CHB	rs4851614	2	103140398	0.175	1	HapMap	1000GP	C	0.53	T	0.47	C/T
JPT	rs1357471	2	103140472	0.05	0.62	HapMap	1000GP	C	0.53	T	0.47	C/T
CHB	rs1357471	2	103140472	0.17	1	HapMap	1000GP	C	0.53	T	0.47	C/T
JPT	rs4241211	2	103143159	0.05	0.62	HapMap	1000GP	T	0.53	G	0.47	T/G
CHB	rs4241211	2	103143159	0.17	1	HapMap	1000GP	T	0.53	G	0.47	T/G
JPT	rs12712156	2	103144020	0.05	0.62	HapMap	1000GP	A	0.53	C	0.47	A/C
CHB	rs12712156	2	103144020	0.163	1	HapMap	1000GP	A	0.53	C	0.47	A/C
CHB	rs3849364	2	103144242	0.17	1	HapMap	1000GP	T	0.53	C	0.47	T/C
JPT	rs3849364	2	103144242	0.05	0.62	HapMap	1000GP	T	0.53	C	0.47	T/C
JPT	rs3849365	2	103144391	0.05	0.615	HapMap	1000GP	G	0.53	A	0.47	G/A
CHB	rs3849365	2	103144391	0.17	1	HapMap	1000GP	G	0.53	A	0.47	G/A
CHB	rs1005042	2	103145359	0.186	1	HapMap	1000GP	A	0.53	G	0.47	A/G
JPT	rs1005042	2	103145359	0.05	0.615	HapMap	1000GP	A	0.53	G	0.47	A/G
JPT	rs4851018	2	103146615	0.05	0.62	HapMap	1000GP	C	0.53	T	0.47	C/T
CHB	rs4851018	2	103146615	0.17	1	HapMap	1000GP	C	0.53	T	0.47	C/T
CHB	rs6737119	2	103151109	0.158	1	HapMap	1000GP	G	0.53	A	0.47	G/A
JPT	rs6737119	2	103151109	0.05	0.62	HapMap	1000GP	G	0.53	A	0.47	G/A
CHB	rs6709284	2	103151164	0.17	1	HapMap	1000GP	C	0.53	G	0.47	C/G
JPT	rs6709284	2	103151164	0.05	0.62	HapMap	1000GP	C	0.53	G	0.47	C/G

JPT	rs2177317	2	103151319	0.05	0.62	HapMap	1000GP	A	0.53	G	0.47	A/G
CHB	rs2177317	2	103151319	0.17	1	HapMap	1000GP	A	0.53	G	0.47	A/G
JPT	rs4851617	2	103152060	0.05	0.62	HapMap	1000GP	C	0.53	T	0.47	C/T
CHB	rs4851617	2	103152060	0.17	1	HapMap	1000GP	C	0.53	T	0.47	C/T
JPT	rs4292112	2	103153780	0.05	0.62	HapMap	1000GP	G	0.53	A	0.47	G/A
CHB	rs4292112	2	103153780	0.17	1	HapMap	1000GP	G	0.53	A	0.47	G/A
JPT	rs10490202	2	103160832	0.05	0.62	HapMap	1000GP	C	0.53	G	0.47	C/G
CHB	rs10490202	2	103160832	0.17	1	HapMap	1000GP	C	0.53	G	0.47	C/G
CHB	rs7581853	2	103167724	0.17	1	HapMap	1000GP	C	0.53	T	0.47	C/T
CHB	rs950880	2	102932562	0.111	1	HapMap	1000GP	C	0.56	A	0.44	C/A
JPT	rs950880	2	102932562	0.21	1	HapMap	1000GP	C	0.56	A	0.44	C/A
CHB	rs13001325	2	102939036	0.111	1	HapMap	1000GP	C	0.56	T	0.44	C/T
JPT	rs13001325	2	102939036	0.21	1	HapMap	1000GP	C	0.56	T	0.44	C/T
CHB	rs12479210	2	102949161	0.111	1	HapMap	1000GP	C	0.56	T	0.44	C/T
JPT	rs12479210	2	102949161	0.21	1	HapMap	1000GP	C	0.56	T	0.44	C/T
CHB	rs13017455	2	102964742	0.111	1	HapMap	1000GP	C	0.56	T	0.44	C/T
JPT	rs13017455	2	102964742	0.21	1	HapMap	1000GP	C	0.56	T	0.44	C/T
CHB	rs1024798	2	103141651	0.155	1	HapMap	1000GP	G	0.56	C	0.44	G/C
JPT	rs1024798	2	103141651	0.111	1	HapMap	1000GP	G	0.56	C	0.44	G/C
JPT	rs2871474	2	103151441	0.111	1	HapMap	1000GP	G	0.56	A	0.44	G/A
CHB	rs2871474	2	103151441	0.155	1	HapMap	1000GP	G	0.56	A	0.44	G/A
CHB	rs11685483	2	103159093	0.155	1	HapMap	1000GP	A	0.56	C	0.44	A/C
JPT	rs11685483	2	103159093	0.111	1	HapMap	1000GP	A	0.56	C	0.44	A/C
JPT	rs6739426	2	103160443	0.111	1	HapMap	1000GP	A	0.56	G	0.44	A/G
CHB	rs6739426	2	103160443	0.155	1	HapMap	1000GP	A	0.56	G	0.44	A/G
JPT	rs11899041	2	103161053	0.111	1	HapMap	1000GP	T	0.56	A	0.44	T/A
CHB	rs11899041	2	103161053	0.155	1	HapMap	1000GP	T	0.56	A	0.44	T/A
CHB	rs1303960	2	103165832	0.155	1	HapMap	1000GP	G	0.56	A	0.44	G/A
JPT	rs1303960	2	103165832	0.111	1	HapMap	1000GP	G	0.56	A	0.44	G/A
JPT	rs6543119	2	102963072	0.21	1	HapMap	1000GP	A	0.57	T	0.43	A/T
CHB	rs6543119	2	102963072	0.111	1	HapMap	1000GP	A	0.57	T	0.43	A/T
JPT	rs6718157	2	103079814	0.105	1	HapMap	1000GP	A	0.57	T	0.43	A/T
CHB	rs6718157	2	103079814	0.141	1	HapMap	1000GP	A	0.57	T	0.43	A/T
CHB	rs6737668	2	103093081	0.148	1	HapMap	1000GP	C	0.57	T	0.43	C/T

JPT	rs6737668	2	103093081	0.105	1	HapMap	1000GP	C	0.57	T	0.43	C/T
CHB	rs759381	2	103094323	0.141	1	HapMap	1000GP	A	0.57	T	0.43	A/T
JPT	rs759381	2	103094323	0.117	1	HapMap	1000GP	A	0.57	T	0.43	A/T
CHB	rs6724322	2	103125182	0.148	1	HapMap	1000GP	C	0.57	T	0.43	C/T
JPT	rs6724322	2	103125182	0.111	1	HapMap	1000GP	C	0.57	T	0.43	C/T
CHB	rs4851609	2	103128866	0.148	1	HapMap	1000GP	T	0.57	C	0.43	T/C
JPT	rs4851609	2	103128866	0.111	1	HapMap	1000GP	T	0.57	C	0.43	T/C
JPT	rs2192758	2	103132269	0.111	1	HapMap	1000GP	C	0.57	G	0.43	C/G
CHB	rs2192758	2	103132269	0.148	1	HapMap	1000GP	C	0.57	G	0.43	C/G
CHB	rs2192757	2	103132378	0.148	1	HapMap	1000GP	C	0.57	T	0.43	C/T
JPT	rs2192757	2	103132378	0.111	1	HapMap	1000GP	C	0.57	T	0.43	C/T
CHB	rs6714379	2	103133310	0.144	1	HapMap	1000GP	A	0.57	G	0.43	A/G
JPT	rs6714379	2	103133310	0.109	1	HapMap	1000GP	A	0.57	G	0.43	A/G
CHB	rs4851610	2	103134652	0.148	1	HapMap	1000GP	C	0.57	G	0.43	C/G
JPT	rs4851610	2	103134652	0.111	1	HapMap	1000GP	C	0.57	G	0.43	C/G
CHB	rs1523203	2	103135759	0.148	1	HapMap	1000GP	A	0.57	G	0.43	A/G
JPT	rs1523203	2	103135759	0.111	1	HapMap	1000GP	A	0.57	G	0.43	A/G
JPT	rs4851611	2	103135938	0.111	1	HapMap	1000GP	A	0.57	T	0.43	A/T
CHB	rs4851611	2	103135938	0.148	1	HapMap	1000GP	A	0.57	T	0.43	A/T
CHB	rs4851613	2	103137990	0.148	1	HapMap	1000GP	T	0.57	C	0.43	T/C
JPT	rs4851613	2	103137990	0.111	1	HapMap	1000GP	T	0.57	C	0.43	T/C
CHB	rs6750971	2	103138825	0.148	1	HapMap	1000GP	A	0.57	G	0.43	A/G
JPT	rs6750971	2	103138825	0.111	1	HapMap	1000GP	A	0.57	G	0.43	A/G
JPT	rs11123935	2	103139751	0.111	1	HapMap	1000GP	A	0.57	G	0.43	A/G
CHB	rs11123935	2	103139751	0.148	1	HapMap	1000GP	A	0.57	G	0.43	A/G
CHB	rs997049	2	102782433	0.047	0.603	HapMap	1000GP	T	0.58	A	0.42	T/A
JPT	rs2310220	2	102951851	0.095	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs2310220	2	102951851	0.135	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs2058622	2	102985424	0.107	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs2058622	2	102985424	0.127	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs3771170	2	102985980	0.105	1	HapMap	1000GP	T	0.58	A	0.42	T/A
CHB	rs3771170	2	102985980	0.124	1	HapMap	1000GP	T	0.58	A	0.42	T/A
JPT	rs2058623	2	102986170	0.107	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs2058623	2	102986170	0.124	1	HapMap	1000GP	C	0.58	T	0.42	C/T

CHB	rs1465321	2	102986618	0.127	1	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs1465321	2	102986618	0.108	1	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs2270297	2	102992675	0.105	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs2270297	2	102992675	0.135	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs6753717	2	102993161	0.135	1	HapMap	1000GP	A	0.58	C	0.42	A/C
JPT	rs6753717	2	102993161	0.105	1	HapMap	1000GP	A	0.58	C	0.42	A/C
JPT	rs6750020	2	102994714	0.109	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs6750020	2	102994714	0.144	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs17027037	2	102994884	0.038	0.642	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs17027037	2	102994884	0.173	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs2080289	2	102995020	0.173	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs2080289	2	102995020	0.038	0.642	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs11683700	2	102996805	0.191	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs4851570	2	103006387	0.038	0.642	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs4851570	2	103006387	0.173	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs4851007	2	103024813	0.105	1	HapMap	1000GP	T	0.58	G	0.42	T/G
CHB	rs4851007	2	103024813	0.141	1	HapMap	1000GP	T	0.58	G	0.42	T/G
CHB	rs4851575	2	103025203	0.141	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs4851575	2	103025203	0.105	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs4851008	2	103026611	0.105	1	HapMap	1000GP	G	0.58	C	0.42	G/C
CHB	rs4851008	2	103026611	0.141	1	HapMap	1000GP	G	0.58	C	0.42	G/C
CHB	rs1807782	2	103033147	0.141	1	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs1807782	2	103033147	0.105	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs3771156	2	103036677	0.033	0.62	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs3771156	2	103036677	0.173	1	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs3755268	2	103038527	0.105	1	HapMap	1000GP	C	0.58	G	0.42	C/G
CHB	rs3755268	2	103038527	0.141	1	HapMap	1000GP	C	0.58	G	0.42	C/G
CHB	rs3817465	2	103039584	0.141	1	HapMap	1000GP	A	0.58	T	0.42	A/T
JPT	rs3817465	2	103039584	0.105	1	HapMap	1000GP	A	0.58	T	0.42	A/T
JPT	rs887971	2	103041167	0.173	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs887971	2	103041167	0.033	0.62	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs2160232	2	103046880	0.105	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs2160232	2	103046880	0.148	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs6716784	2	103048467	0.138	1	HapMap	1000GP	T	0.58	G	0.42	T/G

JPT	rs6716784	2	103048467	0.103	1	HapMap	1000GP	T	0.58	G	0.42	T/G
CHB	rs6543134	2	103050458	0.141	1	HapMap	1000GP	T	0.58	G	0.42	T/G
JPT	rs6543134	2	103050458	0.117	1	HapMap	1000GP	T	0.58	G	0.42	T/G
JPT	rs2110735	2	103050925	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs2110735	2	103050925	0.141	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs11681718	2	103051144	0.173	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs11681718	2	103051144	0.033	0.613	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs4851582	2	103051558	0.033	0.62	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs4851582	2	103051558	0.178	1	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs2110734	2	103052206	0.113	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs2110734	2	103052206	0.141	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs6746271	2	103052995	0.141	1	HapMap	1000GP	G	0.58	C	0.42	G/C
JPT	rs6746271	2	103052995	0.105	1	HapMap	1000GP	G	0.58	C	0.42	G/C
CHB	rs2058658	2	103054803	0.141	1	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs2058658	2	103054803	0.105	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs4851009	2	103055644	0.141	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs4851009	2	103055644	0.105	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs17027179	2	103057159	0.033	0.62	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs17027179	2	103057159	0.173	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs10490203	2	103059237	0.033	0.62	HapMap	1000GP	T	0.58	G	0.42	T/G
JPT	rs10490203	2	103059237	0.173	1	HapMap	1000GP	T	0.58	G	0.42	T/G
JPT	rs1558650	2	103060024	0.113	1	HapMap	1000GP	T	0.58	A	0.42	T/A
CHB	rs1558650	2	103060024	0.141	1	HapMap	1000GP	T	0.58	A	0.42	T/A
JPT	rs4851583	2	103060300	0.173	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs4851584	2	103060313	0.084	0.752	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs4851584	2	103060313	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs11694360	2	103061147	0.173	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs11123928	2	103061286	0.173	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs7597017	2	103062116	0.173	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs6734736	2	103062880	0.103	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs6734736	2	103062880	0.12	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs6543137	2	103065908	0.084	0.752	HapMap	1000GP	T	0.58	G	0.42	T/G
JPT	rs6543137	2	103065908	0.105	1	HapMap	1000GP	T	0.58	G	0.42	T/G
CHB	rs7603250	2	103068834	0.084	0.752	HapMap	1000GP	T	0.58	A	0.42	T/A

JPT	rs7603250	2	103068834	0.105	1	HapMap	1000GP	T	0.58	A	0.42	T/A
JPT	rs2075185	2	103070988	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs2075185	2	103070988	0.141	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs4070554	2	103074493	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs4070554	2	103074493	0.141	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs6761825	2	103075561	0.105	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs6761825	2	103075561	0.141	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs6705001	2	103076210	0.141	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs6705001	2	103076210	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs6543141	2	103076351	0.141	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs6543141	2	103076351	0.105	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs4241210	2	103078740	0.141	1	HapMap	1000GP	G	0.58	A	0.42	G/A
JPT	rs4241210	2	103078740	0.105	1	HapMap	1000GP	G	0.58	A	0.42	G/A
CHB	rs6720564	2	103079297	0.141	1	HapMap	1000GP	T	0.58	C	0.42	T/C
JPT	rs6720564	2	103079297	0.105	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs17027230	2	103079330	0.038	0.636	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs17027230	2	103079330	0.171	1	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs6717915	2	103079619	0.099	1	HapMap	1000GP	A	0.58	C	0.42	A/C
CHB	rs6717915	2	103079619	0.137	1	HapMap	1000GP	A	0.58	C	0.42	A/C
CHB	rs917996	2	103082273	0.141	1	HapMap	1000GP	C	0.58	A	0.42	C/A
JPT	rs917996	2	103082273	0.105	1	HapMap	1000GP	C	0.58	A	0.42	C/A
CHB	rs990171	2	103086770	0.141	1	HapMap	1000GP	A	0.58	C	0.42	A/C
JPT	rs990171	2	103086770	0.105	1	HapMap	1000GP	A	0.58	C	0.42	A/C
JPT	rs1474309	2	103091001	0.173	1	HapMap	1000GP	C	0.58	T	0.42	C/T
CHB	rs1474309	2	103091001	0.033	0.62	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs17027258	2	103091540	0.178	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs1468791	2	103092021	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs1468791	2	103092021	0.141	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs7597819	2	103092906	0.105	1	HapMap	1000GP	A	0.58	G	0.42	A/G
CHB	rs7597819	2	103092906	0.141	1	HapMap	1000GP	A	0.58	G	0.42	A/G
JPT	rs10469840	2	103093243	0.105	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs10469840	2	103093243	0.144	1	HapMap	1000GP	T	0.58	C	0.42	T/C
CHB	rs10193407	2	103139298	0.148	1	HapMap	1000GP	C	0.58	T	0.42	C/T
JPT	rs10193407	2	103139298	0.111	1	HapMap	1000GP	C	0.58	T	0.42	C/T

JPT	rs4577297	2	102918018	0.092	1	HapMap	1000GP	G	0.59	A	0.41	G/A
CHB	rs4577297	2	102918018	0.13	1	HapMap	1000GP	G	0.59	A	0.41	G/A
CHB	rs953934	2	102932293	0.141	1	HapMap	1000GP	C	0.59	T	0.41	C/T
JPT	rs953934	2	102932293	0.095	1	HapMap	1000GP	C	0.59	T	0.41	C/T
CHB	rs1420103	2	102948632	0.135	1	HapMap	1000GP	A	0.59	C	0.41	A/C
JPT	rs1420103	2	102948632	0.095	1	HapMap	1000GP	A	0.59	C	0.41	A/C
CHB	rs3821204	2	102960281	0.091	1	HapMap	1000GP	C	0.59	G	0.41	C/G
JPT	rs3821204	2	102960281	0.182	1	HapMap	1000GP	C	0.59	G	0.41	C/G
JPT	rs12469506	2	102965871	0.182	1	HapMap	1000GP	C	0.59	T	0.41	C/T
CHB	rs12469506	2	102965871	0.091	1	HapMap	1000GP	C	0.59	T	0.41	C/T
CHB	rs11693955	2	103029165	0.033	0.62	HapMap	1000GP	A	0.59	T	0.41	A/T
JPT	rs11693955	2	103029165	0.173	1	HapMap	1000GP	A	0.59	T	0.41	A/T
CHB	rs887972	2	103040945	0.033	0.62	HapMap	1000GP	G	0.59	A	0.41	G/A
JPT	rs887972	2	103040945	0.173	1	HapMap	1000GP	G	0.59	A	0.41	G/A
CHB	rs873022	2	102955683	0.083	1	HapMap	1000GP	G	0.6	T	0.4	G/T
JPT	rs873022	2	102955683	0.182	1	HapMap	1000GP	G	0.6	T	0.4	G/T
JPT	rs3771177	2	102955860	0.182	1	HapMap	1000GP	G	0.6	T	0.4	G/T
CHB	rs3771177	2	102955860	0.083	1	HapMap	1000GP	G	0.6	T	0.4	G/T
CHB	rs3732129	2	102957532	0.083	1	HapMap	1000GP	T	0.6	C	0.4	T/C
JPT	rs3732129	2	102957532	0.182	1	HapMap	1000GP	T	0.6	C	0.4	T/C
CHB	rs3771172	2	102985812	0.091	1	HapMap	1000GP	C	0.6	T	0.4	C/T
JPT	rs3771172	2	102985812	0.165	1	HapMap	1000GP	C	0.6	T	0.4	C/T
CHB	rs3771171	2	102985950	0.084	1	HapMap	1000GP	T	0.6	C	0.4	T/C
JPT	rs3771171	2	102985950	0.165	1	HapMap	1000GP	T	0.6	C	0.4	T/C
CHB	rs2160202	2	102986154	0.084	1	HapMap	1000GP	G	0.6	A	0.4	G/A
JPT	rs2160202	2	102986154	0.169	1	HapMap	1000GP	G	0.6	A	0.4	G/A
CHB	rs7566063	2	103112565	0.132	0.677	HapMap	1000GP	C	0.6	A	0.4	C/A
JPT	rs7566063	2	103112565	0.102	0.604	HapMap	1000GP	C	0.6	A	0.4	C/A
JPT	rs7591878	2	103112658	0.151	0.764	HapMap	1000GP	G	0.6	A	0.4	G/A
CHB	rs7591878	2	103112658	0.12	0.654	HapMap	1000GP	G	0.6	A	0.4	G/A
JPT	rs6543154	2	103114334	0.102	0.604	HapMap	1000GP	T	0.6	C	0.4	T/C
CHB	rs6543154	2	103114334	0.132	0.677	HapMap	1000GP	T	0.6	C	0.4	T/C
JPT	rs6543155	2	103114895	0.123	0.737	HapMap	1000GP	G	0.6	A	0.4	G/A
CHB	rs6543155	2	103114895	0.139	0.68	HapMap	1000GP	G	0.6	A	0.4	G/A

JPT	rs11123934	2	103115568	0.102	0.604	HapMap	1000GP	G	0.6	A	0.4	G/A
CHB	rs11123934	2	103115568	0.132	0.677	HapMap	1000GP	G	0.6	A	0.4	G/A
CHB	rs1030026	2	103098178	0.142	0.667	HapMap	1000GP	A	0.62	C	0.38	A/C
CHB	rs2140316	2	103098676	0.142	0.667	HapMap	1000GP	T	0.62	A	0.38	T/A
CHB	rs12468355	2	102861250	0.222	0.835	HapMap	1000GP	T	0.66	G	0.34	T/G
JPT	rs12468355	2	102861250	0.144	0.665	HapMap	1000GP	T	0.66	G	0.34	T/G
JPT	rs1558626	2	102862070	0.144	0.665	HapMap	1000GP	T	0.66	A	0.34	T/A
CHB	rs1558626	2	102862070	0.211	0.836	HapMap	1000GP	T	0.66	A	0.34	T/A
CHB	rs1558624	2	102862233	0.211	0.836	HapMap	1000GP	A	0.66	G	0.34	A/G
JPT	rs1558624	2	102862233	0.144	0.665	HapMap	1000GP	A	0.66	G	0.34	A/G
CHB	rs1558623	2	102862402	0.211	0.836	HapMap	1000GP	T	0.66	A	0.34	T/A
JPT	rs1558623	2	102862402	0.144	0.665	HapMap	1000GP	T	0.66	A	0.34	T/A
JPT	rs17689452	2	102864681	0.144	0.665	HapMap	1000GP	A	0.66	G	0.34	A/G
CHB	rs17689452	2	102864681	0.211	0.836	HapMap	1000GP	A	0.66	G	0.34	A/G
CHB	rs10186746	2	102866377	0.211	0.836	HapMap	1000GP	G	0.66	A	0.34	G/A
JPT	rs10186746	2	102866377	0.144	0.665	HapMap	1000GP	G	0.66	A	0.34	G/A
JPT	rs7572871	2	102853838	0.049	1	HapMap	1000GP	G	0.7	A	0.3	G/A
JPT	rs12712153	2	103111761	0.09	1	HapMap	1000GP	C	0.71	T	0.29	C/T
JPT	rs11687071	2	103111920	0.09	1	HapMap	1000GP	G	0.71	A	0.29	G/A
JPT	rs6543153	2	103114203	0.032	0.607	HapMap	1000GP	T	0.71	C	0.29	T/C
JPT	rs7573566	2	103115205	0.09	1	HapMap	1000GP	T	0.71	C	0.29	T/C
JPT	rs12987295	2	103115838	0.09	1	HapMap	1000GP	G	0.71	A	0.29	G/A
JPT	rs12995030	2	103116466	0.09	1	HapMap	1000GP	C	0.71	G	0.29	C/G
JPT	rs6728288	2	103117268	0.09	1	HapMap	1000GP	A	0.71	T	0.29	A/T
JPT	rs2075192	2	103118228	0.09	1	HapMap	1000GP	A	0.71	G	0.29	A/G
JPT	rs2075191	2	103118299	0.09	1	HapMap	1000GP	G	0.71	T	0.29	G/T
JPT	rs2075190	2	103118559	0.09	1	HapMap	1000GP	A	0.71	T	0.29	A/T
JPT	rs2075189	2	103118689	0.09	1	HapMap	1000GP	C	0.71	G	0.29	C/G
JPT	rs11690932	2	103119029	0.09	1	HapMap	1000GP	G	0.71	A	0.29	G/A
JPT	rs4851605	2	103120868	0.09	1	HapMap	1000GP	A	0.71	G	0.29	A/G
JPT	rs4851606	2	103120889	0.09	1	HapMap	1000GP	G	0.71	A	0.29	G/A
JPT	rs7600901	2	102915571	0.053	1	HapMap	1000GP	A	0.73	G	0.27	A/G
JPT	rs7605606	2	103121536	0.08	1	HapMap	1000GP	G	0.73	A	0.27	G/A
CHB	rs3755292	2	102769137	0.057	1	HapMap	1000GP	T	0.74	G	0.26	T/G

CHB	rs871656	2	102771282	0.057	1	HapMap	1000GP	T	0.75	A	0.25	T/A
CHB	rs2287048	2	102773999	0.066	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CHB	rs1468789	2	103092503	0.045	1	HapMap	1000GP	C	0.76	T	0.24	C/T
CHB	rs1882510	2	102883618	0.052	1	HapMap	1000GP	C	0.77	T	0.23	C/T
JPT	rs3755294	2	102768376	0.058	1	HapMap	1000GP	G	0.82	A	0.18	G/A
CHB	rs12465829	2	103072320	0.034	1	HapMap	1000GP	T	0.82	C	0.18	T/C
JPT	rs12465829	2	103072320	0.058	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CHB	rs10200410	2	102870871	0.396	0.776	HapMap	1000GP	G	0.83	A	0.17	G/A
CHB	rs1345301	2	102875587	0.396	0.776	HapMap	1000GP	A	0.83	G	0.17	A/G
CHB	rs2310243	2	102877560	0.396	0.776	HapMap	1000GP	A	0.83	G	0.17	A/G
CHB	rs13405355	2	102878206	0.396	0.776	HapMap	1000GP	C	0.83	T	0.17	C/T
JPT	rs17026901	2	102890386	0.03	0.826	HapMap	1000GP	T	0.83	C	0.17	T/C
JPT	rs10206291	2	103038863	0.85	1	HapMap	1000GP	T	0.83	C	0.17	T/C
CHB	rs10206291	2	103038863	0.564	0.892	HapMap	1000GP	T	0.83	C	0.17	T/C
CHB	rs10208196	2	102996345	0.564	0.892	HapMap	1000GP	G	0.84	A	0.16	G/A
JPT	rs10208196	2	102996345	0.849	1	HapMap	1000GP	G	0.84	A	0.16	G/A
CHB	rs3213732	2	102998279	0.564	0.892	HapMap	1000GP	A	0.84	G	0.16	A/G
JPT	rs3213732	2	102998279	0.85	1	HapMap	1000GP	A	0.84	G	0.16	A/G
JPT	rs6760621	2	102999952	0.84	1	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs6760621	2	102999952	0.558	0.889	HapMap	1000GP	T	0.84	C	0.16	T/C
JPT	rs6706002	2	103006104	0.85	1	HapMap	1000GP	A	0.84	G	0.16	A/G
CHB	rs6706002	2	103006104	0.564	0.892	HapMap	1000GP	A	0.84	G	0.16	A/G
CHB	rs4851571	2	103019000	0.564	0.892	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs4851571	2	103019000	0.85	1	HapMap	1000GP	C	0.84	T	0.16	C/T
CHB	rs4851572	2	103019031	0.564	0.892	HapMap	1000GP	G	0.84	A	0.16	G/A
JPT	rs4851572	2	103019031	0.85	1	HapMap	1000GP	G	0.84	A	0.16	G/A
CHB	rs2110662	2	103020139	0.564	0.892	HapMap	1000GP	A	0.84	T	0.16	A/T
JPT	rs2110662	2	103020139	0.85	1	HapMap	1000GP	A	0.84	T	0.16	A/T
CHB	rs7594402	2	103021267	0.564	0.892	HapMap	1000GP	A	0.84	T	0.16	A/T
JPT	rs7594402	2	103021267	0.85	1	HapMap	1000GP	A	0.84	T	0.16	A/T
JPT	rs6710034	2	103023678	0.85	1	HapMap	1000GP	G	0.84	A	0.16	G/A
CHB	rs6710034	2	103023678	0.564	0.892	HapMap	1000GP	G	0.84	A	0.16	G/A
CHB	rs7589142	2	103024660	0.736	0.899	HapMap	1000GP	T	0.84	C	0.16	T/C
JPT	rs7589142	2	103024660	1	1	HapMap	1000GP	T	0.84	C	0.16	T/C

CHB	rs10203558	2	103027640	0.562	0.891	HapMap	1000GP	T	0.84	C	0.16	T/C
JPT	rs10203558	2	103027640	0.841	1	HapMap	1000GP	T	0.84	C	0.16	T/C
JPT	rs4851576	2	103028895	0.85	1	HapMap	1000GP	C	0.84	T	0.16	C/T
CHB	rs4851576	2	103028895	0.564	0.892	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs4851577	2	103028921	0.85	1	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs4851577	2	103028921	0.564	0.892	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs4851579	2	103028984	0.564	0.892	HapMap	1000GP	G	0.84	A	0.16	G/A
JPT	rs4851579	2	103028984	0.85	1	HapMap	1000GP	G	0.84	A	0.16	G/A
JPT	rs1592458	2	103031749	0.85	1	HapMap	1000GP	A	0.84	T	0.16	A/T
CHB	rs1592458	2	103031749	0.564	0.892	HapMap	1000GP	A	0.84	T	0.16	A/T
JPT	rs2160201	2	103033961	0.822	1	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs2160201	2	103033961	0.778	1	HapMap	1000GP	T	0.84	C	0.16	T/C
JPT	rs2293224	2	103035779	0.85	1	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs2293224	2	103035779	0.564	0.892	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs1420100	2	103037002	0.564	0.892	HapMap	1000GP	C	0.84	A	0.16	C/A
JPT	rs1420100	2	103037002	0.85	1	HapMap	1000GP	C	0.84	A	0.16	C/A
JPT	rs3771155	2	103037826	0.85	1	HapMap	1000GP	A	0.84	G	0.16	A/G
CHB	rs3771155	2	103037826	0.564	0.892	HapMap	1000GP	A	0.84	G	0.16	A/G
CHB	rs3771154	2	103039360	0.564	0.892	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs3771154	2	103039360	0.85	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs6759479	2	103040047	0.85	1	HapMap	1000GP	A	0.84	C	0.16	A/C
CHB	rs6759479	2	103040047	0.564	0.892	HapMap	1000GP	A	0.84	C	0.16	A/C
JPT	rs6543133	2	103040177	0.179	0.628	HapMap	1000GP	A	0.84	T	0.16	A/T
CHB	rs7559845	2	103046214	0.564	0.892	HapMap	1000GP	T	0.84	G	0.16	T/G
JPT	rs7559845	2	103046214	0.85	1	HapMap	1000GP	T	0.84	G	0.16	T/G
CHB	rs3755265	2	103052816	0.564	0.892	HapMap	1000GP	C	0.84	A	0.16	C/A
JPT	rs3755265	2	103052816	0.85	1	HapMap	1000GP	C	0.84	A	0.16	C/A
JPT	rs4479442	2	103054074	0.833	1	HapMap	1000GP	A	0.84	T	0.16	A/T
CHB	rs4479442	2	103054074	0.541	0.883	HapMap	1000GP	A	0.84	T	0.16	A/T
CHB	rs13021177	2	103056493	0.564	0.892	HapMap	1000GP	A	0.84	G	0.16	A/G
JPT	rs13021177	2	103056493	0.85	1	HapMap	1000GP	A	0.84	G	0.16	A/G
JPT	rs3771202	2	102772669	0.034	1	HapMap	1000GP	C	0.85	G	0.15	C/G
JPT	rs2080312	2	102774810	0.03	1	HapMap	1000GP	A	0.85	G	0.15	A/G
JPT	rs3917245	2	102775155	0.027	1	HapMap	1000GP	G	0.85	A	0.15	G/A

JPT	rs3917246	2	102775164	0.027	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs1041973	2	102955468	0.52	0.79	HapMap	1000GP	C	0.85	A	0.15	C/A
CHB	rs10208293	2	102966310	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs10208293	2	102966310	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs13424006	2	102967236	1	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs13424006	2	102967236	1	1	HapMap	1000GP	T	0.85	C	0.15	T/C
JPT	rs6751967	2	102967413	1	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs6751967	2	102967413	1	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs6749114	2	102967587	1	1	HapMap	1000GP	A	0.85	C	0.15	A/C
JPT	rs6749114	2	102967587	1	1	HapMap	1000GP	A	0.85	C	0.15	A/C
CHB	rs10170583	2	102974764	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs10170583	2	102974764	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
CHB	rs10176664	2	102976172	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs10176664	2	102976172	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs1974675	2	102986375	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
CHB	rs1974675	2	102986375	1	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs17027352	2	103138836	0.442	0.766	HapMap	1000GP	C	0.85	T	0.15	C/T
CHB	rs17027352	2	103138836	0.385	0.68	HapMap	1000GP	C	0.85	T	0.15	C/T
CHB	rs7576682	2	103143312	0.375	0.66	HapMap	1000GP	G	0.86	A	0.14	G/A
JPT	rs7576682	2	103143312	0.299	0.757	HapMap	1000GP	G	0.86	A	0.14	G/A
CHB	rs3849363	2	103143548	0.385	0.68	HapMap	1000GP	T	0.86	G	0.14	T/G
JPT	rs3849363	2	103143548	0.442	0.766	HapMap	1000GP	T	0.86	G	0.14	T/G
CHB	rs13388541	2	103147818	0.388	0.655	HapMap	1000GP	T	0.86	C	0.14	T/C
JPT	rs13388541	2	103147818	0.437	0.763	HapMap	1000GP	T	0.86	C	0.14	T/C
CHB	rs10183491	2	103151587	0.385	0.68	HapMap	1000GP	T	0.86	G	0.14	T/G
JPT	rs10183491	2	103151587	0.442	0.766	HapMap	1000GP	T	0.86	G	0.14	T/G
JPT	rs17027415	2	103154594	0.442	0.766	HapMap	1000GP	C	0.86	A	0.14	C/A
CHB	rs17027415	2	103154594	0.385	0.68	HapMap	1000GP	C	0.86	A	0.14	C/A
JPT	rs13027294	2	102860074	0.595	1	HapMap	1000GP	G	0.87	C	0.13	G/C
CHB	rs13027294	2	102860074	0.547	1	HapMap	1000GP	G	0.87	C	0.13	G/C
CHB	rs11677452	2	102865236	0.627	0.879	HapMap	1000GP	A	0.87	T	0.13	A/T
JPT	rs11677452	2	102865236	0.457	0.707	HapMap	1000GP	A	0.87	T	0.13	A/T
CHB	rs9646944	2	102865875	0.627	0.879	HapMap	1000GP	G	0.87	C	0.13	G/C
JPT	rs9646944	2	102865875	0.457	0.707	HapMap	1000GP	G	0.87	C	0.13	G/C

CHB	rs13418548	2	102917239	0.223	1	HapMap	1000GP	C	0.88	T	0.12	C/T
JPT	rs13418548	2	102917239	0.329	1	HapMap	1000GP	C	0.88	T	0.12	C/T
CHB	rs950881	2	102932512	0.369	1	HapMap	1000GP	G	0.88	T	0.12	G/T
JPT	rs950881	2	102932512	0.574	1	HapMap	1000GP	G	0.88	T	0.12	G/T
CHB	rs13408569	2	102955056	0.632	1	HapMap	1000GP	G	0.88	C	0.12	G/C
JPT	rs13408569	2	102955056	0.753	1	HapMap	1000GP	G	0.88	C	0.12	G/C
CHB	rs13408661	2	102955082	0.632	1	HapMap	1000GP	G	0.88	A	0.12	G/A
JPT	rs13408661	2	102955082	0.753	1	HapMap	1000GP	G	0.88	A	0.12	G/A
JPT	rs10173081	2	102957348	0.753	1	HapMap	1000GP	C	0.88	T	0.12	C/T
CHB	rs10173081	2	102957348	0.632	1	HapMap	1000GP	C	0.88	T	0.12	C/T
CHB	rs17027029	2	102990648	0.632	1	HapMap	1000GP	G	0.88	C	0.12	G/C
JPT	rs17027029	2	102990648	0.753	1	HapMap	1000GP	G	0.88	C	0.12	G/C
JPT	rs3771164	2	102991786	0.753	1	HapMap	1000GP	A	0.88	T	0.12	A/T
CHB	rs3771164	2	102991786	0.632	1	HapMap	1000GP	A	0.88	T	0.12	A/T
JPT	rs3732127	2	103013750	0.753	1	HapMap	1000GP	G	0.88	C	0.12	G/C
CHB	rs3732127	2	103013750	0.632	1	HapMap	1000GP	G	0.88	C	0.12	G/C
JPT	rs12991737	2	103018128	0.752	1	HapMap	1000GP	T	0.88	A	0.12	T/A
CHB	rs12991737	2	103018128	0.754	1	HapMap	1000GP	T	0.88	A	0.12	T/A
CHB	rs10181785	2	103025274	0.632	1	HapMap	1000GP	C	0.88	T	0.12	C/T
JPT	rs10181785	2	103025274	0.753	1	HapMap	1000GP	C	0.88	T	0.12	C/T
CHB	rs12712148	2	103025547	0.632	1	HapMap	1000GP	G	0.88	A	0.12	G/A
JPT	rs12712148	2	103025547	0.676	1	HapMap	1000GP	G	0.88	A	0.12	G/A
CHB	rs7586983	2	103028066	0.632	1	HapMap	1000GP	C	0.88	T	0.12	C/T
JPT	rs7586983	2	103028066	0.753	1	HapMap	1000GP	C	0.88	T	0.12	C/T
CHB	rs2272127	2	103039873	0.632	1	HapMap	1000GP	C	0.88	G	0.12	C/G
JPT	rs2272127	2	103039873	0.718	1	HapMap	1000GP	C	0.88	G	0.12	C/G
CHB	rs10166330	2	103050390	0.632	1	HapMap	1000GP	C	0.89	T	0.11	C/T
JPT	rs10166330	2	103050390	0.753	1	HapMap	1000GP	C	0.89	T	0.11	C/T
CHB	rs11465736	2	103067930	0.462	1	HapMap	1000GP	C	0.89	T	0.11	C/T
JPT	rs11465736	2	103067930	0.752	1	HapMap	1000GP	C	0.89	T	0.11	C/T
JPT	rs10169676	2	103074919	0.753	1	HapMap	1000GP	G	0.89	A	0.11	G/A
CHB	rs10169676	2	103074919	0.632	1	HapMap	1000GP	G	0.89	A	0.11	G/A
JPT	rs17027246	2	103080055	0.753	1	HapMap	1000GP	C	0.89	G	0.11	C/G
CHB	rs17027246	2	103080055	0.603	1	HapMap	1000GP	C	0.89	G	0.11	C/G

CHB	rs741284	2	103083324	0.632	1	HapMap	1000GP	G	0.89	C	0.11	G/C
JPT	rs741284	2	103083324	0.753	1	HapMap	1000GP	G	0.89	C	0.11	G/C
JPT	rs10172116	2	103087573	0.753	1	HapMap	1000GP	C	0.89	T	0.11	C/T
CHB	rs10172116	2	103087573	0.632	1	HapMap	1000GP	C	0.89	T	0.11	C/T
CHB	rs13030642	2	103091585	0.632	1	HapMap	1000GP	C	0.89	A	0.11	C/A
JPT	rs13030642	2	103091585	0.753	1	HapMap	1000GP	C	0.89	A	0.11	C/A
JPT	rs11892768	2	103096936	0.6	1	HapMap	1000GP	C	0.89	T	0.11	C/T
CHB	rs11892768	2	103096936	0.546	1	HapMap	1000GP	C	0.89	T	0.11	C/T
CHB	rs7579846	2	103112585	0.546	1	HapMap	1000GP	A	0.89	C	0.11	A/C
JPT	rs7579846	2	103112585	0.6	1	HapMap	1000GP	A	0.89	C	0.11	A/C
JPT	rs10208027	2	103121372	0.455	1	HapMap	1000GP	G	0.89	T	0.11	G/T
CHB	rs10208027	2	103121372	0.546	1	HapMap	1000GP	G	0.89	T	0.11	G/T
JPT	rs10185897	2	102966790	0.455	1	HapMap	1000GP	C	0.9	A	0.1	C/A
CHB	rs10185897	2	102966790	0.223	1	HapMap	1000GP	C	0.9	A	0.1	C/A
JPT	rs10196556	2	103075079	0.753	1	HapMap	1000GP	C	0.9	T	0.1	C/T
CHB	rs10196556	2	103075079	0.462	1	HapMap	1000GP	C	0.9	T	0.1	C/T
JPT	rs2302622	2	102836521	0.005	0.684	HapMap	1000GP	G	0.91	C	0.09	G/C
CHB	rs2302622	2	102836521	0.009	0.658	HapMap	1000GP	G	0.91	C	0.09	G/C
JPT	rs17820338	2	102809182	0.005	1	HapMap	1000GP	G	0.95	C	0.05	G/C
CHB	rs17820338	2	102809182	0.012	1	HapMap	1000GP	G	0.95	C	0.05	G/C
CHB	rs1558648	2	102810168	0.014	1	HapMap	1000GP	T	0.95	G	0.05	T/G
JPT	rs1558648	2	102810168	0.005	1	HapMap	1000GP	T	0.95	G	0.05	T/G
JPT	rs17769234	2	102811716	0.005	1	HapMap	1000GP	T	0.95	C	0.05	T/C
CHB	rs17769234	2	102811716	0.011	1	HapMap	1000GP	T	0.95	C	0.05	T/C
JPT	rs17026757	2	102813912	0.002	1	HapMap	1000GP	A	0.95	C	0.05	A/C
CHB	rs17026757	2	102813912	0.011	1	HapMap	1000GP	A	0.95	C	0.05	A/C
CHB	rs12996377	2	102830478	0.014	1	HapMap	1000GP	T	0.95	A	0.05	T/A
JPT	rs12996377	2	102830478	0.005	1	HapMap	1000GP	T	0.95	A	0.05	T/A
CHB	rs7582378	2	103162263	0.147	1	HapMap	1000GP	C	0.95	A	0.05	C/A
CHB	rs3917306	2	102788839	0.006	0.749	HapMap	1000GP	A	0.96	G	0.04	A/G
JPT	rs6728945	2	102986471	0.07	1	HapMap	1000GP	T	0.96	C	0.04	T/C
CHB	rs6728945	2	102986471	0.202	1	HapMap	1000GP	T	0.96	C	0.04	T/C
CHB	rs3917322	2	102793246	0.008	1	HapMap	1000GP	A	0.97	G	0.03	A/G
CHB	rs3917326	2	102794326	0.008	1	HapMap	1000GP	C	0.97	T	0.03	C/T

JPT	rs1882511	2	102883721	0.01	1	HapMap	1000GP	G	0.97	A	0.03	G/A
JPT	rs10200945	2	102884757	0.01	1	HapMap	1000GP	A	0.97	T	0.03	A/T
JPT	rs1922288	2	102888565	0.01	1	HapMap	1000GP	T	0.97	C	0.03	T/C
JPT	rs9308855	2	102890795	0.01	1	HapMap	1000GP	A	0.97	G	0.03	A/G
JPT	rs1115281	2	102891107	0.01	1	HapMap	1000GP	C	0.97	G	0.03	C/G
JPT	rs10179570	2	102891632	0.01	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CHB	rs17026916	2	102900381	0.006	1	HapMap	1000GP	A	0.97	T	0.03	A/T
CHB	rs985523	2	102954376	0.301	1	HapMap	1000GP	G	0.97	A	0.03	G/A
JPT	rs985523	2	102954376	0.185	1	HapMap	1000GP	G	0.97	A	0.03	G/A
CHB	rs6719130	2	102958236	0.301	1	HapMap	1000GP	C	0.97	T	0.03	C/T
JPT	rs6719130	2	102958236	0.185	1	HapMap	1000GP	C	0.97	T	0.03	C/T
CHB	rs3771167	2	102986188	0.274	1	HapMap	1000GP	A	0.97	G	0.03	A/G
JPT	rs3771167	2	102986188	0.133	1	HapMap	1000GP	A	0.97	G	0.03	A/G
JPT	rs11465623	2	102993039	0.005	1	HapMap	1000GP	G	0.97	T	0.03	G/T
JPT	rs11465673	2	103035375	0.005	1	HapMap	1000GP	T	0.97	C	0.03	T/C
JPT	rs11465689	2	103040167	0.005	1	HapMap	1000GP	C	0.97	A	0.03	C/A
JPT	rs11465711	2	103060092	0.005	1	HapMap	1000GP	T	0.97	C	0.03	T/C
JPT	rs17821875	2	103071030	0.005	1	HapMap	1000GP	A	0.97	G	0.03	A/G
JPT	rs6753066	2	103095946	0.005	1	HapMap	1000GP	G	0.97	C	0.03	G/C
JPT	rs6756536	2	103096400	0.005	1	HapMap	1000GP	G	0.97	T	0.03	G/T
JPT	rs6543145	2	103096436	0.005	1	HapMap	1000GP	C	0.97	A	0.03	C/A
JPT	rs7582118	2	103096999	0.005	1	HapMap	1000GP	C	0.97	T	0.03	C/T
JPT	rs7607856	2	103097036	0.005	1	HapMap	1000GP	G	0.97	A	0.03	G/A
JPT	rs6747752	2	103097679	0.005	1	HapMap	1000GP	A	0.97	C	0.03	A/C
JPT	rs6751282	2	103098207	0.005	1	HapMap	1000GP	A	0.97	G	0.03	A/G
JPT	rs6736822	2	103098403	0.005	1	HapMap	1000GP	C	0.97	T	0.03	C/T
JPT	rs6741464	2	103099887	0.005	1	HapMap	1000GP	C	0.97	T	0.03	C/T
CHB	rs6543147	2	103099945	0.009	1	HapMap	1000GP	G	0.97	A	0.03	G/A
JPT	rs6543147	2	103099945	0.005	1	HapMap	1000GP	G	0.97	A	0.03	G/A
JPT	rs2080316	2	103104229	0.005	1	HapMap	1000GP	A	0.97	G	0.03	A/G
JPT	rs7558013	2	102992806	0.221	1	HapMap	1000GP	G	0.98	T	0.02	G/T
CHB	rs7558013	2	102992806	0.222	1	HapMap	1000GP	G	0.98	T	0.02	G/T
JPT	rs11465698	2	103054577	0.185	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs11465698	2	103054577	0.223	1	HapMap	1000GP	T	0.98	C	0.02	T/C

JPT	rs6543135	2	103062406	0.185	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs6543135	2	103062406	0.223	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs1880000	2	103099953	0.147	1	HapMap	1000GP	T	0.98	C	0.02	T/C
JPT	rs1880000	2	103099953	0.122	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs6749440	2	103101846	0.147	1	HapMap	1000GP	C	0.98	T	0.02	C/T
JPT	rs6749440	2	103101846	0.122	1	HapMap	1000GP	C	0.98	T	0.02	C/T
JPT	rs1403549	2	103110745	0.122	1	HapMap	1000GP	G	0.98	C	0.02	G/C
CHB	rs1403549	2	103110745	0.147	1	HapMap	1000GP	G	0.98	C	0.02	G/C
JPT	rs17027327	2	103122513	0.122	1	HapMap	1000GP	C	0.98	A	0.02	C/A
CHB	rs17027327	2	103122513	0.147	1	HapMap	1000GP	C	0.98	A	0.02	C/A
CHB	rs7587856	2	103144305	0.147	1	HapMap	1000GP	C	0.98	A	0.02	C/A
CHB	rs9677607	2	103149520	0.147	1	HapMap	1000GP	A	0.98	T	0.02	A/T
CHB	rs7593444	2	103158561	0.147	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CHB	rs17027421	2	103159882	0.146	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs17027428	2	103163175	0.147	1	HapMap	1000GP	G	0.98	A	0.02	G/A
JPT	rs17027428	2	103163175	0.122	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CHB	rs17027430	2	103163237	0.147	1	HapMap	1000GP	T	0.98	C	0.02	T/C
JPT	rs17027430	2	103163237	0.122	1	HapMap	1000GP	T	0.98	C	0.02	T/C
JPT	rs1523197	2	103163732	0.122	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs1523197	2	103163732	0.147	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs2310294	2	103165706	0.147	1	HapMap	1000GP	A	0.98	G	0.02	A/G
JPT	rs2310294	2	103165706	0.122	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs1989399	2	103166742	0.147	1	HapMap	1000GP	G	0.98	A	0.02	G/A
JPT	rs1989399	2	103166742	0.122	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CHB	rs723292	2	103166804	0.147	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs3917256	2	102776855	0.002	1	HapMap	1000GP	C	0.99	T	0.01	C/T
CHB	rs3917281	2	102780653	0.002	1	HapMap	1000GP	G	0.99	T	0.01	G/T
CHB	rs11895033	2	102799751	0.072	1	HapMap	1000GP	T	0.99	C	0.01	T/C
CHB	rs4851550	2	102800046	0.002	1	HapMap	1000GP	A	0.99	G	0.01	A/G
JPT	rs11904409	2	102803184	0.003	1	HapMap	1000GP	G	0.99	A	0.01	G/A
JPT	rs12619169	2	103011084	0.002	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CHB	rs12619169	2	103011084	0.002	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CHB	rs952437	2	102897159	0.073	1	HapMap	1000GP	C	0.9965	T	0.0035	C/T
CHB	rs17639215	2	102953444	0.073	1	HapMap	1000GP	G	0.9983	A	0.0017	G/A

CHB	rs11465596	2	102987093	0.072	1	HapMap	1000GP	C	0.9983	A	0.0017	C/A
JPT	rs7606834	2	102811400	0.066	1	HapMap	1000GP	A	1	T	0	A/T
JPT	rs952438	2	102897385	0.06	1	HapMap	1000GP	G	1	A	0	G/A
CEU	rs17026762	2	102814372	0.017	1	HapMap	1000GP	A	NA	G	.	A/G
CEU	rs1861245	2	102966906	1	1	HapMap	1000GP	A	NA	G	.	A/G
CEU	rs7559566	2	103028041	0.761	1	HapMap	1000GP	G	NA	T	.	G/T
CEU	rs10208196	2	102996345	0.754	1	HapMap	1000GP	G	0.54	A	0.46	G/A
CEU	rs3213732	2	102998279	0.759	1	HapMap	1000GP	A	0.54	G	0.46	A/G
CEU	rs6760621	2	102999952	0.74	1	HapMap	1000GP	T	0.54	C	0.46	T/C
CEU	rs6706002	2	103006104	0.759	1	HapMap	1000GP	A	0.54	G	0.46	A/G
CEU	rs4851571	2	103019000	0.759	1	HapMap	1000GP	C	0.54	T	0.46	C/T
CEU	rs4851572	2	103019031	0.759	1	HapMap	1000GP	G	0.54	A	0.46	G/A
CEU	rs2110662	2	103020139	0.759	1	HapMap	1000GP	A	0.54	T	0.46	A/T
CEU	rs7594402	2	103021267	0.759	1	HapMap	1000GP	A	0.54	T	0.46	A/T
CEU	rs6710034	2	103023678	0.759	1	HapMap	1000GP	G	0.54	A	0.46	G/A
CEU	rs10203558	2	103027640	0.754	1	HapMap	1000GP	T	0.54	C	0.46	T/C
CEU	rs10200952	2	103027651	0.722	1	HapMap	1000GP	A	0.54	C	0.46	A/C
CEU	rs4851576	2	103028895	0.759	1	HapMap	1000GP	C	0.54	T	0.46	C/T
CEU	rs4851577	2	103028921	0.759	1	HapMap	1000GP	T	0.54	C	0.46	T/C
CEU	rs4851579	2	103028984	0.759	1	HapMap	1000GP	G	0.54	A	0.46	G/A
CEU	rs1592458	2	103031749	0.759	1	HapMap	1000GP	A	0.54	T	0.46	A/T
CEU	rs2293224	2	103035779	0.759	1	HapMap	1000GP	T	0.54	C	0.46	T/C
CEU	rs1420100	2	103037002	0.759	1	HapMap	1000GP	C	0.54	A	0.46	C/A
CEU	rs3771155	2	103037826	0.754	1	HapMap	1000GP	A	0.54	G	0.46	A/G
CEU	rs10206291	2	103038863	0.759	1	HapMap	1000GP	T	0.54	C	0.46	T/C
CEU	rs3771154	2	103039360	0.759	1	HapMap	1000GP	C	0.54	T	0.46	C/T
CEU	rs6759479	2	103040047	0.759	1	HapMap	1000GP	A	0.54	C	0.46	A/C
CEU	rs7559845	2	103046214	0.759	1	HapMap	1000GP	T	0.54	G	0.46	T/G
CEU	rs3755265	2	103052816	0.754	1	HapMap	1000GP	C	0.54	A	0.46	C/A
CEU	rs4479442	2	103054074	0.759	1	HapMap	1000GP	A	0.54	T	0.46	A/T
CEU	rs13021177	2	103056493	0.759	1	HapMap	1000GP	A	0.54	G	0.46	A/G
CEU	rs10200410	2	102870871	0.573	0.788	HapMap	1000GP	G	0.55	A	0.45	G/A
CEU	rs1345301	2	102875587	0.573	0.788	HapMap	1000GP	A	0.55	G	0.45	A/G
CEU	rs2310243	2	102877560	0.573	0.788	HapMap	1000GP	A	0.55	G	0.45	A/G

CEU	rs13405355	2	102878206	0.573	0.788	HapMap	1000GP	C	0.55	T	0.45	C/T
CEU	rs13424006	2	102967236	1	1	HapMap	1000GP	T	0.59	C	0.41	T/C
CEU	rs6751967	2	102967413	1	1	HapMap	1000GP	T	0.59	C	0.41	T/C
CEU	rs6749114	2	102967587	1	1	HapMap	1000GP	A	0.59	C	0.41	A/C
CEU	rs10170583	2	102974764	1	1	HapMap	1000GP	G	0.59	A	0.41	G/A
CEU	rs10176664	2	102976172	1	1	HapMap	1000GP	G	0.59	A	0.41	G/A
CEU	rs1974675	2	102986375	0.954	1	HapMap	1000GP	G	0.59	A	0.41	G/A
CEU	rs6543119	2	102963072	0.414	1	HapMap	1000GP	A	0.62	T	0.38	A/T
CEU	rs13017455	2	102964742	0.414	1	HapMap	1000GP	C	0.62	T	0.38	C/T
CEU	rs12468355	2	102861250	0.238	0.611	HapMap	1000GP	T	0.63	G	0.37	T/G
CEU	rs1558626	2	102862070	0.345	0.774	HapMap	1000GP	T	0.63	A	0.37	T/A
CEU	rs1558623	2	102862402	0.345	0.774	HapMap	1000GP	T	0.63	A	0.37	T/A
CEU	rs17689452	2	102864681	0.345	0.774	HapMap	1000GP	A	0.63	G	0.37	A/G
CEU	rs1035126	2	103019981	0.337	0.656	HapMap	1000GP	C	0.63	T	0.37	C/T
CEU	rs2080288	2	103022166	0.337	0.656	HapMap	1000GP	G	0.63	A	0.37	G/A
CEU	rs4851578	2	103028951	0.341	0.649	HapMap	1000GP	T	0.63	G	0.37	T/G
CEU	rs7602207	2	103032366	0.359	0.653	HapMap	1000GP	C	0.63	G	0.37	C/G
CEU	rs6543144	2	103092575	0.337	0.656	HapMap	1000GP	A	0.63	G	0.37	A/G
CEU	rs10186746	2	102866377	0.437	0.882	HapMap	1000GP	G	0.64	A	0.36	G/A
CEU	rs11465700	2	103057668	0.337	0.656	HapMap	1000GP	G	0.64	A	0.36	G/A
CEU	rs10169192	2	103072211	0.337	0.656	HapMap	1000GP	A	0.64	G	0.36	A/G
CEU	rs2310301	2	103072935	0.337	0.656	HapMap	1000GP	C	0.64	T	0.36	C/T
CEU	rs6543140	2	103074274	0.337	0.656	HapMap	1000GP	G	0.64	T	0.36	G/T
CEU	rs13390895	2	103075499	0.337	0.656	HapMap	1000GP	G	0.64	A	0.36	G/A
CEU	rs4851591	2	103077423	0.337	0.656	HapMap	1000GP	T	0.64	C	0.36	T/C
CEU	rs7561351	2	103077780	0.337	0.656	HapMap	1000GP	A	0.64	G	0.36	A/G
CEU	rs13393175	2	103078849	0.337	0.656	HapMap	1000GP	T	0.64	G	0.36	T/G
CEU	rs6734203	2	103080066	0.301	0.626	HapMap	1000GP	G	0.64	C	0.36	G/C
CEU	rs6543142	2	103082006	0.36	0.705	HapMap	1000GP	T	0.64	C	0.36	T/C
CEU	rs10200945	2	102884757	0.245	0.637	HapMap	1000GP	A	0.65	T	0.35	A/T
CEU	rs1115281	2	102891107	0.245	0.637	HapMap	1000GP	C	0.65	G	0.35	C/G
CEU	rs950880	2	102932562	0.293	0.92	HapMap	1000GP	C	0.65	A	0.35	C/A
CEU	rs13001325	2	102939036	0.268	0.909	HapMap	1000GP	C	0.65	T	0.35	C/T
CEU	rs12479210	2	102949161	0.293	0.92	HapMap	1000GP	C	0.65	T	0.35	C/T

CEU	rs10208293	2	102966310	0.576	1	HapMap	1000GP	G	0.72	A	0.28	G/A
CEU	rs7600901	2	102915571	0.097	0.635	HapMap	1000GP	A	0.73	G	0.27	A/G
CEU	rs887972	2	103040945	0.313	1	HapMap	1000GP	G	0.73	A	0.27	G/A
CEU	rs887971	2	103041167	0.316	1	HapMap	1000GP	T	0.73	C	0.27	T/C
CEU	rs2310220	2	102951851	0.273	1	HapMap	1000GP	G	0.74	A	0.26	G/A
CEU	rs17027258	2	103091540	0.301	1	HapMap	1000GP	A	0.74	G	0.26	A/G
CEU	rs1420103	2	102948632	0.273	1	HapMap	1000GP	A	0.75	C	0.25	A/C
CEU	rs873022	2	102955683	0.301	1	HapMap	1000GP	G	0.75	T	0.25	G/T
CEU	rs3771177	2	102955860	0.301	1	HapMap	1000GP	G	0.75	T	0.25	G/T
CEU	rs3732129	2	102957532	0.301	1	HapMap	1000GP	T	0.75	C	0.25	T/C
CEU	rs3821204	2	102960281	0.301	1	HapMap	1000GP	C	0.75	G	0.25	C/G
CEU	rs12469506	2	102965871	0.301	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs3771172	2	102985812	0.301	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs3771171	2	102985950	0.285	1	HapMap	1000GP	T	0.75	C	0.25	T/C
CEU	rs2160202	2	102986154	0.296	1	HapMap	1000GP	G	0.75	A	0.25	G/A
CEU	rs7558013	2	102992806	0.604	1	HapMap	1000GP	G	0.75	T	0.25	G/T
CEU	rs17027037	2	102994884	0.301	1	HapMap	1000GP	A	0.75	G	0.25	A/G
CEU	rs2080289	2	102995020	0.301	1	HapMap	1000GP	G	0.75	A	0.25	G/A
CEU	rs11683700	2	102996805	0.308	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs4851570	2	103006387	0.301	1	HapMap	1000GP	A	0.75	G	0.25	A/G
CEU	rs11693955	2	103029165	0.301	1	HapMap	1000GP	A	0.75	T	0.25	A/T
CEU	rs3771156	2	103036677	0.301	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs11681718	2	103051144	0.301	1	HapMap	1000GP	A	0.75	G	0.25	A/G
CEU	rs4851582	2	103051558	0.301	1	HapMap	1000GP	T	0.75	C	0.25	T/C
CEU	rs17027179	2	103057159	0.301	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs10490203	2	103059237	0.301	1	HapMap	1000GP	T	0.75	G	0.25	T/G
CEU	rs11694360	2	103061147	0.177	0.732	HapMap	1000GP	G	0.75	A	0.25	G/A
CEU	rs11123928	2	103061286	0.177	0.732	HapMap	1000GP	G	0.75	A	0.25	G/A
CEU	rs7597017	2	103062116	0.185	0.73	HapMap	1000GP	A	0.75	G	0.25	A/G
CEU	rs6543135	2	103062406	0.708	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs17027230	2	103079330	0.301	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs3771202	2	102772669	0.104	0.712	HapMap	1000GP	C	0.77	G	0.23	C/G
CEU	rs3917245	2	102775155	0.112	0.732	HapMap	1000GP	G	0.77	A	0.23	G/A
CEU	rs3917246	2	102775164	0.112	0.732	HapMap	1000GP	T	0.77	C	0.23	T/C

CEU	rs759381	2	103094323	0.26	1	HapMap	1000GP	A	0.77	T	0.23	A/T
CEU	rs4851008	2	103026611	0.209	1	HapMap	1000GP	G	0.78	C	0.22	G/C
CEU	rs12712153	2	103111761	0.227	0.893	HapMap	1000GP	C	0.78	T	0.22	C/T
CEU	rs11687071	2	103111920	0.232	0.898	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs7566063	2	103112565	0.237	0.898	HapMap	1000GP	C	0.78	A	0.22	C/A
CEU	rs7591878	2	103112658	0.227	0.893	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs6543153	2	103114203	0.232	0.898	HapMap	1000GP	T	0.78	C	0.22	T/C
CEU	rs6543154	2	103114334	0.222	0.893	HapMap	1000GP	T	0.78	C	0.22	T/C
CEU	rs6543155	2	103114895	0.222	0.893	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs7573566	2	103115205	0.232	0.898	HapMap	1000GP	T	0.78	C	0.22	T/C
CEU	rs11123934	2	103115568	0.232	0.898	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs12987295	2	103115838	0.232	0.898	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs12995030	2	103116466	0.248	0.898	HapMap	1000GP	C	0.78	G	0.22	C/G
CEU	rs6728288	2	103117268	0.232	0.898	HapMap	1000GP	A	0.78	T	0.22	A/T
CEU	rs2075192	2	103118228	0.232	0.898	HapMap	1000GP	A	0.78	G	0.22	A/G
CEU	rs2075191	2	103118299	0.184	0.872	HapMap	1000GP	G	0.78	T	0.22	G/T
CEU	rs2075190	2	103118559	0.232	0.898	HapMap	1000GP	A	0.78	T	0.22	A/T
CEU	rs2075189	2	103118689	0.237	0.898	HapMap	1000GP	C	0.78	G	0.22	C/G
CEU	rs11690932	2	103119029	0.232	0.898	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs4851605	2	103120868	0.258	0.894	HapMap	1000GP	A	0.78	G	0.22	A/G
CEU	rs4851606	2	103120889	0.237	0.898	HapMap	1000GP	G	0.78	A	0.22	G/A
CEU	rs3917256	2	102776855	0.094	0.712	HapMap	1000GP	C	0.79	T	0.21	C/T
CEU	rs2058622	2	102985424	0.167	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs3771170	2	102985980	0.137	0.855	HapMap	1000GP	T	0.79	A	0.21	T/A
CEU	rs2058623	2	102986170	0.175	1	HapMap	1000GP	C	0.79	T	0.21	C/T
CEU	rs1465321	2	102986618	0.167	1	HapMap	1000GP	T	0.79	C	0.21	T/C
CEU	rs2270297	2	102992675	0.209	1	HapMap	1000GP	T	0.79	C	0.21	T/C
CEU	rs6753717	2	102993161	0.209	1	HapMap	1000GP	A	0.79	C	0.21	A/C
CEU	rs6750020	2	102994714	0.209	1	HapMap	1000GP	G	0.79	A	0.21	G/A
CEU	rs4851007	2	103024813	0.209	1	HapMap	1000GP	T	0.79	G	0.21	T/G
CEU	rs4851575	2	103025203	0.209	1	HapMap	1000GP	G	0.79	A	0.21	G/A
CEU	rs1807782	2	103033147	0.209	1	HapMap	1000GP	C	0.79	T	0.21	C/T
CEU	rs3755268	2	103038527	0.209	1	HapMap	1000GP	C	0.79	G	0.21	C/G
CEU	rs3817465	2	103039584	0.209	1	HapMap	1000GP	A	0.79	T	0.21	A/T

CEU	rs11694658	2	103045020	0.195	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs2160232	2	103046880	0.237	1	HapMap	1000GP	G	0.79	A	0.21	G/A
CEU	rs6716784	2	103048467	0.196	1	HapMap	1000GP	T	0.79	G	0.21	T/G
CEU	rs6543134	2	103050458	0.187	1	HapMap	1000GP	T	0.79	G	0.21	T/G
CEU	rs2110735	2	103050925	0.209	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs2110734	2	103052206	0.201	1	HapMap	1000GP	C	0.79	T	0.21	C/T
CEU	rs6746271	2	103052995	0.213	1	HapMap	1000GP	G	0.79	C	0.21	G/C
CEU	rs2058658	2	103054803	0.209	1	HapMap	1000GP	T	0.79	C	0.21	T/C
CEU	rs4851009	2	103055644	0.209	1	HapMap	1000GP	G	0.79	A	0.21	G/A
CEU	rs1558650	2	103060024	0.209	1	HapMap	1000GP	T	0.79	A	0.21	T/A
CEU	rs6734736	2	103062880	0.122	1	HapMap	1000GP	C	0.79	T	0.21	C/T
CEU	rs4070554	2	103074493	0.209	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs6761825	2	103075561	0.209	1	HapMap	1000GP	T	0.79	C	0.21	T/C
CEU	rs6705001	2	103076210	0.209	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs6543141	2	103076351	0.209	1	HapMap	1000GP	G	0.79	A	0.21	G/A
CEU	rs4241210	2	103078740	0.209	1	HapMap	1000GP	G	0.79	A	0.21	G/A
CEU	rs6720564	2	103079297	0.209	1	HapMap	1000GP	T	0.79	C	0.21	T/C
CEU	rs6717915	2	103079619	0.209	1	HapMap	1000GP	A	0.79	C	0.21	A/C
CEU	rs6718157	2	103079814	0.201	1	HapMap	1000GP	A	0.79	T	0.21	A/T
CEU	rs917996	2	103082273	0.209	1	HapMap	1000GP	C	0.79	A	0.21	C/A
CEU	rs990171	2	103086770	0.201	1	HapMap	1000GP	A	0.79	C	0.21	A/C
CEU	rs1468791	2	103092021	0.209	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs7597819	2	103092906	0.209	1	HapMap	1000GP	A	0.79	G	0.21	A/G
CEU	rs6737668	2	103093081	0.209	1	HapMap	1000GP	C	0.79	T	0.21	C/T
CEU	rs10469840	2	103093243	0.221	1	HapMap	1000GP	T	0.79	C	0.21	T/C
CEU	rs13027294	2	102860074	0.159	1	HapMap	1000GP	G	0.8	C	0.2	G/C
CEU	rs11677452	2	102865236	0.21	1	HapMap	1000GP	A	0.8	T	0.2	A/T
CEU	rs9646944	2	102865875	0.21	1	HapMap	1000GP	G	0.8	C	0.2	G/C
CEU	rs11685483	2	103159093	0.145	0.859	HapMap	1000GP	A	0.8	C	0.2	A/C
CEU	rs6739426	2	103160443	0.145	0.859	HapMap	1000GP	A	0.8	G	0.2	A/G
CEU	rs11899041	2	103161053	0.145	0.859	HapMap	1000GP	T	0.8	A	0.2	T/A
CEU	rs1303960	2	103165832	0.145	0.859	HapMap	1000GP	G	0.8	A	0.2	G/A
CEU	rs9989842	2	103123633	0.145	0.859	HapMap	1000GP	C	0.81	G	0.19	C/G
CEU	rs9989749	2	103123642	0.145	0.859	HapMap	1000GP	G	0.81	A	0.19	G/A

CEU	rs6751949	2	103125138	0.145	0.859	HapMap	1000GP	G	0.81	A	0.19	G/A
CEU	rs6724322	2	103125182	0.145	0.859	HapMap	1000GP	C	0.81	T	0.19	C/T
CEU	rs4851607	2	103125632	0.157	0.827	HapMap	1000GP	C	0.81	T	0.19	C/T
CEU	rs10195948	2	103125736	0.134	0.843	HapMap	1000GP	T	0.81	C	0.19	T/C
CEU	rs12712155	2	103127963	0.145	0.859	HapMap	1000GP	A	0.81	T	0.19	A/T
CEU	rs4851609	2	103128866	0.145	0.859	HapMap	1000GP	T	0.81	C	0.19	T/C
CEU	rs11676371	2	103129692	0.123	0.828	HapMap	1000GP	G	0.81	C	0.19	G/C
CEU	rs2192758	2	103132269	0.145	0.859	HapMap	1000GP	C	0.81	G	0.19	C/G
CEU	rs2192757	2	103132378	0.156	0.864	HapMap	1000GP	C	0.81	T	0.19	C/T
CEU	rs6714379	2	103133310	0.147	0.857	HapMap	1000GP	A	0.81	G	0.19	A/G
CEU	rs1523203	2	103135759	0.156	0.864	HapMap	1000GP	A	0.81	G	0.19	A/G
CEU	rs4851611	2	103135938	0.156	0.864	HapMap	1000GP	A	0.81	T	0.19	A/T
CEU	rs4851613	2	103137990	0.157	0.868	HapMap	1000GP	T	0.81	C	0.19	T/C
CEU	rs6750971	2	103138825	0.156	0.864	HapMap	1000GP	A	0.81	G	0.19	A/G
CEU	rs10193407	2	103139298	0.156	0.864	HapMap	1000GP	C	0.81	T	0.19	C/T
CEU	rs11123935	2	103139751	0.156	0.864	HapMap	1000GP	A	0.81	G	0.19	A/G
CEU	rs1024798	2	103141651	0.145	0.859	HapMap	1000GP	G	0.81	C	0.19	G/C
CEU	rs6724213	2	103151219	0.13	0.822	HapMap	1000GP	A	0.81	C	0.19	A/C
CEU	rs2871474	2	103151441	0.145	0.859	HapMap	1000GP	G	0.81	A	0.19	G/A
CEU	rs2287048	2	102773999	0.227	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs17027029	2	102990648	0.181	1	HapMap	1000GP	G	0.82	C	0.18	G/C
CEU	rs3771164	2	102991786	0.178	1	HapMap	1000GP	A	0.82	T	0.18	A/T
CEU	rs12991737	2	103018128	0.198	1	HapMap	1000GP	T	0.82	A	0.18	T/A
CEU	rs10181785	2	103025274	0.193	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs12712148	2	103025547	0.193	1	HapMap	1000GP	G	0.82	A	0.18	G/A
CEU	rs7586983	2	103028066	0.193	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs2272127	2	103039873	0.21	1	HapMap	1000GP	C	0.82	G	0.18	C/G
CEU	rs10166330	2	103050390	0.193	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs11465736	2	103067930	0	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs10169676	2	103074919	0.193	1	HapMap	1000GP	G	0.82	A	0.18	G/A
CEU	rs741284	2	103083324	0.193	1	HapMap	1000GP	G	0.82	C	0.18	G/C
CEU	rs10172116	2	103087573	0.164	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs13030642	2	103091585	0.193	1	HapMap	1000GP	C	0.82	A	0.18	C/A
CEU	rs3732127	2	103013750	0.193	1	HapMap	1000GP	G	0.83	C	0.17	G/C

CEU	rs2241132	2	102804035	0.086	1	HapMap	1000GP	C	0.84	A	0.16	C/A
CEU	rs1882510	2	102883618	0.209	1	HapMap	1000GP	C	0.84	T	0.16	C/T
CEU	rs4851610	2	103134652	0.077	0.81	HapMap	1000GP	C	0.84	G	0.16	C/G
CEU	rs950881	2	102932512	0.046	1	HapMap	1000GP	G	0.85	T	0.15	G/T
CEU	rs1558648	2	102810168	0.1	0.792	HapMap	1000GP	T	0.86	G	0.14	T/G
CEU	rs12996377	2	102830478	0.12	0.827	HapMap	1000GP	T	0.86	A	0.14	T/A
CEU	rs7572871	2	102853838	0.053	0.719	HapMap	1000GP	G	0.86	A	0.14	G/A
CEU	rs11690644	2	102914214	0.181	1	HapMap	1000GP	A	0.86	G	0.14	A/G
CEU	rs985523	2	102954376	0.322	1	HapMap	1000GP	G	0.86	A	0.14	G/A
CEU	rs13408569	2	102955056	0.159	1	HapMap	1000GP	G	0.86	C	0.14	G/C
CEU	rs13408661	2	102955082	0.159	1	HapMap	1000GP	G	0.86	A	0.14	G/A
CEU	rs10173081	2	102957348	0.159	1	HapMap	1000GP	C	0.86	T	0.14	C/T
CEU	rs6719130	2	102958236	0.322	1	HapMap	1000GP	C	0.86	T	0.14	C/T
CEU	rs3771167	2	102986188	0.277	1	HapMap	1000GP	A	0.86	G	0.14	A/G
CEU	rs6728945	2	102986471	0.31	1	HapMap	1000GP	T	0.86	C	0.14	T/C
CEU	rs17639215	2	102953444	0.322	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs12989197	2	102962739	0.056	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs12996097	2	102963628	0.056	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs13028993	2	102963949	0.056	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CEU	rs17696376	2	102965153	0.193	1	HapMap	1000GP	C	0.87	T	0.13	C/T
CEU	rs12999542	2	102965392	0.056	1	HapMap	1000GP	A	0.87	C	0.13	A/C
CEU	rs4851567	2	102972807	0.193	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs12105808	2	102974222	0.198	1	HapMap	1000GP	A	0.87	T	0.13	A/T
CEU	rs11465596	2	102987093	0.301	1	HapMap	1000GP	C	0.87	A	0.13	C/A
CEU	rs6759588	2	103040159	0.241	1	HapMap	1000GP	A	0.87	G	0.13	A/G
CEU	rs11465698	2	103054577	0.264	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CEU	rs1880000	2	103099953	0.245	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CEU	rs6749440	2	103101846	0.245	1	HapMap	1000GP	C	0.87	T	0.13	C/T
CEU	rs1403549	2	103110745	0.245	1	HapMap	1000GP	G	0.87	C	0.13	G/C
CEU	rs17027327	2	103122513	0.245	1	HapMap	1000GP	C	0.87	A	0.13	C/A
CEU	rs7587856	2	103144305	0.242	1	HapMap	1000GP	C	0.87	A	0.13	C/A
CEU	rs9677607	2	103149520	0.245	1	HapMap	1000GP	A	0.87	T	0.13	A/T
CEU	rs7593444	2	103158561	0.245	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs17027421	2	103159882	0.252	1	HapMap	1000GP	A	0.87	G	0.13	A/G

CEU	rs7582378	2	103162263	0.245	1	HapMap	1000GP	C	0.87	A	0.13	C/A
CEU	rs17027428	2	103163175	0.245	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs17027430	2	103163237	0.245	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CEU	rs1523197	2	103163732	0.245	1	HapMap	1000GP	A	0.87	G	0.13	A/G
CEU	rs2310294	2	103165706	0.245	1	HapMap	1000GP	A	0.87	G	0.13	A/G
CEU	rs1989399	2	103166742	0.245	1	HapMap	1000GP	G	0.87	A	0.13	G/A
CEU	rs723292	2	103166804	0.245	1	HapMap	1000GP	A	0.87	G	0.13	A/G
CEU	rs1476984	2	102912269	0.176	1	HapMap	1000GP	C	0.88	T	0.12	C/T
CEU	rs13425475	2	103025181	0.188	1	HapMap	1000GP	G	0.88	A	0.12	G/A
CEU	rs6724273	2	103080103	0.21	1	HapMap	1000GP	T	0.88	A	0.12	T/A
CEU	rs13008334	2	103167031	0.05	0.721	HapMap	1000GP	A	0.88	G	0.12	A/G
CEU	rs11465623	2	102993039	0.05	1	HapMap	1000GP	G	0.89	T	0.11	G/T
CEU	rs11465673	2	103035375	0.034	1	HapMap	1000GP	T	0.89	C	0.11	T/C
CEU	rs17821875	2	103071030	0.056	1	HapMap	1000GP	A	0.89	G	0.11	A/G
CEU	rs6753066	2	103095946	0.047	1	HapMap	1000GP	G	0.9	C	0.1	G/C
CEU	rs6756536	2	103096400	0.047	1	HapMap	1000GP	G	0.9	T	0.1	G/T
CEU	rs6543145	2	103096436	0.047	1	HapMap	1000GP	C	0.9	A	0.1	C/A
CEU	rs7582118	2	103096999	0.047	1	HapMap	1000GP	C	0.9	T	0.1	C/T
CEU	rs7607856	2	103097036	0.047	1	HapMap	1000GP	G	0.9	A	0.1	G/A
CEU	rs6747752	2	103097679	0.047	1	HapMap	1000GP	A	0.9	C	0.1	A/C
CEU	rs6751282	2	103098207	0.047	1	HapMap	1000GP	A	0.9	G	0.1	A/G
CEU	rs6736822	2	103098403	0.047	1	HapMap	1000GP	C	0.9	T	0.1	C/T
CEU	rs6741464	2	103099887	0.047	1	HapMap	1000GP	C	0.9	T	0.1	C/T
CEU	rs6543147	2	103099945	0.047	1	HapMap	1000GP	G	0.9	A	0.1	G/A
CEU	rs2080316	2	103104229	0.047	1	HapMap	1000GP	A	0.9	G	0.1	A/G
CEU	rs17027352	2	103138836	0.042	1	HapMap	1000GP	C	0.9	T	0.1	C/T
CEU	rs7576682	2	103143312	0.026	1	HapMap	1000GP	G	0.9	A	0.1	G/A
CEU	rs3849363	2	103143548	0.047	1	HapMap	1000GP	T	0.9	G	0.1	T/G
CEU	rs13388541	2	103147818	0.042	1	HapMap	1000GP	T	0.9	C	0.1	T/C
CEU	rs10183491	2	103151587	0.047	1	HapMap	1000GP	T	0.9	G	0.1	T/G
CEU	rs17027415	2	103154594	0.047	1	HapMap	1000GP	C	0.9	A	0.1	C/A
CEU	rs4851553	2	102811808	0.073	0.766	HapMap	1000GP	A	0.91	G	0.09	A/G
CEU	rs1362347	2	102919585	0.015	1	HapMap	1000GP	C	0.91	T	0.09	C/T
CEU	rs13001301	2	102938998	0.015	1	HapMap	1000GP	C	0.91	T	0.09	C/T

CEU	rs17695648	2	102948181	0.015	1	HapMap	1000GP	A	0.91	G	0.09	A/G
CEU	rs3755278	2	102952217	0.015	1	HapMap	1000GP	T	0.91	C	0.09	T/C
CEU	rs13016771	2	102959080	0.015	1	HapMap	1000GP	G	0.91	A	0.09	G/A
CEU	rs2228139	2	102781649	0.045	0.684	HapMap	1000GP	C	0.92	G	0.08	C/G
CEU	rs3917299	2	102786086	0.045	0.684	HapMap	1000GP	A	0.92	G	0.08	A/G
CEU	rs3917268	2	102778862	0.015	1	HapMap	1000GP	A	0.95	T	0.05	A/T
CEU	rs3917291	2	102782166	0.04	1	HapMap	1000GP	G	0.95	A	0.05	G/A
CEU	rs3917314	2	102790863	0.04	1	HapMap	1000GP	A	0.95	C	0.05	A/C
CEU	rs3917320	2	102792875	0.04	1	HapMap	1000GP	A	0.95	C	0.05	A/C
CEU	rs12995229	2	102846907	0.039	1	HapMap	1000GP	A	0.95	G	0.05	A/G
CEU	rs2041747	2	102788409	0.023	1	HapMap	1000GP	G	0.96	A	0.04	G/A
CEU	rs9808381	2	102816909	0.023	1	HapMap	1000GP	C	0.96	T	0.04	C/T
CEU	rs1922300	2	102819594	0.023	1	HapMap	1000GP	C	0.96	T	0.04	C/T
CEU	rs13021607	2	102824726	0.042	1	HapMap	1000GP	G	0.96	A	0.04	G/A
CEU	rs10490570	2	102827739	0.04	1	HapMap	1000GP	C	0.96	T	0.04	C/T
CEU	rs12989930	2	102829822	0.04	1	HapMap	1000GP	T	0.96	C	0.04	T/C
CEU	rs13002813	2	102831280	0.04	1	HapMap	1000GP	T	0.96	C	0.04	T/C
CEU	rs13028635	2	102832284	0.04	1	HapMap	1000GP	C	0.96	T	0.04	C/T
CEU	rs13033782	2	102843833	0.039	1	HapMap	1000GP	G	0.96	A	0.04	G/A
CEU	rs13017475	2	102853208	0.04	1	HapMap	1000GP	C	0.96	T	0.04	C/T
CEU	rs12993937	2	102855831	0.054	1	HapMap	1000GP	G	0.96	T	0.04	G/T
CEU	rs13018912	2	102864310	0.04	1	HapMap	1000GP	G	0.96	T	0.04	G/T
CEU	rs12997225	2	102864748	0.04	1	HapMap	1000GP	A	0.96	C	0.04	A/C
CEU	rs13015695	2	102888441	0.04	1	HapMap	1000GP	C	0.96	A	0.04	C/A
CEU	rs12989419	2	102900754	0.013	1	HapMap	1000GP	A	0.96	C	0.04	A/C
CEU	rs13024772	2	102902173	0.013	1	HapMap	1000GP	G	0.96	A	0.04	G/A
CEU	rs13407644	2	102905351	0.013	1	HapMap	1000GP	A	0.96	G	0.04	A/G
CEU	rs13017541	2	102906176	0.015	1	HapMap	1000GP	C	0.96	T	0.04	C/T
CEU	rs13024003	2	102907761	0.015	1	HapMap	1000GP	G	0.96	C	0.04	G/C
CEU	rs12465829	2	103072320	0.039	1	HapMap	1000GP	T	0.96	C	0.04	T/C
CEU	rs17824661	2	103162027	0.031	1	HapMap	1000GP	A	0.96	C	0.04	A/C
CEU	rs17696274	2	102963227	0.039	1	HapMap	1000GP	C	0.97	G	0.03	C/G
CEU	rs11465677	2	103035764	0.008	1	HapMap	1000GP	G	0.97	A	0.03	G/A
CEU	rs12987260	2	103055634	0	1	HapMap	1000GP	G	0.97	T	0.03	G/T

CEU	rs10196556	2	103075079	0	1	HapMap	1000GP	C	0.97	T	0.03	C/T
CEU	rs3917236	2	102772268	0.008	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs2080312	2	102774810	0.008	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CEU	rs17026899	2	102890137	0.008	1	HapMap	1000GP	A	0.98	C	0.02	A/C
CEU	rs1200327	2	102900355	0.031	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CEU	rs13029918	2	102957291	0.013	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CEU	rs12997015	2	103042401	0	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CEU	rs3917226	2	102769457	0.008	1	HapMap	1000GP	A	0.99	T	0.01	A/T
CEU	rs3917270	2	102779392	0.008	1	HapMap	1000GP	A	0.99	G	0.01	A/G
CEU	rs3917271	2	102779509	0.008	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CEU	rs3917298	2	102785255	0.008	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CEU	rs3917312	2	102790182	0.008	1	HapMap	1000GP	G	0.99	C	0.01	G/C
CEU	rs3917313	2	102790240	0.008	1	HapMap	1000GP	T	0.99	C	0.01	T/C
CEU	rs3917327	2	102794379	0.008	1	HapMap	1000GP	C	0.99	G	0.01	C/G
CEU	rs3917333	2	102796783	0.008	1	HapMap	1000GP	T	0.99	A	0.01	T/A
CEU	rs3917334	2	102796880	0.008	1	HapMap	1000GP	G	0.99	T	0.01	G/T
CEU	rs7562706	2	102810899	0.008	1	HapMap	1000GP	G	0.99	T	0.01	G/T
CEU	rs7606834	2	102811400	0.008	1	HapMap	1000GP	A	0.99	T	0.01	A/T
CEU	rs7596051	2	102817675	0.008	1	HapMap	1000GP	C	0.99	T	0.01	C/T
CEU	rs6713939	2	102823188	0.008	1	HapMap	1000GP	C	0.99	T	0.01	C/T
CEU	rs6730496	2	102839010	0.008	1	HapMap	1000GP	A	0.99	G	0.01	A/G
CEU	rs6752537	2	102841912	0.026	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CEU	rs13428595	2	102850317	0.008	1	HapMap	1000GP	T	0.99	G	0.01	T/G
CEU	rs11465674	2	103035434	0.008	1	HapMap	1000GP	T	0.99	G	0.01	T/G
CEU	rs11465731	2	103066939	0.008	1	HapMap	1000GP	G	0.99	A	0.01	G/A
YRI	rs3917321	2	102793221	0.023	1	HapMap	1000GP	A	NA	G	NA	A/G
YRI	rs3917302	2	102787096	0.024	1	HapMap	1000GP	C	NA	T	NA	C/T
YRI	rs1861245	2	102966906	1	1	HapMap	1000GP	A	NA	G	NA	A/G
YRI	rs11465679	2	103036409	0.023	1	HapMap	1000GP	A	NA	G	NA	A/G
YRI	rs10208293	2	102966310	0.489	1	HapMap	1000GP	G	0.55	A	0.45	G/A
YRI	rs6734742	2	102967857	0.852	1	HapMap	1000GP	C	0.66	T	0.34	C/T
YRI	rs6752482	2	102967858	0.827	1	HapMap	1000GP	T	0.66	C	0.34	T/C
YRI	rs10176664	2	102976172	0.916	1	HapMap	1000GP	G	0.67	A	0.33	G/A
YRI	rs1974675	2	102986375	0.951	1	HapMap	1000GP	G	0.67	A	0.33	G/A

YRI	rs10170583	2	102974764	0.956	1	HapMap	1000GP	G	0.68	A	0.32	G/A
YRI	rs10181869	2	102801852	0.072	0.686	HapMap	1000GP	C	0.7	A	0.3	C/A
YRI	rs6543117	2	102929445	0.072	1	HapMap	1000GP	A	0.7	G	0.3	A/G
YRI	rs6751977	2	102967430	0.806	1	HapMap	1000GP	T	0.7	C	0.3	T/C
YRI	rs13408569	2	102955056	0.216	1	HapMap	1000GP	G	0.73	C	0.27	G/C
YRI	rs13408661	2	102955082	0.216	1	HapMap	1000GP	G	0.73	A	0.27	G/A
YRI	rs10173081	2	102957348	0.216	1	HapMap	1000GP	C	0.73	T	0.27	C/T
YRI	rs1882511	2	102883721	0.043	0.749	HapMap	1000GP	G	0.74	A	0.26	G/A
YRI	rs1922288	2	102888565	0.043	0.749	HapMap	1000GP	T	0.75	C	0.25	T/C
YRI	rs9308855	2	102890795	0.043	0.749	HapMap	1000GP	A	0.75	G	0.25	A/G
YRI	rs13424006	2	102967236	1	1	HapMap	1000GP	T	0.76	C	0.24	T/C
YRI	rs6751967	2	102967413	1	1	HapMap	1000GP	T	0.76	C	0.24	T/C
YRI	rs6749114	2	102967587	1	1	HapMap	1000GP	A	0.76	C	0.24	A/C
YRI	rs7572871	2	102853838	0.056	0.674	HapMap	1000GP	G	0.77	A	0.23	G/A
YRI	rs10185897	2	102966790	0.145	0.881	HapMap	1000GP	C	0.77	A	0.23	C/A
YRI	rs17026825	2	102836665	0.046	0.616	HapMap	1000GP	A	0.78	T	0.22	A/T
YRI	rs1024791	2	102837910	0.046	0.616	HapMap	1000GP	T	0.78	C	0.22	T/C
YRI	rs3771186	2	102840411	0.047	0.623	HapMap	1000GP	G	0.78	A	0.22	G/A
YRI	rs10198860	2	102842633	0.051	0.634	HapMap	1000GP	T	0.78	A	0.22	T/A
YRI	rs13416449	2	102842665	0.045	0.607	HapMap	1000GP	A	0.78	G	0.22	A/G
YRI	rs12105808	2	102974222	0.07	1	HapMap	1000GP	A	0.79	T	0.21	A/T
YRI	rs10166535	2	102809860	0.042	0.601	HapMap	1000GP	G	0.8	T	0.2	G/T
YRI	rs3821206	2	102817648	0.042	0.601	HapMap	1000GP	C	0.8	T	0.2	C/T
YRI	rs4851567	2	102972807	0.077	1	HapMap	1000GP	G	0.8	A	0.2	G/A
YRI	rs13425475	2	103025181	0.064	0.806	HapMap	1000GP	G	0.81	A	0.19	G/A
YRI	rs13415651	2	103052038	0.043	0.749	HapMap	1000GP	G	0.82	C	0.18	G/C
YRI	rs10202399	2	103019317	0.038	0.729	HapMap	1000GP	G	0.83	T	0.17	G/T
YRI	rs13001325	2	102939036	0.376	0.901	HapMap	1000GP	C	0.84	T	0.16	C/T
YRI	rs12479210	2	102949161	0.466	1	HapMap	1000GP	C	0.84	T	0.16	C/T
YRI	rs6736287	2	103017996	0.036	0.713	HapMap	1000GP	T	0.84	C	0.16	T/C
YRI	rs2310239	2	102824201	0.051	1	HapMap	1000GP	G	0.85	A	0.15	G/A
YRI	rs950880	2	102932562	0.466	1	HapMap	1000GP	C	0.85	A	0.15	C/A
YRI	rs2075185	2	103070988	0.054	0.666	HapMap	1000GP	A	0.85	G	0.15	A/G
YRI	rs10179570	2	102891632	0.031	1	HapMap	1000GP	T	0.87	C	0.13	T/C

YRI	rs3917299	2	102786086	0.016	0.645	HapMap	1000GP	A	0.88	G	0.12	A/G
YRI	rs4070554	2	103074493	0.054	0.666	HapMap	1000GP	A	0.88	G	0.12	A/G
YRI	rs6761825	2	103075561	0.054	0.666	HapMap	1000GP	T	0.88	C	0.12	T/C
YRI	rs6720564	2	103079297	0.054	0.666	HapMap	1000GP	T	0.88	C	0.12	T/C
YRI	rs2058622	2	102985424	0.053	0.662	HapMap	1000GP	A	0.89	G	0.11	A/G
YRI	rs1465321	2	102986618	0.053	0.662	HapMap	1000GP	T	0.89	C	0.11	T/C
YRI	rs2160232	2	103046880	0.058	1	HapMap	1000GP	G	0.89	A	0.11	G/A
YRI	rs6705001	2	103076210	0.054	0.666	HapMap	1000GP	A	0.89	G	0.11	A/G
YRI	rs6543141	2	103076351	0.054	0.666	HapMap	1000GP	G	0.89	A	0.11	G/A
YRI	rs4241210	2	103078740	0.054	0.666	HapMap	1000GP	G	0.89	A	0.11	G/A
YRI	rs6717915	2	103079619	0.054	0.666	HapMap	1000GP	A	0.89	C	0.11	A/C
YRI	rs6718157	2	103079814	0.054	0.666	HapMap	1000GP	A	0.89	T	0.11	A/T
YRI	rs917996	2	103082273	0.054	0.666	HapMap	1000GP	C	0.89	A	0.11	C/A
YRI	rs1468791	2	103092021	0.054	0.666	HapMap	1000GP	A	0.89	G	0.11	A/G
YRI	rs13001301	2	102938998	0.173	1	HapMap	1000GP	C	0.9	T	0.1	C/T
YRI	rs17695648	2	102948181	0.227	1	HapMap	1000GP	A	0.9	G	0.1	A/G
YRI	rs3755278	2	102952217	0.227	1	HapMap	1000GP	T	0.9	C	0.1	T/C
YRI	rs6716784	2	103048467	0.07	1	HapMap	1000GP	T	0.9	G	0.1	T/G
YRI	rs2110735	2	103050925	0.054	0.666	HapMap	1000GP	A	0.9	G	0.1	A/G
YRI	rs2110734	2	103052206	0.066	0.672	HapMap	1000GP	C	0.9	T	0.1	C/T
YRI	rs4851009	2	103055644	0.054	0.666	HapMap	1000GP	G	0.9	A	0.1	G/A
YRI	rs3917245	2	102775155	0.028	1	HapMap	1000GP	G	0.91	A	0.09	G/A
YRI	rs13018912	2	102864310	0.155	0.826	HapMap	1000GP	G	0.91	T	0.09	G/T
YRI	rs12997225	2	102864748	0.155	0.826	HapMap	1000GP	A	0.91	C	0.09	A/C
YRI	rs13015695	2	102888441	0.137	0.811	HapMap	1000GP	C	0.91	A	0.09	C/A
YRI	rs2310220	2	102951851	0.342	1	HapMap	1000GP	G	0.92	A	0.08	G/A
YRI	rs17696376	2	102965153	0.023	1	HapMap	1000GP	C	0.92	T	0.08	C/T
YRI	rs11465623	2	102993039	0.036	0.609	HapMap	1000GP	G	0.93	T	0.07	G/T
YRI	rs3771156	2	103036677	0.143	0.711	HapMap	1000GP	C	0.93	T	0.07	C/T
YRI	rs11465689	2	103040167	0.036	0.609	HapMap	1000GP	C	0.93	A	0.07	C/A
YRI	rs10208920	2	103054132	0.039	1	HapMap	1000GP	C	0.93	T	0.07	C/T
YRI	rs9308858	2	103056004	0.039	1	HapMap	1000GP	C	0.93	T	0.07	C/T
YRI	rs17027177	2	103057056	0.039	1	HapMap	1000GP	T	0.93	C	0.07	T/C
YRI	rs13401597	2	103060818	0.041	1	HapMap	1000GP	C	0.93	G	0.07	C/G

YRI	rs13406732	2	103137911	0.035	1	HapMap	1000GP	C	0.93	A	0.07	C/A
YRI	rs3917242	2	102774268	0.015	1	HapMap	1000GP	T	0.94	C	0.06	T/C
YRI	rs3917268	2	102778862	0.065	0.695	HapMap	1000GP	A	0.94	T	0.06	A/T
YRI	rs3917275	2	102779944	0.011	1	HapMap	1000GP	A	0.94	G	0.06	A/G
YRI	rs3755282	2	102854882	0.007	1	HapMap	1000GP	C	0.94	T	0.06	C/T
YRI	rs12993937	2	102855831	0.071	1	HapMap	1000GP	G	0.94	T	0.06	G/T
YRI	rs952437	2	102897159	0.007	1	HapMap	1000GP	C	0.94	T	0.06	C/T
YRI	rs12989419	2	102900754	0.071	1	HapMap	1000GP	A	0.94	C	0.06	A/C
YRI	rs13024772	2	102902173	0.071	1	HapMap	1000GP	G	0.94	A	0.06	G/A
YRI	rs13017541	2	102906176	0.071	1	HapMap	1000GP	C	0.94	T	0.06	C/T
YRI	rs884517	2	102906457	0.019	1	HapMap	1000GP	T	0.94	C	0.06	T/C
YRI	rs13024003	2	102907761	0.048	1	HapMap	1000GP	G	0.94	C	0.06	G/C
YRI	rs873022	2	102955683	0.2	1	HapMap	1000GP	G	0.94	T	0.06	G/T
YRI	rs3771177	2	102955860	0.2	1	HapMap	1000GP	G	0.94	T	0.06	G/T
YRI	rs3732129	2	102957532	0.2	1	HapMap	1000GP	T	0.94	C	0.06	T/C
YRI	rs3821204	2	102960281	0.2	1	HapMap	1000GP	C	0.94	G	0.06	C/G
YRI	rs12469506	2	102965871	0.2	1	HapMap	1000GP	C	0.94	T	0.06	C/T
YRI	rs3771171	2	102985950	0.2	1	HapMap	1000GP	T	0.94	C	0.06	T/C
YRI	rs2160202	2	102986154	0.2	1	HapMap	1000GP	G	0.94	A	0.06	G/A
YRI	rs11683700	2	102996805	0.085	0.717	HapMap	1000GP	C	0.94	T	0.06	C/T
YRI	rs887972	2	103040945	0.15	0.714	HapMap	1000GP	G	0.94	A	0.06	G/A
YRI	rs11681718	2	103051144	0.143	0.711	HapMap	1000GP	A	0.94	G	0.06	A/G
YRI	rs11465711	2	103060092	0.071	1	HapMap	1000GP	T	0.94	C	0.06	T/C
YRI	rs17821875	2	103071030	0.071	1	HapMap	1000GP	A	0.94	G	0.06	A/G
YRI	rs3917239	2	102773548	0.023	1	HapMap	1000GP	C	0.95	T	0.05	C/T
YRI	rs17026775	2	102815794	0.011	1	HapMap	1000GP	C	0.95	T	0.05	C/T
YRI	rs11678722	2	102829807	0.047	1	HapMap	1000GP	C	0.95	T	0.05	C/T
YRI	rs985523	2	102954376	0.035	1	HapMap	1000GP	G	0.95	A	0.05	G/A
YRI	rs6719130	2	102958236	0.035	1	HapMap	1000GP	C	0.95	T	0.05	C/T
YRI	rs3771172	2	102985812	0.2	1	HapMap	1000GP	C	0.95	T	0.05	C/T
YRI	rs3771167	2	102986188	0.027	1	HapMap	1000GP	A	0.95	G	0.05	A/G
YRI	rs7566063	2	103112565	0.012	1	HapMap	1000GP	C	0.95	A	0.05	C/A
YRI	rs7591878	2	103112658	0.013	1	HapMap	1000GP	G	0.95	A	0.05	G/A
YRI	rs2228139	2	102781649	0.028	1	HapMap	1000GP	C	0.96	G	0.04	C/G

YRI	rs3771196	2	102815727	0.023	1	HapMap	1000GP	T	0.96	A	0.04	T/A
YRI	rs6733727	2	102839219	0.024	1	HapMap	1000GP	T	0.96	C	0.04	T/C
YRI	rs17026874	2	102861682	0.007	1	HapMap	1000GP	T	0.96	C	0.04	T/C
YRI	rs17026878	2	102862835	0.007	1	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs17026889	2	102882916	0.007	1	HapMap	1000GP	G	0.96	C	0.04	G/C
YRI	rs7340445	2	102901879	0.007	1	HapMap	1000GP	G	0.96	A	0.04	G/A
YRI	rs12987260	2	103055634	0.138	1	HapMap	1000GP	G	0.96	T	0.04	G/T
YRI	rs6708944	2	103123951	0.015	1	HapMap	1000GP	G	0.96	C	0.04	G/C
YRI	rs6737329	2	103128892	0.015	1	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs6752045	2	103128931	0.015	1	HapMap	1000GP	A	0.96	T	0.04	A/T
YRI	rs7597566	2	103159938	0.011	1	HapMap	1000GP	G	0.96	A	0.04	G/A
YRI	rs10195375	2	102806641	0.01	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs10201203	2	102814004	0.011	1	HapMap	1000GP	A	0.97	G	0.03	A/G
YRI	rs10201417	2	102814233	0.011	1	HapMap	1000GP	A	0.97	G	0.03	A/G
YRI	rs7596051	2	102817675	0.054	0.666	HapMap	1000GP	C	0.97	T	0.03	C/T
YRI	rs10184622	2	102825818	0.011	1	HapMap	1000GP	G	0.97	A	0.03	G/A
YRI	rs10179283	2	102826350	0.011	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs10168021	2	102827446	0.011	1	HapMap	1000GP	C	0.97	A	0.03	C/A
YRI	rs10207764	2	102835474	0.011	1	HapMap	1000GP	C	0.97	T	0.03	C/T
YRI	rs6730496	2	102839010	0.057	0.67	HapMap	1000GP	A	0.97	G	0.03	A/G
YRI	rs11903870	2	102886180	0.074	0.711	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs7594361	2	102932332	0.007	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs13397711	2	102934427	0.011	1	HapMap	1000GP	C	0.97	G	0.03	C/G
YRI	rs10174243	2	102940014	0.015	1	HapMap	1000GP	G	0.97	A	0.03	G/A
YRI	rs1420103	2	102948632	0.096	1	HapMap	1000GP	A	0.97	C	0.03	A/C
YRI	rs17639215	2	102953444	0.027	1	HapMap	1000GP	G	0.97	A	0.03	G/A
YRI	rs11465695	2	103041764	0.096	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs10177895	2	103049529	0.019	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs11889853	2	103080313	0.096	1	HapMap	1000GP	A	0.97	C	0.03	A/C
YRI	rs6729198	2	103096712	0.074	1	HapMap	1000GP	C	0.97	T	0.03	C/T
YRI	rs6543154	2	103114334	0.026	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs11123934	2	103115568	0.026	1	HapMap	1000GP	G	0.97	A	0.03	G/A
YRI	rs6714379	2	103133310	0.023	1	HapMap	1000GP	A	0.97	G	0.03	A/G
YRI	rs3917248	2	102775377	0.007	1	HapMap	1000GP	G	0.98	A	0.02	G/A

YRI	rs3917255	2	102776730	0.012	1	HapMap	1000GP	T	0.98	A	0.02	T/A
YRI	rs3917305	2	102788760	0.011	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10181153	2	102801109	0.007	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs6722601	2	102813173	0.011	1	HapMap	1000GP	G	0.98	T	0.02	G/T
YRI	rs13405631	2	102828620	0.019	1	HapMap	1000GP	T	0.98	C	0.02	T/C
YRI	rs7567539	2	102839839	0.011	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10209002	2	102860848	0.011	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs13423746	2	102883673	0.011	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10175804	2	102890163	0.011	1	HapMap	1000GP	T	0.98	C	0.02	T/C
YRI	rs10180574	2	102892822	0.013	1	HapMap	1000GP	A	0.98	G	0.02	A/G
YRI	rs10211352	2	102896894	0.011	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10200993	2	102908695	0.012	1	HapMap	1000GP	T	0.98	G	0.02	T/G
YRI	rs4577297	2	102918018	0.023	1	HapMap	1000GP	G	0.98	A	0.02	G/A
YRI	rs13429528	2	102948868	0.019	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10181632	2	102956150	0.019	1	HapMap	1000GP	A	0.98	G	0.02	A/G
YRI	rs10168510	2	102963125	0.019	1	HapMap	1000GP	G	0.98	T	0.02	G/T
YRI	rs10193102	2	102963340	0.019	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10178584	2	102994251	0.019	1	HapMap	1000GP	C	0.98	G	0.02	C/G
YRI	rs13388673	2	103032668	0.019	1	HapMap	1000GP	A	0.98	G	0.02	A/G
YRI	rs11465669	2	103034292	0.004	1	HapMap	1000GP	T	0.98	C	0.02	T/C
YRI	rs10199166	2	103066430	0.024	1	HapMap	1000GP	T	0.98	C	0.02	T/C
YRI	rs9631044	2	103070622	0.019	1	HapMap	1000GP	G	0.98	A	0.02	G/A
YRI	rs13386538	2	103077527	0.02	1	HapMap	1000GP	A	0.98	T	0.02	A/T
YRI	rs10169647	2	103081470	0.019	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10190130	2	103094638	0.019	1	HapMap	1000GP	A	0.98	G	0.02	A/G
YRI	rs6724322	2	103125182	0.023	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs13423747	2	103128429	0.015	1	HapMap	1000GP	A	0.98	G	0.02	A/G
YRI	rs4851609	2	103128866	0.023	1	HapMap	1000GP	T	0.98	C	0.02	T/C
YRI	rs13417556	2	103130158	0.019	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs10180466	2	103132946	0.019	1	HapMap	1000GP	G	0.98	A	0.02	G/A
YRI	rs3917240	2	102773553	0.023	1	HapMap	1000GP	A	0.99	G	0.01	A/G
YRI	rs3917241	2	102774015	0	1	HapMap	1000GP	G	0.99	A	0.01	G/A
YRI	rs3917270	2	102779392	0.047	1	HapMap	1000GP	A	0.99	G	0.01	A/G
YRI	rs3732133	2	102794278	0.05	1	HapMap	1000GP	C	0.99	T	0.01	C/T

YRI	rs11465628	2	102993700	0.004	1	HapMap	1000GP	G	0.99	C	0.01	G/C
YRI	rs11465671	2	103034582	0	1	HapMap	1000GP	A	0.99	G	0.01	A/G
YRI	rs11895701	2	103055977	0.011	1	HapMap	1000GP	G	0.99	T	0.01	G/T
YRI	rs11465717	2	103061890	0.007	1	HapMap	1000GP	C	0.99	T	0.01	C/T
YRI	rs11465738	2	103068545	0.004	1	HapMap	1000GP	G	0.99	A	0.01	G/A
YRI	rs3917313	2	102790240	0.047	1	HapMap	1000GP	T	0.9959	C	0.0041	T/C
YRI	rs3917341	2	102783439	0.004	1	HapMap	1000GP	A	1	G	0	A/G
YRI	rs1922300	2	102819594	0	1	HapMap	1000GP	C	1	T	0	C/T

Table 4: SNPs in high LD with rs4742165

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs10117792	9	6148778	0.211	0.659	HapMap	HapMap	T	0.837	C	0.163	T/C
JPT	rs10117792	9	6148778	0.417	0.726	HapMap	HapMap	T	0.918	C	0.082	T/C
MKK	rs10117792	9	6148778	0.551	0.791	HapMap	HapMap	T	0.867	C	0.133	T/C
CHD	rs10117792	9	6148778	0.404	0.674	HapMap	HapMap	T	0.882	C	0.118	T/C
MEX	rs10117792	9	6148778	0.741	1	HapMap	HapMap	T	0.949	C	0.051	T/C
GIH	rs10117792	9	6148778	0.884	1	HapMap	HapMap	T	0.949	C	0.051	T/C
CEU	rs10117792	9	6148778	0.8	1	HapMap	HapMap	T	0.912	C	0.088	T/C
CEU	rs10118795	9	6230658	0.217	1	HapMap	HapMap	T	0.345	C	0.655	T/C
GIH	rs10118795	9	6230658	0.085	1	HapMap	HapMap	T	0.358	C	0.642	T/C
JPT	rs10118795	9	6230658	0.05	1	HapMap	HapMap	T	0.535	C	0.465	T/C
CEU	rs10119713	9	6153823	0.109	1	HapMap	HapMap	G	0.545	A	0.455	G/A
CHD	rs10119713	9	6153823	0.152	0.784	HapMap	HapMap	G	0.676	A	0.324	G/A
GIH	rs10119713	9	6153823	0.073	1	HapMap	HapMap	G	0.608	A	0.392	G/A
JPT	rs10119713	9	6153823	0.131	0.698	HapMap	HapMap	G	0.808	A	0.192	G/A
MKK	rs10119713	9	6153823	0.066	0.802	HapMap	HapMap	G	0.434	A	0.566	G/A
MEX	rs10119713	9	6153823	0.052	0.693	HapMap	HapMap	G	0.66	A	0.34	G/A
GIH	rs10120134	9	6078457	0.004	1	HapMap	HapMap	G	0.926	A	0.074	G/A
JPT	rs10120134	9	6078457	0.041	0.632	HapMap	HapMap	G	0.698	A	0.302	G/A
MEX	rs10120935	9	6355852	0.001	1	HapMap	HapMap	G	0.98	C	0.02	G/C
MEX	rs10121888	9	6304179	0.001	1	HapMap	HapMap	T	0.02	C	0.98	T/C
LWK	rs10121888	9	6304179	0.102	0.793	HapMap	HapMap	T	0.039	C	0.961	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MKK	rs10121888	9	6304179	0.007	1	HapMap	HapMap	T	0.047	C	0.953	T/C
ASW	rs10121888	9	6304179	0.04	1	HapMap	HapMap	T	0.104	C	0.896	T/C
GIH	rs10121888	9	6304179	0.001	1	HapMap	HapMap	T	0.017	C	0.983	T/C
CEU	rs10124250	9	6151686	0.109	1	HapMap	HapMap	C	0.549	T	0.451	C/T
MEX	rs10124250	9	6151686	0.059	0.703	HapMap	HapMap	C	0.68	T	0.32	C/T
CHB	rs10124250	9	6151686	0.13	0.619	HapMap	HapMap	C	0.726	T	0.274	C/T
CHD	rs10124250	9	6151686	0.183	0.804	HapMap	HapMap	C	0.706	T	0.294	C/T
GIH	rs10124250	9	6151686	0.075	1	HapMap	HapMap	C	0.614	T	0.386	C/T
JPT	rs10124250	9	6151686	0.163	0.718	HapMap	HapMap	C	0.837	T	0.163	C/T
MKK	rs10124250	9	6151686	0.066	0.802	HapMap	HapMap	C	0.434	T	0.566	C/T
ASW	rs1037885	9	6320915	0.04	0.626	HapMap	HapMap	G	0.245	A	0.755	G/A
GIH	rs1037885	9	6320915	0.001	1	HapMap	HapMap	G	0.017	A	0.983	G/A
MEX	rs1037885	9	6320915	0.001	1	HapMap	HapMap	G	0.03	A	0.97	G/A
GIH	rs1048274	9	6246292	0.039	1	HapMap	HapMap	G	0.545	A	0.455	G/A
MKK	rs1048274	9	6246292	0.057	0.698	HapMap	HapMap	G	0.535	A	0.465	G/A
CEU	rs10491836	9	6321421	0.052	1	HapMap	HapMap	C	0.717	A	0.283	C/A
ASW	rs10491836	9	6321421	0.041	0.663	HapMap	HapMap	C	0.736	A	0.264	C/A
GIH	rs10491836	9	6321421	0.008	1	HapMap	HapMap	C	0.864	A	0.136	C/A
MEX	rs10491836	9	6321421	0.013	1	HapMap	HapMap	C	0.82	A	0.18	C/A
MKK	rs10491836	9	6321421	0.025	0.718	HapMap	HapMap	C	0.739	A	0.261	C/A
MEX	rs10491837	9	6357615	0.001	1	HapMap	HapMap	A	0.98	G	0.02	A/G
YRI	rs1052335	9	6320380	0.105	0.645	HapMap	HapMap	A	0.907	C	0.093	A/C
LWK	rs1052335	9	6320380	0.019	1	HapMap	HapMap	A	0.928	C	0.072	A/C
MEX	rs1052335	9	6320380	0.04	0.671	HapMap	HapMap	A	0.6	C	0.4	A/C
JPT	rs1052335	9	6320380	0.004	0.615	HapMap	HapMap	A	0.843	C	0.157	A/C
ASW	rs1052335	9	6320380	0.303	1	HapMap	HapMap	A	0.925	C	0.075	A/C
MKK	rs106033	9	6002734	0.069	0.638	HapMap	HapMap	A	0.556	C	0.444	A/C
CEU	rs10733522	9	5982192	0.001	1	HapMap	HapMap	C	0.009	T	0.991	C/T
MEX	rs10733522	9	5982192	0.003	1	HapMap	HapMap	C	0.06	T	0.94	C/T
GIH	rs10733522	9	5982192	0.006	1	HapMap	HapMap	C	0.108	T	0.892	C/T
CHB	rs10733522	9	5982192	0.116	0.758	HapMap	HapMap	C	0.307	T	0.693	C/T
CHB	rs10739082	9	5971901	0.116	0.758	HapMap	HapMap	A	0.321	G	0.679	A/G
GIH	rs10739082	9	5971901	0.006	1	HapMap	HapMap	A	0.103	G	0.897	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs10739082	9	5971901	0.001	1	HapMap	HapMap	A	0.009	G	0.991	A/G
MEX	rs10739082	9	5971901	0.003	1	HapMap	HapMap	A	0.06	G	0.94	A/G
ASW	rs10739083	9	6057122	0.024	1	HapMap	HapMap	T	0.896	C	0.104	T/C
CHD	rs10739083	9	6057122	0.027	1	HapMap	HapMap	T	0.812	C	0.188	T/C
JPT	rs10739083	9	6057122	0.007	1	HapMap	HapMap	T	0.86	C	0.14	T/C
MKK	rs10739090	9	6277142	0.001	1	HapMap	HapMap	C	0.01	A	0.99	C/A
MEX	rs10739090	9	6277142	0.001	1	HapMap	HapMap	C	0.02	A	0.98	C/A
LWK	rs10739090	9	6277142	0.138	1	HapMap	HapMap	C	0.033	A	0.967	C/A
YRI	rs10739090	9	6277142	0.03	1	HapMap	HapMap	C	0.013	A	0.987	C/A
ASW	rs10739090	9	6277142	0.019	1	HapMap	HapMap	C	0.047	A	0.953	C/A
GIH	rs10739090	9	6277142	0.001	1	HapMap	HapMap	C	0.017	A	0.983	C/A
MEX	rs10758732	9	5981772	0.005	1	HapMap	HapMap	C	0.08	T	0.92	C/T
CEU	rs10758732	9	5981772	0.001	1	HapMap	HapMap	C	0.04	T	0.96	C/T
CHB	rs10758732	9	5981772	0.076	0.683	HapMap	HapMap	C	0.331	T	0.669	C/T
GIH	rs10758732	9	5981772	0.014	1	HapMap	HapMap	C	0.222	T	0.778	C/T
CEU	rs10758734	9	5990551	0.001	1	HapMap	HapMap	T	0.009	C	0.991	T/C
GIH	rs10758734	9	5990551	0.013	1	HapMap	HapMap	T	0.216	C	0.784	T/C
MEX	rs10758734	9	5990551	0.005	1	HapMap	HapMap	T	0.08	C	0.92	T/C
CHB	rs10758736	9	6001757	0.023	1	HapMap	HapMap	G	0.798	A	0.202	G/A
CHD	rs10758736	9	6001757	0.031	1	HapMap	HapMap	G	0.794	A	0.206	G/A
MEX	rs10758739	9	6013927	0.051	0.639	HapMap	HapMap	T	0.7	C	0.3	T/C
CHB	rs10758739	9	6013927	0.017	0.889	HapMap	HapMap	T	0.815	C	0.185	T/C
MEX	rs10815335	9	5988919	0.005	1	HapMap	HapMap	T	0.08	C	0.92	T/C
CHB	rs10815335	9	5988919	0.092	0.729	HapMap	HapMap	T	0.339	C	0.661	T/C
GIH	rs10815335	9	5988919	0.014	1	HapMap	HapMap	T	0.222	C	0.778	T/C
CEU	rs10815335	9	5988919	0.001	1	HapMap	HapMap	T	0.009	C	0.991	T/C
CHD	rs10815337	9	5991599	0.018	1	HapMap	HapMap	T	0.871	C	0.129	T/C
JPT	rs10815347	9	6054103	0.006	1	HapMap	HapMap	G	0.884	A	0.116	G/A
LWK	rs10815347	9	6054103	0.003	1	HapMap	HapMap	G	0.989	A	0.011	G/A
MEX	rs10815347	9	6054103	0.087	0.729	HapMap	HapMap	G	0.75	A	0.25	G/A
ASW	rs10815347	9	6054103	0.004	1	HapMap	HapMap	G	0.953	A	0.047	G/A
CHD	rs10815347	9	6054103	0.024	1	HapMap	HapMap	G	0.833	A	0.167	G/A
CHB	rs10815357	9	6134025	0.265	0.678	HapMap	HapMap	A	0.839	G	0.161	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
GIH	rs10815357	9	6134025	0.159	0.692	HapMap	HapMap	A	0.875	G	0.125	A/G
CHB	rs10815358	9	6134065	0.265	0.678	HapMap	HapMap	G	0.851	A	0.149	G/A
GIH	rs10815358	9	6134065	0.162	0.697	HapMap	HapMap	G	0.874	A	0.126	G/A
JPT	rs10815388	9	6222242	0.05	1	HapMap	HapMap	C	0.535	T	0.465	C/T
CEU	rs10815388	9	6222242	0.217	1	HapMap	HapMap	C	0.341	T	0.659	C/T
GIH	rs10815388	9	6222242	0.085	1	HapMap	HapMap	C	0.358	T	0.642	C/T
MKK	rs10815393	9	6230324	0.005	0.601	HapMap	HapMap	T	0.906	C	0.094	T/C
ASW	rs10815393	9	6230324	0.046	1	HapMap	HapMap	T	0.827	C	0.173	T/C
CEU	rs10815393	9	6230324	0.041	1	HapMap	HapMap	T	0.768	C	0.232	T/C
GIH	rs10815393	9	6230324	0.006	1	HapMap	HapMap	T	0.885	C	0.115	T/C
MEX	rs10815393	9	6230324	0.007	0.819	HapMap	HapMap	T	0.867	C	0.133	T/C
CEU	rs10815398	9	6262766	0.025	0.626	HapMap	HapMap	C	0.354	A	0.646	C/A
GIH	rs10815398	9	6262766	0.039	1	HapMap	HapMap	C	0.455	A	0.545	C/A
GIH	rs10815402	9	6283715	0.036	1	HapMap	HapMap	G	0.568	A	0.432	G/A
ASW	rs10815402	9	6283715	0.23	0.671	HapMap	HapMap	G	0.877	A	0.123	G/A
CEU	rs10975412	9	6039547	0.016	1	HapMap	HapMap	A	0.858	G	0.142	A/G
CHB	rs10975412	9	6039547	0.004	1	HapMap	HapMap	A	0.958	G	0.042	A/G
GIH	rs10975412	9	6039547	0.016	1	HapMap	HapMap	A	0.756	G	0.244	A/G
MEX	rs10975412	9	6039547	0.011	1	HapMap	HapMap	A	0.851	G	0.149	A/G
MEX	rs10975413	9	6039843	0.01	1	HapMap	HapMap	A	0.857	G	0.143	A/G
CEU	rs10975413	9	6039843	0.016	1	HapMap	HapMap	A	0.858	G	0.142	A/G
CHB	rs10975413	9	6039843	0.004	1	HapMap	HapMap	A	0.958	G	0.042	A/G
GIH	rs10975413	9	6039843	0.015	1	HapMap	HapMap	A	0.756	G	0.244	A/G
GIH	rs10975416	9	6041924	0.015	1	HapMap	HapMap	T	0.756	G	0.244	T/G
MEX	rs10975416	9	6041924	0.009	1	HapMap	HapMap	T	0.87	G	0.13	T/G
CEU	rs10975416	9	6041924	0.016	1	HapMap	HapMap	T	0.858	G	0.142	T/G
CHB	rs10975416	9	6041924	0.004	1	HapMap	HapMap	T	0.958	G	0.042	T/G
JPT	rs10975422	9	6063817	0.001	1	HapMap	HapMap	G	0.988	C	0.012	G/C
CHD	rs10975422	9	6063817	0.001	1	HapMap	HapMap	G	0.994	C	0.006	G/C
ASW	rs10975422	9	6063817	0.019	1	HapMap	HapMap	G	0.952	C	0.048	G/C
CHB	rs10975422	9	6063817	0.001	1	HapMap	HapMap	G	0.988	C	0.012	G/C
YRI	rs10975438	9	6103103	0.103	0.743	HapMap	HapMap	C	0.965	T	0.035	C/T
MKK	rs10975438	9	6103103	0.127	0.825	HapMap	HapMap	C	0.976	T	0.024	C/T

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
GIH	rs10975444	9	6109329	0.139	0.822	HapMap	HapMap	A	0.812	G	0.188	A/G
ASW	rs10975444	9	6109329	0.019	1	HapMap	HapMap	A	0.934	G	0.066	A/G
CHB	rs10975444	9	6109329	0.201	0.796	HapMap	HapMap	A	0.774	G	0.226	A/G
ASW	rs10975450	9	6123672	0.018	1	HapMap	HapMap	A	0.933	T	0.067	A/T
CHB	rs10975450	9	6123672	0.232	0.804	HapMap	HapMap	A	0.775	T	0.225	A/T
GIH	rs10975450	9	6123672	0.182	0.835	HapMap	HapMap	A	0.843	T	0.157	A/T
YRI	rs10975454	9	6125411	0.025	1	HapMap	HapMap	C	0.924	A	0.076	C/A
LWK	rs10975454	9	6125411	0.006	1	HapMap	HapMap	C	0.978	A	0.022	C/A
MKK	rs10975454	9	6125411	0.007	1	HapMap	HapMap	C	0.948	A	0.052	C/A
JPT	rs10975454	9	6125411	0.007	1	HapMap	HapMap	C	0.878	A	0.122	C/A
GIH	rs10975454	9	6125411	0.008	1	HapMap	HapMap	C	0.858	A	0.142	C/A
CHD	rs10975454	9	6125411	0.025	1	HapMap	HapMap	C	0.827	A	0.173	C/A
CHB	rs10975454	9	6125411	0.017	1	HapMap	HapMap	C	0.863	A	0.137	C/A
CEU	rs10975463	9	6139006	0.014	1	HapMap	HapMap	A	0.903	G	0.097	A/G
LWK	rs10975463	9	6139006	0.023	1	HapMap	HapMap	A	0.917	G	0.083	A/G
MEX	rs10975463	9	6139006	0.003	1	HapMap	HapMap	A	0.96	G	0.04	A/G
MKK	rs10975463	9	6139006	0.02	1	HapMap	HapMap	A	0.871	G	0.129	A/G
YRI	rs10975463	9	6139006	0.028	1	HapMap	HapMap	A	0.925	G	0.075	A/G
MEX	rs10975501	9	6223221	0.002	1	HapMap	HapMap	A	0.041	C	0.959	A/C
CEU	rs10975501	9	6223221	0.005	0.757	HapMap	HapMap	A	0.05	C	0.95	A/C
GIH	rs10975501	9	6223221	0	1	HapMap	HapMap	A	0.006	C	0.994	A/C
MKK	rs10975501	9	6223221	0.037	1	HapMap	HapMap	A	0.213	C	0.787	A/C
JPT	rs10975514	9	6236144	0.053	1	HapMap	HapMap	G	0.561	A	0.439	G/A
GIH	rs10975514	9	6236144	0.039	1	HapMap	HapMap	G	0.545	A	0.455	G/A
CEU	rs10975514	9	6236144	0.043	1	HapMap	HapMap	G	0.694	A	0.306	G/A
JPT	rs10975516	9	6237693	0.02	0.666	HapMap	HapMap	G	0.57	A	0.43	G/A
GIH	rs10975516	9	6237693	0.039	1	HapMap	HapMap	G	0.545	A	0.455	G/A
GIH	rs10975519	9	6243571	0.043	1	HapMap	HapMap	C	0.529	T	0.471	C/T
JPT	rs10975519	9	6243571	0.069	1	HapMap	HapMap	C	0.589	T	0.411	C/T
MKK	rs10975519	9	6243571	0.058	0.684	HapMap	HapMap	C	0.525	T	0.475	C/T
GIH	rs10975520	9	6243710	0.039	1	HapMap	HapMap	G	0.545	C	0.455	G/C
JPT	rs10975527	9	6278738	0.418	0.727	HapMap	HapMap	G	0.93	T	0.07	G/T
MEX	rs10975527	9	6278738	0	1	HapMap	HapMap	G	0.99	T	0.01	G/T

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
GIH	rs10975539	9	6298729	0.007	1	HapMap	HapMap	C	0.875	T	0.125	C/T
LWK	rs10975539	9	6298729	0.001	1	HapMap	HapMap	C	0.994	T	0.006	C/T
MKK	rs10975539	9	6298729	0.002	1	HapMap	HapMap	C	0.986	T	0.014	C/T
CEU	rs10975539	9	6298729	0.027	1	HapMap	HapMap	C	0.792	T	0.208	C/T
ASW	rs10975539	9	6298729	0.014	1	HapMap	HapMap	C	0.894	T	0.106	C/T
CHD	rs10975543	9	6307385	0.05	1	HapMap	HapMap	C	0.006	T	0.994	C/T
MEX	rs10975543	9	6307385	0.001	1	HapMap	HapMap	C	0.01	T	0.99	C/T
MKK	rs10975543	9	6307385	0.002	1	HapMap	HapMap	C	0.014	T	0.986	C/T
ASW	rs10975543	9	6307385	0.022	1	HapMap	HapMap	C	0.049	T	0.951	C/T
GIH	rs10975543	9	6307385	0.001	1	HapMap	HapMap	C	0.017	T	0.983	C/T
LWK	rs10975543	9	6307385	0.078	1	HapMap	HapMap	C	0.017	T	0.983	C/T
CHD	rs10975552	9	6341834	0.047	1	HapMap	HapMap	T	0.718	C	0.282	T/C
GIH	rs10975552	9	6341834	0.029	1	HapMap	HapMap	T	0.625	C	0.375	T/C
LWK	rs10975552	9	6341834	0.03	0.614	HapMap	HapMap	T	0.761	C	0.239	T/C
MEX	rs10975552	9	6341834	0.023	1	HapMap	HapMap	T	0.73	C	0.27	T/C
MKK	rs10975552	9	6341834	0.022	0.684	HapMap	HapMap	T	0.745	C	0.255	T/C
CEU	rs10975552	9	6341834	0.073	1	HapMap	HapMap	T	0.628	C	0.372	T/C
CHB	rs10975552	9	6341834	0.033	1	HapMap	HapMap	T	0.738	C	0.262	T/C
MEX	rs10975556	9	6353043	0.191	1	HapMap	HapMap	C	0.99	G	0.01	C/G
CEU	rs10975556	9	6353043	0.579	0.86	HapMap	HapMap	C	0.938	G	0.062	C/G
MKK	rs10975556	9	6353043	0.001	1	HapMap	HapMap	C	0.99	G	0.01	C/G
YRI	rs10975558	9	6354449	0.049	1	HapMap	HapMap	C	0.854	T	0.146	C/T
ASW	rs10975558	9	6354449	0.052	1	HapMap	HapMap	C	0.811	T	0.189	C/T
MKK	rs10975558	9	6354449	0.012	0.72	HapMap	HapMap	C	0.848	T	0.152	C/T
MEX	rs10975558	9	6354449	0.009	1	HapMap	HapMap	C	0.86	T	0.14	C/T
CEU	rs10975558	9	6354449	0.052	1	HapMap	HapMap	C	0.721	T	0.279	C/T
GIH	rs10975558	9	6354449	0.008	1	HapMap	HapMap	C	0.858	T	0.142	C/T
CHB	rs11506678	9	6030282	0.004	1	HapMap	HapMap	C	0.958	A	0.042	C/A
GIH	rs11506678	9	6030282	0.013	1	HapMap	HapMap	C	0.784	A	0.216	C/A
MEX	rs11506678	9	6030282	0.002	1	HapMap	HapMap	C	0.97	A	0.03	C/A
LWK	rs11787939	9	6212553	0.098	0.776	HapMap	HapMap	G	0.606	A	0.394	G/A
MKK	rs11787939	9	6212553	0.033	0.781	HapMap	HapMap	G	0.713	A	0.287	G/A
YRI	rs11787939	9	6212553	0.056	0.612	HapMap	HapMap	G	0.664	A	0.336	G/A

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs11787939	9	6212553	0.007	1	HapMap	HapMap	G	0.956	A	0.044	G/A
CHD	rs11793017	9	6068204	0.02	1	HapMap	HapMap	C	0.853	T	0.147	C/T
GIH	rs11793017	9	6068204	0.015	1	HapMap	HapMap	C	0.767	T	0.233	C/T
JPT	rs11793017	9	6068204	0.007	1	HapMap	HapMap	C	0.876	T	0.124	C/T
LWK	rs11793017	9	6068204	0.007	0.831	HapMap	HapMap	C	0.961	T	0.039	C/T
CHB	rs11793017	9	6068204	0.013	1	HapMap	HapMap	C	0.881	T	0.119	C/T
MKK	rs11793017	9	6068204	0.01	1	HapMap	HapMap	C	0.934	T	0.066	C/T
YRI	rs11793017	9	6068204	0.038	1	HapMap	HapMap	C	0.889	T	0.111	C/T
MKK	rs12000491	9	6247367	0.026	1	HapMap	HapMap	T	0.839	C	0.161	T/C
YRI	rs12000491	9	6247367	0.059	0.767	HapMap	HapMap	T	0.732	C	0.268	T/C
ASW	rs12000491	9	6247367	0.086	1	HapMap	HapMap	T	0.811	C	0.189	T/C
GIH	rs12000491	9	6247367	0.001	1	HapMap	HapMap	T	0.989	C	0.011	T/C
MEX	rs12000491	9	6247367	0.001	1	HapMap	HapMap	T	0.97	C	0.03	T/C
CEU	rs12000491	9	6247367	0.004	1	HapMap	HapMap	T	0.965	C	0.035	T/C
ASW	rs12003769	9	6158335	0.427	0.759	HapMap	HapMap	T	0.821	C	0.179	T/C
CEU	rs12003769	9	6158335	0.815	1	HapMap	HapMap	T	0.907	C	0.093	T/C
CHB	rs12003769	9	6158335	0.307	0.827	HapMap	HapMap	T	0.827	C	0.173	T/C
CHD	rs12003769	9	6158335	0.433	0.678	HapMap	HapMap	T	0.888	C	0.112	T/C
GIH	rs12003769	9	6158335	0.884	1	HapMap	HapMap	T	0.949	C	0.051	T/C
JPT	rs12003769	9	6158335	0.499	0.779	HapMap	HapMap	T	0.913	C	0.087	T/C
MEX	rs12003769	9	6158335	0.791	1	HapMap	HapMap	T	0.94	C	0.06	T/C
MKK	rs12003769	9	6158335	0.384	0.842	HapMap	HapMap	T	0.801	C	0.199	T/C
YRI	rs12237914	9	6296896	0.025	0.687	HapMap	HapMap	A	0.821	G	0.179	A/G
CEU	rs12237914	9	6296896	0.128	0.817	HapMap	HapMap	A	0.593	G	0.407	A/G
GIH	rs12237914	9	6296896	0.076	1	HapMap	HapMap	A	0.615	G	0.385	A/G
CHD	rs12337790	9	6015559	0.101	1	HapMap	HapMap	T	0.988	C	0.012	T/C
GIH	rs12337790	9	6015559	0.012	1	HapMap	HapMap	T	0.807	C	0.193	T/C
LWK	rs12337790	9	6015559	0.048	1	HapMap	HapMap	T	0.839	C	0.161	T/C
MEX	rs12337790	9	6015559	0.001	1	HapMap	HapMap	T	0.98	C	0.02	T/C
CHB	rs12337790	9	6015559	0.004	1	HapMap	HapMap	T	0.97	C	0.03	T/C
LWK	rs12339889	9	5998989	0.015	1	HapMap	HapMap	C	0.944	G	0.056	C/G
GIH	rs12339889	9	5998989	0.006	1	HapMap	HapMap	C	0.886	G	0.114	C/G
MEX	rs12339889	9	5998989	0.001	1	HapMap	HapMap	C	0.98	G	0.02	C/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs12339889	9	5998989	0.004	1	HapMap	HapMap	C	0.97	G	0.03	C/G
YRI	rs12339889	9	5998989	0.134	0.612	HapMap	HapMap	C	0.929	G	0.071	C/G
CEU	rs12349559	9	6135491	0.815	1	HapMap	HapMap	T	0.898	C	0.102	T/C
CHB	rs12349559	9	6135491	0.505	0.85	HapMap	HapMap	T	0.869	C	0.131	T/C
ASW	rs12349559	9	6135491	0.427	0.759	HapMap	HapMap	T	0.84	C	0.16	T/C
CHD	rs12349559	9	6135491	0.54	0.785	HapMap	HapMap	T	0.905	C	0.095	T/C
MEX	rs12349559	9	6135491	0.791	1	HapMap	HapMap	T	0.94	C	0.06	T/C
MKK	rs12349559	9	6135491	0.56	0.761	HapMap	HapMap	T	0.878	C	0.122	T/C
YRI	rs12349559	9	6135491	0.338	0.814	HapMap	HapMap	T	0.881	C	0.119	T/C
JPT	rs12349559	9	6135491	0.79	1	HapMap	HapMap	T	0.942	C	0.058	T/C
GIH	rs12349559	9	6135491	0.884	1	HapMap	HapMap	T	0.949	C	0.051	T/C
GIH	rs12378118	9	6023278	0.004	1	HapMap	HapMap	G	0.932	A	0.068	G/A
MEX	rs12378118	9	6023278	0.016	1	HapMap	HapMap	G	0.78	A	0.22	G/A
ASW	rs12378311	9	6078903	0.019	1	HapMap	HapMap	G	0.934	C	0.066	G/C
GIH	rs12378311	9	6078903	0.119	0.673	HapMap	HapMap	G	0.847	C	0.153	G/C
JPT	rs12378311	9	6078903	0.002	1	HapMap	HapMap	G	0.942	C	0.058	G/C
GIH	rs12551256	9	6221239	0.05	1	HapMap	HapMap	A	0.483	G	0.517	A/G
CEU	rs12551256	9	6221239	0.076	1	HapMap	HapMap	A	0.566	G	0.434	A/G
JPT	rs12551256	9	6221239	0.047	1	HapMap	HapMap	A	0.541	G	0.459	A/G
ASW	rs1317230	9	6241012	0.224	0.779	HapMap	HapMap	C	0.896	A	0.104	C/A
JPT	rs1317230	9	6241012	0.02	0.666	HapMap	HapMap	C	0.57	A	0.43	C/A
GIH	rs1317230	9	6241012	0.037	1	HapMap	HapMap	C	0.557	A	0.443	C/A
CEU	rs1322166	9	6299862	0.07	1	HapMap	HapMap	C	0.332	T	0.668	C/T
GIH	rs1322166	9	6299862	0.009	1	HapMap	HapMap	C	0.153	T	0.847	C/T
MKK	rs1322166	9	6299862	0.049	0.781	HapMap	HapMap	C	0.374	T	0.626	C/T
MEX	rs1322166	9	6299862	0.018	1	HapMap	HapMap	C	0.24	T	0.76	C/T
GIH	rs13291323	9	6175360	0	1	HapMap	HapMap	T	0.994	C	0.006	T/C
ASW	rs13291323	9	6175360	0.009	1	HapMap	HapMap	T	0.972	C	0.028	T/C
CEU	rs13291323	9	6175360	0.008	0.921	HapMap	HapMap	T	0.951	C	0.049	T/C
LWK	rs13291323	9	6175360	0.012	1	HapMap	HapMap	T	0.956	C	0.044	T/C
MEX	rs13291323	9	6175360	0.001	1	HapMap	HapMap	T	0.98	C	0.02	T/C
MKK	rs13291323	9	6175360	0.002	0.727	HapMap	HapMap	T	0.979	C	0.021	T/C
ASW	rs13293142	9	6160924	0.008	0.741	HapMap	HapMap	A	0.962	C	0.038	A/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs13293142	9	6160924	0.008	0.921	HapMap	HapMap	A	0.947	C	0.053	A/C
MEX	rs13293142	9	6160924	0.001	1	HapMap	HapMap	A	0.98	C	0.02	A/C
GIH	rs13293142	9	6160924	0	1	HapMap	HapMap	A	0.994	C	0.006	A/C
CEU	rs13296741	9	6177395	0.01	0.996	HapMap	HapMap	G	0.941	T	0.059	G/T
CHB	rs13296741	9	6177395	0.115	1	HapMap	HapMap	G	0.982	T	0.018	G/T
MKK	rs13296741	9	6177395	0.004	0.999	HapMap	HapMap	G	0.975	T	0.025	G/T
MEX	rs13296741	9	6177395	0.003	1	HapMap	HapMap	G	0.958	T	0.042	G/T
ASW	rs13296741	9	6177395	0.009	1	HapMap	HapMap	G	0.962	T	0.038	G/T
JPT	rs13296741	9	6177395	0.002	1	HapMap	HapMap	G	0.976	T	0.024	G/T
CHD	rs13296741	9	6177395	0.001	1	HapMap	HapMap	G	0.988	T	0.012	G/T
GIH	rs13296741	9	6177395	0	1	HapMap	HapMap	G	0.989	T	0.011	G/T
GIH	rs13298872	9	6348385	0	1	HapMap	HapMap	G	0.994	A	0.006	G/A
ASW	rs13298872	9	6348385	0.019	1	HapMap	HapMap	G	0.953	A	0.047	G/A
MEX	rs13298872	9	6348385	0.001	1	HapMap	HapMap	G	0.98	A	0.02	G/A
MKK	rs13298872	9	6348385	0.001	1	HapMap	HapMap	G	0.99	A	0.01	G/A
YRI	rs13298872	9	6348385	0.006	1	HapMap	HapMap	G	0.982	A	0.018	G/A
CEU	rs1330124	9	6043098	0.016	1	HapMap	HapMap	A	0.858	C	0.142	A/C
CHB	rs1330124	9	6043098	0.004	1	HapMap	HapMap	A	0.958	C	0.042	A/C
GIH	rs1330124	9	6043098	0.015	1	HapMap	HapMap	A	0.761	C	0.239	A/C
MKK	rs1330124	9	6043098	0.029	1	HapMap	HapMap	A	0.822	C	0.178	A/C
ASW	rs1330380	9	6300829	0.019	1	HapMap	HapMap	C	0.047	A	0.953	C/A
GIH	rs1330380	9	6300829	0.001	1	HapMap	HapMap	C	0.017	A	0.983	C/A
MKK	rs1330380	9	6300829	0.001	1	HapMap	HapMap	C	0.007	A	0.993	C/A
YRI	rs1330380	9	6300829	0.03	1	HapMap	HapMap	C	0.013	A	0.987	C/A
MEX	rs1330380	9	6300829	0.001	1	HapMap	HapMap	C	0.02	A	0.98	C/A
LWK	rs1330380	9	6300829	0.138	1	HapMap	HapMap	C	0.033	A	0.967	C/A
MKK	rs1330383	9	6241507	0.05	0.666	HapMap	HapMap	G	0.545	T	0.455	G/T
JPT	rs1330383	9	6241507	0.047	1	HapMap	HapMap	G	0.564	T	0.436	G/T
GIH	rs1330383	9	6241507	0.039	1	HapMap	HapMap	G	0.545	T	0.455	G/T
CEU	rs1332290	9	6245881	0.025	0.626	HapMap	HapMap	T	0.353	G	0.647	T/G
GIH	rs1332290	9	6245881	0.04	1	HapMap	HapMap	T	0.46	G	0.54	T/G
MKK	rs1332290	9	6245881	0.115	0.601	HapMap	HapMap	T	0.703	G	0.297	T/G
ASW	rs1342326	9	6180076	0.062	0.726	HapMap	HapMap	A	0.679	C	0.321	A/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs1342326	9	6180076	0.03	1	HapMap	HapMap	A	0.832	C	0.168	A/C
GIH	rs1342326	9	6180076	0.008	1	HapMap	HapMap	A	0.858	C	0.142	A/C
YRI	rs1342326	9	6180076	0.144	1	HapMap	HapMap	A	0.668	C	0.332	A/C
LWK	rs1342326	9	6180076	0.12	0.774	HapMap	HapMap	A	0.556	C	0.444	A/C
MEX	rs1342326	9	6180076	0.012	1	HapMap	HapMap	A	0.84	C	0.16	A/C
ASW	rs1342328	9	6200785	0.034	1	HapMap	HapMap	A	0.906	G	0.094	A/G
GIH	rs1342328	9	6200785	0.001	1	HapMap	HapMap	A	0.983	G	0.017	A/G
LWK	rs1342328	9	6200785	0.028	1	HapMap	HapMap	A	0.9	G	0.1	A/G
MKK	rs1342328	9	6200785	0.012	1	HapMap	HapMap	A	0.916	G	0.084	A/G
GIH	rs1381038	9	6323156	0.001	1	HapMap	HapMap	C	0.017	A	0.983	C/A
ASW	rs1381038	9	6323156	0.04	0.626	HapMap	HapMap	C	0.255	A	0.745	C/A
MEX	rs1381038	9	6323156	0.001	1	HapMap	HapMap	C	0.03	A	0.97	C/A
MKK	rs1381038	9	6323156	0.015	1	HapMap	HapMap	C	0.101	A	0.899	C/A
GIH	rs1381039	9	6332682	0.001	1	HapMap	HapMap	A	0.017	G	0.983	A/G
MEX	rs1381039	9	6332682	0.001	1	HapMap	HapMap	A	0.031	G	0.969	A/G
CEU	rs1381039	9	6332682	0.006	1	HapMap	HapMap	A	0.031	G	0.969	A/G
JPT	rs1411341	9	6108982	0.007	1	HapMap	HapMap	T	0.878	C	0.122	T/C
CHB	rs1411341	9	6108982	0.017	1	HapMap	HapMap	T	0.863	C	0.137	T/C
CHD	rs1411341	9	6108982	0.024	1	HapMap	HapMap	T	0.833	C	0.167	T/C
GIH	rs1411341	9	6108982	0.009	1	HapMap	HapMap	T	0.841	C	0.159	T/C
LWK	rs1411341	9	6108982	0.048	1	HapMap	HapMap	T	0.839	C	0.161	T/C
CEU	rs1411948	9	5972797	0.008	0.921	HapMap	HapMap	G	0.925	A	0.075	G/A
GIH	rs1411948	9	5972797	0.001	1	HapMap	HapMap	G	0.972	A	0.028	G/A
LWK	rs1411948	9	5972797	0.003	1	HapMap	HapMap	G	0.989	A	0.011	G/A
MKK	rs1411948	9	5972797	0.002	1	HapMap	HapMap	G	0.982	A	0.018	G/A
YRI	rs1411948	9	5972797	0.015	1	HapMap	HapMap	G	0.965	A	0.035	G/A
ASW	rs1412420	9	6245152	0.029	1	HapMap	HapMap	A	0.075	G	0.925	A/G
MEX	rs1412420	9	6245152	0.001	1	HapMap	HapMap	A	0.02	G	0.98	A/G
GIH	rs1412420	9	6245152	0	1	HapMap	HapMap	A	0.006	G	0.994	A/G
CEU	rs1412420	9	6245152	0.004	0.676	HapMap	HapMap	A	0.044	G	0.956	A/G
LWK	rs1412424	9	6079129	0.021	0.904	HapMap	HapMap	G	0.906	C	0.094	G/C
MEX	rs1412424	9	6079129	0.001	1	HapMap	HapMap	G	0.99	C	0.01	G/C
CHD	rs1412426	9	6178652	0.638	0.918	HapMap	HapMap	A	0.085	C	0.915	A/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
GIH	rs1412426	9	6178652	0.12	1	HapMap	HapMap	A	0.284	C	0.716	A/C
JPT	rs1412426	9	6178652	0.499	0.779	HapMap	HapMap	A	0.052	C	0.948	A/C
ASW	rs1412426	9	6178652	0.063	0.705	HapMap	HapMap	A	0.642	C	0.358	A/C
LWK	rs1412426	9	6178652	0.04	0.7	HapMap	HapMap	A	0.756	C	0.244	A/C
CHB	rs1412426	9	6178652	0.273	0.611	HapMap	HapMap	A	0.077	C	0.923	A/C
CEU	rs1412426	9	6178652	0.149	1	HapMap	HapMap	A	0.336	C	0.664	A/C
MKK	rs1412426	9	6178652	0.092	0.897	HapMap	HapMap	A	0.546	C	0.454	A/C
MKK	rs1478940	9	6058048	0.024	1	HapMap	HapMap	C	0.85	A	0.15	C/A
LWK	rs1478940	9	6058048	0.024	1	HapMap	HapMap	C	0.911	A	0.089	C/A
MEX	rs1478940	9	6058048	0	1	HapMap	HapMap	C	0.99	A	0.01	C/A
ASW	rs1478940	9	6058048	0.019	1	HapMap	HapMap	C	0.925	A	0.075	C/A
CEU	rs1478940	9	6058048	0.001	1	HapMap	HapMap	C	0.991	A	0.009	C/A
ASW	rs1551761	9	6303518	0.046	1	HapMap	HapMap	C	0.17	G	0.83	C/G
GIH	rs1551761	9	6303518	0.001	1	HapMap	HapMap	C	0.017	G	0.983	C/G
MKK	rs1551761	9	6303518	0.015	1	HapMap	HapMap	C	0.101	G	0.899	C/G
MEX	rs1551761	9	6303518	0.001	1	HapMap	HapMap	C	0.031	G	0.969	C/G
ASW	rs16924068	9	6154596	0.015	1	HapMap	HapMap	C	0.971	T	0.029	C/T
YRI	rs16924068	9	6154596	0.019	1	HapMap	HapMap	C	0.932	T	0.068	C/T
YRI	rs16924081	9	6159135	0.038	1	HapMap	HapMap	G	0.889	A	0.111	G/A
MKK	rs16924081	9	6159135	0.018	1	HapMap	HapMap	G	0.88	A	0.12	G/A
LWK	rs16924081	9	6159135	0.039	0.967	HapMap	HapMap	G	0.856	A	0.144	G/A
MEX	rs16924081	9	6159135	0.001	1	HapMap	HapMap	G	0.97	A	0.03	G/A
GIH	rs16924081	9	6159135	0.002	1	HapMap	HapMap	G	0.96	A	0.04	G/A
ASW	rs16924081	9	6159135	0.024	1	HapMap	HapMap	G	0.925	A	0.075	G/A
CHD	rs16924081	9	6159135	0.101	1	HapMap	HapMap	G	0.988	A	0.012	G/A
CHB	rs16924081	9	6159135	0.232	1	HapMap	HapMap	G	0.976	A	0.024	G/A
MKK	rs16924144	9	6211246	0.032	0.774	HapMap	HapMap	T	0.717	C	0.283	T/C
JPT	rs16924144	9	6211246	0.015	1	HapMap	HapMap	T	0.75	C	0.25	T/C
LWK	rs16924144	9	6211246	0.035	1	HapMap	HapMap	T	0.878	C	0.122	T/C
CEU	rs16924144	9	6211246	0.05	1	HapMap	HapMap	T	0.69	C	0.31	T/C
GIH	rs16924144	9	6211246	0.023	1	HapMap	HapMap	T	0.676	C	0.324	T/C
YRI	rs16924161	9	6220912	0.012	1	HapMap	HapMap	T	0.969	C	0.031	T/C
ASW	rs16924161	9	6220912	0.014	1	HapMap	HapMap	T	0.953	C	0.047	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MEX	rs16924161	9	6220912	0.008	1	HapMap	HapMap	T	0.89	C	0.11	T/C
JPT	rs16924161	9	6220912	0.073	1	HapMap	HapMap	T	0.506	C	0.494	T/C
LWK	rs16924161	9	6220912	0.022	1	HapMap	HapMap	T	0.994	C	0.006	T/C
CHD	rs16924161	9	6220912	0.061	1	HapMap	HapMap	T	0.659	C	0.341	T/C
ASW	rs16924241	9	6246144	0.008	0.741	HapMap	HapMap	C	0.962	G	0.038	C/G
LWK	rs16924241	9	6246144	0.007	0.831	HapMap	HapMap	C	0.961	G	0.039	C/G
ASW	rs16924243	9	6247054	0.086	1	HapMap	HapMap	T	0.811	C	0.189	T/C
CEU	rs16924243	9	6247054	0.004	1	HapMap	HapMap	T	0.965	C	0.035	T/C
GIH	rs16924243	9	6247054	0.001	1	HapMap	HapMap	T	0.989	C	0.011	T/C
MEX	rs16924243	9	6247054	0.001	1	HapMap	HapMap	T	0.97	C	0.03	T/C
MKK	rs16924243	9	6247054	0.026	1	HapMap	HapMap	T	0.839	C	0.161	T/C
YRI	rs16924243	9	6247054	0.059	0.767	HapMap	HapMap	T	0.73	C	0.27	T/C
YRI	rs16924277	9	6269324	0.015	1	HapMap	HapMap	C	0.965	T	0.035	C/T
MKK	rs16924277	9	6269324	0	1	HapMap	HapMap	C	0.997	T	0.003	C/T
ASW	rs16924277	9	6269324	0.034	1	HapMap	HapMap	C	0.925	T	0.075	C/T
LWK	rs16924301	9	6296093	0.004	1	HapMap	HapMap	A	0.983	G	0.017	A/G
JPT	rs16924301	9	6296093	0.004	0.615	HapMap	HapMap	A	0.831	G	0.169	A/G
ASW	rs16924301	9	6296093	0.176	1	HapMap	HapMap	A	0.943	G	0.057	A/G
GIH	rs16924301	9	6296093	0.016	1	HapMap	HapMap	A	0.744	G	0.256	A/G
YRI	rs16924301	9	6296093	0.06	1	HapMap	HapMap	A	0.96	G	0.04	A/G
MKK	rs16924301	9	6296093	0.004	1	HapMap	HapMap	A	0.972	G	0.028	A/G
MKK	rs16924356	9	6321610	0.017	0.656	HapMap	HapMap	G	0.776	A	0.224	G/A
MEX	rs16924356	9	6321610	0.013	1	HapMap	HapMap	G	0.82	A	0.18	G/A
ASW	rs16924356	9	6321610	0.041	0.663	HapMap	HapMap	G	0.736	A	0.264	G/A
GIH	rs16924356	9	6321610	0.008	1	HapMap	HapMap	G	0.864	A	0.136	G/A
CEU	rs16924356	9	6321610	0.052	1	HapMap	HapMap	G	0.717	A	0.283	G/A
MKK	rs16924360	9	6321840	0.014	1	HapMap	HapMap	T	0.906	G	0.094	T/G
MEX	rs16924360	9	6321840	0.001	1	HapMap	HapMap	T	0.98	G	0.02	T/G
LWK	rs16924360	9	6321840	0.02	0.668	HapMap	HapMap	T	0.85	G	0.15	T/G
GIH	rs16924360	9	6321840	0	1	HapMap	HapMap	T	0.994	G	0.006	T/G
MKK	rs16924434	9	6348334	0.005	1	HapMap	HapMap	A	0.965	G	0.035	A/G
MEX	rs16924434	9	6348334	0.009	1	HapMap	HapMap	A	0.87	G	0.13	A/G
CHD	rs16924434	9	6348334	0.047	1	HapMap	HapMap	A	0.718	G	0.282	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs16924434	9	6348334	0.033	1	HapMap	HapMap	A	0.738	G	0.262	A/G
CEU	rs16924434	9	6348334	0.011	1	HapMap	HapMap	A	0.898	G	0.102	A/G
ASW	rs16924434	9	6348334	0	1	HapMap	HapMap	A	0.991	G	0.009	A/G
CEU	rs17498168	9	6227186	0.378	0.811	HapMap	HapMap	T	0.965	C	0.035	T/C
MEX	rs17498196	9	6227547	0.006	0.77	HapMap	HapMap	A	0.87	C	0.13	A/C
GIH	rs17498196	9	6227547	0.007	1	HapMap	HapMap	A	0.875	C	0.125	A/C
MKK	rs17498196	9	6227547	0.002	1	HapMap	HapMap	A	0.983	C	0.017	A/C
ASW	rs17498196	9	6227547	0.014	1	HapMap	HapMap	A	0.906	C	0.094	A/C
CEU	rs17498196	9	6227547	0.041	1	HapMap	HapMap	A	0.765	C	0.235	A/C
CEU	rs1755531	9	6114250	0.013	1	HapMap	HapMap	T	0.129	G	0.871	T/G
CHB	rs1755531	9	6114250	0.002	1	HapMap	HapMap	T	0.03	G	0.97	T/G
GIH	rs1755531	9	6114250	0.016	1	HapMap	HapMap	T	0.25	G	0.75	T/G
MEX	rs1755531	9	6114250	0.009	1	HapMap	HapMap	T	0.13	G	0.87	T/G
MKK	rs1755531	9	6114250	0.032	1	HapMap	HapMap	T	0.186	G	0.814	T/G
ASW	rs17580721	9	6007252	0.004	1	HapMap	HapMap	A	0.962	G	0.038	A/G
MEX	rs17580721	9	6007252	0.003	1	HapMap	HapMap	A	0.96	G	0.04	A/G
CEU	rs17580721	9	6007252	0.016	1	HapMap	HapMap	A	0.832	G	0.168	A/G
CHD	rs17580721	9	6007252	0.001	1	HapMap	HapMap	A	0.994	G	0.006	A/G
GIH	rs17580721	9	6007252	0.003	1	HapMap	HapMap	A	0.943	G	0.057	A/G
CHD	rs17705436	9	6300908	0.001	1	HapMap	HapMap	C	0.994	G	0.006	C/G
GIH	rs17705436	9	6300908	0.007	1	HapMap	HapMap	C	0.869	G	0.131	C/G
ASW	rs17705436	9	6300908	0.014	1	HapMap	HapMap	C	0.896	G	0.104	C/G
CEU	rs17705436	9	6300908	0.043	1	HapMap	HapMap	C	0.743	G	0.257	C/G
MKK	rs17705436	9	6300908	0.002	1	HapMap	HapMap	C	0.986	G	0.014	C/G
GIH	rs17756142	9	6291578	0.007	1	HapMap	HapMap	A	0.875	C	0.125	A/C
MEX	rs17756142	9	6291578	0.009	0.925	HapMap	HapMap	A	0.86	C	0.14	A/C
ASW	rs17756142	9	6291578	0.014	1	HapMap	HapMap	A	0.896	C	0.104	A/C
MKK	rs17756142	9	6291578	0.002	1	HapMap	HapMap	A	0.986	C	0.014	A/C
CHD	rs17756142	9	6291578	0.004	1	HapMap	HapMap	A	0.97	C	0.03	A/C
CEU	rs17756142	9	6291578	0.043	1	HapMap	HapMap	A	0.735	C	0.265	A/C
GIH	rs1888703	9	5973508	0.008	1	HapMap	HapMap	T	0.132	G	0.868	T/G
CHB	rs1888703	9	5973508	0.116	0.758	HapMap	HapMap	T	0.315	G	0.685	T/G
CEU	rs1888909	9	6187392	0.208	1	HapMap	HapMap	T	0.288	C	0.712	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
ASW	rs1888909	9	6187392	0.11	0.646	HapMap	HapMap	T	0.462	C	0.538	T/C
CHB	rs1888909	9	6187392	0.232	1	HapMap	HapMap	T	0.036	C	0.964	T/C
CHD	rs1888909	9	6187392	0.417	1	HapMap	HapMap	T	0.047	C	0.953	T/C
YRI	rs1888909	9	6187392	0.212	0.89	HapMap	HapMap	T	0.535	C	0.465	T/C
GIH	rs1888909	9	6187392	0.151	1	HapMap	HapMap	T	0.239	C	0.761	T/C
JPT	rs1888909	9	6187392	0.585	1	HapMap	HapMap	T	0.035	C	0.965	T/C
MKK	rs1888909	9	6187392	0.148	0.699	HapMap	HapMap	T	0.308	C	0.692	T/C
ASW	rs1891385	9	6209845	0	1	HapMap	HapMap	A	0.991	C	0.009	A/C
CEU	rs1891385	9	6209845	0.012	1	HapMap	HapMap	A	0.894	C	0.106	A/C
CHD	rs1891385	9	6209845	0.035	1	HapMap	HapMap	A	0.771	C	0.229	A/C
LWK	rs1891385	9	6209845	0.045	1	HapMap	HapMap	A	0.989	C	0.011	A/C
MEX	rs1891385	9	6209845	0.005	1	HapMap	HapMap	A	0.93	C	0.07	A/C
MKK	rs1891385	9	6209845	0.006	1	HapMap	HapMap	A	0.955	C	0.045	A/C
JPT	rs189309	9	6101393	0.014	1	HapMap	HapMap	T	0.215	C	0.785	T/C
CHB	rs189309	9	6101393	0.063	0.65	HapMap	HapMap	T	0.393	C	0.607	T/C
GIH	rs189309	9	6101393	0.038	1	HapMap	HapMap	T	0.557	C	0.443	T/C
MEX	rs189309	9	6101393	0.022	0.609	HapMap	HapMap	T	0.48	C	0.52	T/C
CEU	rs1929994	9	6214308	0.007	1	HapMap	HapMap	T	0.956	C	0.044	T/C
LWK	rs1929994	9	6214308	0.048	1	HapMap	HapMap	T	0.839	C	0.161	T/C
MKK	rs1929994	9	6214308	0.024	0.938	HapMap	HapMap	T	0.831	C	0.169	T/C
CHB	rs1970089	9	6114359	0.002	1	HapMap	HapMap	T	0.03	C	0.97	T/C
GIH	rs1970089	9	6114359	0.016	1	HapMap	HapMap	T	0.241	C	0.759	T/C
MEX	rs1970089	9	6114359	0.009	1	HapMap	HapMap	T	0.14	C	0.86	T/C
CEU	rs1970089	9	6114359	0.013	1	HapMap	HapMap	T	0.125	C	0.875	T/C
MKK	rs1970089	9	6114359	0.033	1	HapMap	HapMap	T	0.191	C	0.809	T/C
MEX	rs1993912	9	5977781	0.001	1	HapMap	HapMap	A	0.98	C	0.02	A/C
CHB	rs1993912	9	5977781	0.004	1	HapMap	HapMap	A	0.97	C	0.03	A/C
GIH	rs1993912	9	5977781	0.004	1	HapMap	HapMap	A	0.92	C	0.08	A/C
LWK	rs1993912	9	5977781	0.03	1	HapMap	HapMap	A	0.894	C	0.106	A/C
ASW	rs2000199	9	6258893	0.158	0.705	HapMap	HapMap	G	0.509	A	0.491	G/A
CEU	rs2000199	9	6258893	0.013	1	HapMap	HapMap	G	0.075	A	0.925	G/A
GIH	rs2000199	9	6258893	0.001	1	HapMap	HapMap	G	0.017	A	0.983	G/A
MEX	rs2000199	9	6258893	0.005	1	HapMap	HapMap	G	0.09	A	0.91	G/A

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MKK	rs2000199	9	6258893	0.043	0.752	HapMap	HapMap	G	0.36	A	0.64	G/A
ASW	rs2026991	9	6256440	0.158	0.705	HapMap	HapMap	A	0.509	G	0.491	A/G
CEU	rs2026991	9	6256440	0.013	1	HapMap	HapMap	A	0.075	G	0.925	A/G
GIH	rs2026991	9	6256440	0.001	1	HapMap	HapMap	A	0.017	G	0.983	A/G
MEX	rs2026991	9	6256440	0.005	1	HapMap	HapMap	A	0.09	G	0.91	A/G
MKK	rs2026991	9	6256440	0.045	0.76	HapMap	HapMap	A	0.367	G	0.633	A/G
ASW	rs2039386	9	6258204	0.146	0.794	HapMap	HapMap	G	0.396	C	0.604	G/C
CEU	rs2039386	9	6258204	0.013	1	HapMap	HapMap	G	0.075	C	0.925	G/C
GIH	rs2039386	9	6258204	0.001	1	HapMap	HapMap	G	0.017	C	0.983	G/C
MEX	rs2039386	9	6258204	0.004	1	HapMap	HapMap	G	0.08	C	0.92	G/C
JPT	rs2054314	9	6281125	0.001	1	HapMap	HapMap	T	0.006	C	0.994	T/C
MEX	rs2054314	9	6281125	0.003	1	HapMap	HapMap	T	0.07	C	0.93	T/C
MKK	rs2054314	9	6281125	0.016	0.608	HapMap	HapMap	T	0.236	C	0.764	T/C
CHB	rs2054314	9	6281125	0.001	1	HapMap	HapMap	T	0.012	C	0.988	T/C
CEU	rs2054314	9	6281125	0.014	1	HapMap	HapMap	T	0.078	C	0.922	T/C
GIH	rs2054314	9	6281125	0.001	1	HapMap	HapMap	T	0.028	C	0.972	T/C
CEU	rs2066362	9	6209176	0.026	1	HapMap	HapMap	G	0.835	T	0.165	G/T
GIH	rs2066362	9	6209176	0.013	1	HapMap	HapMap	G	0.784	T	0.216	G/T
MEX	rs2066362	9	6209176	0.014	1	HapMap	HapMap	G	0.82	T	0.18	G/T
JPT	rs2069264	9	6124787	0.007	1	HapMap	HapMap	T	0.878	C	0.122	T/C
LWK	rs2069264	9	6124787	0.033	1	HapMap	HapMap	T	0.883	C	0.117	T/C
YRI	rs2069264	9	6124787	0.028	0.679	HapMap	HapMap	T	0.839	C	0.161	T/C
ASW	rs2069264	9	6124787	0.041	0.663	HapMap	HapMap	T	0.764	C	0.236	T/C
CHB	rs2069264	9	6124787	0.018	1	HapMap	HapMap	T	0.857	C	0.143	T/C
GIH	rs2069264	9	6124787	0.008	1	HapMap	HapMap	T	0.852	C	0.148	T/C
CHD	rs2069264	9	6124787	0.025	1	HapMap	HapMap	T	0.824	C	0.176	T/C
CEU	rs2169282	9	6340235	0.089	1	HapMap	HapMap	A	0.389	G	0.611	A/G
CHD	rs2169282	9	6340235	0.047	1	HapMap	HapMap	A	0.282	G	0.718	A/G
GIH	rs2169282	9	6340235	0.03	1	HapMap	HapMap	A	0.386	G	0.614	A/G
MEX	rs2169282	9	6340235	0.02	1	HapMap	HapMap	A	0.26	G	0.74	A/G
MKK	rs2169282	9	6340235	0.067	0.761	HapMap	HapMap	A	0.462	G	0.538	A/G
CHB	rs2169282	9	6340235	0.033	1	HapMap	HapMap	A	0.262	G	0.738	A/G
CEU	rs2210463	9	6217752	0.287	1	HapMap	HapMap	A	0.699	G	0.301	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
GIH	rs2210463	9	6217752	0.094	1	HapMap	HapMap	A	0.665	G	0.335	A/G
JPT	rs2210463	9	6217752	0.056	1	HapMap	HapMap	A	0.482	G	0.518	A/G
MKK	rs2210463	9	6217752	0.099	0.729	HapMap	HapMap	A	0.58	G	0.42	A/G
CEU	rs2210464	9	6213903	0.446	1	HapMap	HapMap	A	0.757	T	0.243	A/T
MKK	rs2210464	9	6213903	0.187	0.626	HapMap	HapMap	A	0.78	T	0.22	A/T
JPT	rs2210464	9	6213903	0.052	1	HapMap	HapMap	A	0.477	T	0.523	A/T
MKK	rs2290913	9	6320321	0	1	HapMap	HapMap	T	0.996	A	0.004	T/A
JPT	rs2290913	9	6320321	0.006	1	HapMap	HapMap	T	0.936	A	0.064	T/A
CHD	rs2290913	9	6320321	0.014	1	HapMap	HapMap	T	0.894	A	0.106	T/A
ASW	rs2295843	9	6318871	0.004	1	HapMap	HapMap	G	0.991	A	0.009	G/A
CHB	rs2295843	9	6318871	0.115	1	HapMap	HapMap	G	0.994	A	0.006	G/A
JPT	rs2295843	9	6318871	0.19	1	HapMap	HapMap	G	0.994	A	0.006	G/A
MEX	rs2295843	9	6318871	0	1	HapMap	HapMap	G	0.99	A	0.01	G/A
CHD	rs2295843	9	6318871	0.256	1	HapMap	HapMap	G	0.971	A	0.029	G/A
CHD	rs2381413	9	6157017	0.177	0.8	HapMap	HapMap	C	0.7	G	0.3	C/G
GIH	rs2381413	9	6157017	0.075	1	HapMap	HapMap	C	0.614	G	0.386	C/G
JPT	rs2381413	9	6157017	0.163	0.718	HapMap	HapMap	C	0.831	G	0.169	C/G
MEX	rs2381413	9	6157017	0.052	0.693	HapMap	HapMap	C	0.66	G	0.34	C/G
MKK	rs2381413	9	6157017	0.064	0.796	HapMap	HapMap	C	0.427	G	0.573	C/G
CEU	rs2381413	9	6157017	0.1	1	HapMap	HapMap	C	0.54	G	0.46	C/G
CHB	rs2381413	9	6157017	0.151	0.776	HapMap	HapMap	C	0.69	G	0.31	C/G
ASW	rs2381422	9	6271211	0.058	1	HapMap	HapMap	C	0.123	T	0.877	C/T
LWK	rs2381422	9	6271211	0.096	0.675	HapMap	HapMap	C	0.05	T	0.95	C/T
GIH	rs2381422	9	6271211	0.001	1	HapMap	HapMap	C	0.017	T	0.983	C/T
MKK	rs2381422	9	6271211	0.002	1	HapMap	HapMap	C	0.014	T	0.986	C/T
MEX	rs2381422	9	6271211	0.001	1	HapMap	HapMap	C	0.02	T	0.98	C/T
CEU	rs2381438	9	6332855	0.006	1	HapMap	HapMap	G	0.031	A	0.969	G/A
GIH	rs2381438	9	6332855	0.001	1	HapMap	HapMap	G	0.017	A	0.983	G/A
MEX	rs2381438	9	6332855	0.001	1	HapMap	HapMap	G	0.031	A	0.969	G/A
ASW	rs2381438	9	6332855	0.046	0.621	HapMap	HapMap	G	0.274	A	0.726	G/A
CHD	rs2890704	9	6174165	0.417	1	HapMap	HapMap	T	0.047	C	0.953	T/C
GIH	rs2890704	9	6174165	0.445	1	HapMap	HapMap	T	0.097	C	0.903	T/C
MEX	rs2890704	9	6174165	0.587	1	HapMap	HapMap	T	0.03	C	0.97	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MKK	rs2890704	9	6174165	0.484	0.851	HapMap	HapMap	T	0.168	C	0.832	T/C
YRI	rs2890704	9	6174165	0.567	0.886	HapMap	HapMap	T	0.292	C	0.708	T/C
JPT	rs2890704	9	6174165	0.585	1	HapMap	HapMap	T	0.035	C	0.965	T/C
LWK	rs2890704	9	6174165	0.499	0.767	HapMap	HapMap	T	0.228	C	0.772	T/C
CEU	rs2890704	9	6174165	0.683	1	HapMap	HapMap	T	0.119	C	0.881	T/C
CHB	rs2890704	9	6174165	0.232	1	HapMap	HapMap	T	0.036	C	0.964	T/C
ASW	rs2890704	9	6174165	0.541	0.802	HapMap	HapMap	T	0.198	C	0.802	T/C
ASW	rs2890707	9	6321324	0.04	0.626	HapMap	HapMap	A	0.255	G	0.745	A/G
GIH	rs2890707	9	6321324	0.001	1	HapMap	HapMap	A	0.017	G	0.983	A/G
MEX	rs2890707	9	6321324	0.001	1	HapMap	HapMap	A	0.03	G	0.97	A/G
MKK	rs2890707	9	6321324	0.015	1	HapMap	HapMap	A	0.101	G	0.899	A/G
MEX	rs340890	9	6090169	0.016	1	HapMap	HapMap	C	0.735	T	0.265	C/T
MKK	rs340890	9	6090169	0.019	0.615	HapMap	HapMap	C	0.724	T	0.276	C/T
CHD	rs340890	9	6090169	0.014	0.612	HapMap	HapMap	C	0.759	T	0.241	C/T
YRI	rs340890	9	6090169	0.018	1	HapMap	HapMap	C	0.942	T	0.058	C/T
MEX	rs340892	9	6088662	0.022	0.609	HapMap	HapMap	T	0.48	G	0.52	T/G
GIH	rs340892	9	6088662	0.027	1	HapMap	HapMap	T	0.636	G	0.364	T/G
CHB	rs340892	9	6088662	0.063	0.65	HapMap	HapMap	T	0.392	G	0.608	T/G
MEX	rs340899	9	6099080	0.024	0.617	HapMap	HapMap	C	0.47	T	0.53	C/T
CHB	rs340899	9	6099080	0.063	0.65	HapMap	HapMap	C	0.399	T	0.601	C/T
GIH	rs340899	9	6099080	0.034	1	HapMap	HapMap	C	0.585	T	0.415	C/T
MEX	rs340900	9	6098921	0.022	0.609	HapMap	HapMap	T	0.48	C	0.52	T/C
CHB	rs340900	9	6098921	0.063	0.65	HapMap	HapMap	T	0.393	C	0.607	T/C
GIH	rs340900	9	6098921	0.034	1	HapMap	HapMap	T	0.585	C	0.415	T/C
MKK	rs340904	9	6096779	0.029	1	HapMap	HapMap	C	0.175	A	0.825	C/A
CHB	rs340904	9	6096779	0.002	1	HapMap	HapMap	C	0.03	A	0.97	C/A
GIH	rs340904	9	6096779	0.015	1	HapMap	HapMap	C	0.244	A	0.756	C/A
CEU	rs340904	9	6096779	0.013	1	HapMap	HapMap	C	0.124	A	0.876	C/A
MEX	rs340904	9	6096779	0.009	1	HapMap	HapMap	C	0.13	A	0.87	C/A
CEU	rs340908	9	6118897	0.013	1	HapMap	HapMap	T	0.124	C	0.876	T/C
CHB	rs340908	9	6118897	0.002	1	HapMap	HapMap	T	0.03	C	0.97	T/C
GIH	rs340908	9	6118897	0.015	1	HapMap	HapMap	T	0.244	C	0.756	T/C
MKK	rs340908	9	6118897	0.029	1	HapMap	HapMap	T	0.175	C	0.825	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MEX	rs340908	9	6118897	0.009	1	HapMap	HapMap	T	0.13	C	0.87	T/C
MEX	rs340921	9	6080160	0.009	1	HapMap	HapMap	G	0.133	T	0.867	G/T
MKK	rs340921	9	6080160	0.027	1	HapMap	HapMap	G	0.164	T	0.836	G/T
GIH	rs340921	9	6080160	0.015	1	HapMap	HapMap	G	0.244	T	0.756	G/T
CHB	rs340921	9	6080160	0.004	1	HapMap	HapMap	G	0.036	T	0.964	G/T
CEU	rs340921	9	6080160	0.013	1	HapMap	HapMap	G	0.125	T	0.875	G/T
CHB	rs340923	9	6078628	0.003	1	HapMap	HapMap	G	0.03	A	0.97	G/A
GIH	rs340923	9	6078628	0.015	1	HapMap	HapMap	G	0.239	A	0.761	G/A
MEX	rs340923	9	6078628	0.009	1	HapMap	HapMap	G	0.14	A	0.86	G/A
MKK	rs340923	9	6078628	0.018	0.692	HapMap	HapMap	G	0.22	A	0.78	G/A
CEU	rs340923	9	6078628	0.013	1	HapMap	HapMap	G	0.124	A	0.876	G/A
YRI	rs340930	9	6076676	0.05	0.642	HapMap	HapMap	T	0.054	G	0.946	T/G
LWK	rs340930	9	6076676	0.161	1	HapMap	HapMap	T	0.039	G	0.961	T/G
ASW	rs340930	9	6076676	0.062	1	HapMap	HapMap	T	0.01	G	0.99	T/G
CHB	rs340933	9	6075078	0.004	1	HapMap	HapMap	T	0.037	G	0.963	T/G
GIH	rs340933	9	6075078	0.015	1	HapMap	HapMap	T	0.241	G	0.759	T/G
MEX	rs340933	9	6075078	0.01	1	HapMap	HapMap	T	0.135	G	0.865	T/G
CEU	rs340933	9	6075078	0.014	1	HapMap	HapMap	T	0.125	G	0.875	T/G
CEU	rs340934	9	6071804	0.014	1	HapMap	HapMap	G	0.119	T	0.881	G/T
JPT	rs340934	9	6071804	0.001	1	HapMap	HapMap	G	0.017	T	0.983	G/T
GIH	rs340934	9	6071804	0.013	1	HapMap	HapMap	G	0.216	T	0.784	G/T
MEX	rs340934	9	6071804	0.008	1	HapMap	HapMap	G	0.13	T	0.87	G/T
MKK	rs340934	9	6071804	0.027	1	HapMap	HapMap	G	0.163	T	0.837	G/T
CHD	rs343470	9	6034937	0.035	0.787	HapMap	HapMap	T	0.324	C	0.676	T/C
LWK	rs343470	9	6034937	0.015	1	HapMap	HapMap	T	0.056	C	0.944	T/C
CHB	rs343471	9	6033593	0.122	0.6	HapMap	HapMap	T	0.78	C	0.22	T/C
ASW	rs343471	9	6033593	0.026	1	HapMap	HapMap	T	0.923	C	0.077	T/C
CEU	rs343471	9	6033593	0.001	1	HapMap	HapMap	T	0.991	C	0.009	T/C
CHB	rs343473	9	6064936	0.005	1	HapMap	HapMap	A	0.054	G	0.946	A/G
JPT	rs343473	9	6064936	0.001	1	HapMap	HapMap	A	0.023	G	0.977	A/G
MEX	rs343474	9	6063843	0.027	0.632	HapMap	HapMap	A	0.44	G	0.56	A/G
CHD	rs343474	9	6063843	0.024	1	HapMap	HapMap	A	0.163	G	0.837	A/G
JPT	rs343474	9	6063843	0.008	1	HapMap	HapMap	A	0.145	G	0.855	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs343474	9	6063843	0.017	0.889	HapMap	HapMap	A	0.179	G	0.821	A/G
CEU	rs343477	9	5999761	0.097	0.67	HapMap	HapMap	G	0.712	A	0.288	G/A
MEX	rs343477	9	5999761	0.053	0.671	HapMap	HapMap	G	0.68	A	0.32	G/A
CEU	rs343484	9	6015606	0.058	0.609	HapMap	HapMap	G	0.659	A	0.341	G/A
MEX	rs343484	9	6015606	0.088	1	HapMap	HapMap	G	0.612	A	0.388	G/A
CEU	rs343485	9	6016180	0.058	0.609	HapMap	HapMap	T	0.659	G	0.341	T/G
MEX	rs343485	9	6016180	0.097	1	HapMap	HapMap	T	0.633	G	0.367	T/G
GIH	rs343485	9	6016180	0.035	1	HapMap	HapMap	T	0.426	G	0.574	T/G
CEU	rs343489	9	6054299	0.016	1	HapMap	HapMap	C	0.858	G	0.142	C/G
CHB	rs343489	9	6054299	0.004	1	HapMap	HapMap	C	0.958	G	0.042	C/G
GIH	rs343489	9	6054299	0.015	1	HapMap	HapMap	C	0.761	G	0.239	C/G
MEX	rs343489	9	6054299	0.009	1	HapMap	HapMap	C	0.87	G	0.13	C/G
MKK	rs343489	9	6054299	0.023	1	HapMap	HapMap	C	0.857	G	0.143	C/G
CEU	rs343491	9	6054640	0.016	1	HapMap	HapMap	G	0.858	C	0.142	G/C
CHB	rs343491	9	6054640	0.004	1	HapMap	HapMap	G	0.958	C	0.042	G/C
GIH	rs343491	9	6054640	0.015	1	HapMap	HapMap	G	0.761	C	0.239	G/C
MEX	rs343491	9	6054640	0.009	1	HapMap	HapMap	G	0.87	C	0.13	G/C
MKK	rs343491	9	6054640	0.023	1	HapMap	HapMap	G	0.857	C	0.143	G/C
GIH	rs343494	9	6060342	0.029	1	HapMap	HapMap	C	0.381	T	0.619	C/T
MEX	rs343494	9	6060342	0.026	0.624	HapMap	HapMap	C	0.54	T	0.46	C/T
CHD	rs343497	9	6057744	0.024	1	HapMap	HapMap	C	0.829	T	0.171	C/T
JPT	rs343497	9	6057744	0.007	1	HapMap	HapMap	C	0.866	T	0.134	C/T
MEX	rs343497	9	6057744	0.027	0.632	HapMap	HapMap	C	0.56	T	0.44	C/T
CHB	rs343497	9	6057744	0.01	0.699	HapMap	HapMap	C	0.833	T	0.167	C/T
GIH	rs343500	9	6005011	0.006	1	HapMap	HapMap	T	0.898	C	0.102	T/C
MEX	rs343500	9	6005011	0.001	1	HapMap	HapMap	T	0.97	C	0.03	T/C
CHB	rs343500	9	6005011	0.136	0.613	HapMap	HapMap	T	0.78	C	0.22	T/C
CEU	rs343500	9	6005011	0.001	1	HapMap	HapMap	T	0.991	C	0.009	T/C
CHB	rs371454	9	6068614	0.004	1	HapMap	HapMap	C	0.042	T	0.958	C/T
GIH	rs371454	9	6068614	0.015	1	HapMap	HapMap	C	0.244	T	0.756	C/T
MEX	rs371454	9	6068614	0.009	1	HapMap	HapMap	C	0.13	T	0.87	C/T
MKK	rs371454	9	6068614	0.023	1	HapMap	HapMap	C	0.147	T	0.853	C/T
YRI	rs371454	9	6068614	0.157	0.63	HapMap	HapMap	C	0.133	T	0.867	C/T

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs371454	9	6068614	0.014	1	HapMap	HapMap	C	0.133	T	0.867	C/T
CHB	rs376382	9	6124999	0.02	1	HapMap	HapMap	C	0.167	T	0.833	C/T
CHD	rs376382	9	6124999	0.026	1	HapMap	HapMap	C	0.182	T	0.818	C/T
GIH	rs376382	9	6124999	0.031	1	HapMap	HapMap	C	0.392	T	0.608	C/T
JPT	rs376382	9	6124999	0.007	1	HapMap	HapMap	C	0.122	T	0.878	C/T
CEU	rs380568	9	6045531	0.016	1	HapMap	HapMap	T	0.863	C	0.137	T/C
CHB	rs380568	9	6045531	0.004	1	HapMap	HapMap	T	0.958	C	0.042	T/C
GIH	rs380568	9	6045531	0.016	1	HapMap	HapMap	T	0.75	C	0.25	T/C
MEX	rs380568	9	6045531	0.009	1	HapMap	HapMap	T	0.87	C	0.13	T/C
MKK	rs380568	9	6045531	0.012	1	HapMap	HapMap	T	0.918	C	0.082	T/C
ASW	rs3847261	9	6299188	0.101	1	HapMap	HapMap	T	0.25	A	0.75	T/A
GIH	rs3847261	9	6299188	0.001	1	HapMap	HapMap	T	0.017	A	0.983	T/A
MEX	rs3847261	9	6299188	0.001	1	HapMap	HapMap	T	0.031	A	0.969	T/A
MKK	rs3847261	9	6299188	0.018	1	HapMap	HapMap	T	0.115	A	0.885	T/A
ASW	rs3847262	9	6318947	0.093	1	HapMap	HapMap	T	0.264	C	0.736	T/C
GIH	rs3847262	9	6318947	0.001	1	HapMap	HapMap	T	0.017	C	0.983	T/C
MEX	rs3847262	9	6318947	0.001	1	HapMap	HapMap	T	0.03	C	0.97	T/C
MKK	rs3847262	9	6318947	0.016	1	HapMap	HapMap	T	0.108	C	0.892	T/C
MEX	rs386775	9	6134486	0.002	1	HapMap	HapMap	T	0.03	C	0.97	T/C
CHB	rs386775	9	6134486	0.001	1	HapMap	HapMap	T	0.012	C	0.988	T/C
GIH	rs386775	9	6134486	0.011	1	HapMap	HapMap	T	0.188	C	0.812	T/C
MKK	rs386775	9	6134486	0.023	0.886	HapMap	HapMap	T	0.178	C	0.822	T/C
CHD	rs386880	9	6134333	0.052	1	HapMap	HapMap	C	0.304	T	0.696	C/T
GIH	rs386880	9	6134333	0.026	1	HapMap	HapMap	C	0.352	T	0.648	C/T
JPT	rs386880	9	6134333	0.011	1	HapMap	HapMap	C	0.188	T	0.812	C/T
MKK	rs386880	9	6134333	0.05	0.666	HapMap	HapMap	C	0.455	T	0.545	C/T
MEX	rs387149	9	6135022	0.016	1	HapMap	HapMap	C	0.22	T	0.78	C/T
LWK	rs387149	9	6135022	0.237	0.804	HapMap	HapMap	C	0.386	T	0.614	C/T
CHB	rs387149	9	6135022	0.036	0.604	HapMap	HapMap	C	0.494	T	0.506	C/T
CEU	rs387149	9	6135022	0.031	1	HapMap	HapMap	C	0.308	T	0.692	C/T
CHB	rs3939286	9	6200099	0.232	1	HapMap	HapMap	T	0.036	C	0.964	T/C
CHD	rs3939286	9	6200099	0.417	1	HapMap	HapMap	T	0.047	C	0.953	T/C
YRI	rs3939286	9	6200099	0.206	0.895	HapMap	HapMap	T	0.54	C	0.46	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MKK	rs3939286	9	6200099	0.141	0.817	HapMap	HapMap	T	0.391	C	0.609	T/C
GIH	rs3939286	9	6200099	0.151	1	HapMap	HapMap	T	0.239	C	0.761	T/C
JPT	rs3939286	9	6200099	0.585	1	HapMap	HapMap	T	0.029	C	0.971	T/C
ASW	rs3939286	9	6200099	0.136	0.676	HapMap	HapMap	T	0.462	C	0.538	T/C
CEU	rs3939286	9	6200099	0.208	1	HapMap	HapMap	T	0.283	C	0.717	T/C
ASW	rs3955036	9	6271660	0.019	1	HapMap	HapMap	G	0.953	A	0.047	G/A
GIH	rs3955036	9	6271660	0	1	HapMap	HapMap	G	0.994	A	0.006	G/A
MEX	rs3955036	9	6271660	0.001	1	HapMap	HapMap	G	0.98	A	0.02	G/A
MKK	rs3955036	9	6271660	0.001	1	HapMap	HapMap	G	0.989	A	0.011	G/A
CHB	rs406322	9	6136121	0.02	1	HapMap	HapMap	C	0.839	T	0.161	C/T
CHD	rs406322	9	6136121	0.03	1	HapMap	HapMap	C	0.8	T	0.2	C/T
GIH	rs406322	9	6136121	0.013	1	HapMap	HapMap	C	0.784	T	0.216	C/T
JPT	rs406322	9	6136121	0.008	1	HapMap	HapMap	C	0.888	T	0.112	C/T
CEU	rs406322	9	6136121	0.035	1	HapMap	HapMap	C	0.748	T	0.252	C/T
ASW	rs406322	9	6136121	0.04	1	HapMap	HapMap	C	0.858	T	0.142	C/T
MKK	rs409038	9	6124750	0.05	0.611	HapMap	HapMap	A	0.497	G	0.503	A/G
JPT	rs409038	9	6124750	0.007	1	HapMap	HapMap	A	0.134	G	0.866	A/G
GIH	rs409038	9	6124750	0.031	1	HapMap	HapMap	A	0.392	G	0.608	A/G
CHD	rs409038	9	6124750	0.027	1	HapMap	HapMap	A	0.188	G	0.812	A/G
CHB	rs409038	9	6124750	0.022	1	HapMap	HapMap	A	0.173	G	0.827	A/G
CHB	rs413382	9	6132948	0.001	1	HapMap	HapMap	C	0.018	A	0.982	C/A
MEX	rs413382	9	6132948	0.009	1	HapMap	HapMap	C	0.13	A	0.87	C/A
GIH	rs413382	9	6132948	0.016	1	HapMap	HapMap	C	0.25	A	0.75	C/A
MKK	rs413382	9	6132948	0.016	0.618	HapMap	HapMap	C	0.232	A	0.768	C/A
CEU	rs413382	9	6132948	0.019	1	HapMap	HapMap	C	0.142	A	0.858	C/A
GIH	rs418014	9	6110336	0.032	1	HapMap	HapMap	C	0.403	T	0.597	C/T
JPT	rs418014	9	6110336	0.007	1	HapMap	HapMap	C	0.134	T	0.866	C/T
CHB	rs418014	9	6110336	0.02	1	HapMap	HapMap	C	0.167	T	0.833	C/T
CHD	rs418014	9	6110336	0.027	1	HapMap	HapMap	C	0.188	T	0.812	C/T
ASW	rs4361812	9	6355737	0.014	1	HapMap	HapMap	C	0.934	A	0.066	C/A
CEU	rs4361812	9	6355737	0.027	1	HapMap	HapMap	C	0.841	A	0.159	C/A
GIH	rs4361812	9	6355737	0.007	1	HapMap	HapMap	C	0.875	A	0.125	C/A
MEX	rs4361812	9	6355737	0.005	1	HapMap	HapMap	C	0.93	A	0.07	C/A

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
GIH	rs4367609	9	6155405	1	1	HapMap	HapMap	C	0.955	T	0.045	C/T
MKK	rs4367609	9	6155405	0.384	0.842	HapMap	HapMap	C	0.801	T	0.199	C/T
CHD	rs4367609	9	6155405	0.473	0.822	HapMap	HapMap	C	0.923	T	0.077	C/T
CEU	rs4367609	9	6155405	0.815	1	HapMap	HapMap	C	0.906	T	0.094	C/T
JPT	rs4367609	9	6155405	0.585	1	HapMap	HapMap	C	0.948	T	0.052	C/T
MEX	rs4367609	9	6155405	0.791	1	HapMap	HapMap	C	0.95	T	0.05	C/T
ASW	rs4367609	9	6155405	0.358	0.736	HapMap	HapMap	C	0.821	T	0.179	C/T
CHB	rs4395943	9	5981006	0.116	0.758	HapMap	HapMap	T	0.31	C	0.69	T/C
GIH	rs4395943	9	5981006	0.006	1	HapMap	HapMap	T	0.108	C	0.892	T/C
CEU	rs4395943	9	5981006	0.001	1	HapMap	HapMap	T	0.009	C	0.991	T/C
MEX	rs4395943	9	5981006	0.003	1	HapMap	HapMap	T	0.06	C	0.94	T/C
GIH	rs448115	9	6124642	0.031	1	HapMap	HapMap	G	0.392	A	0.608	G/A
CHD	rs448115	9	6124642	0.029	1	HapMap	HapMap	G	0.194	A	0.806	G/A
JPT	rs448115	9	6124642	0.007	1	HapMap	HapMap	G	0.134	A	0.866	G/A
CHB	rs448115	9	6124642	0.022	1	HapMap	HapMap	G	0.173	A	0.827	G/A
MKK	rs451361	9	6039892	0.003	1	HapMap	HapMap	G	0.976	A	0.024	G/A
ASW	rs451361	9	6039892	0.014	1	HapMap	HapMap	G	0.972	A	0.028	G/A
CEU	rs451361	9	6039892	0.001	1	HapMap	HapMap	G	0.991	A	0.009	G/A
MEX	rs451361	9	6039892	0	1	HapMap	HapMap	G	0.99	A	0.01	G/A
YRI	rs451361	9	6039892	0.028	1	HapMap	HapMap	G	0.929	A	0.071	G/A
GIH	rs459525	9	6022924	0.035	1	HapMap	HapMap	C	0.426	T	0.574	C/T
MKK	rs459525	9	6022924	0.053	0.709	HapMap	HapMap	C	0.441	T	0.559	C/T
MKK	rs4740840	9	6219110	0.092	0.724	HapMap	HapMap	A	0.566	G	0.434	A/G
JPT	rs4740840	9	6219110	0.052	1	HapMap	HapMap	A	0.477	G	0.523	A/G
GIH	rs4740840	9	6219110	0.094	1	HapMap	HapMap	A	0.665	G	0.335	A/G
CEU	rs4740840	9	6219110	0.287	1	HapMap	HapMap	A	0.699	G	0.301	A/G
GIH	rs4742170	9	6232950	0.085	1	HapMap	HapMap	C	0.358	T	0.642	C/T
JPT	rs4742170	9	6232950	0.047	1	HapMap	HapMap	C	0.541	T	0.459	C/T
CEU	rs4742170	9	6232950	0.208	1	HapMap	HapMap	C	0.354	T	0.646	C/T
GIH	rs544253	9	6132157	0.024	1	HapMap	HapMap	A	0.665	C	0.335	A/C
CHD	rs544253	9	6132157	0.022	0.605	HapMap	HapMap	A	0.659	C	0.341	A/C
LWK	rs544253	9	6132157	0.022	1	HapMap	HapMap	A	0.994	C	0.006	A/C
MKK	rs544253	9	6132157	0.004	1	HapMap	HapMap	A	0.969	C	0.031	A/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
YRI	rs544253	9	6132157	0.006	1	HapMap	HapMap	A	0.978	C	0.022	A/C
CHD	rs6477029	9	6017931	0.024	1	HapMap	HapMap	T	0.833	C	0.167	T/C
CHB	rs6477029	9	6017931	0.01	0.699	HapMap	HapMap	T	0.821	C	0.179	T/C
MEX	rs6477029	9	6017931	0.103	1	HapMap	HapMap	T	0.66	C	0.34	T/C
CHB	rs6477037	9	6108174	0.017	1	HapMap	HapMap	T	0.863	C	0.137	T/C
LWK	rs6477037	9	6108174	0.048	1	HapMap	HapMap	T	0.839	C	0.161	T/C
CHD	rs6477037	9	6108174	0.025	1	HapMap	HapMap	T	0.827	C	0.173	T/C
GIH	rs6477037	9	6108174	0.009	1	HapMap	HapMap	T	0.841	C	0.159	T/C
JPT	rs6477037	9	6108174	0.007	1	HapMap	HapMap	T	0.876	C	0.124	T/C
CHB	rs6477040	9	6123074	0.017	1	HapMap	HapMap	C	0.863	T	0.137	C/T
ASW	rs6477040	9	6123074	0.048	0.687	HapMap	HapMap	C	0.736	T	0.264	C/T
YRI	rs6477040	9	6123074	0.039	0.625	HapMap	HapMap	C	0.765	T	0.235	C/T
JPT	rs6477040	9	6123074	0.007	1	HapMap	HapMap	C	0.878	T	0.122	C/T
GIH	rs6477040	9	6123074	0.008	1	HapMap	HapMap	C	0.852	T	0.148	C/T
LWK	rs6477040	9	6123074	0.054	1	HapMap	HapMap	C	0.822	T	0.178	C/T
CHD	rs6477040	9	6123074	0.024	1	HapMap	HapMap	C	0.829	T	0.171	C/T
MKK	rs6477040	9	6123074	0.05	1	HapMap	HapMap	C	0.732	T	0.268	C/T
CHB	rs694796	9	6122621	0.002	1	HapMap	HapMap	A	0.03	G	0.97	A/G
GIH	rs7021445	9	6346657	0.001	1	HapMap	HapMap	C	0.017	T	0.983	C/T
MEX	rs7021445	9	6346657	0.001	1	HapMap	HapMap	C	0.02	T	0.98	C/T
CHD	rs7024677	9	6076073	0.025	1	HapMap	HapMap	C	0.824	T	0.176	C/T
JPT	rs7024677	9	6076073	0.007	1	HapMap	HapMap	C	0.878	T	0.122	C/T
LWK	rs7024677	9	6076073	0.007	1	HapMap	HapMap	C	0.972	T	0.028	C/T
MKK	rs7024677	9	6076073	0.007	1	HapMap	HapMap	C	0.948	T	0.052	C/T
YRI	rs7024677	9	6076073	0.028	1	HapMap	HapMap	C	0.929	T	0.071	C/T
GIH	rs7024677	9	6076073	0.015	1	HapMap	HapMap	C	0.761	T	0.239	C/T
JPT	rs7025417	9	6230084	0.05	1	HapMap	HapMap	T	0.465	C	0.535	T/C
CEU	rs7025417	9	6230084	0.395	1	HapMap	HapMap	T	0.739	C	0.261	T/C
LWK	rs7032572	9	6162380	0.056	1	HapMap	HapMap	A	0.817	G	0.183	A/G
MEX	rs7032572	9	6162380	0.01	0.973	HapMap	HapMap	A	0.857	G	0.143	A/G
YRI	rs7032572	9	6162380	0.041	1	HapMap	HapMap	A	0.907	G	0.093	A/G
ASW	rs7032572	9	6162380	0.046	1	HapMap	HapMap	A	0.846	G	0.154	A/G
MKK	rs7032572	9	6162380	0.015	1	HapMap	HapMap	A	0.901	G	0.099	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs7032572	9	6162380	0.024	1	HapMap	HapMap	A	0.857	G	0.143	A/G
GIH	rs7032572	9	6162380	0.011	1	HapMap	HapMap	A	0.812	G	0.188	A/G
CEU	rs7033258	9	6224131	0.217	1	HapMap	HapMap	G	0.341	A	0.659	G/A
GIH	rs7033258	9	6224131	0.085	1	HapMap	HapMap	G	0.358	A	0.642	G/A
JPT	rs7033258	9	6224131	0.052	1	HapMap	HapMap	G	0.529	A	0.471	G/A
ASW	rs7034801	9	6312415	0.093	1	HapMap	HapMap	C	0.255	A	0.745	C/A
MKK	rs7034801	9	6312415	0.016	1	HapMap	HapMap	C	0.105	A	0.895	C/A
GIH	rs7034801	9	6312415	0.001	1	HapMap	HapMap	C	0.017	A	0.983	C/A
MEX	rs7034801	9	6312415	0.001	1	HapMap	HapMap	C	0.03	A	0.97	C/A
GIH	rs7034861	9	6284824	0.001	1	HapMap	HapMap	C	0.017	T	0.983	C/T
MEX	rs7034861	9	6284824	0.001	1	HapMap	HapMap	C	0.03	T	0.97	C/T
MKK	rs7034861	9	6284824	0.015	1	HapMap	HapMap	C	0.101	T	0.899	C/T
ASW	rs7034861	9	6284824	0.046	1	HapMap	HapMap	C	0.17	T	0.83	C/T
CHD	rs7035152	9	6036694	0.021	1	HapMap	HapMap	G	0.847	T	0.153	G/T
MEX	rs7035152	9	6036694	0.057	0.678	HapMap	HapMap	G	0.7	T	0.3	G/T
CEU	rs7035594	9	6115353	0.013	1	HapMap	HapMap	A	0.124	T	0.876	A/T
MEX	rs7035594	9	6115353	0.009	1	HapMap	HapMap	A	0.14	T	0.86	A/T
CHB	rs7035594	9	6115353	0.002	1	HapMap	HapMap	A	0.03	T	0.97	A/T
GIH	rs7035594	9	6115353	0.015	1	HapMap	HapMap	A	0.244	T	0.756	A/T
ASW	rs7035741	9	6279504	0.058	1	HapMap	HapMap	C	0.123	T	0.877	C/T
GIH	rs7035741	9	6279504	0.001	1	HapMap	HapMap	C	0.017	T	0.983	C/T
LWK	rs7035741	9	6279504	0.096	0.675	HapMap	HapMap	C	0.05	T	0.95	C/T
MEX	rs7035741	9	6279504	0.001	1	HapMap	HapMap	C	0.02	T	0.98	C/T
MKK	rs7035741	9	6279504	0.002	1	HapMap	HapMap	C	0.014	T	0.986	C/T
CEU	rs7037276	9	6237430	0.013	1	HapMap	HapMap	C	0.071	T	0.929	C/T
GIH	rs7037276	9	6237430	0	1	HapMap	HapMap	C	0.006	T	0.994	C/T
MEX	rs7037276	9	6237430	0.001	1	HapMap	HapMap	C	0.03	T	0.97	C/T
LWK	rs7037276	9	6237430	0.076	0.637	HapMap	HapMap	C	0.044	T	0.956	C/T
YRI	rs7037276	9	6237430	0.122	1	HapMap	HapMap	C	0.044	T	0.956	C/T
MKK	rs7037276	9	6237430	0.001	1	HapMap	HapMap	C	0.011	T	0.989	C/T
LWK	rs7037534	9	6245511	0.016	1	HapMap	HapMap	T	0.939	A	0.061	T/A
ASW	rs7037534	9	6245511	0.04	1	HapMap	HapMap	T	0.906	A	0.094	T/A
LWK	rs7040888	9	6103735	0.037	1	HapMap	HapMap	T	0.872	C	0.128	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
JPT	rs7040888	9	6103735	0.007	1	HapMap	HapMap	T	0.878	C	0.122	T/C
GIH	rs7040888	9	6103735	0.01	1	HapMap	HapMap	T	0.835	C	0.165	T/C
CHB	rs7040888	9	6103735	0.017	1	HapMap	HapMap	T	0.863	C	0.137	T/C
CHD	rs7040888	9	6103735	0.024	1	HapMap	HapMap	T	0.829	C	0.171	T/C
GIH	rs7041863	9	6317690	0.001	1	HapMap	HapMap	A	0.017	C	0.983	A/C
MKK	rs7041863	9	6317690	0.015	1	HapMap	HapMap	A	0.101	C	0.899	A/C
CHD	rs7041863	9	6317690	0.001	1	HapMap	HapMap	A	0.006	C	0.994	A/C
MEX	rs7041863	9	6317690	0.001	1	HapMap	HapMap	A	0.03	C	0.97	A/C
ASW	rs7041863	9	6317690	0.093	1	HapMap	HapMap	A	0.245	C	0.755	A/C
MEX	rs7042561	9	6101473	0.001	1	HapMap	HapMap	G	0.99	A	0.01	G/A
LWK	rs7042561	9	6101473	0.021	0.904	HapMap	HapMap	G	0.906	A	0.094	G/A
MKK	rs7043459	9	6256718	0.032	1	HapMap	HapMap	C	0.804	T	0.196	C/T
MEX	rs7043459	9	6256718	0.003	1	HapMap	HapMap	C	0.96	T	0.04	C/T
MEX	rs7045164	9	6317778	0.001	1	HapMap	HapMap	T	0.02	C	0.98	T/C
YRI	rs7045164	9	6317778	0.03	1	HapMap	HapMap	T	0.013	C	0.987	T/C
LWK	rs7045164	9	6317778	0.138	1	HapMap	HapMap	T	0.033	C	0.967	T/C
GIH	rs7045164	9	6317778	0.001	1	HapMap	HapMap	T	0.017	C	0.983	T/C
ASW	rs7045164	9	6317778	0.019	1	HapMap	HapMap	T	0.047	C	0.953	T/C
MKK	rs7045164	9	6317778	0.001	1	HapMap	HapMap	T	0.01	C	0.99	T/C
ASW	rs7046661	9	6199199	0.063	0.705	HapMap	HapMap	C	0.642	G	0.358	C/G
CEU	rs7046661	9	6199199	0.143	1	HapMap	HapMap	C	0.35	G	0.65	C/G
MKK	rs7046661	9	6199199	0.091	0.898	HapMap	HapMap	C	0.545	G	0.455	C/G
GIH	rs7046661	9	6199199	0.116	1	HapMap	HapMap	C	0.29	G	0.71	C/G
CHD	rs7046661	9	6199199	0.699	1	HapMap	HapMap	C	0.077	G	0.923	C/G
LWK	rs7046661	9	6199199	0.036	0.678	HapMap	HapMap	C	0.761	G	0.239	C/G
CHB	rs7046661	9	6199199	0.236	0.705	HapMap	HapMap	C	0.06	G	0.94	C/G
JPT	rs7046661	9	6199199	0.499	0.779	HapMap	HapMap	C	0.047	G	0.953	C/G
GIH	rs7047921	9	6245319	0.039	1	HapMap	HapMap	G	0.545	A	0.455	G/A
MKK	rs7047921	9	6245319	0.057	0.698	HapMap	HapMap	G	0.535	A	0.465	G/A
GIH	rs719724	9	6355614	0.033	1	HapMap	HapMap	T	0.401	A	0.599	T/A
MEX	rs719724	9	6355614	0.031	1	HapMap	HapMap	T	0.337	A	0.663	T/A
CHD	rs719724	9	6355614	0.044	1	HapMap	HapMap	T	0.271	A	0.729	T/A
CHB	rs719724	9	6355614	0.031	1	HapMap	HapMap	T	0.265	A	0.735	T/A

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs719724	9	6355614	0.097	1	HapMap	HapMap	T	0.41	A	0.59	T/A
MEX	rs721352	9	6322901	0.018	1	HapMap	HapMap	A	0.24	C	0.76	A/C
MKK	rs721352	9	6322901	0.049	0.689	HapMap	HapMap	A	0.434	C	0.566	A/C
GIH	rs721352	9	6322901	0.009	1	HapMap	HapMap	A	0.153	C	0.847	A/C
CEU	rs721352	9	6322901	0.067	1	HapMap	HapMap	A	0.314	C	0.686	A/C
CHB	rs7425	9	6001335	0.017	0.889	HapMap	HapMap	T	0.81	C	0.19	T/C
CHD	rs7425	9	6001335	0.024	1	HapMap	HapMap	T	0.829	C	0.171	T/C
GIH	rs7850988	9	6325760	0.008	1	HapMap	HapMap	A	0.864	T	0.136	A/T
LWK	rs7850988	9	6325760	0.033	0.654	HapMap	HapMap	A	0.767	T	0.233	A/T
MEX	rs7850988	9	6325760	0.013	1	HapMap	HapMap	A	0.82	T	0.18	A/T
MKK	rs7850988	9	6325760	0.016	0.662	HapMap	HapMap	A	0.79	T	0.21	A/T
CEU	rs7850988	9	6325760	0.052	1	HapMap	HapMap	A	0.728	T	0.272	A/T
ASW	rs7850988	9	6325760	0.035	0.635	HapMap	HapMap	A	0.745	T	0.255	A/T
GIH	rs7851246	9	6352365	0.009	1	HapMap	HapMap	G	0.847	A	0.153	G/A
MKK	rs7851246	9	6352365	0.014	0.61	HapMap	HapMap	G	0.78	A	0.22	G/A
LWK	rs7851246	9	6352365	0.03	0.614	HapMap	HapMap	G	0.761	A	0.239	G/A
MEX	rs7851246	9	6352365	0.009	1	HapMap	HapMap	G	0.86	A	0.14	G/A
CEU	rs7851246	9	6352365	0.052	1	HapMap	HapMap	G	0.721	A	0.279	G/A
CHD	rs7852365	9	6058910	0.001	1	HapMap	HapMap	C	0.994	T	0.006	C/T
CHB	rs7852365	9	6058910	0.002	1	HapMap	HapMap	C	0.982	T	0.018	C/T
JPT	rs7852365	9	6058910	0.001	1	HapMap	HapMap	C	0.988	T	0.012	C/T
YRI	rs7855264	9	6291923	0.03	1	HapMap	HapMap	A	0.009	G	0.991	A/G
LWK	rs7855264	9	6291923	0.138	1	HapMap	HapMap	A	0.033	G	0.967	A/G
GIH	rs7859139	9	6296294	0.001	1	HapMap	HapMap	G	0.017	A	0.983	G/A
MEX	rs7859139	9	6296294	0.001	1	HapMap	HapMap	G	0.03	A	0.97	G/A
CHD	rs7859139	9	6296294	0.001	1	HapMap	HapMap	G	0.006	A	0.994	G/A
ASW	rs7859139	9	6296294	0.046	1	HapMap	HapMap	G	0.17	A	0.83	G/A
MKK	rs7859139	9	6296294	0.018	1	HapMap	HapMap	G	0.115	A	0.885	G/A
MKK	rs7861831	9	6254463	0.033	1	HapMap	HapMap	C	0.804	T	0.196	C/T
MEX	rs7861831	9	6254463	0.003	1	HapMap	HapMap	C	0.96	T	0.04	C/T
CHB	rs7865727	9	6080276	0.127	0.601	HapMap	HapMap	T	0.976	C	0.024	T/C
ASW	rs7865727	9	6080276	0.004	1	HapMap	HapMap	T	0.972	C	0.028	T/C
MKK	rs7865727	9	6080276	0.008	1	HapMap	HapMap	T	0.944	C	0.056	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MEX	rs7865727	9	6080276	0.001	1	HapMap	HapMap	T	0.98	C	0.02	T/C
JPT	rs7865727	9	6080276	0.001	1	HapMap	HapMap	T	0.994	C	0.006	T/C
CEU	rs8172	9	6247898	0.013	1	HapMap	HapMap	A	0.08	G	0.92	A/G
GIH	rs8172	9	6247898	0.001	1	HapMap	HapMap	A	0.017	G	0.983	A/G
MEX	rs8172	9	6247898	0.005	1	HapMap	HapMap	A	0.09	G	0.91	A/G
MKK	rs8172	9	6247898	0.051	0.753	HapMap	HapMap	A	0.399	G	0.601	A/G
JPT	rs8172	9	6247898	0.001	1	HapMap	HapMap	A	0.006	G	0.994	A/G
ASW	rs8172	9	6247898	0.158	0.705	HapMap	HapMap	A	0.509	G	0.491	A/G
CEU	rs821164	9	6080989	0.012	1	HapMap	HapMap	C	0.121	G	0.879	C/G
GIH	rs821164	9	6080989	0.015	1	HapMap	HapMap	C	0.241	G	0.759	C/G
MEX	rs821164	9	6080989	0.009	1	HapMap	HapMap	C	0.14	G	0.86	C/G
CHB	rs821164	9	6080989	0.002	1	HapMap	HapMap	C	0.03	G	0.97	C/G
CEU	rs899381	9	6024076	0.001	1	HapMap	HapMap	T	0.991	C	0.009	T/C
GIH	rs899381	9	6024076	0.013	0.898	HapMap	HapMap	T	0.75	C	0.25	T/C
MEX	rs899381	9	6024076	0.003	1	HapMap	HapMap	T	0.95	C	0.05	T/C
MKK	rs928413	9	6203387	0.126	0.808	HapMap	HapMap	G	0.413	A	0.587	G/A
YRI	rs928413	9	6203387	0.206	1	HapMap	HapMap	G	0.588	A	0.412	G/A
JPT	rs928413	9	6203387	0.79	1	HapMap	HapMap	G	0.047	A	0.953	G/A
ASW	rs928413	9	6203387	0.139	0.799	HapMap	HapMap	G	0.538	A	0.462	G/A
CEU	rs928413	9	6203387	0.208	1	HapMap	HapMap	G	0.288	A	0.712	G/A
CHB	rs928413	9	6203387	0.236	0.705	HapMap	HapMap	G	0.048	A	0.952	G/A
CHD	rs928413	9	6203387	0.587	0.847	HapMap	HapMap	G	0.088	A	0.912	G/A
GIH	rs928413	9	6203387	0.098	0.79	HapMap	HapMap	G	0.233	A	0.767	G/A
JPT	rs928414	9	6226350	0.052	1	HapMap	HapMap	G	0.529	A	0.471	G/A
CEU	rs928414	9	6226350	0.208	1	HapMap	HapMap	G	0.35	A	0.65	G/A
GIH	rs928414	9	6226350	0.085	1	HapMap	HapMap	G	0.358	A	0.642	G/A
GIH	rs9408638	9	6086931	0.016	1	HapMap	HapMap	A	0.25	G	0.75	A/G
CEU	rs9408638	9	6086931	0.013	1	HapMap	HapMap	A	0.124	G	0.876	A/G
CHB	rs9408638	9	6086931	0.002	1	HapMap	HapMap	A	0.03	G	0.97	A/G
MEX	rs9408638	9	6086931	0.009	1	HapMap	HapMap	A	0.13	G	0.87	A/G
MKK	rs9408638	9	6086931	0.03	1	HapMap	HapMap	A	0.18	G	0.82	A/G
CEU	rs992969	9	6199697	0.208	1	HapMap	HapMap	A	0.283	G	0.717	A/G
JPT	rs992969	9	6199697	0.585	1	HapMap	HapMap	A	0.029	G	0.971	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
LWK	rs992969	9	6199697	0.395	0.78	HapMap	HapMap	A	0.278	G	0.722	A/G
MKK	rs992969	9	6199697	0.321	0.761	HapMap	HapMap	A	0.196	G	0.804	A/G
GIH	rs992969	9	6199697	0.167	1	HapMap	HapMap	A	0.222	G	0.778	A/G
ASW	rs992969	9	6199697	0.259	0.745	HapMap	HapMap	A	0.33	G	0.67	A/G
CHB	rs992969	9	6199697	0.232	1	HapMap	HapMap	A	0.036	G	0.964	A/G
CHD	rs992969	9	6199697	0.417	1	HapMap	HapMap	A	0.047	G	0.953	A/G
YRI	rs992969	9	6199697	0.315	0.792	HapMap	HapMap	A	0.363	G	0.637	A/G
CEU	rs993951	9	6294401	0.128	0.817	HapMap	HapMap	A	0.589	G	0.411	A/G
GIH	rs993951	9	6294401	0.07	1	HapMap	HapMap	A	0.597	G	0.403	A/G
CHB	rs996029	9	6212302	0.115	1	HapMap	HapMap	T	0.006	G	0.994	T/G
CHD	rs996029	9	6212302	0.001	1	HapMap	HapMap	T	0.006	G	0.994	T/G
MKK	rs996029	9	6212302	0.007	1	HapMap	HapMap	T	0.049	G	0.951	T/G
MKK	rs16924159	9	6219417	0.033	0.77	HapMap	HapMap	G	0.712	A	0.288	G/A
JPT	rs16924159	9	6219417	0.015	1	HapMap	HapMap	G	0.783	A	0.217	G/A
GIH	rs17496153	9	6060037	0.002	1	HapMap	HapMap	G	0.96	C	0.04	G/C
CHD	rs17496153	9	6060037	0.001	1	HapMap	HapMap	G	0.994	C	0.006	G/C
ASW	rs17496153	9	6060037	0.004	1	HapMap	HapMap	G	0.971	C	0.029	G/C
CEU	rs17496153	9	6060037	0.01	0.996	HapMap	HapMap	G	0.867	C	0.133	G/C
JPT	rs2079	9	6156653	0.008	1	HapMap	HapMap	G	0.901	A	0.099	G/A
CHB	rs2079	9	6156653	0.02	1	HapMap	HapMap	G	0.821	A	0.179	G/A
CEU	rs2079	9	6156653	0.073	1	HapMap	HapMap	G	0.633	A	0.367	G/A
GIH	rs2079	9	6156653	0.021	1	HapMap	HapMap	G	0.699	A	0.301	G/A
CHD	rs2079	9	6156653	0.032	1	HapMap	HapMap	G	0.788	A	0.212	G/A
ASW	rs2079	9	6156653	0.11	1	HapMap	HapMap	G	0.731	A	0.269	G/A
MKK	rs2079	9	6156653	0.04	1	HapMap	HapMap	G	0.773	A	0.227	G/A
MEX	rs2079	9	6156653	0.021	1	HapMap	HapMap	G	0.75	A	0.25	G/A
GIH	rs12339713	9	5968437	0.004	1	HapMap	HapMap	C	0.92	T	0.08	C/T
LWK	rs12339713	9	5968437	0.046	1	HapMap	HapMap	C	0.844	T	0.156	C/T
LWK	rs4742172	9	6266733	0.124	0.816	HapMap	HapMap	C	0.045	T	0.955	C/T
GIH	rs4742172	9	6266733	0.001	1	HapMap	HapMap	C	0.017	T	0.983	C/T
ASW	rs4742172	9	6266733	0.058	1	HapMap	HapMap	C	0.132	T	0.868	C/T
MKK	rs4742172	9	6266733	0.003	1	HapMap	HapMap	C	0.025	T	0.975	C/T
MEX	rs4742172	9	6266733	0.001	1	HapMap	HapMap	C	0.02	T	0.98	C/T

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
MKK	rs7863536	9	6154771	0.529	0.752	HapMap	HapMap	C	0.877	A	0.123	C/A
JPT	rs7863536	9	6154771	0.585	1	HapMap	HapMap	C	0.948	A	0.052	C/A
GIH	rs7863536	9	6154771	1	1	HapMap	HapMap	C	0.955	A	0.045	C/A
YRI	rs7863536	9	6154771	0.378	0.899	HapMap	HapMap	C	0.891	A	0.109	C/A
CHD	rs7863536	9	6154771	0.43	0.753	HapMap	HapMap	C	0.918	A	0.082	C/A
ASW	rs7863536	9	6154771	0.508	1	HapMap	HapMap	C	0.865	A	0.135	C/A
ASW	rs2169285	9	6270786	0.125	0.732	HapMap	HapMap	A	0.42	G	0.58	A/G
GIH	rs2169285	9	6270786	0.001	1	HapMap	HapMap	A	0.03	G	0.97	A/G
JPT	rs7044468	9	6120398	0.005	1	HapMap	1000GP	A	NA	G	NA	A/G
CHB	rs7044468	9	6120398	0.007	0.794	HapMap	1000GP	A	NA	G	NA	A/G
JPT	rs10758750	9	6230513	0.048	1	HapMap	1000GP	C	0.5	G	0.5	C/G
JPT	rs10815383	9	6230670	0.048	1	HapMap	1000GP	C	0.5	G	0.5	C/G
JPT	rs16924171	9	6233279	0.05	1	HapMap	1000GP	A	0.5	T	0.5	A/T
JPT	rs7019575	9	6243935	0.047	1	HapMap	1000GP	G	0.5	C	0.5	G/C
JPT	rs7034720	9	6234546	0.051	1	HapMap	1000GP	C	0.51	A	0.49	C/A
JPT	rs1375	9	6235753	0.052	1	HapMap	1000GP	G	0.51	T	0.49	G/T
JPT	rs4237164	9	6236501	0.052	1	HapMap	1000GP	T	0.51	G	0.49	T/G
JPT	rs10975509	9	6237263	0.053	1	HapMap	1000GP	G	0.51	A	0.49	G/A
JPT	rs1929992	9	6251588	0.047	1	HapMap	1000GP	T	0.51	C	0.49	T/C
JPT	rs10435816	9	6225535	0.055	1	HapMap	1000GP	A	0.52	G	0.48	A/G
JPT	rs10975497	9	6226592	0.062	1	HapMap	1000GP	C	0.52	T	0.48	C/T
JPT	rs10975498	9	6226688	0.052	1	HapMap	1000GP	T	0.52	C	0.48	T/C
JPT	rs10815397	9	6265256	0.051	1	HapMap	1000GP	C	0.52	G	0.48	C/G
JPT	rs1113573	9	6253301	0.02	0.666	HapMap	1000GP	T	0.54	C	0.46	T/C
JPT	rs7044343	9	6254208	0.038	1	HapMap	1000GP	C	0.54	T	0.46	C/T
JPT	rs7871381	9	6254900	0.047	1	HapMap	1000GP	G	0.54	A	0.46	G/A
CHB	rs10758733	9	5992100	0.051	0.69	HapMap	1000GP	C	0.55	T	0.45	C/T
CHB	rs1475614	9	5992594	0.051	0.69	HapMap	1000GP	G	0.55	C	0.45	G/C
CHB	rs4742145	9	5995278	0.068	0.689	HapMap	1000GP	G	0.55	A	0.45	G/A
JPT	rs1412421	9	6255010	0.058	1	HapMap	1000GP	A	0.55	C	0.45	A/C
CHB	rs10975386	9	5982246	0.05	0.659	HapMap	1000GP	T	0.56	C	0.44	T/C
JPT	rs10975555	9	6360299	0.049	1	HapMap	1000GP	C	0.6	G	0.4	C/G
CHB	rs10975555	9	6360299	0.055	1	HapMap	1000GP	C	0.6	G	0.4	C/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs340910	9	6128620	0.063	0.65	HapMap	1000GP	A	0.68	G	0.32	A/G
CHB	rs407153	9	6133014	0.059	0.634	HapMap	1000GP	C	0.68	T	0.32	C/T
CHB	rs4389996	9	5991399	0.092	0.729	HapMap	1000GP	C	0.69	T	0.31	C/T
CHB	rs182908	9	6098381	0.063	0.65	HapMap	1000GP	A	0.69	C	0.31	A/C
CHB	rs436300	9	6112044	0.063	0.65	HapMap	1000GP	G	0.69	C	0.31	G/C
CHB	rs444826	9	6114483	0.063	0.65	HapMap	1000GP	G	0.69	C	0.31	G/C
CHB	rs340916	9	6126372	0.07	0.668	HapMap	1000GP	T	0.69	C	0.31	T/C
CHB	rs16924328	9	6324744	0.037	1	HapMap	1000GP	T	0.69	C	0.31	T/C
CHB	rs10975553	9	6352819	0.033	1	HapMap	1000GP	T	0.69	C	0.31	T/C
CHB	rs7022186	9	6359144	0.033	1	HapMap	1000GP	T	0.69	C	0.31	T/C
CHB	rs4742181	9	6363694	0.031	1	HapMap	1000GP	A	0.7	G	0.3	A/G
CHB	rs719725	9	6365683	0.031	1	HapMap	1000GP	A	0.7	C	0.3	A/C
CHB	rs2291055	9	5988333	0.116	0.758	HapMap	1000GP	C	0.71	T	0.29	C/T
CHB	rs6477024	9	5990450	0.122	0.761	HapMap	1000GP	C	0.71	T	0.29	C/T
CHB	rs7851749	9	5993652	0.116	0.758	HapMap	1000GP	T	0.71	A	0.29	T/A
CHB	rs7875450	9	5996739	0.116	0.758	HapMap	1000GP	C	0.71	T	0.29	C/T
CHB	rs4740834	9	5979717	0.116	0.758	HapMap	1000GP	C	0.72	T	0.28	C/T
CHB	rs4742142	9	5981316	0.116	0.758	HapMap	1000GP	C	0.72	T	0.28	C/T
CHB	rs4742143	9	5981647	0.116	0.758	HapMap	1000GP	T	0.72	A	0.28	T/A
CHB	rs10815330	9	5983481	0.147	0.776	HapMap	1000GP	G	0.72	C	0.28	G/C
JPT	rs7044750	9	5983655	0.008	1	HapMap	1000GP	G	0.72	A	0.28	G/A
CHB	rs2381360	9	5990250	0.116	0.758	HapMap	1000GP	T	0.72	G	0.28	T/G
CHB	rs10733523	9	5992256	0.116	0.758	HapMap	1000GP	C	0.72	T	0.28	C/T
CHB	rs1331379	9	6003377	0.116	0.758	HapMap	1000GP	C	0.72	T	0.28	C/T
CHB	rs186913	9	6008826	0.125	0.766	HapMap	1000GP	T	0.72	C	0.28	T/C
CHB	rs7875812	9	6364533	0.033	1	HapMap	1000GP	A	0.72	T	0.28	A/T
JPT	rs343493	9	6071061	0.011	0.971	HapMap	1000GP	A	0.73	G	0.27	A/G
JPT	rs340920	9	6090484	0.01	1	HapMap	1000GP	T	0.75	G	0.25	T/G
JPT	rs1116795	9	6155226	0.183	0.728	HapMap	1000GP	G	0.77	T	0.23	G/T
CHB	rs1116795	9	6155226	0.163	0.783	HapMap	1000GP	G	0.77	T	0.23	G/T
JPT	rs2225537	9	6160578	0.163	0.718	HapMap	1000GP	C	0.77	T	0.23	C/T
JPT	rs10491835	9	6325345	0.004	0.615	HapMap	1000GP	G	0.8	A	0.2	G/A
JPT	rs7872052	9	6026757	0.007	0.753	HapMap	1000GP	T	0.82	C	0.18	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs7872052	9	6026757	0.01	0.699	HapMap	1000GP	T	0.82	C	0.18	T/C
CHB	rs343469	9	6046486	0.136	0.613	HapMap	1000GP	A	0.84	G	0.16	A/G
CHB	rs340889	9	6100476	0.025	1	HapMap	1000GP	G	0.84	C	0.16	G/C
JPT	rs340889	9	6100476	0.008	1	HapMap	1000GP	G	0.84	C	0.16	G/C
CHB	rs13299104	9	6101432	0.201	0.796	HapMap	1000GP	C	0.84	T	0.16	C/T
CHB	rs439190	9	6114076	0.02	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs439190	9	6114076	0.007	1	HapMap	1000GP	C	0.84	T	0.16	C/T
CHB	rs391813	9	6114094	0.004	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs372482	9	6119872	0.007	1	HapMap	1000GP	G	0.84	A	0.16	G/A
CHB	rs372482	9	6119872	0.02	1	HapMap	1000GP	G	0.84	A	0.16	G/A
CHB	rs442246	9	6121504	0.022	1	HapMap	1000GP	G	0.84	T	0.16	G/T
JPT	rs442246	9	6121504	0.007	1	HapMap	1000GP	G	0.84	T	0.16	G/T
CHB	rs13289987	9	6121900	0.218	0.803	HapMap	1000GP	T	0.84	A	0.16	T/A
CHB	rs381702	9	6122331	0.024	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs381702	9	6122331	0.007	1	HapMap	1000GP	C	0.84	T	0.16	C/T
CHB	rs693838	9	6122556	0.022	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs693838	9	6122556	0.007	1	HapMap	1000GP	C	0.84	T	0.16	C/T
CHB	rs13293742	9	6129017	0.201	0.796	HapMap	1000GP	T	0.84	C	0.16	T/C
CHB	rs10739086	9	6130822	0.022	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs10739086	9	6130822	0.006	1	HapMap	1000GP	C	0.84	T	0.16	C/T
JPT	rs10758743	9	6066175	0.007	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs694965	9	6117329	0.02	1	HapMap	1000GP	C	0.85	T	0.15	C/T
JPT	rs694965	9	6117329	0.007	1	HapMap	1000GP	C	0.85	T	0.15	C/T
CHB	rs381486	9	6118911	0.02	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs381486	9	6118911	0.007	1	HapMap	1000GP	G	0.85	A	0.15	G/A
CHB	rs340909	9	6128646	0.02	1	HapMap	1000GP	G	0.85	A	0.15	G/A
JPT	rs340909	9	6128646	0.007	1	HapMap	1000GP	G	0.85	A	0.15	G/A
CHB	rs16924009	9	6129374	0.218	0.803	HapMap	1000GP	A	0.85	T	0.15	A/T
JPT	rs489464	9	6132664	0.007	1	HapMap	1000GP	A	0.85	T	0.15	A/T
CHB	rs489464	9	6132664	0.019	1	HapMap	1000GP	A	0.85	T	0.15	A/T
CHB	rs386412	9	6132904	0.02	1	HapMap	1000GP	T	0.85	A	0.15	T/A
JPT	rs386412	9	6132904	0.007	1	HapMap	1000GP	T	0.85	A	0.15	T/A
CHB	rs369756	9	6146441	0.019	1	HapMap	1000GP	G	0.85	T	0.15	G/T

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
JPT	rs369756	9	6146441	0.004	1	HapMap	1000GP	G	0.85	T	0.15	G/T
JPT	rs4579584	9	6166919	0.004	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs4579584	9	6166919	0.016	1	HapMap	1000GP	T	0.85	C	0.15	T/C
CHB	rs10758742	9	6064670	0.008	0.636	HapMap	1000GP	C	0.86	G	0.14	C/G
JPT	rs10758742	9	6064670	0.006	1	HapMap	1000GP	C	0.86	G	0.14	C/G
CHB	rs4740837	9	6089527	0.017	1	HapMap	1000GP	C	0.87	T	0.13	C/T
JPT	rs4740837	9	6089527	0.007	1	HapMap	1000GP	C	0.87	T	0.13	C/T
CHB	rs10975436	9	6108729	0.017	1	HapMap	1000GP	T	0.87	C	0.13	T/C
JPT	rs10975436	9	6108729	0.007	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CHB	rs7024136	9	6110470	0.017	1	HapMap	1000GP	A	0.87	C	0.13	A/C
JPT	rs7024136	9	6110470	0.006	1	HapMap	1000GP	A	0.87	C	0.13	A/C
JPT	rs7869888	9	6111007	0.007	1	HapMap	1000GP	C	0.87	T	0.13	C/T
CHB	rs7869888	9	6111007	0.017	1	HapMap	1000GP	C	0.87	T	0.13	C/T
CHB	rs7869064	9	6111078	0.002	1	HapMap	1000GP	G	0.87	T	0.13	G/T
CHB	rs7043663	9	6111603	0.017	1	HapMap	1000GP	C	0.87	T	0.13	C/T
JPT	rs7043663	9	6111603	0.008	1	HapMap	1000GP	C	0.87	T	0.13	C/T
JPT	rs7048296	9	6120702	0.007	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CHB	rs7048296	9	6120702	0.018	1	HapMap	1000GP	T	0.87	C	0.13	T/C
JPT	rs10975446	9	6123309	0.005	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CHB	rs10975446	9	6123309	0.018	1	HapMap	1000GP	T	0.87	C	0.13	T/C
JPT	rs6477038	9	6127921	0.007	1	HapMap	1000GP	A	0.87	C	0.13	A/C
CHB	rs6477038	9	6127921	0.017	1	HapMap	1000GP	A	0.87	C	0.13	A/C
CHB	rs4742158	9	6128137	0.017	1	HapMap	1000GP	A	0.87	C	0.13	A/C
JPT	rs4742158	9	6128137	0.007	1	HapMap	1000GP	A	0.87	C	0.13	A/C
CHB	rs13296527	9	6127082	0.297	0.685	HapMap	1000GP	G	0.89	T	0.11	G/T
CHB	rs13290080	9	6117291	0.265	0.678	HapMap	1000GP	G	0.9	A	0.1	G/A
JPT	rs10975465	9	6155014	0.79	1	HapMap	1000GP	G	0.92	A	0.08	G/A
CHB	rs10975465	9	6155014	0.463	0.83	HapMap	1000GP	G	0.92	A	0.08	G/A
JPT	rs10815363	9	6174316	0.822	1	HapMap	1000GP	T	0.92	C	0.08	T/C
CHB	rs10815363	9	6174316	0.648	1	HapMap	1000GP	T	0.92	C	0.08	T/C
JPT	rs1012715	9	6151320	0.585	1	HapMap	1000GP	C	0.93	A	0.07	C/A
JPT	rs12352464	9	6157329	0.487	1	HapMap	1000GP	C	0.93	T	0.07	C/T
JPT	rs6477048	9	6161253	0.585	1	HapMap	1000GP	C	0.93	T	0.07	C/T

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs4742166	9	6188124	0.273	0.611	HapMap	1000GP	G	0.93	C	0.07	G/C
JPT	rs4742166	9	6188124	0.499	0.779	HapMap	1000GP	G	0.93	C	0.07	G/C
CHB	rs1412425	9	6188740	0.346	0.761	HapMap	1000GP	A	0.93	C	0.07	A/C
JPT	rs1412425	9	6188740	0.61	0.781	HapMap	1000GP	A	0.93	C	0.07	A/C
JPT	rs2095044	9	6192796	0.499	0.779	HapMap	1000GP	T	0.93	C	0.07	T/C
CHB	rs2095044	9	6192796	0.273	0.611	HapMap	1000GP	T	0.93	C	0.07	T/C
CHB	rs10815370	9	6194831	0.273	0.611	HapMap	1000GP	C	0.93	A	0.07	C/A
JPT	rs10815370	9	6194831	0.499	0.779	HapMap	1000GP	C	0.93	A	0.07	C/A
JPT	rs4742167	9	6195285	0.499	0.779	HapMap	1000GP	C	0.93	T	0.07	C/T
CHB	rs4742167	9	6195285	0.273	0.611	HapMap	1000GP	C	0.93	T	0.07	C/T
JPT	rs1929996	9	6187636	0.499	0.779	HapMap	1000GP	C	0.94	G	0.06	C/G
CHB	rs1929996	9	6187636	0.354	0.767	HapMap	1000GP	C	0.94	G	0.06	C/G
CHB	rs7848215	9	6213468	0.236	0.705	HapMap	1000GP	C	0.94	T	0.06	C/T
JPT	rs7848215	9	6213468	0.616	0.785	HapMap	1000GP	C	0.94	T	0.06	C/T
JPT	rs10815362	9	6173798	0.79	1	HapMap	1000GP	T	0.95	C	0.05	T/C
CHB	rs10815362	9	6173798	0.475	1	HapMap	1000GP	T	0.95	C	0.05	T/C
CHB	rs2150970	9	6201364	0.354	0.767	HapMap	1000GP	G	0.95	A	0.05	G/A
JPT	rs2150970	9	6201364	0.79	1	HapMap	1000GP	G	0.95	A	0.05	G/A
JPT	rs12683048	9	6160944	0.004	1	HapMap	1000GP	T	0.96	C	0.04	T/C
CHB	rs12683048	9	6160944	0.005	1	HapMap	1000GP	T	0.96	C	0.04	T/C
JPT	rs2381416	9	6193455	0.585	1	HapMap	1000GP	C	0.96	A	0.04	C/A
CHB	rs2381416	9	6193455	0.127	0.601	HapMap	1000GP	C	0.96	A	0.04	C/A
CHB	rs12352918	9	5992351	0.004	1	HapMap	1000GP	G	0.97	C	0.03	G/C
CHB	rs12341021	9	6009656	0.004	1	HapMap	1000GP	C	0.97	G	0.03	C/G
CHB	rs10124484	9	6046505	0.004	1	HapMap	1000GP	T	0.97	G	0.03	T/G
CHB	rs12351447	9	6046950	0.002	1	HapMap	1000GP	T	0.97	G	0.03	T/G
CHB	rs343490	9	6064575	0.004	1	HapMap	1000GP	A	0.97	G	0.03	A/G
CHB	rs343496	9	6068077	0.004	1	HapMap	1000GP	A	0.97	T	0.03	A/T
CHB	rs343476	9	6072597	0.004	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CHB	rs343475	9	6073013	0.004	1	HapMap	1000GP	C	0.97	G	0.03	C/G
CHB	rs189348	9	6073194	0.004	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CHB	rs378952	9	6078146	0.004	1	HapMap	1000GP	C	0.97	T	0.03	C/T
CHB	rs454664	9	6078763	0.004	1	HapMap	1000GP	A	0.97	G	0.03	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs401834	9	6078991	0.004	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CHB	rs340925	9	6088398	0.004	1	HapMap	1000GP	T	0.97	G	0.03	T/G
CHB	rs340922	9	6088815	0.004	1	HapMap	1000GP	A	0.97	C	0.03	A/C
JPT	rs10758748	9	6187862	0.585	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CHB	rs10758748	9	6187862	0.232	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CHB	rs12339713	9	5978437	0.002	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs11793956	9	5987402	0.001	1	HapMap	1000GP	T	0.98	A	0.02	T/A
CHB	rs7859471	9	6023626	0.004	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs340919	9	6090704	0.002	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs340918	9	6091048	0.002	1	HapMap	1000GP	A	0.98	C	0.02	A/C
CHB	rs695013	9	6091565	0.002	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs531759	9	6091996	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs639247	9	6092089	0.002	1	HapMap	1000GP	T	0.98	G	0.02	T/G
CHB	rs420445	9	6092154	0.001	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CHB	rs503384	9	6092804	0.004	1	HapMap	1000GP	T	0.98	A	0.02	T/A
JPT	rs503384	9	6092804	0.001	1	HapMap	1000GP	T	0.98	A	0.02	T/A
CHB	rs398561	9	6093132	0.002	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CHB	rs2150969	9	6093990	0.002	1	HapMap	1000GP	C	0.98	G	0.02	C/G
CHB	rs437389	9	6099531	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs340906	9	6106086	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs340905	9	6106169	0.003	1	HapMap	1000GP	A	0.98	C	0.02	A/C
CHB	rs340903	9	6107113	0.002	1	HapMap	1000GP	C	0.98	G	0.02	C/G
CHB	rs340901	9	6108398	0.002	1	HapMap	1000GP	G	0.98	C	0.02	G/C
CHB	rs974936	9	6111703	0.002	1	HapMap	1000GP	A	0.98	C	0.02	A/C
CHB	rs441616	9	6113940	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs375560	9	6114744	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs1556470	9	6115538	0.003	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs374672	9	6119038	0.002	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CHB	rs443175	9	6123556	0.003	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs1332291	9	6124101	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs1537285	9	6124584	0.002	1	HapMap	1000GP	T	0.98	G	0.02	T/G
CHB	rs1332292	9	6124862	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs7039066	9	6125539	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CHB	rs340915	9	6126588	0.002	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs340914	9	6126799	0.004	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs340913	9	6127330	0.002	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CHB	rs340912	9	6127851	0.002	1	HapMap	1000GP	A	0.98	G	0.02	A/G
CHB	rs340907	9	6129637	0.002	1	HapMap	1000GP	A	0.98	C	0.02	A/C
CHB	rs1888906	9	6131460	0.002	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CHB	rs4742159	9	6131612	0.002	1	HapMap	1000GP	A	0.98	T	0.02	A/T
CHB	rs376690	9	6134926	0.002	1	HapMap	1000GP	C	0.98	T	0.02	C/T
JPT	rs16924291	9	6293305	0.001	1	HapMap	1000GP	C	0.98	A	0.02	C/A
CHB	rs986295	9	6069435	0.002	1	HapMap	1000GP	G	0.99	A	0.01	G/A
JPT	rs986295	9	6069435	0.001	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CHB	rs10975453	9	6135000	0.003	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CHB	rs12684265	9	6327828	0.002	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CHB	rs12683480	9	6349964	0.002	1	HapMap	1000GP	G	0.99	A	0.01	G/A
JPT	rs17496153	9	6070037	0.19	1	HapMap	1000GP	G	0.9965	C	0.0035	G/C
JPT	rs10975442	9	6116768	0.001	1	HapMap	1000GP	G	0.9983	A	0.0017	G/A
CHB	rs10975442	9	6116768	0.001	1	HapMap	1000GP	G	0.9983	A	0.0017	G/A
CHB	rs12380605	9	6118873	0.001	1	HapMap	1000GP	A	0.9983	T	0.0017	A/T
CHB	rs2094756	9	6135696	0.018	1	HapMap	1000GP	A	1	C	0	A/C
JPT	rs2094756	9	6135696	0.007	1	HapMap	1000GP	A	1	C	0	A/C
CHB	rs13302749	9	6171731	0.155	1	HapMap	1000GP	T	1	C	0	T/C
JPT	rs7048482	9	6225659	0.001	1	HapMap	1000GP	G	1	A	0	G/A
JPT	rs4742172	9	6276733	0	1	HapMap	1000GP	C	1	T	0	C/T
CEU	rs7019575	9	6243935	0.113	1	HapMap	1000GP	G	0.54	C	0.46	G/C
CEU	rs450108	9	6153485	0.089	1	HapMap	1000GP	T	0.59	C	0.41	T/C
CEU	rs1116795	9	6155226	0.109	1	HapMap	1000GP	G	0.59	T	0.41	G/T
CEU	rs2225537	9	6160578	0.105	1	HapMap	1000GP	C	0.59	T	0.41	C/T
CEU	rs10975553	9	6352819	0.07	1	HapMap	1000GP	T	0.6	C	0.4	T/C
CEU	rs7022186	9	6359144	0.076	1	HapMap	1000GP	T	0.6	C	0.4	T/C
CEU	rs719725	9	6365683	0.076	1	HapMap	1000GP	A	0.6	C	0.4	A/C
CEU	rs7875812	9	6364533	0.076	1	HapMap	1000GP	A	0.63	T	0.37	A/T
CEU	rs731585	9	6342328	0.065	1	HapMap	1000GP	G	0.65	A	0.35	G/A
CEU	rs343481	9	6024285	0.055	0.601	HapMap	1000GP	C	0.66	G	0.34	C/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs1113573	9	6253301	0.019	0.612	HapMap	1000GP	T	0.67	C	0.33	T/C
CEU	rs10758733	9	5992100	0.104	0.676	HapMap	1000GP	C	0.68	T	0.32	C/T
CEU	rs16924159	9	6229417	0.038	1	HapMap	1000GP	G	0.68	A	0.32	G/A
CEU	rs1375	9	6235753	0.208	1	HapMap	1000GP	G	0.69	T	0.31	G/T
CEU	rs10975386	9	5982246	0.115	0.792	HapMap	1000GP	T	0.7	C	0.3	T/C
CEU	rs1475614	9	5992594	0.104	0.676	HapMap	1000GP	G	0.7	C	0.3	G/C
CEU	rs340911	9	6128446	0.025	1	HapMap	1000GP	C	0.7	G	0.3	C/G
CEU	rs16924171	9	6233279	0.217	1	HapMap	1000GP	A	0.7	T	0.3	A/T
CEU	rs7034720	9	6234546	0.194	1	HapMap	1000GP	C	0.7	A	0.3	C/A
CEU	rs10758764	9	6326825	0.068	1	HapMap	1000GP	T	0.7	A	0.3	T/A
CEU	rs10758741	9	6054645	0.08	0.649	HapMap	1000GP	G	0.71	A	0.29	G/A
CEU	rs10758743	9	6066175	0.131	0.827	HapMap	1000GP	T	0.71	C	0.29	T/C
CEU	rs4742179	9	6324376	0.067	1	HapMap	1000GP	A	0.71	C	0.29	A/C
CEU	rs10758742	9	6064670	0.134	0.821	HapMap	1000GP	C	0.72	G	0.28	C/G
CEU	rs1929996	9	6187636	0.149	1	HapMap	1000GP	C	0.72	G	0.28	C/G
CEU	rs4742166	9	6188124	0.147	1	HapMap	1000GP	G	0.72	C	0.28	G/C
CEU	rs1412425	9	6188740	0.153	1	HapMap	1000GP	A	0.72	C	0.28	A/C
CEU	rs10815370	9	6194831	0.143	1	HapMap	1000GP	C	0.72	A	0.28	C/A
CEU	rs4742167	9	6195285	0.143	1	HapMap	1000GP	C	0.72	T	0.28	C/T
CEU	rs10975509	9	6237263	0.249	1	HapMap	1000GP	G	0.72	A	0.28	G/A
CEU	rs10975498	9	6226688	0.306	1	HapMap	1000GP	T	0.73	C	0.27	T/C
CEU	rs2006682	9	6227045	0.03	1	HapMap	1000GP	G	0.73	C	0.27	G/C
CEU	rs10435816	9	6225535	0.287	1	HapMap	1000GP	A	0.74	G	0.26	A/G
CEU	rs10975497	9	6226592	0.304	1	HapMap	1000GP	C	0.74	T	0.26	C/T
CEU	rs10758750	9	6230513	0.289	1	HapMap	1000GP	C	0.74	G	0.26	C/G
CEU	rs10815383	9	6230670	0.29	1	HapMap	1000GP	C	0.74	G	0.26	C/G
CEU	rs16924428	9	6351111	0.05	1	HapMap	1000GP	A	0.74	G	0.26	A/G
CEU	rs369756	9	6146441	0.033	1	HapMap	1000GP	G	0.75	T	0.25	G/T
CEU	rs7848215	9	6213468	0.191	1	HapMap	1000GP	C	0.75	T	0.25	C/T
CEU	rs2095044	9	6192796	0.208	1	HapMap	1000GP	T	0.76	C	0.24	T/C
CEU	rs2381416	9	6193455	0.199	1	HapMap	1000GP	C	0.76	A	0.24	C/A
CEU	rs10815397	9	6265256	0.206	0.7	HapMap	1000GP	C	0.76	G	0.24	C/G
CEU	rs744567	9	6292602	0.041	1	HapMap	1000GP	C	0.77	G	0.23	C/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs12339348	9	6233082	0.041	1	HapMap	1000GP	A	0.78	T	0.22	A/T
CEU	rs17582919	9	6233376	0.041	1	HapMap	1000GP	T	0.78	C	0.22	T/C
CEU	rs10975507	9	6236977	0.041	1	HapMap	1000GP	A	0.78	T	0.22	A/T
CEU	rs343490	9	6064575	0.016	1	HapMap	1000GP	A	0.81	G	0.19	A/G
CEU	rs343496	9	6068077	0.014	1	HapMap	1000GP	A	0.81	T	0.19	A/T
CEU	rs343476	9	6072597	0.014	1	HapMap	1000GP	T	0.81	C	0.19	T/C
CEU	rs343475	9	6073013	0.014	1	HapMap	1000GP	C	0.81	G	0.19	C/G
CEU	rs189348	9	6073194	0.014	1	HapMap	1000GP	T	0.81	C	0.19	T/C
CEU	rs378952	9	6078146	0.014	1	HapMap	1000GP	C	0.81	T	0.19	C/T
CEU	rs1332291	9	6124101	0.014	1	HapMap	1000GP	T	0.81	C	0.19	T/C
CEU	rs340918	9	6091048	0.013	1	HapMap	1000GP	A	0.82	C	0.18	A/C
CEU	rs695013	9	6091565	0.013	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs531759	9	6091996	0.012	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs639247	9	6092089	0.013	1	HapMap	1000GP	T	0.82	G	0.18	T/G
CEU	rs420445	9	6092154	0.013	1	HapMap	1000GP	G	0.82	A	0.18	G/A
CEU	rs503507	9	6092757	0.013	1	HapMap	1000GP	G	0.82	A	0.18	G/A
CEU	rs503384	9	6092804	0.014	1	HapMap	1000GP	T	0.82	A	0.18	T/A
CEU	rs425489	9	6093790	0.014	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs2150969	9	6093990	0.014	1	HapMap	1000GP	C	0.82	G	0.18	C/G
CEU	rs437389	9	6099531	0.013	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs340896	9	6102891	0.013	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs340906	9	6106086	0.012	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs340905	9	6106169	0.013	1	HapMap	1000GP	A	0.82	C	0.18	A/C
CEU	rs340903	9	6107113	0.013	1	HapMap	1000GP	C	0.82	G	0.18	C/G
CEU	rs340901	9	6108398	0.013	1	HapMap	1000GP	G	0.82	C	0.18	G/C
CEU	rs974936	9	6111703	0.013	1	HapMap	1000GP	A	0.82	C	0.18	A/C
CEU	rs441616	9	6113940	0.012	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs1556470	9	6115538	0.012	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs374672	9	6119038	0.013	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs443175	9	6123556	0.012	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs1537285	9	6124584	0.013	1	HapMap	1000GP	T	0.82	G	0.18	T/G
CEU	rs1332292	9	6124862	0.013	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs7039066	9	6125539	0.011	1	HapMap	1000GP	T	0.82	C	0.18	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs340915	9	6126588	0.013	1	HapMap	1000GP	A	0.82	G	0.18	A/G
CEU	rs340914	9	6126799	0.011	1	HapMap	1000GP	A	0.82	G	0.18	A/G
CEU	rs340913	9	6127330	0.013	1	HapMap	1000GP	T	0.82	C	0.18	T/C
CEU	rs340912	9	6127851	0.012	1	HapMap	1000GP	A	0.82	G	0.18	A/G
CEU	rs340907	9	6129637	0.013	1	HapMap	1000GP	A	0.82	C	0.18	A/C
CEU	rs10114457	9	6130940	0.014	1	HapMap	1000GP	A	0.82	G	0.18	A/G
CEU	rs1888906	9	6131460	0.013	1	HapMap	1000GP	G	0.82	A	0.18	G/A
CEU	rs4742159	9	6131612	0.013	1	HapMap	1000GP	A	0.82	T	0.18	A/T
CEU	rs376690	9	6134926	0.013	1	HapMap	1000GP	C	0.82	T	0.18	C/T
CEU	rs16924291	9	6293305	0.017	1	HapMap	1000GP	C	0.84	A	0.16	C/A
CEU	rs16924328	9	6324744	0.011	1	HapMap	1000GP	T	0.87	C	0.13	T/C
CEU	rs4579584	9	6166919	0.005	1	HapMap	1000GP	T	0.88	C	0.12	T/C
CEU	rs10815362	9	6173798	0.659	1	HapMap	1000GP	T	0.91	C	0.09	T/C
CEU	rs10758748	9	6187862	0.744	1	HapMap	1000GP	T	0.91	C	0.09	T/C
CEU	rs2150970	9	6201364	0.683	1	HapMap	1000GP	G	0.91	A	0.09	G/A
CEU	rs7859471	9	6023626	0.008	0.921	HapMap	1000GP	T	0.93	C	0.07	T/C
CEU	rs13300552	9	6095799	0.011	1	HapMap	1000GP	T	0.93	C	0.07	T/C
CEU	rs13298861	9	6150279	0.015	1	HapMap	1000GP	A	0.93	T	0.07	A/T
CEU	rs10975464	9	6151609	0.014	1	HapMap	1000GP	G	0.93	C	0.07	G/C
CEU	rs4742143	9	5981647	0.001	1	HapMap	1000GP	T	0.94	A	0.06	T/A
CEU	rs1012715	9	6151320	0.815	1	HapMap	1000GP	C	0.94	A	0.06	C/A
CEU	rs10975465	9	6155014	0.815	1	HapMap	1000GP	G	0.94	A	0.06	G/A
CEU	rs12352464	9	6157329	0.8	1	HapMap	1000GP	C	0.94	T	0.06	C/T
CEU	rs12352510	9	6157433	0.815	1	HapMap	1000GP	C	0.94	T	0.06	C/T
CEU	rs6477048	9	6161253	0.815	1	HapMap	1000GP	C	0.94	T	0.06	C/T
CEU	rs13302008	9	6162881	0.014	1	HapMap	1000GP	T	0.94	C	0.06	T/C
CEU	rs7863536	9	6164771	0.815	1	HapMap	1000GP	C	0.94	A	0.06	C/A
CEU	rs10118918	9	6170162	0.815	1	HapMap	1000GP	T	0.94	G	0.06	T/G
CEU	rs1041538	9	6270359	0.013	1	HapMap	1000GP	A	0.94	G	0.06	A/G
CEU	rs1041537	9	6271238	0.013	1	HapMap	1000GP	A	0.94	G	0.06	A/G
CEU	rs10123059	9	6275456	0.013	1	HapMap	1000GP	T	0.94	C	0.06	T/C
CEU	rs10758754	9	6277740	0.013	1	HapMap	1000GP	G	0.94	A	0.06	G/A
CEU	rs2169284	9	6278071	0.012	1	HapMap	1000GP	A	0.94	G	0.06	A/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs2169285	9	6280786	0.013	1	HapMap	1000GP	A	0.94	G	0.06	A/G
CEU	rs10739091	9	6292919	0.008	0.884	HapMap	1000GP	A	0.94	T	0.06	A/T
CEU	rs4389996	9	5991399	0.001	1	HapMap	1000GP	C	0.95	T	0.05	C/T
CEU	rs10118537	9	6135155	0.003	1	HapMap	1000GP	A	0.95	T	0.05	A/T
CEU	rs7048482	9	6225659	0.005	1	HapMap	1000GP	G	0.95	A	0.05	G/A
CEU	rs13298301	9	6187242	0.008	0.921	HapMap	1000GP	A	0.96	G	0.04	A/G
CEU	rs13284060	9	6202701	0.004	0.676	HapMap	1000GP	A	0.96	C	0.04	A/C
CEU	rs11794419	9	6222110	0.006	1	HapMap	1000GP	T	0.97	C	0.03	T/C
CEU	rs1854709	9	6251455	0.004	0.676	HapMap	1000GP	T	0.97	C	0.03	T/C
CEU	rs7047769	9	6267718	0.004	1	HapMap	1000GP	C	0.97	T	0.03	C/T
CEU	rs980850	9	6269458	0.004	0.676	HapMap	1000GP	G	0.97	C	0.03	G/C
CEU	rs2381440	9	6373548	0.001	1	HapMap	1000GP	G	0.97	A	0.03	G/A
CEU	rs4740834	9	5979717	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs4742142	9	5981316	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs10815330	9	5983481	0.001	1	HapMap	1000GP	G	0.98	C	0.02	G/C
CEU	rs7044750	9	5983655	0.001	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CEU	rs2291055	9	5988333	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs2381360	9	5990250	0.001	1	HapMap	1000GP	T	0.98	G	0.02	T/G
CEU	rs6477024	9	5990450	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs10733523	9	5992256	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs12352918	9	5992351	0.001	1	HapMap	1000GP	G	0.98	C	0.02	G/C
CEU	rs7851749	9	5993652	0.001	1	HapMap	1000GP	T	0.98	A	0.02	T/A
CEU	rs7875450	9	5996739	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs1331379	9	6003377	0.001	1	HapMap	1000GP	C	0.98	T	0.02	C/T
CEU	rs186913	9	6008826	0.001	1	HapMap	1000GP	T	0.98	C	0.02	T/C
CEU	rs7852538	9	6026472	0.002	1	HapMap	1000GP	G	0.98	A	0.02	G/A
CEU	rs343480	9	6023030	0.001	1	HapMap	1000GP	A	0.99	G	0.01	A/G
CEU	rs343482	9	6024347	0.001	1	HapMap	1000GP	T	0.99	G	0.01	T/G
CEU	rs343469	9	6046486	0.001	1	HapMap	1000GP	A	0.99	G	0.01	A/G
CEU	rs13290235	9	6052352	0.004	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CEU	rs7866793	9	6055039	0.001	1	HapMap	1000GP	T	0.99	C	0.01	T/C
CEU	rs7857802	9	6075321	0.001	1	HapMap	1000GP	G	0.99	A	0.01	G/A
CEU	rs10975442	9	6116768	0.002	1	HapMap	1000GP	G	0.996	A	0.004	G/A

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
CEU	rs12336478	9	6247287	0.001	1	HapMap	1000GP	G	1	A	0	G/A
YRI	rs1969732	9	6278604	0.015	1	HapMap	1000GP	A	NA	G	NA	A/G
YRI	rs2381416	9	6193455	0.138	0.865	HapMap	1000GP	C	0.61	A	0.39	C/A
YRI	rs343481	9	6024285	0.042	0.663	HapMap	1000GP	C	0.64	G	0.36	C/G
YRI	rs2095044	9	6192796	0.052	0.625	HapMap	1000GP	T	0.66	C	0.34	T/C
YRI	rs1412425	9	6188740	0.037	0.633	HapMap	1000GP	A	0.72	C	0.28	A/C
YRI	rs2150970	9	6201364	0.542	1	HapMap	1000GP	G	0.72	A	0.28	G/A
YRI	rs10815370	9	6194831	0.082	1	HapMap	1000GP	C	0.73	A	0.27	C/A
YRI	rs10758748	9	6187862	0.567	0.886	HapMap	1000GP	T	0.75	C	0.25	T/C
YRI	rs7047769	9	6267718	0.038	1	HapMap	1000GP	C	0.76	T	0.24	C/T
YRI	rs2079	9	6166653	0.049	0.714	HapMap	1000GP	G	0.78	A	0.22	G/A
YRI	rs10975424	9	6077716	0.056	0.787	HapMap	1000GP	T	0.83	C	0.17	T/C
YRI	rs401834	9	6078991	0.137	0.604	HapMap	1000GP	T	0.83	C	0.17	T/C
YRI	rs343476	9	6072597	0.157	0.63	HapMap	1000GP	T	0.84	C	0.16	T/C
YRI	rs343475	9	6073013	0.137	0.604	HapMap	1000GP	C	0.84	G	0.16	C/G
YRI	rs189348	9	6073194	0.137	0.604	HapMap	1000GP	T	0.84	C	0.16	T/C
YRI	rs378952	9	6078146	0.157	0.63	HapMap	1000GP	C	0.84	T	0.16	C/T
YRI	rs10815340	9	6005037	0.031	0.935	HapMap	1000GP	T	0.85	G	0.15	T/G
YRI	rs343496	9	6068077	0.157	0.63	HapMap	1000GP	A	0.85	T	0.15	A/T
YRI	rs6477038	9	6127921	0.02	0.62	HapMap	1000GP	A	0.87	C	0.13	A/C
YRI	rs10118918	9	6170162	0.55	1	HapMap	1000GP	T	0.87	G	0.13	T/G
YRI	rs2094756	9	6135696	0.012	1	HapMap	1000GP	A	0.88	C	0.12	A/C
YRI	rs12352464	9	6157329	0.382	0.9	HapMap	1000GP	C	0.88	T	0.12	C/T
YRI	rs1012715	9	6151320	0.402	0.902	HapMap	1000GP	C	0.89	A	0.11	C/A
YRI	rs10975465	9	6155014	0.397	1	HapMap	1000GP	G	0.89	A	0.11	G/A
YRI	rs12352510	9	6157433	0.396	1	HapMap	1000GP	C	0.89	T	0.11	C/T
YRI	rs13302008	9	6162881	0.045	1	HapMap	1000GP	T	0.9	C	0.1	T/C
YRI	rs1888910	9	6190650	0.024	1	HapMap	1000GP	C	0.9	T	0.1	C/T
YRI	rs13298861	9	6150279	0.026	1	HapMap	1000GP	A	0.92	T	0.08	A/T
YRI	rs10975464	9	6151609	0.028	1	HapMap	1000GP	G	0.93	C	0.07	G/C
YRI	rs7854452	9	6132673	0.018	1	HapMap	1000GP	G	0.94	A	0.06	G/A
YRI	rs7850282	9	6217232	0.03	1	HapMap	1000GP	A	0.94	G	0.06	A/G
YRI	rs7042708	9	6023059	0.044	0.601	HapMap	1000GP	C	0.95	G	0.05	C/G

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
YRI	rs1556471	9	6170677	0.007	1	HapMap	1000GP	A	0.95	G	0.05	A/G
YRI	rs1332293	9	6172604	0.018	1	HapMap	1000GP	G	0.95	A	0.05	G/A
YRI	rs1854709	9	6251455	0.029	1	HapMap	1000GP	T	0.95	C	0.05	T/C
YRI	rs2000198	9	6268569	0.031	1	HapMap	1000GP	T	0.95	C	0.05	T/C
YRI	rs980850	9	6269458	0.029	1	HapMap	1000GP	G	0.95	C	0.05	G/C
YRI	rs980849	9	6269689	0.03	1	HapMap	1000GP	T	0.95	C	0.05	T/C
YRI	rs10123132	9	6275720	0.03	1	HapMap	1000GP	T	0.95	C	0.05	T/C
YRI	rs10758763	9	6326371	0.03	1	HapMap	1000GP	T	0.95	C	0.05	T/C
YRI	rs7865566	9	5990717	0.009	1	HapMap	1000GP	A	0.96	G	0.04	A/G
YRI	rs480246	9	6095728	0.05	0.642	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs1888907	9	6131376	0.05	0.642	HapMap	1000GP	A	0.96	G	0.04	A/G
YRI	rs4567097	9	6159523	0.018	1	HapMap	1000GP	G	0.96	T	0.04	G/T
YRI	rs1322167	9	6282089	0.03	1	HapMap	1000GP	A	0.96	T	0.04	A/T
YRI	rs7858373	9	6301948	0.03	1	HapMap	1000GP	T	0.96	G	0.04	T/G
YRI	rs1407357	9	6302126	0.031	1	HapMap	1000GP	C	0.96	G	0.04	C/G
YRI	rs1407358	9	6302297	0.03	1	HapMap	1000GP	T	0.96	G	0.04	T/G
YRI	rs1923359	9	6310773	0.03	1	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs1330379	9	6310933	0.03	1	HapMap	1000GP	T	0.96	C	0.04	T/C
YRI	rs10491835	9	6325345	0.06	1	HapMap	1000GP	G	0.96	A	0.04	G/A
YRI	rs7040374	9	6348594	0.03	1	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs4742180	9	6352776	0.031	1	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs10758768	9	6354290	0.03	1	HapMap	1000GP	A	0.96	T	0.04	A/T
YRI	rs7350177	9	6357262	0.03	1	HapMap	1000GP	C	0.96	T	0.04	C/T
YRI	rs6477071	9	6358849	0.03	1	HapMap	1000GP	T	0.96	C	0.04	T/C
YRI	rs13302749	9	6171731	0.01	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs12000756	9	6188025	0.012	1	HapMap	1000GP	A	0.97	C	0.03	A/C
YRI	rs1969733	9	6278591	0.015	1	HapMap	1000GP	T	0.97	C	0.03	T/C
YRI	rs1535425	9	6278774	0.015	1	HapMap	1000GP	C	0.97	T	0.03	C/T
YRI	rs7859105	9	6288641	0.015	1	HapMap	1000GP	C	0.97	A	0.03	C/A
YRI	rs7042279	9	6324234	0.003	1	HapMap	1000GP	G	0.97	A	0.03	G/A
YRI	rs1599369	9	6349335	0.015	1	HapMap	1000GP	A	0.97	T	0.03	A/T
YRI	rs4740837	9	6089527	0.012	1	HapMap	1000GP	C	0.98	T	0.02	C/T
YRI	rs13300552	9	6095799	0.036	1	HapMap	1000GP	T	0.98	C	0.02	T/C

ANC	LD_SNP	CHR	BP	RSQ	DPRIME	LD SOURCE	FREQ SOURCE	A1	A1 FREQ	A2	A2 FREQ	ALLELES
YRI	rs7048296	9	6120702	0.012	1	HapMap	1000GP	T	0.98	C	0.02	T/C
YRI	rs7041151	9	6326934	0.015	1	HapMap	1000GP	T	0.98	A	0.02	T/A
YRI	rs12339585	9	6272584	0.012	1	HapMap	1000GP	C	0.99	T	0.01	C/T

Other Embodiments

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literature cited herein are expressly incorporated in their entirety by reference.

WHAT IS CLAIMED IS:

1. A method of treating a patient suffering from an interleukin-33 (IL-33)-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

2. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs4988956 (SEQ ID NO: 1) or at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

3. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs4988956 (SEQ ID NO: 1) or at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each G allele at polymorphism rs4988956 (SEQ ID NO: 1) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

4. The method of claim 2 or 3, further comprising administering an IL-33 axis binding antagonist to the patient.

5. The method of any one of claims 1-4, further comprising determining the level of periostin in a sample derived from the patient.

6. The method of claim 5, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

7. The method of claim 5, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

8. The method of any one of claims 1-7, wherein the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) has a D' value greater than or equal to 0.6 to polymorphism rs4988956 (SEQ ID NO: 1).

9. The method of claim 8, wherein the D' value is greater than or equal to 0.8.

10. The method of any one of claims 1-9, wherein the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1) is a polymorphism in Table 3.

11. The method of any one of claims 1-10, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

12. The method of any one of claims 1-10, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

13. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

14. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10204137 (SEQ ID NO: 2) or at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

15. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10204137 (SEQ ID NO: 2) or at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each A allele at polymorphism rs10204137 (SEQ ID NO: 2) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

16. The method of claim 14 or 15, further comprising administering an IL-33 axis binding antagonist to the patient.

17. The method of any one of claims 13-16, further comprising determining the level of periostin in a sample derived from the patient.

18. The method of claim 17, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

19. The method of claim 17, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

20. The method of any one of claims 13-19, wherein the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) has a D' value greater than or equal to 0.6 to polymorphism rs10204137 (SEQ ID NO: 2).

21. The method of claim 20, wherein the D' value is greater than or equal to 0.8.

22. The method of any one of claims 13-21, wherein the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2) is a polymorphism in Table 3.

23. The method of any one of claims 13-22, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

24. The method of any one of claims 13-22, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

25. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

26. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10192036 (SEQ ID NO: 3) or at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an

equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

27. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10192036 (SEQ ID NO: 3) or at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each C allele at polymorphism rs10192036 (SEQ ID NO: 3) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

28. The method of claim 26 or 27, further comprising administering an IL-33 axis binding antagonist to the patient.

29. The method of any one of claims 25-28, further comprising determining the level of periostin in a sample derived from the patient.

30. The method of claim 29, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

31. The method of claim 29, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

32. The method of any one of claims 25-31, wherein the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) has a D' value greater than or equal to 0.6 to polymorphism rs10192036 (SEQ ID NO: 3).

33. The method of claim 32, wherein the D' value is greater than or equal to 0.8.

34. The method of any one of claims 25-33, wherein the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3) is a polymorphism in Table 3.

35. The method of any one of claims 25-34, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

36. The method of any one of claims 25-34, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

37. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

38. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10192157 (SEQ ID NO: 4) or at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

39. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10192157 (SEQ ID NO: 4) or at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each C allele at polymorphism rs10192157 (SEQ ID NO: 4) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

40. The method of claim 38 or 39, further comprising administering an IL-33 axis binding antagonist to the patient.

41. The method of any one of claims 37-40, further comprising determining the level of periostin in a sample derived from the patient.

42. The method of claim 41, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

43. The method of claim 41, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

44. The method of any one of claims 37-43, wherein the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) has a D' value greater than or equal to 0.6 to polymorphism rs10192157 (SEQ ID NO: 4).

45. The method of claim 44, wherein the D' value is greater than or equal to 0.8.

46. The method of any one of claims 37-45, wherein the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4) is a polymorphism in Table 3.

47. The method of any one of claims 37-46, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

48. The method of any one of claims 37-46, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4).

49. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

50. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs10206753 (SEQ ID NO: 5) or at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

51. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs10206753 (SEQ ID NO: 5) or at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each T allele at polymorphism rs10206753 (SEQ ID NO:

5) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

52. The method of claim 50 or 51, further comprising administering an IL-33 axis binding antagonist to the patient.

53. The method of any one of claims 49-52, further comprising determining the level of periostin in a sample derived from the patient.

54. The method of claim 53, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

55. The method of claim 53, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

56. The method of any one of claims 49-55, wherein the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) has a D' value greater than or equal to 0.6 to polymorphism rs10206753 (SEQ ID NO: 5).

57. The method of claim 56, wherein the D' value is greater than or equal to 0.8.

58. The method of any one of claims 49-57, wherein the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5) is a polymorphism in Table 3.

59. The method of any one of claims 49-58, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

60. The method of any one of claims 49-58, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

61. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

62. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at polymorphism rs4742165 (SEQ ID NO: 6) or at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if the genotype of the patient comprises a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

63. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at polymorphism rs4742165 (SEQ ID NO: 6) or at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of each T allele at polymorphism rs4742165 (SEQ ID NO: 6) or each equivalent allele at the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

64. The method of claim 62 or 63, further comprising administering an IL-33 axis binding antagonist to the patient.

65. The method of any one of claims 61-64, further comprising determining the level of periostin in a sample derived from the patient.

66. The method of claim 65, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

67. The method of claim 65, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

68. The method of any one of claims 61-67, wherein the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) has a D' value greater than or equal to 0.6 to polymorphism rs4742165 (SEQ ID NO: 6).

69. The method of claim 68, wherein the D' value is greater than or equal to 0.8.

70. The method of any one of claims 61-69, wherein the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6) is a polymorphism in Table 4.

71. The method of any one of claims 61-70, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

72. The method of any one of claims 61-70, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

73. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the genotype of the patient has been determined to comprise two or more of the following: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

74. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising determining the genotype at two or more polymorphisms selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), rs4742165 (SEQ ID NO: 6), and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) in a sample derived from the patient, wherein the patient is at increased risk of an IL-33-mediated disorder if:

(a) the genotype of the patient comprises a G allele at polymorphism rs4988956 (SEQ ID NO: 1);

(b) the genotype of the patient comprises an A allele at polymorphism rs10204137 (SEQ ID NO: 2);

(c) the genotype of the patient comprises a C allele at polymorphism rs10192036 (SEQ ID NO: 3);

(d) the genotype of the patient comprises a C allele at polymorphism rs10192157 (SEQ ID NO: 4); (e) the genotype of the patient comprises a T allele at polymorphism rs10206753 (SEQ ID NO: 5)

(f) the genotype of the patient comprises a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or

(g) the genotype of the patient comprises an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

75. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining in a sample derived from a patient suffering from an IL-33-mediated disorder the genotype at two or more polymorphisms selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), rs4742165 (SEQ ID NO: 6), and a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6); and

(b) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the genotype, wherein the presence of:

(i) each G allele at polymorphism rs4988956 (SEQ ID NO: 1);

(ii) each A allele at polymorphism rs10204137 (SEQ ID NO: 2);

(iii) each C allele at polymorphism rs10192036 (SEQ ID NO: 3);

(iv) each C allele at polymorphism rs10192157 (SEQ ID NO: 4);

(v) each T allele at polymorphism rs10206753 (SEQ ID NO: 5);

(vi) each T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or

(vii) each equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6)

indicates that the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist.

76. The method of any one of claims 73-75, wherein the genotype of the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and an A allele at polymorphism rs10204137 (SEQ ID NO: 2).

77. The method of any one of claims 73-75, wherein the genotype of the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) and a C allele at polymorphism rs10192036 (SEQ ID NO: 3).

78. The method of any one of claims 76-77, wherein the genotype of the patient has been determined to further comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or a T allele at polymorphism rs10206753 (SEQ ID NO: 5).

79. The method of claim 78, wherein the genotype of the patient has been determined to further comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) and a T allele at polymorphism rs10206753 (SEQ ID NO: 5).

80. The method of any one of claims 73-79, wherein the genotype of the patient has been determined to comprise: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at

polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); and a T allele at polymorphism rs4742165 (SEQ ID NO: 6).

81. The method of any one of claims 74-80, further comprising administering an IL-33 axis binding antagonist to the patient.

82. The method of any one of claims 73-81, further comprising determining the level of periostin in a sample derived from the patient.

83. The method of claim 82, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

84. The method of claim 82, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

85. The method of any one of claims 73-81, wherein the polymorphism in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) has a D' value greater than or equal to 0.6 to the selected polymorphism.

86. The method of claim 85, wherein the D' value is greater than or equal to 0.8.

87. The method of any one of claims 73-86, wherein the polymorphism in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6) is a polymorphism in Table 3 or Table 4.

88. The method of any one of claims 73-87, wherein the equivalent allele is the minor allele of the polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

89. The method of any one of claims 73-87, wherein the equivalent allele is the major allele of the polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

90. A method of selecting a therapy for a patient having an IL-33-mediated disorder, the method comprising:

(a) determining the level of periostin in a sample derived from the patient;

(b) comparing the level of periostin in the sample derived from the patient to a reference level of periostin; and

(c) selecting a therapy comprising an IL-33 axis binding antagonist if the level of periostin in the sample is at or below the reference level.

91. The method of claim 90, further comprising administering a therapy comprising an IL-33 axis binding antagonist to the patient.

92. A method of treating a patient suffering from an IL-33-mediated disorder, the method comprising administering to the patient a therapy comprising an IL-33 axis binding antagonist, wherein the level of soluble ST2 (sST2) in a sample derived from the patient has been determined to be at or above a reference level of sST2.

93. A method of determining whether a patient is at increased risk of an IL-33-mediated disorder, the method comprising:

(a) determining the level of sST2 in a sample derived from the patient; and

(b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2, wherein the patient is at an increased risk of an IL-33-mediated disorder if the level of sST2 in the sample derived from the patient is at or above the reference level.

94. A method of selecting a therapy for a patient having an IL-33-mediated disorder, the method comprising:

(a) determining the level of sST2 in a sample derived from the patient;

(b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2; and

(c) selecting a therapy comprising an IL-33 axis binding antagonist if the level of sST2 in the sample is at or above the reference level.

95. A method of determining whether a patient suffering from an IL-33-mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist, the method comprising:

(a) determining the level of sST2 in a sample derived from the patient;

(b) comparing the level of sST2 in the sample derived from the patient to a reference level of sST2; and

(c) identifying the patient as likely to respond to treatment comprising an IL-33 axis binding antagonist based on the level of sST2 in the sample derived from the patient,

wherein the patient has an increased likelihood of being responsive to treatment comprising an IL-33 axis binding antagonist if the level of sST2 in the sample is at or above the reference level.

96. The method of any one of claims 93-95, further comprising administering a therapy comprising an IL-33 axis binding antagonist to the patient.

97. A method for assessing a treatment response of a patient treated with an IL-33 axis binding antagonist, the method comprising:

(a) determining the level of sST2 in a sample derived from the patient at a time point during or after administration of the IL-33 axis binding antagonist; and

(b) maintaining, adjusting, or stopping the treatment of the patient based on a comparison of the level of sST2 in the sample derived from the patient with a reference level of sST2,

wherein a change in the level of sST2 in the sample derived from the patient compared to the reference level is indicative of a response to treatment with the IL-33 axis binding antagonist.

98. The method of claim 97, wherein the change is an increase in the level of sST2 and treatment is maintained.

99. The method of claim 97, wherein the change is a decrease in the level of sST2 and treatment is stopped.

100. A method for monitoring the response of a patient treated with a IL-33 axis binding antagonist, the method comprising:

(a) determining the level of sST2 in a sample derived from the patient at a time point during or after administration of the IL-33 axis binding antagonist; and

(b) comparing the level of sST2 in the sample derived from the patient with a reference level of sST2, thereby monitoring the response in the patient undergoing treatment with the IL-33 axis binding antagonist.

101. The method of any one of claims 92-100, further comprising determining the level of periostin in a sample derived from the patient.

102. The method of claim 101, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or below a reference level of periostin.

103. The method of claim 101, wherein the patient has an increased likelihood of being responsive to treatment with an IL-33 axis binding antagonist if the level of periostin in the sample is at or above a reference level of periostin.

104. The method of any one of claims 92-103, wherein the level of sST2 is a level of sST2 protein.

105. The method of claim 104, wherein the sample derived from the patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof.

106. The method of claim 105, wherein the sample derived from the patient is a serum sample.

107. The method of any one of claims 92-106, wherein the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs4742165 (SEQ ID NO: 6).

108. The method of any one of claims 92-107, wherein the reference level of sST2 is a level of sST2 determined from a group of individuals, wherein each member of the group has a genotype comprising two G alleles at polymorphism rs3771166 (SEQ ID NO: 8).

109. The method of claim 107 or 108, wherein the group of individuals is suffering from asthma.

110. The method of any one of claims 107-109, wherein the reference level of sST2 is a median level.

111. The method of claim 107-110, wherein the group of individuals is a group of female individuals and the patient is female.

112. The method of claim 107-110, wherein the group of individuals is a group of male individuals and the patient is male.

113. The method of any one of claims 1, 4, 13, 16, 25, 28, 37, 40, 49, 52, 61, 64, 73, 81, 91, 92, 96, 97, and 100, wherein the IL-33 axis binding antagonist is administered in combination with a tryptase-beta binding antagonist, a chemoattractant receptor-homologous molecule expressed on Th2 cells (CRTH2) binding antagonist, an interleukin-13 (IL-13) binding antagonist, an interleukin-17 (IL-17) binding antagonist, a JAK1 antagonist, and/or an interleukin-5 (IL-5) binding antagonist.

114. The method of any one of claims 1, 3-13, 15-25, 27-37, 39-49, 51-61, 63-73, 75-92, and 93-112, wherein the IL-33 axis binding antagonist is an IL-33 binding antagonist, an ST2 binding antagonist, or an IL-1RAcP binding antagonist.

115. The method of claim 114, wherein:

(a) the IL-33 binding antagonist is an anti-IL33 antibody or antigen-binding fragment thereof;

(b) the ST2 binding antagonist is an ST2-Fc protein, an anti-ST2 antibody, or antigen-binding fragment thereof; or

(c) the IL-1RAcP binding antagonist is an anti-IL-1RAcP antibody.

116. The method of any one of claims 1-115, wherein the IL-33-mediated disorder is selected from the group consisting of an inflammatory condition, an immune disorder, a fibrotic disorder, an eosinophilic disorder, an infection, pain, a central nervous system disorder, a solid tumor, and an ophthalmologic disorder.

117. The method of claim 116, wherein the inflammatory condition is selected from the group consisting of asthma, sepsis, septic shock, atopic dermatitis, allergic rhinitis, rheumatoid arthritis, and chronic obstructive pulmonary disease (COPD).

118. The method of claim 116, wherein the immune disorder is selected from the group consisting of asthma, rheumatoid arthritis, allergy, anaphylaxis, anaphylactic shock, allergic rhinitis, psoriasis, inflammatory bowel disease (IBD), Crohn's disease, diabetes, and liver disease.

119. The method of claim 116, wherein the fibrotic disease is idiopathic pulmonary fibrosis (IPF).

120. The method of claim 116, wherein the eosinophilic disorder is an eosinophil-associated gastrointestinal disorder (EGID).

121. The method of claim 120, wherein the EGID is eosinophilic esophagitis.

122. The method of claim 116, wherein the infection is a helminth infection, a protozoan infection, or a viral infection.

123. The method of claim 122, wherein the protozoan infection is a *Leishmania major* infection.

124. The method of claim 122, wherein the viral infection is a respiratory syncytial virus (RSV) infection or an influenza infection.

125. The method of claim 116, wherein the pain is inflammatory pain.

126. The method of claim 116, wherein the central nervous system disorder is Alzheimer's disease.

127. The method of claim 116, wherein the solid tumor is selected from the group consisting of breast tumor, colon tumor, prostate tumor, lung tumor, kidney tumor, liver tumor, pancreas tumor, stomach tumor, intestinal tumor, brain tumor, bone tumor, and skin tumor.

128. The method of claim 116, wherein the ophthalmologic disorder is age-related macular degeneration (AMD), geographic atrophy (GA), or retinopathy of the eye.

129. The method of any one of claims 6, 7, 18, 19, 30, 31, 42, 43, 54, 55, 66, 67, 83, 84, 102, and 103 , wherein the reference level of periostin is between about 23 ng/ml and about 50 ng/ml.

130. The method of any one of claims 2-12, 14-24, 26-36, 38-48, 50-60, 62-72, and 74-129, wherein the sample derived from the patient is a whole blood sample, a serum sample, a plasma sample, or a combination thereof.

131. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

132. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

133. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a G allele at polymorphism rs4988956 (SEQ ID NO: 1) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4988956 (SEQ ID NO: 1).

134. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

135. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

136. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise an A allele at polymorphism rs10204137 (SEQ ID NO: 2) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10204137 (SEQ ID NO: 2).

137. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

138. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

139. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192036 (SEQ ID NO: 3) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192036 (SEQ ID NO: 3).

140. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4)..

141. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4)..

142. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a C allele at polymorphism rs10192157 (SEQ ID NO: 4) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10192157 (SEQ ID NO: 4)..

143. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

144. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient

has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

145. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs10206753 (SEQ ID NO: 5) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs10206753 (SEQ ID NO: 5).

146. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

147. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

148. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise a T allele at polymorphism rs4742165 (SEQ ID NO: 6) or an equivalent allele at a polymorphism in linkage disequilibrium with polymorphism rs4742165 (SEQ ID NO: 6).

149. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to comprise two or more of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

150. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise twoor more of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T

allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

151. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to comprise two or more of the following alleles: a G allele at polymorphism rs4988956 (SEQ ID NO: 1); an A allele at polymorphism rs10204137 (SEQ ID NO: 2); a C allele at polymorphism rs10192036 (SEQ ID NO: 3); a C allele at polymorphism rs10192157 (SEQ ID NO: 4); a T allele at polymorphism rs10206753 (SEQ ID NO: 5); a T allele at polymorphism rs4742165 (SEQ ID NO: 6); and/or an equivalent allele at a polymorphism that is in linkage disequilibrium with a polymorphism selected from the group consisting of rs4988956 (SEQ ID NO: 1), rs10204137 (SEQ ID NO: 2), rs10192036 (SEQ ID NO: 3), rs10192157 (SEQ ID NO: 4), rs10206753 (SEQ ID NO: 5), and rs4742165 (SEQ ID NO: 6).

152. An IL-33 axis binding antagonist for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient, prior to any administration of an IL-33 axis binding antagonist, has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level.

153. Use of an effective amount of an IL-33 axis binding antagonist in the manufacture of a medicament for use in treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level.

154. A composition comprising an effective amount of an IL-33 axis binding antagonist for use in a method of treating a patient suffering from an IL-33-mediated disorder, wherein the patient has been determined to have a level of sST2 in a sample derived from the patient at or above a reference level.

Figures 1A-1B

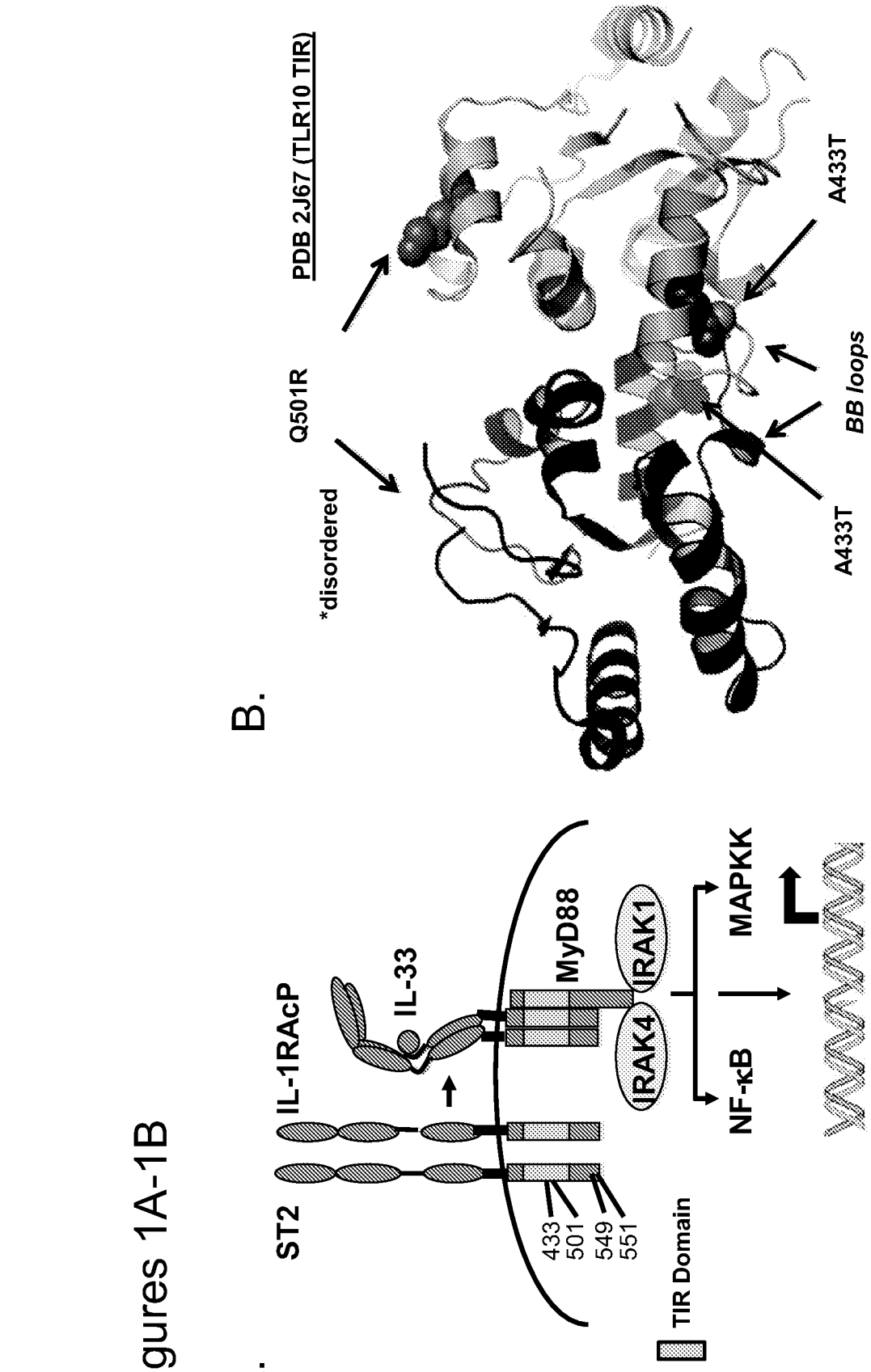


Figure 1C

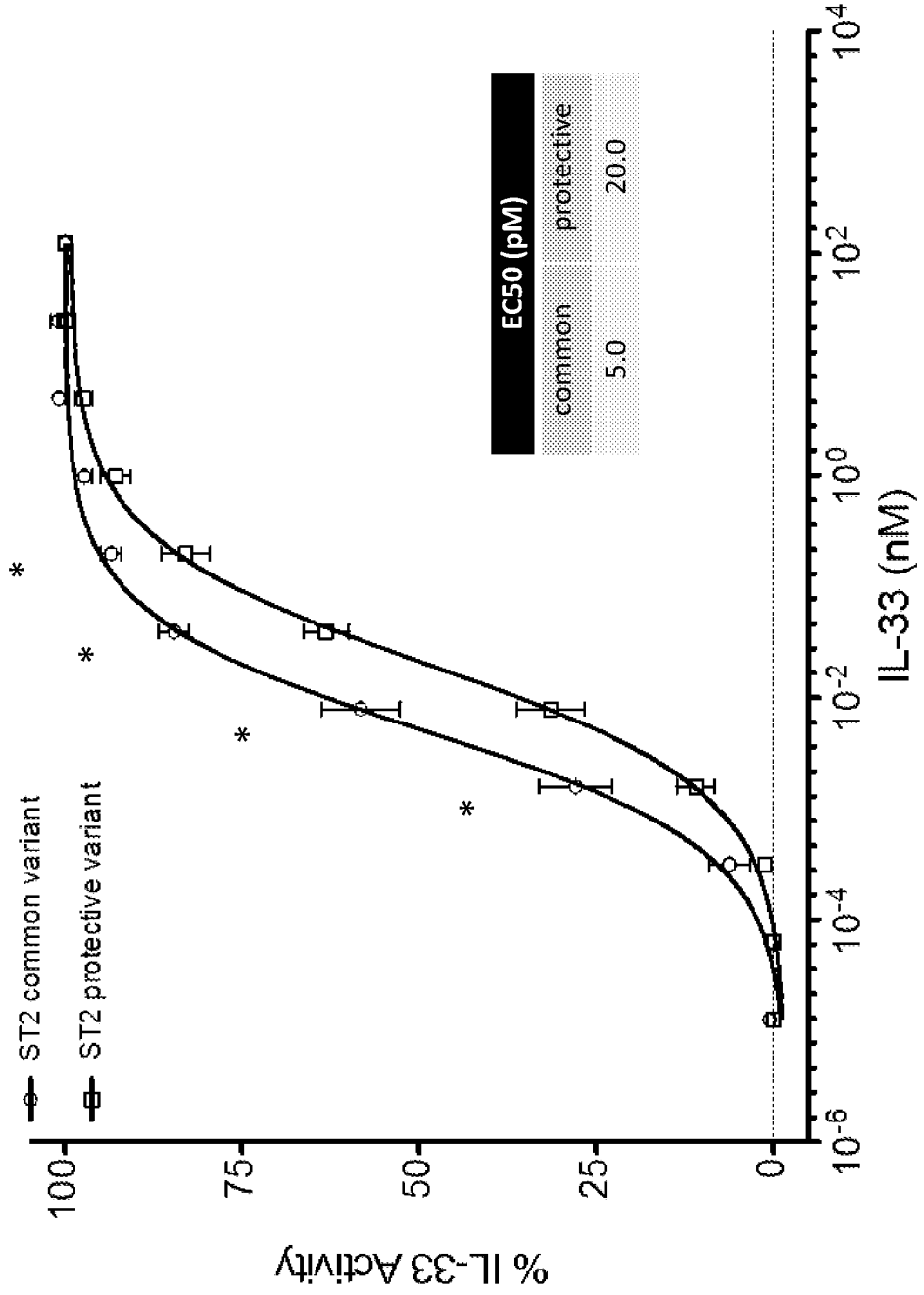

ST2 common variant
ST2 protective variant
EC50 (pM)
common
protective
5.0
20.0
% IL-33 Activity
IL-33 (nM)
100
75
50
25
0
10-6
10-4
10-2
100
102
104
*
*
*
*

Figure 1D

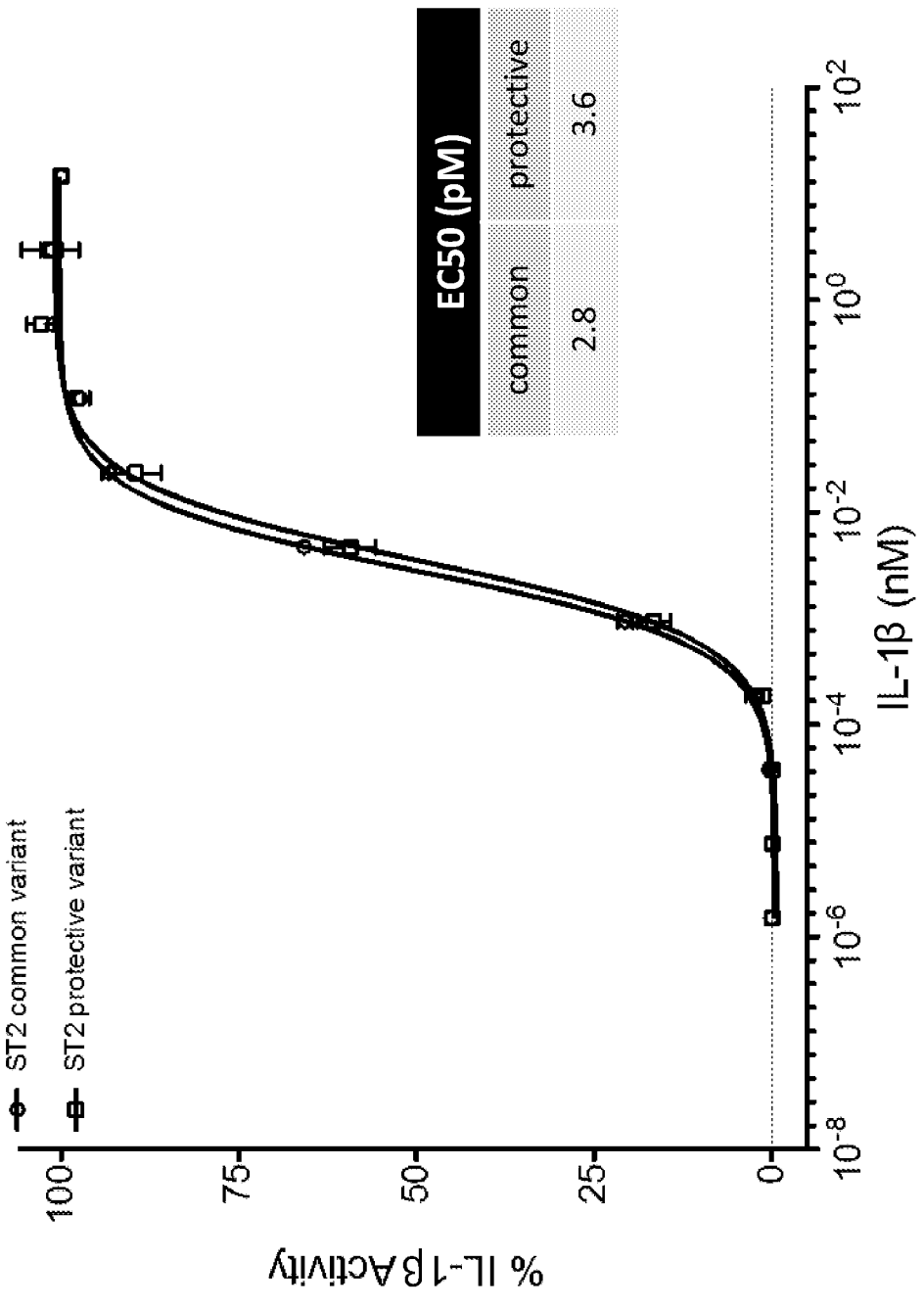
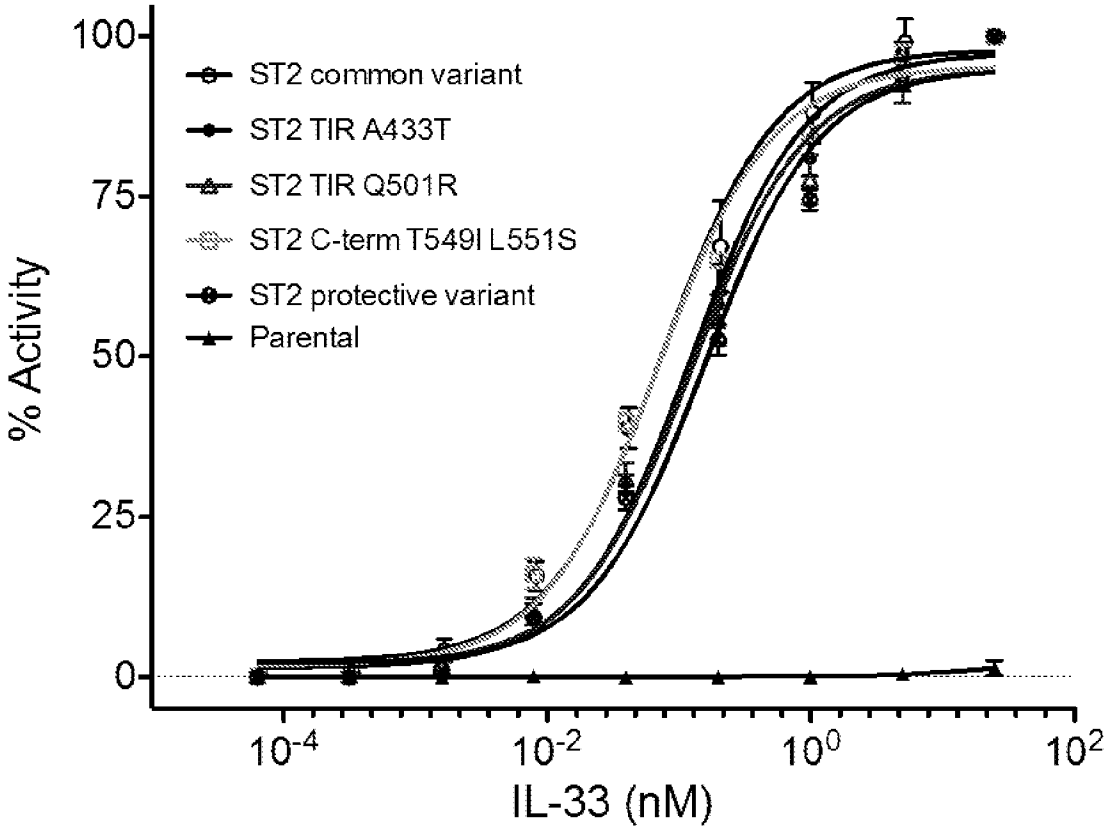
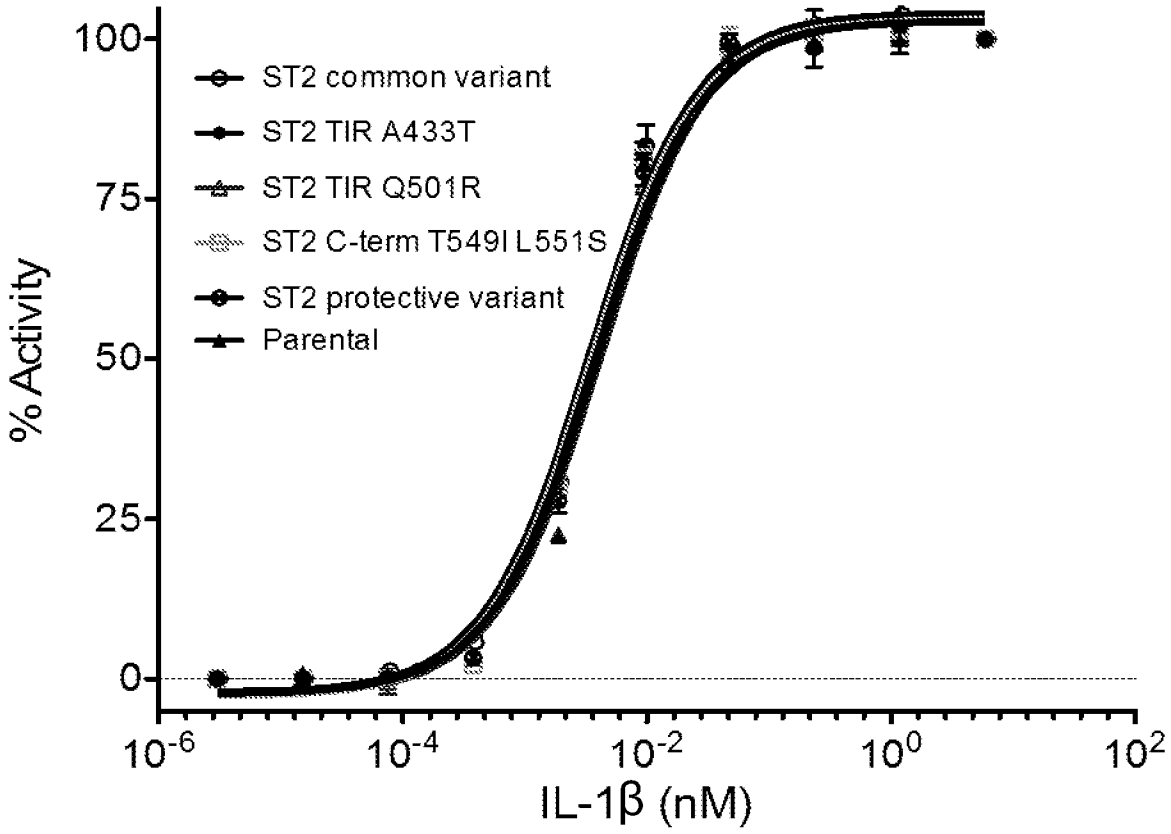

ST2 common variant
ST2 protective variant
EC50 (pM)
common
protective
2.8
3.6
% IL-1β Activity
IL-1β (nM)
100
75
50
25
0
10-8
10-6
10-4
10-2
100
102

Figure 2A



EC50 (pM)					
common	TIR A433T	TIR Q501R	C-term T549I L551S	protective	Parental
74	122	126	69	155	> 100,000

Figure 2B



EC50 (pM)					
common	TIR A433T	TIR Q501R	C-term T549I L551S	protective	Parental
3.4	3.6	4.3	3.5	3.7	4.0

Figure 3A

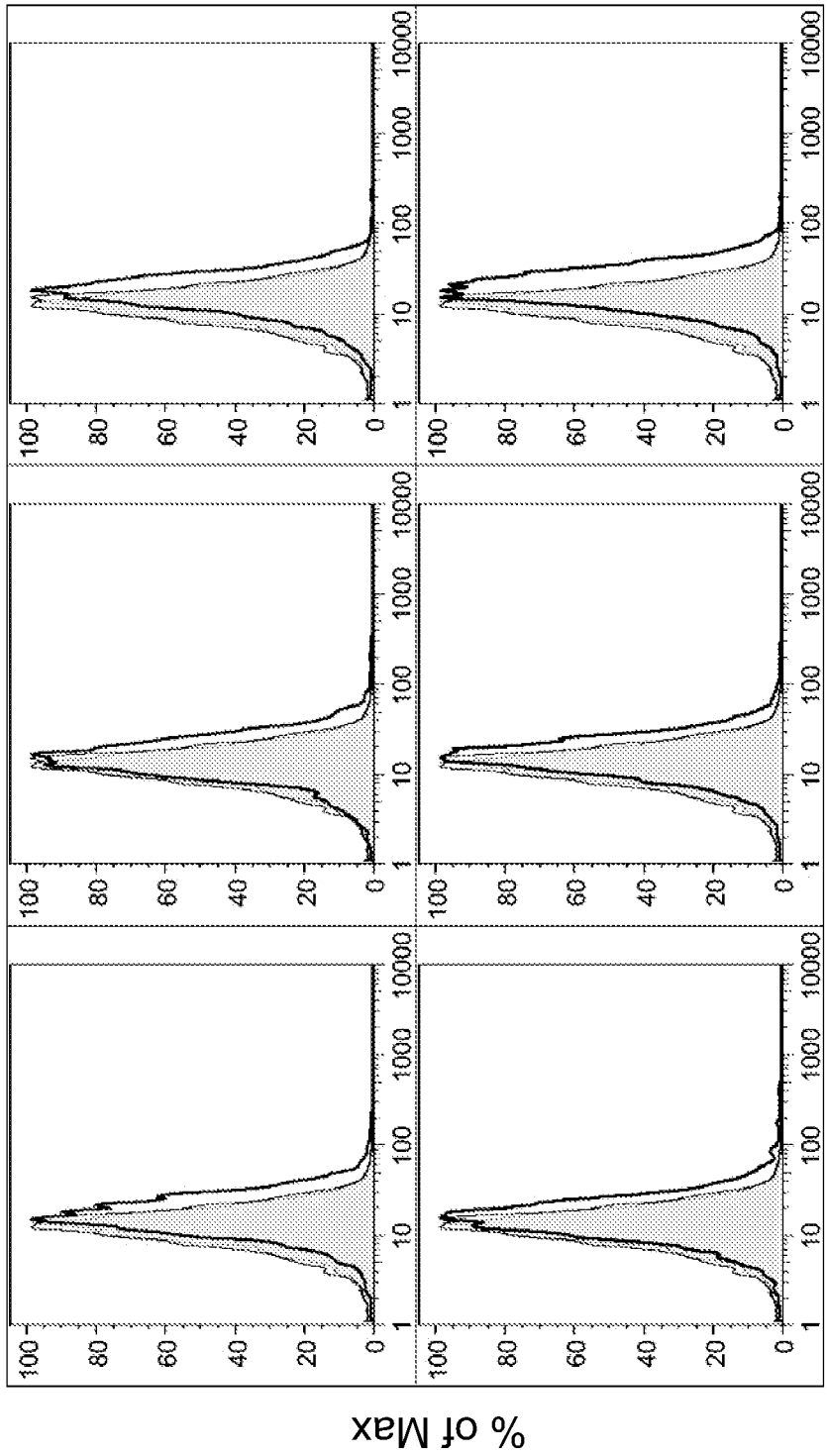


Figure 3B

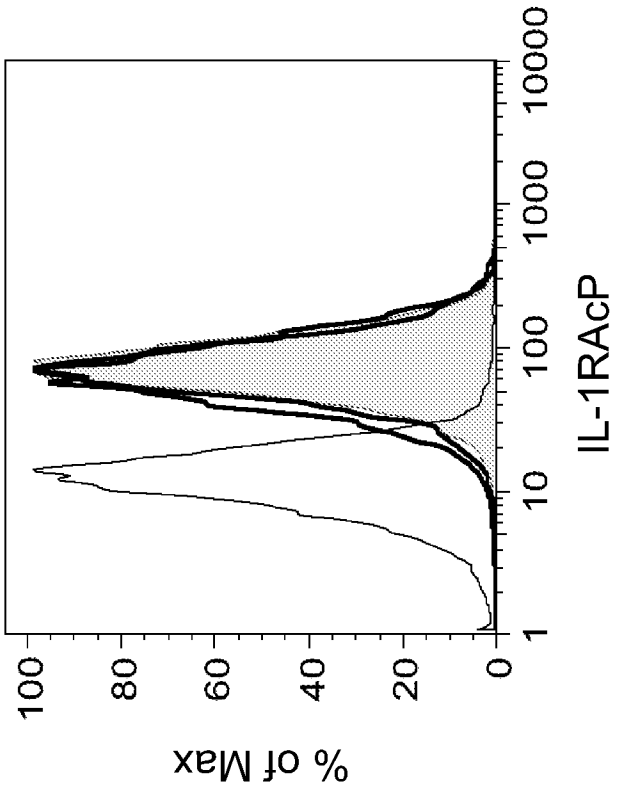

common
protective
parental
isotype
% of Max
100
80
60
40
20
0
1
10
100
1000
10000
IL-1RAcP

Figure 3C

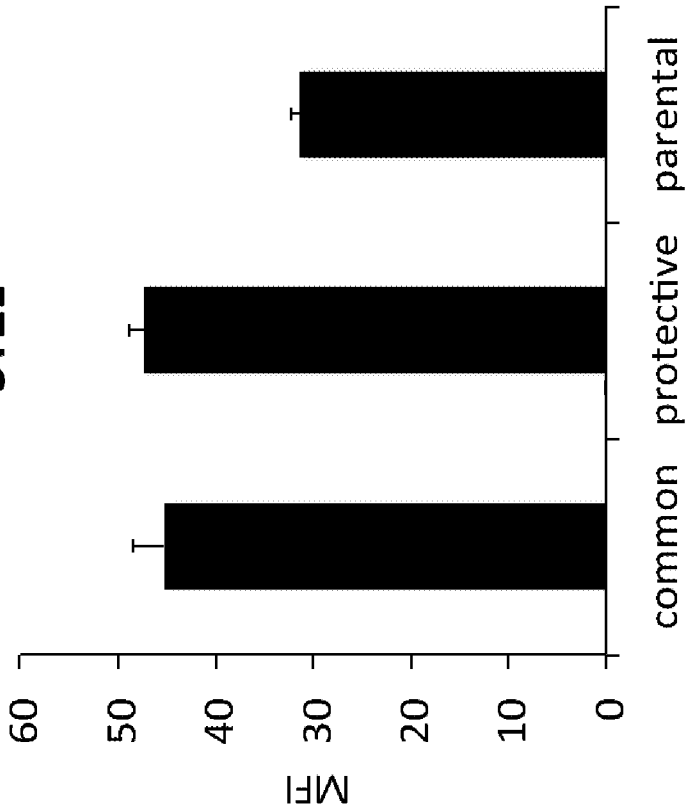


Figure 3D

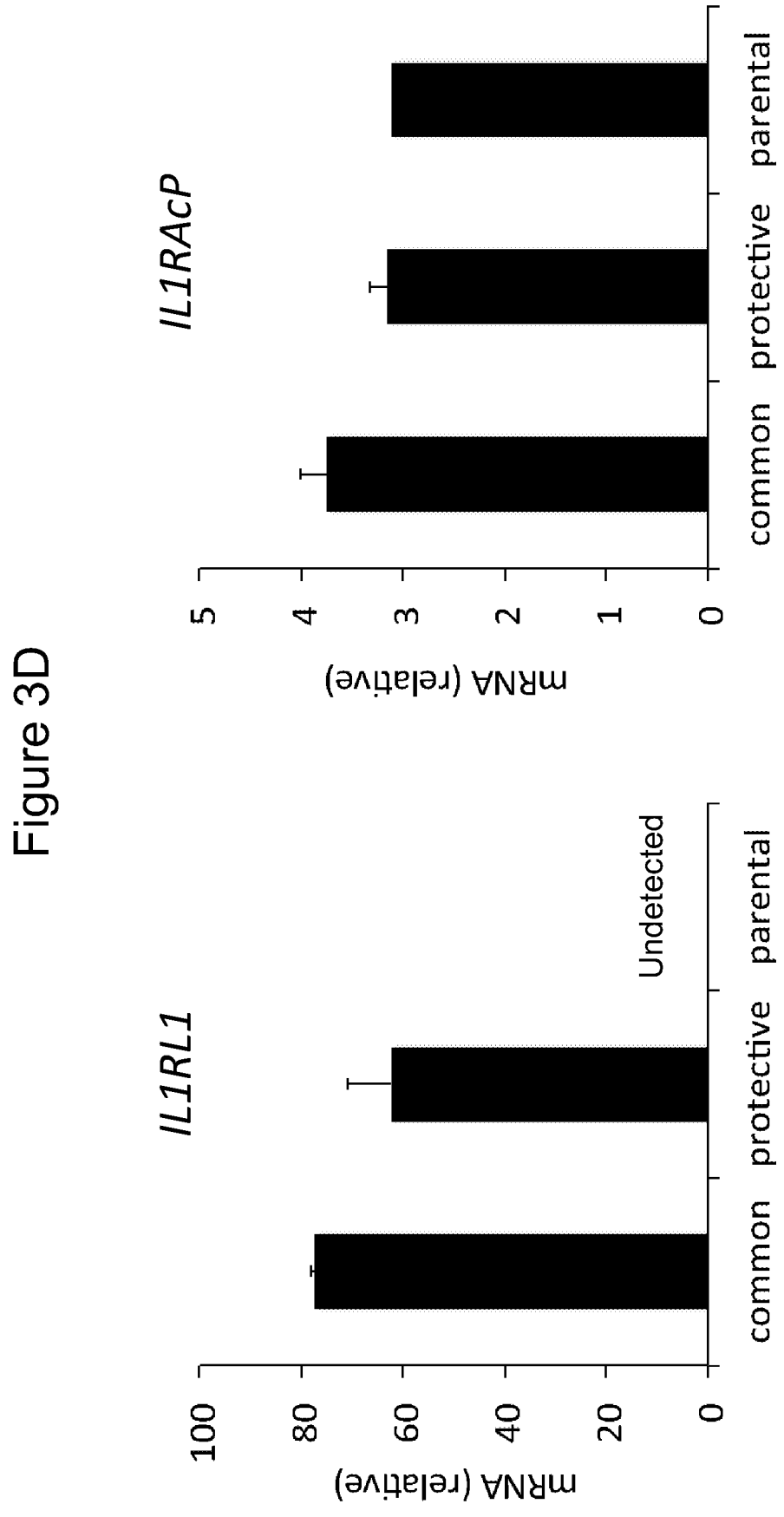
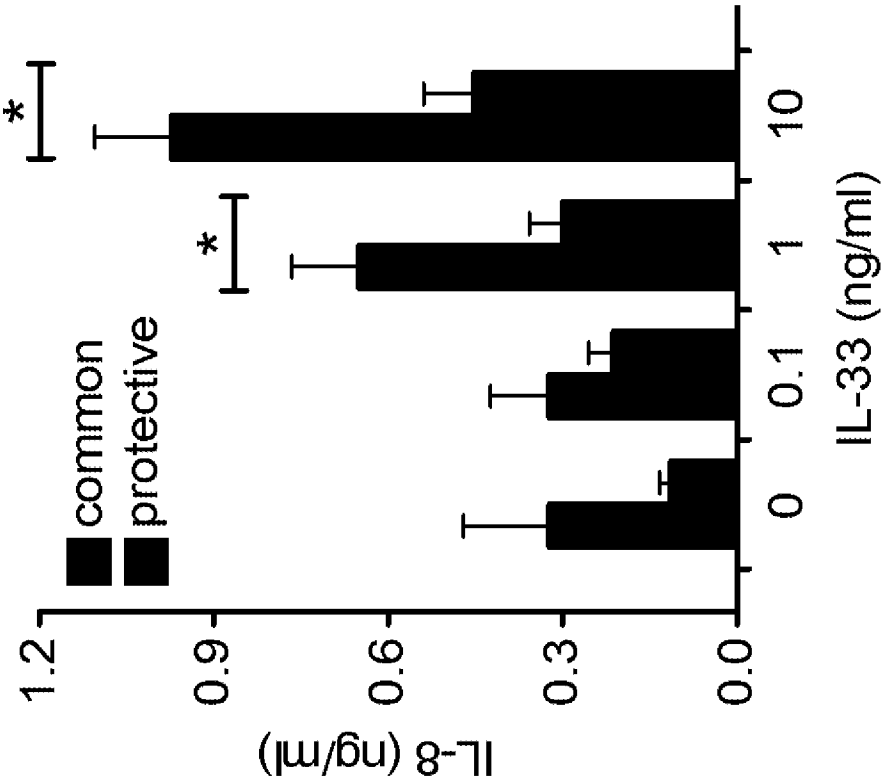

IL1RL1
mRNA (relative)
100
80
60
40
20
0
Undetected
common
protective
parental
IL1RAcP
mRNA (relative)
5
4
3
2
1
0
common
protective
parental

Figure 4



Figures 5A-5B

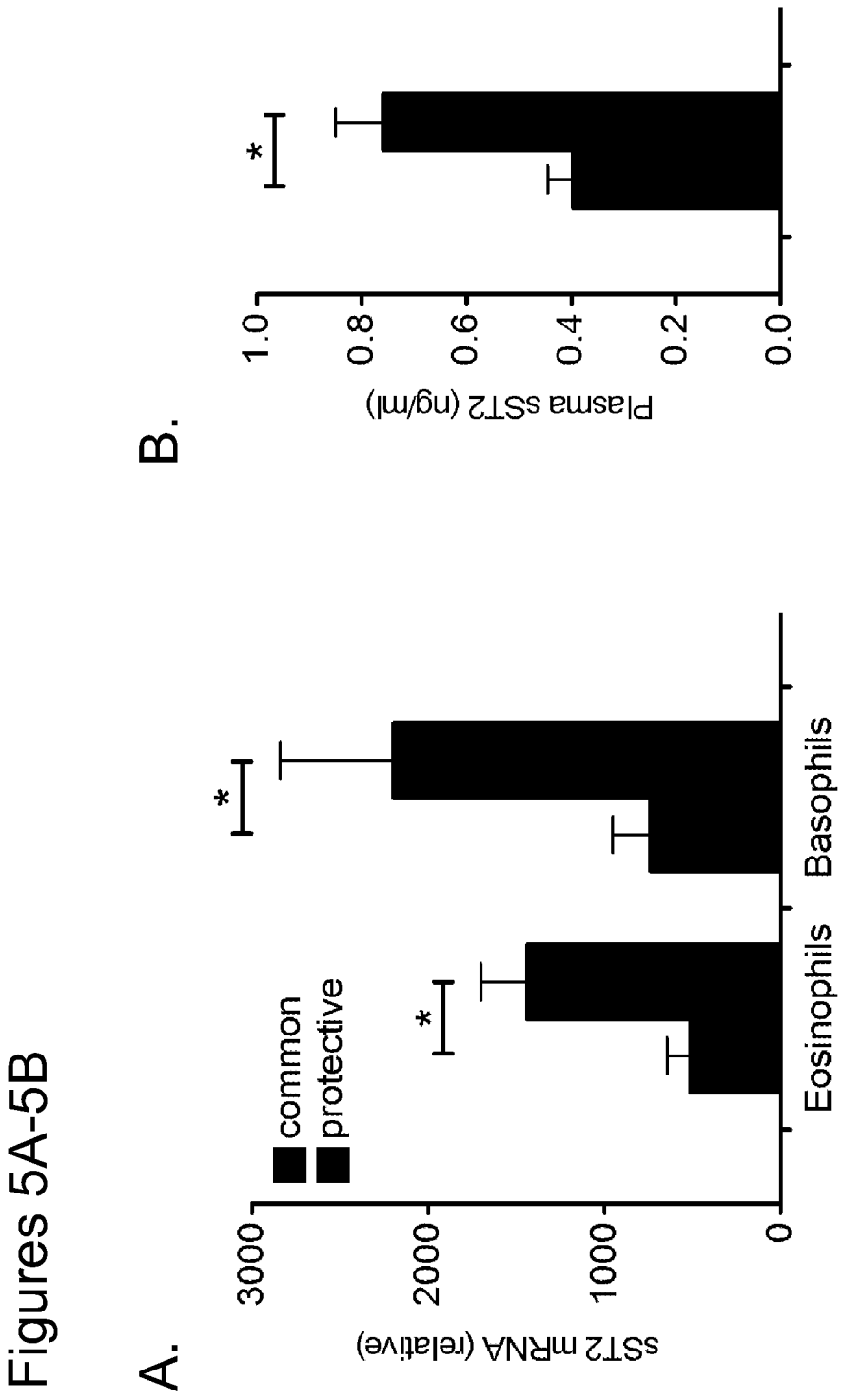
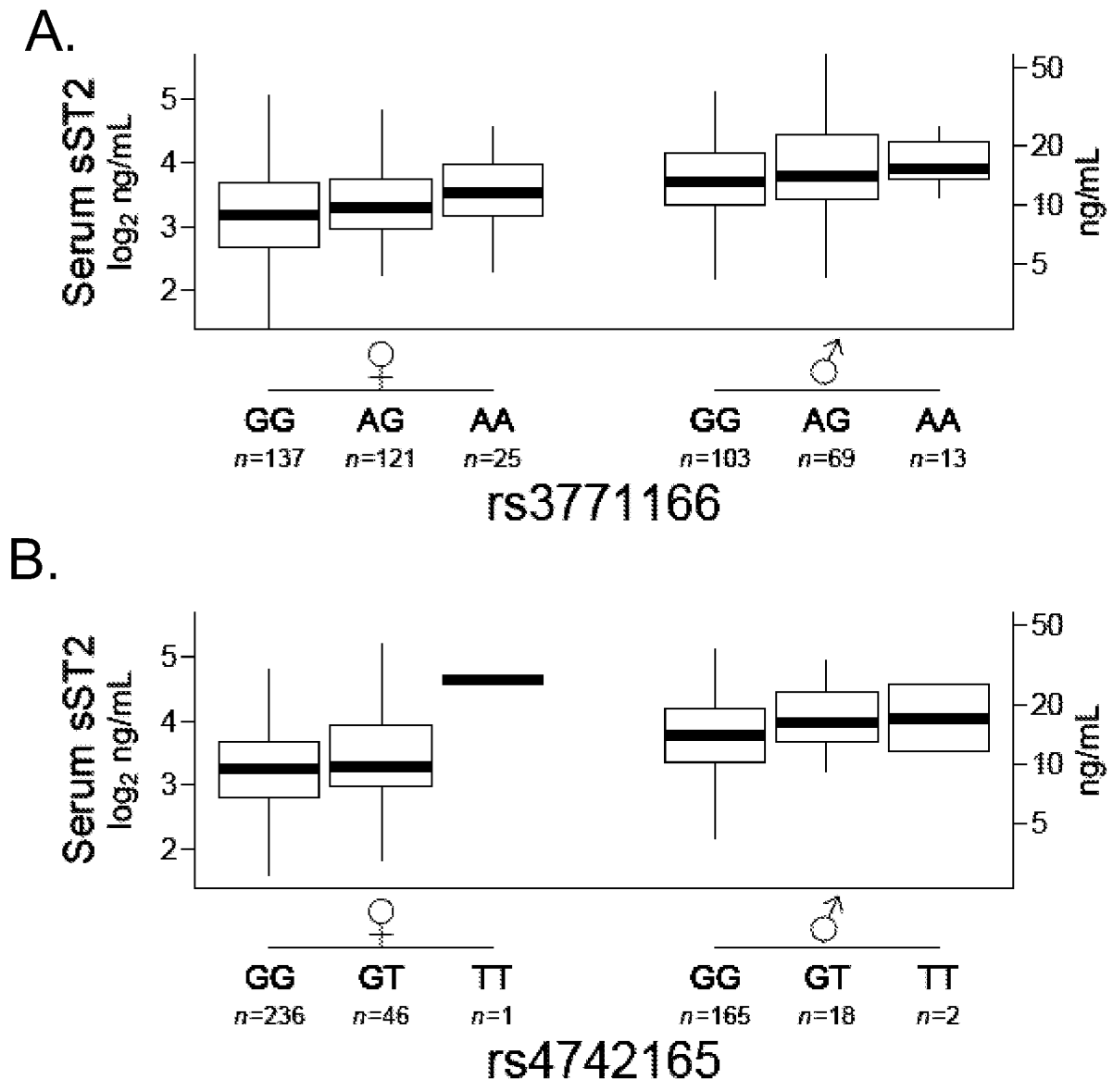


Figure 6

	CHR	SNP	Location/ function	All vs. control		Periostin High vs. control		Periostin Low vs. control		MAF		
				P	OR	P	OR	P	OR	CTRL	HI	LO
ST2	2	rs3771166#	intronic	5.83E-05	0.70	0.009	0.73	4.17E-05	0.63	0.38	0.34	0.30
ST2	2	rs10204137	Q>R	2.97E-05	0.68	0.007	0.72	2.34E-05	0.62	0.38	0.34	0.30
ST2	2	rs10206753	L>S	5.77E-05	0.70	0.013	0.74	2.97E-05	0.63	0.38	0.34	0.31
ST2	2	rs10192157	T>I	7.41E-05	0.70	0.012	0.74	4.78E-05	0.64	0.38	0.34	0.31
ST2	2	rs4988956	A>T	7.70E-05	0.70	0.012	0.74	5.19E-05	0.64	0.38	0.34	0.31

Figures 7A-7B



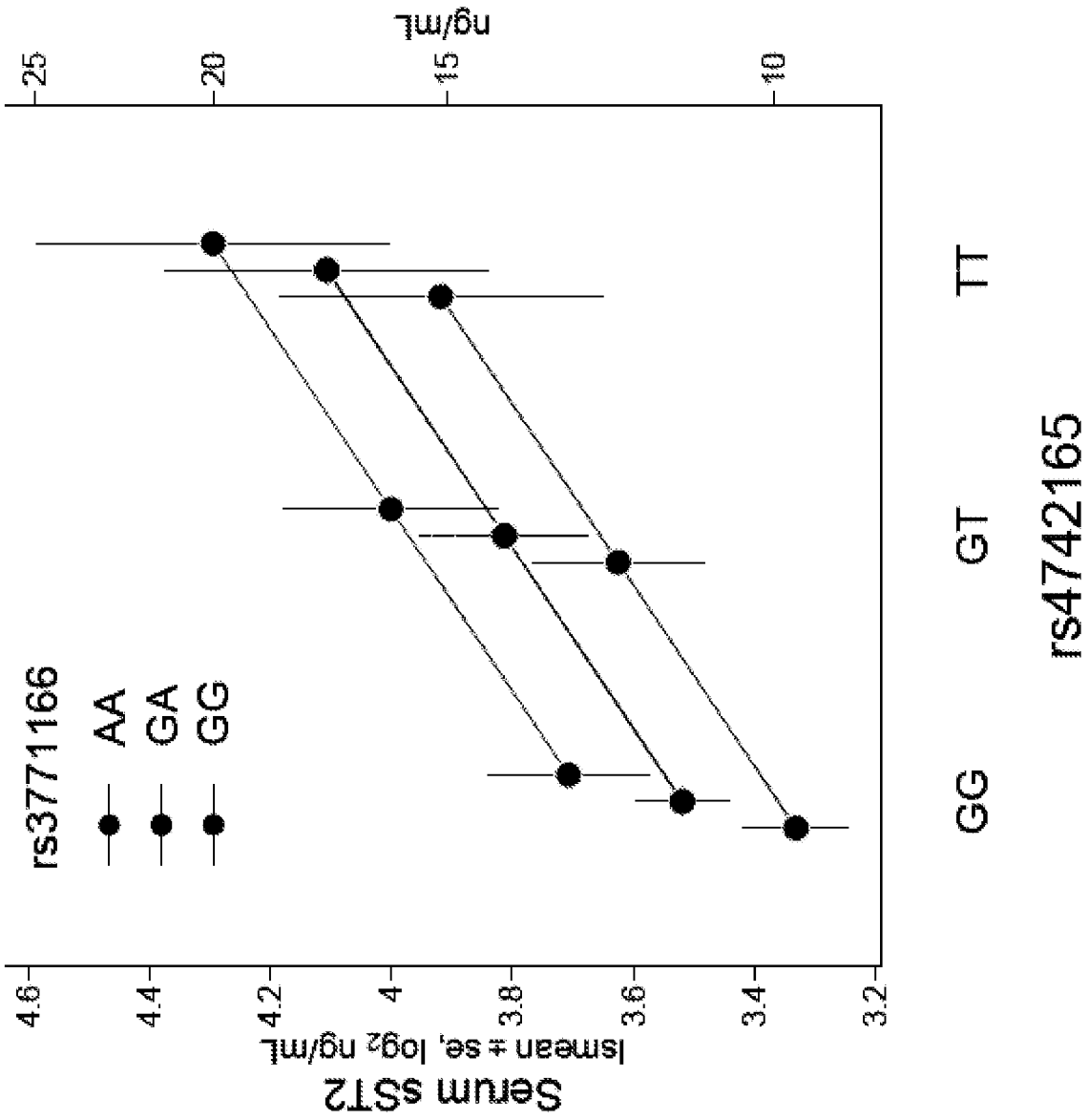

Serum sST2
lsmean ± se, log2 ng/mL
4.6
4.4
4.2
4
3.8
3.6
3.4
3.2
ng/mL
25
20
15
10
rs3771166
AA
GA
GG
GG
GT
TT
rs4742165

Figure 7C

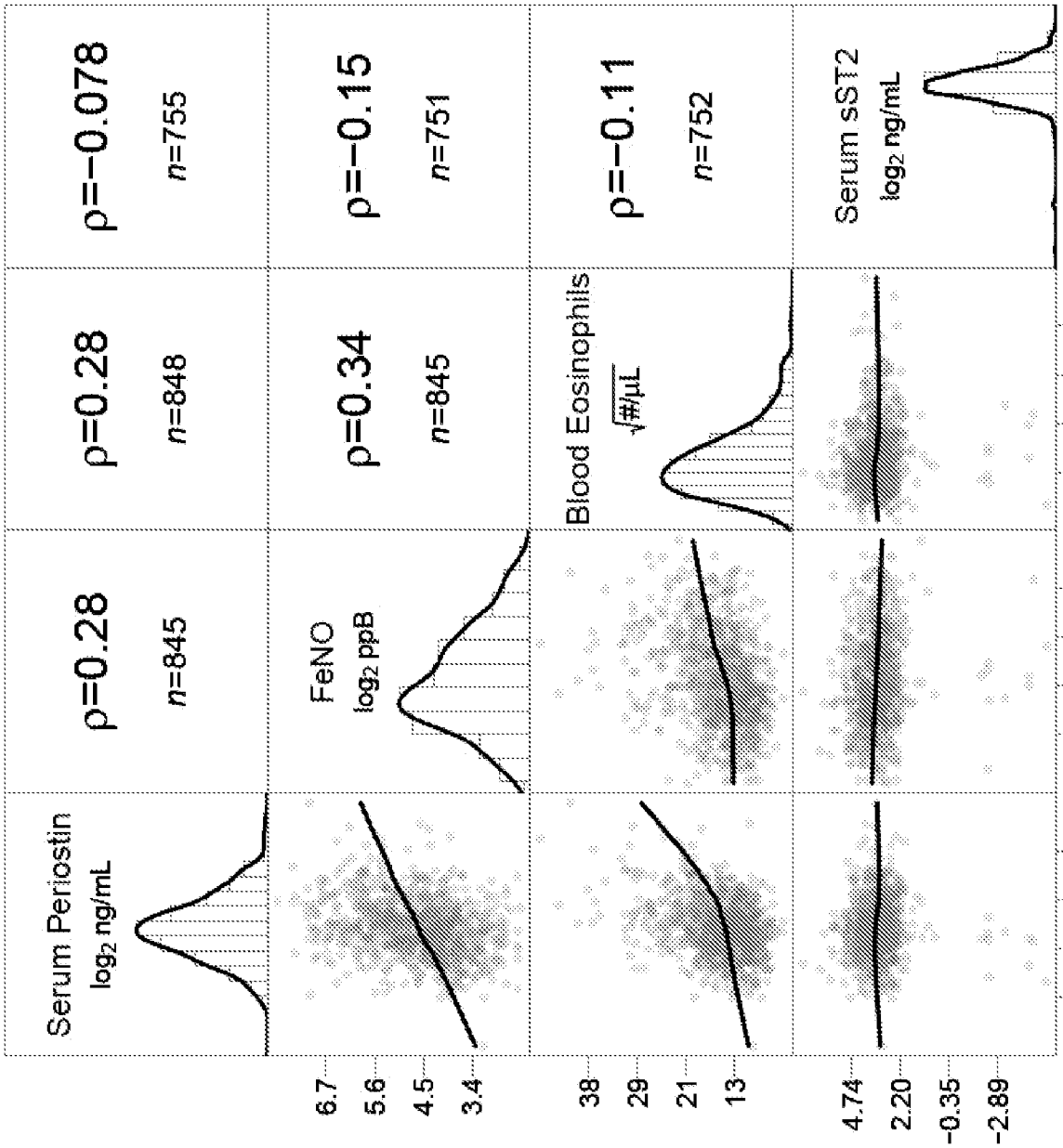

Serum Periostin
log2 ng/mL
ρ=0.28
n=845
ρ=0.28
n=848
ρ=−0.078
n=755
FeNO
log2 ppB
ρ=0.34
n=845
ρ=−0.15
n=751
Blood Eosinophils
√#/μL
ρ=−0.11
n=752
Serum sST2
log2 ng/mL
6.7
5.6
4.5
3.4
38
29
21
13
4.74
2.20
−0.35
−2.89
4.7 5.4 6.1 6.8
3.4 4.5 5.6 6.7
13 21 29 38

Figure 8

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2015/059982

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68 G01N33/68
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q G01N

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

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

EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2011/031600 A1 (SCHERING CORP [US]; RANKIN ANDREW L [US]; PFLANZ STEFAN [US]; MUMM JOH) 17 March 2011 (2011-03-17) paragraphs [0043], [0045]; claim 1 ----- -/--	1-60, 73-89, 113-145, 149-151

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
25 January 2016	04/05/2016

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Knudsen, Henrik

1

Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2015/059982

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-60, 73-89, 131-145, 149-151(completely); 113-130(partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-60, 73-89, 131-145, 149-151(completely); 113-130(partially)

Method of treating a patient suffering from an IL-33 mediated disorder comprising administering an IL-33 axis binding antagonist wherein the genotype of the patient has been determined to comprise a G at rs4988956; an A at rs10204137; a C at rs10192036; a C at rs10192157; or a T at rs10206753 or has been determined to comprise an equivalent allele at a polymorphism in linkage disequilibrium with one of said polymorphisms. Method of determining whether a patient is at increased risk of an IL-33 mediated disorder comprising determining whether one of the above alleles is present. Method of determining whether a patient suffering from an IL-33 mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist.

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2. claims: 61-72, 146-148(completely); 113-130(partially)

Method of treating a patient suffering from an IL-33 mediated disorder comprising administering an IL-33 axis binding antagonist wherein the genotype of the patient has been determined to comprise a T at rs4742165 or has been determined to comprise an equivalent allele at a polymorphism in linkage disequilibrium with one of said polymorphisms. Method of determining whether a patient is at increased risk of an IL-33 mediated disorder comprising determining whether one of the above alleles is present. Method of determining whether a patient suffering from an IL-33 mediated disorder is likely to respond to treatment comprising an IL-33 axis binding antagonist comprising determining whether one of the above alleles is present

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3. claims: 90, 91(completely); 113-130(partially)

Method for selecting a therapy for a patient having an IL-33 mediated disorder comprising determining the level of periostin in a sample from the patient and selecting a therapy comprising an IL-33 axis binding antagonist if the level of periostin is at or below the reference level.

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4. claims: 92-112, 152-154(completely); 113-130(partially)

Method of treating a patient suffering from an IL-33 mediated disorder comprising administering an IL-33 axis binding antagonist wherein the level of sST2 in a sample is determined to be at or above a reference level. Method of determining whether a patient is at increased risk of an IL-33 mediated disorder comprising determining whether the

level of sST2 is at or above a reference level. Method of selecting a therapy for a patient having an IL-33 mediated disorder, determining whether the patient is likely to respond to a therapy comprising an IL-33 axis binding antagonist, assessing a treatment response comprising determining the sST2 level and selecting a therapy comprising an IL-33 axis binding antagonist if the level of sST2 is above or at the reference level.

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	M. A. K. SEDHOM ET AL: "Neutralisation of the interleukin-33/ST2 pathway ameliorates experimental colitis through enhancement of mucosal healing in mice", GUT, vol. 62, no. 12, 1 December 2013 (2013-12-01), pages 1714-1723, XP055243814, UK ISSN: 0017-5749, DOI: 10.1136/gutjnl-2011-301785 page 1715, left-hand column, last paragraph page 1717, right-hand column, last paragraph	1-60, 73-89, 113-145, 149-151
A	CHUAN QIU ET AL: "Anti-interleukin-33 inhibits cigarette smoke-induced lung inflammation in mice", IMMUNOLOGY., vol. 138, no. 1, 13 January 2013 (2013-01-13), pages 76-82, XP055243811, GB ISSN: 0019-2805, DOI: 10.1111/imm.12020 page 79, left-hand column, paragraph 3	1-60, 73-89, 113-145, 149-151
A	WO 2007/143295 A2 (CRITICAL CARE DIAGNOSTICS INC [US]; SNIDER JAMES [US]; JACOBSON SVEN []) 13 December 2007 (2007-12-13) page 8; claim 1	1-60, 73-89, 113-145, 149-151
Y	KAKKAR R ET AL: "The IL-33/ST2 pathway: Therapeutic target and novel biomarker", NATURE REVIEWS. DRUG DISCOVERY, NATURE PUBLISHING GROUP, GB, vol. 7, no. 10, 1 January 2008 (2008-01-01), pages 827-840, XP002530680, ISSN: 1474-1784, DOI: 10.1038/NRD2660 abstract	1,3-37, 39-60, 73-89, 113-145, 149-151

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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JENNIFER E. HO ET AL: "Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling", JOURNAL OF CLINICAL INVESTIGATION, vol. 123, no. 10, 1 October 2013 (2013-10-01), pages 4208-4218, XP055242886, US ISSN: 0021-9738, DOI: 10.1172/JCI67119	2,38
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X	LOUBNA AKHABIR ET AL: "Lung expression quantitative trait loci data set identifies important functional polymorphisms in the asthma-associated IL1RL1 region", JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY, vol. 134, no. 3, 1 September 2014 (2014-09-01), pages 729-731, XP055243813, AMSTERDAM, NL ISSN: 0091-6749, DOI: 10.1016/j.jaci.2014.02.039	2
Y	table 1	1,3-37, 39-60, 73-89, 113-145, 149-151

X,P	VLADIMIR RAMIREZ-CARROZZI ET AL: "Functional analysis of protective IL1RL1 variants associated with asthma risk", JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY, vol. 135, no. 4, 1 April 2015 (2015-04-01) , pages 1080-1083.e3, XP055243121, AMSTERDAM, NL ISSN: 0091-6749, DOI: 10.1016/j.jaci.2014.10.028 the whole document	1-60, 73-89, 113-145, 149-151

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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	Sawa Ito ET AL: "Transplantation: ST2: the biomarker at the heart of GVHD severity", Blood, 1 January 2015 (2015-01-01), pages 10-11, XP055243196, DOI: 10.1182/blood-2014-11-611780 Retrieved from the Internet: URL:http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4281822/ [retrieved on 2016-01-20] abstract -----	1
X,P	TAE YOUNG JANG ET AL: "Interleukin-33 and Mast Cells Bridge Innate and Adaptive Immunity: From the Allergologist's Perspective", INTERNATIONAL NEUROUROLOGY JOURNAL, vol. 19, no. 3, 22 September 2015 (2015-09-22), pages 142-150, XP055243774, DOI: 10.5213/inj.2015.19.3.142 page 143, right-hand column -----	1

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2015/059982

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