

BREAST CANCER RISK ASSESSMENT

FIELD OF THE INVENTION

The present disclosure relates to methods and systems for assessing the risk of a
5 human female subject for developing breast cancer.

BACKGROUND OF THE INVENTION

For decades, women have been told that they have an increased risk of breast cancer if they have a family history of the disease (Collaborative Group on Hormonal
10 Factors in Breast Cancer, 2001), and more recently, women have been told that they have increased risk of breast cancer if they have mammographically dense breasts (Cappello et al., 2019) among other factors (Hopper et al., 2018). Genetic risk derived from common changes throughout the genome can also be used to predict risk of breast cancer (Mavaddat et al., 2015), but this information is not readily available to women.
15 This fragmented approach to risk prediction can result in women being given inaccurate risk information and can mean that women get conflicting and confusing advice.

About 22% of women report having at least one first-degree relative with breast cancer (Nickson et al., 2018; Ziogas et al., 2000) and 20% report having a family
20 history in at least one second-degree relative (Ziogas et al., 2000). The magnitude of familial risk depends on the closeness of the genetic relationship, the age at diagnosis of the affected relative and the age of the at-risk woman. Familial risk is best captured by algorithms that model major genes and underlying genetic risk using multi-generational pedigree data (Antoniou et al., 2008; Tyrer et al., 2004; Berry et al., 1997).
25 Cancer family clinics use these tools when managing the small proportion of women who have several affected relatives and where there is the time and commitment to collect and validate extensive family cancer data. However, this approach is not feasible on a population basis using current methods.

Mammographic density is the bright regions on a mammogram and can be
30 measured on a continuous scale using a computer-assisted method (e.g. Cumulus) (Byng et al., 1998) or assigned to categories by radiologists' visual inspection (e.g. BI-RADS) (Sak et al., 2015). Age- and body mass index-adjusted percent mammographic density is strongly associated with risk of breast cancer (Boyd et al., 2002). The issue of mammographically dense breasts has become important, especially in the United
35 States, where mammographically dense breasts are defined as BI-RADS categories C or D (Sickles and Bassett, 2013), which are the equivalent of having a percent

mammographic density greater than 50%. Over 40% of women in the United States have dense breasts, more so at young ages.

Mammography clinics in most states of the United States are now required by law to notify women if they have mammographically dense breasts. Women receiving a
5 dense breast notification are encouraged to discuss this and other breast cancer risk factors with their healthcare provider to decide if additional screening options are necessary. Unfortunately, most women are unaware of the other risk factors and most healthcare professionals are reluctant to pursue more aggressive screening modalities based on mammographic density alone.

10 The first major susceptibility genes for breast cancer (BRCA1 and BRCA2) were discovered over 20 years ago (Wendt and Margolin, 2019), and since then TP53, STK11, CD1 and PTEN have been identified. The approximately 1 in 600 women with mutations in BRCA1 or BRCA2 have, on average, a lifetime breast cancer risk of >50% (Kuchenbaecker et al., 2017), much greater than the population average risk of
15 about 10%. The rarity of these mutations means they have limited impact on population health.

A single-nucleotide polymorphism (SNP) is a nucleotide substitution that has an allele frequency of >1% in the population. Large collaborative studies have identified SNPs that are independently associated with breast cancer risk. These associations are
20 small, with the odds ratio per risk allele typically being 1.1 or less (Michailidou et al., 2017), and empirically appear to multiply. These susceptibility SNPs can be used to create a polygenic risk score (PRS) that can predict risk of disease.

Despite available tools, there is a need for improved comprehensive breast cancer risk assessment methods.

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SUMMARY OF THE INVENTION

The present inventors have developed a model to accurately predict breast cancer risk for unaffected women. This approach is of practical importance for both clinical and population health. Women at very high risk of breast cancer can be
30 identified and given more frequent or alternative modes of screening, and women at very low risk of breast cancer can be identified as candidates for less frequent screening, with a concomitant financial benefit to population-based screening programs.

In a first aspect, the present invention provides a computer-implemented method
35 for assessing the risk of a human female subject developing breast cancer, the method comprising:

determining a genetic risk score based on genetic data derived from a biological sample taken from the female subject;

determining a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;

5 determining a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;

determining a body mass index risk score based on the body mass index and menopause status of the subject;

10 calculating a risk modifier score, the risk modifier score being a function of the polygenetic risk score, mammographic density risk score, first-degree family history risk score, second-degree family history risk score and body mass index risk score;

calculating at least two cumulative risk scores of the female subject developing breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer

15 incidence value based on the subjects age and ethnicity, and

calculating the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.

In an embodiment, the genetic risk score is determined by $\ln(\text{PRS}) \times \beta_{\text{PRS}}$, where the PRS is the polygenic risk score that represents the female subject's genetic predisposition to breast cancer, and β_{PRS} is the natural logarithm of the relative risk associated with a one-unit increase in $\ln(\text{PRS})$.

20 In an embodiment, the genetic risk score is determined using at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 313, at least 350, at least 400, at least 450, at least 500, at least 550, at least 600, at least 650, at least 700, at least 750, at least 800, at least 825, at least 850, at least 3,820 or all of the polymorphism provided in one or more of Tables 8 to 18, or a polymorphism in linkage disequilibrium with one or more thereof.

In an embodiment, the genetic risk score is determined using the 313 polymorphism of Table 17.

30 In an embodiment, the genetic risk score is determined using the 3,820 polymorphisms of Table 18.

In an embodiment, the first-degree family history risk score (fh_risk_1) is based on the subjects age and the number and youngest age affected of the subjects first-degree relatives with invasive breast cancer., such as determined using Table 1.

35 In an embodiment, the first-degree family history risk score is $\ln(\text{fh_risk_1})$.

In an embodiment, the second-degree family history risk score (fh_risk_2) is based on the subjects age and the subject's number of second-degree relatives with invasive breast cancer, such as determined using Table 2.

In an embodiment, the second-degree family history risk score is $\ln(\text{fh_risk_2})$.

5 In an embodiment, the body mass index risk score is determined using $\text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}})$ if pre-menopausal, or $\text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}})$ if post-menopausal, where mean_{BMI} is the mean body mass index in the population in which the test is used, $\text{intercept}_{\text{PRE}}$ is the equation intercept for pre-menopausal women and $\text{intercept}_{\text{POST}}$ is the equation intercept for
10 post-menopausal women.

In an embodiment, the mammographic density risk score is determined using $(\sqrt{\text{percent_density}} - \sqrt{\text{mean}_{\text{DENS}}}) \times \beta_{\text{DENS}}$, where $\text{mean}_{\text{DENS}}$ is the mean percent density in the population in which the test is used, and β_{DENS} is the natural logarithm of the relative risk associated with a one-unit increase in the square root of percent
15 density.

In an embodiment, the risk modifier score (risk_mod1) is determined using:

$$\begin{aligned} \ln \text{risk1} &= \ln(\text{PRS}) \times \beta_{\text{PRS}} \\ &+ (\sqrt{\text{percent_density}} - \sqrt{\text{mean}_{\text{DENS}}}) \times \beta_{\text{DENS}} \\ &+ \ln(\text{fh_risk_1}) \\ 20 \quad &+ \ln(\text{fh_risk_2}) \\ &+ \text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}}) \text{ if pre-menopausal} \\ &+ \text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}}) \text{ if post-menopausal} \end{aligned}$$

then:

$$25 \quad \text{risk_mod1} = e^{\ln \text{risk1}}.$$

In an embodiment, the at least two cumulative risk scores are selected from:

$$\begin{aligned} \text{cumul1_b} &= 1 - e^{-\text{risk_mod1} \times \text{incid_b}} \\ \text{cumul1_b_N} &= 1 - e^{-\text{risk_mod1} \times \text{incid_b_N}} \\ 30 \quad \text{cumul1_full_life} &= 1 - e^{-\text{risk_mod1} \times \text{incid_full_life}} \end{aligned}$$

where:

N is the number of years of risk to calculate

incid_b = is the ethnicity-specific cumulative breast cancer incidence up to current age,

35 incid_bN5 = is the ethnicity-specific cumulative breast cancer incidence up to current age plus 5N years, and

incid_full_life is the ethnicity-specific cumulative breast cancer incidence up to 90 years.

In an embodiment, breast cancer risk score is determined using either of:

$$5 \quad brisk1_N = \frac{(cumul1_b_N - cumul1_b)}{(1 - cumul1_b)}$$

or

$$10 \quad brisk1_rem_life = \frac{(cumul1_full_life - cumul1_b)}{(1 - cumul1_b)}$$

In an embodiment, the mammographic density risk score is a BI-RADS category.

In an embodiment, the risk modifier score (*risk_mod2*) is determined using:

$$\begin{aligned} 15 \quad \lnrisk1 &= \ln(PRS) \times \beta_{PRS} \\ &+ X \text{ if BI-RADS category is A or B} \\ &+ Y \text{ if BI-RADS category is C or D} \\ &+ \ln(fh_risk_1) \\ &+ \ln(fh_risk_2) \\ 20 \quad &+ intercept_{PRE} + ((\ln(bmi/5) - \ln(mean_{BMI}/5)) \times \beta_{PRE}) \text{ if pre-menopausal} \\ &+ intercept_{POST} + ((\ln(bmi/5) - \ln(mean_{BMI}/5)) \times \beta_{POST}) \text{ if post-menopausal} \end{aligned}$$

wherein, X is between -0.05 and -0.25, or between -0.1 and -0.2 or is -0.15, and Y is between 0.14 and 0.34, or between 0.19 and 0.29, or is 0.24,

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then:

$$risk_mod2 = e^{\lnrisk2}.$$

In an embodiment, the at least two cumulative risk scores are selected from:

$$\begin{aligned} 30 \quad cumul2_b &= 1 - e^{-risk_mod2 \times incid_b} \\ cumul2_b_N &= 1 - e^{-risk_mod2 \times incid_b_N} \\ cumul2_full_life &= 1 - e^{-risk_mod2 \times incid_full_life} \end{aligned}$$

where:

35 N is the number of years of risk to calculate,

incid_b = is the ethnicity-specific cumulative breast cancer incidence up to current age,

incid_b_N5 = is the ethnicity-specific cumulative breast cancer incidence up to current age plus 5N years, and

5 incid_full_life is the ethnicity-specific cumulative breast cancer incidence up to 90 years (i.e. full-lifetime risk).

In an embodiment, the breast cancer risk score is determined using either of:

$$brisk2_N = \frac{(cumul2_b_N - cumul2_b)}{(1 - cumul2_b)}$$

10

or

$$brisk2_rem_life = \frac{(cumul2_full_life - cumul2_b)}{(1 - cumul2_b)}$$

15 In an embodiment, the method further comprises comparing the score to a pre-determined threshold.

In an embodiment, the method further comprises outputting the breast cancer risk score.

20 In second aspect, the present invention provides a computer-implemented method for assessing the risk of a human female subject developing breast cancer, the method comprising:

determining a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;

determining a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;

25 determining a body mass index risk score based on the body mass index and menopause status of the subject;

calculating a risk modifier score, the risk modifier score being a function of the mammographic density risk score, first-degree family history risk score, second-degree family history risk score and body mass index risk score;

30 calculating at least two cumulative risk scores of the female subject developing breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer incidence value based on the subjects age and ethnicity, and

calculating the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.

The embodiments above are also relevant to this method apart from the determining a genetic risk score. Thus,

$$\begin{aligned} \text{Inrisk1} &= (\text{sqrt}(\text{percent_density}) - \text{sqrt}(\text{meanDENS})) \times \beta_{\text{DENS}} \\ &+ \ln(\text{fh_risk_1}) \\ &+ \ln(\text{fh_risk_2}) \\ &+ \text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}}) \text{ if pre-menopausal} \\ &+ \text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}}) \text{ if post-menopausal,} \end{aligned}$$

10

or

$$\begin{aligned} \text{Inrisk1} &= X \text{ if BI-RADS category is A or B} \\ &+ Y \text{ if BI-RADS category is C or D} \\ &+ \ln(\text{fh_risk_1}) \\ &+ \ln(\text{fh_risk_2}) \\ &+ \text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}}) \text{ if pre-menopausal} \\ &+ \text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}}) \text{ if post-menopausal} \end{aligned}$$

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In a further aspect, the present invention provides a computer readable storage

medium storing executable code, wherein when a processor executes the code, the processor is caused to perform the method of the invention.

In another aspect, the present invention provides a device for assessing the risk of a human female subject developing breast cancer, the device comprising:

a processor; and

a memory device storing executable code, the memory being accessible to the processor;

wherein when caused to execute the executable code stored in the memory device, the processor is caused to:

determine a genetic risk score based on genetic data derived from a biological

sample taken from the female subject;

determine a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;

determine a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;

determine a body mass index risk score based on the body mass index and menopause status of the subject;

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calculate a risk modifier score, the risk modifier score being a function of the polygenetic risk score, mammographic density risk score, first-degree family history risk score, second-degree family history risk score and body mass index risk score

calculate at least two cumulative risk scores of the female subject developing
5 breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer incidence value based on the subjects age and ethnicity, and

calculate the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.

10 Embodiments of the first aspect are relevant to this aspect.

In another aspect, the present invention provides a device for assessing the risk of a human female subject developing breast cancer, the device comprising:

a processor; and

a memory device storing executable code, the memory being accessible to the
15 processor;

wherein when caused to execute the executable code stored in the memory device, the processor is caused to:

determine a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;

20 determine a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;

determine a body mass index risk score based on the body mass index and menopause status of the subject;

calculate a risk modifier score, the risk modifier score being a function of the
25 mammographic density risk score, first-degree family history risk score, second-degree family history risk score and body mass index risk score

calculate at least two cumulative risk scores of the female subject developing breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer
30 incidence value based on the subjects age and ethnicity, and

calculate the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.

Embodiments of the second aspect are relevant to this aspect.

In an embodiment, the device further comprises a display component, wherein
35 the processor is further caused to display the breast cancer risk score of the female subject for developing breast cancer on the display component.

In an embodiment, the device further comprises a communications module, wherein the processor is further caused to communicate the breast cancer risk score of the female subject for developing breast cancer to an external device via the communications module.

5 In an aspect, the present invention provides a method for assessing the risk of a human female subject for developing breast cancer comprising:

i) determining the age, ethnicity, family history of breast cancer incorporating number of first-degree relatives who have had breast cancer, the age of the youngest first-degree relative at diagnosis with breast cancer, the number of second-degree
10 relatives who have had breast cancer, country of residence, mammographic breast density, body mass index (BMI) and menopausal status,

ii) determining the genotype of the human female subject at 50 or more polymorphic loci associated with a risk of a human female subject for developing breast cancer,

15 iii) determining a breast cancer risk score based on i) and ii).

In an aspect, the present invention provides a method for assessing the risk of a human female subject for developing breast cancer comprising:

i) determining the age, ethnicity, family history of breast cancer incorporating number of first-degree relatives who have had breast cancer, the age of the youngest
20 first-degree relative at diagnosis with breast cancer, the number of second-degree relatives who have had breast cancer, mammographic breast density, body mass index (BMI) and menopausal status,

ii) determining the genotype of the human female subject at 50 or more polymorphic loci associated with a risk of a human female subject for developing
25 breast cancer,

iii) determining a breast cancer risk score based on i) and ii).

Embodiments of the first aspect are relevant to the above two aspects.

In an aspect, the present invention provides a method for assessing the risk of a human female subject for developing breast cancer comprising:

30 i) determining the age, ethnicity, family history of breast cancer incorporating number of first-degree relatives who have had breast cancer, the age of the youngest first-degree relative at diagnosis with breast cancer, the number of second-degree relatives who have had breast cancer, country of residence, mammographic breast density, body mass index (BMI) and menopausal status,

35 ii) determining a breast cancer risk score based on i).

In an aspect, the present invention provides a method for assessing the risk of a human female subject for developing breast cancer comprising:

- i) determining the age, ethnicity, family history of breast cancer incorporating number of first-degree relatives who have had breast cancer, the age of the youngest
5 first-degree relative at diagnosis with breast cancer, the number of second-degree relatives who have had breast cancer, mammographic breast density, body mass index (BMI) and menopausal status,
- ii) determining a breast cancer risk score based on i).

Embodiments of the second aspect are relevant to the above two aspects.

- 10 In an embodiment, the results of the assessment indicate that the female should be subjected to more frequent screening and/or prophylactic anti-breast cancer therapy.

In an embodiment, if it is determined that the subject has a risk of developing breast cancer, the subject is more likely to be responsive to oestrogen inhibition therapy than non-responsive.

- 15 In an embodiment, the breast cancer is oestrogen receptor positive or oestrogen receptor negative.

Also provided is a method for determining the need for routine diagnostic testing of a human female subject for breast cancer comprising assessing the risk of the subject for developing breast cancer using a method of the invention.

- 20 In an embodiment, an risk score greater than about 20% lifetime risk indicates that the subject should be enrolled in a screening breast MRI and mammography program.

- In an aspect, the present invention provides a method of screening for breast cancer in a human female subject, the method comprising assessing the risk of the
25 subject for developing breast cancer using a method of the invention, and routinely screening for breast cancer in the subject if they are assessed as having a risk for developing breast cancer.

- In an aspect, the present invention provides a method for determining the need of a human female subject for prophylactic anti-breast cancer therapy comprising
30 assessing the risk of the subject for developing breast cancer using a method of the invention.

In an embodiment, an risk score greater than about 1.66% 5-year risk indicates that oestrogen receptor antagonist therapy should be offered to the subject.

- In an aspect, the present invention provides a method for preventing breast
35 cancer in a human female subject, the method comprising assessing the risk of the subject for developing breast cancer using a method of the invention, and administering

an anti-breast cancer therapy to the subject if they are assessed as having a risk for developing breast cancer.

In an embodiment, the therapy inhibits oestrogen.

5 In an aspect, the present invention provides an anti-breast cancer therapy for use in preventing breast cancer in a human female subject at risk thereof, wherein the subject is assessed as having a risk for developing breast cancer using a method of the invention.

10 In an aspect, the present invention provides a method for stratifying a group of human female subjects for a clinical trial of a candidate therapy, the method comprising assessing the individual risk of the subjects for developing breast cancer using a method of the invention, and using the results of the assessment to select subjects more likely to be responsive to the therapy.

Any embodiment herein shall be taken to apply *mutatis mutandis* to any other embodiment unless specifically stated otherwise.

15 The present invention is not to be limited in scope by the specific embodiments described herein, which are intended for the purpose of exemplification only. Functionally equivalent products, compositions and methods are clearly within the scope of the invention, as described herein.

20 Throughout this specification, unless specifically stated otherwise or the context requires otherwise, reference to a single step, composition of matter, group of steps or group of compositions of matter shall be taken to encompass one and a plurality (i.e. one or more) of those steps, compositions of matter, groups of steps or group of compositions of matter.

The invention is hereinafter described by way of the following non-limiting
25 Examples and with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE ACCOMPANYING DRAWINGS

Figure 1. Calibration plots of expected versus observed odds ratio (OR) of the respective risk models.

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DETAILED DESCRIPTION OF THE INVENTION

General Techniques and Definitions

Unless specifically defined otherwise, all technical and scientific terms used herein shall be taken to have the same meaning as commonly understood by one of
35 ordinary skill in the art (e.g., oncology, breast cancer analysis, molecular genetics, risk assessment and clinical studies).

Unless otherwise indicated, the molecular, and immunological techniques utilized in the present disclosure are standard procedures, well known to those skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular Cloning, John Wiley and Sons (1984), J. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present), Ed Harlow and David Lane (editors) Antibodies: A Laboratory Manual, Cold Spring Harbour Laboratory, (1988), and J.E. Coligan et al. (editors) Current Protocols in Immunology, John Wiley & Sons (including all updates until present).

It is to be understood that this disclosure is not limited to particular embodiments, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting. As used in this specification and the appended claims, terms in the singular and the singular forms "a," "an" and "the," for example, optionally include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "a probe" optionally includes a plurality of probe molecules; similarly, depending on the context, use of the term "a nucleic acid" optionally includes, as a practical matter, many copies of that nucleic acid molecule.

As used herein, the term "about", unless stated to the contrary, refers to +/- 10%, more preferably +/- 5%, more preferably +/- 1%, of the designated value.

The methods of the present disclosure can be used to assess risk of a human female subject developing breast cancer. As used herein, the term "breast cancer" encompasses any type of breast cancer that can develop in a female subject. For example, the breast cancer may be characterised as Luminal A (ER+ and/or PR+, HER2-, low Ki67), Luminal B (ER+ and/or PR+, HER2+ (or HER2- with high Ki67), Triple negative/basal-like (ER-, PR-, HER2-) or HER2 type (ER-, PR-, HER2+). In another example, the breast cancer may be resistant to therapy or therapies such as alkylating agents, platinum agents, taxanes, vinca agents, anti-estrogen drugs, aromatase inhibitors, ovarian suppression agents, endocrine/hormonal agents, bisphosphonate therapy agents or targeted biological therapy agents. As used herein, "breast cancer" also encompasses a phenotype that displays a predisposition towards developing breast cancer in an individual. A phenotype that displays a predisposition

for breast cancer, can, for example, show a higher likelihood that the cancer will develop in an individual with the phenotype than in members of a relevant general population under a given set of environmental conditions (diet, physical activity regime, geographic location, etc.).

5 As used herein, "biological sample" refers to any sample comprising nucleic acids, especially DNA, from or derived from a human patient, e.g., bodily fluids (blood, saliva, urine etc.), biopsy, tissue, and/or waste from the patient. Thus, tissue biopsies, stool, sputum, saliva, blood, lymph, or the like can easily be screened for polymorphisms, as can essentially any tissue of interest that contains the appropriate
10 nucleic acids. In one embodiment, the biological sample is a cheek cell sample. These samples are typically taken, following informed consent, from a patient by standard medical laboratory methods. The sample may be in a form taken directly from the patient, or may be at least partially processed (purified) to remove at least some non-nucleic acid material.

15 A "polymorphism" is a locus that is variable; that is, within a population, the nucleotide sequence at a polymorphism has more than one version or allele. One example of a polymorphism is a "single nucleotide polymorphism", which is a polymorphism at a single nucleotide position in a genome (the nucleotide at the specified position varies between individuals or populations). Other examples include a
20 deletion or insertion of one or more base pairs at the polymorphism locus.

As used herein, the term "SNP" or "single nucleotide polymorphism" refers to a genetic variation between individuals; e.g., a single nitrogenous base position in the DNA of organisms that is variable. As used herein, "SNPs" is the plural of SNP. Of course, when one refers to DNA herein, such reference may include derivatives of the
25 DNA such as amplicons, RNA transcripts thereof, etc.

The term "allele" refers to one of two or more different nucleotide sequences that occur or are encoded at a specific locus, or two or more different polypeptide sequences encoded by such a locus. For example, a first allele can occur on one chromosome, while a second allele occurs on a second homologous chromosome, e.g.,
30 as occurs for different chromosomes of a heterozygous individual, or between different homozygous or heterozygous individuals in a population. An allele "positively" correlates with a trait when it is linked to it and when presence of the allele is an indicator that the trait or trait form will occur in an individual comprising the allele. An allele "negatively" correlates with a trait when it is linked to it and when presence of
35 the allele is an indicator that a trait or trait form will not occur in an individual comprising the allele.

A marker polymorphism or allele is "correlated" or "associated" with a specified phenotype (breast cancer susceptibility, etc.) when it can be statistically linked (positively or negatively) to the phenotype. Methods for determining whether a polymorphism or allele is statistically linked are known to those in the art. That is, the specified polymorphism occurs more commonly in a case population (e.g., breast cancer patients) than in a control population (e.g., individuals that do not have breast cancer). This correlation is often inferred as being causal in nature, but it need not be, simple genetic linkage to (association with) a locus for a trait that underlies the phenotype is sufficient for correlation/association to occur.

- 10 The phrase "linkage disequilibrium" (LD) is used to describe the statistical correlation between two neighbouring polymorphic genotypes. Typically, LD refers to the correlation between the alleles of a random gamete at the two loci, assuming Hardy-Weinberg equilibrium (statistical independence) between gametes. LD is quantified with either Lewontin's parameter of association (D') or with Pearson correlation coefficient (r) (Devlin and Risch, 1995). Two loci with a LD value of 1 are said to be in complete LD. At the other extreme, two loci with a LD value of 0 are termed to be in linkage equilibrium. Linkage disequilibrium is calculated following the application of the expectation maximization algorithm (EM) for the estimation of haplotype frequencies (Slatkin and Excoffier, 1996). LD values according to the present disclosure for neighbouring genotypes/loci are selected above 0.1, preferably, above 0.2, more preferably above 0.5, more preferably, above 0.6, still more preferably, above 0.7, preferably, above 0.8, more preferably above 0.9, ideally about 1.0.

- Another way one of skill in the art can readily identify polymorphisms in linkage disequilibrium with the polymorphisms of the present disclosure is determining the LOD score for two loci. LOD stands for "logarithm of the odds", a statistical estimate of whether two genes, or a gene and a disease gene, are likely to be located near each other on a chromosome and are therefore likely to be inherited. A LOD score of between about 2 - 3 or higher is generally understood to mean that two genes are located close to each other on the chromosome. The present inventors have found that many of the polymorphisms in linkage disequilibrium with the polymorphisms of the present disclosure have a LOD score of between about 2 – 50. Accordingly, in an embodiment, LOD values according to the present disclosure for neighbouring genotypes/loci are selected at least above 2, at least above 3, at least above 4, at least above 5, at least above 6, at least above 7, at least above 8, at least above 9, at least above 10, at least above 20 at least above 30, at least above 40, at least above 50.

In another embodiment, polymorphisms in linkage disequilibrium with the polymorphisms of the present disclosure can have a specified genetic recombination distance of less than or equal to about 20 centimorgan (cM) or less. For example, 15 cM or less, 10 cM or less, 9 cM or less, 8 cM or less, 7 cM or less, 6 cM or less, 5 cM or less, 4 cM or less, 3 cM or less, 2 cM or less, 1 cM or less, 0.75 cM or less, 0.5 cM or less, 0.25 cM or less, or 0.1 cM or less. For example, two linked loci within a single chromosome segment can undergo recombination during meiosis with each other at a frequency of less than or equal to about 20%, about 19%, about 18%, about 17%, about 16%, about 15%, about 14%, about 13%, about 12%, about 11%, about 10%, about 9%, about 8%, about 7%, about 6%, about 5%, about 4%, about 3%, about 2%, about 1%, about 0.75%, about 0.5%, about 0.25%, or about 0.1% or less.

In another embodiment, polymorphisms in linkage disequilibrium with the polymorphisms of the present disclosure are within at least 100 kb (which correlates in humans to about 0.1 cM, depending on local recombination rate), at least 50 kb, at least 20 kb or less of each other.

For example, one approach for the identification of surrogate markers for a particular polymorphism involves a simple strategy that presumes that polymorphisms surrounding the target polymorphism are in linkage disequilibrium and can therefore provide information about disease susceptibility. Thus, as described herein, surrogate markers can therefore be identified from publicly available databases, such as HAPMAP, by searching for polymorphisms fulfilling certain criteria which have been found in the scientific community to be suitable for the selection of surrogate marker candidates.

"Allele frequency" refers to the frequency (proportion or percentage) at which an allele is present at a locus within an individual, within a line or within a population of lines. For example, for an allele "A," diploid individuals of genotype "AA", "Aa" or "aa" have allele frequencies of 1.0, 0.5, or 0.0, respectively. One can estimate the allele frequency within a line or population (e.g., cases or controls) by averaging the allele frequencies of a sample of individuals from that line or population. Similarly, one can calculate the allele frequency within a population of lines by averaging the allele frequencies of lines that make up the population.

In an embodiment, the term "allele frequency" is used to define the minor allele frequency (MAF) or effect allele frequency. MAF refers to the frequency at which the least common allele occurs in a given population. The effect allele is that linked to breast cancer risk.

An individual is "homozygous" if the individual has only one type of allele at a given locus (e.g., a diploid individual has a copy of the same allele at a locus for each of two homologous chromosomes). An individual is "heterozygous" if more than one allele type is present at a given locus (e.g., a diploid individual with one copy each of two different alleles). The term "homogeneity" indicates that members of a group have the same genotype at one or more specific loci. In contrast, the term "heterogeneity" is used to indicate that individuals within the group differ in genotype at one or more specific loci.

A "locus" is a chromosomal position or region. For example, a polymorphic locus is a position or region where a polymorphic nucleic acid, trait determinant, gene or marker is located. In a further example, a "gene locus" is a specific chromosome location (region) in the genome of a species where a specific gene can be found.

A "marker", "molecular marker" or "marker nucleic acid" refers to a nucleotide sequence or encoded product thereof (e.g., a protein) used as a point of reference when identifying a locus or a linked locus. A marker can be derived from genomic nucleotide sequence or from expressed nucleotide sequences (e.g., from an RNA, nRNA, mRNA, a cDNA, etc.), or from an encoded polypeptide. The term also refers to nucleic acid sequences complementary to or flanking the marker sequences, such as nucleic acids used as probes or primer pairs capable of amplifying the marker sequence. A "marker probe" is a nucleic acid sequence or molecule that can be used to identify the presence of a marker locus, e.g., a nucleic acid probe that is complementary to a marker locus sequence. Nucleic acids are "complementary" when they specifically hybridize in solution, e.g., according to Watson-Crick base pairing rules. A "marker locus" is a locus that can be used to track the presence of a second linked locus, e.g., a linked or correlated locus that encodes or contributes to the population variation of a phenotypic trait. For example, a marker locus can be used to monitor segregation of alleles at a locus, such as a QTL, that are genetically or physically linked to the marker locus. Thus, a "marker allele," alternatively an "allele of a marker locus" is one of a plurality of polymorphic nucleotide sequences found at a marker locus in a population that is polymorphic for the marker locus. Each of the identified markers is expected to be in close physical and genetic proximity (resulting in physical and/or genetic linkage) to a genetic element, e.g., a QTL, that contributes to the relevant phenotype. Markers corresponding to genetic polymorphisms between members of a population can be detected by methods well-established in the art. These include, e.g., DNA sequencing, PCR-based sequence specific amplification methods, detection of restriction fragment length polymorphisms (RFLP), detection of isozyme markers, detection of allele

specific hybridization (ASH), detection of single nucleotide extension, detection of amplified variable sequences of the genome, detection of self-sustained sequence replication, detection of simple sequence repeats (SSRs), detection of single nucleotide polymorphisms (SNPs), or detection of amplified fragment length polymorphisms (AFLPs).

The term "amplifying" in the context of nucleic acid amplification is any process whereby additional copies of a selected nucleic acid (or a transcribed form thereof) are produced. Typical amplification methods include various polymerase based replication methods, including the polymerase chain reaction (PCR), ligase mediated methods such as the ligase chain reaction (LCR) and RNA polymerase based amplification (e.g., by transcription) methods.

An "amplicon" is an amplified nucleic acid, e.g., a nucleic acid that is produced by amplifying a template nucleic acid by any available amplification method (e.g., PCR, LCR, transcription, or the like).

A "gene" is one or more sequence(s) of nucleotides in a genome that together encode one or more expressed molecules, e.g., an RNA, or polypeptide. The gene can include coding sequences that are transcribed into RNA which may then be translated into a polypeptide sequence, and can include associated structural or regulatory sequences that aid in replication or expression of the gene.

A "genotype" is the genetic constitution of an individual (or group of individuals) at one or more genetic loci. Genotype is defined by the allele(s) of one or more known loci of the individual, typically, the compilation of alleles inherited from its parents.

A "haplotype" is the genotype of an individual at a plurality of genetic loci on a single DNA strand. Typically, the genetic loci described by a haplotype are physically and genetically linked, i.e., on the same chromosome strand.

A "set" of markers, probes or primers refers to a collection or group of markers probes, primers, or the data derived therefrom, used for a common purpose, e.g., identifying an individual with a specified genotype (e.g., risk of developing breast cancer). Frequently, data corresponding to the markers, probes or primers, or derived from their use, is stored in an electronic medium. While each of the members of a set possess utility with respect to the specified purpose, individual markers selected from the set as well as subsets including some, but not all of the markers, are also effective in achieving the specified purpose.

The polymorphisms and genes, and corresponding marker probes, amplicons or primers described above can be embodied in any system herein, either in the form of

physical nucleic acids, or in the form of system instructions that include sequence information for the nucleic acids. For example, the system can include primers or amplicons corresponding to (or that amplify a portion of) a gene or polymorphism described herein. As in the methods above, the set of marker probes or primers
5 optionally detects a plurality of polymorphisms in a plurality of said genes or genetic loci. Thus, for example, the set of marker probes or primers detects at least one polymorphism in each of these polymorphisms or genes, or any other polymorphism, gene or locus defined herein. Any such probe or primer can include a nucleotide sequence of any such polymorphism or gene, or a complementary nucleic acid thereof,
10 or a transcribed product thereof (e.g., a nRNA or mRNA form produced from a genomic sequence, e.g., by transcription or splicing).

As used herein, “risk assessment” refers to a process by which a subject’s risk of developing breast cancer can be assessed. A risk assessment will typically involve obtaining information relevant to the subject’s risk of developing breast cancer,
15 assessing that information, and quantifying the subject’s risk of developing breast cancer, for example, by producing a risk score.

As used herein, “receiver operating characteristic curves” (ROC) refer to a graphical plot of the sensitivity vs. (1 – specificity) for a binary classifier system as its discrimination threshold is varied. The ROC can also be represented equivalently by
20 plotting the fraction of true positives (TPR = true positive rate) vs. the fraction of false positives (FPR = false positive rate). Also known as a Relative Operating Characteristic curve, because it is a comparison of two operating characteristics (TPR & FPR) as the criterion changes. ROC analysis provides tools to select possibly optimal models and to discard suboptimal ones independently from (and prior to
25 specifying) the cost context or the class distribution. Methods of using in the context of the disclosure will be clear to those skilled in the art.

As used herein, the terms “routinely screening for breast cancer” and “more frequent screening” are relative terms, and are based on a comparison to the level of screening recommended to a subject who has no identified risk of developing breast
30 cancer.

Clinical Risk Assessments

The present invention comprises, preferably consists of, the analysis of the following clinical factors; age, ethnicity, family history of breast cancer (incorporating
35 number of first-degree relatives who have had breast cancer, the youngest age of first-degree relative at diagnosis with breast cancer, the number of second degree relatives

who have had breast cancer), country of residence, mammographic breast density (for example as a BI-RADS score or percentage breast density), body mass index (BMI) and menopausal status.

Clinical information can be self-reported by the female subject. For example,
5 the subject may complete a questionnaire designed to obtain clinical information regarding the above factors. In another example, subject to obtaining informed consent from the female subject, clinical information can be obtained from medical records by interrogating a relevant database comprising the clinical information.

In an embodiment, the clinical risk assessment procedure provides an estimate
10 of the risk of the human female subject developing breast cancer during the next N-year period (for example 5-year risk).

In another embodiment, the clinical risk assessment procedure provides an estimate of the risk of the human female subject developing breast cancer from her current age up to age 90 years (i.e. remaining lifetime risk).

15 In another embodiment, performing the clinical risk assessment uses a model which calculates the absolute risk of developing breast cancer. For example, the absolute risk of developing breast cancer can be calculated using cancer incidence rates.

In an embodiment, the clinical risk assessment provides a 5-year absolute risk of
20 developing breast cancer. In another embodiment, the clinical risk assessment provides a 10-year absolute risk of developing breast cancer.

“Family history of breast cancer” is used in the context of the present disclosure to refer to the history of breast cancer amongst the female subject’s first and/or second degree relatives. For example, “family history of breast cancer” can be used to refer to
25 the history of breast cancer amongst only first-degree relatives. Put another way, the first clinical risk assessment procedure can take into consideration the female subjects family history of breast cancer amongst first-degree relatives. In the context of the present disclosure, a “first-degree relative” is a family member who shares about 50 percent of their genes with the female subject. Examples of first-degree relatives
30 include parents, offspring, and full-siblings. A “second degree relative” is a family member who shares about 25 percent of their genes with the female subject. Examples of second-degree relatives include uncles, aunts, nephews, nieces, grandparents, grandchildren, and half-siblings.

In another embodiment, the female subject’s family history of breast cancer is
35 based on the female subject’s first degree-relatives and second degree relatives.

In an embodiment, the subjects first-degree relative risk (fh_risk_1) is based on age and the number and age of first-degree relatives with invasive breast cancer. In an embodiment, fh_risk_1 is determined as outlined in Table 1.

5 **Table 1.** Look up table for determining fh_risk_1.

Number of affected first-degree relatives	Age (yrs)	Age of affected first-degree relative (yrs)	fh_risk_1
0	All ages	N/A	0.94
1	<40	<40	4.90
1	<40	40–49	2.90
1	<40	50–59	2.60
1	<40	≥60	1.90
1	40–49	<40	2.94
1	40–49	40–49	2.34
1	40–49	50–59	2.14
1	40–49	≥60	1.64
1	50–59	<40	2.05
1	50–59	40–49	1.85
1	50–59	50–59	1.55
1	50–59	≥60	1.55
1	≥60	<40	1.37
1	≥60	40–49	1.37
1	≥60	50–59	1.37
1	≥60	≥60	1.37
1	<35	Unknown	2.84
1	35–39	Unknown	2.43
1	40–44	Unknown	2.00
1	45–49	Unknown	1.94
1	50–54	Unknown	1.84
1	55–59	Unknown	1.74
1	60–64	Unknown	1.55
1	65–69	Unknown	1.46
1	≥70	Unknown	1.37
≥2	<50	At least one <40	13.50
≥2	<50	Both ≥40	7.80
≥2	≥50	At least one <40	3.90
≥2	≥50	Both ≥40	2.60
≥2	<45	Unknown	5.00
≥2	45–54	Unknown	3.50
≥2	55–64	Unknown	2.70
≥2	≥65	Unknown	2.30

In an embodiment, the subjects second-degree relative risk (fh_risk_2) is based on age and the number and age of first-degree relatives with invasive breast cancer. In an embodiment, fh_risk_1 is determined as outlined in Table 2.

Table 2. Look up table for determining fh_risk_2.

Number of affected second-degree relatives	Age (years)	fh_risk_2
0	All ages	0.97
1	<40	1.7
1	40–49	1.4
1	50–59	1.3
1	≥60	1.2
≥2	<55	2.1
≥2	≥55	1.6

5 As the skilled person would appreciate, the fh_risk_1 and fh_risk_2 values in Table 1 and 2 can be modified without necessarily affecting the performance of the method. Thus, in an embodiment, one or more or all of the fh_risk_1 and fh_risk_2 values can be varied +/- 10%, more preferably +/- 5%, more preferably +/- 1%, of the designated value on a relative basis.

10 As used herein, “based on” means that values are assigned to, for example, the subject’s age and family history of breast cancer, but then any suitable calculations are conducted to determine clinical risk.

Breast density can be measured using any method known in the art. For example, breast density can be estimated based on radiographic appearance of the breast on a mammogram. As will be known to those skilled in the art, dense breast tissue appears light on a mammogram and comprises epithelial and stromal tissue whereas non-dense tissue, comprising fat, appears dark. Thus, in some embodiments, breast density is assessed using a mammogram.

15 In an embodiment, breast density is assessed using higher pixel brightness thresholds.

In an embodiment, breast density is assessed using percent dense area. Percent dense area is calculated by dividing the area of dense breast tissue by the total breast area identified in a breast image, for example in a mammogram.

In an embodiment, breast density is assessed using Cumulus percent dense area.

25 In another embodiment breast density is assessed using Cumulus percent dense area and non-dense area. “Cumulus” is a software package for semi-automated measurement of dense area from mammograms and is described in (Byng et al., 1994).

In an embodiment, breast density is assessed using a BI-RADS score. “BI-RADS” is an acronym for Breast Imaging-Reporting and Data System, which is a system of standardized numerical codes typically assigned by a radiologist after interpreting a mammogram and is used to communicate a subject’s risk of developing breast cancer. A BI-RADS score can also be obtained using automated computerised methods. Typical BI-RADS Assessment Categories (BI-RADS Atlas) are:

- 0: Incomplete;
- 1: Negative;
- 2: Benign;
- 3: Probably benign;
- 4: Suspicious;
- 5: Highly suggestive of malignancy; and
- 6: Known biopsy – proven malignancy.

In an embodiment, BI-RADS is scored as an A, B, C or D using the following criteria as described by Sickles and Bassett (2013):

A: Almost entirely fatty indicates that the breasts are almost entirely composed of fat. About 1 in 10 women has this result.

B: Scattered areas of fibroglandular density indicates there are some scattered areas of density, but the majority of the breast tissue is nondense. About 4 in 10 women have this result.

C: Heterogeneously dense indicates that there are some areas of nondense tissue, but that the majority of the breast tissue is dense. About 4 in 10 women have this result.

D: Extremely dense indicates that nearly all of the breast tissue is dense. About 1 in 10 women has this result.

Body mass index (BMI) is a value derived from the mass (weight) and height of a person. The BMI is defined as the body mass divided by the square of the body height, and is expressed in units of kg/m^2 , resulting from mass in kilograms and height in metres.

Menopausal status is typically determined if it has been over a year since the subjects last period. In an embodiment, the subject is scored as a 1 if it has been over a year since the subjects last period and otherwise scored as 0.

In an embodiment, ethnicity is taken into consideration by using ethnicity-specific population-based breast cancer incidence data. This is derived from publically available country- and ethnicity-specific population-based breast cancer incidence data. For example, in Tables 3 to 7, incid is the breast cancer incidence per 100,000 women

- per year at a given age, incid_b is the sum of the breast cancer incidence from birth to the given age; incid_b_N is the sum of the breast cancer incidence from birth to the given age plus N years and incid_full_life is the sum of the breast cancer incidence from birth to age 90 years, for different populations and ethnicities. Incidence data can
- 5 be obtained from the relevant National agencies, for example, the Office of National Statistics in England (www.ons.gov.uk), the Surveillance, Epidemiology, and End Results Program in the United States (seer.cancer.gov) and the Australian Institute of Health and Welfare in Australia (www.aihw.gov.au).

- 10 **Table 3.** Look up table for Caucasian United Kingdom specific population-based breast cancer incidence data.

Age	Incidence	incid	incid_b	incid_b_5	incid_b_10	incid_full_life
0	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
1	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
2	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
3	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
4	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
5	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
6	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
7	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
8	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
9	0.0	0.000000	0.000000	0.000000	0.000000	0.172625
10	0.0	0.000000	0.000000	0.000000	0.000015	0.172625
11	0.0	0.000000	0.000000	0.000000	0.000030	0.172625
12	0.0	0.000000	0.000000	0.000000	0.000045	0.172625
13	0.0	0.000000	0.000000	0.000000	0.000060	0.172625
14	0.0	0.000000	0.000000	0.000000	0.000075	0.172625
15	0.0	0.000000	0.000000	0.000015	0.000181	0.172625
16	0.0	0.000000	0.000000	0.000030	0.000287	0.172625
17	0.0	0.000000	0.000000	0.000045	0.000393	0.172625
18	0.0	0.000000	0.000000	0.000060	0.000499	0.172625
19	0.0	0.000000	0.000000	0.000075	0.000605	0.172625
20	1.5	0.000015	0.000015	0.000181	0.000924	0.172625
21	1.5	0.000015	0.000030	0.000287	0.001243	0.172625
22	1.5	0.000015	0.000045	0.000393	0.001562	0.172625
23	1.5	0.000015	0.000060	0.000499	0.001881	0.172625
24	1.5	0.000015	0.000075	0.000605	0.002200	0.172625
25	10.6	0.000106	0.000181	0.000924	0.002868	0.172625
26	10.6	0.000106	0.000287	0.001243	0.003536	0.172625

27	10.6	0.000106	0.000393	0.001562	0.004204	0.172625
28	10.6	0.000106	0.000499	0.001881	0.004872	0.172625
29	10.6	0.000106	0.000605	0.002200	0.005540	0.172625
30	31.9	0.000319	0.000924	0.002868	0.006794	0.172625
31	31.9	0.000319	0.001243	0.003536	0.008048	0.172625
32	31.9	0.000319	0.001562	0.004204	0.009302	0.172625
33	31.9	0.000319	0.001881	0.004872	0.010556	0.172625
34	31.9	0.000319	0.002200	0.005540	0.011810	0.172625
35	66.8	0.000668	0.002868	0.006794	0.013972	0.172625
36	66.8	0.000668	0.003536	0.008048	0.016134	0.172625
37	66.8	0.000668	0.004204	0.009302	0.018296	0.172625
38	66.8	0.000668	0.004872	0.010556	0.020458	0.172625
39	66.8	0.000668	0.005540	0.011810	0.022620	0.172625
40	125.4	0.001254	0.006794	0.013972	0.025364	0.172625
41	125.4	0.001254	0.008048	0.016134	0.028108	0.172625
42	125.4	0.001254	0.009302	0.018296	0.030852	0.172625
43	125.4	0.001254	0.010556	0.020458	0.033596	0.172625
44	125.4	0.001254	0.011810	0.022620	0.036340	0.172625
45	216.2	0.002162	0.013972	0.025364	0.039212	0.172625
46	216.2	0.002162	0.016134	0.028108	0.042084	0.172625
47	216.2	0.002162	0.018296	0.030852	0.044956	0.172625
48	216.2	0.002162	0.020458	0.033596	0.047828	0.172625
49	216.2	0.002162	0.022620	0.036340	0.050700	0.172625
50	274.4	0.002744	0.025364	0.039212	0.053966	0.172625
51	274.4	0.002744	0.028108	0.042084	0.057232	0.172625
52	274.4	0.002744	0.030852	0.044956	0.060498	0.172625
53	274.4	0.002744	0.033596	0.047828	0.063764	0.172625
54	274.4	0.002744	0.036340	0.050700	0.067030	0.172625
55	287.2	0.002872	0.039212	0.053966	0.071126	0.172625
56	287.2	0.002872	0.042084	0.057232	0.075222	0.172625
57	287.2	0.002872	0.044956	0.060498	0.079318	0.172625
58	287.2	0.002872	0.047828	0.063764	0.083414	0.172625
59	287.2	0.002872	0.050700	0.067030	0.087510	0.172625
60	326.6	0.003266	0.053966	0.071126	0.091148	0.172625
61	326.6	0.003266	0.057232	0.075222	0.094786	0.172625
62	326.6	0.003266	0.060498	0.079318	0.098424	0.172625
63	326.6	0.003266	0.063764	0.083414	0.102062	0.172625
64	326.6	0.003266	0.067030	0.087510	0.105700	0.172625
65	409.6	0.004096	0.071126	0.091148	0.109556	0.172625
66	409.6	0.004096	0.075222	0.094786	0.113412	0.172625
67	409.6	0.004096	0.079318	0.098424	0.117268	0.172625
68	409.6	0.004096	0.083414	0.102062	0.121124	0.172625

69	409.6	0.004096	0.087510	0.105700	0.124980	0.172625
70	363.8	0.003638	0.091148	0.109556	0.129197	0.172625
71	363.8	0.003638	0.094786	0.113412	0.133414	0.172625
72	363.8	0.003638	0.098424	0.117268	0.137631	0.172625
73	363.8	0.003638	0.102062	0.121124	0.141848	0.172625
74	363.8	0.003638	0.105700	0.124980	0.146065	0.172625
75	385.6	0.003856	0.109556	0.129197	0.150475	0.172625
76	385.6	0.003856	0.113412	0.133414	0.154885	0.172625
77	385.6	0.003856	0.117268	0.137631	0.159295	0.172625
78	385.6	0.003856	0.121124	0.141848	0.163705	0.172625
79	385.6	0.003856	0.124980	0.146065	0.168115	0.172625
80	421.7	0.004217	0.129197	0.150475	0.172625	0.172625
81	421.7	0.004217	0.133414	0.154885		0.172625
82	421.7	0.004217	0.137631	0.159295		0.172625
83	421.7	0.004217	0.141848	0.163705		0.172625
84	421.7	0.004217	0.146065	0.168115		0.172625
85	441.0	0.004410	0.150475	0.172625		0.172625
86	441.0	0.004410				0.172625
87	441.0	0.004410				0.172625
88	441.0	0.004410				0.172625
89	441.0	0.004410				0.172625
90	451.0	0.004510				0.172625

Table 4. Look up table for Caucasian Australian specific population-based breast cancer incidence data.

Age	Incidence	incid	incid_b	incid_b_5	incid_b_10	incid_full_life
0	0.0	0.000000	0.000000	0.000000	0.000000	0.159749
1	0.0	0.000000	0.000000	0.000000	0.000000	0.159749
2	0.0	0.000000	0.000000	0.000000	0.000000	0.159749
3	0.0	0.000000	0.000000	0.000000	0.000000	0.159749
4	0.0	0.000000	0.000000	0.000000	0.000000	0.159749
5	0.0	0.000000	0.000000	0.000000	0.000003	0.159749
6	0.0	0.000000	0.000000	0.000000	0.000006	0.159749
7	0.0	0.000000	0.000000	0.000000	0.000010	0.159749
8	0.0	0.000000	0.000000	0.000000	0.000013	0.159749
9	0.0	0.000000	0.000000	0.000000	0.000016	0.159749
10	0.0	0.000000	0.000000	0.000003	0.000026	0.159749
11	0.0	0.000000	0.000000	0.000006	0.000035	0.159749
12	0.0	0.000000	0.000000	0.000010	0.000044	0.159749
13	0.0	0.000000	0.000000	0.000013	0.000054	0.159749

14	0.0	0.000000	0.000000	0.000016	0.000063	0.159749
15	0.3	0.000003	0.000003	0.000026	0.000154	0.159749
16	0.3	0.000003	0.000006	0.000035	0.000244	0.159749
17	0.3	0.000003	0.000010	0.000044	0.000335	0.159749
18	0.3	0.000003	0.000013	0.000054	0.000425	0.159749
19	0.3	0.000003	0.000016	0.000063	0.000516	0.159749
20	0.9	0.000009	0.000026	0.000154	0.000772	0.159749
21	0.9	0.000009	0.000035	0.000244	0.001027	0.159749
22	0.9	0.000009	0.000044	0.000335	0.001283	0.159749
23	0.9	0.000009	0.000054	0.000425	0.001539	0.159749
24	0.9	0.000009	0.000063	0.000516	0.001795	0.159749
25	9.1	0.000091	0.000154	0.000772	0.002395	0.159749
26	9.1	0.000091	0.000244	0.001027	0.002994	0.159749
27	9.1	0.000091	0.000335	0.001283	0.003594	0.159749
28	9.1	0.000091	0.000425	0.001539	0.004193	0.159749
29	9.1	0.000091	0.000516	0.001795	0.004793	0.159749
30	25.6	0.000256	0.000772	0.002395	0.006065	0.159749
31	25.6	0.000256	0.001027	0.002994	0.007338	0.159749
32	25.6	0.000256	0.001283	0.003594	0.008610	0.159749
33	25.6	0.000256	0.001539	0.004193	0.009882	0.159749
34	25.6	0.000256	0.001795	0.004793	0.011155	0.159749
35	60.0	0.000600	0.002395	0.006065	0.013250	0.159749
36	60.0	0.000600	0.002994	0.007338	0.015345	0.159749
37	60.0	0.000600	0.003594	0.008610	0.017440	0.159749
38	60.0	0.000600	0.004193	0.009882	0.019535	0.159749
39	60.0	0.000600	0.004793	0.011155	0.021630	0.159749
40	127.2	0.001272	0.006065	0.013250	0.024190	0.159749
41	127.2	0.001272	0.007338	0.015345	0.026749	0.159749
42	127.2	0.001272	0.008610	0.017440	0.029309	0.159749
43	127.2	0.001272	0.009882	0.019535	0.031868	0.159749
44	127.2	0.001272	0.011155	0.021630	0.034428	0.159749
45	209.5	0.002095	0.013250	0.024190	0.037170	0.159749
46	209.5	0.002095	0.015345	0.026749	0.039912	0.159749
47	209.5	0.002095	0.017440	0.029309	0.042654	0.159749
48	209.5	0.002095	0.019535	0.031868	0.045396	0.159749
49	209.5	0.002095	0.021630	0.034428	0.048138	0.159749
50	255.9	0.002559	0.024190	0.037170	0.051618	0.159749
51	255.9	0.002559	0.026749	0.039912	0.055099	0.159749
52	255.9	0.002559	0.029309	0.042654	0.058580	0.159749
53	255.9	0.002559	0.031868	0.045396	0.062060	0.159749
54	255.9	0.002559	0.034428	0.048138	0.065541	0.159749
55	274.2	0.002742	0.037170	0.051618	0.069581	0.159749

56	274.2	0.002742	0.039912	0.055099	0.073621	0.159749
57	274.2	0.002742	0.042654	0.058580	0.077661	0.159749
58	274.2	0.002742	0.045396	0.062060	0.081701	0.159749
59	274.2	0.002742	0.048138	0.065541	0.085741	0.159749
60	348.1	0.003481	0.051618	0.069581	0.089865	0.159749
61	348.1	0.003481	0.055099	0.073621	0.093989	0.159749
62	348.1	0.003481	0.058580	0.077661	0.098113	0.159749
63	348.1	0.003481	0.062060	0.081701	0.102237	0.159749
64	348.1	0.003481	0.065541	0.085741	0.106361	0.159749
65	404.0	0.004040	0.069581	0.089865	0.109943	0.159749
66	404.0	0.004040	0.073621	0.093989	0.113526	0.159749
67	404.0	0.004040	0.077661	0.098113	0.117109	0.159749
68	404.0	0.004040	0.081701	0.102237	0.120692	0.159749
69	404.0	0.004040	0.085741	0.106361	0.124275	0.159749
70	412.4	0.004124	0.089865	0.109943	0.127558	0.159749
71	412.4	0.004124	0.093989	0.113526	0.130842	0.159749
72	412.4	0.004124	0.098113	0.117109	0.134125	0.159749
73	412.4	0.004124	0.102237	0.120692	0.137409	0.159749
74	412.4	0.004124	0.106361	0.124275	0.140693	0.159749
75	358.3	0.003583	0.109943	0.127558	0.143869	0.159749
76	358.3	0.003583	0.113526	0.130842	0.147045	0.159749
77	358.3	0.003583	0.117109	0.134125	0.150221	0.159749
78	358.3	0.003583	0.120692	0.137409	0.153397	0.159749
79	358.3	0.003583	0.124275	0.140693	0.156573	0.159749
80	328.4	0.003284	0.127558	0.143869	0.159749	0.159749
81	328.4	0.003284	0.130842	0.147045		0.159749
82	328.4	0.003284	0.134125	0.150221		0.159749
83	328.4	0.003284	0.137409	0.153397		0.159749
84	328.4	0.003284	0.140693	0.156573		0.159749
85	317.6	0.003176	0.143869	0.159749		0.159749
86	317.6	0.003176				0.159749
87	317.6	0.003176				0.159749
88	317.6	0.003176				0.159749
89	317.6	0.003176				0.159749
90	317.6	0.003176				0.159749

Table 5. Look up table for Caucasian United States specific population-based breast cancer incidence data.

Age	incidence	incid	incid_b	incid_b_5	incid_b_10	incid_life
0	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
3	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
4	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
5	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
6	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
7	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
8	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
9	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
10	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
11	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
12	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
13	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
14	0.0000	0.0000	0.0000	0.0000	0.0000	0.1850
15	0.0000	0.0000	0.0000	0.0000	0.0001	0.1850
16	0.0000	0.0000	0.0000	0.0000	0.0002	0.1850
17	0.0000	0.0000	0.0000	0.0000	0.0003	0.1850
18	0.0000	0.0000	0.0000	0.0000	0.0004	0.1850
19	0.0000	0.0000	0.0000	0.0000	0.0006	0.1850
20	0.9000	0.0000	0.0000	0.0001	0.0009	0.1850
21	0.9000	0.0000	0.0000	0.0002	0.0012	0.1850
22	0.9000	0.0000	0.0000	0.0003	0.0015	0.1850
23	0.9000	0.0000	0.0000	0.0004	0.0018	0.1850
24	0.9000	0.0000	0.0000	0.0006	0.0021	0.1850
25	10.1000	0.0001	0.0001	0.0009	0.0027	0.1850
26	10.1000	0.0001	0.0002	0.0012	0.0034	0.1850
27	10.1000	0.0001	0.0003	0.0015	0.0040	0.1850
28	10.1000	0.0001	0.0004	0.0018	0.0047	0.1850
29	10.1000	0.0001	0.0006	0.0021	0.0053	0.1850
30	31.1000	0.0003	0.0009	0.0027	0.0067	0.1850
31	31.1000	0.0003	0.0012	0.0034	0.0081	0.1850
32	31.1000	0.0003	0.0015	0.0040	0.0095	0.1850
33	31.1000	0.0003	0.0018	0.0047	0.0108	0.1850
34	31.1000	0.0003	0.0021	0.0053	0.0122	0.1850

35	64.4000	0.0006	0.0027	0.0067	0.0144	0.1850
36	64.4000	0.0006	0.0034	0.0081	0.0165	0.1850
37	64.4000	0.0006	0.0040	0.0095	0.0187	0.1850
38	64.4000	0.0006	0.0047	0.0108	0.0208	0.1850
39	64.4000	0.0006	0.0053	0.0122	0.0230	0.1850
40	137.6000	0.0014	0.0067	0.0144	0.0255	0.1850
41	137.6000	0.0014	0.0081	0.0165	0.0280	0.1850
42	137.6000	0.0014	0.0095	0.0187	0.0305	0.1850
43	137.6000	0.0014	0.0108	0.0208	0.0331	0.1850
44	137.6000	0.0014	0.0122	0.0230	0.0356	0.1850
45	215.8000	0.0022	0.0144	0.0255	0.0384	0.1850
46	215.8000	0.0022	0.0165	0.0280	0.0412	0.1850
47	215.8000	0.0022	0.0187	0.0305	0.0441	0.1850
48	215.8000	0.0022	0.0208	0.0331	0.0469	0.1850
49	215.8000	0.0022	0.0230	0.0356	0.0498	0.1850
50	251.4000	0.0025	0.0255	0.0384	0.0533	0.1850
51	251.4000	0.0025	0.0280	0.0412	0.0568	0.1850
52	251.4000	0.0025	0.0305	0.0441	0.0603	0.1850
53	251.4000	0.0025	0.0331	0.0469	0.0638	0.1850
54	251.4000	0.0025	0.0356	0.0498	0.0673	0.1850
55	283.8000	0.0028	0.0384	0.0533	0.0717	0.1850
56	283.8000	0.0028	0.0412	0.0568	0.0761	0.1850
57	283.8000	0.0028	0.0441	0.0603	0.0806	0.1850
58	283.8000	0.0028	0.0469	0.0638	0.0850	0.1850
59	283.8000	0.0028	0.0498	0.0673	0.0894	0.1850
60	351.4000	0.0035	0.0533	0.0717	0.0945	0.1850
61	351.4000	0.0035	0.0568	0.0761	0.0997	0.1850
62	351.4000	0.0035	0.0603	0.0806	0.1048	0.1850
63	351.4000	0.0035	0.0638	0.0850	0.1099	0.1850
64	351.4000	0.0035	0.0673	0.0894	0.1151	0.1850
65	441.0000	0.0044	0.0717	0.0945	0.1202	0.1850
66	441.0000	0.0044	0.0761	0.0997	0.1253	0.1850
67	441.0000	0.0044	0.0806	0.1048	0.1304	0.1850
68	441.0000	0.0044	0.0850	0.1099	0.1355	0.1850
69	441.0000	0.0044	0.0894	0.1151	0.1406	0.1850
70	513.8000	0.0051	0.0945	0.1202	0.1453	0.1850
71	513.8000	0.0051	0.0997	0.1253	0.1499	0.1850
72	513.8000	0.0051	0.1048	0.1304	0.1545	0.1850
73	513.8000	0.0051	0.1099	0.1355	0.1591	0.1850
74	513.8000	0.0051	0.1151	0.1406	0.1637	0.1850
75	511.4000	0.0051	0.1202	0.1453	0.1673	0.1850
76	511.4000	0.0051	0.1253	0.1499	0.1708	0.1850

77	511.4000	0.0051	0.1304	0.1545	0.1743	0.1850
78	511.4000	0.0051	0.1355	0.1591	0.1779	0.1850
79	511.4000	0.0051	0.1406	0.1637	0.1814	0.1850
80	462.0000	0.0046	0.1453	0.1673	0.1850	0.1850
81	462.0000	0.0046	0.1499	0.1708		0.1850
82	462.0000	0.0046	0.1545	0.1743		0.1850
83	462.0000	0.0046	0.1591	0.1779		0.1850
84	462.0000	0.0046	0.1637	0.1814		0.1850
85	353.7000	0.0035	0.1673	0.1850		0.1850
86	353.7000	0.0035				0.1850
87	353.7000	0.0035				0.1850
88	353.7000	0.0035				0.1850
89	353.7000	0.0035				0.1850
90	353.7000	0.0035				0.1850

Table 6. Look up table for African-American United States specific population-based breast cancer incidence data.

Age	incidence	incid	incid_b	incid_b_5	incid_b_10	incid_life
0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
2.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
3.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
4.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
5.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
6.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
7.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
8.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
9.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
10.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1707
11.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1707
12.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1707
13.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1707
14.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1707
15.0000	0.3000	0.0000	0.0000	0.0000	0.0003	0.1707
16.0000	0.3000	0.0000	0.0000	0.0001	0.0004	0.1707
17.0000	0.3000	0.0000	0.0000	0.0001	0.0006	0.1707
18.0000	0.3000	0.0000	0.0000	0.0001	0.0007	0.1707
19.0000	0.3000	0.0000	0.0000	0.0001	0.0008	0.1707
20.0000	2.2000	0.0000	0.0000	0.0003	0.0012	0.1707
21.0000	2.2000	0.0000	0.0001	0.0004	0.0016	0.1707

22.0000	2.2000	0.0000	0.0001	0.0006	0.0019	0.1707
23.0000	2.2000	0.0000	0.0001	0.0007	0.0023	0.1707
24.0000	2.2000	0.0000	0.0001	0.0008	0.0027	0.1707
25.0000	14.3000	0.0001	0.0003	0.0012	0.0034	0.1707
26.0000	14.3000	0.0001	0.0004	0.0016	0.0041	0.1707
27.0000	14.3000	0.0001	0.0006	0.0019	0.0047	0.1707
28.0000	14.3000	0.0001	0.0007	0.0023	0.0054	0.1707
29.0000	14.3000	0.0001	0.0008	0.0027	0.0061	0.1707
30.0000	36.4000	0.0004	0.0012	0.0034	0.0075	0.1707
31.0000	36.4000	0.0004	0.0016	0.0041	0.0088	0.1707
32.0000	36.4000	0.0004	0.0019	0.0047	0.0101	0.1707
33.0000	36.4000	0.0004	0.0023	0.0054	0.0114	0.1707
34.0000	36.4000	0.0004	0.0027	0.0061	0.0127	0.1707
35.0000	69.6000	0.0007	0.0034	0.0075	0.0146	0.1707
36.0000	69.6000	0.0007	0.0041	0.0088	0.0166	0.1707
37.0000	69.6000	0.0007	0.0047	0.0101	0.0185	0.1707
38.0000	69.6000	0.0007	0.0054	0.0114	0.0205	0.1707
39.0000	69.6000	0.0007	0.0061	0.0127	0.0224	0.1707
40.0000	131.3000	0.0013	0.0075	0.0146	0.0245	0.1707
41.0000	131.3000	0.0013	0.0088	0.0166	0.0266	0.1707
42.0000	131.3000	0.0013	0.0101	0.0185	0.0287	0.1707
43.0000	131.3000	0.0013	0.0114	0.0205	0.0308	0.1707
44.0000	131.3000	0.0013	0.0127	0.0224	0.0329	0.1707
45.0000	193.7000	0.0019	0.0146	0.0245	0.0356	0.1707
46.0000	193.7000	0.0019	0.0166	0.0266	0.0382	0.1707
47.0000	193.7000	0.0019	0.0185	0.0287	0.0408	0.1707
48.0000	193.7000	0.0019	0.0205	0.0308	0.0434	0.1707
49.0000	193.7000	0.0019	0.0224	0.0329	0.0461	0.1707
50.0000	210.7000	0.0021	0.0245	0.0356	0.0495	0.1707
51.0000	210.7000	0.0021	0.0266	0.0382	0.0530	0.1707
52.0000	210.7000	0.0021	0.0287	0.0408	0.0564	0.1707
53.0000	210.7000	0.0021	0.0308	0.0434	0.0599	0.1707
54.0000	210.7000	0.0021	0.0329	0.0461	0.0634	0.1707
55.0000	263.1000	0.0026	0.0356	0.0495	0.0675	0.1707
56.0000	263.1000	0.0026	0.0382	0.0530	0.0716	0.1707
57.0000	263.1000	0.0026	0.0408	0.0564	0.0758	0.1707
58.0000	263.1000	0.0026	0.0434	0.0599	0.0799	0.1707
59.0000	263.1000	0.0026	0.0461	0.0634	0.0841	0.1707
60.0000	345.5000	0.0035	0.0495	0.0675	0.0886	0.1707
61.0000	345.5000	0.0035	0.0530	0.0716	0.0931	0.1707
62.0000	345.5000	0.0035	0.0564	0.0758	0.0976	0.1707
63.0000	345.5000	0.0035	0.0599	0.0799	0.1021	0.1707

64.0000	345.5000	0.0035	0.0634	0.0841	0.1066	0.1707
65.0000	414.0000	0.0041	0.0675	0.0886	0.1109	0.1707
66.0000	414.0000	0.0041	0.0716	0.0931	0.1152	0.1707
67.0000	414.0000	0.0041	0.0758	0.0976	0.1196	0.1707
68.0000	414.0000	0.0041	0.0799	0.1021	0.1239	0.1707
69.0000	414.0000	0.0041	0.0841	0.1066	0.1282	0.1707
70.0000	450.6000	0.0045	0.0886	0.1109	0.1323	0.1707
71.0000	450.6000	0.0045	0.0931	0.1152	0.1364	0.1707
72.0000	450.6000	0.0045	0.0976	0.1196	0.1405	0.1707
73.0000	450.6000	0.0045	0.1021	0.1239	0.1446	0.1707
74.0000	450.6000	0.0045	0.1066	0.1282	0.1486	0.1707
75.0000	433.1000	0.0043	0.1109	0.1323	0.1523	0.1707
76.0000	433.1000	0.0043	0.1152	0.1364	0.1560	0.1707
77.0000	433.1000	0.0043	0.1196	0.1405	0.1597	0.1707
78.0000	433.1000	0.0043	0.1239	0.1446	0.1634	0.1707
79.0000	433.1000	0.0043	0.1282	0.1486	0.1670	0.1707
80.0000	407.8000	0.0041	0.1323	0.1523	0.1707	0.1707
81.0000	407.8000	0.0041	0.1364	0.1560		0.1707
82.0000	407.8000	0.0041	0.1405	0.1597		0.1707
83.0000	407.8000	0.0041	0.1446	0.1634		0.1707
84.0000	407.8000	0.0041	0.1486	0.1670		0.1707
85.0000	368.1000	0.0037	0.1523	0.1707		0.1707
86.0000	368.1000	0.0037				0.1707
87.0000	368.1000	0.0037				0.1707
88.0000	368.1000	0.0037				0.1707
89.0000	368.1000	0.0037				0.1707
90.0000	368.1000	0.0037				0.1707

Table 7. Look up table for Hispanic United States specific population-based breast cancer incidence data.

Age	incidence	incid	incid_b	incid_b_5	incid_b_10	incid_life
0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
2.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
3.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
4.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
5.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
6.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
7.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
8.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280

9.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
10.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1280
11.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1280
12.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1280
13.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1280
14.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.1280
15.0000	0.3000	0.0000	0.0000	0.0000	0.0002	0.1280
16.0000	0.3000	0.0000	0.0000	0.0001	0.0003	0.1280
17.0000	0.3000	0.0000	0.0000	0.0001	0.0004	0.1280
18.0000	0.3000	0.0000	0.0000	0.0001	0.0005	0.1280
19.0000	0.3000	0.0000	0.0000	0.0001	0.0005	0.1280
20.0000	1.9000	0.0000	0.0000	0.0002	0.0008	0.1280
21.0000	1.9000	0.0000	0.0001	0.0003	0.0010	0.1280
22.0000	1.9000	0.0000	0.0001	0.0004	0.0012	0.1280
23.0000	1.9000	0.0000	0.0001	0.0005	0.0015	0.1280
24.0000	1.9000	0.0000	0.0001	0.0005	0.0017	0.1280
25.0000	8.5000	0.0001	0.0002	0.0008	0.0022	0.1280
26.0000	8.5000	0.0001	0.0003	0.0010	0.0027	0.1280
27.0000	8.5000	0.0001	0.0004	0.0012	0.0031	0.1280
28.0000	8.5000	0.0001	0.0005	0.0015	0.0036	0.1280
29.0000	8.5000	0.0001	0.0005	0.0017	0.0041	0.1280
30.0000	23.4000	0.0002	0.0008	0.0022	0.0051	0.1280
31.0000	23.4000	0.0002	0.0010	0.0027	0.0062	0.1280
32.0000	23.4000	0.0002	0.0012	0.0031	0.0072	0.1280
33.0000	23.4000	0.0002	0.0015	0.0036	0.0082	0.1280
34.0000	23.4000	0.0002	0.0017	0.0041	0.0093	0.1280
35.0000	47.6000	0.0005	0.0022	0.0051	0.0107	0.1280
36.0000	47.6000	0.0005	0.0027	0.0062	0.0121	0.1280
37.0000	47.6000	0.0005	0.0031	0.0072	0.0136	0.1280
38.0000	47.6000	0.0005	0.0036	0.0082	0.0150	0.1280
39.0000	47.6000	0.0005	0.0041	0.0093	0.0164	0.1280
40.0000	103.4000	0.0010	0.0051	0.0107	0.0182	0.1280
41.0000	103.4000	0.0010	0.0062	0.0121	0.0200	0.1280
42.0000	103.4000	0.0010	0.0072	0.0136	0.0218	0.1280
43.0000	103.4000	0.0010	0.0082	0.0150	0.0236	0.1280
44.0000	103.4000	0.0010	0.0093	0.0164	0.0254	0.1280
45.0000	143.8000	0.0014	0.0107	0.0182	0.0276	0.1280
46.0000	143.8000	0.0014	0.0121	0.0200	0.0297	0.1280
47.0000	143.8000	0.0014	0.0136	0.0218	0.0319	0.1280
48.0000	143.8000	0.0014	0.0150	0.0236	0.0340	0.1280
49.0000	143.8000	0.0014	0.0164	0.0254	0.0362	0.1280
50.0000	179.1000	0.0018	0.0182	0.0276	0.0388	0.1280

51.0000	179.1000	0.0018	0.0200	0.0297	0.0415	0.1280
52.0000	179.1000	0.0018	0.0218	0.0319	0.0442	0.1280
53.0000	179.1000	0.0018	0.0236	0.0340	0.0469	0.1280
54.0000	179.1000	0.0018	0.0254	0.0362	0.0496	0.1280
55.0000	215.0000	0.0022	0.0276	0.0388	0.0529	0.1280
56.0000	215.0000	0.0022	0.0297	0.0415	0.0563	0.1280
57.0000	215.0000	0.0022	0.0319	0.0442	0.0596	0.1280
58.0000	215.0000	0.0022	0.0340	0.0469	0.0630	0.1280
59.0000	215.0000	0.0022	0.0362	0.0496	0.0663	0.1280
60.0000	268.0000	0.0027	0.0388	0.0529	0.0700	0.1280
61.0000	268.0000	0.0027	0.0415	0.0563	0.0738	0.1280
62.0000	268.0000	0.0027	0.0442	0.0596	0.0775	0.1280
63.0000	268.0000	0.0027	0.0469	0.0630	0.0813	0.1280
64.0000	268.0000	0.0027	0.0496	0.0663	0.0850	0.1280
65.0000	335.0000	0.0034	0.0529	0.0700	0.0879	0.1280
66.0000	335.0000	0.0034	0.0563	0.0738	0.0908	0.1280
67.0000	335.0000	0.0034	0.0596	0.0775	0.0936	0.1280
68.0000	335.0000	0.0034	0.0630	0.0813	0.0965	0.1280
69.0000	335.0000	0.0034	0.0663	0.0850	0.0994	0.1280
70.0000	374.1000	0.0037	0.0700	0.0879	0.1023	0.1280
71.0000	374.1000	0.0037	0.0738	0.0908	0.1052	0.1280
72.0000	374.1000	0.0037	0.0775	0.0936	0.1081	0.1280
73.0000	374.1000	0.0037	0.0813	0.0965	0.1110	0.1280
74.0000	374.1000	0.0037	0.0850	0.0994	0.1139	0.1280
75.0000	288.1000	0.0029	0.0879	0.1023	0.1162	0.1280
76.0000	288.1000	0.0029	0.0908	0.1052	0.1186	0.1280
77.0000	288.1000	0.0029	0.0936	0.1081	0.1209	0.1280
78.0000	288.1000	0.0029	0.0965	0.1110	0.1233	0.1280
79.0000	288.1000	0.0029	0.0994	0.1139	0.1256	0.1280
80.0000	289.0000	0.0029	0.1023	0.1162	0.1280	0.1280
81.0000	289.0000	0.0029	0.1052	0.1186		0.1280
82.0000	289.0000	0.0029	0.1081	0.1209		0.1280
83.0000	289.0000	0.0029	0.1110	0.1233		0.1280
84.0000	289.0000	0.0029	0.1139	0.1256		0.1280
85.0000	235.2000	0.0024	0.1162	0.1280		0.1280
86.0000	235.2000	0.0024				0.1280
87.0000	235.2000	0.0024				0.1280
88.0000	235.2000	0.0024				0.1280
89.0000	235.2000	0.0024				0.1280
90.0000	235.2000	0.0024				0.1280

Genetic Risk Assessment

Various exemplary polymorphisms associated with breast cancer are discussed in the present disclosure. These polymorphisms vary in terms of penetrance and many would be understood by those of skill in the art to be low penetrance polymorphisms.

5 The term “penetrance” is used in the context of the present disclosure to refer to the frequency at which a particular polymorphism manifests itself within female subjects with breast cancer. “High penetrance” polymorphisms will almost always be apparent in a female subject with breast cancer while “low penetrance” polymorphisms will only sometimes be apparent. In an embodiment polymorphisms assessed as part of
10 a genetic risk assessment according to the present disclosure are low penetrance polymorphisms.

In an embodiment, the genetic risk assessment is performed by analysing the genotype of the subject at 72 or more loci for polymorphisms associated with breast cancer. In an embodiment, the genetic risk assessment is performed by analysing the
15 genotype of the subject at 150 or more loci for polymorphisms associated with breast cancer. In an embodiment, the genetic risk assessment is performed by analysing the genotype of the subject at 200 or more loci for polymorphisms associated with breast cancer. In an embodiment, the genetic risk assessment is performed by analysing the genotype of the subject at 313 or more loci for polymorphisms associated with breast
20 cancer. In an embodiment, the genetic risk assessment is performed by analysing the genotype of the subject at 1,500 or more loci for polymorphisms associated with breast cancer. In an embodiment, the genetic risk assessment is performed by analysing the genotype of the subject at 3,820 or more loci for polymorphisms associated with breast cancer.

25 In an embodiment, when performing the methods of the present disclosure to assess risk of breast cancer, at least 67 of the polymorphisms are selected from Table 79 or a polymorphism in linkage disequilibrium with one or more thereof and the remaining polymorphisms are selected from Table 8, or a polymorphism in linkage disequilibrium with one or more thereof. In another embodiment, when performing the
30 methods of the present disclosure at least 68, at least 69, at least 70 of the polymorphisms are selected from Table 9 or a polymorphism in linkage disequilibrium with one or more thereof and the remaining polymorphisms are selected from Table 8, or a polymorphism in linkage disequilibrium with one or more thereof. In one embodiment, at least 72, at least 73, at least 74, at least 75, at least 76, at least 77, at
35 least 78, at least 79, at least 80, at least 81, at least 82, at least 83, at least 84, at least 85, at least 86, at least 87, at least 88 of the polymorphisms shown in Table 8, or a

polymorphism in linkage disequilibrium with one or more thereof are assessed. In further embodiments, at least 67, at least 68, at least 69, at least 70 of the polymorphisms shown in Table 8, or a polymorphism in linkage disequilibrium with one or more thereof are assessed. In further embodiments, at least 70, at least 71, at least 72, at least 73, at least 74, at least 75, at least 76, at least 77, at least 78, at least 79, at least 80, at least 81, at least 82, at least 83, at least 84, at least 85, at least 86, at least 87, at least 88 polymorphisms are assessed, wherein at least 67, at least 68, at least 69, at least 70 polymorphisms shown in Table 9, or a polymorphism in linkage disequilibrium with one or more thereof are assessed, with any remaining polymorphisms being selected from Table 8, or a polymorphism in linkage disequilibrium with one or more thereof.

In some embodiments, when performing the methods of the present disclosure to assess risk of breast cancer, one or more polymorphisms are selected from Table 14 or a polymorphism in linkage disequilibrium with one or more thereof. In an embodiment, at least 50 of the polymorphisms are selected from Table 14, or a polymorphism in linkage disequilibrium with one or more thereof. In an embodiment, at least 60, at least 70, at least 80, at least 90, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200 of the polymorphisms are selected from Table 14, or a polymorphism in linkage disequilibrium with one or more thereof. In an embodiment, at least 100 of the polymorphisms are selected from Table 14, or a polymorphism in linkage disequilibrium with one or more thereof. In an embodiment, at least 150 of the polymorphisms are selected from Table 14, or a polymorphism in linkage disequilibrium with one or more thereof. In an embodiment, at least 200 of the polymorphisms are selected from Table 14, or a polymorphism in linkage disequilibrium with one or more thereof.

In an embodiment, when determining breast cancer risk, the methods of the present disclosure comprise detecting at least 50, at least 100, or at least 150 polymorphisms shown in Table 14, or a polymorphism in linkage disequilibrium with one or more thereof. In an embodiment, when determining breast cancer risk, the methods of the present disclosure comprise detecting all of the 203 polymorphisms shown in Table 14, or a polymorphism in linkage disequilibrium with one or more thereof.

In an embodiment, when determining breast cancer risk, the methods of the present disclosure comprise detecting at least 50, 80, 100, 150 of the polymorphisms

shown in Table 14, or a polymorphism in linkage disequilibrium with one or more thereof.

In another embodiment, when determining breast cancer risk, the methods of the present disclosure encompass assessing all of the polymorphisms shown in Table 8 or
5 Table 14 or a polymorphism in linkage disequilibrium with one or more thereof.

Table 8, Table 9, and Table 14 recite overlapping polymorphisms. It will be appreciated that when selecting polymorphisms for assessment the same polymorphism will not be selected twice. For convenience, the polymorphisms in Table 8 have been separated into Tables 9 and 10. Table 9 lists polymorphisms common across
10 Caucasians, African American and Hispanic populations. Table 10 lists polymorphisms that are not common across Caucasian, African American and Hispanic populations.

In a further embodiment, between 72 and 88, between 73 and 87, between 74 and 86, between 75 and 85, between 76 and 84, between 75 and 83, between 76 and 82,
15 between 77 and 81, between 78 and 80 polymorphisms are assessed, wherein at least 60, at least 61, at least 62, at least 63, at least 64, at least 65, at least 66, at least 67, at least 68, at least 69, at least 70, of the polymorphisms shown in Table 9, or a polymorphism in linkage disequilibrium with one or more thereof are assessed, with any remaining polymorphisms being selected from Table 8, or a polymorphism in
20 linkage disequilibrium with one or more thereof.

In an embodiment, when performing the methods of the present disclosure to assess risk of breast cancer, the 313 polymorphisms provided in Table 17 or a polymorphism in linkage disequilibrium with one or more thereof are assessed. In an embodiment, the subject is Caucasian.

25 In an embodiment, when performing the methods of the present disclosure to assess risk of breast cancer, the 3,820 polymorphisms provided in Table 18 or a polymorphism in linkage disequilibrium with one or more thereof are assessed. In an embodiment, the subject is Caucasian.

In an embodiment, a panel of polymorphisms described in WO 2010/139006,
30 WO2016/049694 or Mavaddat et al. (2019) is used.

Polymorphisms in linkage disequilibrium with those specifically mentioned herein are easily identified by those of skill in the art, such as using the HAPMAP database as described in WO 2016/049694.

Ethnic Genotype Variation

It is known to those of skill in the art that genotypic variation exists between different populations. This phenomenon is referred to as human genetic variation. Human genetic variation is often observed between populations from different ethnic
5 backgrounds. Such variation is rarely consistent and is often directed by various combinations of environmental and lifestyle factors. As a result of genetic variation, it is often difficult to identify a population of genetic markers such as polymorphisms that remain informative across various populations such as populations from different ethnic backgrounds.

10 A selection of polymorphisms that are common to at least three ethnic backgrounds and remain informative for assessing the risk for developing breast cancer are disclosed herein.

In an embodiment, the methods of the present disclosure can be used for assessing the risk for developing breast cancer in human female subjects from various
15 ethnic backgrounds. For example, the female subject can be classified as Caucasoid, Australoid, Mongoloid and Negroid based on physical anthropology.

In an embodiment, the human female subject can be Caucasian, African American, Hispanic, Asian, Indian, or Latina. In a preferred embodiment, the human female subject is Caucasian, African American or Hispanic. Accordingly, ethnicity can
20 be taken into consideration as part of the clinical and/or genetic risk assessments.

In one embodiment, the human female subject is Caucasian and at least 72, at least 73, at least 74, at least 75, at least 76, at least 77, polymorphisms selected from Table 11, or a polymorphism in linkage disequilibrium with one or more thereof are assessed. Alternatively, all of the 77 polymorphisms selected from Table 11 or a
25 polymorphism in linkage disequilibrium with one or more thereof are assessed.

In another embodiment, the human female subject is Negroid or African American and at least 70, at least 71, at least 72, at least 73, or at least 74 polymorphisms selected from Table 12, or a polymorphism in linkage disequilibrium with one or more thereof are assessed. Alternatively, at least 74 polymorphisms
30 selected from Table 12 or a polymorphism in linkage disequilibrium with one or more thereof are assessed.

In another embodiment, the human female subject is Negroid or African American and at least 70, at least 71, at least 72, at least 73, or at least 74 polymorphisms shown in Table 15, or a polymorphism in linkage disequilibrium with
35 one or more thereof are assessed. In one embodiment, the human female subject is Negroid or African American and the methods described herein comprise detecting all

of the 74 polymorphisms shown in Table 15, or a polymorphism in linkage disequilibrium with one or more thereof.

In a further embodiment, the human female subject is Hispanic and at least 67, at least 68, at least 69, at least 70, or at least 71 polymorphisms selected from Table 13, or a polymorphism in linkage disequilibrium with one or more thereof are assessed. Alternatively, at least 71 polymorphisms selected from Table 13 or a polymorphism in linkage disequilibrium with one or more thereof are assessed.

In another embodiment, the human female subject can be Hispanic and at least 67, at least 68, at least 69, at least 70, or at least 71 polymorphisms shown in Table 16, or a polymorphism in linkage disequilibrium with one or more thereof are assessed. In one embodiment, the human female subject can be Hispanic and the methods described herein comprise detecting all of the 71 polymorphisms shown in Table 16, or a polymorphism in linkage disequilibrium with one or more thereof.

It is well known that over time there has been blending of different ethnic origins. However, in practice this does not influence the ability of a skilled person to practice the invention.

A female subject of predominantly European origin, either direct or indirect through ancestry, with white skin is considered Caucasian in the context of the present disclosure. A Caucasian may have, for example, at least 75% Caucasian ancestry (for example, but not limited to, the female subject having at least three Caucasian grandparents).

A female subject of predominantly central or southern African origin, either direct or indirect through ancestry, is considered Negroid in the context of the present disclosure. A Negroid may have, for example, at least 75% Negroid ancestry. An American female subject with predominantly Negroid ancestry and black skin is considered African American in the context of the present disclosure. An African American may have, for example, at least 75% Negroid ancestry. Similar principle applies to, for example, females of Negroid ancestry living in other countries (for example Great Britain, Canada and The Netherlands).

A female subject predominantly originating from Spain or a Spanish-speaking country, such as a country of Central or Southern America, either direct or indirect through ancestry, is considered Hispanic in the context of the present disclosure. An Hispanic may have, for example, at least 75% Hispanic ancestry.

The terms "ethnicity" and "race" can be used interchangeably in the context of the present disclosure. In an embodiment, the genetic risk assessment can readily be practiced based on what ethnicity the subject considers themselves to be. Thus, in an

embodiment, the ethnicity of the human female subject is self-reported by the subject. As an example, female subjects can be asked to identify their ethnicity in response to this question: “To what ethnic group do you belong?”. In another example, the ethnicity of the female subject is derived from medical records after obtaining the
 5 appropriate consent from the subject or from the opinion or observations of a clinician.

Table 8. Examples of polymorphisms indicative of breast cancer risk (n=88).

#	Polymorphism	Genomic region	Chromosome	Position	Nearest Gene	Caucasian	African American	Hispanic
1	rs616488	1p36.22	1	10,566,215	<i>PEX14</i>			
2	rs11552449	1p13.2	1	114,448,389	<i>SYT6</i>			
3	rs11249433	1p11.2	1	121,280,613	<i>FCGR1B</i>			
4	rs6678914	1q32.1	1	202,187,176	<i>LGR6</i>			
5	rs4245739	1q32.1	1	204,518,842	<i>MDM4</i>			
6	rs12710696	2p24.1	2	19,320,803	<i>OSR1</i>			
7	rs4849887	2q14.2	2	120,487,546	<i>INHBB</i>			
8	rs2016394	2q31.1	2	172,972,971	<i>DLX2</i>			
9	rs1550623	2q31.1	2	174,212,894	<i>CDCA7</i>			
10	rs1045485	2q33.1	2	202,149,589	<i>CASP8</i>			
11	rs13387042	2q35	2	217,905,832	<i>TNP1</i>			
12	rs16857609	2q35	2	218,296,508	<i>TNSI</i>			
13	rs6762644	3p26.1	3	4,742,276	<i>ITPR1</i>			
14	rs4973768	3p24.1	3	27,416,013	<i>SLC4A7</i>			
15	rs12493607	3p24.1	3	30,682,939	<i>TGFBR2</i>			
16	rs9790517	4q24	4	106,084,778	<i>TET2</i>			
17	rs6828523	4q34.1	4	175,846,426	<i>ADAM29</i>			
18	rs10069690	5p15.33	5	1,279,790	<i>TERT</i>			
19	rs10941679	5p12	5	44,706,498	<i>MRPS30</i>			
20	rs10472076	5q11.2	5	58,184,061	<i>RAB3C</i>			
21	rs1353747	5q11.2	5	58,337,481	<i>PDE4D</i>			
22	rs1432679	5q33.3	5	158,244,083	<i>EBF1</i>			
23	rs11242675	6p25.3	6	1,318,878	<i>FOXQ1</i>			
24	rs204247	6p23	6	13,722,523	<i>RANBP9</i>			
25	rs17529111	6q14	6	81418669	<i>FAM46A</i>			
26	rs2046210	6q25.1	6	151,948,366	<i>C6orf97</i>			
27	rs720475	7q35	7	144,074,929	<i>ARHGEF5</i>			
28	rs9693444	8p12	8	29,509,616	<i>DUSP4</i>			
29	rs6472903	8q21.11	8	76,230,301	<i>HNF4G</i>			
30	rs2943559	8q21.11	8	76,417,937	<i>HNF4G</i>			

31	rs13281615	8q24.21	8	128,355,618	<i>POU5F1B</i>			
32	rs11780156	8q24.21	8	129,194,641	<i>MYC</i>			
33	rs1011970	9p21.3	9	22,062,134	<i>CDKN2B</i>			
34	rs10759243	9q31.2	9	110,306,115	<i>KLF4</i>			
35	rs865686	9q31.2	9	110,888,478	<i>KLF4</i>			
36	rs2380205	10p15.1	10	5,886,734	<i>ANKRD16</i>			
37	rs7072776	10p12.31	10	22,032,942	<i>MLLT10</i>			
38	rs11814448	10p12.31	10	22,315,843	<i>DNAJC1</i>			
39	rs10995190	10q21.2	10	64,278,682	<i>ZNF365</i>			
40	rs704010	10q22.3	10	80,841,148	<i>ZMIZ1</i>			
41	rs7904519	10q25.2	10	114,773,927	<i>TCF7L2</i>			
42	rs2981579	10q26.13	10	123,337,335	<i>FGFR2</i>			
43	rs11199914	10q26.12	10	123,093,901	<i>FGFR2</i>			
44	rs3817198	11p15.5	11	1,909,006	<i>LSP1</i>			
45	rs3903072	11q13.1	11	65,583,066	<i>SNX32</i>			
46	rs554219	11q13.3	11	69,331,642	<i>CCND1</i>			
47	rs75915166	11q13.3	11	69,379,161	<i>FGF3</i>			
48	rs11820646	11q24.3	11	129,461,171	<i>BARX2</i>			
49	rs12422552	12p13.1	12	14,413,931	<i>ATF7IP</i>			
50	rs10771399	12p11.22	12	28,155,080	<i>PTHLH</i>			
51	rs17356907	12q22	12	96,027,759	<i>NTN4</i>			
52	rs1292011	12q24.21	12	115,836,522	<i>TBX3</i>			
53	rs11571833	13q13.1	13	32,972,626	<i>BRCA2</i>			
54	rs2236007	14q13.3	14	37,132,769	<i>PAX9</i>			
55	rs999737	14q23	14	68,567,965	<i>RAD51L1</i>			
56	rs2588809	14q24.1	14	68,660,428	<i>RAD51B</i>			
57	rs941764	14q32.11	14	91,841,069	<i>CCDC88C</i>			
58	rs3803662	16q12.1	16	52,586,341	<i>TOX3</i>			
59	rs17817449	16q12.2	16	53,813,367	<i>FTO</i>			
60	rs11075995	16q12.2	16	53,855,291	<i>FTO</i>			
61	rs13329835	16q23.2	16	80,650,805	<i>CDYL2</i>			
62	rs6504950	17q22	17	53,056,471	<i>STXBP4</i>			
63	rs527616	18q11.2	18	24,337,424	<i>AQP4</i>			
64	rs1436904	18q11.2	18	24,570,667	<i>CHST9</i>			
65	rs8170	19p13.11	19	17,389,704	<i>BABAM1</i>			
66	rs4808801	19p13.11	19	18,571,141	<i>ELL</i>			
67	rs3760982	19q13.31	19	44,286,513	<i>KCNN4</i>			
68	rs2823093	21q21.1	21	16,520,832	<i>NRIP1</i>			
69	rs132390	22q12.2	22	29,621,477	<i>EMID1</i>			
70	rs6001930	22q13.1	22	40,876,234	<i>SGSM3</i>			

71	rs7696175	4p14	4	38819365	<i>TLR1</i>			
72	rs4415084	5p12	5	44662413	<i>FGF10</i>			
73	rs7726159	5p15.33	5	1,282,204	<i>TERT</i>			
74	rs2736108	5p15.33	5	1,297,373	<i>TERT</i>			
75	rs889312	5q11.2	5	56,031,884	<i>MAP3K1</i>			
76	rs2067980	5q11.2	5	44982215	<i>MRPS30</i>			
77	rs2180341	6q22.3	6	127279485	<i>RNF146</i>			
78	rs9485370	6q25	6	149285665	<i>TAB2</i>			
79	RS12662670	6q25.1	6	151,597,721	<i>ESR1</i>			
80	rs3757318	6q25.1	6	151,914,113	<i>C6orf97</i>			
81	rs17157903	7q22	7	103987589	<i>RELN</i>			
82	rs10822013	10q21.2	10	62492218	<i>ZNF365</i>			
83	rs2981582	10q26	10	121592803	<i>FGFR2</i>			
84	rs614367	11q13.3	11	69513996	<i>CCND1</i>			
85	rs78540526	11q13.3	11	69,516,650	<i>CCND1</i>			
86	rs2363956	19P13	19	17,283,315	<i>ANKLE1</i>			
87	rs2284378	20q11.22	20	32,588,095	<i>DYNLRB1</i>			
88	rs17879961	22q12.1	22	28,725,099	<i>CHEK2157T</i>			
Total						77	78	82

Table 9. Examples of polymorphisms common across Caucasian, African American and Hispanic populations (n=70)

#	Polymorphism	Genomic region	Chromosome	Position	Nearest Gene	Caucasian	African American	Hispanic
1	rs616488	1p36.22	1	10,566,215	<i>PEX14</i>			
2	rs11552449	1p13.2	1	114,448,389	<i>SYT6</i>			
3	rs11249433	1p11.2	1	121,280,613	<i>FCGR1B</i>			
4	rs6678914	1q32.1	1	202,187,176	<i>LGR6</i>			
5	rs4245739	1q32.1	1	204,518,842	<i>MDM4</i>			
6	rs12710696	2p24.1	2	19,320,803	<i>OSR1</i>			
7	rs4849887	2q14.2	2	120,487,546	<i>INHBB</i>			
8	rs2016394	2q31.1	2	172,972,971	<i>DLX2</i>			
9	rs1550623	2q31.1	2	174,212,894	<i>CDCA7</i>			
10	rs1045485	2q33.1	2	202,149,589	<i>CASP8</i>			
11	rs13387042	2q35	2	217,905,832	<i>TNP1</i>			
12	rs16857609	2q35	2	218,296,508	<i>TNSI</i>			
13	rs6762644	3p26.1	3	4,742,276	<i>ITPR1</i>			
14	rs4973768	3p24.1	3	27,416,013	<i>SLC4A7</i>			
15	rs12493607	3p24.1	3	30,682,939	<i>TGFBR2</i>			
16	rs9790517	4q24	4	106,084,778	<i>TET2</i>			

17	rs6828523	4q34.1	4	175,846,426	ADAM29			
18	rs10069690	5p15.33	5	1,279,790	TERT			
19	rs10941679	5p12	5	44,706,498	MRPS30			
20	rs10472076	5q11.2	5	58,184,061	RAB3C			
21	rs1353747	5q11.2	5	58,337,481	PDE4D			
22	rs1432679	5q33.3	5	158,244,083	EBF1			
23	rs11242675	6p25.3	6	1,318,878	FOXQ1			
24	rs204247	6p23	6	13,722,523	RANBP9			
25	rs17529111	6q14	6	814,186,69	FAM46A			
26	rs2046210	6q25.1	6	151,948,366	C6orf97			
27	rs720475	7q35	7	144,074,929	ARHGEF5			
28	rs9693444	8p12	8	29,509,616	DUSP4			
29	rs6472903	8q21.11	8	76,230,301	HNF4G			
30	rs2943559	8q21.11	8	76,417,937	HNF4G			
31	rs13281615	8q24.21	8	128,355,618	POU5F1B			
32	rs11780156	8q24.21	8	129,194,641	MYC			
33	rs1011970	9p21.3	9	22,062,134	CDKN2B			
34	rs10759243	9q31.2	9	110,306,115	KLF4			
35	rs865686	9q31.2	9	110,888,478	KLF4			
36	rs2380205	10p15.1	10	5,886,734	ANKRD16			
37	rs7072776	10p12.31	10	22,032,942	MLLT10			
38	rs11814448	10p12.31	10	22,315,843	DNAJC1			
39	rs10995190	10q21.2	10	64,278,682	ZNF365			
40	rs704010	10q22.3	10	80,841,148	ZMIZ1			
41	rs7904519	10q25.2	10	114,773,927	TCF7L2			
42	rs2981579	10q26.13	10	123,337,335	FGFR2			
43	rs11199914	10q26.12	10	123,093,901	FGFR2			
44	rs3817198	11p15.5	11	1,909,006	LSP1			
45	rs3903072	11q13.1	11	65,583,066	SNX32			
46	rs554219	11q13.3	11	69,331,642	CCND1			
47	rs75915166	11q13.3	11	69,379,161	FGF3			
48	rs11820646	11q24.3	11	129,461,171	BARX2			
49	rs12422552	12p13.1	12	14,413,931	ATF7IP			
50	rs10771399	12p11.22	12	28,155,080	PTHLH			
51	rs17356907	12q22	12	96,027,759	NTN4			
52	rs1292011	12q24.21	12	115,836,522	TBX3			
53	rs11571833	13q13.1	13	32,972,626	BRCA2			
54	rs2236007	14q13.3	14	37,132,769	PAX9			
55	rs999737	14q23	14	68567965	RAD51L1			
56	rs2588809	14q24.1	14	68,660,428	RAD51B			

57	rs941764	14q32.11	14	91,841,069	CCDC88C			
58	rs3803662	16q12.1	16	52,586,341	TOX3			
59	rs17817449	16q12.2	16	53,813,367	FTO			
60	rs11075995	16q12.2	16	53,855,291	FTO			
61	rs13329835	16q23.2	16	80,650,805	CDYL2			
62	rs6504950	17q22	17	53,056,471	STXBP4			
63	rs527616	18q11.2	18	24,337,424	AQP4			
64	rs1436904	18q11.2	18	24,570,667	CHST9			
65	rs8170	19p13.11	19	17,389,704	BABAMI			
66	rs4808801	19p13.11	19	18,571,141	ELL			
67	rs3760982	19q13.31	19	44,286,513	KCNN4			
68	rs2823093	21q21.1	21	16,520,832	NRIP1			
69	rs132390	22q12.2	22	29,621,477	EMID1			
70	rs6001930	22q13.1	22	40,876,234	SGSM3			

Table 10. Examples of polymorphisms not common across Caucasian, African American and Hispanic populations (n=18)

Polymorphism	Genomic region	Chromosome	Position	Nearest Gene	Caucasian	African American	Hispanic
rs7696175	4p14	4	38819365	TLR1			
rs4415084	5p12	5	44662413	FGF10			
rs7726159	5p15.33	5	1,282,204	TERT			
rs2736108	5p15.33	5	1,297,373	TERT			
rs889312	5q11.2	5	56,031,884	MAP3K1			
rs2067980	5q11.2	5	44982215	MRPS30			
rs2180341	6q22.3	6	127279485	RNF146			
rs9485370	6q25	6	149285665	TAB2			
RS12662670	6q25.1	6	151,597,721	ESR1			
rs3757318	6q25.1	6	151,914,113	C6orf97			
rs17157903	7q22	7	103987589	RELN			
rs10822013	10q21.2	10	62492218	ZNF365			
rs2981582	10q26	10	121592803	FGFR2			
rs614367	11q13.3	11	69513996	CCND1			
rs78540526	11q13.3	11	69,516,650	CCND1			
rs2363956	19P13	19	17,283,315	ANKLE1			
rs2284378	20q11.22	20	32,588,095	DYNLRB1			
rs17879961	22q12.1	22	28,725,099	CHEK2157T			

5 Legend

	Common to Caucasian, African American and Hispanic
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	Caucasian
	African American
	Hispanic

Table 11. Examples of Caucasian polymorphisms (n=77). Alleles represented as major/minor (e.g. for rs616488 A is the common allele and G less common). Minor allele odds ratios below 1 mean the minor allele is not the risk allele, whereas when above 1 the minor allele is the risk allele.

Polymorphism	Chromosome	Alleles	Minor allele frequency	OR Minor Allele	μ	Adjusted Risk Score					
rs616488	1	A/G	0.33	0.9417	0.96	AA	1.04	GA	0.98	GG	0.92
rs11552449	1	C/T	0.17	1.0810	1.03	CC	0.97	TC	1.05	TT	1.14
rs11249433	1	A/G	0.40	1.0993	1.08	AA	0.93	GA	1.02	GG	1.12
rs6678914	1	G/A	0.414	0.9890	0.99	GG	1.01	AG	1.00	AA	0.99
rs4245739	1	A/C	0.258	1.0291	1.02	AA	0.99	CA	1.01	CC	1.04
rs12710696	2	G/A	0.357	1.0387	1.03	GG	0.97	AG	1.01	AA	1.05
rs4849887	2	C/T	0.098	0.9187	0.98	CC	1.02	TC	0.93	TT	0.86
rs2016394	2	G/A	0.48	0.9504	0.95	GG	1.05	AG	1.00	AA	0.95
rs1550623	2	A/G	0.16	0.9445	0.98	AA	1.02	GA	0.96	GG	0.91
rs1045485	2	G/C	0.13	0.9644	0.99	GG	1.01	CG	0.97	CC	0.94
rs13387042	2	A/G	0.49	0.8794	0.89	AA	1.13	GA	0.99	GG	0.87
rs16857609	2	C/T	0.26	1.0721	1.04	CC	0.96	TC	1.03	TT	1.11
rs6762644	3	A/G	0.4	1.0661	1.05	AA	0.95	GA	1.01	GG	1.08
rs4973768	3	C/T	0.47	1.0938	1.09	CC	0.92	TC	1.00	TT	1.10
rs12493607	3	G/C	0.35	1.0529	1.04	GG	0.96	CG	1.01	CC	1.07
rs9790517	4	C/T	0.23	1.0481	1.02	CC	0.98	TC	1.03	TT	1.07
rs6828523	4	C/A	0.13	0.9056	0.98	CC	1.03	AC	0.93	AA	0.84
rs10069690	5	C/T	0.26	1.0242	1.01	CC	0.99	TC	1.01	TT	1.04
rs7726159	5	C/A	0.338	1.0359	1.02	CC	0.98	AC	1.01	AA	1.05
rs2736108	5	C/T	0.292	0.9379	0.96	CC	1.04	TC	0.97	TT	0.91
rs10941679	5	A/G	0.25	1.1198	1.06	AA	0.94	GA	1.06	GG	1.18
rs889312	5	A/C	0.28	1.1176	1.07	AA	0.94	CA	1.05	CC	1.17
rs10472076	5	T/C	0.38	1.0419	1.03	TT	0.97	CT	1.01	CC	1.05
rs1353747	5	T/G	0.095	0.9213	0.99	TT	1.02	GT	0.94	GG	0.86
rs1432679	5	A/G	0.43	1.0670	1.06	AA	0.94	GA	1.01	GG	1.08
rs11242675	6	T/C	0.39	0.9429	0.96	TT	1.05	CT	0.99	CC	0.93
rs204247	6	A/G	0.43	1.0503	1.04	AA	0.96	GA	1.01	GG	1.06
rs17529111	6	A/G	0.218	1.0457	1.02	AA	0.98	GA	1.03	GG	1.07
rs12662670	6	T/G	0.073	1.1392	1.02	TT	0.98	GT	1.12	GG	1.27
rs2046210	6	G/A	0.34	1.0471	1.03	GG	0.97	AG	1.01	AA	1.06

rs720475	7	G/A	0.25	0.9452	0.97	GG	1.03	AG	0.97	AA	0.92
rs9693444	8	C/A	0.32	1.0730	1.05	CC	0.95	AC	1.02	AA	1.10
rs6472903	8	T/G	0.18	0.9124	0.97	TT	1.03	GT	0.94	GG	0.86
rs2943559	8	A/G	0.07	1.1334	1.02	AA	0.98	GA	1.11	GG	1.26
rs13281615	8	A/G	0.41	1.0950	1.08	AA	0.93	GA	1.01	GG	1.11
rs11780156	8	C/T	0.16	1.0691	1.02	CC	0.98	TC	1.05	TT	1.12
rs1011970	9	G/T	0.17	1.0502	1.02	GG	0.98	TG	1.03	TT	1.08
rs10759243	9	C/A	0.39	1.0542	1.04	CC	0.96	AC	1.01	AA	1.07
rs865686	9	T/G	0.38	0.8985	0.92	TT	1.08	GT	0.97	GG	0.87
rs2380205	10	C/T	0.44	0.9771	0.98	CC	1.02	TC	1.00	TT	0.97
rs7072776	10	G/A	0.29	1.0581	1.03	GG	0.97	AG	1.02	AA	1.08
rs11814448	10	A/C	0.02	1.2180	1.01	AA	0.99	CA	1.21	CC	1.47
rs10995190	10	G/A	0.16	0.8563	0.95	GG	1.05	AG	0.90	AA	0.77
rs704010	10	C/T	0.38	1.0699	1.05	CC	0.95	TC	1.02	TT	1.09
rs7904519	10	A/G	0.46	1.0584	1.05	AA	0.95	GA	1.00	GG	1.06
rs2981579	10	G/A	0.4	1.2524	1.21	GG	0.83	AG	1.03	AA	1.29
rs11199914	10	C/T	0.32	0.9400	0.96	CC	1.04	TC	0.98	TT	0.92
rs3817198	11	T/C	0.31	1.0744	1.05	TT	0.96	CT	1.03	CC	1.10
rs3903072	11	G/T	0.47	0.9442	0.95	GG	1.05	TG	1.00	TT	0.94
rs554219	11	C/G	0.112	1.1238	1.03	CC	0.97	GC	1.09	GG	1.23
rs78540526	11	C/T	0.032	1.1761	1.01	CC	0.99	TC	1.16	TT	1.37
rs75915166	11	C/A	0.059	1.0239	1.00	CC	1.00	AC	1.02	AA	1.05
rs11820646	11	C/T	0.41	0.9563	0.96	CC	1.04	TC	0.99	TT	0.95
rs12422552	12	G/C	0.26	1.0327	1.02	GG	0.98	CG	1.02	CC	1.05
rs10771399	12	A/G	0.12	0.8629	0.97	AA	1.03	GA	0.89	GG	0.77
rs17356907	12	A/G	0.3	0.9078	0.95	AA	1.06	GA	0.96	GG	0.87
rs1292011	12	A/G	0.42	0.9219	0.94	AA	1.07	GA	0.99	GG	0.91
rs11571833	13	A/T	0.008	1.2609	1.00	AA	1.00	TA	1.26	TT	1.58
rs2236007	14	G/A	0.21	0.9203	0.97	GG	1.03	AG	0.95	AA	0.88
rs999737	14	C/T	0.23	0.9239	0.97	CC	1.04	TC	0.96	TT	0.88
rs2588809	14	C/T	0.16	1.0667	1.02	CC	0.98	TC	1.04	TT	1.11
rs941764	14	A/G	0.34	1.0636	1.04	AA	0.96	GA	1.02	GG	1.08
rs3803662	16	G/A	0.26	1.2257	1.12	GG	0.89	AG	1.09	AA	1.34
rs17817449	16	T/G	0.4	0.9300	0.94	TT	1.06	GT	0.98	GG	0.92
rs11075995	16	A/T	0.241	1.0368	1.02	AA	0.98	TA	1.02	TT	1.06
rs13329835	16	A/G	0.22	1.0758	1.03	AA	0.97	GA	1.04	GG	1.12
rs6504950	17	G/A	0.28	0.9340	0.96	GG	1.04	AG	0.97	AA	0.91
rs527616	18	G/C	0.38	0.9573	0.97	GG	1.03	CG	0.99	CC	0.95
rs1436904	18	T/G	0.4	0.9466	0.96	TT	1.04	GT	0.99	GG	0.94
rs2363956	19	G/T	0.487	1.0264	1.03	GG	0.97	TG	1.00	TT	1.03

rs8170	19	G/A	0.19	1.0314	1.01	GG	0.99	AG	1.02	AA	1.05
rs4808801	19	A/G	0.35	0.9349	0.95	AA	1.05	GA	0.98	GG	0.92
rs3760982	19	G/A	0.46	1.0553	1.05	GG	0.95	AG	1.00	AA	1.06
rs2823093	21	G/A	0.27	0.9274	0.96	GG	1.04	AG	0.96	AA	0.89
rs17879961	22	A/G	0.005	1.3632	1.00	AA	1.00	GA	1.36	GG	1.85
rs132390	22	T/C	0.036	1.1091	1.01	TT	0.99	CT	1.10	CC	1.22
rs6001930	22	T/C	0.11	1.1345	1.03	TT	0.97	CT	1.10	CC	1.25

Table 12. Examples of African American polymorphisms (n=78). Alleles represented as risk/reference (non-risk) (e.g., for rs616488 A is the risk allele).

Polymorphism	Chromosome	Alleles	Risk allele frequency	OR Risk Allele	μ	Adjusted Risk Score					
rs616488	1	A/G	0.86	1.03	1.05	AA	0.95	AG	0.98	GG	1.01
rs11552449	1	C/T	0.037	0.9	0.99	CC	1.01	CT	0.91	TT	0.82
rs11249433	1	A/G	0.13	0.99	1.00	AA	1.00	AG	0.99	GG	0.98
rs6678914	1	G/A	0.66	1	1.00	GG	1.00	GA	1.00	AA	1.00
rs4245739	1	A/C	0.24	0.97	0.99	AA	1.01	AC	0.98	CC	0.95
rs12710696	2	G/A	0.53	1.06	1.06	GG	0.94	GA	1.00	AA	1.06
rs4849887	2	C/T	0.7	1.16	1.24	CC	0.81	CT	0.94	TT	1.09
rs2016394	2	G/A	0.72	1.05	1.07	GG	0.93	GA	0.98	AA	1.03
rs1550623	2	A/G	0.71	1.1	1.15	AA	0.87	AG	0.96	GG	1.05
rs1045485	2	G/C	0.93	0.99	0.98	GG	1.02	GC	1.01	CC	1.00
rs13387042	2	A/G	0.72	1.12	1.18	AA	0.85	AG	0.95	GG	1.06
rs16857609	2	C/T	0.24	1.17	1.08	CC	0.92	CT	1.08	TT	1.26
rs6762644	3	A/G	0.46	1.05	1.05	AA	0.96	AG	1.00	GG	1.05
rs4973768	3	C/T	0.36	1.04	1.03	CC	0.97	CT	1.01	TT	1.05
rs12493607	3	G/C	0.14	1.04	1.01	GG	0.99	GC	1.03	CC	1.07
rs9790517	4	C/T	0.084	0.88	0.98	CC	1.02	CT	0.90	TT	0.79
rs6828523	4	C/A	0.65	1	1.00	CC	1.00	CA	1.00	AA	1.00
rs4415084	5	C/T	0.61	1.1	1.13	CC	0.89	CT	0.98	TT	1.07
rs10069690	5	C/T	0.57	1.13	1.15	CC	0.87	CT	0.98	TT	1.11
rs10941679	5	A/G	0.21	1.04	1.02	AA	0.98	AG	1.02	GG	1.06
rs889312	5	A/C	0.33	1.07	1.05	AA	0.96	AC	1.02	CC	1.09
rs10472076	5	T/C	0.28	0.95	0.97	TT	1.03	TC	0.98	CC	0.93
rs1353747	5	T/G	0.98	1.01	1.02	TT	0.98	TG	0.99	GG	1.00
rs1432679	5	A/G	0.79	1.07	1.11	AA	0.90	AG	0.96	GG	1.03
rs11242675	6	T/C	0.51	1.06	1.06	TT	0.94	TC	1.00	CC	1.06
rs204247	6	A/G	0.34	1.13	1.09	AA	0.92	AG	1.04	GG	1.17
rs17529111	6	A/G	0.075	0.99	1.00	AA	1.00	AG	0.99	GG	0.98
rs9485370	6	G/T	0.78	1.13	1.21	GG	0.82	GT	0.93	TT	1.05

rs3757318	6	G/A	0.038	1.11	1.01	GG	0.99	GA	1.10	AA	1.22
rs2046210	6	G/A	0.6	0.99	0.99	GG	1.01	GA	1.00	AA	0.99
rs720475	7	G/A	0.88	0.99	0.98	GG	1.02	GA	1.01	AA	1.00
rs9693444	8	C/A	0.37	1.06	1.04	CC	0.96	CA	1.01	AA	1.08
rs6472903	8	T/G	0.9	1.02	1.04	TT	0.96	TG	0.98	GG	1.00
rs2943559	8	A/G	0.22	1.07	1.03	AA	0.97	AG	1.04	GG	1.11
rs13281615	8	A/G	0.43	1.06	1.05	AA	0.95	AG	1.01	GG	1.07
rs11780156	8	C/T	0.052	0.84	0.98	CC	1.02	CT	0.85	TT	0.72
rs1011970	9	G/T	0.32	1.06	1.04	GG	0.96	GT	1.02	TT	1.08
rs10759243	9	C/A	0.59	1.02	1.02	CC	0.98	CA	1.00	AA	1.02
rs865686	9	T/G	0.51	1.09	1.09	TT	0.91	TG	1.00	GG	1.09
rs2380205	10	C/T	0.42	0.98	0.98	CC	1.02	CT	1.00	TT	0.98
rs7072776	10	G/A	0.49	1.04	1.04	GG	0.96	GA	1.00	AA	1.04
rs11814448	10	A/C	0.61	1.04	1.05	AA	0.95	AC	0.99	CC	1.03
rs10822013	10	T/C	0.23	1	1.00	TT	1.00	TC	1.00	CC	1.00
rs10995190	10	G/A	0.83	0.98	0.97	GG	1.03	GA	1.01	AA	0.99
rs704010	10	C/T	0.11	0.98	1.00	CC	1.00	CT	0.98	TT	0.96
rs7904519	10	A/G	0.78	1.13	1.21	AA	0.82	AG	0.93	GG	1.05
rs2981579	10	G/A	0.59	1.18	1.22	GG	0.82	GA	0.96	AA	1.14
rs2981582	10	G/A	0.49	1.05	1.05	GG	0.95	GA	1.00	AA	1.05
rs11199914	10	C/T	0.48	0.97	0.97	CC	1.03	CT	1.00	TT	0.97
rs3817198	11	T/C	0.17	0.98	0.99	TT	1.01	TC	0.99	CC	0.97
rs3903072	11	G/T	0.82	0.99	0.98	GG	1.02	GT	1.01	TT	1.00
rs554219	11	C/G	0.22	1	1.00	CC	1.00	CG	1.00	GG	1.00
rs614367	11	G/A	0.13	0.96	0.99	GG	1.01	GA	0.97	AA	0.93
rs75915166	11	C/A	0.015	1.44	1.01	CC	0.99	CA	1.42	AA	2.05
rs11820646	11	C/T	0.78	0.98	0.97	CC	1.03	CT	1.01	TT	0.99
rs12422552	12	G/C	0.41	1.02	1.02	GG	0.98	GC	1.00	CC	1.02
rs10771399	12	A/G	0.96	1.19	1.40	AA	0.72	AG	0.85	GG	1.01
rs17356907	12	A/G	0.79	1.02	1.03	AA	0.97	AG	0.99	GG	1.01
rs1292011	12	A/G	0.55	1.03	1.03	AA	0.97	AG	1.00	GG	1.03
rs11571833	13	A/T	0.003	0.95	1.00	AA	1.00	AT	0.95	TT	0.90
rs2236007	14	G/A	0.93	0.9	0.82	GG	1.22	GA	1.09	AA	0.98
rs999737	14	C/T	0.95	1.03	1.06	CC	0.95	CT	0.97	TT	1.00
rs2588809	14	C/T	0.29	1.01	1.01	CC	0.99	CT	1.00	TT	1.01
rs941764	14	A/G	0.7	1.1	1.14	AA	0.87	AG	0.96	GG	1.06
rs3803662	16	G/A	0.51	0.99	0.99	GG	1.01	GA	1.00	AA	0.99
rs17817449	16	T/G	0.6	1.05	1.06	TT	0.94	TG	0.99	GG	1.04
rs11075995	16	A/T	0.18	1.07	1.03	AA	0.98	AT	1.04	TT	1.12
rs13329835	16	A/G	0.63	1.08	1.10	AA	0.91	AG	0.98	GG	1.06

rs6504950	17	G/A	0.65	1.06	1.08	GG	0.93	GA	0.98	AA	1.04
rs527616	18	G/C	0.86	0.98	0.97	GG	1.04	GC	1.01	CC	0.99
rs1436904	18	T/G	0.75	0.98	0.97	TT	1.03	TG	1.01	GG	0.99
rs8170	19	G/A	0.19	1.13	1.05	GG	0.95	GA	1.08	AA	1.22
rs4808801	19	A/G	0.33	1.01	1.01	AA	0.99	AG	1.00	GG	1.01
rs3760982	19	G/A	0.47	1	1.00	GG	1.00	GA	1.00	AA	1.00
rs2284378	20	C/T	0.16	1.06	1.02	CC	0.98	CT	1.04	TT	1.10
rs2823093	21	G/A	0.57	1.03	1.03	GG	0.97	GA	1.00	AA	1.03
rs132390	22	T/C	0.052	0.88	0.99	TT	1.01	TC	0.89	CC	0.78
rs6001930	22	T/C	0.13	1.02	1.01	TT	0.99	TC	1.01	CC	1.04

Table 13. Examples of Hispanic polymorphisms (n=82). Alleles represented as major/minor (e.g. for rs616488 A is the common allele and G less common). Minor allele odds ratios below 1 means the minor allele is not the risk allele, whereas when above 1 the minor allele is the risk allele.

Polymorphism	Chromosome	Alleles	Minor allele frequency	OR Minor Allele	μ	Adjusted Risk Score					
						AA	1.04	GA	0.98	GG	0.92
rs616488	1	A/G	0.33	0.9417	0.96	AA	1.04	GA	0.98	GG	0.92
rs11552449	1	C/T	0.17	1.0810	1.03	CC	0.97	TC	1.05	TT	1.14
rs11249433	1	A/G	0.40	1.0993	1.08	AA	0.93	GA	1.02	GG	1.12
rs6678914	1	G/A	0.414	0.9890	0.99	GG	1.01	AG	1.00	AA	0.99
rs4245739	1	A/C	0.258	1.0291	1.02	AA	0.99	CA	1.01	CC	1.04
rs12710696	2	G/A	0.357	1.0387	1.03	GG	0.97	AG	1.01	AA	1.05
rs4849887	2	C/T	0.098	0.9187	0.98	CC	1.02	TC	0.93	TT	0.86
rs2016394	2	G/A	0.48	0.9504	0.95	GG	1.05	AG	1.00	AA	0.95
rs1550623	2	A/G	0.16	0.9445	0.98	AA	1.02	GA	0.96	GG	0.91
rs1045485	2	G/C	0.13	0.9644	0.99	GG	1.01	CG	0.97	CC	0.94
rs13387042	2	A/G	0.49	0.8794	0.89	AA	1.13	GA	0.99	GG	0.87
rs16857609	2	C/T	0.26	1.0721	1.04	CC	0.96	TC	1.03	TT	1.11
rs6762644	3	A/G	0.4	1.0661	1.05	AA	0.95	GA	1.01	GG	1.08
rs4973768	3	C/T	0.47	1.0938	1.09	CC	0.92	TC	1.00	TT	1.10
rs12493607	3	G/C	0.35	1.0529	1.04	GG	0.96	CG	1.01	CC	1.07
rs7696175	4	T/C	0.38	1.14	1.11	TT	0.90	CT	1.03	CC	1.17
rs9790517	4	C/T	0.23	1.0481	1.02	CC	0.98	TC	1.03	TT	1.07
rs6828523	4	C/A	0.13	0.9056	0.98	CC	1.03	AC	0.93	AA	0.84
rs10069690	5	C/T	0.26	1.0242	1.01	CC	0.99	TC	1.01	TT	1.04
rs7726159	5	C/A	0.338	1.0359	1.02	CC	0.98	AC	1.01	AA	1.05
rs2736108	5	C/T	0.292	0.9379	0.96	CC	1.04	TC	0.97	TT	0.91
rs10941679	5	A/G	0.25	1.1198	1.06	AA	0.94	GA	1.06	GG	1.18
rs889312	5	A/C	0.28	1.1176	1.07	AA	0.94	CA	1.05	CC	1.17

rs10472076	5	T/C	0.38	1.0419	1.03	TT	0.97	CT	1.01	CC	1.05
rs2067980	5	G/A	0.16	1	1.00	GG	1.00	AG	1.00	AA	1.00
rs1353747	5	T/G	0.095	0.9213	0.99	TT	1.02	GT	0.94	GG	0.86
rs1432679	5	A/G	0.43	1.0670	1.06	AA	0.94	GA	1.01	GG	1.08
rs11242675	6	T/C	0.39	0.9429	0.96	TT	1.05	CT	0.99	CC	0.93
rs204247	6	A/G	0.43	1.0503	1.04	AA	0.96	GA	1.01	GG	1.06
rs17529111	6	A/G	0.218	1.0457	1.02	AA	0.98	GA	1.03	GG	1.07
rs2180341	6	G/A	0.23	0.9600	0.98	GG	1.02	AG	0.98	AA	0.94
rs12662670	6	T/G	0.073	1.1392	1.02	TT	0.98	GT	1.12	GG	1.27
rs2046210	6	G/A	0.34	1.0471	1.03	GG	0.97	AG	1.01	AA	1.06
rs17157903	7	T/C	0.09	0.93	0.99	TT	1.01	CT	0.94	CC	0.88
rs720475	7	G/A	0.25	0.9452	0.97	GG	1.03	AG	0.97	AA	0.92
rs9693444	8	C/A	0.32	1.0730	1.05	CC	0.95	AC	1.02	AA	1.10
rs6472903	8	T/G	0.18	0.9124	0.97	TT	1.03	GT	0.94	GG	0.86
rs2943559	8	A/G	0.07	1.1334	1.02	AA	0.98	GA	1.11	GG	1.26
rs13281615	8	A/G	0.41	1.0950	1.08	AA	0.93	GA	1.01	GG	1.11
rs11780156	8	C/T	0.16	1.0691	1.02	CC	0.98	TC	1.05	TT	1.12
rs1011970	9	G/T	0.17	1.0502	1.02	GG	0.98	TG	1.03	TT	1.08
rs10759243	9	C/A	0.39	1.0542	1.04	CC	0.96	AC	1.01	AA	1.07
rs865686	9	T/G	0.38	0.8985	0.92	TT	1.08	GT	0.97	GG	0.87
rs2380205	10	C/T	0.44	0.9771	0.98	CC	1.02	TC	1.00	TT	0.97
rs7072776	10	G/A	0.29	1.0581	1.03	GG	0.97	AG	1.02	AA	1.08
rs11814448	10	A/C	0.02	1.2180	1.01	AA	0.99	CA	1.21	CC	1.47
rs10995190	10	G/A	0.16	0.8563	0.95	GG	1.05	AG	0.90	AA	0.77
rs704010	10	C/T	0.38	1.0699	1.05	CC	0.95	TC	1.02	TT	1.09
rs7904519	10	A/G	0.46	1.0584	1.05	AA	0.95	GA	1.00	GG	1.06
rs2981579	10	G/A	0.4	1.2524	1.21	GG	0.83	AG	1.03	AA	1.29
rs2981582	10	T/C	0.42	1.1900	1.17	TT	0.86	CT	1.02	CC	1.21
rs11199914	10	C/T	0.32	0.9400	0.96	CC	1.04	TC	0.98	TT	0.92
rs3817198	11	T/C	0.31	1.0744	1.05	TT	0.96	CT	1.03	CC	1.10
rs3903072	11	G/T	0.47	0.9442	0.95	GG	1.05	TG	1.00	TT	0.94
rs554219	11	C/G	0.112	1.1238	1.03	CC	0.97	GC	1.09	GG	1.23
rs78540526	11	C/T	0.032	1.1761	1.01	CC	0.99	TC	1.16	TT	1.37
rs75915166	11	C/A	0.059	1.0239	1.00	CC	1.00	AC	1.02	AA	1.05
rs11820646	11	C/T	0.41	0.9563	0.96	CC	1.04	TC	0.99	TT	0.95
rs12422552	12	G/C	0.26	1.0327	1.02	GG	0.98	CG	1.02	CC	1.05
rs10771399	12	A/G	0.12	0.8629	0.97	AA	1.03	GA	0.89	GG	0.77
rs17356907	12	A/G	0.3	0.9078	0.95	AA	1.06	GA	0.96	GG	0.87
rs1292011	12	A/G	0.42	0.9219	0.94	AA	1.07	GA	0.99	GG	0.91
rs11571833	13	A/T	0.008	1.2609	1.00	AA	1.00	TA	1.26	TT	1.58

rs2236007	14	G/A	0.21	0.9203	0.97	GG	1.03	AG	0.95	AA	0.88
rs999737	14	C/T	0.23	0.9239	0.97	CC	1.04	TC	0.96	TT	0.88
rs2588809	14	C/T	0.16	1.0667	1.02	CC	0.98	TC	1.04	TT	1.11
rs941764	14	A/G	0.34	1.0636	1.04	AA	0.96	GA	1.02	GG	1.08
rs3803662	16	G/A	0.26	1.2257	1.12	GG	0.89	AG	1.09	AA	1.34
rs17817449	16	T/G	0.4	0.9300	0.94	TT	1.06	GT	0.98	GG	0.92
rs11075995	16	A/T	0.241	1.0368	1.02	AA	0.98	TA	1.02	TT	1.06
rs13329835	16	A/G	0.22	1.0758	1.03	AA	0.97	GA	1.04	GG	1.12
rs6504950	17	G/A	0.28	0.9340	0.96	GG	1.04	AG	0.97	AA	0.91
rs527616	18	G/C	0.38	0.9573	0.97	GG	1.03	CG	0.99	CC	0.95
rs1436904	18	T/G	0.4	0.9466	0.96	TT	1.04	GT	0.99	GG	0.94
rs2363956	19	G/T	0.487	1.0264	1.03	GG	0.97	TG	1.00	TT	1.03
rs8170	19	G/A	0.19	1.0314	1.01	GG	0.99	AG	1.02	AA	1.05
rs4808801	19	A/G	0.35	0.9349	0.95	AA	1.05	GA	0.98	GG	0.92
rs3760982	19	G/A	0.46	1.0553	1.05	GG	0.95	AG	1.00	AA	1.06
rs2823093	21	G/A	0.27	0.9274	0.96	GG	1.04	AG	0.96	AA	0.89
rs17879961	22	A/G	0.005	1.3632	1.00	AA	1.00	GA	1.36	GG	1.85
rs132390	22	T/C	0.036	1.1091	1.01	TT	0.99	CT	1.10	CC	1.22
rs6001930	22	T/C	0.11	1.1345	1.03	TT	0.97	CT	1.10	CC	1.25

Table 14. Expanded list of polymorphisms indicative of breast cancer risk (n=203).

“*” indicates a 21 base pair deletion, “**” indicates a 36 base pair deletion, “***” indicates a 14 base pair insertion, and “****” indicates a 31 kb deletion. “Odds Ratio minor allele” values below 1 means that the minor allele is not the risk allele, whereas when above 1 the minor allele is the risk allele.

Polymorphism	Location	Major allele/ minor allele	Minor allele frequency	Odds ratio minor allele
12:120832146:C:T	12q24.31	C/T	0.16	1.05
12:85009437:T:C	12q21.31	T/C	0.34	0.95
17:44252468:G:A	17q21.31	G/A	0.19	0.95
4:84370124	4q21.23	TA/TAA	0.47	1.04
chr17:29230520	17q11.2	GGT/G	0.27	0.97
chr22:39359355	22q13.1	I/D****	0.10	1.10
rs10022462	4q22.1	C/T	0.44	1.04
rs10069690	5p15.33	C/T	0.26	1.06
rs1011970	9p21.3	G/T	0.16	1.07
rs10472076	5q11.2	T/C	0.38	1.03
rs10474352	5q14.3	C/T	0.16	0.94
rs1053338	3p14.1	A/G	0.14	1.05

rs10623258	14q32.33	C/CTT	0.45	1.04
rs10759243	9q31.2	C/A	0.29	1.06
rs10760444	9q33.3	A/G	0.43	1.03
rs10816625	9q31.2	A/G	0.06	1.11
rs10941679	5p12	A/G	0.25	1.15
rs10995201	10q21.2	A/G	0.16	0.90
rs11075995	16q12.2	T/A	0.24	1.03
rs11076805	16p13.3	C/A	0.26	0.97
rs11117758	1q41	G/A	0.21	0.95
rs11199914	10q26.12	C/T	0.32	0.96
rs11242675	6p25.3	T/C	0.37	1.00
rs11249433	1p11.2	A/G	0.41	1.11
rs113577745	2p25.1	C/G	0.10	1.08
rs113701136	19q12	C/T	0.32	1.03
rs11374964	11q22.3	G/GA	0.42	1.00
rs11389348	20q12	G/GT	0.38	0.96
rs11552449	1p13.2	C/T	0.17	1.04
rs11571833	13q13.1	A/T	0.01	1.35
rs116095464	5p15.33	T/C	0.05	1.06
rs11627032	14q32.12	T/C	0.25	0.96
rs117618124	18q12.1	T/C	0.05	0.89
rs11780156	8q24.21	C/T	0.17	1.05
rs11814448	10p12.31	A/C	0.02	1.12
rs11820646	11q24.3	C/T	0.40	0.96
rs11977670	7q34	G/A	0.43	1.06
rs12048493	1q21.2	A/C	0.38	1.04
rs12207986	6q14.1	A/G	0.47	0.97
rs12405132	1q21.1	C/T	0.37	0.97
rs12422552	12p13.1	G/C	0.26	1.06
rs12479355	2q36.3	A/G	0.21	0.96
rs12493607	3p24.1	G/C	0.34	1.05
rs12546444	8q23.1	A/T	0.10	0.93
rs12624860	20q13.2	C/G	0.24	1.04
rs12710696	2p24.1	C/T	0.37	1.03
rs1292011	12q24.21	A/G	0.42	0.92
rs13066793	3p12.1	A/G	0.09	0.94
rs13162653	5p15.1	G/T	0.45	0.99
rs132390	22q12.2	T/C	0.04	1.04
rs13267382	8q23.3	G/A	0.36	1.03
rs13281615	8q24.21	A/G	0.41	1.11
rs13294895	9q31.2	C/T	0.18	1.06
rs13329835	16q23.2	A/G	0.23	1.07
rs13365225	8p11.23	A/G	0.18	0.91
rs1353747	5q11.2	T/G	0.09	0.96
rs140850326	1p32.3	I/D*	0.49	0.97
rs140936696	10q23.33	C/CAA	0.18	1.04
rs1432679	5q33.3	T/C	0.43	1.08
rs1436904	18q11.2	T/G	0.40	0.95
rs151090251	15q22.33	D/I***	0.05	1.08

rs1550623	2q31.1	A/G	0.15	0.95
rs16857609	2q35	C/T	0.26	1.06
rs16991615	20p12.3	G/A	0.06	1.10
rs1707302	1p34.1	G/A	0.34	0.96
rs17156577	7p15.1	T/C	0.11	1.05
rs17268829	7q21.3	T/C	0.28	1.05
rs17356907	12q22	A/G	0.30	0.91
rs17426269	1p22.3	G/A	0.15	1.05
rs17529111	6q14.1	T/C	0.22	1.02
rs17817449	16q12.2	T/G	0.41	0.95
rs17879961	22q12.1	A/G	0.005	1.26
rs1830298	2q33.1	T/C	0.28	1.06
rs1895062	9q33.1	A/G	0.41	0.94
rs2012709	5p13.3	C/T	0.48	1.02
rs2016394	2q31.1	G/A	0.47	0.95
rs204247	6p23	A/G	0.44	1.04
rs2223621	6p22.3	C/T	0.38	1.04
rs2236007	14q13.3	G/A	0.21	0.93
rs2284378	20q11.22	C/T	0.32	1.00
rs2290203	15q26.1	G/A	0.21	0.94
rs2380205	10p15.1	C/T	0.44	0.98
rs2432539	16q13	G/A	0.40	1.03
rs2588809	14q24.1	C/T	0.17	1.06
rs2594714	19p13.12	G/A	0.23	0.97
rs2747652	6q25	C/T	0.48	0.94
rs2787486	17q22	A/C	0.30	0.93
rs2823093	21q21.1	G/A	0.27	0.94
rs28512361	22q13.31	G/A	0.11	1.05
rs28539243	16q12.2	G/A	0.49	1.05
rs2943559	8q21.11	A/G	0.08	1.10
rs2965183	19p13.11	G/A	0.35	1.04
rs2981578	10q26.13	T/C	0.47	1.23
rs2992756	1p36.13	C/T	0.49	1.06
rs310302	8p21.2	G/A	0.40	1.04
rs3215401	5p15.33	A/AG	0.31	0.93
rs322144	19p13.2	C/G	0.47	0.98
rs34005590	2q35	C/A	0.05	0.82
rs34207738	3q23	CTT/C	0.41	1.06
rs35054928	10q26.13	G/GC	0.40	1.27
rs35383942	1q32.1	C/T	0.06	1.12
rs35951924	5q11.1	A/AT	0.32	0.95
rs36194942	18q12.1	A/AT	0.30	0.98
rs3757322	6q25	T/G	0.32	1.08
rs3760982	19q13.31	G/A	0.46	1.05
rs3817198	11p15.5	T/C	0.32	1.05
rs3819405	6p22.3	C/T	0.33	0.96
rs3903072	11q13.1	G/T	0.47	0.97
rs4233486	1p34.2	T/C	0.36	0.97
rs4245739	1q32.1	A/C	0.26	1.02

rs4442975	2q35	G/T	0.50	0.89
rs4496150	16q24.2	C/A	0.25	0.96
rs4562056	5q35.1	G/T	0.33	1.05
rs45631563	10q26.13	A/T	0.05	0.81
rs4577244	2p23.2	C/T	0.23	1.01
rs4593472	7q32.3	C/T	0.35	0.97
rs4784227	16q12.1	C/T	0.24	1.23
rs4808801	19p13.11	A/G	0.34	0.93
rs4849887	2q14.1	C/T	0.10	0.91
rs4951011	1q32.1	A/G	0.16	1.04
rs4971059	1q22	G/A	0.35	1.05
rs4973768	3p24.1	C/T	0.50	1.11
rs514192	8q22.3	T/A	0.32	1.05
rs527616	18q11.2	G/C	0.38	0.97
rs554219	11q13.3	C/G	0.13	1.21
rs58058861	3q26.31	G/A	0.21	1.06
rs58847541	8q24.13	G/A	0.15	1.08
rs6001930	22q13.1	T/C	0.10	1.12
rs6062356	20q13.33	T/G	0.15	1.06
rs6122906	20q13.13	A/G	0.18	1.05
rs616488	1p36.22	A/G	0.33	0.94
rs62355902	5q11.2	A/T	0.16	1.18
rs6472903	8q21.11	T/G	0.17	0.94
rs6507583	18q12.3	A/G	0.07	0.92
rs6562760	13q22.1	G/A	0.24	0.95
rs6569648	6q23.1	T/C	0.24	0.94
rs6596100	5q31.1	C/T	0.25	0.94
rs6597981	11p15	G/A	0.48	0.96
rs6678914	1q32.1	G/A	0.41	1.00
rs66823261	8p23.3	T/C	0.22	1.03
rs6725517	2p23.3	A/G	0.41	0.96
rs67397200	19p13.11	C/G	0.30	1.03
rs676256	9q31.2	T/C	0.38	0.91
rs6762644	3p26.1	A/G	0.38	1.05
rs67958007	10p14	TG/T	0.12	0.19
rs6796502	3p21.31	G/A	0.10	0.92
rs6805189	3p13	T/C	0.48	0.97
rs6815814	4p14	A/C	0.26	1.06
rs6828523	4q34.1	C/A	0.12	0.91
rs6882649	5q22.1	T/G	0.34	0.97
rs6964587	7q21.2	G/T	0.39	1.03
rs704010	10q22.3	C/T	0.38	1.07
rs7072776	10p12.31	G/A	0.29	1.05
rs71338792	19q13.22	A/AT	0.23	1.05
rs71557345	6p22.2	G/A	0.07	0.92
rs71559437	7q22.1	G/A	0.12	0.93
rs71801447	2q13	CTTATGTT/C	0.06	1.09
rs720475	7q35	G/A	0.25	0.96
rs72749841	5q11.1	T/C	0.16	0.93

rs72755295	1q43	A/G	0.03	1.05
rs72826962	17q21.2	C/T	0.01	1.20
rs7297051	12p11.22	C/T	0.24	0.89
rs73161324	22q13.2	C/T	0.06	1.06
rs738321	22q13.1	C/G	0.38	0.95
rs745570	17q25.3	G/A	0.50	1.03
rs74911261	11q22.3	G/A	0.03	1.01
rs7529522	1p12	T/C	0.23	1.06
rs75915166	11q13.3	C/A	0.06	1.28
rs7707921	5q14.2	A/T	0.25	0.96
rs77528541	4q28.1	G/T	0.13	0.95
rs78269692	19p13.13	T/C	0.05	1.09
rs7904519	10q25.2	A/G	0.46	1.03
rs7971	7p15.3	A/G	0.35	0.96
rs79724016	1p34.2	T/G	0.03	0.93
rs8176636	9q34.2	I/D**	0.20	1.03
rs9257408	6p22.1	G/C	0.41	1.02
rs9348512	6p24.3	C/A	0.33	1.00
rs9358466	6p22.3	T/C	0.43	0.97
rs9397437	6q25	G/A	0.07	1.17
rs941764	14q32.11	A/G	0.35	1.03
rs9485372	6q25.1	G/A	0.19	0.96
rs9693444	8p12	C/A	0.32	1.06
rs9790517	4q24	C/T	0.23	1.04
rs9833888	3p12.1	G/T	0.22	1.06
rs999737	14q24.1	C/T	0.23	0.91
rs2981582	10q26	T/C		
rs3803662	16q12.1	G/A		
rs889312	5q11.2	A/C		
rs13387042	2q35	A/G		
rs4415084	5p12	C/T		
rs1045485	2q33.1	G/C		
rs2736108	5p15.33	C/T		
rs7726159	5p15.33	C/A		
rs12662670	6q25.1	T/G		
rs2046210	6q25.1	G/A		
rs865686	9q31.2	T/G		
rs2981579	10q26.13	G/A		
rs10995190	10q21.2	G/A		
rs78540526	11q13.3	C/T		
rs10771399	12p11.22	A/G		
rs6504950	17q22	G/A		
rs2363956	19p13	G/T		
rs8170	19p13.11	G/A		

Table 15. Optimised list of African American polymorphisms (n=74).

Polymorphism	Chromosome	Major allele/ minor allele
rs11249433	1	G/A
rs4245739	1	C/A
rs616488	1	A/G
rs6678914	1	G/A
rs1045485	2	C/G
rs12710696	2	A/G
rs13387042	2	A/G
rs1550623	2	A/G
rs16857609	2	A/G
rs2016394	2	G/A
rs4849887	2	G/A
rs12493607	3	G/C
rs4973768	3	A/G
rs6762644	3	G/A
rs6828523	4	C/A
rs9790517	4	A/G
rs10069690	5	A/G
rs10472076	5	G/A
rs10941679	5	G/A
rs1353747	5	A/C
rs1432679	5	G/A
rs4415084	5	T/C
rs889312	5	C/A
rs11242675	6	A/G
rs17529111	6	G/A
rs204247	6	G/A
rs2046210	6	A/G
rs3757318	6	A/G
rs720475	7	G/A
rs11780156	8	A/G
rs13281615	8	G/A
rs2943559	8	G/A
rs6472903	8	A/C
rs9693444	8	A/C
rs1011970	9	A/C
rs10759243	9	A/C
rs865686	9	A/C
rs10995190	10	G/A
rs11199914	10	G/A
rs11814448	10	C/A
rs2380205	10	G/A
rs2981579	10	A/G

rs2981582	10	A/G
rs704010	10	A/G
rs7072776	10	A/G
rs7904519	10	G/A
rs11820646	11	G/A
rs3817198	11	G/A
rs3903072	11	C/A
rs554219	11	G/C
rs614367	11	A/G
rs75915166	11	A/C
rs10771399	12	A/G
rs12422552	12	C/G
rs1292011	12	A/G
rs17356907	12	A/G
rs11571833	13	A/T
rs2236007	14	G/A
rs2588809	14	A/G
rs941764	14	G/A
rs999737	14	G/A
rs11075995	16	A/T
rs13329835	16	G/A
rs17817449	16	A/C
rs3803662	16	A/G
rs6504950	17	G/A
rs1436904	18	A/C
rs527616	18	C/G
rs3760982	19	A/G
rs4808801	19	A/G
rs8170	19	A/G
rs2823093	21	G/A
rs132390	22	G/A
rs6001930	22	G/A

Table 16. Optimised list of Hispanic polymorphisms (n=71).

Polymorphism	Chromosome	Major allele/ minor allele
rs11249433	1	C/T
rs11552449	1	T/C
rs4245739	1	A/C
rs616488	1	G/A
rs6678914	1	A/G
rs12710696	2	T/C
rs13387042	2	A/G
rs1550623	2	G/A

rs16857609	2	T/C
rs2016394	2	A/G
rs4849887	2	T/C
rs12493607	3	G/G
rs4973768	3	T/C
rs6762644	3	C/A
rs6828523	4	A/C
rs7696175	4	T/C
rs9790517	4	T/C
rs10069690	5	T/C
rs10472076	5	C/T
rs10941679	5	G/A
rs1353747	5	G/T
rs1432679	5	C/T
rs2067980	5	G/A
rs889312	5	C/A
rs11242675	6	C/T
rs140068132	6	G/A
rs204247	6	G/A
rs2046210	6	A/G
rs2180341	6	G/A
rs17157903	7	T/C
rs720475	7	A/G
rs11780156	8	T/C
rs13281615	8	G/A
rs2943559	8	G/A
rs6472903	8	G/T
rs9693444	8	A/C
rs1011970	9	T/G
rs10759243	9	A/C
rs865686	9	T/G
rs10995190	10	G/A
rs11199914	10	T/C
rs11814448	10	C/A
rs2380205	10	C/T
rs2981579	10	T/C
rs2981582	10	T/C
rs704010	10	T/C
rs7072776	10	A/G
rs11820646	11	T/C
rs3817198	11	C/T
rs3903072	11	T/G
rs10771399	12	T/C
rs12422552	12	C/G
rs1292011	12	A/G
rs17356907	12	G/A
rs2236007	14	A/G
rs2588809	14	T/C
rs941764	14	G/A

rs999737	14	C/T
rs11075995	16	A/T
rs13329835	16	G/A
rs17817449	16	G/T
rs3803662	16	T/C
rs6504950	17	G/A
rs1436904	18	G/T
rs527616	18	C/G
rs2363956	19	C/A
rs3760982	19	A/G
rs4808801	19	G/A
rs8170	19	A/G
rs2823093	21	G/A
rs6001930	22	C/T

Table 17. 313 polymorphism panel.

Chromosome	SNP	GRCh37 Position (hg19)	GRCh38 Position (hg38)	RS Number	Effect Allele	Reference Allele	Effect Allele Frequency	β Overall Breast Cancer	OR Overall Breast Cancer	μ
1	1_7917076_G_A	7917076	7857016	rs707475	A	G	0.3899	-0.0409	0.9599	0.9690
1	1_10566215_A_G	10566215	10506158	rs616488	G	A	0.3290	-0.0586	0.9431	0.9629
1	1_18807339_T_C	18807339	18480845	rs2992756	C	T	0.5145	-0.0564	0.9452	0.9444
1	1_41380440_C_T	41380440	40914768	rs4233486	T	C	0.6438	0.0426	1.0435	1.0568
1	1_41389220_T_C	41389220	40923548	rs114282204	C	T	0.0169	0.1550	1.1677	1.0057
1	1_46670206_TC_T	46670206	46204534	1:46670206_TC_T	T	TC	0.2973	0.0447	1.0457	1.0274
1	1_51467096_CT_C	51467096	51001424	1:51467096_CT_C	C	CT	0.4800	0.0374	1.0381	1.0369
1	1_88156923_G_A	88156923	87691240	rs17426269	A	G	0.1487	0.0494	1.0506	1.0151
1	1_88428199_C_A	88428199	87962516	rs2151842	A	C	0.2477	-0.0387	0.9620	0.9813
1	1_100880328_A_T	100880328	100414772	rs612683	T	A	0.4097	0.0373	1.0380	1.0314
1	1_110198129_CAAA_C	110198129	109655507	1:110198129_CAA A_C	C	CAAA	0.7755	0.0458	1.0469	1.0740
1	1_114445880_G_A	114445880	113903258	rs7513707	A	G	0.1664	0.0621	1.0641	1.0214
1	1_118141492_A_C	118141492	117598870	rs12406858	C	A	0.2657	0.0452	1.0462	1.0247
1	1_120257110_T_C	120257110	119714487	rs637868	C	T	0.5309	0.0385	1.0393	1.0421
1	1_121280613_A_G	121280613	121538815	rs11249433	G	A	0.4053	0.0881	1.0921	1.0761
1	1_121287994_A_G	121287994	121546196	rs111458676	G	A	0.1060	-0.0673	0.9349	0.9862
1	1_145604302_C_CT	145604302	145830811	rs143384623	CT	C	0.3515	-0.0399	0.9609	0.9727
1	1_149906413_T_C	149906413	149934520	rs11205303	C	T	0.4017	0.0548	1.0563	1.0458
1	1_155556971_G_A	155556971	155587180	rs12091730	A	G	0.2302	0.0499	1.0512	1.0237
1	1_168171052_CA_C	168171052	168201814	rs761575824	C	CA	0.1097	-0.0680	0.9343	0.9856

1	1_172328767_T_TA	172328767	172359627	rs11463354	TA	T	0.3305	-0.0435	0.9574	0.9721
1	1_201437832_C_T	201437832	201468704	rs35383942	T	C	0.0559	0.0917	1.0960	1.0108
1	1_202184600_C_T	202184600	202215472	rs6686987	T	C	0.3992	-0.0065	0.9935	0.9948
1	1_203770448_T_A	203770448	203801320	rs7514172	A	T	0.2715	0.0498	1.0511	1.0279
1	1_204502514_T_TTC TGAAACAGGG	204502514	204533386	rs11268668	TTCGTGAA ACAGGG	T	0.8028	-0.0321	0.9684	0.9499
1	1_208076291_G_A	208076291	207902946	rs2785646	A	G	0.3337	-0.0366	0.9641	0.9762
1	1_217053815_T_G	217053815	216880473	rs2576261	G	T	0.3280	0.0417	1.0426	1.0281
1	1_217220574_G_A	217220574	217047232	rs11117758	A	G	0.2107	-0.0440	0.9570	0.9819
1	1_220671050_C_T	220671050	220497708	rs11118563	T	C	0.2415	0.0418	1.0427	1.0207
1	1_242034263_A_G	242034263	241870961	rs72755295	G	A	0.0305	0.1428	1.1535	1.0094
2	2_10138983_T_C	10138983	9998855	rs78425380	C	T	0.1160	0.0603	1.0622	1.0145
2	2_19315675_T_A	19315675	19115914	rs6743383	A	T	0.5599	-0.0331	0.9674	0.9639
2	2_25129473_A_G	25129473	24906604	rs6725517	G	A	0.4082	-0.0427	0.9582	0.9662
2	2_29179452_G_C	29179452	28956586	rs12472404	C	G	0.2287	-0.0066	0.9934	0.9970
2	2_29615233_T_C	29615233	29392367	rs4322799	C	T	0.2622	-0.0427	0.9582	0.9782
2	2_39699510_C_CT	39699510	39472369	rs553796823	CT	C	0.4659	-0.0402	0.9606	0.9636
2	2_70172587_G_A	70172587	69945455	rs6756513	A	G	0.2787	-0.0412	0.9596	0.9776
2	2_88358825_G_C	88358825	88059306	rs1036759	C	G	0.3081	0.0473	1.0484	1.0301
2	2_121058254_A_G	121058254	120300678	rs6746250	G	A	0.7047	-0.0334	0.9672	0.9542
2	2_121089731_T_C	121089731	120332155	rs17625845	C	T	0.1943	-0.0427	0.9582	0.9838
2	2_121159205_G_A	121159205	120401629	rs10164550	A	G	0.3527	-0.0440	0.9570	0.9699
2	2_121246568_T_C	121246568	120488992	rs10179592	C	T	0.8970	0.0992	1.1043	1.1958
2	2_172974566_C_G	172974566	172109838	rs17726078	G	C	0.4743	-0.0473	0.9538	0.9567
2	2_174212910_A_G	174212910	173348182	rs1550622	G	A	0.8450	0.0593	1.0611	1.1059
2	2_192381934_C_T	192381934	191517208	rs2356656	T	C	0.8588	0.0316	1.0321	1.0559
2	2_202204741_T_C	202204741	201340018	rs10197246	C	T	0.7210	-0.0492	0.9520	0.9320

2	2_217920769_G_T	217920769	217056046	rs4442975	T	G	0.5001	-0.1318	0.8765	0.8803
2	2_217955896_GA_G	217955896	217091173	2:217955896_GA_ G	G	GA	0.0382	-0.2016	0.8174	0.9861
2	2_218292158_C_G	218292158	217427435	rs11693806	G	C	0.7309	-0.0757	0.9271	0.8963
2	2_218714845_G_A	218714845	217850122	rs3791977	A	G	0.3917	-0.0431	0.9578	0.9672
2	2_241388857_C_A	241388857	240449440	rs4676356	A	C	0.9772	-0.1232	0.8841	0.7863
3	3_4742251_A_G	4742251	4700567	rs6762558	G	A	0.3802	0.0616	1.0635	1.0489
3	3_27353716_C_A	27353716	27312225	rs552647	A	C	0.5259	0.0748	1.0777	1.0834
3	3_27388664_C_G	27388664	27347173	rs622255657	G	C	0.2735	0.0502	1.0515	1.0284
3	3_29294845_C_T	29294845	29253354	rs112476261	T	C	0.0163	-0.1281	0.8798	0.9961
3	3_30684907_C_T	30684907	30643415	rs17838698	T	C	0.2975	0.0592	1.0610	1.0366
3	3_46888198_T_C	46888198	46846708	rs56387622	C	T	0.1032	-0.0806	0.9226	0.9841
3	3_49709912_C_CT	49709912	49672479	rs371314787	CT	C	0.2873	-0.0367	0.9640	0.9794
3	3_55970777_A_AT	55970777	55936749	rs138866686	AT	A	0.0305	-0.1195	0.8874	0.9932
3	3_59373745_C_T	59373745	59388019	rs2886671	T	C	0.4294	-0.0394	0.9614	0.9671
3	3_63887449_T_TTG	63887449	63901773		TTG	T	0.1297	0.0648	1.0669	1.0174
3	3_71620370_T_G	71620370	71571219	rs9825432	G	T	0.6382	-0.0374	0.9633	0.9537
3	3_87037543_A_G	87037543	86988393	rs13066793	G	A	0.0921	-0.0723	0.9303	0.9872
3	3_99403877_G_A	99403877	99685033	rs639355	A	G	0.4852	-0.0376	0.9631	0.9645
3	3_141112859_CTT_C	141112859	141394017	3:141112859_CTT_ C	C	CTT	0.4149	0.0551	1.0566	1.0476
3	3_172285237_G_A	172285237	172567447	rs58058861	A	G	0.2131	0.0422	1.0431	1.0185
3	3_189774456_C_T	189774456	190056667	rs9882792	T	C	0.2235	-0.0478	0.9533	0.9792
4	4_38784633_G_T	38784633	38783012	rs10012017	T	G	0.2493	0.0489	1.0501	1.0251
4	4_84370124_TAA_T A	84370124	83448971	rs774021038	TA	TAA	0.5324	-0.0464	0.9547	0.9523
4	4_89240476_G_A	89240476	88319324	rs17014016	A	G	0.4395	0.0352	1.0358	1.0317
4	4_92594859_TTCTT TC_T	92594859	91673708	rs775780062	T	TTCTTTC	0.4445	-0.0407	0.9601	0.9649

4	4	4_106069013_G_T	106069013	105147856	rs62331150	T	G	0.2289	0.0471	1.0482	1.0222
4	4	4_126752992_A_AA T	126752992	125831837		AAT	A	0.5167	-0.0377	0.9630	0.9621
4	4	4_143467195_C_T	143467195	142546042	rs56039025	T	C	0.1115	-0.0569	0.9447	0.9877
4	4	4_151218296_CATA TTT_C	151218296	150297144	rs745707748	C	CATATTT	0.6533	0.0388	1.0396	1.0524
4	4	4_175842495_G_A	175842495	174921344	rs28436676	A	G	0.1161	-0.0898	0.9141	0.9802
4	4	4_175847436_C_A	175847436	174926285	rs62334414	A	C	0.3433	0.0348	1.0354	1.0245
4	4	4_187503758_A_T	187503758	186582604		T	A	0.4471	0.0357	1.0363	1.0328
5	5	5_345109_T_C	345109	344994	rs62641919	C	T	0.0544	0.0840	1.0876	1.0096
5	5	5_1279790_C_T	1279790	1279675	rs10069690	T	C	0.2592	0.0617	1.0636	1.0333
5	5	5_1296255_A_AG	1296255	1296140	rs3215401	AG	A	0.3072	-0.0549	0.9466	0.9674
5	5	5_1353077_T_C	1353077	1352962	rs62329727	C	T	0.0121	0.1552	1.1679	1.0041
5	5	5_2777029_G_A	2777029	2776915	rs4866496	A	G	0.4139	0.0391	1.0399	1.0333
5	5	5_16231194_G_C	16231194	16231085	rs17611291	C	G	0.5594	-0.0426	0.9583	0.9539
5	5	5_32579616_TCA_T	32579616	32579510	rs770436441	T	TCA	0.4844	0.0363	1.0370	1.0361
5	5	5_44508264_G_GT	44508264	44508162	rs138335036	GT	G	0.1265	-0.1177	0.8890	0.9721
5	5	5_44619502_A_G	44619502	44619400	rs187108781	G	A	0.1549	-0.1101	0.8957	0.9680
5	5	5_44649944_C_T	44649944	44649842	rs4613718	T	C	0.6010	0.0492	1.0504	1.0615
5	5	5_44706498_A_G	44706498	44706396	rs10941679	G	A	0.2481	0.0497	1.0510	1.0254
5	5	5_44853593_G_C	44853593	44853491	rs17343002	C	G	0.3081	-0.0336	0.9670	0.9797
5	5	5_52679539_C_CA	52679539	53383709		CA	C	0.0998	0.0571	1.0588	1.0118
5	5	5_55662540_C_CT	55662540	56366713	rs553874618	CT	C	0.3631	-0.0458	0.9552	0.9678
5	5	5_55965167_C_T	55965167	56669340	rs889310	T	C	0.5576	0.0394	1.0402	1.0453
5	5	5_56023083_T_G	56023083	56727256	rs16886165	G	T	0.1583	0.1366	1.1464	1.0469
5	5	5_56042972_C_T	56042972	56747145	rs76250845	T	C	0.0521	0.0865	1.0904	1.0094
5	5	5_56045081_T_C	56045081	56749254	rs11949391	C	T	0.1655	-0.0564	0.9452	0.9819
5	5	5_58241712_C_T	58241712	58945885	rs113778879	T	C	0.5750	-0.0434	0.9575	0.9518

5	5	71965007	G_A	71965007	72669180	rs3010266	A	G	0.2572	-0.0410	0.9598	0.9794
5	5	73234583	T_C	73234583	73938758	rs157557	C	T	0.3213	-0.0363	0.9644	0.9772
5	5	77155397	GT_G	77155397	77859573	rs767431357	G	GT	0.3466	-0.0408	0.9600	0.9725
5	5	79180995	G_GA	79180995	79885172	rs34525310	GA	G	0.1755	0.0328	1.0333	1.0117
5	5	81512947	TA_T	81512947	82217128	5:81512947_TA_T	T	TA	0.2503	-0.0598	0.9420	0.9712
5	5	90789470	G_A	90789470	91493653	rs332529	A	G	0.1580	-0.0564	0.9452	0.9827
5	5	104300273	G_T	104300273	104964572	rs17157372	T	G	0.1810	-0.0487	0.9525	0.9829
5	5	122478676	C_A	122478676	123142982	rs335160	A	C	0.7448	-0.0386	0.9621	0.9444
5	5	122705244	C_T	122705244	123369550	rs1428387	T	C	0.0306	0.0944	1.0990	1.0061
5	5	131640536	A_G	131640536	132304843	rs6860806	G	A	0.5427	0.0392	1.0400	1.0439
5	5	132407058	C_T	132407058	133071366	rs6596100	T	C	0.2450	-0.0388	0.9619	0.9814
5	5	158244083	C_T	158244083	158817075	rs1432679	T	C	0.5683	-0.0677	0.9345	0.9270
5	5	169591460	T_C	169591460	170164456	rs10074269	C	T	0.3345	0.0412	1.0421	1.0283
5	5	173358154	G_A	173358154	173931151	rs6864691	A	G	0.4074	0.0365	1.0372	1.0305
5	5	176134882	T_C	176134882	176707881	rs4868701	C	T	0.5422	0.0363	1.0370	1.0405
6	6	13713366	G_C	13713366	13713134	rs418053	C	G	0.5691	-0.0553	0.9462	0.9397
6	6	16399557	C_T	16399557	16399326	rs3819405	T	C	0.3299	-0.0373	0.9634	0.9760
6	6	18783140	G_A	18783140	18782909	rs12211970	A	G	0.6200	0.0326	1.0331	1.0415
6	6	20537845	CA_C	20537845	20537614	rs769485514	C	CA	0.4733	-0.0391	0.9617	0.9640
6	6	21923810	T_C	21923810	21923579	rs9358466	C	T	0.4303	-0.0321	0.9684	0.9730
6	6	27425644	G_C	27425644	27457865	rs34196306	C	G	0.0815	-0.0737	0.9290	0.9885
6	6	43227141	G_A	43227141	43259403	rs111342015	A	G	0.0985	-0.0640	0.9380	0.9878
6	6	82263549	AAT_A	82263549	81553832	rs10623112	A	AAT	0.4262	0.0477	1.0489	1.0421
6	6	85912194	CAA_C	85912194	85202476	6:85912194_CAA_C	C	CAA	0.0604	0.0762	1.0792	1.0096
6	6	87803819	T_C	87803819	87094101	rs73754909	C	T	0.2770	0.0383	1.0390	1.0217
6	6	130341728	C_CT	130341728	130020583	rs55941023	CT	C	0.7116	0.0472	1.0483	1.0700

6	6_149595505_T_C	149595505	149274369	rs2121348	C	T	0.2061	-0.0476	0.9535	0.9809
6	6_151949806_A_C	151949806	151628671	rs6913578	C	A	0.3083	0.0703	1.0728	1.0454
6	6_151955914_A_G	151955914	151634779	rs60954078	G	A	0.0713	0.1449	1.1559	1.0224
6	6_152022664_CAAA_AAAA_C	152022664	151701529	6:152022664_CAA_AAAA_C	C	CAAAAAA	0.6119	0.0137	1.0138	1.0170
6	6_152023191_G_A	152023191	151702056	rs851984	A	G	0.3965	0.0626	1.0646	1.0519
6	6_152055978_A_T	152055978	151734843	rs6904031	T	A	0.0627	0.0740	1.0768	1.0096
6	6_152432902_C_T	152432902	152111767	rs910416	T	C	0.5146	0.0649	1.0671	1.0702
6	6_169006947_C_G	169006947	168606267	rs9364472	G	C	0.5202	-0.0308	0.9697	0.9687
6	6_170332621_T_C	170332621	170017397	rs6940159	C	T	0.6158	0.0373	1.0380	1.0474
7	7_21940960_A_G	21940960	21901342	rs7971	G	A	0.3515	-0.0467	0.9544	0.9682
7	7_25569548_C_T	25569548	25529928	rs289997	T	C	0.1667	-0.0486	0.9526	0.9842
7	7_28869017_G_A	28869017	28829400	rs74765302	A	G	0.1072	-0.0572	0.9444	0.9881
7	7_55192256_A_C	55192256	55124563	rs13244925	C	A	0.5497	-0.0349	0.9657	0.9626
7	7_91459189_A_ATT	91459189	91829875		ATT	A	0.3286	0.0452	1.0462	1.0306
7	7_94113799_T_C	94113799	94484487	rs17268829	C	T	0.2792	0.0449	1.0459	1.0258
7	7_98005235_G_A	98005235	98375923	rs4439053	A	G	0.1627	-0.0467	0.9544	0.9852
7	7_99948655_T_G	99948655	100351032	rs111963714	G	T	0.2109	0.0420	1.0429	1.0182
7	7_101552440_G_A	101552440	101909160	rs71559437	A	G	0.1255	-0.0568	0.9448	0.9862
7	7_102481842_T_C	102481842	102841395	rs7800548	C	T	0.3416	0.0418	1.0427	1.0294
7	7_130656911_C_T	130656911	130972152	rs12706954	T	C	0.3734	-0.0476	0.9535	0.9656
7	7_130674481_G_A	130674481	130989722	rs68056147	A	G	0.2971	0.0416	1.0425	1.0254
7	7_139943702_CT_C	139943702	140243902	rs201664599	C	CT	0.5381	0.0582	1.0599	1.0655
7	7_144048902_G_T	144048902	144351809	rs62485509	T	G	0.2284	-0.0563	0.9453	0.9751
8	8_170692_T_C	170692	220692	rs66823261	C	T	0.2227	0.0477	1.0489	1.0219
8	8_17787610_CT_C	17787610	17930101	8:17787610_CT_C	C	CT	0.6230	-0.0377	0.9630	0.9544
8	8_23447496_A_G	23447496	23589983	rs1028016	G	A	0.6487	-0.0389	0.9618	0.9511

8	8	23663653_C_A	23663653	23806140	rs310295	A	C	0.4032	0.0335	1.0341	1.0277
8	8	29509616_A_C	29509616	29652100	rs9693444	C	A	0.6756	-0.0601	0.9417	0.9227
8	8	36858483_A_G	36858483	37000965	rs13365225	G	A	0.1820	-0.0760	0.9268	0.9735
8	8	76230943_A_G	76230943	75318708	rs1511243	G	A	0.8282	0.0755	1.0784	1.1341
8	8	76333056_C_T	76333056	75420821	rs72658084	T	C	0.0878	0.1129	1.1195	1.0211
8	8	76378165_G_T	76378165	75465930	rs1533366	T	G	0.3595	-0.0391	0.9617	0.9726
8	8	102483100_T_C	102483100	101470872	rs62517052	C	T	0.0967	0.0593	1.0611	1.0118
8	8	106358620_A_T	106358620	105346392	rs12546444	T	A	0.1003	-0.0745	0.9282	0.9856
8	8	117209548_A_G	117209548	116197325	rs13267382	G	A	0.6445	-0.0417	0.9592	0.9480
8	8	120862186_A_G	120862186	119849946	rs62526620	G	A	0.1318	0.0527	1.0541	1.0143
8	8	124563705_T_C	124563705	123551465	rs35542655	C	T	0.1458	0.0477	1.0489	1.0143
8	8	124571581_G_A	124571581	123559341	rs12541094	A	G	0.4173	0.0340	1.0346	1.0291
8	8	124739913_T_G	124739913	123727673	rs7842619	G	T	0.3985	0.0466	1.0477	1.0384
8	8	128213561_C_CA	128213561	127201316	rs35961416	CA	C	0.4153	-0.0430	0.9579	0.9653
8	8	128370949_C_G	128370949	127358703	rs12550713	G	C	0.4020	0.0642	1.0663	1.0540
8	8	128372172_A_G	128372172	127359926	rs10096351	G	A	0.5446	0.0597	1.0615	1.0681
8	8	129199566_G_A	129199566	128187320	rs1016578	A	G	0.1717	0.0615	1.0634	1.0219
8	8	143669254_A_G	143669254	142587893	rs7830152	G	A	0.3390	-0.0346	0.9660	0.9771
9	9	6880263_A_G	6880263	6880263	rs10975870	G	A	0.2855	0.0348	1.0354	1.0203
9	9	21964882_CAAAA	21964882	21964883	rs745322029	C	CAAAA	0.3184	0.0550	1.0565	1.0363
9	9	22041998_C_G	22041998	22041999	rs17694493	G	C	0.1393	0.0289	1.0293	1.0082
9	9	36928288_T_C	36928288	36928291	rs4880038	C	T	0.5349	0.0249	1.0252	1.0272
9	9	87782211_T_C	87782211	85167296	rs665889	C	T	0.5094	0.0361	1.0368	1.0378
9	9	98362587_T_C	98362587	95600305	rs10120432	C	T	0.0940	0.0576	1.0593	1.0112
9	9	110303808_TAA_T	110303808	107541527	9:110303808_TAA_T	T	TAA	0.2065	0.0797	1.0830	1.0346
9	9	110837073_A_G	110837073	108074792	rs10816625	G	A	0.0630	0.1158	1.1228	1.0155

9	9_110837176_C_T	110837176	108074895	rs13294895	T	C	0.1750	0.0653	1.0675	1.0238
9	9_110849525_G_T	110849525	108087244	rs7848334	T	G	0.5977	0.0153	1.0154	1.0185
9	9_110885479_C_T	110885479	108123199	rs6309065	T	C	0.6222	0.0877	1.0917	1.1173
9	9_119313486_A_G	119313486	116551207	rs1895062	G	A	0.4087	-0.0462	0.9549	0.9634
9	9_129424719_A_G	129424719	126662440	rs3861871	G	A	0.4577	-0.0382	0.9625	0.9660
9	9_136146597_C_T	136146597	133271182	rs550057	T	C	0.2727	0.0400	1.0408	1.0224
10	10_5794652_A_G	5794652	5752689	rs55910451	G	A	0.2137	0.0470	1.0481	1.0207
10	10_13892298_G_A	13892298	13850298	rs10796139	A	G	0.4376	0.0371	1.0378	1.0334
10	10_22032942_A_G	22032942	21744013	rs7072776	G	A	0.7085	-0.0580	0.9436	0.9217
10	10_22477776_ACC_A	22477776	22188847	rs762131501	A	ACC	0.0202	0.1687	1.1838	1.0074
10	10_22861490_A_C	22861490	22572561	rs10764337	C	A	0.9370	0.0875	1.0914	1.1787
10	10_38523626_C_A	38523626	38234698	rs2384736	A	C	0.3698	0.0404	1.0412	1.0307
10	10_64299890_A_G	64299890	62540131	rs10995201	G	A	0.1603	-0.1345	0.8742	0.9601
10	10_64819996_G_T	64819996	63060236	rs6479868	T	G	0.1958	0.0472	1.0483	1.0190
10	10_71335574_C_T	71335574	69575818	rs111833376	T	C	0.3179	-0.0404	0.9604	0.9750
10	10_80851257_G_T	80851257	79091500	rs719338	T	G	0.6172	-0.0805	0.9227	0.9068
10	10_80886726_A_G	80886726	79126969	rs4980029	G	A	0.1631	0.0762	1.0792	1.0260
10	10_95292187_CAA_C	95292187	93532430	10:95292187_CAA_C	C	CAA	0.8234	-0.0512	0.9501	0.9195
10	10_114777670_C_T	114777670	113017911	rs10885405	T	C	0.4631	0.0472	1.0483	1.0453
10	10_115128491_T_C	115128491	113368732	rs12250948	C	T	0.7846	-0.0592	0.9425	0.9118
10	10_123095209_G_A	123095209	121335695	rs9421410	A	G	0.3269	-0.0538	0.9476	0.9660
10	10_123340107_A_G	123340107	121580593	rs45631580	G	A	0.0656	0.1508	1.1628	1.0215
10	10_123340431_GC_G	123340431	121580917	10:123340431_GC_G	G	GC				
10	10_123349324_A_T	123349324	121589810	rs45631563	T	A	0.0484	-0.2609	0.7704	0.9779
11	11_433617_T_C	433617	433617	rs7394715	C	T	0.7969	-0.0437	0.9572	0.9330

11	11_803017_A_G	803017	803017	rs6597981	G	A	0.5167	0.0457	1.0468	1.0489
11	11_1895708_C_A	1895708	1874478	rs4980386	A	C	0.3924	-0.0762	0.9266	0.9432
11	11_18664241_T_G	18664241	18642694	rs10832963	G	T	0.7293	0.0461	1.0472	1.0700
11	11_42844441_C_T	42844441	42822891	rs4472923	T	C	0.3279	-0.0336	0.9670	0.9784
11	11_44368892_G_A	44368892	44347342	rs10838267	A	G	0.5495	0.0374	1.0381	1.0423
11	11_46318032_C_G	46318032	46296481	rs77047825	G	C	0.0659	-0.0748	0.9279	0.9905
11	11_65553492_C_A	65553492	65786021	rs12287832	A	C	0.1867	0.0425	1.0434	1.0163
11	11_65572431_G_A	65572431	65804960	rs10896047	A	G	0.4886	-0.0347	0.9659	0.9670
11	11_69328130_A_T	69328130	69513362	rs35039974	T	A	0.2130	-0.0423	0.9586	0.9824
11	11_69330983_G_A	69330983	69516215	rs661204	A	G	0.1250	0.1022	1.1076	1.0271
11	11_69331418_C_T	69331418	69516650	rs78540526	T	C	0.0753	0.1782	1.1951	1.0296
11	11_103614438_T_G	103614438	103743710	rs7125780	G	T	0.6572	0.0147	1.0148	1.0196
11	11_108267402_C_CA	108267402	108396675	rs199504893	CA	C	0.4173	-0.0022	0.9978	0.9982
11	11_111696440_T_C	111696440	111825716	rs610437	C	T	0.6221	-0.0396	0.9612	0.9523
11	11_116727936_A_T	116727936	116857220	rs625145	T	A	0.2046	-0.0423	0.9586	0.9831
11	11_122966626_A_G	122966626	123095918	rs7121616	G	A	0.2922	-0.0383	0.9624	0.9782
11	11_129243417_T_G	129243417	129373522	rs7939702	G	T	0.8620	-0.0543	0.9471	0.9110
11	11_129461016_A_G	129461016	129591121	rs11822830	G	A	0.6016	0.0453	1.0463	1.0565
12	12_293626_A_G	293626	184460	rs797736	G	A	0.3711	0.0401	1.0409	1.0306
12	12_14413931_G_C	14413931	14260997	rs12422552	C	G	0.2619	0.0484	1.0496	1.0261
12	12_28149568_C_T	28149568	27996635	rs788458	T	C	0.1170	-0.0620	0.9399	0.9860
12	12_28174817_C_T	28174817	28021884	rs7297051	T	C	0.2421	-0.0856	0.9180	0.9607
12	12_28347382_C_T	28347382	28194449	rs11049431	T	C	0.2153	-0.0521	0.9492	0.9783
12	12_29140260_G_A	29140260	28987327	rs1027113	A	G	0.9126	0.0647	1.0668	1.1257
12	12_57146069_T_G	57146069	56752285	rs2277339	G	T	0.1037	-0.0579	0.9437	0.9884
12	12_70798355_A_T	70798355	70404575	rs2870876	T	A	0.1810	0.0469	1.0480	1.0175
12	12_83064195_G_GA	83064195	82670416	rs111622698	GA	G	0.0992	0.0671	1.0694	1.0138

12	12	12_85004551_C_T	85004551	84610772	rs10862899	T	C	0.4955	0.0348	1.0354	1.0354
12	12	12_96027759_A_G	96027759	95633983	rs17356907	G	A	0.2963	-0.0867	0.9170	0.9514
12	12	12_103097887_C_T	103097887	102704109	rs7132703	T	C	0.1175	0.0546	1.0561	1.0132
12	12	12_111600134_G_T	111600134	111162330	rs11065822	T	G	0.3715	-0.0442	0.9568	0.9681
12	12	12_115108136_T_C	115108136	114670331	rs1061657	C	T	0.2615	0.0465	1.0476	1.0251
12	12	12_115796577_A_G	115796577	115358772	rs11067551	G	A	0.1959	-0.0428	0.9581	0.9837
12	12	12_115835836_T_C	115835836	115398031	rs2454399	C	T	0.4171	-0.0813	0.9219	0.9359
12	12	12_120832146_C_T	120832146	120394343	rs206966	T	C	0.1593	0.0516	1.0530	1.0169
13	13	13_32839990_G_A	32839990	32265853	rs56404467	A	G	0.0174	0.0424	1.0433	1.0015
13	13	13_32972626_A_T	32972626	32398489	rs11571833	T	A	0.0079	0.2687	1.3083	1.0049
13	13	13_43501356_A_G	43501356	42927220	rs9315973	G	A	0.8303	0.0517	1.0531	1.0901
13	13	13_73806982_T_C	73806982	73232845	rs12870942	C	T	0.3153	0.0345	1.0351	1.0223
13	13	13_73960952_A_G	73960952	73386815	rs2181965	G	A	0.7618	0.0399	1.0407	1.0630
14	14	14_37128564_C_A	37128564	36659359	rs34914085	A	C	0.2122	-0.0733	0.9293	0.9702
14	14	14_37228504_C_T	37228504	36759299	rs2253012	T	C	0.4434	0.0390	1.0398	1.0356
14	14	14_68660428_T_C	68660428	68193711	rs2588809	C	T	0.8345	-0.0474	0.9537	0.9242
14	14	14_68979835_T_C	68979835	68513118	rs11624333	C	T	0.2581	-0.0911	0.9129	0.9556
14	14	14_91751788_TC_T	91751788	91285444	14_91751788_TC_T	T	TC	0.6934	0.0380	1.0387	1.0544
14	14	14_91841069_A_G	91841069	91374725	rs941764	G	A	0.3444	0.0513	1.0526	1.0366
14	14	14_93070286_C_T	93070286	92603941	rs78440108	T	C	0.1709	-0.0577	0.9439	0.9809
14	14	14_105213978_T_G	105213978	104747641	rs4983544	G	T	0.4588	0.0399	1.0407	1.0377
15	15	15_46680811_C_A	46680811	46388613	rs187010898	A	C	0.0115	-0.1973	0.8209	0.9959
15	15	15_50694306_A_G	50694306	50402109	rs4774565	G	A	0.3446	-0.0417	0.9592	0.9720
15	15	15_66630569_G_A	66630569	66338231	rs8042593	A	G	0.6413	-0.0369	0.9638	0.9541
15	15	15_67457698_A_G	67457698	67165360	rs35874463	G	A	0.0496	0.0782	1.0813	1.0081
15	15	15_75750383_T_C	75750383	75458042	rs8035987	C	T	0.2604	-0.0413	0.9595	0.9790
15	15	15_91512267_G_T	91512267	90969037	rs2290202	T	G	0.1353	-0.0589	0.9428	0.9846

15	15_100905819_A_C	100905819	100365614	rs144767203	C	A	0.1100	-0.0608	0.9410	0.9871
16	16_4008542_CAAA A_C	4008542	3958541	16_4008542_CAAA AA_C	C	CAAAAA	0.8213	-0.0329	0.9676	0.9475
16	16_4106788_C_A	4106788	4056787	rs11076805	A	C	0.2643	-0.0300	0.9704	0.9844
16	16_6963972_C_G	6963972	6913971	rs12709163	G	C	0.7835	0.0354	1.0360	1.0573
16	16_10706580_G_A	10706580	10612723	rs34872983	A	G	0.0695	-0.0740	0.9287	0.9901
16	16_23007047_G_T	23007047	22995726	rs75753503	T	G	0.0236	0.1218	1.1295	1.0061
16	16_52538825_C_A	52538825	52504913	rs35668161	A	C	0.2562	0.1147	1.1215	1.0632
16	16_52599188_C_T	52599188	52565276	rs4784227	T	C	0.2406	0.1070	1.1129	1.0551
16	16_53809123_C_T	53809123	53775211	rs55872725	T	C	0.4201	-0.0704	0.9320	0.9437
16	16_53861139_C_T	53861139	53827227	rs6499648	T	C	0.7604	-0.0338	0.9668	0.9501
16	16_53861592_G_A	53861592	53827680	rs7184573	A	G	0.3663	-0.0337	0.9669	0.9759
16	16_54682064_G_A	54682064	54648152	rs28539243	A	G	0.4850	0.0477	1.0489	1.0480
16	16_80648296_A_G	80648296	80614399	rs7500067	G	A	0.2303	0.0839	1.0875	1.0407
16	16_85145977_T_C	85145977	85112371	rs9931038	C	T	0.4856	-0.0211	0.9791	0.9798
16	16_87086492_T_C	87086492	87052886	rs12449271	C	T	0.2586	-0.0469	0.9542	0.9764
17	17_29168077_G_T	29168077	30841059	rs79461387	T	G	0.2613	-0.0568	0.9448	0.9713
17	17_39251123_T_C	39251123	41094871	rs150537328	C	T	0.0682	0.0799	1.0832	1.0114
17	17_40127060_T_C	40127060	41975042	rs11296	C	T	0.0570	0.0174	1.0176	1.0020
17	17_40485239_G_T	40485239	42333221	rs17881320	T	G	0.0874	-0.0571	0.9445	0.9903
17	17_40744470_G_A	40744470	42592452	rs149370081	A	G	0.0124	0.2017	1.2235	1.0055
17	17_43212339_C_CT	43212339	45134972	rs545502941	CT	C	0.2284	0.0438	1.0448	1.0206
17	17_44283858_G_A	44283858	46206492	rs2668667	A	G	0.1895	-0.0540	0.9474	0.9802
17	17_53209774_A_C	53209774	55132413	rs2787486	C	A	0.3023	-0.0793	0.9238	0.9544
17	17_77781725_A_G	77781725	79807926	rs745570	G	A	0.5038	-0.0401	0.9607	0.9608
18	18_11696613_C_T	11696613	11696614	rs16976596	T	C	0.1379	-0.0381	0.9626	0.9897
18	18_20634253_C_T	20634253	23054290	rs11665269	T	C	0.6403	-0.0415	0.9593	0.9486

18	18_24125857_T_C	24125857	26545893	rs11111207	C	T	0.4214	0.0346	1.0352	1.0299
18	18_24337424_C_G	24337424	26757460	rs527616	G	C	0.6205	0.0455	1.0466	1.0586
18	18_24518050_AT_A	24518050	26938086	18_24518050_AT_A	A	AT	0.2773	-0.0599	0.9419	0.9680
18	18_25407513_C_G	25407513	27827549	rs8092192	G	C	0.7126	0.0399	1.0407	1.0589
18	18_29981526_G_A	29981526	32401563	rs72931898	A	G	0.0474	-0.1058	0.8996	0.9905
18	18_42411803_G_C	42411803	44831838	rs9954058	C	G	0.0717	-0.0877	0.9160	0.9880
18	18_42888797_T_C	42888797	45308832	rs9952980	C	T	0.3519	-0.0542	0.9472	0.9632
19	19_13249921_G_T	13249921	13139107	rs117922601	T	G	0.0513	0.0956	1.1003	1.0103
19	19_17393925_C_A	17393925	17283116	rs56069439	A	C	0.2958	0.0378	1.0385	1.0229
19	19_18569492_C_T	18569492	18458682	rs10164323	T	C	0.3481	-0.0719	0.9306	0.9523
19	19_19517054_C_CG	19517054	19406245	rs140702307	CGGGCG	C	0.3537	0.0437	1.0447	1.0318
19	19_44283031_T_C	44283031	43778879	rs56681946	C	T	0.3519	0.0619	1.0639	1.0454
19	19_46166073_T_C	46166073	45662815	rs4399645	C	T	0.6074	-0.0360	0.9646	0.9575
19	19_55816678_C_T	55816678	55305310	rs1172821	T	C	0.3626	-0.0359	0.9647	0.9746
20	20_5948227_G_A	5948227	5967581	rs16991615	A	G	0.0628	0.0760	1.0790	1.0099
20	20_11379842_T_C	11379842	11399194	rs1154723	C	T	0.9483	0.0844	1.0881	1.1740
20	20_41613706_C_G	41613706	42985066	rs6030585	G	C	0.7928	0.0315	1.0320	1.0514
20	20_52296849_G_A	52296849	53680310	rs13039563	A	G	0.2400	0.0440	1.0450	1.0217
21	21_16364756_T_G	16364756	14992435	rs2822999	G	T	0.1732	0.0646	1.0667	1.0233
21	21_16566350_A_G	16566350	15194030	rs2823130	G	A	0.0873	0.0595	1.0613	1.0107
21	21_16574455_C_A	16574455	15202135	rs2403907	A	C	0.3167	-0.0707	0.9317	0.9572
21	21_47762932_G_A	47762932	46343018	rs4818836	A	G	0.0355	0.0946	1.0992	1.0071
22	22_19766137_C_T	19766137	19778614	rs9798754	T	C	0.3798	-0.0367	0.9640	0.9728
22	22_29121087_A_G	29121087	28725099	rs17879961	G	A	0.0054	0.1839	1.2019	1.0022
22	22_29135543_G_A	29135543	28739555	rs5997390	A	G	0.0870	0.0654	1.0676	1.0118

22	22_29203724_C_T	29203724	28807736	rs34134147	T	C	0.0209	0.1405	1.1508	1.0063
22	22_29551872_A_G	29551872	29155884	rs132289	G	A	0.9846	-0.1716	0.8423	0.7136
22	22_38583315_AAAA G AAAAGAAAG	38583315	38187308		AAAAGAA AG	AAAAG	0.2805	-0.0471	0.9540	0.9744
22	22_39343916_T_A	39343916	38947911	rs750715	A	T	0.2541	0.0407	1.0415	1.0212
22	22_40904707_CT_C	40904707	40508703	22:40904707_CT_C	C	CT	0.1099	0.1148	1.1216	1.0269
22	22_43433100_C_T	43433100	43037094	rs9611990	T	C	0.1144	-0.0600	0.9418	0.9867
22	22_45319953_G_A	45319953	44924073	rs112855987	A	G	0.4166	-0.0134	0.9867	0.9889
22	22_46283297_G_A	46283297	45887417	rs28512361	A	G	0.1117	0.0736	1.0764	1.0171

Table 18. 3,820 polymorphism panel.

Chromosome	SNP	GRCh37 Position (hg19)	GRCh38 Position (hg38)	RS Number	Effect Allele	Reference Allele	Effect Allele Frequency	β Overall Breast Cancer	OR Overall Breast Cancer	μ
1	1_4693695_C_T	4693695	4633635	rs74051909	T	C	0.2718	-0.0086	0.9914	0.9954
1	1_5470084_A_G	5470084	5410024	rs61763346	G	A	0.0367	0.0163	1.0164	1.0012
1	1_7598422_TA_T	7598422	7538362	1:7598422_TA_T	T	TA	0.0579	-0.0078	0.9922	0.9991
1	1_7799738_A_G	7799738	7739678	rs59214896	G	A	0.2085	0.0002	1.0002	1.0001
1	1_7801288_G_A	7801288	7741228	rs2032563	A	G	0.1975	0.0008	1.0008	1.0003
1	1_7911221_A_G	7911221	7851161	rs79479445	G	A	0.0630	-0.0003	0.9997	1.0000
1	1_7917076_G_A	7917076	7857016	rs707475	A	G	0.3899	-0.0137	0.9864	0.9894
1	1_8095500_T_G	8095500	8035440	rs225132	G	T	0.1821	-0.0132	0.9869	0.9952
1	1_9280040_C_T	9280040	9219981	rs10864397	T	C	0.5749	0.0039	1.0039	1.0045
1	1_10315413_G_A	10315413	10255355	rs112432872	A	G	0.0514	0.0000	1.0000	1.0000
1	1_10525841_T_C	10525841	10465784	rs34132699	C	T	0.2568	0.0000	1.0000	1.0000
1	1_10554505_A_G	10554505	10494448	rs597438	G	A	0.7029	0.0050	1.0050	1.0071
1	1_10565488_C_T	10565488	10505431	rs1755594	T	C	0.6348	0.0000	1.0000	1.0000
1	1_10566215_A_G	10566215	10506158	rs616488	G	A	0.3290	-0.0246	0.9757	0.9841
1	1_10570721_G_A	10570721	10510664	rs2480784	A	G	0.0676	-0.0038	0.9962	0.9995
1	1_10612820_G_C	10612820	10552763	rs9430149	C	G	0.3149	-0.0010	0.9990	0.9994
1	1_10614233_C_T	10614233	10554176	rs35612158	T	C	0.1803	0.0062	1.0062	1.0022
1	1_10629772_G_T	10629772	10569715	rs76431309	T	G	0.0536	0.0000	1.0000	1.0000
1	1_10633489_A_G	10633489	10573432	rs78507554	G	A	0.1476	0.0000	1.0000	1.0000
1	1_10704688_C_T	10704688	10644631	rs11587145	T	C	0.1333	0.0083	1.0083	1.0022

1	1_11843224_C_T	11843224	11783167	rs116276371	T	C	0.0265	0.0054	1.0054	1.0003
1	1_14507831_C_T	14507831	14181336	rs12065331	T	C	0.3179	0.0063	1.0063	1.0040
1	1_15296282_T_G	15296282	14969786	rs4575078	G	T	0.2643	0.0067	1.0067	1.0036
1	1_15693556_A_T	15693556	15367060	rs2496346	T	A	0.1854	0.0035	1.0035	1.0013
1	1_15719028_A_G	15719028	15392532	rs12734304	G	A	0.1302	0.0059	1.0059	1.0015
1	1_16075981_C_T	16075981	15749486	rs11585750	T	C	0.3254	0.0086	1.0086	1.0056
1	1_17733996_G_A	17733996	17407500	rs3193024	A	G	0.1119	-0.0077	0.9923	0.9983
1	1_18800547_A_G	18800547	18474053	rs2992734	G	A	0.7428	0.0000	1.0000	1.0000
1	1_18807339_T_C	18807339	18480845	rs2992756	C	T	0.5145	-0.0098	0.9902	0.9900
1	1_18807953_C_A	18807953	18481459	rs11261022	A	C	0.3691	-0.0097	0.9903	0.9929
1	1_18808292_C_A	18808292	18481798	rs2992753	A	C	0.6357	-0.0172	0.9829	0.9784
1	1_18809916_G_A	18809916	18483422	rs12061708	A	G	0.3226	-0.0070	0.9930	0.9955
1	1_21262731_G_A	21262731	20936238	rs72652973	A	G	0.0113	-0.0196	0.9806	0.9996
1	1_22370457_CT_C	22370457	22043964	1:22370457_C T_C	C	CT	0.1770	-0.0010	0.9990	0.9996
1	1_22439520_T_C	22439520	22113027	rs4654783	C	T	0.6978	0.0044	1.0044	1.0062
1	1_22485467_A_G	22485467	22158974	rs2807365	G	A	0.3350	-0.0021	0.9979	0.9986
1	1_22585468_G_A	22585468	22258975	rs76843148	A	G	0.0560	0.0057	1.0057	1.0006
1	1_23068465_C_T	23068465	22741972	rs6669666	T	C	0.2068	-0.0028	0.9972	0.9988
1	1_23098679_C_T	23098679	22772186	rs114804938	T	C	0.0189	0.0203	1.0205	1.0008
1	1_23862653_A_G	23862653	23536161	rs760607	G	A	0.3939	0.0065	1.0065	1.0051
1	1_24565083_C_T	24565083	24238593	rs11249049	T	C	0.2619	-0.0075	0.9925	0.9961
1	1_24593061_T_C	24593061	24266571	rs72874872	C	T	0.0425	0.0033	1.0033	1.0003
1	1_25197155_G_A	25197155	24870664	rs4648881	A	G	0.4848	0.0032	1.0032	1.0031
1	1_25220498_G_T	25220498	24894007	rs11249197	T	G	0.4802	0.0000	1.0000	1.0000
1	1_25241056_G_A	25241056	24914565	rs2282718	A	G	0.3977	-0.0123	0.9878	0.9903
1	1_25251706_T_C	25251706	24925215	rs742232	C	T	0.5531	0.0006	1.0006	1.0007

1	1_26758602_T_C	26758602	26432111	rs3811462	C	T	0.7850	0.0052	1.0052	1.0082
1	1_27304568_A_G	27304568	26978077	rs2993063	G	A	0.7725	-0.0001	0.9999	0.9998
1	1_27557607_G_A	27557607	27231116	rs4609452	A	G	0.8161	-0.0069	0.9931	0.9888
1	1_32407833_C_T	32407833	31942232	rs139994937	T	C	0.0612	-0.0242	0.9761	0.9971
1	1_32551080_G_A	32551080	32085479	rs72666734	A	G	0.0631	-0.0108	0.9893	0.9986
1	1_33727981_C_CT	33727981	33262380	rs34542197	CT	C	0.7619	0.0126	1.0127	1.0194
1	1_35619907_G_A	35619907	35154306	rs2878436	A	G	0.8952	-0.0151	0.9850	0.9733
1	1_36588402_G_A	36588402	36122801	rs11263857	A	G	0.1021	0.0108	1.0109	1.0022
1	1_39976128_T_C	39976128	39510456	rs1180325	C	T	0.4332	-0.0039	0.9961	0.9966
1	1_40398728_C_T	40398728	39933056	rs7554235	T	C	0.2564	0.0081	1.0081	1.0042
1	1_40435999_A_G	40435999	39970327	rs2131311	G	A	0.7259	-0.0053	0.9947	0.9923
1	1_41332388_C_T	41332388	40866716	rs12049459	T	C	0.3185	0.0065	1.0065	1.0042
1	1_41351322_A_G	41351322	40885650	rs111473215	G	A	0.3118	-0.0049	0.9951	0.9970
1	1_41380170_A_AG	41380170	40914498	rs769225960	AG	A	0.8630	0.0010	1.0010	1.0017
1	1_41380440_C_T	41380440	40914768	rs4233486	T	C	0.6438	0.0157	1.0158	1.0205
1	1_41389220_T_C	41389220	40923548	rs114282204	C	T	0.0169	0.0531	1.0545	1.0018
1	1_41887180_GT_G	41887180	41421508	1:41887180_G T_G	G	GT	0.5612	-0.0035	0.9965	0.9961
1	1_41909856_C_T	41909856	41444185	rs7534137	T	C	0.1359	0.0037	1.0037	1.0010
1	1_42018135_G_A	42018135	41552464	rs144427343	A	G	0.0478	0.0048	1.0048	1.0005
1	1_42058260_G_C	42058260	41592589	rs116351921	C	G	0.0777	0.0204	1.0206	1.0032
1	1_42140601_C_T	42140601	41674930	rs56394244	T	C	0.0336	-0.0415	0.9593	0.9973
1	1_42176600_C_T	42176600	41710929	rs36021639	T	C	0.0841	0.0005	1.0005	1.0001
1	1_42204512_A_G	42204512	41738841	rs77615557	G	A	0.0567	0.0158	1.0159	1.0018
1	1_44514883_G_C	44514883	44049211	rs2108201	C	G	0.6371	-0.0083	0.9917	0.9895
1	1_44564405_G_A	44564405	44098733	rs12756908	A	G	0.3317	-0.0022	0.9978	0.9985
1	1_44926646_T_C	44926646	44460974	rs946960	C	T	0.2722	0.0000	1.0000	1.0000

1	1_44935232_T_TAT TC	44935232	44469560	rs35387836	TATTC	T	0.3280	-0.0017	0.9983	0.9989
1	1_45842878_C_G	45842878	45377206	rs76179004	G	C	0.0470	-0.0018	0.9982	0.9998
1	1_45939591_C_T	45939591	45473919	rs1765709	T	C	0.4998	0.0000	1.0000	1.0000
1	1_46487168_T_C	46487168	46021496	rs946526	C	T	0.9570	0.0101	1.0102	1.0195
1	1_46526185_A_G	46526185	46060513	rs72677528	G	A	0.0604	0.0012	1.0012	1.0001
1	1_46600917_A_G	46600917	46135245	rs1707302	G	A	0.6633	0.0073	1.0073	1.0097
1	1_46670206_TC_T	46670206	46204534	1:46670206_T C_T	T	TC	0.2973	0.0050	1.0050	1.0030
1	1_46701282_G_A	46701282	46235610	rs12129542	A	G	0.7452	0.0000	1.0000	1.0000
1	1_46776759_A_T	46776759	46311087	rs61273183	T	A	0.5999	0.0000	1.0000	1.0000
1	1_46823917_A_G	46823917	46358245	rs6674538	G	A	0.2891	0.0003	1.0003	1.0002
1	1_46842079_TA_T	46842079	46376407	1:46842079_T A_T	T	TA	0.3065	0.0195	1.0197	1.0121
1	1_50771882_T_C	50771882	50306210	rs12070259	C	T	0.0459	0.0093	1.0093	1.0009
1	1_51129510_AATC _A	51129510	50663838	1:51129510_A ATC_A	A	AATC	0.0324	0.0157	1.0158	1.0010
1	1_51467096_CT_C	51467096	51001424	1:51467096_C T_C	C	CT	0.4800	0.0057	1.0057	1.0055
1	1_51478336_T_A	51478336	51012664	rs35311109	A	T	0.2917	0.0077	1.0077	1.0045
1	1_56363704_CT_C	56363704	55898031	1:56363704_C T_C	C	CT	0.2643	0.0053	1.0053	1.0028
1	1_58592530_C_T	58592530	58126858	rs6659357	T	C	0.2020	0.0031	1.0031	1.0013
1	1_58891310_A_G	58891310	58425638	rs724564	G	A	0.1220	-0.0176	0.9826	0.9957
1	1_59981754_ATTAT GCCTTC_A	59981754	59516082	1:59981754_A TTATGCCTTC_A	A	ATTATG CCCTTC	0.1190	0.0000	1.0000	1.0000
1	1_61000020_A_C	61000020	60534348	rs142036730	C	A	0.0155	-0.0201	0.9801	0.9994

1	1_61681136_TA_T	61681136	61215464	1:61681136_T A_T	T	TA	0.0830	-0.0112	0.9889	0.9982
1	1_61894902_A_G	61894902	61429230	rs2207791	G	A	0.4727	-0.0002	0.9998	0.9998
1	1_61895257_C_A	61895257	61429585	rs6587924	A	C	0.5013	0.0000	1.0000	1.0000
1	1_61911157_G_A	61911157	61445485	rs2261980	A	G	0.2298	0.0054	1.0054	1.0025
1	1_62382617_A_C	62382617	61916945	rs6587949	C	A	0.6255	0.0093	1.0093	1.0117
1	1_62445706_A_G	62445706	61980034	rs885581	G	A	0.4111	-0.0065	0.9935	0.9947
1	1_63635787_C_CA	63635787	63170116	rs71813788	CA	C	0.0876	0.0035	1.0035	1.0006
1	1_63638791_G_A	63638791	63173120	rs6588016	A	G	0.5140	-0.0034	0.9966	0.9965
1	1_63818393_C_T	63818393	63352722	rs6675284	T	C	0.4145	-0.0036	0.9964	0.9970
1	1_64124310_T_A	64124310	63658639	rs59784071	A	T	0.0437	0.0000	1.0000	1.0000
1	1_64536417_G_A	64536417	64070745	rs113619373	A	G	0.0207	0.0179	1.0181	1.0007
1	1_66128239_G_T	66128239	65662556	rs6664626	T	G	0.1402	0.0074	1.0074	1.0021
1	1_66341400_C_T	66341400	65875717	rs12759968	T	C	0.1740	0.0040	1.0040	1.0014
1	1_66359367_C_CA TATATAT	66359367	65893684	rs375308081	CATATAT AT	C	0.2583	0.0032	1.0032	1.0017
1	1_66389097_C_T	66389097	65923414	rs4655809	T	C	0.3597	0.0086	1.0086	1.0062
1	1_69746553_A_G	69746553	69280870	rs114230792	G	A	0.0387	0.0072	1.0072	1.0006
1	1_69881944_G_T	69881944	69416261	rs12027709	T	G	0.1287	0.0096	1.0096	1.0025
1	1_72002778_T_C	72002778	71537095	rs78725171	C	T	0.0555	0.0135	1.0136	1.0015
1	1_72511514_AT_A	72511514	72045831	rs764149303	A	AT	0.2675	-0.0042	0.9958	0.9978
1	1_76067119_ATGA CGGGT_A	76067119	75601434	1:76067119_A TGACGGGT_A	A	ATGACG GGT	0.2029	0.0083	1.0083	1.0034
1	1_76073887_C_CA	76073887	75608202	rs148880761	CA	C	0.2091	0.0028	1.0028	1.0012
1	1_76962558_C_G	76962558	76496873	rs75325512	G	C	0.0503	-0.0152	0.9849	0.9985
1	1_78464526_C_CT AAA	78464526	77998842		CTAAA	C	0.7818	-0.0026	0.9974	0.9959

1	1_81567342_T_C	81567342	81101657	rs10518651	C	T	0.0694	-0.0107	0.9894	0.9985
1	1_84223168_A_G	84223168	83757485	rs6663583	G	A	0.8653	0.0123	1.0124	1.0215
1	1_84265575_G_T	84265575	83799892	rs761405	T	G	0.5554	0.0056	1.0056	1.0062
1	1_86474446_C_T	86474446	86008763	rs58845753	T	C	0.0245	-0.0207	0.9795	0.9990
1	1_87688394_A_G	87688394	87222711	rs10873824	G	A	0.7330	0.0093	1.0093	1.0137
1	1_87849060_TA_T	87849060	87383377	1:87849060_T A_T	T	TA	0.7309	-0.0046	0.9954	0.9933
1	1_87850495_T_C	87850495	87384812	rs1415174	C	T	0.7559	0.0000	1.0000	1.0000
1	1_87856591_CT_C	87856591	87390908		C	CT	0.1534	-0.0106	0.9895	0.9968
1	1_87890934_T_TAC CAGTGCCTTCTCTG AGAAATGCAGCTAAA CAC	87890934	87425251	rs144893360	TACCAGT GCCTTCT CTTGAGA ATGCAGC TAAACAC	T	0.3945	0.0107	1.0108	1.0085
1	1_88119395_T_C	88119395	87653712	rs28404364	C	T	0.6191	0.0067	1.0067	1.0083
1	1_88156923_G_A	88156923	87691240	rs17426269	A	G	0.1487	0.0171	1.0172	1.0051
1	1_88189692_C_G	88189692	87724009	rs305461	G	C	0.2365	0.0032	1.0032	1.0015
1	1_88207421_A_G	88207421	87741738	rs6700541	G	A	0.1774	0.0000	1.0000	1.0000
1	1_88343731_G_GG TGTT	88343731	87878048	rs143643147	GGTGTT	G	0.0452	0.0157	1.0158	1.0014
1	1_88428199_C_A	88428199	87962516	rs2151842	A	C	0.2477	-0.0149	0.9852	0.9927
1	1_88429257_T_C	88429257	87963574	rs3008452	C	T	0.4701	-0.0028	0.9972	0.9974
1	1_88764449_C_T	88764449	88298766	rs17326377	T	C	0.0400	-0.0131	0.9870	0.9990
1	1_90602741_A_T	90602741	90137183	rs12567673	T	A	0.1726	0.0025	1.0025	1.0009
1	1_92273253_C_G	92273253	91807696	rs284156	G	C	0.4087	0.0070	1.0070	1.0058
1	1_93811023_G_A	93811023	93345466	rs76909542	A	G	0.0122	-0.0182	0.9820	0.9996
1	1_95028119_C_T	95028119	94562563	rs2022032	T	C	0.2719	0.0008	1.0008	1.0004
1	1_96786288_C_T	96786288	96320732	rs113194393	T	C	0.0152	0.0053	1.0053	1.0002

1	1_97032073_TA_T	97032073	96566517	rs755722246	T	TA	0.0113	0.0142	1.0143	1.0003
1	1_99933338_T_C	99933338	99467782	rs12144940	C	T	0.2423	0.0045	1.0045	1.0022
1	1_100781169_T_C	100781169	100315613	rs3119188	C	T	0.1472	0.0031	1.0031	1.0009
1	1_100880328_A_T	100880328	100414772	rs612683	T	A	0.4097	0.0148	1.0149	1.0123
1	1_101687757_G_A	101687757	101222201	rs10875362	A	G	0.4019	0.0085	1.0085	1.0069
1	1_101702825_A_G	101702825	101237269	rs3753194	G	A	0.0588	0.0128	1.0129	1.0015
1	1_102596334_T_C	102596334	102130778	rs34470656	C	T	0.2019	-0.0065	0.9935	0.9974
1	1_102718900_G_C	102718900	102253344	rs77712548	C	G	0.0103	0.0331	1.0337	1.0007
1	1_107295378_C_T	107295378	106752756	rs74979491	T	C	0.0322	-0.0101	0.9900	0.9994
1	1_108657357_A_A	108657357	108114735	ATT	ATT	A	0.8258	-0.0098	0.9902	0.9840
1	1_109692641_G_A	109692641	109150019	rs610249	A	G	0.5630	0.0037	1.0037	1.0042
1	1_109725239_C_T	109725239	109182617	rs621414	T	C	0.5694	0.0022	1.0022	1.0025
1	1_109727653_CT_C	109727653	109185031	1:109727653_CT_C	C	CT	0.1273	-0.0152	0.9849	0.9962
1	1_110093159_C_CT	110093159	109550537	rs370352103	CT	C	0.1534	-0.0079	0.9921	0.9976
1	1_110195901_T_C	110195901	109653279	rs115450622	C	T	0.0242	-0.0093	0.9907	0.9996
1	1_110198129_CAA_A_C	110198129	109655507	1:110198129_CAA_C	C	CAAA	0.7755	0.0155	1.0156	1.0244
1	1_110212534_T_C	110212534	109669912	rs687643	C	T	0.4872	0.0077	1.0077	1.0075
1	1_110218716_C_T	110218716	109676094	rs620077	T	C	0.9133	0.0042	1.0042	1.0077
1	1_112949872_C_T	112949872	112407250	rs72697071	T	C	0.0767	0.0039	1.0039	1.0006
1	1_114096460_A_G	114096460	113553838	rs4274063	G	A	0.3074	0.0003	1.0003	1.0002
1	1_114173410_A_G	114173410	113630788	rs1230666	G	A	0.8723	-0.0122	0.9879	0.9790
1	1_114422976_T_A	114422976	113880354		A	T	0.7454	-0.0036	0.9964	0.9947
1	1_114445880_G_A	114445880	113903258	rs7513707	A	G	0.1664	0.0249	1.0252	1.0084
1	1_114813581_G_A	114813581	114270959	rs7541732	A	G	0.1149	-0.0019	0.9981	0.9996

1	1_114939944_A_G	114939944	114397322	rs35834438	G	A	0.0599	-0.0191	0.9811	0.9977
1	1_116286496_G_T	116286496	115743875	rs145128079	T	G	0.0106	-0.0090	0.9910	0.9998
1	1_116296125_C_C A	116296125	115753504	rs11440911	CA	C	0.9776	-0.0215	0.9787	0.9588
1	1_116304301_G_T	116304301	115761680	rs12023881	T	G	0.3231	0.0030	1.0030	1.0019
1	1_116310967_T_C	116310967	115768346	rs4074536	C	T	0.2852	0.0015	1.0015	1.0009
1	1_116807794_C_T	116807794	116265172	rs6699946	T	C	0.6082	-0.0081	0.9919	0.9902
1	1_118141340_T_A	118141340	117598718	rs12731593	A	T	0.2288	0.0015	1.0015	1.0007
1	1_118141492_A_C	118141492	117598870	rs12406858	C	A	0.2657	0.0112	1.0113	1.0060
1	1_118195233_T_C	118195233	117652611	rs319497	C	T	0.2691	0.0096	1.0096	1.0052
1	1_118238892_G_G T	118238892	117696270	rs61416637	GT	G	0.3530	-0.0025	0.9975	0.9982
1	1_118942949_G_C	118942949	118400326	rs61837306	C	G	0.1407	-0.0112	0.9889	0.9969
1	1_119030698_A_C	119030698	118488075	rs10923574	C	A	0.3256	-0.0078	0.9922	0.9949
1	1_120257110_T_C	120257110	119714487	rs637868	C	T	0.5309	0.0114	1.0115	1.0122
1	1_120261388_G_T	120261388	119718765	rs839616	T	G	0.3904	0.0004	1.0004	1.0003
1	1_120385937_C_G	120385937	119843314	rs2994823	G	C	0.0800	-0.0079	0.9921	0.9987
1	1_120392239_C_G	120392239	119849616	rs12734865	G	C	0.0700	-0.0068	0.9932	0.9991
1	1_120436751_T_C	120436751	119894128	rs35273427	C	T	0.0594	0.0311	1.0316	1.0038
1	1_121232045_A_T	121232045	121490247	rs116450554	T	A	0.0641	-0.0251	0.9752	0.9968
1	1_121280613_A_G	121280613	121538815	rs11249433	G	A	0.4053	0.0597	1.0615	1.0505
1	1_121287994_A_G	121287994	121546196	rs111458676	G	A	0.1060	-0.0341	0.9665	0.9929
1	1_121288049_A_G	121288049	121546251	rs12135688	G	A	0.0939	0.0000	1.0000	1.0000
1	1_121288913_C_G	121288913	121547115	rs11249430	G	C	0.4982	0.0056	1.0056	1.0056
1	1_121343930_G_C	121343930	121602132	rs146695762	C	G	0.0346	0.0190	1.0192	1.0013
1	1_121347829_A_G	121347829	121606031	rs12733576	G	A	0.0115	-0.0018	0.9982	1.0000
1	1_145365316_G_A	145365316	146069686	rs61813408	A	G	0.3721	-0.0119	0.9882	0.9912

1	1_145577585_C_G	145577585	145857483	rs12756687	G	C	0.5936	-0.0034	0.9966	0.9960
1	1_145604302_C_CT	145604302	145830811	rs143384623	CT	C	0.3515	-0.0148	0.9853	0.9897
1	1_145604791_G_T	145604791	145830322	rs36107432	T	G	0.3692	-0.0002	0.9998	0.9999
1	1_145661932_A_G	145661932	145773146	rs35353761	G	A	0.2419	-0.0020	0.9980	0.9990
1	1_149892872_A_G	149892872	149920979	rs11205277	G	A	0.4313	0.0049	1.0049	1.0042
1	1_149906413_T_C	149906413	149934520	rs11205303	C	T	0.4017	0.0321	1.0326	1.0264
1	1_151328794_T_A	151328794	151356318	rs744536	A	T	0.6283	0.0034	1.0034	1.0043
1	1_155046402_G_T	155046402	155073926	rs72702268	T	G	0.0179	-0.0294	0.9710	0.9990
1	1_155123837_G_C	155123837	155151361	rs6676150	C	G	0.3965	0.0000	1.0000	1.0000
1	1_155155608_A_G	155155608	155183132	rs4971099	G	A	0.4411	0.0000	1.0000	1.0000
1	1_155184975_A_G	155184975	155215184	rs2990223	G	A	0.5932	0.0095	1.0095	1.0114
1	1_155195071_ATT AT_A	155195071	155225280	rs139558368	A	ATTAT	0.4418	-0.0009	0.9991	0.9992
1	1_155219452_C_T	155219452	155249661	rs147869881	T	C	0.0303	0.0365	1.0372	1.0023
1	1_155358506_CT_C	155358506	155388715	1:155358506_ CT_C	C	CT	0.3305	0.0001	1.0001	1.0001
1	1_155556971_G_A	155556971	155587180	rs12091730	A	G	0.2302	0.0196	1.0198	1.0091
1	1_155848692_T_A	155848692	155878901	rs2025575	A	T	0.7961	0.0000	1.0000	1.0000
1	1_156146546_C_T	156146546	156176755	rs76381440	T	C	0.0155	-0.0054	0.9946	0.9998
1	1_156153043_A_G	156153043	156183252	rs11264454	G	A	0.4240	0.0098	1.0098	1.0084
1	1_156158777_G_A	156158777	156188986	rs114417629	A	G	0.1410	0.0042	1.0042	1.0012
1	1_156187024_TA_T	156187024	156217233	1:156187024_ TA_T	T	TA	0.3352	0.0002	1.0002	1.0001
1	1_156662700_G_A	156662700	156692908	rs114082130	A	G	0.0529	0.0071	1.0071	1.0008
1	1_156768568_G_A	156768568	156798776	rs150411804	A	G	0.0368	0.0333	1.0339	1.0025
1	1_157224242_C_A	157224242	157254452	rs190475459	A	C	0.0132	-0.0371	0.9636	0.9990
1	1_157634687_A_C	157634687	157664897	rs150038704	C	A	0.0279	0.0221	1.0223	1.0012

1	1_157873941_CA_CAAAA	157873941	157904151		CAAAA	CA	0.0295	-0.0093	0.9907	0.9995
1	1_165885282_G_A	165885282	165916045	rs35899976	A	G	0.2257	0.0110	1.0111	1.0050
1	1_167820337_T_G	167820337	167851099	rs149612953	G	T	0.0501	-0.0016	0.9984	0.9998
1	1_167918583_T_C	167918583	167949345	rs145940992	C	T	0.0183	-0.0028	0.9972	0.9999
1	1_168086743_C_T	168086743	168117505	rs4657734	T	C	0.3464	-0.0085	0.9915	0.9941
1	1_168095701_G_G	168095701	168126463	rs138538350	GT	G	0.1269	-0.0091	0.9909	0.9977
1	1_168171052_CA_C	168171052	168201814	rs761575824	C	CA	0.1097	-0.0332	0.9673	0.9929
1	1_168539624_G_C	168539624	168570386	rs7354947	C	G	0.3904	0.0032	1.0032	1.0025
1	1_168542393_T_C	168542393	168573155	rs55748465	C	T	0.1069	0.0112	1.0113	1.0024
1	1_169180229_CT_C	169180229	169210991		C	CT	0.4365	-0.0036	0.9964	0.9969
1	1_169457028_A_G	169457028	169487790	rs12138875	G	A	0.3873	-0.0031	0.9969	0.9976
1	1_169460645_A_G	169460645	169491407	rs12143031	G	A	0.1902	0.0005	1.0005	1.0002
1	1_169574722_T_G	169574722	169605484	rs2205894	G	T	0.3179	0.0036	1.0036	1.0023
1	1_171131262_T_TA	171131262	171162123	rs148297052	TAAAAA	T	0.0372	0.0079	1.0079	1.0006
1	1_172328767_T_TA	172328767	172359627	rs11463354	TA	T	0.3305	-0.0147	0.9854	0.9904
1	1_172331059_A_G	172331059	172361919	rs1894633	G	A	0.3305	-0.0026	0.9974	0.9983
1	1_172415351_GA_G	172415351	172446211	rs200139225	G	GA	0.5047	0.0013	1.0013	1.0013
1	1_172452463_CAG_C	172452463	172483323		C	CAG	0.6726	0.0071	1.0071	1.0096
1	1_177902387_C_A	177902387	177933252	rs61745560	A	C	0.2483	0.0010	1.0010	1.0005
1	1_177903281_T_A	177903281	177934146	rs500142	A	T	0.6890	-0.0054	0.9946	0.9926
1	1_183773076_A_G	183773076	183803942	rs3814327	G	A	0.3331	0.0052	1.0052	1.0035
1	1_186732170_G_A	186732170	186763038	rs56160832	A	G	0.1097	0.0052	1.0052	1.0011

1	1_186787603_CGT GTGTGTGT_C	186787603	186818471	1:186787603_ CGTGTGTGTG T_C	C	CGTGTG TGTGT	0.1264	0.0034	1.0034	1.0009
1	1_187858446_G_A	187858446	187889315	rs80807	A	G	0.7220	0.0008	1.0008	1.0012
1	1_187884585_C_T	187884585	187915454	rs1548791	T	C	0.7875	0.0071	1.0071	1.0113
1	1_188666269_G_A	188666269	188697138	rs28819695	A	G	0.4820	-0.0030	0.9970	0.9971
1	1_188700606_G_C	188700606	188731475	rs73055028	C	G	0.4309	-0.0066	0.9934	0.9943
1	1_193938198_A_G	193938198	193969068	rs657308	G	A	0.6068	0.0000	1.0000	1.0000
1	1_199438261_TAA _T	199438261	199469133	1:199438261_ TAA_T	T	TAA	0.5507	-0.0020	0.9980	0.9978
1	1_199679378_A_G	199679378	199710250	rs17699358	G	A	0.3911	0.0078	1.0078	1.0061
1	1_201437832_C_T	201437832	201468704	rs35383942	T	C	0.0559	0.0357	1.0363	1.0041
1	1_201630517_G_A	201630517	201661389	rs724221	A	G	0.4446	-0.0103	0.9898	0.9909
1	1_201662222_A_G	201662222	201693094	rs2007411	G	A	0.4454	0.0018	1.0018	1.0016
1	1_202184600_C_T	202184600	202215472	rs6686987	T	C	0.3992	0.0000	1.0000	1.0000
1	1_202196697_G_A	202196697	202227569	rs12032080	A	G	0.4011	0.0000	1.0000	1.0000
1	1_202442574_G_A	202442574	202473446	rs3767418	A	G	0.0597	0.0305	1.0310	1.0037
1	1_202570918_G_A	202570918	202601790	rs61820902	A	G	0.0563	0.0150	1.0151	1.0017
1	1_203770448_T_A	203770448	203801320	rs7514172	A	T	0.2715	0.0157	1.0158	1.0086
1	1_203842355_T_A	203842355	203873227		A	T	0.1268	0.0074	1.0074	1.0019
1	1_204061744_G_A	204061744	204092616	rs7528560	A	G	0.1270	-0.0011	0.9989	0.9997
1	1_204423559_G_A	204423559	204454431	rs151283122	A	G	0.0169	-0.0332	0.9673	0.9989
1	1_204490311_A_T	204490311	204521183	rs11586387	T	A	0.0165	0.0144	1.0145	1.0005
1	1_204491551_C_C AG	204491551	204522423	rs35946963	CAG	C	0.7402	0.0000	1.0000	1.0000
1	1_205556426_T_C	205556426	205587298	rs6593954	C	T	0.3123	-0.0024	0.9976	0.9985
1	1_208076291_G_A	208076291	207902946	rs2785646	A	G	0.3337	-0.0095	0.9905	0.9937

1	1_208142894_A_G	208142894	207969549	rs35303635	G	A	0.3694	-0.0004	0.9996	0.9997
1	1_210042456_T_C	210042456	209869111	rs111119358	C	T	0.1594	0.0000	1.0000	1.0000
1	1_210042983_G_A	210042983	209869638	rs2206043	A	G	0.1460	0.0000	1.0000	1.0000
1	1_210050756_T_G	210050756	209877411	rs76610459	G	T	0.1567	0.0000	1.0000	1.0000
1	1_210796591_T_C	210796591	210623247	rs7548424	C	T	0.9069	0.0153	1.0154	1.0282
1	1_211828151_G_A	211828151	211654809	rs7526473	A	G	0.4251	-0.0075	0.9925	0.9937
1	1_213722114_T_C	213722114	213548771	rs320394	C	T	0.8421	0.0082	1.0082	1.0139
1	1_214154719_G_T	214154719	213981376	rs2075423	T	G	0.3536	0.0086	1.0086	1.0061
1	1_214524613_T_C	214524613	214351270	rs7414346	C	T	0.5900	-0.0040	0.9960	0.9953
1	1_214623189_TAA AAAA_TAAAAAA	214623189	214449846		TAAAAAA A	TAAAA A	0.4513	-0.0098	0.9902	0.9912
1	1_215226642_T_A	215226642	215053299	rs121118830	A	T	0.0413	0.0355	1.0361	1.0030
1	1_216871412_A_G	216871412	216698070	rs17043393	G	A	0.1576	0.0059	1.0059	1.0019
1	1_217053815_T_G	217053815	216880473	rs2576261	G	T	0.3280	0.0179	1.0181	1.0119
1	1_217200883_G_A	217200883	217027541	rs2377360	A	G	0.7529	0.0000	1.0000	1.0000
1	1_217220574_G_A	217220574	217047232	rs111117758	A	G	0.2107	-0.0075	0.9925	0.9969
1	1_217236895_T_G	217236895	217063553	rs1416526	G	T	0.1565	-0.0017	0.9983	0.9995
1	1_219168079_A_T	219168079	218994737	rs67056850	T	A	0.3367	-0.0034	0.9966	0.9977
1	1_220583106_A_C	220583106	220409764	rs1890461	C	A	0.7727	-0.0097	0.9903	0.9851
1	1_220675924_G_T	220675924	220502582	rs111118564	T	G	0.6814	-0.0022	0.9978	0.9970
1	1_220684965_A_A T	220684965	220511623	rs11417702	AT	A	0.7491	-0.0020	0.9980	0.9970
1	1_220731475_AAA T_A	220731475	220558133	rs369215403	A	AAAT	0.7125	-0.0033	0.9967	0.9953
1	1_220824115_G_C	220824115	220650773	rs12123306	C	G	0.4324	-0.0016	0.9984	0.9986
1	1_221436185_C_G	221436185	221262843	rs9431466	G	C	0.6529	-0.0010	0.9990	0.9987
1	1_221898651_A_G	221898651	221725309	rs116232610	G	A	0.0209	0.0202	1.0204	1.0009

1	1_223922062_A_G	223922062	223734360	rs7517684	G	A	0.1398	0.0027	1.0027	1.0008
1	1_223937520_C_A	223937520	223749818	rs12563713	A	C	0.0825	0.0084	1.0084	1.0014
1	1_224180489_C_T	224180489	223992787	rs11799363	T	C	0.2025	0.0096	1.0096	1.0039
1	1_228178296_T_G	228178296	227990595	rs112479896	G	T	0.0664	-0.0032	0.9968	0.9996
1	1_228856469_C_T	228856469	228720722	rs76436368	T	C	0.0757	-0.0043	0.9957	0.9994
1	1_228974769_C_T	228974769	228839022	rs1389138	T	C	0.1384	0.0000	1.0000	1.0000
1	1_229934838_A_T	229934838	229799091	rs581850	T	A	0.5172	0.0000	1.0000	1.0000
1	1_230622709_C_T	230622709	230486963	rs853022	T	C	0.7638	0.0000	1.0000	1.0000
1	1_230849190_C_T	230849190	230713444	rs7539020	T	C	0.3710	-0.0060	0.9940	0.9956
1	1_230851628_G_A	230851628	230715882	rs6683321	A	G	0.1760	-0.0021	0.9979	0.9993
1	1_230852551_C_T	230852551	230716805	rs1977414	T	C	0.2840	-0.0027	0.9973	0.9985
1	1_231711128_AT_A	231711128	231575382	1:231711128_AT_A	A	AT	0.1655	0.0105	1.0106	1.0035
1	1_231974202_T_G	231974202	231838456	rs76945478	G	T	0.0377	-0.0093	0.9907	0.9993
1	1_232002834_T_C	232002834	231867088	rs55696805	C	T	0.0417	-0.0055	0.9945	0.9995
1	1_232004691_G_T	232004691	231868945	rs9432019	T	G	0.6021	-0.0099	0.9901	0.9882
1	1_232235709_G_A	232235709	232099963	rs12146088	A	G	0.0186	0.0045	1.0045	1.0002
1	1_232908177_C_A	232908177	232772431	rs2814544	A	C	0.0756	-0.0183	0.9819	0.9973
1	1_233060511_T_C	233060511	232924765	rs1555394	C	T	0.2302	-0.0102	0.9899	0.9953
1	1_233063389_C_T	233063389	232927643	rs7546587	T	C	0.2488	-0.0003	0.9997	0.9999
1	1_233476712_T_C	233476712	233340966	rs4649217	C	T	0.3304	-0.0078	0.9922	0.9949
1	1_233560466_C_G	233560466	233424720	rs6692313	G	C	0.7789	-0.0129	0.9872	0.9801
1	1_233717882_C_T	233717882	233582136	rs4649337	T	C	0.0121	0.0173	1.0175	1.0004
1	1_240217696_C_G	240217696	240054396	rs75280320	G	C	0.2445	-0.0098	0.9902	0.9952
1	1_242034263_A_G	242034263	241870961	rs72755295	G	A	0.0305	0.0897	1.0938	1.0057
1	1_242047847_A_G	242047847	241884545	rs4149991	G	A	0.1061	0.0017	1.0017	1.0004
1	1_243143385_G_A	243143385	242980083	rs7417508	A	G	0.3746	-0.0005	0.9995	0.9996

1	1_243487861_G_A	243487861	243324559	rs12058508	A	G		0.2760	0.0018	1.0018	1.0010
1	1_243492643_C_T	243492643	243329341	rs2490400	T	C		0.7709	0.0076	1.0076	1.0118
1	1_244150083_C_T	244150083	243986781	rs472967	T	C		0.5380	-0.0045	0.9955	0.9952
1	1_247358075_C_T	247358075	247194773	rs12136392	T	C		0.1513	0.0017	1.0017	1.0005
1	1_247772275_G_C	247772275	247608973	rs80281736	C	G		0.2255	-0.0035	0.9965	0.9984
2	2_609177_A_G	609177	609177	rs2947415	G	A		0.8259	0.0000	1.0000	1.0000
2	2_620989_G_A	620989	620989	rs6753148	A	G		0.6244	0.0000	1.0000	1.0000
2	2_621954_T_C	621954	621954	rs1320332	C	T		0.8229	-0.0191	0.9811	0.9691
2	2_1047592_CACA_AACA	1047592	1051906	rs114056577	AACA	CACA		0.0198	0.0095	1.0095	1.0004
2	2_1140472_C_T	1140472	1144786	rs7584432	T	C		0.3275	-0.0079	0.9921	0.9949
2	2_1821846_C_G	1821846	1818074	rs34526459	G	C		0.2901	0.0015	1.0015	1.0009
2	2_3408669_G_A	3408669	3404898	rs7355558	A	G		0.1233	0.0073	1.0073	1.0018
2	2_5495963_C_T	5495963	5355830	rs11677035	T	C		0.4933	0.0057	1.0057	1.0056
2	2_6121326_AACACACACAC_A	6121326	5981194	2:6121326_AA CACACACAC_A	A	AACACA CACAC		0.7392	-0.0036	0.9964	0.9947
2	2_7188646_T_C	7188646	7048515	rs2460410	C	T		0.5504	-0.0008	0.9992	0.9991
2	2_7202628_TA_T	7202628	7062497	rs762471000	T	TA		0.4727	-0.0054	0.9946	0.9949
2	2_9841449_T_C	9841449	9701320	rs12613334	C	T		0.5896	0.0038	1.0038	1.0045
2	2_10028920_T_G	10028920	9888791	rs1620983	G	T		0.6215	-0.0041	0.9959	0.9949
2	2_10081789_A_G	10081789	9941660	rs76907460	G	A		0.2294	-0.0131	0.9870	0.9940
2	2_10109664_A_G	10109664	9969535	rs17364282	G	A		0.0145	-0.0289	0.9715	0.9992
2	2_10125007_T_C	10125007	9984879	rs115538162	C	T		0.0337	-0.0024	0.9976	0.9998
2	2_10138983_T_C	10138983	9998855	rs78425380	C	T		0.1160	0.0245	1.0248	1.0058
2	2_10619416_C_CA TAT	10619416	10479290	rs113100467	CATAT	C		0.1082	0.0091	1.0091	1.0020
2	2_11118159_A_T	11118159	10978033	rs6432156	T	A		0.0162	-0.0281	0.9723	0.9991

2	2_11681043_G_T	11681043	11540917	rs13021546	T	G	0.7171	0.0017	1.0017	1.0024
2	2_11701843_G_A	11701843	11561717	rs113084984	A	G	0.2301	-0.0026	0.9974	0.9988
2	2_12035555_G_C	12035555	11895429	rs64332241	C	G	0.6899	-0.0047	0.9953	0.9935
2	2_13083482_T_A	13083482	12943356	rs779385	A	T	0.1642	0.0007	1.0007	1.0002
2	2_13281213_T_C	13281213	13141088	rs112377288	C	T	0.0860	-0.0051	0.9949	0.9991
2	2_13619816_A_G	13619816	13479691	rs64332387	G	A	0.3212	0.0052	1.0052	1.0034
2	2_14594985_C_G	14594985	14454861	rs6758768	G	C	0.4516	-0.0074	0.9926	0.9934
2	2_17275801_C_T	17275801	17094534	rs4832704	T	C	0.0812	0.0149	1.0150	1.0024
2	2_18033944_G_A	18033944	17852677	rs60957847	A	G	0.1479	-0.0033	0.9967	0.9990
2	2_18081917_C_T	18081917	17900650	rs146177537	T	C	0.0513	-0.0040	0.9960	0.9996
2	2_18898271_G_A	18898271	18717005	rs12996938	A	G	0.0544	0.0136	1.0137	1.0015
2	2_18936729_GTAT ATTA_G	18936729	18755463	2:18936729_G TATATTA_G	G	GTATAT TA	0.6657	-0.0073	0.9927	0.9903
2	2_19297503_T_TA ACA	19297503	19097742	rs151210220	TAACA	T	0.3769	-0.0054	0.9946	0.9959
2	2_19302429_G_A	19302429	19102668	rs4283375	A	G	0.5597	-0.0005	0.9995	0.9994
2	2_19315675_T_A	19315675	19115914	rs6743383	A	T	0.5599	-0.0037	0.9963	0.9959
2	2_19320803_T_C	19320803	19121042	rs12710696	C	T	0.6341	0.0000	1.0000	1.0000
2	2_20406245_C_T	20406245	20206484	rs3771254	T	C	0.0887	-0.0208	0.9794	0.9964
2	2_20592798_G_A	20592798	20393037	rs343155	A	G	0.2576	0.0139	1.0140	1.0072
2	2_20769210_G_T	20769210	20569450	rs57203893	T	G	0.0535	0.0165	1.0166	1.0018
2	2_23361864_T_C	23361864	23138993	rs188194202	C	T	0.0123	-0.0137	0.9864	0.9997
2	2_25129473_A_G	25129473	24906604	rs6725517	G	A	0.4082	-0.0174	0.9828	0.9860
2	2_25155419_C_T	25155419	24932550	rs75503394	T	C	0.0874	-0.0043	0.9957	0.9993
2	2_25266649_T_TC	25266649	25043780	rs190535084	TC	T	0.1964	-0.0022	0.9978	0.9991
2	2_25400559_G_T	25400559	25177690	rs13022041	T	G	0.3258	0.0000	1.0000	1.0000
2	2_25455389_G_A	25455389	25232520	rs7522208	A	G	0.2052	-0.0021	0.9979	0.9991

2	2_25473311_G_A	25473311	25250442	rs13427672	A	G	0.4313	0.0059	1.0059	1.0051
2	2_25485152_C_G	25485152	25262283	rs58552784	G	C	0.2523	0.0054	1.0054	1.0027
2	2_25526632_C_T	25526632	25303763	rs34635462	T	C	0.3970	-0.0105	0.9896	0.9917
2	2_25605972_C_T	25605972	25383103	rs35010208	T	C	0.2664	0.0000	1.0000	1.0000
2	2_26109750_TTTTA	26109750	25886881		T	TTTTA	0.7152	0.0063	1.0063	1.0091
2	2_28549701_C_G	28549701	28326834	rs2002406	G	C	0.0863	0.0000	1.0000	1.0000
2	2_29045868_CTT_C	29045868	28823002	2:29045868_C TT_C	C	CTT	0.0820	0.0000	1.0000	1.0000
2	2_29179452_G_C	29179452	28956586	rs12472404	C	G	0.2287	0.0000	1.0000	1.0000
2	2_29198141_A_G	29198141	28975275	rs11674944	G	A	0.2340	0.0000	1.0000	1.0000
2	2_29542948_C_T	29542948	29320082	rs4666201	T	C	0.7034	-0.0031	0.9969	0.9957
2	2_29586343_C_A	29586343	29363477	rs13010090	A	C	0.2468	-0.0009	0.9991	0.9996
2	2_29593022_AATC	29593022	29370156	2:29593022_A ATC_A	A	AATC	0.0489	-0.0043	0.9957	0.9996
2	2_29604977_G_T	29604977	29382111	rs7608573	T	G	0.2548	-0.0078	0.9922	0.9960
2	2_29615233_T_C	29615233	29392367	rs4322799	C	T	0.2622	-0.0098	0.9902	0.9949
2	2_31597032_C_A	31597032	31374166	rs12712316	A	C	0.0236	0.0036	1.0036	1.0002
2	2_32769544_TTTTC	32769544	32544477	2:32769544_T TTTC_T	T	TTTTC	0.0148	-0.0064	0.9936	0.9998
2	2_32907914_G_T	32907914	32682847	rs61397127	T	G	0.8131	0.0020	1.0020	1.0033
2	2_32969116_T_C	32969116	32744049	rs3769581	C	T	0.2696	0.0019	1.0019	1.0010
2	2_33074113_T_C	33074113	32849046	rs72789809	C	T	0.0647	-0.0091	0.9909	0.9988
2	2_33441564_G_C	33441564	33216497	rs17012691	C	G	0.0249	0.0202	1.0204	1.0010
2	2_33621242_G_GT	33621242	33396175	rs555691297	GT	G	0.1296	0.0019	1.0019	1.0005
2	2_33625577_AGTT TTTGGTACTTT_A	33625577	33400510	2:33625577_A GTTTTGGTAC TTT_A	A	AGTTT TGGTAC TTT	0.1364	0.0004	1.0004	1.0001

2	2_33629266_C_A	33629266	33404199	rs148685563	A	C	0.0144	0.0203	1.0205	1.0006
2	2_34387201_C_G	34387201	34162134	rs77303967	G	C	0.0136	-0.0445	0.9565	0.9988
2	2_39699510_C_CT	39699510	39472369	rs553796823	CT	C	0.4659	-0.0147	0.9854	0.9865
2	2_40527128_T_G	40527128	40299988	rs727477	G	T	0.3029	-0.0098	0.9902	0.9941
2	2_40555273_G_T	40555273	40328133	rs72943146	T	G	0.0310	0.0152	1.0153	1.0009
2	2_42099286_C_T	42099286	41872146	rs4594493	T	C	0.2734	-0.0044	0.9956	0.9976
2	2_42137215_G_A	42137215	41910075	rs6734260	A	G	0.5073	-0.0034	0.9966	0.9966
2	2_42158304_A_C	42158304	41931164	rs17029056	C	A	0.2150	-0.0036	0.9964	0.9985
2	2_43505230_C_T	43505230	43278091	rs145471010	T	C	0.0209	0.0175	1.0177	1.0007
2	2_43531812_A_AT	43531812	43304673	rs538548562	AT	A	0.1771	0.0013	1.0013	1.0005
2	2_45814226_T_A	45814226	45587087	rs7609316	A	T	0.1391	-0.0043	0.9957	0.9988
2	2_46065571_C_G	46065571	45838432	rs79942805	G	C	0.0401	-0.0119	0.9882	0.9991
2	2_46583593_G_A	46583593	46356454	rs2278753	A	G	0.3435	-0.0057	0.9943	0.9961
2	2_46595363_G_A	46595363	46368224	rs4145836	A	G	0.1153	-0.0055	0.9945	0.9987
2	2_46650458_T_C	46650458	46423319	rs78809850	C	T	0.0190	-0.0246	0.9757	0.9991
2	2_47248466_A_G	47248466	47021327	rs7565217	G	A	0.0937	-0.0097	0.9903	0.9982
2	2_48709948_T_C	48709948	48482809	rs113361760	C	T	0.0106	0.0053	1.0053	1.0001
2	2_49141322_A_C	49141322	48914183	rs17037825	C	A	0.0506	0.0166	1.0167	1.0017
2	2_51818904_T_C	51818904	51591766	rs113497123	C	T	0.0275	0.0084	1.0084	1.0005
2	2_53039116_AT_A	53039116	52811978	rs35688857	A	AT	0.1129	-0.0153	0.9848	0.9966
2	2_54830389_C_G	54830389	54603252	rs116707394	G	C	0.0265	0.0193	1.0195	1.0010
2	2_55132603_T_C	55132603	54905466	rs78860519	C	T	0.0330	-0.0176	0.9826	0.9988
2	2_56787003_G_A	56787003	56559868	rs2194795	A	G	0.5982	0.0064	1.0064	1.0077
2	2_58006573_A_G	58006573	57779438	rs74338168	G	A	0.0704	0.0076	1.0076	1.0011
2	2_58455206_AT_A	58455206	58228071	rs11461396	AT	AT	0.5157	0.0007	1.0007	1.0007
2	2_58844708_A_T	58844708	58617573	rs7582795	T	A	0.2366	-0.0064	0.9936	0.9970

2	2_60641329_G_A	60641329	60414194	rs13028240	A	G	0.2906	-0.0123	0.9878	0.9929
2	2_60669068_A_AT G	60669068	60441933	rs3028025	ATG	A	0.6875	0.0035	1.0035	1.0048
2	2_62845873_G_T	62845873	62618738	rs116622237	T	G	0.0733	0.0090	1.0090	1.0013
2	2_64894053_T_TTT G	64894053	64666919	rs35123788	TTTG	T	0.1676	-0.0192	0.9810	0.9936
2	2_65618119_A_G	65618119	65390985	rs268128	G	A	0.9514	0.0182	1.0184	1.0353
2	2_65980103_T_C	65980103	65752969	rs139124371	C	T	0.0195	0.0100	1.0101	1.0004
2	2_66105510_A_G	66105510	65878376	rs58378948	G	A	0.1573	-0.0055	0.9945	0.9983
2	2_67560500_G_A	67560500	67333368	rs148972021	A	G	0.0762	-0.0004	0.9996	0.9999
2	2_68106897_G_C	68106897	67879765	rs13004783	C	G	0.4432	0.0102	1.0103	1.0091
2	2_68111722_C_T	68111722	67884590	rs7573637	T	C	0.4848	0.0007	1.0007	1.0007
2	2_68655836_A_G	68655836	68428704	rs34352314	G	A	0.0450	-0.0130	0.9871	0.9988
2	2_68665012_A_G	68665012	68437880	rs11126187	G	A	0.8846	0.0035	1.0035	1.0062
2	2_69247526_CTGTT T_C	69247526	69020394	rs151058084	C	CTGTTT	0.1010	-0.0149	0.9852	0.9970
2	2_69250632_G_A	69250632	69023500	rs66686620	A	G	0.1424	-0.0017	0.9983	0.9995
2	2_69386671_G_GA	69386671	69159539	rs5831961	GA	G	0.1302	-0.0069	0.9931	0.9982
2	2_69396387_G_A	69396387	69169255	rs10188804	A	G	0.4007	0.0044	1.0044	1.0035
2	2_69429294_G_A	69429294	69202162	rs62134902	A	G	0.1475	-0.0069	0.9931	0.9980
2	2_69495157_C_A	69495157	69268025	rs62134957	A	C	0.0513	-0.0230	0.9773	0.9977
2	2_69905400_C_G	69905400	69678268	rs6546540	G	C	0.4163	-0.0014	0.9986	0.9988
2	2_69918942_A_G	69918942	69691810	rs12620484	G	A	0.5395	-0.0063	0.9937	0.9932
2	2_70149873_G_A	70149873	69922741	rs80352135	A	G	0.2008	-0.0075	0.9925	0.9970
2	2_70165966_G_A	70165966	69938834	rs7349311	A	G	0.1829	-0.0034	0.9966	0.9988
2	2_71048778_G_T	71048778	70821647	rs73937022	T	G	0.0428	0.0066	1.0066	1.0006
2	2_72206150_G_T	72206150	71979020	rs114669536	T	G	0.0192	0.0149	1.0150	1.0006

2	2_74153422_C_G	74153422	73926295	rs11683738	G	C	0.1733	0.0008	1.0008	1.0003
2	2_76465046_C_T	76465046	76237920	rs12470208	T	C	0.5538	-0.0058	0.9942	0.9936
2	2_77276201_C_T	77276201	77049075	rs1838878	T	C	0.0979	-0.0134	0.9867	0.9974
2	2_85347751_G_A	85347751	85120628	rs75975689	A	G	0.1569	0.0008	1.0008	1.0003
2	2_85357265_G_A	85357265	85130142	rs116666195	A	G	0.0154	0.0264	1.0268	1.0008
2	2_85394611_A_G	85394611	85167488	rs11691849	G	A	0.3662	-0.0106	0.9895	0.9923
2	2_85409239_G_A	85409239	85182116	rs147597376	A	G	0.0224	0.0005	1.0005	1.0000
2	2_86586325_C_CT	86586325	86359202	rs58938847	CT	C	0.4419	0.0002	1.0002	1.0002
2	2_86808935_CA_C	86808935	86581812	2:86808935_C_A_C	C	CA	0.5093	0.0011	1.0011	1.0011
2	2_88358825_G_C	88358825	88059306	rs1036759	C	G	0.3081	0.0221	1.0223	1.0138
2	2_89045587_C_T	89045587	88746070	rs4972012	T	C	0.3180	-0.0006	0.9994	0.9996
2	2_89127937_A_C	89127937	88828424	rs2848119	C	A	0.5833	-0.0023	0.9977	0.9973
2	2_96640703_T_C	96640703	95974955	rs7563714	C	T	0.9520	-0.0006	0.9994	0.9989
2	2_101878882_C_T	101878882	101262420	rs74642933	T	C	0.0963	0.0064	1.0064	1.0012
2	2_102279803_C_CT TTATTTA	102279803	101663341	rs373462994	CTTTATTT A	C	0.5640	0.0000	1.0000	1.0000
2	2_102334926_AT_ A	102334926	101718464	2:102334926_ AT_A	A	AT	0.3797	0.0037	1.0037	1.0028
2	2_102849214_T_C	102849214	102232754	rs76394402	C	T	0.0223	-0.0021	0.9979	0.9999
2	2_105307941_C_T	105307941	104691483	rs10178865	T	C	0.0275	-0.0068	0.9932	0.9996
2	2_107543335_G_A	107543335	106926879	rs62152998	A	G	0.0160	0.0195	1.0197	1.0006
2	2_108642171_A_C	108642171	108025715	rs71419398	C	A	0.1336	-0.0027	0.9973	0.9993
2	2_111597589_C_T	111597589	110840012	rs6707257	T	C	0.1722	0.0038	1.0038	1.0013
2	2_111629125_G_T	111629125	110871548	rs13029175	T	G	0.3148	0.0051	1.0051	1.0032
2	2_111796986_G_G A	111796986	111039409	rs200239486	GA	G	0.3177	-0.0015	0.9985	0.9990

2	2_111900904_G_T	111900904	111143327	rs75543804	T	G	0.0306	0.0236	1.0239	1.0015
2	2_111919346_A_C	111919346	111161769	rs686952	C	A	0.6962	0.0037	1.0037	1.0052
2	2_111946084_C_C	111946084	111188507	rs532558450	CA	C	0.5343	0.0026	1.0026	1.0028
2	2_111988486_TAA	111988486	111230909		T	TAA	0.2286	-0.0049	0.9951	0.9978
2	2_111988486_TAA	111988486	111230909		TA	TAA	0.2775	0.0006	1.0006	1.0003
2	2_113847915_G_A	113847915	113090338	rs28730394	A	G	0.0131	0.0096	1.0096	1.0003
2	2_115405865_T_C	115405865	114648288	rs74419649	C	T	0.1150	-0.0034	0.9966	0.9992
2	2_118156200_C_T	118156200	117398624	rs11123419	T	C	0.3276	0.0071	1.0071	1.0047
2	2_118211834_C_T	118211834	117454258	rs34973731	T	C	0.1212	0.0087	1.0087	1.0021
2	2_118669853_C_T	118669853	117912277	rs7583655	T	C	0.2571	0.0055	1.0055	1.0028
2	2_118755669_A_G	118755669	117998093	rs17512698	G	A	0.5054	-0.0033	0.9967	0.9967
2	2_119510491_C_G	119510491	118752915		G	C	0.9331	0.0039	1.0039	1.0073
2	2_119901805_G_T	119901805	119144229	rs13433007	T	G	0.3223	0.0070	1.0070	1.0045
2	2_121058254_A_G	121058254	120300678	rs6746250	G	A	0.7047	-0.0118	0.9883	0.9835
2	2_121069922_C_T	121069922	120312346	rs4849857	T	C	0.7248	0.0000	1.0000	1.0000
2	2_121070582_G_A	121070582	120313006	rs11684491	A	G	0.5977	0.0000	1.0000	1.0000
2	2_121070811_C_T	121070811	120313235	rs11673874	T	C	0.7132	0.0000	1.0000	1.0000
2	2_121070858_CG_	121070858	120313282	rs745439348	C	CG	0.5894	0.0000	1.0000	1.0000
2	2_121079515_A_C	121079515	120321939	rs4528762	C	A	0.2648	0.0000	1.0000	1.0000
2	2_121088182_G_A	121088182	120330606	rs11903787	A	G	0.2408	-0.0031	0.9969	0.9985
2	2_121089731_T_C	121089731	120332155	rs17625845	C	T	0.1943	-0.0162	0.9839	0.9938
2	2_121095920_T_C	121095920	120338344	rs7589138	C	T	0.4180	0.0000	1.0000	1.0000
2	2_121125114_G_C	121125114	120367538	rs10198584	C	G	0.6077	0.0042	1.0042	1.0051
2	2_121125289_C_T	121125289	120367713	rs1992131	T	C	0.1188	0.0010	1.0010	1.0002

2	2_121126279_G_A	121126279	120368703	rs12622286	A	G	0.6601	0.0029	1.0029	1.0038
2	2_121159205_G_A	121159205	120401629	rs10164550	A	G	0.3527	-0.0147	0.9854	0.9897
2	2_121160898_C_T	121160898	120403322	rs76476871	T	C	0.0873	0.0117	1.0118	1.0021
2	2_121238571_AGT GT_AGT	121238571	120480995	2:121238571_ AGT_A	AGT	AGTGT	0.8845	0.0077	1.0077	1.0137
2	2_121246568_T_C	121246568	120488992	rs10179592	C	T	0.8970	0.0563	1.0579	1.1066
2	2_121852657_C_T	121852657	121095081	rs13409556	T	C	0.0263	-0.0056	0.9944	0.9997
2	2_121854954_C_G	121854954	121097378	rs28374086	G	C	0.0189	-0.0043	0.9957	0.9998
2	2_122966476_C_T	122966476	122208900	rs56080854	T	C	0.1588	0.0037	1.0037	1.0012
2	2_123784114_A_G	123784114	123026538	rs115470088	G	A	0.0197	0.0000	1.0000	1.0000
2	2_124310905_C_T	124310905	123553329	rs13398935	T	C	0.0745	0.0094	1.0094	1.0014
2	2_124766981_G_A	124766981	124009404	rs12478765	A	G	0.2546	0.0083	1.0083	1.0042
2	2_128302536_A_G	128302536	127544961	rs148135359	G	A	0.1450	-0.0070	0.9930	0.9980
2	2_129915194_GTT GAC_G	129915194	129157621	rs775250244	G	GTTGAC	0.6350	-0.0120	0.9881	0.9849
2	2_133952040_G_A	133952040	133194468	rs12691834	A	G	0.2580	-0.0030	0.9970	0.9985
2	2_134356301_C_T	134356301	133598730	rs12987374	T	C	0.5358	0.0019	1.0019	1.0020
2	2_135158254_A_G	135158254	134400683	rs13007251	G	A	0.2286	-0.0094	0.9906	0.9957
2	2_135284038_C_A	135284038	134526467	rs479980	A	C	0.5864	-0.0032	0.9968	0.9963
2	2_145205693_G_C	145205693	144448126	rs10187892	C	G	0.5371	0.0063	1.0063	1.0068
2	2_145976169_A_T	145976169	145218601	rs59116697	T	A	0.4184	0.0047	1.0047	1.0039
2	2_146008395_AG_ A	146008395	145250827	rs767604124	A	AG	0.2291	-0.0103	0.9898	0.9953
2	2_153266604_C_T	153266604	152410090	rs73967988	T	C	0.0131	0.0059	1.0059	1.0002
2	2_160750861_T_C	160750861	159894350	rs1511224	C	T	0.4127	0.0013	1.0013	1.0011
2	2_160781240_TG_T	160781240	159924729	rs796929846	T	TG	0.3882	0.0047	1.0047	1.0037
2	2_166297783_G_A	166297783	165441273	rs190067614	A	G	0.0172	0.0104	1.0105	1.0004

2	2_168581285_A_G	168581285	167724775	rs67678493	G	A	0.2472	0.0105	1.0106	1.0052
2	2_168611545_C_G	168611545	167755035	rs115102047	G	C	0.0448	0.0119	1.0120	1.0011
2	2_171504324_C_T	171504324	170647814	rs12151651	T	C	0.1366	0.0039	1.0039	1.0011
2	2_172158381_C_G	172158381	171301871	rs72874644	G	C	0.1048	0.0028	1.0028	1.0006
2	2_172369400_T_C	172369400	171512890	rs10490603	C	T	0.1379	-0.0057	0.9943	0.9984
2	2_172380723_G_C	172380723	171524213	rs11681001	C	G	0.3728	0.0000	1.0000	1.0000
2	2_172382596_G_A	172382596	171526086	rs112352153	A	G	0.1221	-0.0037	0.9963	0.9991
2	2_172424963_C_T	172424963	171568453	rs25422943	T	C	0.5467	-0.0046	0.9954	0.9950
2	2_172425405_AAA GT_A	172425405	171568895	rs765335847	A	AAAGT	0.2350	0.0041	1.0041	1.0019
2	2_172428729_G_A	172428729	171572219	rs2356791	A	G	0.6398	0.0000	1.0000	1.0000
2	2_172972828_G_C	172972828	172108100	rs2357322	C	G	0.3460	0.0000	1.0000	1.0000
2	2_172974566_C_G	172974566	172109838	rs17726078	G	C	0.4743	-0.0258	0.9745	0.9760
2	2_173027109_C_T	173027109	172162381	rs79238150	T	C	0.0175	0.0131	1.0132	1.0005
2	2_173041097_T_C	173041097	172176369	rs13412383	C	T	0.1415	0.0017	1.0017	1.0005
2	2_173296850_G_A	173296850	172432122	rs36055280	A	G	0.3366	0.0020	1.0020	1.0013
2	2_173424800_G_T	173424800	172560072	rs6723492	T	G	0.2097	-0.0042	0.9958	0.9982
2	2_174104508_A_G	174104508	173239780	rs62174362	G	A	0.0375	0.0036	1.0036	1.0003
2	2_174204524_G_C	174204524	173339796	rs7604661	C	G	0.8562	0.0000	1.0000	1.0000
2	2_174212910_A_G	174212910	173348182	rs1550622	G	A	0.8450	0.0222	1.0224	1.0383
2	2_174242984_G_T	174242984	173378256	rs144869769	T	G	0.0308	0.0049	1.0049	1.0003
2	2_174276092_T_C	174276092	173411364	rs7571484	C	T	0.2008	0.0042	1.0042	1.0017
2	2_174584779_C_G	174584779	173720051	rs1371439	G	C	0.0260	0.0148	1.0149	1.0008
2	2_174705699_A_G	174705699	173840971	rs75627816	G	A	0.0130	0.0211	1.0213	1.0006
2	2_177375311_CAG _C	177375311	176510583	2:177375311_ CAG_C	C	CAG	0.1223	0.0000	1.0000	1.0000
2	2_178877989_G_A	178877989	178013262	rs17636214	A	G	0.0399	0.0105	1.0106	1.0008

2	2_180145058_C_G	180145058	179280331	rs77076967	G	C	0.0552	0.0058	1.0058	1.0006
2	2_180438264_T_A	180438264	179573537	rs22222032	A	T	0.0898	0.0021	1.0021	1.0004
2	2_180448523_A_G	180448523	179583796	rs11695089	G	A	0.0868	0.0026	1.0026	1.0005
2	2_180934312_A_T	180934312	180069585	rs71425659	T	A	0.0454	0.0200	1.0202	1.0018
2	2_181000793_T_C	181000793	180136066	rs10175272	C	T	0.2159	0.0106	1.0107	1.0046
2	2_181659051_A_G	181659051	180794324	rs11686097	G	A	0.0759	-0.0052	0.9948	0.9992
2	2_185343431_G_A	185343431	184478704	rs72893750	A	G	0.0155	-0.0030	0.9970	0.9999
2	2_186761497_C_T	186761497	185896770	rs59190502	T	C	0.2421	-0.0067	0.9933	0.9968
2	2_187757692_T_C	187757692	186892965	rs10931260	C	T	0.2638	-0.0012	0.9988	0.9994
2	2_187782375_T_G	187782375	186917648	rs1901341	G	T	0.4504	0.0037	1.0037	1.0033
2	2_188871632_CCCTT	188871632	188006905	2:188871632_ CCCTT_C	C	CCCTT	0.1269	0.0053	1.0053	1.0013
2	2_188872284_T_TA CACACAC	188872284	188007557	rs3060834	TACACAC AC	T	0.7770	-0.0075	0.9925	0.9884
2	2_189684112_A_C	189684112	188819386	rs529161674	C	A	0.0286	-0.0150	0.9851	0.9991
2	2_189805077_C_A	189805077	188940351	rs7588568	A	C	0.2810	-0.0036	0.9964	0.9980
2	2_189882065_T_G	189882065	189017339	rs10175784	G	T	0.4470	-0.0021	0.9979	0.9981
2	2_190037694_CT_C	190037694	189172968	rs762595062	C	CT	0.6987	0.0080	1.0080	1.0113
2	2_190305048_A_T	190305048	189440322	rs75116627	T	A	0.0121	-0.0102	0.9899	0.9998
2	2_190410532_C_T	190410532	189545806	rs74637811	T	C	0.0117	-0.0109	0.9892	0.9997
2	2_191333980_C_CT	191333980	190469254	rs147470027	CT	C	0.0188	0.0000	1.0000	1.0000
2	2_192066082_G_A	192066082	191201356	rs17510839	A	G	0.0414	-0.0037	0.9963	0.9997
2	2_192381934_C_T	192381934	191517208	rs2356656	T	C	0.8588	0.0000	1.0000	1.0000
2	2_194256253_T_C	194256253	193391528	rs147035132	C	T	0.0144	-0.0247	0.9756	0.9993
2	2_195931292_G_A	195931292	195066568	rs1991632	A	G	0.0516	0.0091	1.0091	1.0009
2	2_195954734_A_G	195954734	195090010	rs777717	G	A	0.9244	-0.0107	0.9894	0.9804
2	2_200004974_G_T	200004974	199140251	rs4673248	T	G	0.5721	0.0098	1.0098	1.0113

2	2_201559027_A_G	201559027	200694304	rs116056056	G	A	0.0393	-0.0131	0.9870	0.9990
2	2_201559931_G_A	201559931	200695208	rs868396	A	G	0.1268	0.0034	1.0034	1.0009
2	2_201912518_ACT GTTAAAGGC_A	201912518	201047795	rs758917394	A	ACTGTT AAAGG GC	0.0686	-0.0062	0.9938	0.9992
2	2_201962858_A_T	201962858	201098135	rs145395636	T	A	0.0211	0.0131	1.0132	1.0006
2	2_201990540_T_G	201990540	201125817	rs13015648	G	T	0.0638	0.0195	1.0197	1.0025
2	2_202004676_C_T	202004676	201139953	rs6759004	T	C	0.1525	-0.0004	0.9996	0.9999
2	2_202096254_C_T	202096254	201231531	rs17860411	T	C	0.0139	0.0090	1.0090	1.0003
2	2_202123430_C_T	202123430	201258707	rs3769821	T	C	0.6670	-0.0067	0.9933	0.9911
2	2_202170655_T_C	202170655	201305932	rs10200279	C	T	0.7139	-0.0050	0.9950	0.9929
2	2_202198589_C_T	202198589	201333866	rs566570823	T	C	0.0261	0.0116	1.0117	1.0006
2	2_202204741_T_C	202204741	201340018	rs10197246	C	T	0.7210	-0.0149	0.9852	0.9788
2	2_202242307_C_G	202242307	201377584	rs7616	G	C	0.0674	-0.0069	0.9931	0.9991
2	2_202379828_T_A	202379828	201515105	rs59278883	A	T	0.0763	-0.0133	0.9868	0.9980
2	2_202395302_TA_T	202395302	201530579	2:202395302_ TA_T	T	TA	0.7456	-0.0014	0.9986	0.9979
2	2_202531264_T_C	202531264	201666541	rs62193398	C	T	0.4174	0.0119	1.0120	1.0100
2	2_205638110_CAT_ C	205638110	204773387	rs7599107	C	CAT	0.0337	0.0062	1.0062	1.0004
2	2_205860163_C_T	205860163	204995440	rs199556273	T	C	0.4595	-0.0021	0.9979	0.9981
2	2_205901702_TA_T	205901702	205036979	2:205901702_ TA_T	T	TA	0.1110	0.0148	1.0149	1.0033
2	2_205922601_T_TA	205922601	205057878	rs35436581	TA	T	0.3386	-0.0100	0.9900	0.9933
2	2_205991363_G_A	205991363	205126639	rs112373916	A	G	0.0783	-0.0014	0.9986	0.9998
2	2_207521558_T_C	207521558	206656834	rs6749661	C	T	0.1822	0.0044	1.0044	1.0016
2	2_208087325_G_C	208087325	207222601	rs10203899	C	G	0.0566	-0.0075	0.9925	0.9992
2	2_208977402_A_G	208977402	208112678	rs55999272	G	A	0.3754	-0.0057	0.9943	0.9957

2	2_211620445_T_C	211620445	210755721	rs2193619	C	T	0.1325	-0.0050	0.9950	0.9987
2	2_213414265_A_G	213414265	212549541	rs13427822	G	A	0.2724	0.0066	1.0066	1.0036
2	2_214087853_G_A	214087853	213223129	rs62186589	A	G	0.2095	-0.0036	0.9964	0.9985
2	2_215928972_G_C	215928972	215064249	rs1523721	C	G	0.5767	0.0007	1.0007	1.0008
2	2_217001090_A_A AAAAAG	217001090	216136367	rs564652267	AAAAAAG	A	0.7472	-0.0094	0.9906	0.9861
2	2_217004038_TAC_T	217004038	216139315	rs759482711	T	TAC	0.4694	-0.0015	0.9985	0.9986
2	2_217030284_A_G	217030284	216165561	rs16855522	G	A	0.1326	0.0083	1.0083	1.0022
2	2_217290060_C_T	217290060	216425337	rs2738280	T	C	0.0388	-0.0200	0.9802	0.9985
2	2_217582016_C_T	217582016	216717293	rs9646854	T	C	0.0616	-0.0018	0.9982	0.9998
2	2_217858641_G_A	217858641	216993918	rs76546018	A	G	0.0308	-0.0032	0.9968	0.9998
2	2_217859657_G_A	217859657	216994934	rs10191184	A	G	0.1268	-0.0078	0.9922	0.9980
2	2_217894234_G_A	217894234	217029511	rs12465506	A	G	0.4956	-0.0013	0.9987	0.9987
2	2_217912437_C_T	217912437	217047714	rs77549302	T	C	0.0522	0.0000	1.0000	1.0000
2	2_217914253_A_G	217914253	217049530	rs10178467	G	A	0.0302	0.0000	1.0000	1.0000
2	2_217920769_G_T	217920769	217056046	rs4442975	T	G	0.5001	-0.1078	0.8978	0.9004
2	2_217936015_T_C	217936015	217071292	rs12622536	C	T	0.4074	0.0000	1.0000	1.0000
2	2_217955896_GA_G	217955896	217091173	2:217955896_ GA_G	G	GA	0.0382	-0.1086	0.8971	0.9922
2	2_217963060_C_A	217963060	217098337	rs34005590	A	C	0.0499	-0.0277	0.9727	0.9973
2	2_217965655_T_A	217965655	217100932	rs2372964	A	T	0.7946	0.0000	1.0000	1.0000
2	2_217965676_T_A	217965676	217100953	rs78464992	A	T	0.0532	-0.0059	0.9941	0.9994
2	2_217967717_C_A	217967717	217102994	rs2372965	A	C	0.7609	0.0000	1.0000	1.0000
2	2_218148853_C_T	218148853	217284130	rs148721366	T	C	0.0198	0.0108	1.0109	1.0004
2	2_218159244_T_C	218159244	217294521	rs6752033	C	T	0.8291	0.0009	1.0009	1.0015
2	2_218174384_TGA	218174384	217309661	rs758533999	T	TGA	0.1402	-0.0003	0.9997	0.9999

2	2_218181721_T_C	218181721	217316998	rs79286679	C	T	0.1243	-0.0016	0.9984	0.9996
2	2_218219226_G_A	218219226	217354503	rs55848226	A	G	0.1058	-0.0127	0.9874	0.9973
2	2_218262547_G_A	218262547	217397824	rs899278	A	G	0.0243	0.0367	1.0374	1.0018
2	2_218292158_C_G	218292158	217427435	rs11693806	G	C	0.7309	-0.0341	0.9665	0.9516
2	2_218303958_G_A	218303958	217439235	rs2568176	A	G	0.2905	0.0189	1.0191	1.0111
2	2_218677711_G_A	218677711	217812988	rs78297591	A	G	0.1009	-0.0023	0.9977	0.9995
2	2_218714845_G_A	218714845	217850122	rs3791977	A	G	0.3917	-0.0144	0.9857	0.9888
2	2_218722506_C_G	218722506	217857783	rs3791959	G	C	0.3298	0.0061	1.0061	1.0040
2	2_218723455_A_G	218723455	217858732	rs6436017	G	A	0.5098	0.0010	1.0010	1.0010
2	2_219963550_C_T	219963550	219098828	rs11692085	T	C	0.6393	-0.0011	0.9989	0.9986
2	2_222865746_T_C	222865746	222001027	rs1030280	C	T	0.7345	0.0017	1.0017	1.0025
2	2_222904550_AC_A	222904550	222039831	rs775726741	A	AC	0.1549	-0.0024	0.9976	0.9993
2	2_227226952_A_G	227226952	226362236	rs12479355	G	A	0.2105	-0.0010	0.9990	0.9996
2	2_227228251_T_C	227228251	226363535	rs76367336	C	T	0.1191	-0.0020	0.9980	0.9995
2	2_227254695_A_G	227254695	226389979	rs13020901	G	A	0.3354	0.0053	1.0053	1.0036
2	2_227274762_C_G	227274762	226410046	rs2396351	G	C	0.6559	0.0054	1.0054	1.0071
2	2_227344207_C_T	227344207	226479491	rs13029395	T	C	0.1710	0.0084	1.0084	1.0029
2	2_227346475_G_A	227346475	226481759	rs192188884	A	G	0.1275	-0.0041	0.9959	0.9990
2	2_227358407_A_G	227358407	226493691	rs148731541	G	A	0.0311	-0.0148	0.9853	0.9991
2	2_233520942_T_C	233520942	232656232	rs12694911	C	T	0.5332	0.0058	1.0058	1.0062
2	2_236025273_G_C	236025273	235116629	rs13398186	C	G	0.2216	-0.0068	0.9932	0.9970
2	2_238277795_A_G	238277795	237369152	rs2646260	G	A	0.2355	-0.0042	0.9958	0.9980
2	2_238299230_G_A	238299230	237390587	rs12052971	A	G	0.2542	-0.0008	0.9992	0.9996
2	2_238508099_T_C	238508099	237599456	rs1316476	C	T	0.2817	0.0023	1.0023	1.0013
2	2_238509759_G_A	238509759	237601116	rs11894280	A	G	0.0788	0.0005	1.0005	1.0001

2	2_238511029_T_C	238511029	237602386	rs4663260	C	T	0.0660	0.0011	1.0011	1.0011	1.0001
2	2_238581009_T_C	238581009	237672366	rs7562075	C	T	0.6830	-0.0089	0.9911	0.9911	0.9879
2	2_239479931_G_A	239479931	238571290	rs11690762	A	G	0.3851	0.0011	1.0011	1.0011	1.0008
2	2_239506956_A_G	239506956	238598315	rs143887241	G	A	0.0119	-0.0295	0.9709	0.9709	0.9993
2	2_240987052_A_C	240987052	240047635	rs79166293	C	A	0.0397	-0.0130	0.9871	0.9871	0.9990
2	2_241313213_A_T	241313213	240373796	rs34352794	T	A	0.2720	-0.0011	0.9989	0.9989	0.9994
2	2_241341294_G_G GGAGAAGAA	241341294	240401877	rs11271854	GGGAGA AGAA	G	0.2739	-0.0059	0.9941	0.9941	0.9968
2	2_241344383_C_G	241344383	240404966	rs10195442	G	C	0.1856	-0.0016	0.9984	0.9984	0.9994
2	2_241388857_C_A	241388857	240449440	rs4676356	A	C	0.9772	-0.0686	0.9337	0.9337	0.8746
3	3_118118_C_G	118118	76435	rs12633924	G	C	0.1908	0.0000	1.0000	1.0000	1.0000
3	3_253679_C_T	253679	211996	rs17329688	T	C	0.1394	-0.0051	0.9949	0.9949	0.9986
3	3_1882270_C_T	1882270	1840586	rs6807710	T	C	0.5197	0.0044	1.0044	1.0044	1.0046
3	3_4733966_C_CA	4733966	4692282	rs34151611	CA	C	0.5524	0.0045	1.0045	1.0045	1.0050
3	3_4742251_A_G	4742251	4700567	rs6762558	G	A	0.3802	0.0284	1.0288	1.0288	1.0220
3	3_4764437_T_C	4764437	4722753	rs55864359	C	T	0.4512	0.0013	1.0013	1.0013	1.0012
3	3_4869622_T_C	4869622	4827938	rs3805026	C	T	0.1911	0.0190	1.0192	1.0192	1.0073
3	3_6885152_G_C	6885152	6843465	rs150612085	C	G	0.0138	0.0000	1.0000	1.0000	1.0000
3	3_8557875_T_A	8557875	8516189	rs6802843	A	T	0.5070	0.0000	1.0000	1.0000	1.0000
3	3_8615277_G_A	8615277	8573591	rs164966	A	G	0.7860	0.0082	1.0082	1.0082	1.0130
3	3_9318416_T_G	9318416	9276732	rs17050210	G	T	0.6254	0.0105	1.0106	1.0106	1.0132
3	3_10258192_G_C	10258192	10216508	rs696322	C	G	0.0744	0.0000	1.0000	1.0000	1.0000
3	3_10261294_A_G	10261294	10219610	rs3895947	G	A	0.7695	0.0000	1.0000	1.0000	1.0000
3	3_10310878_T_G	10310878	10269194	rs2270455	G	T	0.1009	-0.0017	0.9983	0.9983	0.9997
3	3_10326169_G_A	10326169	10284485	rs171407	A	G	0.5327	-0.0098	0.9902	0.9902	0.9896
3	3_11050452_T_C	11050452	11008766	rs2950800	C	T	0.7306	0.0033	1.0033	1.0033	1.0048
3	3_11055624_C_T	11055624	11013938	rs2933308	T	C	0.3922	-0.0028	0.9972	0.9972	0.9978

3	3_11059996_A_G	11059996	11018310	rs1728803	G	A	0.6018	0.0026	1.0026	1.0031
3	3_12329452_C_T	12329452	12287953	rs17029006	T	C	0.2779	0.0124	1.0125	1.0069
3	3_12508167_C_T	12508167	12466668	rs6793530	T	C	0.3351	0.0138	1.0139	1.0093
3	3_13611731_G_GC	13611731	13570231	rs3832210	GC	G	0.0564	0.0232	1.0235	1.0026
3	3_14137393_A_G	14137393	14095893	rs77027159	G	A	0.0213	0.0350	1.0356	1.0015
3	3_14347085_T_C	14347085	14305585	rs9837707	C	T	0.9547	-0.0105	0.9896	0.9802
3	3_15384049_A_G	15384049	15342542	rs74716230	G	A	0.0340	-0.0062	0.9938	0.9996
3	3_16788466_A_G	16788466	16746959	rs13067457	G	A	0.6642	0.0105	1.0106	1.0141
3	3_18129387_C_G	18129387	18087895	rs115551171	G	C	0.0182	-0.0101	0.9900	0.9996
3	3_18463734_G_C	18463734	18422242	rs141634179	C	G	0.0239	-0.0269	0.9735	0.9987
3	3_22410483_T_C	22410483	22368992	rs9872825	C	T	0.9383	0.0222	1.0224	1.0426
3	3_23684104_G_A	23684104	23642613	rs6768220	A	G	0.6912	0.0000	1.0000	1.0000
3	3_24284559_GAAA_AA_G	24284559	24243068	3:24284559_G AAAAA_G	G	GAAAA	0.8040	0.0037	1.0037	1.0060
3	3_24308707_TAGT_C_T	24308707	24267216	rs766138533	T	TAGTC	0.1787	0.0056	1.0056	1.0020
3	3_24958946_A_G	24958946	24917455	rs73049478	G	A	0.0625	0.0138	1.0139	1.0017
3	3_25554733_G_A	25554733	25513242	rs10446417	A	G	0.0714	-0.0021	0.9979	0.9997
3	3_27045315_A_G	27045315	27003824	rs11710754	G	A	0.3345	0.0070	1.0070	1.0047
3	3_27116801_C_T	27116801	27075310	rs61548819	T	C	0.4146	0.0000	1.0000	1.0000
3	3_27142557_G_GA	27142557	27101066		GA	G	0.4960	0.0000	1.0000	1.0000
3	3_27187022_G_A	27187022	27145531	rs17317121	A	G	0.0583	0.0010	1.0010	1.0001
3	3_27246771_G_T	27246771	27205280	rs34629416	T	G	0.2283	0.0000	1.0000	1.0000
3	3_27256049_G_T	27256049	27214558	rs6805966	T	G	0.4801	0.0044	1.0044	1.0042
3	3_27307298_CT_C	27307298	27265807	3:27307298_C T_C	C	CT	0.5032	0.0000	1.0000	1.0000
3	3_27347117_A_AT	27347117	27305626	rs63334461	AT	A	0.4680	0.0000	1.0000	1.0000

3	3_27353716_C_A	27353716	27312225	rs552647	A	C		0.5259	0.0363	1.0370	1.0393
3	3_27368425_C_T	27368425	27326934	rs1352941	T	C		0.5000	0.0000	1.0000	1.0000
3	3_27388664_C_G	27388664	27347173	rs62255657	G	C		0.2735	0.0273	1.0277	1.0152
3	3_27392625_T_A	27392625	27351134	rs73055736	A	T		0.4212	-0.0122	0.9879	0.9898
3	3_27413566_C_T	27413566	27372075	rs4973766	T	C		0.4568	0.0000	1.0000	1.0000
3	3_27432206_T_C	27432206	27390715	rs6551196	C	T		0.5611	0.0092	1.0092	1.0104
3	3_27520500_A_G	27520500	27479009	rs12054243	G	A		0.3612	-0.0015	0.9985	0.9989
3	3_27785427_T_C	27785427	27743936	rs74614983	C	T		0.0217	-0.0028	0.9972	0.9999
3	3_27817597_G_A	27817597	27776106	rs141629957	A	G		0.0170	-0.0054	0.9946	0.9998
3	3_27830509_G_A	27830509	27789018	rs12491073	A	G		0.1494	-0.0001	0.9999	1.0000
3	3_29229732_A_G	29229732	29188241	rs73058397	G	A		0.0276	0.0000	1.0000	1.0000
3	3_29254155_T_C	29254155	29212664	rs111292208	C	T		0.0259	0.0000	1.0000	1.0000
3	3_29294845_C_T	29294845	29253354	rs112476261	T	C		0.0163	-0.0497	0.9515	0.9984
3	3_29359952_T_C	29359952	29318461	rs57440162	C	T		0.3673	0.0044	1.0044	1.0032
3	3_30283362_C_T	30283362	30241871	rs17564259	T	C		0.0727	-0.0017	0.9983	0.9998
3	3_30307462_G_A	30307462	30265971	rs112847401	A	G		0.0603	-0.0083	0.9917	0.9990
3	3_30549108_G_A	30549108	30507616	rs73050822	A	G		0.1014	-0.0014	0.9986	0.9997
3	3_30582035_C_T	30582035	30540543	rs150163739	T	C		0.0236	0.0090	1.0090	1.0004
3	3_30664321_G_A	30664321	30622829	rs7644802	A	G		0.4627	-0.0027	0.9973	0.9975
3	3_30670425_G_C	30670425	30628933	rs5020833	C	G		0.3217	0.0000	1.0000	1.0000
3	3_30675880_A_T	30675880	30634388	rs1431131	T	A		0.3596	0.0025	1.0025	1.0018
3	3_30677116_G_A	30677116	30635624	rs952411	A	G		0.6135	0.0032	1.0032	1.0039
3	3_30684097_G_A	30684097	30642605	rs35263707	A	G		0.3253	0.0108	1.0109	1.0071
3	3_30684907_C_T	30684907	30643415	rs17838698	T	C		0.2975	0.0108	1.0109	1.0065
3	3_30689303_T_G	30689303	30647811	rs7613040	G	T		0.6414	0.0031	1.0031	1.0040
3	3_35009348_G_A	35009348	34967856	rs75736174	A	G		0.0939	0.0032	1.0032	1.0006
3	3_35113193_C_T	35113193	35071701	rs11129635	T	C		0.0944	0.0022	1.0022	1.0004

3	3_37516184_C_T	37516184	37474693	rs2162683	T	C	0.3410	0.0000	1.0000	1.0000
3	3_46532543_C_T	46532543	46491053	rs79600837	T	C	0.1402	0.0043	1.0043	1.0012
3	3_46687519_C_T	46687519	46646029	rs13319345	T	C	0.3520	-0.0042	0.9958	0.9971
3	3_46866866_G_A	46866866	46825376	rs6796502	A	G	0.1008	-0.0278	0.9726	0.9945
3	3_46891310_G_C	46891310	46849820	rs57459864	C	G	0.1576	-0.0113	0.9888	0.9965
3	3_47210979_G_T	47210979	47169489	rs184445588	T	G	0.0139	-0.0062	0.9938	0.9998
3	3_47695680_T_G	47695680	47654190	rs186117953	G	T	0.0104	-0.0136	0.9865	0.9997
3	3_48007463_C_T	48007463	47965973	rs75420707	T	C	0.0271	0.0000	1.0000	1.0000
3	3_48261969_C_T	48261969	48220479	rs36019664	T	C	0.0277	-0.0098	0.9902	0.9995
3	3_48294816_C_G	48294816	48253326	rs35010013	G	C	0.0399	-0.0131	0.9870	0.9990
3	3_48839507_T_A	48839507	48802074	rs145663361	A	T	0.0148	-0.0263	0.9740	0.9992
3	3_49166460_C_T	49166460	49129027	rs61729152	T	C	0.0214	-0.0138	0.9863	0.9994
3	3_49518299_A_G	49518299	49480866	rs71615484	G	A	0.3599	-0.0084	0.9916	0.9940
3	3_49710514_CCGG_G_C	49710514	49673081	3:49710514_C CGGG_C	C	CCGGG	0.2870	-0.0093	0.9907	0.9947
3	3_49789921_C_CA	49789921	49752488	rs547649546	CA	C	0.5004	-0.0046	0.9954	0.9954
3	3_49843723_T_C	49843723	49806290	rs3819325	C	T	0.4751	0.0000	1.0000	1.0000
3	3_52529317_C_T	52529317	52495301	rs79914724	T	C	0.0121	0.0000	1.0000	1.0000
3	3_53217413_A_G	53217413	53183397	rs2306572	G	A	0.2391	-0.0059	0.9941	0.9972
3	3_53846588_TTTTG_T	53846588	53812561	3:53846588_T TTTG_T	T	TTTTG	0.0192	-0.0197	0.9805	0.9993
3	3_54648537_A_C	54648537	54614510	rs34592432	C	A	0.1662	0.0021	1.0021	1.0007
3	3_54695858_C_G	54695858	54661831	rs75606245	G	C	0.0994	0.0067	1.0067	1.0013
3	3_55072187_C_T	55072187	55038160	rs358493	T	C	0.3416	0.0061	1.0061	1.0042
3	3_55553097_C_T	55553097	55519069	rs62251462	T	C	0.0465	-0.0100	0.9900	0.9991
3	3_55561657_A_G	55561657	55527629	rs62251466	G	A	0.0361	-0.0067	0.9933	0.9995
3	3_55970777_A_AT	55970777	55936749	rs138866686	AT	A	0.0305	-0.0327	0.9678	0.9980

3	3_59361172_C_CT	59361172	59375446	rs11429792	CT	C	0.6917	0.0077	1.0077	1.0107
3	3_59373745_C_T	59373745	59388019	rs2886671	T	C	0.4294	-0.0127	0.9874	0.9892
3	3_59693450_C_A	59693450	59707724	rs56915453	A	C	0.1236	0.0043	1.0043	1.0011
3	3_59771038_CT_C	59771038	59785312	3:59771038_C_T_C	C	CT	0.7385	0.0020	1.0020	1.0030
3	3_59832595_C_G	59832595	59846869	rs633189	G	C	0.6362	0.0117	1.0118	1.0150
3	3_59856766_T_C	59856766	59871040	rs57341675	C	T	0.1136	-0.0018	0.9982	0.9996
3	3_60553783_A_G	60553783	60568050	rs4679551	G	A	0.1666	-0.0059	0.9941	0.9980
3	3_61466213_C_G	61466213	61480539	rs1975730	G	C	0.8646	-0.0044	0.9956	0.9924
3	3_61486355_AAG_A	61486355	61500681	3:61486355_A_AG_A	A	AAG	0.1962	0.0089	1.0089	1.0035
3	3_62650762_C_T	62650762	62665087	rs62242517	T	C	0.1347	0.0000	1.0000	1.0000
3	3_63491051_A_G	63491051	63505375	rs17068857	G	A	0.1693	-0.0075	0.9925	0.9975
3	3_63493054_G_GA	63493054	63507378	rs71743220	GA	G	0.2023	-0.0067	0.9933	0.9973
3	3_63743823_T_C	63743823	63758147	rs74886078	C	T	0.0215	-0.0065	0.9935	0.9997
3	3_63887449_T_TTG	63887449	63901773		TTG	T	0.1297	0.0166	1.0167	1.0043
3	3_63986046_CT_C	63986046	64000370	3:63986046_C_T_C	C	CT	0.1669	0.0132	1.0133	1.0044
3	3_64019206_A_G	64019206	64033530	rs6785145	G	A	0.4264	0.0040	1.0040	1.0034
3	3_64029383_A_G	64029383	64043707	rs831574	G	A	0.3435	0.0000	1.0000	1.0000
3	3_64116494_T_G	64116494	64130818	rs55796057	G	T	0.1891	0.0009	1.0009	1.0003
3	3_64182827_G_A	64182827	64197151	rs57476258	A	G	0.1613	0.0041	1.0041	1.0013
3	3_64370063_T_G	64370063	64384387	rs7653442	G	T	0.2405	0.0069	1.0069	1.0033
3	3_64371596_C_CG_GTT	64371596	64385920	rs144435498	CGTT	C	0.1179	0.0056	1.0056	1.0013
3	3_65461535_C_T	65461535	65475860	rs7614228	T	C	0.2396	-0.0076	0.9924	0.9964
3	3_65641268_G_C	65641268	65655593	rs1156024	C	G	0.3312	0.0067	1.0067	1.0045

3	3_65650331_T_G	65650331	65664656	rs36091678	G	T	0.3453	0.0006	1.0006	1.0004
3	3_66458047_G_GC A	66458047	66407623	rs796133473	GCA	G	0.5826	0.0086	1.0086	1.0101
3	3_67454299_T_C	67454299	67403875	rs55672035	C	T	0.4504	-0.0066	0.9934	0.9941
3	3_71476825_G_C	71476825	71427674	rs6549389	C	G	0.7313	-0.0046	0.9954	0.9933
3	3_71531467_T_C	71531467	71482316	rs35483362	C	T	0.4758	-0.0123	0.9878	0.9884
3	3_72334204_CCTCC CAA_C	72334204	72285053	3:72334204_C CTCCAA_C	C	CCTCCC AA	0.4389	0.0037	1.0037	1.0033
3	3_72352464_T_TAC ACATGGCCACCGA	72352464	72303313		TACACAT GGCCACC GA	T	0.4850	0.0000	1.0000	1.0000
3	3_72457221_A_G	72457221	72408070	rs6549455	G	A	0.6395	0.0087	1.0087	1.0112
3	3_73330742_G_A	73330742	73281591	rs112563751	A	G	0.0362	0.0000	1.0000	1.0000
3	3_73343559_A_C	73343559	73294408	rs7647925	C	A	0.5262	-0.0136	0.9865	0.9858
3	3_80126605_T_C	80126605	80077455	rs73128241	C	T	0.0264	0.0038	1.0038	1.0002
3	3_81234859_G_T	81234859	81185708	rs1477676	T	G	0.7525	-0.0102	0.9899	0.9848
3	3_85724423_A_G	85724423	85675273	rs147473479	G	A	0.0115	0.0423	1.0432	1.0010
3	3_85768032_TTTAT TATTATTATTA_T	85768032	85718882	3:85768032_T TTATTATTATT ATTA_T	T	TTTATT ATTATT ATTA	0.3170	0.0004	1.0004	1.0003
3	3_86195124_A_G	86195124	86145974	rs6549075	G	A	0.6825	0.0040	1.0040	1.0055
3	3_86203809_G_T	86203809	86154659	rs9833726	T	G	0.1383	-0.0112	0.9889	0.9969
3	3_86499424_G_A	86499424	86450274	rs148727437	A	G	0.0148	0.0000	1.0000	1.0000
3	3_87037543_A_G	87037543	86988393	rs13066793	G	A	0.0921	-0.0277	0.9727	0.9950
3	3_87842066_T_C	87842066	87792916	rs1873209	C	T	0.3376	0.0075	1.0075	1.0051
3	3_87995951_G_A	87995951	87946801	rs2915293	A	G	0.6973	-0.0014	0.9986	0.9980
3	3_88196211_A_C	88196211	88147061	rs9861443	C	A	0.7295	-0.0045	0.9955	0.9935
3	3_98830472_A_G	98830472	99111628	rs34972210	G	A	0.1172	0.0076	1.0076	1.0018

3	3_99184544_C_T	99184544	99465700	rs2700628	T	C	0.0955	0.0012	1.0012	1.0002
3	3_99212523_G_T	99212523	99493679	rs35583542	T	G	0.1039	0.0036	1.0036	1.0007
3	3_99227951_A_T	99227951	99509107	rs115575016	T	A	0.2760	0.0011	1.0011	1.0006
3	3_99269750_T_C	99269750	99550906	rs15133304	C	T	0.2829	0.0014	1.0014	1.0008
3	3_99275637_G_A	99275637	99556793	rs71313557	A	G	0.0373	0.0032	1.0032	1.0002
3	3_99303827_A_C	99303827	99584983	rs13093075	C	A	0.7131	-0.0078	0.9922	0.9889
3	3_99403877_G_A	99403877	99685033	rs639355	A	G	0.4852	-0.0094	0.9906	0.9909
3	3_99425767_A_T	99425767	99706923	rs629120	T	A	0.7823	0.0000	1.0000	1.0000
3	3_99687273_G_A	99687273	99968429	rs4361315	A	G	0.7359	-0.0063	0.9937	0.9908
3	3_103062567_A_T	103062567	103343723	rs73153693	T	A	0.0706	-0.0178	0.9824	0.9975
3	3_107112555_C_G	107112555	107393708	rs10511262	G	C	0.1123	-0.0054	0.9946	0.9988
3	3_110267702_T_G	110267702	110548855	rs80282904	G	T	0.1047	-0.0129	0.9872	0.9973
3	3_111387513_C_G	111387513	111668666	rs146576688	G	C	0.0201	-0.0253	0.9750	0.9990
3	3_114117017_T_G	114117017	114398170	rs16822588	G	T	0.1095	0.0059	1.0059	1.0013
3	3_115528511_A_G	115528511	115809664	rs28636502	G	A	0.1254	-0.0041	0.9959	0.9990
3	3_116345449_C_A	116345449	116626602	rs6438324	A	C	0.4997	0.0037	1.0037	1.0037
3	3_118666410_C_T	118666410	118947563	rs73185814	T	C	0.0376	0.0000	1.0000	1.0000
3	3_118984456_A_T	118984456	119265609	rs77424405	T	A	0.0188	0.0587	1.0605	1.0023
3	3_125060843_C_A	125060843	125341999	rs6804933	A	C	0.7447	-0.0045	0.9955	0.9933
3	3_125074570_TA_T	125074570	125355726	3:125074570_ TA_T	T	TA	0.6995	-0.0044	0.9956	0.9939
3	3_125132642_G_A	125132642	125413798	rs62273093	A	G	0.7271	-0.0054	0.9946	0.9922
3	3_125833260_C_T	125833260	126114417	rs2290053	T	C	0.4932	0.0031	1.0031	1.0031
3	3_125847647_T_C	125847647	126128804	rs6775421	C	T	0.6555	0.0015	1.0015	1.0020
3	3_126056772_C_T	126056772	126337929	rs7619823	T	C	0.4757	0.0110	1.0111	1.0106
3	3_126174838_A_G	126174838	126455995	rs777504	G	A	0.9633	0.0118	1.0119	1.0230
3	3_129060011_A_G	129060011	129341168	rs7374197	G	A	0.5471	0.0082	1.0082	1.0090

3	3_129647253_G_A	129647253	129928410	rs34941175	A	G	0.0624	-0.0186	0.9816	0.9977
3	3_137325391_T_C	137325391	137606549	rs9879724	C	T	0.1892	0.0040	1.0040	1.0015
3	3_138723358_G_A	138723358	139004516	rs138346232	A	G	0.0193	-0.0431	0.9578	0.9984
3	3_139697874_A_G	139697874	139979032	rs73224969	G	A	0.0375	0.0000	1.0000	1.0000
3	3_141063953_C_T	141063953	141345111	rs9838625	T	C	0.4154	0.0000	1.0000	1.0000
3	3_141112859_CTT_C	141112859	141394017	3:141112859_CTT_C	C	CTT	0.4149	0.0258	1.0261	1.0218
3	3_141142691_G_A	141142691	141423849	rs6440006	A	G	0.4347	0.0043	1.0043	1.0037
3	3_141344368_A_T	141344368	141625526	rs9821686	T	A	0.1541	-0.0093	0.9907	0.9971
3	3_141510052_G_T	141510052	141791210	rs2681693	T	G	0.1509	-0.0048	0.9952	0.9986
3	3_141952067_C_C	141952067	142233225	rs10662123	CAAA	C	0.4841	-0.0038	0.9962	0.9963
3	3_142863119_G_A	142863119	143144277	rs4683748	A	G	0.3797	-0.0061	0.9939	0.9954
3	3_142982700_G_A	142982700	143263858	rs6440156	A	G	0.7758	0.0098	1.0098	1.0153
3	3_145444094_C_T	145444094	145726307	rs62269362	T	C	0.3689	0.0011	1.0011	1.0008
3	3_145884210_T_C	145884210	146166423	rs7623263	C	T	0.4239	-0.0028	0.9972	0.9976
3	3_148576368_A_C	148576368	148858581	rs1845415	C	A	0.0183	-0.0341	0.9665	0.9988
3	3_148616863_A_A	148616863	148899076		AAT	A	0.0368	-0.0096	0.9904	0.9993
3	3_150455755_G_A	150455755	150737968	rs502941	A	G	0.8847	0.0089	1.0089	1.0159
3	3_151062093_T_TA	151062093	151344305		TAA	T	0.2725	-0.0081	0.9919	0.9956
3	3_151079960_T_G	151079960	151362172	rs6793061	G	T	0.2412	-0.0044	0.9956	0.9979
3	3_151523713_G_A	151523713	151805925	rs67337703	A	G	0.4022	0.0012	1.0012	1.0010
3	3_151547130_C_T	151547130	151829342	rs9841094	T	C	0.7748	0.0083	1.0083	1.0130
3	3_156357618_CTCT_T_C	156357618	156639829	3:156357618_CTCT_C	C	CTCT	0.2518	-0.0019	0.9981	0.9990
3	3_156399180_G_A	156399180	156681391	rs3851992	A	G	0.4066	0.0071	1.0071	1.0058

3	3_156480941_A_G	156480941	156763152	rs2043108	G	A	0.5862	0.0007	1.0007	1.0008
3	3_156525396_T_A	156525396	156807607	rs1430411	A	T	0.6149	0.0041	1.0041	1.0051
3	3_158019780_GT_G	158019780	158301991	rs759541351	G	GT	0.5195	0.0068	1.0068	1.0071
3	3_158168120_CT_C	158168120	158450331	rs144232662	C	CT	0.2501	0.0000	1.0000	1.0000
3	3_162135821_A_G	162135821	162418033	rs2405502	G	A	0.6713	0.0021	1.0021	1.0028
3	3_163050198_A_G	163050198	163332410	rs77632248	G	A	0.0231	-0.0366	0.9641	0.9983
3	3_166739585_G_A	166739585	167021797	rs2203919	A	G	0.3994	0.0005	1.0005	1.0004
3	3_168674494_A_G	168674494	168956706	rs6781201	G	A	0.1388	0.0050	1.0050	1.0014
3	3_170537091_A_T	170537091	170819302	rs12054015	T	A	0.3180	0.0000	1.0000	1.0000
3	3_170625806_C_T	170625806	170908017	rs2271998	T	C	0.4027	0.0000	1.0000	1.0000
3	3_172081359_G_A	172081359	172363569	rs12152414	A	G	0.0329	0.0025	1.0025	1.0002
3	3_172160206_T_C	172160206	172442416	rs114441197	C	T	0.0117	0.0108	1.0109	1.0003
3	3_172204644_A_G	172204644	172486854	rs1597088	G	A	0.4829	-0.0045	0.9955	0.9957
3	3_172222756_C_T	172222756	172504966	rs7631904	T	C	0.2109	0.0000	1.0000	1.0000
3	3_172227766_CA_C	172227766	172509976	3:172227766_CA_C	C	CA	0.3763	-0.0054	0.9946	0.9960
3	3_172237859_G_T	172237859	172520069	rs3136588	T	G	0.0411	0.0000	1.0000	1.0000
3	3_172285237_G_A	172285237	172567447	rs58058861	A	G	0.2131	0.0105	1.0106	1.0045
3	3_172598961_C_T	172598961	172881171	rs2088658	T	C	0.7522	-0.0048	0.9952	0.9928
3	3_172611899_T_C	172611899	172894109	rs10451925	C	T	0.6812	-0.0015	0.9985	0.9980
3	3_172624366_C_CT	172624366	172906576	rs34346181	CTA	C	0.7093	-0.0046	0.9954	0.9935
3	3_173220074_G_T	173220074	173502284	rs550880	T	G	0.1100	0.0122	1.0123	1.0027
3	3_175862678_A_C	175862678	176144890	rs2902242	C	A	0.1736	0.0047	1.0047	1.0016
3	3_175914226_C_T	175914226	176196438	rs62285838	T	C	0.1394	0.0164	1.0165	1.0046
3	3_176852038_A_T	176852038	177134250	rs7626218	T	A	0.3982	0.0091	1.0091	1.0073

3	3_177427650_A_G	177427650	177709862	rs2133590	G	A	0.3602	-0.0038	0.9962	0.9973
3	3_177522037_T_C	177522037	177804249	rs35370551	C	T	0.1284	0.0009	1.0009	1.0002
3	3_177753655_G_T	177753655	178035867	rs115452163	T	G	0.0288	0.0221	1.0223	1.0013
3	3_179010099_TA_T	179010099	179292311	3:179010099_ TA_T	T	TA	0.6072	-0.0046	0.9954	0.9944
3	3_179020085_T_C	179020085	179302297	rs12634043	C	T	0.6502	-0.0050	0.9950	0.9935
3	3_179673801_A_G	179673801	179956013	rs13097429	G	A	0.1355	0.0000	1.0000	1.0000
3	3_182428424_G_A	182428424	182710636	rs77442660	A	G	0.0872	-0.0132	0.9869	0.9977
3	3_183178910_G_A	183178910	183461122	rs11707996	A	G	0.2023	-0.0097	0.9903	0.9961
3	3_183184794_CTTT TTTT_C	183184794	183467006	rs3074830	C	CTTTTT T	0.2300	-0.0015	0.9985	0.9993
3	3_183888015_G_A	183888015	184170227	rs147393618	A	G	0.0265	0.0145	1.0146	1.0008
3	3_185741991_G_A	185741991	186024202	rs12330780	A	G	0.4783	0.0036	1.0036	1.0035
3	3_185824151_G_C	185824151	186106362	rs77195939	C	G	0.0487	-0.0016	0.9984	0.9998
3	3_185856621_A_C	185856621	186138832	rs57374641	C	A	0.0892	-0.0155	0.9846	0.9973
3	3_185964764_C_T	185964764	186246975	rs6792471	T	C	0.9307	0.0110	1.0111	1.0207
3	3_185966982_C_G	185966982	186249193	rs6799575	G	C	0.0378	-0.0077	0.9923	0.9994
3	3_185991240_C_T	185991240	186273451	rs9290831	T	C	0.0811	-0.0105	0.9896	0.9983
3	3_187310352_C_A	187310352	187592564	rs9868558	A	C	0.2997	0.0073	1.0073	1.0044
3	3_187421181_C_T	187421181	187703393	rs11708364	T	C	0.6379	0.0044	1.0044	1.0056
3	3_187459779_C_T	187459779	187741991	rs3774300	T	C	0.7900	0.0092	1.0092	1.0147
3	3_187756755_G_A	187756755	188038967	rs2378359	A	G	0.8122	-0.0001	0.9999	0.9998
3	3_188976010_C_T	188976010	189258221	rs6801108	T	C	0.1820	0.0000	1.0000	1.0000
3	3_189774456_C_T	189774456	190056667	rs9882792	T	C	0.2235	-0.0144	0.9857	0.9936
3	3_189816756_C_T	189816756	190098967	rs710586	T	C	0.1568	-0.0031	0.9969	0.9990
3	3_191507120_T_C	191507120	191789331	rs75772781	C	T	0.0586	0.0001	1.0001	1.0000
3	3_192380630_G_T	192380630	192662841	rs6784363	T	G	0.6051	0.0048	1.0048	1.0058

3	3_192549113_G_A	192549113	192831324	rs7622135	A	G	0.4785	0.0015	1.0015	1.0014
3	3_192569458_AT_A	192569458	192851669	rs201095372	A	AT	0.4894	0.0024	1.0024	1.0024
3	3_193701697_A_G	193701697	193983908	rs77474546	G	A	0.0892	0.0065	1.0065	1.0012
3	3_195865387_G_A	195865387	196138516	rs7634650	A	G	0.1730	0.0098	1.0098	1.0034
3	3_196104863_C_T	196104863	196377992	rs62409217	T	C	0.1250	0.0104	1.0105	1.0026
3	3_197256058_C_T	197256058	197529187	rs11925979	T	C	0.1169	-0.0030	0.9970	0.9993
3	3_197683078_CCT_C	197683078	197956207	3:197683078_CCT_C	C	CCT	0.1995	0.0034	1.0034	1.0014
4	4_560897_A_T	560897	567108	rs73074224	T	A	0.0434	0.0207	1.0209	1.0018
4	4_1158991_C_A	1158991	1165203	rs17802266	A	C	0.2452	-0.0068	0.9932	0.9967
4	4_6922022_A_G	6922022	6920295	rs116837201	G	A	0.0128	0.0051	1.0051	1.0001
4	4_7292894_T_C	7292894	7291167	rs3846424	C	T	0.7343	0.0035	1.0035	1.0052
4	4_7892228_T_A	7892228	7890501	rs55824910	A	T	0.1545	-0.0073	0.9927	0.9978
4	4_7932704_C_T	7932704	7930977	rs4696808	T	C	0.4867	0.0063	1.0063	1.0062
4	4_7951955_GT_G	7951955	7950228	4:7951955_GT_G	G	GT	0.0311	0.0217	1.0219	1.0014
4	4_8321215_C_A	8321215	8319488	rs4696811	A	C	0.8273	0.0050	1.0050	1.0083
4	4_9575536_G_GT	9575536	9573912	rs35535759	GT	G	0.2572	-0.0112	0.9889	0.9943
4	4_10625018_C_G	10625018	10623394	rs2720360	G	C	0.8126	0.0053	1.0053	1.0087
4	4_12230032_G_A	12230032	12228408	rs62296431	A	G	0.0186	0.0311	1.0316	1.0012
4	4_15011508_C_T	15011508	15009884	rs2643087	T	C	0.0309	-0.0134	0.9867	0.9992
4	4_17042582_C_T	17042582	17040959	rs73245378	T	C	0.2395	0.0077	1.0077	1.0037
4	4_17061476_C_G	17061476	17059853	rs828162	G	C	0.9141	-0.0082	0.9918	0.9851
4	4_17308014_T_G	17308014	17306391	rs73230775	G	T	0.1377	-0.0109	0.9892	0.9970
4	4_17315910_T_C	17315910	17314287	rs13126451	C	T	0.6324	0.0035	1.0035	1.0044
4	4_17386550_A_G	17386550	17384927	rs2031007	G	A	0.2353	0.0049	1.0049	1.0023

4	4_18675840_A_G	18675840	18674217	rs4428281	G	A	0.9536	0.0126	1.0127	1.0243
4	4_18753395_C_T	18753395	18751772	rs1568226	T	C	0.7818	0.0095	1.0095	1.0150
4	4_20064344_T_TA	20064344	20062721	rs201232508	TA	T	0.7154	-0.0056	0.9944	0.9920
4	4_20263484_G_C	20263484	20261861	rs150694043	C	G	0.0105	-0.0442	0.9568	0.9991
4	4_21194184_C_G	21194184	21192561	rs17514618	G	C	0.0271	-0.0075	0.9925	0.9996
4	4_22660580_C_T	22660580	22658957	rs141487006	T	C	0.0125	-0.0295	0.9709	0.9993
4	4_23813109_T_C	23813109	23811486	rs7667050	C	T	0.5279	0.0058	1.0058	1.0062
4	4_23853011_T_C	23853011	23851388	rs7665116	C	T	0.1309	0.0089	1.0089	1.0023
4	4_24209070_G_A	24209070	24207447	rs113743277	A	G	0.0100	-0.0034	0.9966	0.9999
4	4_27680810_A_G	27680810	27679188	rs34258956	G	A	0.0166	0.0224	1.0227	1.0008
4	4_27906865_T_C	27906865	27905243	rs1038442	C	T	0.4591	0.0109	1.0110	1.0101
4	4_31213252_G_A	31213252	31211630	rs2133514	A	G	0.0873	0.0051	1.0051	1.0009
4	4_31229344_CT_CT	31229344	31227722		CTTT	CT	0.0992	0.0000	1.0000	1.0000
4	4_31255491_C_A	31255491	31253869	rs78953893	A	C	0.1294	0.0024	1.0024	1.0006
4	4_31478536_C_A	31478536	31476914	rs410175	A	C	0.8191	0.0053	1.0053	1.0087
4	4_32552249_T_A	32552249	32550627	rs17081562	A	T	0.0142	0.0228	1.0231	1.0007
4	4_38571221_A_G	38571221	38569600	rs11930931	G	A	0.7572	-0.0094	0.9906	0.9859
4	4_38578411_C_G	38578411	38576790	rs7673092	G	C	0.1231	0.0062	1.0062	1.0015
4	4_38751752_G_A	38751752	38750131	rs4540059	A	G	0.1773	0.0050	1.0050	1.0018
4	4_38784633_G_T	38784633	38783012	rs10012017	T	G	0.2493	0.0175	1.0177	1.0088
4	4_38999972_T_C	38999972	38998352	rs112774343	C	T	0.2603	0.0006	1.0006	1.0003
4	4_39909408_G_A	39909408	39907788	rs62309184	A	G	0.2446	0.0044	1.0044	1.0022
4	4_43520590_T_G	43520590	43518573	rs4861284	G	T	0.9255	-0.0065	0.9935	0.9880
4	4_43521885_T_A	43521885	43519868	rs34523991	A	T	0.8171	-0.0064	0.9936	0.9896
4	4_45718837_T_A	45718837	45716820	rs148855431	A	T	0.0422	0.0004	1.0004	1.0000
4	4_45786423_T_C	45786423	45784406	rs114877756	C	T	0.0555	0.0199	1.0201	1.0022

4	4_47658534_A_T	47658534	47656517	rs6447578	T	A	0.4404	0.0013	1.0013	1.0011
4	4_48073073_C_T	48073073	48071056	rs62301688	T	C	0.2784	-0.0066	0.9934	0.9963
4	4_48099439_C_CTT	48099439	48097422	rs4047946	CTT	C	0.6596	0.0003	1.0003	1.0004
4	4_53912593_G_C	53912593	53046426	rs12506630	C	G	0.3736	-0.0115	0.9886	0.9915
4	4_55885742_A_G	55885742	55019575	rs71599662	G	A	0.1979	0.0025	1.0025	1.0010
4	4_55894238_G_A	55894238	55028071	rs13105577	A	G	0.1749	0.0106	1.0107	1.0037
4	4_56387771_C_T	56387771	55521604	rs114924440	T	C	0.0252	0.0325	1.0330	1.0017
4	4_57870386_TTTCA CTGTGTTGGCCAGG CTGGTC_T	57870386	57004220	4:57870386_T TTCACTGTGTT GGCCAGGCTG GTC_T	T	TTTCA TGTGTT GGCCA GGCTG GTC	0.0438	0.0222	1.0224	1.0020
4	4_57879792_C_T	57879792	57013626	rs4865169	T	C	0.5223	0.0076	1.0076	1.0080
4	4_57910940_G_A	57910940	57044774	rs11937978	A	G	0.3279	0.0000	1.0000	1.0000
4	4_57935047_CTT_C TTT	57935047	57068881		CTT	CTT	0.1257	-0.0032	0.9968	0.9992
4	4_58002159_C_T	58002159	57135993	rs114175895	T	C	0.0130	0.0251	1.0254	1.0007
4	4_62017499_G_A	62017499	61151781	rs12508373	A	G	0.2554	0.0029	1.0029	1.0015
4	4_63347138_G_T	63347138	62481420	rs11735362	T	G	0.5269	-0.0042	0.9958	0.9956
4	4_63354303_A_G	63354303	62488585	rs6843214	G	A	0.5877	-0.0029	0.9971	0.9966
4	4_64303165_T_C	64303165	63437447	rs62303365	C	T	0.2643	0.0035	1.0035	1.0019
4	4_68081561_G_A	68081561	67215843	rs62315512	A	G	0.1865	-0.0151	0.9850	0.9944
4	4_68292294_A_G	68292294	67426576	rs148825788	G	A	0.0821	-0.0122	0.9879	0.9980
4	4_70336172_T_C	70336172	69470454	rs2736520	C	T	0.1498	-0.0121	0.9880	0.9964
4	4_73752735_T_A	73752735	72887018	rs76886866	A	T	0.0180	-0.0141	0.9860	0.9995
4	4_74222782_G_A	74222782	73357065	rs55881006	A	G	0.0333	-0.0195	0.9807	0.9987
4	4_74784651_GA_G	74784651	73918934	4:74784651_G A_G	G	GA	0.0546	0.0292	1.0296	1.0032

4	4_77057905_G_T	77057905	76136752	rs4376175	T	G	0.1579	-0.0143	0.9858	0.9955
4	4_78073483_A_G	78073483	77152330	rs6849124	G	A	0.5087	-0.0001	0.9999	0.9999
4	4_78121478_G_C	78121478	77200325	rs4582179	C	G	0.4848	-0.0100	0.9900	0.9904
4	4_83892103_CTGA TT_C	83892103	82970950	rs756255559	C	CTGATT	0.5671	-0.0016	0.9984	0.9982
4	4_84370124_TAA_ TA	84370124	83448971	rs774021038	TA	TAA	0.5324	-0.0176	0.9826	0.9815
4	4_84405745_T_C	84405745	83484592	rs6844460	C	T	0.4946	-0.0071	0.9929	0.9930
4	4_84876371_A_C	84876371	83955218	rs57484869	C	A	0.2697	-0.0025	0.9975	0.9987
4	4_86501825_A_T	86501825	85580672	rs1161259	T	A	0.2594	0.0011	1.0011	1.0006
4	4_86577565_T_C	86577565	85656412	rs2869360	C	T	0.2907	0.0103	1.0104	1.0060
4	4_86616140_C_T	86616140	85694987	rs71599422	T	C	0.0462	-0.0112	0.9889	0.9990
4	4_87225701_G_A	87225701	86304548	rs13132706	A	G	0.2868	-0.0076	0.9924	0.9957
4	4_87272549_AACA C_A	87272549	86351396	rs201445110	A	AACAC	0.5038	0.0015	1.0015	1.0015
4	4_88799710_T_C	88799710	87878558	rs1463104	C	T	0.3454	0.0039	1.0039	1.0027
4	4_88809797_A_G	88809797	87888645		G	A	0.7973	-0.0027	0.9973	0.9957
4	4_88979529_C_A	88979529	88058377	rs2725207	A	C	0.1412	0.0000	1.0000	1.0000
4	4_89023224_G_A	89023224	88102072	rs4693924	A	G	0.0932	-0.0054	0.9946	0.9990
4	4_89240476_G_A	89240476	88319324	rs17014016	A	G	0.4395	0.0145	1.0146	1.0129
4	4_89246214_G_T	89246214	88325062	rs10516806	T	G	0.5286	-0.0005	0.9995	0.9995
4	4_89831258_A_G	89831258	88910107	rs76243762	G	A	0.0703	0.0125	1.0126	1.0018
4	4_89931611_A_G	89931611	89010460	rs72665870	G	A	0.0278	-0.0214	0.9788	0.9988
4	4_90012134_C_T	90012134	89090983	rs13140834	T	C	0.1861	0.0006	1.0006	1.0002
4	4_91026587_A_G	91026587	90105436	rs114957953	G	A	0.0363	0.0104	1.0105	1.0008
4	4_91237099_G_C	91237099	90315948	rs57992896	C	G	0.3138	0.0014	1.0014	1.0009
4	4_91611823_A_G	91611823	90690672	rs17017396	G	A	0.1908	0.0161	1.0162	1.0062

4	4_91836876_G_GT	91836876	90915725		GT	G	0.4405	-0.0017	0.9983	0.9985
4	4_92403085_AAC_A	92403085	91481934	4:92403085_A AC_A	A	AAC	0.0151	0.0178	1.0180	1.0005
4	4_92546996_A_C	92546996	91625845	rs145893239	C	A	0.4554	-0.0068	0.9932	0.9938
4	4_92595386_C_T	92595386	91674235	rs7664260	T	C	0.4696	-0.0061	0.9939	0.9943
4	4_92638157_C_T	92638157	91717006	rs9307101	T	C	0.3757	0.0016	1.0016	1.0012
4	4_95147658_ATT_A	95147658	94226507	4:95147658_A TT_A	A	ATT	0.5661	-0.0031	0.9969	0.9965
4	4_95877957_A_AT	95877957	94956806	rs3839108	AT	A	0.4614	0.0050	1.0050	1.0046
4	4_98651479_A_C	98651479	97730328	rs9991112	C	A	0.4565	0.0020	1.0020	1.0018
4	4_99077721_A_G	99077721	98156570	rs12508039	G	A	0.0352	0.0061	1.0061	1.0004
4	4_99103707_GA_G	99103707	98182556	rs773219786	G	GA	0.3080	-0.0079	0.9921	0.9952
4	4_99428163_C_T	99428163	98507012	rs955931	T	C	0.1535	-0.0045	0.9955	0.9986
4	4_99922538_G_A	99922538	99001387	rs111953321	A	G	0.0369	0.0079	1.0079	1.0006
4	4_100017829_C_T	100017829	99096678	rs113772463	T	C	0.0422	-0.0063	0.9937	0.9995
4	4_100071687_T_C	100071687	99150530	rs6850191	C	T	0.8141	0.0016	1.0016	1.0026
4	4_100293109_C_T	100293109	99371952	rs62305782	T	C	0.1138	0.0100	1.0101	1.0023
4	4_100324473_A_T	100324473	99403316	rs34096752	T	A	0.0614	0.0172	1.0173	1.0021
4	4_101448359_A_G	101448359	100527202	rs72692173	G	A	0.0574	-0.0101	0.9900	0.9988
4	4_101542512_T_G	101542512	100621355	rs72694380	G	T	0.0447	-0.0285	0.9719	0.9975
4	4_104371655_T_C	104371655	103450498	rs10016947	C	T	0.0571	-0.0209	0.9793	0.9976
4	4_106024327_CT_C	106024327	105103170	4:106024327_ CT_C	C	CT	0.0690	0.0000	1.0000	1.0000
4	4_106042993_T_TA	106042993	105121836	rs35457521	TA	T	0.4296	0.0002	1.0002	1.0002
4	4_106044481_C_T	106044481	105123324	rs62331127	T	C	0.2972	0.0002	1.0002	1.0001
4	4_106069013_G_T	106069013	105147856	rs62331150	T	G	0.2289	0.0227	1.0230	1.0105
4	4_106094427_G_A	106094427	105173270	rs2903385	A	G	0.4950	0.0000	1.0000	1.0000

4	4_106356761_C_A	106356761	105435604	rs77928427	A	C	0.2394	0.0174	1.0176	1.0084
4	4_111105528_T_G	111105528	110184372	rs79136024	G	T	0.0506	0.0129	1.0130	1.0013
4	4_113081560_C_C A	113081560	112160404	rs34894300	CA	C	0.3420	-0.0095	0.9905	0.9935
4	4_113109702_T_G	113109702	112188546	rs1045940	G	T	0.4511	-0.0033	0.9967	0.9970
4	4_114703466_T_TA	114703466	113782310	rs112709257	TA	T	0.1913	-0.0029	0.9971	0.9989
4	4_118605518_A_T	118605518	117684363	rs2389389	T	A	0.0722	0.0000	1.0000	1.0000
4	4_118701529_G_A	118701529	117780374	rs28945124	A	G	0.0343	-0.0288	0.9716	0.9981
4	4_121422421_A_G	121422421	120501266	rs72672563	G	A	0.0855	-0.0070	0.9930	0.9988
4	4_122232705_A_G	122232705	121311550	rs9992405	G	A	0.0685	-0.0137	0.9864	0.9981
4	4_122725303_G_A	122725303	121804148	rs6830443	A	G	0.3797	0.0066	1.0066	1.0050
4	4_123612272_C_G	123612272	122691117	rs13103403	G	C	0.2376	0.0049	1.0049	1.0023
4	4_125108130_G_T	125108130	124186975	rs10007609	T	G	0.5310	-0.0095	0.9905	0.9900
4	4_125173747_C_T	125173747	124252592	rs7657011	T	C	0.4276	-0.0009	0.9991	0.9992
4	4_126202299_A_G	126202299	125281144	rs57474540	G	A	0.2946	-0.0043	0.9957	0.9975
4	4_126292075_C_T	126292075	125370920	rs62321344	T	C	0.1911	0.0102	1.0103	1.0039
4	4_126654773_G_T	126654773	125733618	rs9307576	T	G	0.4626	0.0046	1.0046	1.0043
4	4_126708773_T_TA	126708773	125787618	rs5861742	TA	T	0.5477	0.0054	1.0054	1.0059
4	4_126752992_A_A AT	126752992	125831837		AAT	A	0.5167	-0.0018	0.9982	0.9981
4	4_126771475_G_A	126771475	125850320	rs1506162	A	G	0.8163	0.0032	1.0032	1.0052
4	4_126835376_G_A	126835376	125914221	rs4525994	A	G	0.5964	-0.0174	0.9828	0.9795
4	4_126843504_G_T	126843504	125922349	rs77528541	T	G	0.1348	-0.0131	0.9870	0.9965
4	4_126934050_A_G	126934050	126012895	rs62314116	G	A	0.3328	0.0000	1.0000	1.0000
4	4_127515501_A_T	127515501	126594346	rs313107	T	A	0.0939	0.0097	1.0097	1.0018
4	4_127537947_C_A	127537947	126616792	rs1994679	A	C	0.6093	-0.0003	0.9997	0.9996
4	4_130558257_G_T	130558257	129637102	rs6852416	T	G	0.0851	0.0102	1.0103	1.0017

4	4_132497181_GAG A_G	132497181	131576026	rs745490368	G	GAGA	0.0781	0.0148	1.0149	1.0023
4	4_137743220_C_A	137743220	136822066	rs4455476	A	C	0.1742	0.0021	1.0021	1.0007
4	4_143343605_C_T	143343605	142422452	rs6820463	T	C	0.3058	0.0060	1.0060	1.0037
4	4_143467195_C_T	143467195	142546042	rs56039025	T	C	0.1115	-0.0311	0.9694	0.9932
4	4_144406937_A_G	144406937	143485784	rs17017812	G	A	0.2279	0.0057	1.0057	1.0026
4	4_146731529_T_C	146731529	145810377	rs59831926	C	T	0.0985	-0.0209	0.9793	0.9959
4	4_147079249_T_C	147079249	146158097	rs72727929	C	T	0.0578	0.0173	1.0175	1.0020
4	4_149121794_T_C	149121794	148200643	rs6854045	C	T	0.2632	0.0021	1.0021	1.0011
4	4_149134380_T_A	149134380	148213229	rs6857487	A	T	0.4317	0.0038	1.0038	1.0033
4	4_151144895_C_C AATA	151144895	150223743	rs140778874	CAATA	C	0.6647	0.0000	1.0000	1.0000
4	4_151218296_CAT ATT_C	151218296	150297144	rs745707748	C	CATATT T	0.6533	0.0027	1.0027	1.0035
4	4_151268153_G_G TA	151268153	150347001	rs59975091	GTA	G	0.2841	-0.0042	0.9958	0.9976
4	4_151271452_A_G	151271452	150350300	rs13145548	G	A	0.6396	0.0019	1.0019	1.0024
4	4_151281390_C_T	151281390	150360238	rs13128588	T	C	0.3713	0.0055	1.0055	1.0041
4	4_151296384_G_T	151296384	150375232	rs17504352	T	G	0.2950	-0.0017	0.9983	0.9990
4	4_161993005_C_T	161993005	161071853	rs930402	T	C	0.3112	0.0038	1.0038	1.0024
4	4_163461356_A_G	163461356	162540204	rs1131196123	G	A	0.0544	0.0130	1.0131	1.0014
4	4_166052580_C_T	166052580	165131428	rs17585041	T	C	0.0679	0.0202	1.0204	1.0028
4	4_166313062_A_G	166313062	165391910	rs17046389	G	A	0.1487	-0.0133	0.9868	0.9961
4	4_166346355_G_C	166346355	165425203	rs28846814	C	G	0.1476	-0.0007	0.9993	0.9998
4	4_166588797_T_TA	166588797	165667645	rs5863769	TA	T	0.2715	-0.0017	0.9983	0.9991
4	4_166591321_T_C	166591321	165670169	rs2714807	C	T	0.4401	-0.0046	0.9954	0.9960
4	4_169004537_CAA _C	169004537	168083386	4:169004537_ _ CAA_C	C	CAA	0.5367	0.0039	1.0039	1.0042

4	4_171493439_C_T	171493439	170572288	rs415366	T	C	0.6642	-0.0010	0.9990	0.9987
4	4_171536786_C_T	171536786	170615635	rs1596251	T	C	0.4213	0.0006	1.0006	1.0005
4	4_171943596_G_C	171943596	171022445	rs139966312	C	G	0.0315	0.0054	1.0054	1.0003
4	4_172626489_C_T	172626489	171705338	rs1565468	T	C	0.1069	-0.0008	0.9992	0.9998
4	4_174741894_T_C	174741894	173820743	rs4469049	C	T	0.1972	0.0070	1.0070	1.0028
4	4_175716260_C_T	175716260	174795109	rs6830584	T	C	0.9267	0.0070	1.0070	1.0131
4	4_175836048_G_A	175836048	174914897	rs6553847	A	G	0.5730	-0.0115	0.9886	0.9869
4	4_175842495_G_A	175842495	174921344	rs28436676	A	G	0.1161	-0.0281	0.9723	0.9936
4	4_175844668_CATT AT_C	175844668	174923517	4:175844668_ CATTAT_C	C	CATTAT	0.0919	-0.0383	0.9624	0.9931
4	4_175847436_C_A	175847436	174926285	rs62334414	A	C	0.3433	0.0129	1.0130	1.0089
4	4_175857997_A_T	175857997	174936846	rs62334421	T	A	0.3490	0.0000	1.0000	1.0000
4	4_176820922_C_C A	176820922	175899771	rs34037910	CA	C	0.2762	-0.0050	0.9950	0.9972
4	4_180659077_A_G	180659077	179737924	rs112038385	G	A	0.0291	-0.0134	0.9867	0.9992
4	4_182435039_G_A	182435039	181513886	rs6816262	A	G	0.0322	0.0000	1.0000	1.0000
4	4_182543945_T_C	182543945	181622792	rs10002408	C	T	0.9179	-0.0109	0.9892	0.9802
4	4_182602168_A_C	182602168	181681015	rs75399632	C	A	0.0765	-0.0107	0.9894	0.9984
4	4_184355335_G_C	184355335	183434182	rs181139981	C	G	0.0310	-0.0300	0.9704	0.9982
4	4_184357607_G_A	184357607	183436454	rs78515438	A	G	0.0837	0.0038	1.0038	1.0006
4	4_185259670_T_G	185259670	184338517	rs4269220	G	T	0.4643	0.0043	1.0043	1.0040
4	4_185260558_C_C A	185260558	1843339405	rs34156200	CA	C	0.6514	0.0029	1.0029	1.0038
4	4_186838211_A_C	186838211	185917057	rs7671869	C	A	0.4070	-0.0030	0.9970	0.9976
4	4_186847709_G_T	186847709	185926555	rs11733388	T	G	0.3179	-0.0033	0.9967	0.9979
4	4_187503758_A_T	187503758	186582604		T	A	0.4471	0.0094	1.0094	1.0085
4	4_187511304_G_G	187511304	186590150	rs11410853	GT	G	0.4433	0.0032	1.0032	1.0028

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5	5_1297918_T_C	1297918	1297803	rs7449190	C	T	0.8489	-0.0022	0.9978	0.9963
5	5_1299379_C_G	1299379	1299264	rs2735846	G	C	0.5049	-0.0160	0.9841	0.9840
5	5_1318797_T_C	1318797	1318682	rs148487301	C	T	0.0236	0.0000	1.0000	1.0000
5	5_1353077_T_C	1353077	1352962	rs62329727	C	T	0.0121	0.0393	1.0401	1.0010
5	5_1442521_T_C	1442521	1442406	rs2617605	C	T	0.3602	-0.0004	0.9996	0.9997
5	5_1453344_C_A	1453344	1453229	rs2617583	A	C	0.5534	-0.0097	0.9903	0.9893
5	5_2755932_C_T	2755932	2755818	rs4866667	T	C	0.6730	-0.0077	0.9923	0.9897
5	5_2769043_T_G	2769043	2768929	rs6875050	G	T	0.3626	-0.0039	0.9961	0.9972
5	5_2777029_G_A	2777029	2776915	rs4866496	A	G	0.4139	0.0020	1.0020	1.0017
5	5_2777869_T_C	2777869	2777755	rs11960374	C	T	0.3775	0.0062	1.0062	1.0047
5	5_3892571_T_TG	3892571	3892457	rs534632286	TG	T	0.5948	0.0090	1.0090	1.0108
5	5_4106597_C_T	4106597	4106484	rs115682874	T	C	0.0317	-0.0058	0.9942	0.9996
5	5_5308256_C_T	5308256	5308143	rs35614306	T	C	0.0827	0.0158	1.0159	1.0026
5	5_5311838_G_GT	5311838	5311725	rs70965937	GT	G	0.0837	0.0000	1.0000	1.0000
5	5_6574023_C_CA	6574023	6573910	rs35589606	CA	C	0.1240	0.0082	1.0082	1.0020
5	5_6613517_C_T	6613517	6613404	rs3756426	T	C	0.1968	0.0083	1.0083	1.0033
5	5_6677699_G_A	6677699	6677586	rs13166363	A	G	0.2734	-0.0044	0.9956	0.9976
5	5_7225615_A_G	7225615	7225502	rs116151459	G	A	0.0336	0.0104	1.0105	1.0007
5	5_14320462_G_C	14320462	14320353	rs73059540	C	G	0.0731	0.0065	1.0065	1.0010
5	5_14365895_A_G	14365895	14365786	rs43171	G	A	0.5129	-0.0043	0.9957	0.9956
5	5_14380773_T_C	14380773	14380664	rs247136	C	T	0.1727	0.0039	1.0039	1.0014
5	5_14403252_TGTG_T	14403252	14403143	5:14403252_T GTG_T	T	TGTG	0.2617	0.0046	1.0046	1.0024
5	5_15113644_C_CT G	15113644	15113535		CTG	C	0.1534	-0.0121	0.9880	0.9963
5	5_16231194_G_C	16231194	16231085	rs17611291	C	G	0.5594	-0.0088	0.9912	0.9902
5	5_16254310_A_G	16254310	16254201	rs11133838	G	A	0.5814	-0.0130	0.9871	0.9850

5	5_21605146_G_A	21605146	21605037	rs12520587	A	G	0.6025	0.0062	1.0062	1.0075
5	5_22123627_G_C	22123627	22123518	rs62349111	C	G	0.0524	0.0065	1.0065	1.0007
5	5_25664626_G_GA	25664626	25664517	rs35786359	GA	G	0.5266	-0.0046	0.9954	0.9952
5	5_25879426_A_G	25879426	25879317	rs10942144	G	A	0.1715	-0.0139	0.9862	0.9953
5	5_25889346_T_C	25889346	25889237	rs1366468	C	T	0.3980	0.0004	1.0004	1.0003
5	5_27043424_C_T	27043424	27043317	rs77344846	T	C	0.0220	-0.0089	0.9911	0.9996
5	5_27479118_A_G	27479118	27479011	rs193173568	G	A	0.1340	-0.0163	0.9838	0.9957
5	5_27575812_TA_T AA	27575812	27575705		TAA	TA	0.1006	0.0073	1.0073	1.0015
5	5_28288287_G_A	28288287	28288180	rs2468479	A	G	0.1037	0.0066	1.0066	1.0014
5	5_31271073_G_A	31271073	31270966	rs11955971	A	G	0.3547	-0.0103	0.9898	0.9927
5	5_31360086_C_T	31360086	31359979	rs334589	T	C	0.9022	-0.0134	0.9867	0.9761
5	5_32579616_TCA_T	32579616	32579510	rs770436441	T	TCA	0.4844	0.0106	1.0107	1.0104
5	5_32641237_C_T	32641237	32641131	rs818132	T	C	0.4891	0.0050	1.0050	1.0049
5	5_35652823_G_A	35652823	35652721	rs16902377	A	G	0.4071	-0.0068	0.9932	0.9945
5	5_35733285_T_C	35733285	35733183	rs4524534	C	T	0.6405	0.0125	1.0126	1.0162
5	5_36391846_ATTCT _A	36391846	36391744	5:36391846_A TTCT_A	A	ATTCT	0.1480	0.0000	1.0000	1.0000
5	5_38656341_T_A	38656341	38656239	rs10512690	A	T	0.4490	0.0120	1.0121	1.0109
5	5_38789263_A_G	38789263	38789161	rs34836414	G	A	0.2944	-0.0068	0.9932	0.9960
5	5_38820823_C_CA T	38820823	38820721	rs774802178	CAT	C	0.2979	-0.0059	0.9941	0.9965
5	5_39582018_A_C	39582018	39581916	rs114212093	C	A	0.0127	0.0130	1.0131	1.0003
5	5_41638740_G_C	41638740	41638638	rs62360524	C	G	0.0413	-0.0083	0.9917	0.9993
5	5_42529115_CT_C	42529115	42529013	5:42529115_C T_C	C	CT	0.3780	-0.0014	0.9986	0.9989
5	5_43112570_A_T	43112570	43112468	rs13158202	T	A	0.1901	-0.0007	0.9993	0.9997

5	5_43173849_T_TC	43173849	43173747		TC	T		0.2318	0.0091	1.0091	1.0042
5	5_43692598_G_C	43692598	43692496	rs71629192	C	G		0.0492	0.0000	1.0000	1.0000
5	5_44115401_T_G	44115401	44115299	rs36058457	G	T		0.1273	-0.0116	0.9885	0.9971
5	5_44119344_G_A	44119344	44119242	rs62368138	A	G		0.0399	0.0248	1.0251	1.0020
5	5_44302177_A_T	44302177	44302075	rs13186320	T	A		0.5153	0.0064	1.0064	1.0066
5	5_44393569_C_T	44393569	44393467	rs10512852	T	C		0.0975	0.0000	1.0000	1.0000
5	5_44482570_A_AT	44482570	44482468	rs35085334	AT	A		0.7325	-0.0015	0.9985	0.9978
5	5_44486733_T_C	44486733	44486631	rs72748067	C	T		0.0388	-0.0013	0.9987	0.9999
5	5_44499367_TA_T	44499367	44499265	5:44499367_T A_T	T	TA		0.7735	-0.0044	0.9956	0.9932
5	5_44508264_G_GT	44508264	44508162	rs138335056	GT	G		0.1265	-0.0743	0.9284	0.9820
5	5_44609392_C_T	44609392	44609290	rs73093976	T	C		0.1692	0.0000	1.0000	1.0000
5	5_44619502_A_G	44619502	44619400	rs187108781	G	A		0.1549	-0.0154	0.9847	0.9953
5	5_44621050_T_C	44621050	44620948	rs4866915	C	T		0.3804	0.0000	1.0000	1.0000
5	5_44645998_T_C	44645998	44645896	rs36068815	C	T		0.3997	0.0133	1.0134	1.0107
5	5_44649944_C_T	44649944	44649842	rs4613718	T	C		0.6010	0.0000	1.0000	1.0000
5	5_44691395_T_G	44691395	44691293	rs6451770	G	T		0.3837	0.0391	1.0399	1.0308
5	5_44706498_A_G	44706498	44706396	rs10941679	G	A		0.2481	0.0282	1.0286	1.0142
5	5_44800917_A_C	44800917	44800815	rs10462082	C	A		0.5032	0.0091	1.0091	1.0092
5	5_44875005_A_C	44875005	44874903	rs7716600	C	A		0.7825	0.0000	1.0000	1.0000
5	5_44875449_A_G	44875449	44875347	rs62366821	G	A		0.4846	-0.0078	0.9922	0.9925
5	5_44922557_C_T	44922557	44922455	rs112234443	T	C		0.0490	0.0000	1.0000	1.0000
5	5_44929272_A_T	44929272	44929170	rs73963007	T	A		0.0254	0.0000	1.0000	1.0000
5	5_44947702_T_C	44947702	44947600	rs7701656	C	T		0.1262	0.0024	1.0024	1.0006
5	5_44977315_ATAG T_A	44977315	44977213	5:44977315_A TAGT_A	A	ATAGT		0.0722	0.0227	1.0230	1.0033
5	5_44981122_G_A	44981122	44981020	rs144854948	A	G		0.0149	0.0032	1.0032	1.0001

5	5_45018723_G_A	45018723	45018621	rs57909303	A	G	0.1202	0.0030	1.0030	1.0007
5	5_50162499_A_C	50162499	50866665	rs27267	C	A	0.4958	-0.0002	0.9998	0.9998
5	5_50162788_G_A	50162788	50866954	rs27905	A	G	0.7477	-0.0040	0.9960	0.9940
5	5_50172251_C_T	50172251	50876417	rs26089	T	C	0.3643	-0.0003	0.9997	0.9998
5	5_50207118_T_C	50207118	50911284	rs32482	C	T	0.3864	-0.0011	0.9989	0.9992
5	5_50635268_G_A	50635268	51339434	rs78812881	A	G	0.0310	-0.0085	0.9915	0.9995
5	5_51204139_C_CA	51204139	51908305	rs10652826	CAA	C	0.8702	-0.0054	0.9946	0.9906
5	5_52377181_T_A	52377181	53081351	rs3212617	A	T	0.0557	0.0079	1.0079	1.0009
5	5_52499308_G_A	52499308	53203478	rs116520517	A	G	0.0187	0.0237	1.0240	1.0009
5	5_52585565_T_A	52585565	53289735	rs2591892	A	T	0.0295	0.0062	1.0062	1.0004
5	5_52679539_C_CA	52679539	53383709		CA	C	0.0998	0.0231	1.0234	1.0047
5	5_52768800_CAT_C	52768800	53472970	rs756147761	C	CAT	0.2389	-0.0091	0.9909	0.9957
5	5_53222781_A_T	53222781	53926951	rs2253601	T	A	0.8456	-0.0133	0.9868	0.9778
5	5_55621515_G_A	55621515	56325688	rs158489	A	G	0.0979	0.0002	1.0002	1.0000
5	5_55638158_T_C	55638158	56342331	rs56379516	C	T	0.2490	0.0000	1.0000	1.0000
5	5_55662540_C_CT	55662540	56366713	rs553874618	CT	C	0.3631	-0.0141	0.9860	0.9899
5	5_55669065_A_G	55669065	56373238	rs7717167	G	A	0.3041	-0.0052	0.9948	0.9968
5	5_55818087_C_T	55818087	56522260	rs166280	T	C	0.7602	0.0117	1.0118	1.0180
5	5_55883187_C_T	55883187	56587360	rs13155854	T	C	0.5262	-0.0089	0.9911	0.9907
5	5_55912533_G_C	55912533	56616706	rs984113	C	G	0.6186	-0.0231	0.9772	0.9719
5	5_55930546_G_T	55930546	56634719	rs1279628	T	G	0.4470	-0.0004	0.9996	0.9996
5	5_55965167_C_T	55965167	56669340	rs889310	T	C	0.5576	0.0068	1.0068	1.0076
5	5_55965608_G_A	55965608	56669781	rs16885969	A	G	0.2421	-0.0014	0.9986	0.9993
5	5_55989045_G_T	55989045	56693218	rs61657998	T	G	0.1218	0.0000	1.0000	1.0000
5	5_55989304_G_A	55989304	56693477	rs1862624	A	G	0.5749	-0.0055	0.9945	0.9937

5	5_56012629_T_TA	56012629	56716802	rs548650585	TA	T	0.0580	0.0000	1.0000	1.0000
5	5_56023083_T_G	56023083	56727256	rs16886165	G	T	0.1583	0.0909	1.0952	1.0304
5	5_56026500_T_C	56026500	56730673	rs1910020	C	T	0.7238	-0.0055	0.9945	0.9921
5	5_56042972_C_T	56042972	56747145	rs76250845	T	C	0.0521	0.0190	1.0192	1.0020
5	5_56045081_T_C	56045081	56749254	rs11949391	C	T	0.1655	-0.0186	0.9816	0.9939
5	5_56060954_G_A	56060954	56765127	rs112497245	A	G	0.0621	0.0000	1.0000	1.0000
5	5_56068859_AC_A	56068859	56773032	5:56068859_A_C_A	A	AC	0.1679	0.0322	1.0327	1.0110
5	5_56110374_GGACCTGGCCGA_G	56110374	56814547	rs760596453	G	GGACCTGGCCGA A	0.6510	-0.0042	0.9958	0.9946
5	5_56110937_G_C	56110937	56815110	rs72758040	C	G	0.2508	-0.0014	0.9986	0.9993
5	5_56133039_A_G	56133039	56837212	rs72758067	G	A	0.0204	0.0000	1.0000	1.0000
5	5_56153470_T_C	56153470	56857643	rs183088996	C	T	0.0157	0.0002	1.0002	1.0000
5	5_56254772_A_G	56254772	56958945	rs74571895	G	A	0.0540	0.0414	1.0423	1.0046
5	5_56260606_A_G	56260606	56964779	rs6890270	G	A	0.1864	0.0020	1.0020	1.0007
5	5_57186663_G_A	57186663	57890836	rs35100619	A	G	0.0899	0.0074	1.0074	1.0013
5	5_57595040_CTTT_C	57595040	58299213	5:57595040_C_TTT_C	C	CTTT	0.0705	0.0171	1.0172	1.0024
5	5_57600833_G_A	57600833	58305006	rs1202501	A	G	0.2162	0.0014	1.0014	1.0006
5	5_57633272_T_C	57633272	58337445	rs245284	C	T	0.0665	0.0039	1.0039	1.0005
5	5_58177785_G_C	58177785	58881958	rs79517802	C	G	0.0436	-0.0070	0.9930	0.9994
5	5_58184061_T_C	58184061	58888234	rs10472076	C	T	0.3776	0.0070	1.0070	1.0053
5	5_58229580_C_G	58229580	58933753	rs2944383	G	C	0.6057	-0.0012	0.9988	0.9985
5	5_58241712_C_T	58241712	58945885	rs113778879	T	C	0.5750	-0.0029	0.9971	0.9967
5	5_58282789_G_GA_TAT	58282789	58986962		GATAT	G	0.6482	0.0000	1.0000	1.0000
5	5_58306572_A_C	58306572	59010745	rs111567606	C	A	0.0927	-0.0091	0.9909	0.9983

5	5_58365353_T_C	58365353	59069526	rs537267133	C	T	0.0917	-0.0138	0.9863	0.9975
5	5_58427472_C_T	58427472	59131645	rs28373501	T	C	0.7101	0.0022	1.0022	1.0031
5	5_58442025_A_T	58442025	59146198	rs12658004	T	A	0.5177	-0.0026	0.9974	0.9973
5	5_58476117_T_C	58476117	59180291	rs9292195	C	T	0.8508	-0.0064	0.9936	0.9892
5	5_58498540_G_A	58498540	59202714	rs1439	A	G	0.1701	-0.0002	0.9998	0.9999
5	5_58720965_T_C	58720965	59425139	rs2702371	C	T	0.4967	-0.0037	0.9963	0.9963
5	5_58826435_TA_T	58826435	59530609	5:58826435_T A_T	T	TA	0.4063	-0.0003	0.9997	0.9998
5	5_59717871_T_C	59717871	60422044	rs186842595	C	T	0.0165	0.0056	1.0056	1.0002
5	5_60956369_G_C	60956369	61660542	rs79488625	C	G	0.1830	0.0095	1.0095	1.0035
5	5_60971732_G_A	60971732	61675905	rs432733	A	G	0.1555	0.0005	1.0005	1.0002
5	5_63913119_C_T	63913119	64617292	rs2216706	T	C	0.8624	-0.0083	0.9917	0.9858
5	5_64319641_A_AA G	64319641	65023814	rs150001891	AAG	A	0.4476	-0.0012	0.9988	0.9989
5	5_64373628_C_A	64373628	65077801	rs61482254	A	C	0.3235	-0.0056	0.9944	0.9964
5	5_64526683_A_AA TATATAT	64526683	65230856	rs754861492	AATATAT ATAT	A	0.3598	-0.0049	0.9951	0.9965
5	5_64624361_TA_T	64624361	65328534	5:64624361_T A_T	T	TA	0.5104	-0.0037	0.9963	0.9962
5	5_64640912_G_A	64640912	65345085	rs2640717	A	G	0.3778	0.0038	1.0038	1.0029
5	5_64705169_C_CA A	64705169	65409342	rs534131894	CAA	C	0.3855	0.0000	1.0000	1.0000
5	5_66979250_G_T	66979250	67683422	rs6449898	T	G	0.2984	0.0002	1.0002	1.0001
5	5_66983803_C_T	66983803	67687975	rs60493723	T	C	0.2120	0.0048	1.0048	1.0020
5	5_67539174_T_G	67539174	68243346	rs56351136	G	T	0.1307	-0.0110	0.9891	0.9971
5	5_67597321_T_C	67597321	68301493	rs9623	C	T	0.4440	-0.0008	0.9992	0.9993
5	5_67611486_T_C	67611486	68315658	rs184886	C	T	0.7259	0.0024	1.0024	1.0035
5	5_67774099_C_G	67774099	68478272	rs78909682	G	C	0.1032	0.0009	1.0009	1.0002

5	5_68537510_T_G	68537510	69241683	rs114456509	G	T	0.0145	-0.0622	0.9397	0.9982
5	5_71509063_A_G	71509063	72213236	rs62363244	G	A	0.3362	-0.0118	0.9883	0.9921
5	5_71664031_G_A	71664031	72368204	rs17377355	A	G	0.3391	-0.0010	0.9990	0.9993
5	5_71732116_TTA_T	71732116	72436289	5:71732116_T TA_T	T	TTA	0.7400	-0.0011	0.9989	0.9984
5	5_71965007_G_A	71965007	72669180	rs3010266	A	G	0.2572	-0.0133	0.9868	0.9932
5	5_72176643_C_CA A	72176643	72880816	rs35726893	CAA	C	0.4488	0.0008	1.0008	1.0007
5	5_72412780_T_A	72412780	73116953	rs602307	A	T	0.4111	0.0024	1.0024	1.0020
5	5_73226271_T_C	73226271	73930446	rs283629	C	T	0.3545	-0.0124	0.9877	0.9913
5	5_73234583_T_C	73234583	73938758	rs157557	C	T	0.3213	-0.0102	0.9899	0.9935
5	5_73274360_G_C	73274360	73978535	rs425101	C	G	0.3265	0.0000	1.0000	1.0000
5	5_73397165_AATT G_A	73397165	74101340	5:73397165_A ATTG_A	A	AATTG	0.0803	-0.0103	0.9898	0.9984
5	5_77154447_G_C	77154447	77858623	rs6887123	C	G	0.5006	-0.0081	0.9919	0.9919
5	5_77155397_GT_G	77155397	77859573	rs767431357	G	GT	0.3466	-0.0145	0.9856	0.9900
5	5_79180995_G_GA	79180995	79885172	rs34525310	GA	G	0.1755	0.0065	1.0065	1.0023
5	5_79228649_A_G	79228649	79932826	rs6453492	G	A	0.6101	0.0000	1.0000	1.0000
5	5_81091203_A_C	81091203	81795384	rs6885263	C	A	0.1419	-0.0101	0.9900	0.9972
5	5_81146156_T_C	81146156	81850337	rs17241969	C	T	0.0966	0.0000	1.0000	1.0000
5	5_81214843_T_A	81214843	81919024	rs17302470	A	T	0.1449	0.0000	1.0000	1.0000
5	5_81512947_TA_T	81512947	82217128	5:81512947_T A_T	T	TA	0.2503	-0.0379	0.9628	0.9815
5	5_83156500_C_T	83156500	83860681	rs10044480	T	C	0.2915	0.0099	1.0099	1.0058
5	5_83159933_A_G	83159933	83864114	rs56000039	G	A	0.3099	0.0055	1.0055	1.0034
5	5_83165631_C_A	83165631	83869812	rs6452552	A	C	0.7437	0.0106	1.0107	1.0159
5	5_83315048_A_G	83315048	84019229	rs253158	G	A	0.9171	-0.0016	0.9984	0.9971

5	5_83321882_C_T	83321882	84026063	rs442848	T	C	0.9266	-0.0028	0.9972	0.9948
5	5_87544144_C_T	87544144	88248327	rs59198891	T	C	0.0119	0.0294	1.0298	1.0007
5	5_90647770_T_C	90647770	91351953	rs4916712	C	T	0.4600	-0.0003	0.9997	0.9997
5	5_90747018_GA_G	90747018	91451201	5:90747018_G_A_G	G	GA	0.1770	-0.0213	0.9789	0.9926
5	5_90788643_ATATT TC_A	90788643	91492826	5:90788643_A TATTC_A	A	ATATTT C	0.0946	0.0000	1.0000	1.0000
5	5_90789470_G_A	90789470	91493653	rs332529	A	G	0.1580	-0.0086	0.9914	0.9973
5	5_90926353_T_G	90926353	91630536	rs4492142	G	T	0.5074	-0.0058	0.9942	0.9941
5	5_91050109_T_G	91050109	91754292	rs13166131	G	T	0.5488	0.0043	1.0043	1.0047
5	5_92743235_C_T	92743235	93407529	rs73133209	T	C	0.0232	-0.0138	0.9863	0.9994
5	5_94268466_T_C	94268466	94932761	rs32909	C	T	0.3196	-0.0041	0.9959	0.9974
5	5_95147211_C_T	95147211	95811507	rs11953221	T	C	0.0288	0.0241	1.0244	1.0014
5	5_96169897_T_C	96169897	96834194	rs10476692	C	T	0.0659	-0.0066	0.9934	0.9991
5	5_97823498_T_C	97823498	98487794	rs10463479	C	T	0.2807	0.0040	1.0040	1.0023
5	5_103478992_G_T	103478992	104143291	rs140135691	T	G	0.0146	-0.0100	0.9900	0.9997
5	5_104223498_A_T	104223498	104887797	rs1217465	T	A	0.5291	0.0023	1.0023	1.0024
5	5_104300273_G_T	104300273	104964572	rs17157372	T	G	0.1810	-0.0098	0.9902	0.9965
5	5_104302751_A_T	104302751	104967050	rs6596590	T	A	0.1605	-0.0078	0.9922	0.9975
5	5_104331054_T_G	104331054	104995353	rs7445672	G	T	0.8310	0.0004	1.0004	1.0007
5	5_108542241_C_C A	108542241	109206540	rs200459449	CA	C	0.1377	0.0000	1.0000	1.0000
5	5_108572649_A_G	108572649	109236948	rs75073283	G	A	0.0827	0.0000	1.0000	1.0000
5	5_110657114_A_G	110657114	111321416	rs1660930	G	A	0.5854	-0.0046	0.9954	0.9946
5	5_111103258_C_T	111103258	111767561	rs255888	T	C	0.5586	0.0063	1.0063	1.0071
5	5_111217786_G_T	111217786	111882089	rs6882649	T	G	0.6646	0.0059	1.0059	1.0079

5	5_111368597_TAA ATA_T	111368597	112032900	5:111368597_ TAAATA_T	T	TAAATA	0.0499	-0.0110	0.9891	0.9989
5	5_114066225_T_G	114066225	114730528	rs66616485	G	T	0.0688	0.0196	1.0198	1.0027
5	5_114525350_G_T	114525350	115189653	rs17381680	T	G	0.1199	0.0182	1.0184	1.0044
5	5_116745252_TGT G_T	116745252	117409556	5:116745252_ TGTG_T	T	TGTG	0.6591	-0.0013	0.9987	0.9983
5	5_118704975_A_T	118704975	119369280	rs148486181	T	A	0.0436	0.0220	1.0222	1.0019
5	5_120888598_T_A	120888598	121552903	rs9327200	A	T	0.8574	0.0000	1.0000	1.0000
5	5_121789141_G_A	121789141	122453446	rs2737093	A	G	0.1364	0.0068	1.0068	1.0019
5	5_122436528_C_G	122436528	123100833	rs163188	G	C	0.0902	0.0031	1.0031	1.0006
5	5_122442322_A_C	122442322	123106627	rs335143	C	A	0.1824	0.0041	1.0041	1.0015
5	5_122478676_C_A	122478676	123142982	rs335160	A	C	0.7448	-0.0066	0.9934	0.9902
5	5_122705244_C_T	122705244	123369550	rs1428387	T	C	0.0306	0.0286	1.0290	1.0018
5	5_122734724_T_TA	122734724	123399030	rs547152106	TA	T	0.3982	-0.0020	0.9980	0.9984
5	5_124012247_G_A	124012247	124676554	rs114652469	A	G	0.0207	-0.0076	0.9924	0.9997
5	5_124110347_AAC AT_A	124110347	124774654	rs780903759	A	AACAT	0.3674	0.0005	1.0005	1.0004
5	5_125327257_T_C	125327257	125991564	rs78389812	C	T	0.0235	-0.0182	0.9820	0.9992
5	5_125431223_TA_T	125431223	126095530		T	TA	0.9322	-0.0128	0.9873	0.9764
5	5_127418850_C_G	127418850	128083158	rs3812049	G	C	0.7598	-0.0032	0.9968	0.9952
5	5_127596305_G_A	127596305	128260613	rs144549501	A	G	0.0251	-0.0166	0.9835	0.9992
5	5_128290369_G_G TA	128290369	128954676		GTA	G	0.0763	-0.0094	0.9906	0.9986
5	5_128648201_A_G	128648201	129312508	rs151158087	G	A	0.5281	-0.0076	0.9924	0.9920
5	5_128652984_C_T	128652984	129317291	rs113428195	T	C	0.0380	0.0178	1.0180	1.0014
5	5_128664078_A_A TTGTT	128664078	129328385	rs149224778	ATTGTT	A	0.2706	-0.0044	0.9956	0.9976
5	5_131577849_C_CC	131577849	132242156	rs112951115	CCTGCTT	C	0.5289	0.0015	1.0015	1.0016

	TgCTTCT			TCT					
5	5_131640536_A_G	131640536	132304843	rs6860806	G	A	0.5427	0.0084	1.0084
5	5_131667353_A_G	131667353	1323331660	rs273909	G	A	0.1167	-0.0029	0.9971
5	5_131808869_G_A	131808869	132473177	rs2548993	A	G	0.7345	0.0004	1.0004
5	5_131833599_C_T	131833599	132497907	rs736801	T	C	0.3629	0.0101	1.0102
5	5_132407058_C_T	132407058	133071366	rs6596100	T	C	0.2450	-0.0183	0.9819
5	5_135572910_C_A	135572910	136237222	rs889010	A	C	0.5683	-0.0033	0.9967
5	5_135619617_G_T	135619617	136283929	rs1499769	T	G	0.1233	-0.0026	0.9974
5	5_135686384_C_G	135686384	136350696		G	C	0.5218	0.0095	1.0100
5	5_135882597_C_G	135882597	136546908	rs4340911	G	C	0.7011	0.0002	1.0003
5	5_141462248_TA_T	141462248	142082683	5:141462248_TA_T	T	TA	0.0152	-0.0263	0.9740
5	5_141669839_G_T	141669839	142290274	rs10051199	T	G	0.4822	-0.0096	0.9904
5	5_141760963_A_A	141760963	142381398		ATTTTTT GTTTTGT TTTGTTTT	A	0.5510	-0.0001	0.9999
5	5_141764170_T_A	141764170	142384605	rs254442	A	T	0.5106	-0.0098	0.9902
5	5_142756004_A_G	142756004	143376439	rs2963155	G	A	0.2444	-0.0024	0.9976
5	5_142979991_A_C	142979991	143600426	rs153515	C	A	0.4667	-0.0098	0.9902
5	5_143357278_C_T	143357278	143977713	rs318403	T	C	0.5555	0.0087	1.0097
5	5_143837325_G_A	143837325	144457762	rs9324959	A	G	0.4009	-0.0058	0.9954
5	5_144071035_CT_C	144071035	144691472	5:144071035_CT_C	C	CT	0.3330	-0.0063	0.9958
5	5_144691771_G_C	144691771	145312208	rs1597465	C	G	0.3695	-0.0019	0.9986
5	5_144694693_C_T	144694693	145315130	rs112907216	T	C	0.0491	-0.0071	0.9993
5	5_146084418_T_A	146084418	146704855	rs12659673	A	T	0.0940	-0.0137	0.9864
5	5_146330004_T_A	146330004	146950441	rs1036202	A	T	0.1893	-0.0013	0.9987

5	5_146434047_TA_T	146434047	147054484	5:146434047_TA_T	T	TA	0.7610	0.0151	1.0152	1.0233
5	5_148429004_A_G	148429004	149049441	rs36081	G	A	0.4326	0.0044	1.0044	1.0038
5	5_148510232_C_T	148510232	149130669	rs6889911	T	C	0.9733	-0.0120	0.9881	0.9769
5	5_148520923_A_A CACAAGGCCTCGTC CATCT	148520923	149141360	rs3839235	ACACAAG GCCTCGT CCATCT	A	0.7132	-0.0064	0.9936	0.9909
5	5_148621845_G_A	148621845	149242282	rs41291953	A	G	0.0186	-0.0330	0.9675	0.9988
5	5_154041399_G_A	154041399	154661839	rs13177281	A	G	0.1186	-0.0081	0.9919	0.9981
5	5_154355695_C_T	154355695	154976135	rs6890610	T	C	0.2577	-0.0037	0.9963	0.9981
5	5_155470446_T_C	155470446	156043436	rs4704943	C	T	0.2304	-0.0026	0.9974	0.9988
5	5_155497189_C_T	155497189	156070179	rs139257230	T	C	0.1998	-0.0095	0.9905	0.9962
5	5_156489247_G_A	156489247	157062236	rs11952686	A	G	0.0167	-0.0235	0.9768	0.9992
5	5_157616208_A_G	157616208	158189200	rs17055363	G	A	0.1080	-0.0210	0.9792	0.9955
5	5_157641763_C_A	157641763	158214755	rs11741271	A	C	0.1521	0.0019	1.0019	1.0006
5	5_158036093_G_A	158036093	158609085	rs10462916	A	G	0.3136	0.0075	1.0075	1.0047
5	5_158122566_G_A	158122566	158695558	rs79011982	A	G	0.0706	0.0000	1.0000	1.0000
5	5_158136337_T_A	158136337	158709329	rs113926471	A	T	0.0254	0.0020	1.0020	1.0001
5	5_158202753_AAC ACAC_AACACACAC	158202753	158775745		AACACAC AC	C	0.2493	0.0089	1.0089	1.0045
5	5_158244083_C_T	158244083	158817075	rs1432679	T	C	0.5683	-0.0200	0.9802	0.9776
5	5_158261163_C_T	158261163	158834155	rs17715065	T	C	0.5126	-0.0150	0.9851	0.9848
5	5_158263144_G_A	158263144	158836136	rs6885822	A	G	0.1491	0.0000	1.0000	1.0000
5	5_158270225_A_C	158270225	158843217	rs7707918	C	A	0.3943	-0.0060	0.9940	0.9953
5	5_158566745_A_G	158566745	159139737	rs2420354	G	A	0.4272	-0.0022	0.9978	0.9981
5	5_162232358_G_A	162232358	162805352	rs1288205	A	G	0.3070	-0.0048	0.9952	0.9971
5	5_162974403_T_C	162974403	163547397	rs7733433	C	T	0.1876	0.0068	1.0068	1.0026

5	5_165664201_T_C	165664201	166237196	rs62382837	C	T	0.0696	-0.0090	0.9910	0.9988
5	5_166176342_A_C	166176342	166749337	rs114356534	C	A	0.0219	0.0135	1.0136	1.0006
5	5_166259411_G_T	166259411	166832406	rs113755300	T	G	0.0527	-0.0232	0.9771	0.9976
5	5_166337984_T_C	166337984	166910979	rs13180091	C	T	0.1948	-0.0080	0.9920	0.9969
5	5_166361214_G_A	166361214	166934209	rs34067733	A	G	0.1531	0.0120	1.0121	1.0037
5	5_169511279_C_A	169511279	170084275	rs6872596	A	C	0.3805	0.0000	1.0000	1.0000
5	5_169512748_C_A	169512748	170085744	rs17562083	A	C	0.3536	0.0048	1.0048	1.0034
5	5_169534173_A_G	169534173	170107169	rs4315934	G	A	0.5784	-0.0022	0.9978	0.9975
5	5_169543263_AGA TG_AGATGGATG	169543263	170116259		AGATGGA TG	AGATG	0.1940	0.0000	1.0000	1.0000
5	5_169549409_A_A AAGAAG	169549409	170122405	rs141587449	AAAGAAG	A	0.7845	0.0070	1.0070	1.0111
5	5_169591460_T_C	169591460	170164456	rs10074269	C	T	0.3345	0.0147	1.0148	1.0099
5	5_169610853_G_A	169610853	170183849	rs80189533	A	G	0.2548	-0.0058	0.9942	0.9971
5	5_173358154_G_A	173358154	173931151	rs6864691	A	G	0.4074	0.0116	1.0117	1.0095
5	5_173650528_C_A	173650528	174223525	rs10476105	A	C	0.1082	-0.0037	0.9963	0.9992
5	5_173864492_C_A	173864492	174437489	rs35488892	A	C	0.2263	-0.0031	0.9969	0.9986
5	5_173964594_GT_ GTT	173964594	174537591	rs765642088	GTT	GT	0.0996	-0.0106	0.9895	0.9979
5	5_176134882_T_C	176134882	176707881	rs4868701	C	T	0.5422	0.0120	1.0121	1.0131
5	5_179632791_A_G	179632791	180205791	rs4700727	G	A	0.9483	-0.0040	0.9960	0.9924
5	5_179648650_C_T	179648650	180221650	rs139534316	T	C	0.0418	0.0152	1.0153	1.0013
6	6_1106459_G_A	1106459	1106224	rs12208662	A	G	0.0330	0.0171	1.0172	1.0011
6	6_1319312_C_T	1319312	1319077	rs80199833	T	C	0.2001	-0.0104	0.9897	0.9959
6	6_1696841_C_T	1696841	1696607	rs11968464	T	C	0.1022	-0.0089	0.9911	0.9982
6	6_4400365_A_G	4400365	4400131	rs885183	G	A	0.3887	-0.0122	0.9879	0.9906
6	6_4445334_TTTTC	4445334	4445100	rs760592016	T	TTTTC	0.4567	0.0019	1.0019	1.0017

6	6_12448424_C_T	12448424	12448192	rs190929774	T	C	0.0126	-0.0167	0.9834	0.9996
6	6_12860700_C_T	12860700	12860468	rs6924353	T	C	0.0664	-0.0068	0.9932	0.9991
6	6_13192799_G_A	13192799	13192567	rs4273688	A	G	0.1629	0.0115	1.0116	1.0038
6	6_13600459_T_C	13600459	13600227	rs2253217	C	T	0.3137	0.0000	1.0000	1.0000
6	6_13642999_T_C	13642999	13642767	rs3752501	C	T	0.3107	-0.0045	0.9955	0.9972
6	6_13700719_AGTA G_A	13700719	13700487	6:13700719_A GTAG_A	A	AGTAG	0.3723	-0.0128	0.9873	0.9906
6	6_13713366_G_C	13713366	13713134	rs418053	C	G	0.5691	-0.0092	0.9908	0.9896
6	6_13719673_G_A	13719673	13719441	rs412970	A	G	0.4909	0.0000	1.0000	1.0000
6	6_13741516_T_C	13741516	13741284	rs376024	C	T	0.5760	-0.0112	0.9889	0.9872
6	6_14288962_T_TG AATCA	14288962	14288731	rs71552783	TGAATCA	T	0.0835	0.0034	1.0034	1.0006
6	6_14657742_G_A	14657742	14657511	rs10484340	A	G	0.4154	0.0103	1.0104	1.0086
6	6_14665517_T_C	14665517	14665286	rs2092918	C	T	0.3769	0.0014	1.0014	1.0011
6	6_14668667_A_G	14668667	14668436	rs7761066	G	A	0.5444	0.0000	1.0000	1.0000
6	6_14892230_G_A	14892230	14891999	rs837181	A	G	0.7348	0.0074	1.0074	1.0109
6	6_14912686_G_A	14912686	14912455	rs439819	A	G	0.7488	0.0023	1.0023	1.0035
6	6_16399557_C_T	16399557	16399326	rs3819405	T	C	0.3299	-0.0199	0.9803	0.9870
6	6_17096277_G_T	17096277	17096046	rs74443408	T	G	0.1208	-0.0141	0.9860	0.9966
6	6_18520529_A_G	18520529	18520298	rs66680090	G	A	0.2582	0.0086	1.0086	1.0045
6	6_18757303_T_TA	18757303	18757072	rs556702310	TA	T	0.4562	0.0000	1.0000	1.0000
6	6_18783140_G_A	18783140	18782909	rs12211970	A	G	0.6200	0.0071	1.0071	1.0089
6	6_18786308 CCTTC CCTTCT_C	18786308	18786077	6:18786308_C CTTCCCTTCT_C	C	CCTTC CTTCT	0.6704	0.0009	1.0009	1.0012
6	6_19051225_C_A	19051225	19050994	rs1207107	A	C	0.1204	-0.0012	0.9988	0.9997
6	6_20537845_CA_C	20537845	20537614	rs769485514	C	CA	0.4733	-0.0080	0.9920	0.9925

6	6_20634428_G_T	20634428	20634197	rs9465847	T	G	0.1747	0.0000	1.0000	1.0000
6	6_20639604_G_A	20639604	20639373	rs7758612	A	G	0.6946	-0.0032	0.9968	0.9956
6	6_20645999_AATTT T_A	20645999	20645768	6:20645999_A ATTT_A	A	AATTT	0.5640	0.0000	1.0000	1.0000
6	6_20666919_CT_C	20666919	20666688	6:20666919_C T_C	C	CT	0.6369	-0.0005	0.9995	0.9994
6	6_20687802_G_A	20687802	20687571	rs10440832	A	G	0.8056	-0.0045	0.9955	0.9928
6	6_20706418_C_T	20706418	20706187	rs75626419	T	C	0.1159	-0.0088	0.9912	0.9980
6	6_20736237_C_A	20736237	20736006	rs9358361	A	C	0.8370	-0.0010	0.9990	0.9983
6	6_20830700_GAT_ G	20830700	20830469	6:20830700_G AT_G	G	GAT	0.1919	0.0034	1.0034	1.0013
6	6_20899840_C_T	20899840	20899609	rs12154181	T	C	0.2916	0.0021	1.0021	1.0012
6	6_20922863_C_T	20922863	20922632	rs9460577	T	C	0.2856	-0.0031	0.9969	0.9982
6	6_21905726_A_G	21905726	21905495	rs9350395	G	A	0.5920	0.0000	1.0000	1.0000
6	6_21910779_C_T	21910779	21910548	rs138872161	T	C	0.3467	-0.0017	0.9983	0.9988
6	6_21923810_T_C	21923810	21923579	rs9358466	C	T	0.4303	-0.0006	0.9994	0.9995
6	6_21925227_T_A	21925227	21924996	rs9358467	A	T	0.4466	-0.0103	0.9898	0.9909
6	6_21948207_T_C	21948207	21947976	rs10946491	C	T	0.2594	-0.0003	0.9997	0.9998
6	6_21967114_C_T	21967114	21966883	rs79266217	T	C	0.2401	-0.0043	0.9957	0.9979
6	6_22220514_G_A	22220514	22220285	rs74371547	A	G	0.0166	0.0265	1.0269	1.0009
6	6_22968438_T_C	22968438	22968209	rs112016347	C	T	0.0539	-0.0106	0.9895	0.9989
6	6_23019927_C_A	23019927	23019698	rs188165595	A	C	0.0148	-0.0129	0.9872	0.9996
6	6_23446154_G_A	23446154	23445926	rs12529389	A	G	0.2515	-0.0103	0.9898	0.9949
6	6_25148056_C_T	25148056	25147828	rs77078042	T	C	0.0388	-0.0018	0.9982	0.9999
6	6_26759078_C_A	26759078	26742807	rs13195977	A	C	0.1368	-0.0010	0.9990	0.9997
6	6_27274834_C_T	27274834	27307055	rs56114371	T	C	0.0841	-0.0016	0.9984	0.9997
6	6_27425644_G_C	27425644	27457865	rs34196306	C	G	0.0815	-0.0251	0.9752	0.9960

6	6_27848882_T_C	27848882	27881104	rs72847368	C	T	0.0939	0.0056	1.0056	1.0011
6	6_28117602_C_CT	28117602	28149824	rs560097346	CT	C	0.1351	0.0080	1.0080	1.0022
6	6_28897567_TA_T	28897567	28929790	6:28897567_T A_T	T	TA	0.3455	0.0102	1.0103	1.0071
6	6_29369052_G_A	29369052	29401275	rs113838413	A	G	0.0212	0.0174	1.0176	1.0007
6	6_29530628_A_G	29530628	29562851	rs362512	G	A	0.5050	0.0005	1.0005	1.0005
6	6_29861210_G_A	29861210	29893433		A	G	0.0257	-0.0210	0.9792	0.9989
6	6_30454350_G_A	30454350	30486573	rs17189022	A	G	0.0178	0.0000	1.0000	1.0000
6	6_31093776_A_G	31093776	31125999	rs3778639	G	A	0.1049	0.0000	1.0000	1.0000
6	6_31096526_A_G	31096526	31128749	rs9263717	G	A	0.2188	0.0018	1.0018	1.0008
6	6_31274174_C_T	31274174	31306397	rs139101653	T	C	0.0238	-0.0150	0.9851	0.9993
6	6_32583605_A_G	32583605	32615828	rs34341095	G	A	0.4400	-0.0002	0.9998	0.9998
6	6_32583813_G_A	32583813	32616036	rs1846190	A	G	0.2972	-0.0071	0.9929	0.9958
6	6_32584313_C_G	32584313	32616536	rs33932178	G	C	0.3290	-0.0015	0.9985	0.9990
6	6_32600671_C_T	32600671	32632894	rs9272131	T	C	0.0972	-0.0068	0.9932	0.9987
6	6_32693326_A_G	32693326	32725549	rs112269866	G	A	0.6904	0.0025	1.0025	1.0035
6	6_33239869_C_T	33239869	33272092	rs17215231	T	C	0.0795	0.0000	1.0000	1.0000
6	6_33249617_CCTTT T_C	33249617	33281840	6:33249617_C CTTT_C	C	CCTTT	0.3539	0.0000	1.0000	1.0000
6	6_33820658_C_T	33820658	33852881	rs78861422	T	C	0.0349	0.0164	1.0165	1.0012
6	6_33822865_C_T	33822865	33855088	rs9296100	T	C	0.7697	-0.0120	0.9881	0.9817
6	6_34833044_C_T	34833044	34865267	rs35173014	T	C	0.0132	-0.0245	0.9758	0.9994
6	6_35998776_T_G	35998776	36030999	rs13196204	G	T	0.1768	-0.0056	0.9944	0.9980
6	6_36641993_C_A	36641993	36674216	rs148260186	A	C	0.0250	0.0112	1.0113	1.0006
6	6_36644498_T_C	36644498	36676721	rs3829964	C	T	0.4919	0.0125	1.0126	1.0124
6	6_37699029_C_T	37699029	37731253	rs13218687	T	C	0.1384	-0.0054	0.9946	0.9985
6	6_42078871_G_T	42078871	42111133	rs4357133	T	G	0.3103	0.0054	1.0054	1.0034

6	6_43227141_G_A	43227141	43259403	rs111342015	A	G	0.0985	-0.0245	0.9758	0.9952
6	6_43757082_T_A	43757082	43789345	rs4711750	A	T	0.4897	-0.0096	0.9904	0.9907
6	6_45892162_G_A	45892162	45924425	rs4714889	A	G	0.9692	-0.0348	0.9658	0.9348
6	6_46877011_T_A	46877011	46909274	rs1328958	A	T	0.1356	-0.0031	0.9969	0.9992
6	6_46889321_C_A	46889321	46921584	rs76199887	A	C	0.0702	-0.0188	0.9814	0.9974
6	6_46897275_GA_G	46897275	46929538	6:46897275_G A_G	G	GA	0.7599	0.0009	1.0009	1.0014
6	6_47336402_TTTTA TA_T	47336402	47368666	6:47336402_T TTTATA_T	T	TTTTAT A	0.4523	0.0000	1.0000	1.0000
6	6_47898772_C_T	47898772	47931036	rs149063534	T	C	0.0286	0.0061	1.0061	1.0004
6	6_52205511_G_T	52205511	52340713	rs7774765	T	G	0.0548	0.0072	1.0072	1.0008
6	6_52980128_C_T	52980128	53115330	rs6941531	T	C	0.0320	-0.0140	0.9861	0.9991
6	6_52984063_C_A	52984063	53119265	rs9474392	A	C	0.0175	-0.0313	0.9692	0.9989
6	6_54005663_A_G	54005663	54140865	rs816374	G	A	0.2890	-0.0046	0.9954	0.9973
6	6_54700803_G_C	54700803	54836005	rs1393779	C	G	0.4905	0.0009	1.0009	1.0009
6	6_54714635_T_G	54714635	54849837	rs9464149	G	T	0.4778	0.0001	1.0001	1.0001
6	6_54726869_C_T	54726869	54862071	rs931766	T	C	0.5053	0.0089	1.0089	1.0091
6	6_54800275_A_G	54800275	54935477	rs56233640	G	A	0.2546	0.0026	1.0026	1.0013
6	6_55089182_G_A	55089182	55224384	rs10948897	A	G	0.5158	0.0001	1.0001	1.0001
6	6_61948121_C_T	61948121	61289594	rs569725482	T	C	0.0106	0.0381	1.0388	1.0008
6	6_61972502_T_C	61972502	61265212	rs12197273	C	T	0.2801	0.0006	1.0006	1.0003
6	6_64505213_A_G	64505213	63795320	rs756274	G	A	0.3466	0.0008	1.0008	1.0006
6	6_68849351_T_G	68849351	68139459	rs77203199	G	T	0.1700	0.0013	1.0013	1.0004
6	6_69273849_A_G	69273849	68563957	rs62416495	G	A	0.0217	-0.0075	0.9925	0.9997
6	6_69300758_C_T	69300758	68590866	rs117298640	T	C	0.0209	0.0236	1.0239	1.0010
6	6_72994975_C_T	72994975	72285272	rs10455087	T	C	0.1095	0.0036	1.0036	1.0008
6	6_73138812_G_A	73138812	72429110	rs12196354	A	G	0.1700	0.0091	1.0091	1.0031

6	6_73157462_A_G	73157462	72447760	rs6927917	G	A	0.8400	-0.0035	0.9965	0.9941
6	6_73575924_T_C	73575924	72866201	rs2995345	C	T	0.7807	0.0106	1.0107	1.0167
6	6_73588636_T_G	73588636	72878913	rs9442863	G	T	0.2119	-0.0067	0.9933	0.9972
6	6_74819460_G_A	74819460	74109744	rs55976071	A	G	0.1525	-0.0095	0.9905	0.9971
6	6_76267791_AT_A	76267791	75558075	6:76267791_A_T_A	A	AT	0.5132	-0.0048	0.9952	0.9951
6	6_78924045_A_T	78924045	78214328	rs867705	T	A	0.3338	-0.0015	0.9985	0.9990
6	6_79037890_A_G	79037890	78328173	rs611413	G	A	0.1614	-0.0095	0.9905	0.9970
6	6_81105862_T_G	81105862	80396145	rs1836962	G	T	0.5419	0.0014	1.0014	1.0015
6	6_81193866_T_C	81193866	80484149	rs2917619	C	T	0.4972	-0.0030	0.9970	0.9970
6	6_81306990_A_T	81306990	80597273	rs7750052	T	A	0.4540	-0.0018	0.9982	0.9984
6	6_81974654_A_G	81974654	81264937	rs75640685	G	A	0.0564	0.0000	1.0000	1.0000
6	6_82226268_T_A	82226268	81516551	rs117486497	A	T	0.0542	0.0089	1.0089	1.0010
6	6_82263549_AAT_A	82263549	81553832	rs10623112	A	AAT	0.4262	0.0137	1.0138	1.0118
6	6_82280232_T_A	82280232	81570515	rs7771821	A	T	0.2552	0.0046	1.0046	1.0024
6	6_82287685_G_A	82287685	81577968	rs1361549	A	G	0.4150	-0.0100	0.9900	0.9918
6	6_82725389_T_C	82725389	82015672	rs4706918	C	T	0.6471	0.0000	1.0000	1.0000
6	6_85102918_G_A	85102918	84393200	rs62448657	A	G	0.1014	0.0070	1.0070	1.0014
6	6_85689822_A_G	85689822	84980104	rs56413943	G	A	0.1432	0.0007	1.0007	1.0002
6	6_85722437_T_C	85722437	85012719	rs62422908	C	T	0.1067	0.0152	1.0153	1.0033
6	6_85746200_C_A	85746200	85036482	rs142990780	A	C	0.1006	0.0050	1.0050	1.0010
6	6_85991348_A_T	85991348	85281630	rs9450216	T	A	0.0803	0.0017	1.0017	1.0003
6	6_86913286_T_A	86913286	86203568	rs62443510	A	T	0.0927	-0.0014	0.9986	0.9997
6	6_86973861_TC_T	86973861	86264143	6:86973861_T_C_T	T	TC	0.0993	-0.0143	0.9858	0.9972
6	6_87648885_C_G	87648885	86939167	rs862420	G	C	0.1378	0.0026	1.0026	1.0007

6	6_87803819_T_C	87803819	87094101	rs73754909	C	T	0.2770	0.0128	1.0129	1.0072
6	6_87834796_A_G	87834796	87125078	rs11753770	G	A	0.0984	0.0029	1.0029	1.0006
6	6_90141980_A_G	90141980	89432261	rs56170939	G	A	0.1511	0.0147	1.0148	1.0045
6	6_90474544_G_A	90474544	89764825	rs9359863	A	G	0.0524	-0.0012	0.9988	0.9999
6	6_97219145_CA_C	97219145	96771269	rs780491270	C	CA	0.2187	0.0000	1.0000	1.0000
6	6_98462501_G_A	98462501	98014625	rs12529874	A	G	0.0345	-0.0111	0.9890	0.9992
6	6_100048974_T_C	100048974	99601098	rs9385807	C	T	0.1373	0.0030	1.0030	1.0008
6	6_100091541_CAA_A_C	100091541	99643665	6:100091541_CAA_C	C	CAAA	0.2287	0.0026	1.0026	1.0012
6	6_100184696_A_G	100184696	99736820	rs6929136	G	A	0.2023	0.0028	1.0028	1.0011
6	6_100317114_G_A	100317114	99869238	rs6916454	A	G	0.3486	0.0051	1.0051	1.0036
6	6_104762291_T_A	104762291	104314416	rs905538	A	T	0.3253	0.0107	1.0108	1.0070
6	6_110776061_ATG_T_A	110776061	110454858	6:110776061_ATGT_A	A	ATGT	0.0523	-0.0243	0.9760	0.9975
6	6_111236431_G_A	111236431	110915228	rs13203604	A	G	0.1641	-0.0064	0.9936	0.9979
6	6_111313720_A_G	111313720	110992517	rs13203579	G	A	0.2391	-0.0051	0.9949	0.9976
6	6_111492119_T_C	111492119	111170916	rs241768	C	T	0.7090	-0.0045	0.9955	0.9936
6	6_111947938_A_G	111947938	111626735	rs117553096	G	A	0.0257	-0.0287	0.9717	0.9985
6	6_112830623_C_T	112830623	112509421	rs147637256	T	C	0.0279	-0.0170	0.9831	0.9991
6	6_113986557_ATT_A	113986557	113665355	6:113986557_ATT_A	A	ATT	0.6740	0.0038	1.0038	1.0051
6	6_114387136_C_T	114387136	114065972	rs142313879	T	C	0.0159	-0.0125	0.9876	0.9996
6	6_115102204_A_C	115102204	114781040	rs62442934	C	A	0.1357	-0.0218	0.9784	0.9942
6	6_118214194_G_C	118214194	117893031	rs56013995	C	G	0.1824	0.0043	1.0043	1.0016
6	6_119578767_A_G	119578767	119257602	rs147917246	G	A	0.0128	0.0330	1.0336	1.0009
6	6_120623111_T_C	120623111	120301965	rs66945651	C	T	0.5301	-0.0076	0.9924	0.9920
6	6_122329970_C_A	122329970	122008824	rs2684222	A	C	0.7019	0.0102	1.0103	1.0144

6	6_122625590_G_A	122625590	122304445	rs13191873	A	G	0.0596	-0.0232	0.9771	0.9973
6	6_122717777_C_T	122717777	122396632	rs76071582	T	C	0.1109	0.0051	1.0051	1.0011
6	6_122719631_G_T	122719631	122398486	rs516805	T	G	0.7003	-0.0074	0.9926	0.9897
6	6_123366449_A_T	123366449	123045304	rs6940619	T	A	0.2294	-0.0003	0.9997	0.9999
6	6_123825415_T_G	123825415	123504270	rs7746287	G	T	0.8692	-0.0071	0.9929	0.9877
6	6_124613800_TTAC ATTGA_T	124613800	124292654	6:124613800_ TTACATTGA_T	T	TTACAT TGA	0.1758	0.0088	1.0088	1.0031
6	6_125172405_G_A	125172405	124851259	rs1409293	A	G	0.4874	-0.0049	0.9951	0.9952
6	6_125223597_T_G	125223597	124902451	rs11154277	G	T	0.3993	-0.0079	0.9921	0.9937
6	6_127457071_CA_ C	127457071	127135926	6:127457071_ CA_C	C	CA	0.5389	-0.0013	0.9987	0.9986
6	6_127477021_G_G TATA	127477021	127155876	rs139087942	GTATA	G	0.4906	-0.0058	0.9942	0.9943
6	6_129916283_C_C AT	129916283	129595138	rs10633215	CAT	C	0.4745	0.0000	1.0000	1.0000
6	6_129922776_C_CT	129922776	129601631	rs34417139	CT	C	0.3343	-0.0028	0.9972	0.9981
6	6_130341235_T_C	130341235	130020090	rs113898003	C	T	0.2562	0.0051	1.0051	1.0026
6	6_130341728_C_CT	130341728	130020583	rs55941023	CT	C	0.7116	0.0119	1.0120	1.0171
6	6_130349119_C_T	130349119	130027974	rs6569648	T	C	0.7627	0.0174	1.0176	1.0270
6	6_130436472_C_T	130436472	130115327	rs6914419	T	C	0.3643	0.0000	1.0000	1.0000
6	6_132375163_AT_ A	132375163	132054023	6:132375163_ AT_A	A	AT	0.6028	0.0018	1.0018	1.0022
6	6_133703325_A_G	133703325	133382187	rs2235485	G	A	0.1475	0.0119	1.0120	1.0035
6	6_135262565_G_A	135262565	134941427	rs13209279	A	G	0.3406	0.0070	1.0070	1.0048
6	6_135457541_A_G	135457541	135136403	rs1883354	G	A	0.4182	0.0016	1.0016	1.0013
6	6_135492534_C_T	135492534	135171396	rs6903653	T	C	0.3871	0.0046	1.0046	1.0036
6	6_135646235_A_G	135646235	135325097	rs9402703	G	A	0.5649	0.0093	1.0093	1.0106

6	6_138834164_T_C	138834164	138513027	rs6570241	C	T	0.0762	0.0000	1.0000	1.0000
6	6_139134041_G_C	139134041	138812904	rs9403003	C	G	0.2660	-0.0105	0.9896	0.9945
6	6_139153321_GTT_G	139153321	138832184		G	GTT	0.1000	-0.0121	0.9880	0.9976
6	6_139603414_G_A	139603414	139282277	rs9495413	A	G	0.2454	0.0099	1.0099	1.0049
6	6_144311702_C_T	144311702	143990565	rs76161579	T	C	0.0108	-0.0077	0.9923	0.9998
6	6_149595505_T_C	149595505	149274369	rs2121348	C	T	0.2061	-0.0230	0.9773	0.9906
6	6_149601768_G_A	149601768	149280632	rs4897108	A	G	0.2309	0.0000	1.0000	1.0000
6	6_149770179_C_T	149770179	149449043	rs237005	T	C	0.2512	0.0043	1.0043	1.0022
6	6_150576958_G_A	150576958	150255822	rs111766406	A	G	0.0140	0.0000	1.0000	1.0000
6	6_150587307_T_C	150587307	150266171	rs6936991	C	T	0.0270	0.0121	1.0122	1.0007
6	6_150599606_C_T	150599606	150278470	rs12214271	T	C	0.1402	-0.0075	0.9925	0.9979
6	6_150807661_A_G	150807661	150486525	rs9480463	G	A	0.5128	0.0017	1.0017	1.0017
6	6_150812557_T_A	150812557	150491421	rs12207876	A	T	0.1023	-0.0020	0.9980	0.9996
6	6_150894274_G_A	150894274	150573138	rs9480482	A	G	0.1844	-0.0052	0.9948	0.9981
6	6_151214063_TG_T	151214063	150892927	6:151214063_TG_T	T	TG	0.1010	-0.0121	0.9880	0.9976
6	6_151371751_G_A	151371751	151050615	rs6928026	A	G	0.4760	-0.0030	0.9970	0.9972
6	6_151419174_A_G	151419174	151098038	rs9478949	G	A	0.3867	0.0052	1.0052	1.0040
6	6_151932778_A_G	151932778	151611643	rs1023940	G	A	0.4960	0.0000	1.0000	1.0000
6	6_151948366_G_A	151948366	151627231	rs2046210	A	G	0.3403	0.0000	1.0000	1.0000
6	6_151949806_A_C	151949806	151628671	rs6913578	C	A	0.3083	0.0393	1.0401	1.0249
6	6_151950723_C_T	151950723	151629588	rs774781	T	C	0.4098	-0.0059	0.9941	0.9952
6	6_151952332_G_A	151952332	151631197	rs9397437	A	G	0.0688	0.0367	1.0374	1.0052
6	6_151955914_A_G	151955914	151634779	rs60954078	G	A	0.0713	0.0741	1.0769	1.0110
6	6_151965491_G_A	151965491	151644356	rs12197252	A	G	0.0929	0.0000	1.0000	1.0000
6	6_151970639_C_G	151970639	151649504	rs1293960	G	C	0.5758	0.0000	1.0000	1.0000

6	6_151985550_G_A	151985550	151664415	rs851997	A	G	0.3937	0.0045	1.0045	1.0036
6	6_151985574_T_C	151985574	151664439	rs78517863	C	T	0.0824	0.0000	1.0000	1.0000
6	6_152009427_G_A	152009427	151688292	rs79347432	A	G	0.0269	-0.0030	0.9970	0.9998
6	6_152023191_G_A	152023191	151702056	rs851984	A	G	0.3965	0.0457	1.0468	1.0374
6	6_152055978_A_T	152055978	151734843	rs6904031	T	A	0.0627	0.0460	1.0471	1.0059
6	6_152117128_CA_C	152117128	151795993	6:152117128_CA_C	C	CA	0.4525	-0.0086	0.9914	0.9923
6	6_152156935_ATT_A	152156935	1518335800		A	ATT	0.1904	0.0040	1.0040	1.0015
6	6_152163381_A_G	152163381	151842246	rs9340799	G	A	0.3507	0.0000	1.0000	1.0000
6	6_152263860_A_T	152263860	151942725	rs9340898	T	A	0.0239	0.0000	1.0000	1.0000
6	6_152312425_T_G	152312425	151991290	rs79784637	G	T	0.0206	-0.0104	0.9897	0.9996
6	6_152410883_T_G	152410883	152089748	rs1983664	G	T	0.0605	-0.0112	0.9889	0.9987
6	6_152428094_C_C	152428094	152106959	rs538095870	CA	C	0.2291	0.0000	1.0000	1.0000
6	6_152428704_C_G	152428704	152107569	rs1543403	G	C	0.4694	0.0000	1.0000	1.0000
6	6_152432902_C_T	152432902	152111767	rs910416	T	C	0.5146	0.0428	1.0437	1.0455
6	6_152452759_T_C	152452759	152131624	rs6925149	C	T	0.0609	0.0118	1.0119	1.0014
6	6_152465616_AGT_A	152465616	152144481		A	AGT	0.4279	0.0000	1.0000	1.0000
6	6_152474790_T_C	152474790	152153655	rs9397084	C	T	0.2141	0.0055	1.0055	1.0024
6	6_152476784_T_C	152476784	152155649	rs6557199	C	T	0.0354	0.0055	1.0055	1.0004
6	6_153099296_G_C	153099296	152778161	rs137905783	C	G	0.0192	-0.0206	0.9796	0.9992
6	6_155435105_A_C	155435105	155113971	rs9371861	C	A	0.2313	-0.0004	0.9996	0.9998
6	6_157228314_A_G	157228314	156907180	rs28648619	G	A	0.0827	0.0125	1.0126	1.0021
6	6_157331090_C_T	157331090	157009956	rs140842923	T	C	0.0224	0.0176	1.0178	1.0008
6	6_159498130_C_T	159498130	159077098	rs524410	T	C	0.4857	-0.0025	0.9975	0.9976

6	6_159516474_C_CT	159516474	159095442	rs577038023	CT	C	0.1589	0.0155	1.0156	1.0050
6	6_161008833_T_TT CTG	161008833	160587801	rs112021077	TTCTG	T	0.3315	0.0042	1.0042	1.0028
6	6_161087869_A_T	161087869	160666837	rs783148	T	A	0.8573	-0.0047	0.9953	0.9920
6	6_163625614_G_T	163625614	163204582	rs763599	T	G	0.2959	0.0048	1.0048	1.0028
6	6_164143918_G_A	164143918	163722886	rs7766259	A	G	0.8970	0.0065	1.0065	1.0117
6	6_165601875_T_C	165601875	165188386	rs116415103	C	T	0.0205	-0.0017	0.9983	0.9999
6	6_165610793_A_G	165610793	165197304	rs1764051	G	A	0.0701	-0.0014	0.9986	0.9998
6	6_166466348_G_A	166466348	166052860	rs777580	A	G	0.6917	0.0007	1.0007	1.0010
6	6_166497992_TAA TC_T	166497992	166084504	6:166497992_- TAATC_T	T	TAATC	0.4871	0.0019	1.0019	1.0019
6	6_166501349_A_A G	166501349	166087861	rs113289039	AG	A	0.3090	-0.0112	0.9889	0.9931
6	6_166520692_G_A	166520692	166107204	rs2323086	A	G	0.5152	0.0011	1.0011	1.0011
6	6_168292084_GGT GGGTGT_G	168292084	167891404	6:168292084_- GGTGGGTGT_ G	G	GGTGG GTGT	0.9213	-0.0049	0.9951	0.9910
6	6_168336052_G_A	168336052	167935372	rs3800531	A	G	0.3596	-0.0033	0.9967	0.9976
6	6_168378848_T_G	168378848	167978168	rs227249	G	T	0.5552	-0.0051	0.9949	0.9944
6	6_169006947_C_G	169006947	168606267	rs9364472	G	C	0.5202	0.0000	1.0000	1.0000
6	6_169013233_G_A	169013233	168612553	rs4464761	A	G	0.6596	-0.0107	0.9894	0.9860
6	6_169034960_T_G	169034960	168634280	rs2342647	G	T	0.3987	-0.0005	0.9995	0.9996
6	6_169072735_C_T	169072735	168672196	rs58699559	T	C	0.0597	-0.0028	0.9972	0.9997
6	6_169091726_A_C	169091726	168691612	rs11966386	C	A	0.0120	-0.0054	0.9946	0.9999
6	6_169174555_CT_C	169174555	168774460	6:169174555_- CT_C	C	CT	0.8871	-0.0115	0.9886	0.9798
6	6_169186803_ATG _A	169186803	168786708	6:169186803_- ATG_A	A	ATG	0.8213	-0.0009	0.9991	0.9985

6	6_169616697_AT_A	169616697	169216602	6:169616697_AT_A	A	AT	0.5647	-0.0072	0.9928	0.9919
6	6_169630340_G_A	169630340	169230245	rs6605521	A	G	0.5731	-0.0041	0.9959	0.9953
6	6_170332621_T_C	170332621	170017397	rs6940159	C	T	0.6158	0.0190	1.0192	1.0238
6	6_170339055_G_A	170339055	170023831	rs80097054	A	G	0.1077	0.0000	1.0000	1.0000
6	6_170355128_G_A	170355128	170039904	rs114138513	A	G	0.0453	-0.0191	0.9811	0.9983
6	6_170789173_C_T	170789173	170480085	rs57586097	T	C	0.0236	0.0339	1.0345	1.0016
7	7_1512823_G_A	1512823	1473187	rs111256568	A	G	0.0293	-0.0292	0.9712	0.9983
7	7_2768355_A_ATG	2768355	2728721	rs4208	ATG	A	0.2030	-0.0040	0.9960	0.9984
7	7_3563804_C_T	3563804	3524172	rs73035954	T	C	0.2558	-0.0019	0.9981	0.9990
7	7_3576538_G_A	3576538	3536906	rs10234480	A	G	0.6309	-0.0015	0.9985	0.9981
7	7_5240541_T_C	5240541	5200910	rs4591933	C	T	0.6613	-0.0073	0.9927	0.9904
7	7_8820426_G_A	8820426	8780796	rs77450427	A	G	0.0747	0.0032	1.0032	1.0005
7	7_10620231_G_T	10620231	10580604	rs1981581	T	G	0.7575	0.0022	1.0022	1.0033
7	7_10629885_T_C	10629885	10590258	rs10243948	C	T	0.5618	0.0077	1.0077	1.0087
7	7_12592846_A_G	12592846	12553220	rs117012007	G	A	0.0489	0.0227	1.0230	1.0022
7	7_12629758_G_T	12629758	12590133	rs1138910	T	G	0.0952	0.0018	1.0018	1.0003
7	7_12763696_T_A	12763696	12724071	rs10276444	A	T	0.2866	0.0101	1.0102	1.0058
7	7_12771041_T_TTC	12771041	12731416	rs10680080	TTCTC	T	0.3649	0.0006	1.0006	1.0004
7	7_13884782_C_G	13884782	13845157	rs4719382	G	C	0.3517	0.0042	1.0042	1.0030
7	7_16297381_A_G	16297381	16257756	rs11769530	G	A	0.2080	-0.0125	0.9876	0.9948
7	7_17007625_A_T	17007625	16968001	rs1721016	T	A	0.4676	-0.0018	0.9982	0.9983
7	7_17057725_C_G	17057725	17018101	rs13229759	G	C	0.3848	0.0000	1.0000	1.0000
7	7_17066979_T_C	17066979	17027355	rs149535798	C	T	0.0202	-0.0181	0.9821	0.9993
7	7_17074440_G_A	17074440	17034816	rs471475	A	G	0.3963	0.0115	1.0116	1.0092
7	7_17208250_G_A	17208250	17168626	rs75337980	A	G	0.0133	0.0358	1.0364	1.0010

7	7_20508287_CT_C	20508287	20468664	7:20508287_C T_C	C	CT	0.2998	-0.0076	0.9924	0.9955
7	7_20865979_C_A	20865979	20826360	rs12700239	A	C	0.1952	0.0080	1.0080	1.0031
7	7_20885095_C_G	20885095	20845476	rs13245023	G	C	0.0366	0.0054	1.0054	1.0004
7	7_20885792_A_G	20885792	20846173	rs6965314	G	A	0.8525	-0.0054	0.9946	0.9908
7	7_20898650_G_T	20898650	20859031	rs113848802	T	G	0.0211	-0.0105	0.9896	0.9996
7	7_21168014_T_C	21168014	21128395	rs17143912	C	T	0.0775	0.0125	1.0126	1.0020
7	7_21940960_A_G	21940960	21901342	rs7971	G	A	0.3515	-0.0236	0.9767	0.9837
7	7_21941669_A_C	21941669	21902051	rs1128226	C	A	0.3746	-0.0002	0.9998	0.9999
7	7_22014189_CAA_ C	22014189	21974571	rs756053372	C	CAA	0.3789	0.0000	1.0000	1.0000
7	7_22822662_A_T	22822662	22783043	rs12530998	T	A	0.4042	-0.0052	0.9948	0.9958
7	7_22910541_C_T	22910541	22870922	rs117841439	T	C	0.1148	-0.0036	0.9964	0.9992
7	7_23488174_A_C	23488174	23448555	rs12539834	C	A	0.0508	0.0045	1.0045	1.0005
7	7_23523662_AAAT AAT_AAAT	23523662	23484043		AAAT	AAATAA T	0.2545	0.0055	1.0055	1.0028
7	7_23584522_C_A	23584522	23544903	rs11767313	A	C	0.1813	0.0000	1.0000	1.0000
7	7_25163744_A_C	25163744	25124125	rs11267038	C	A	0.0680	-0.0105	0.9896	0.9986
7	7_25569548_C_T	25569548	25529928	rs289997	T	C	0.1667	-0.0063	0.9937	0.9979
7	7_25573204_G_A	25573204	25533584	rs965610	A	G	0.2347	-0.0070	0.9930	0.9967
7	7_25591710_C_T	25591710	25552090	rs73277029	T	C	0.1744	-0.0067	0.9933	0.9977
7	7_25656363_G_C	25656363	25616743	rs73085996	C	G	0.2302	0.0052	1.0052	1.0024
7	7_27509178_A_G	27509178	27469559	rs73077497	G	A	0.0379	0.0262	1.0265	1.0020
7	7_27617028_G_A	27617028	27577409	rs140387951	A	G	0.0410	0.0119	1.0120	1.0010
7	7_28128002_T_C	28128002	28088383	rs7457754	C	T	0.1467	0.0039	1.0039	1.0011
7	7_28209953_GAT_ G	28209953	28170334	7:28209953_G AT_G	G	GAT	0.5268	0.0074	1.0074	1.0078

7	7_28356889_T_C	28356889	28317270	rs17156577	C	T	0.1139	0.0105	1.0106	1.0024
7	7_28627353_C_T	28627353	28587735	rs141085164	T	C	0.0109	-0.0195	0.9807	0.9996
7	7_28652801_A_G	28652801	28613184	rs189567370	G	A	0.0123	-0.0105	0.9896	0.9997
7	7_28856014_T_C	28856014	28816397	rs10486594	C	T	0.1048	-0.0170	0.9831	0.9965
7	7_28938590_G_C	28938590	28898973	rs10250382	C	G	0.5041	0.0073	1.0073	1.0074
7	7_29121211_T_C	29121211	29081595	rs317726	C	T	0.5171	0.0025	1.0025	1.0026
7	7_29468698_G_A	29468698	29429082	rs7785829	A	G	0.6103	0.0141	1.0142	1.0174
7	7_29752475_A_G	29752475	29712859	rs62458273	G	A	0.1310	-0.0045	0.9955	0.9988
7	7_31893072_C_G	31893072	31853458	rs76907223	G	C	0.0619	0.0109	1.0110	1.0014
7	7_33484507_T_G	33484507	33444895	rs1860601	G	T	0.2449	0.0031	1.0031	1.0015
7	7_36706015_A_G	36706015	36666410	rs117705242	G	A	0.0231	-0.0139	0.9862	0.9994
7	7_43291856_T_C	43291856	43252257	rs57648935	C	T	0.3892	-0.0067	0.9933	0.9948
7	7_43299616_T_C	43299616	43260017	rs9639872	C	T	0.3459	0.0000	1.0000	1.0000
7	7_43889991_C_A	43889991	43850392	rs4724250	A	C	0.1457	0.0004	1.0004	1.0001
7	7_44790921_T_C	44790921	44751322	rs55705735	C	T	0.1252	0.0088	1.0088	1.0022
7	7_44961337_G_A	44961337	44921738	rs55738054	A	G	0.0639	0.0194	1.0196	1.0025
7	7_44961407_T_G	44961407	44921808	rs73102191	G	T	0.0148	0.0019	1.0019	1.0001
7	7_47022767_G_A	47022767	46983169	rs6955374	A	G	0.3530	0.0053	1.0053	1.0038
7	7_47100078_C_T	47100078	47060480	rs56017904	T	C	0.1214	-0.0127	0.9874	0.9969
7	7_47673601_T_C	47673601	47634003	rs73697710	C	T	0.0108	0.0203	1.0205	1.0004
7	7_47820962_T_C	47820962	47781364	rs6953528	C	T	0.3646	-0.0063	0.9937	0.9954
7	7_47831912_G_T	47831912	47792314	rs10282416	T	G	0.8159	-0.0018	0.9982	0.9971
7	7_47875564_C_T	47875564	47835966	rs4543454	T	C	0.4036	-0.0064	0.9936	0.9949
7	7_48472383_G_A	48472383	48432786	rs7801736	A	G	0.5402	-0.0027	0.9973	0.9971
7	7_50764404_C_T	50764404	50696707	rs2299156	T	C	0.2009	0.0146	1.0147	1.0059
7	7_50923571_T_C	50923571	50855874	rs17454681	C	T	0.5260	0.0056	1.0056	1.0059
7	7_51166631_A_G	51166631	51098934	rs4948187	G	A	0.3921	-0.0014	0.9986	0.9989

7	7_55192256_A_C	55192256	55124563	rs13244925	C	A	0.5497	-0.0081	0.9919	0.9912
7	7_57401795_C_T	57401795	57334088	rs11767308	T	C	0.0551	0.0000	1.0000	1.0000
7	7_63276830_T_C	63276830	63816452	rs1708651	C	T	0.6040	0.0066	1.0066	1.0080
7	7_67991296_GAGG AAGGA_G	67991296	68526309	7:67991296_G AGGAAGGA_G	G	GAGGA AGGA	0.3327	-0.0014	0.9986	0.9991
7	7_71603177_T_C	71603177	72138192	rs6970190	C	T	0.0210	0.0252	1.0255	1.0011
7	7_73056750_T_C	73056750	73642420	rs6957745	C	T	0.1898	0.0076	1.0076	1.0029
7	7_74110705_A_G	74110705	74696373	rs74910854	G	A	0.0700	0.0102	1.0103	1.0014
7	7_74231353_A_G	74231353	74816826	rs707402	G	A	0.7197	0.0000	1.0000	1.0000
7	7_74279763_C_T	74279763	74863463	rs801066	T	C	0.1925	0.0031	1.0031	1.0012
7	7_74350606_C_CA	74350606	74935609	rs199562542	CA	C	0.2773	0.0000	1.0000	1.0000
7	7_74359358_C_T	74359358	74944369	rs1637365	T	C	0.2792	0.0074	1.0074	1.0042
7	7_75168562_G_A	75168562	75539242	rs1167835	A	G	0.2281	0.0025	1.0025	1.0011
7	7_77062679_A_C	77062679	77433362	rs998994	C	A	0.4996	0.0075	1.0075	1.0075
7	7_77954163_T_A	77954163	78324846	rs798301	A	T	0.4807	0.0000	1.0000	1.0000
7	7_77992996_A_G	77992996	78363679	rs4476926	G	A	0.1428	-0.0139	0.9862	0.9961
7	7_78463911_A_G	78463911	78834595	rs8180745	G	A	0.0463	-0.0162	0.9839	0.9985
7	7_82079457_G_A	82079457	82450141	rs117603127	A	G	0.0139	-0.0582	0.9435	0.9984
7	7_86345495_G_A	86345495	86716179	rs2214653	A	G	0.4112	0.0003	1.0003	1.0002
7	7_86348037_A_G	86348037	86718721	rs2237547	G	A	0.2932	-0.0039	0.9961	0.9977
7	7_86372202_G_A	86372202	86742886	rs12704285	A	G	0.0219	-0.0223	0.9779	0.9990
7	7_86474313_T_C	86474313	86844997	rs1989796	C	T	0.5923	-0.0108	0.9893	0.9873
7	7_86662659_A_C	86662659	87033343	rs6953148	C	A	0.2920	-0.0010	0.9990	0.9994
7	7_88411073_A_G	88411073	88781759	rs3847036	G	A	0.9224	-0.0038	0.9962	0.9930
7	7_89529281_T_C	89529281	89899967	rs148300099	C	T	0.6557	-0.0106	0.9895	0.9862
7	7_89533047_C_G	89533047	89903733	rs11489497	G	C	0.3065	-0.0029	0.9971	0.9982
7	7_90086677_G_GA	90086677	90457563	rs139526283	GA	G	0.1507	0.0116	1.0117	1.0035

7	7_91459189_A_AT T	91459189	91829875		ATT	A	0.3286	0.0151	1.0152	1.0100
7	7_91565914_T_TA	91565914	91936600	rs35469924	TA	T	0.5413	-0.0085	0.9915	0.9909
7	7_94090342_C_T	94090342	94461030	rs78582026	T	C	0.1436	0.0043	1.0043	1.0012
7	7_94113799_T_C	94113799	94484487	rs17268829	C	T	0.2792	0.0112	1.0113	1.0063
7	7_94321785_A_AT T	94321785	94692473		ATT	A	0.3141	0.0023	1.0023	1.0014
7	7_94420291_G_A	94420291	94790979	rs35665648	A	G	0.1820	-0.0055	0.9945	0.9980
7	7_94609593_G_A	94609593	94980281	rs149550563	A	G	0.0106	0.0278	1.0282	1.0006
7	7_94979963_C_T	94979963	95350651	rs17880824	T	C	0.0145	0.0000	1.0000	1.0000
7	7_97686264_A_G	97686264	98056952	rs12704958	G	A	0.0591	0.0230	1.0233	1.0028
7	7_97865802_C_A	97865802	98236490	rs118053816	A	C	0.0205	-0.0165	0.9836	0.9993
7	7_98005235_G_A	98005235	98375923	rs4439053	A	G	0.1627	-0.0150	0.9851	0.9952
7	7_99292372_A_G	99292372	99694749	rs112779675	G	A	0.0179	0.0009	1.0009	1.0000
7	7_99576068_G_A	99576068	99978445	rs12673005	A	G	0.3884	0.0010	1.0010	1.0008
7	7_99893765_C_T	99893765	100296142	rs73161745	T	C	0.2963	0.0016	1.0016	1.0009
7	7_99948655_T_G	99948655	100351032	rs111963714	G	T	0.2109	0.0116	1.0117	1.0049
7	7_100008270_T_C	100008270	100410647	rs192787100	C	T	0.0116	0.0240	1.0243	1.0006
7	7_100035274_G_A	100035274	100437651	rs117911427	A	G	0.0215	0.0085	1.0085	1.0004
7	7_100532911_C_T	100532911	100935285	rs6465777	T	C	0.2644	-0.0034	0.9966	0.9982
7	7_100781615_G_A	100781615	101138334	rs1050813	A	G	0.2012	0.0078	1.0078	1.0032
7	7_101437919_TA_T	101437919	101794639	7:101437919_ TA_T	T	TA	0.3632	-0.0003	0.9997	0.9998
7	7_101552440_G_A	101552440	101909160	rs71559437	A	G	0.1255	-0.0051	0.9949	0.9987
7	7_101556363_C_T	101556363	101913083	rs11974778	T	C	0.2798	-0.0108	0.9893	0.9940
7	7_101561492_C_T	101561492	101918212	rs73185821	T	C	0.0701	-0.0174	0.9828	0.9976
7	7_101591393_G_A	101591393	101948113	rs80173192	A	G	0.0112	-0.0086	0.9914	0.9998

7	7_101842782_A_G	101842782	102199502	rs1297632	G	A	0.9537	0.0055	1.0055	1.0105
7	7_102085389_T_C	102085389	102444942	rs11983129	C	T	0.0725	0.0139	1.0140	1.0020
7	7_102088402_A_G	102088402	102447955	rs6465864	G	A	0.9090	-0.0094	0.9906	0.9831
7	7_102481842_T_C	102481842	102841395	rs7800548	C	T	0.3416	0.0095	1.0095	1.0065
7	7_102607417_G_T	102607417	102966970	rs140632113	T	G	0.0414	0.0137	1.0138	1.0011
7	7_102891784_T_C	102891784	103251337	rs6946892	C	T	0.7472	-0.0083	0.9917	0.9877
7	7_103057977_CT_C	103057977	103417530	7:103057977 - CT_C	C	CT	0.0592	0.0078	1.0078	1.0009
7	7_103451091_A_G	103451091	103810644	rs39332	G	A	0.2259	0.0051	1.0051	1.0023
7	7_106148554_C_A	106148554	106508108	rs75292889	A	C	0.0843	0.0015	1.0015	1.0003
7	7_106715221_C_T	106715221	107074776	rs12669339	T	C	0.4433	0.0044	1.0044	1.0039
7	7_107160253_C_T	107160253	107519808	rs2520253	T	C	0.4695	-0.0088	0.9912	0.9918
7	7_109304110_C_A	109304110	109664053	rs3915078	A	C	0.2788	-0.0019	0.9981	0.9989
7	7_109326883_G_G	109326883	109686826	rs572979797	GA	G	0.3436	-0.0012	0.9988	0.9992
7	7_109373934_A_T	109373934	109733877	rs79862777	T	A	0.3770	0.0000	1.0000	1.0000
7	7_114352862_C_T	114352862	114712807	rs776472	T	C	0.5775	0.0072	1.0072	1.0084
7	7_121950965_A_G	121950965	122310911	rs7779018	G	A	0.4174	-0.0018	0.9982	0.9985
7	7_126090509_C_T	126090509	126450455	rs13247338	T	C	0.1403	-0.0140	0.9861	0.9961
7	7_129217706_C_T	129217706	129577865	rs12673568	T	C	0.5471	0.0000	1.0000	1.0000
7	7_130432913_A_A	130432913	130748154	rs553015785	AT	A	0.4731	0.0102	1.0103	1.0097
7	7_130607688_C_T	130607688	130922929	rs73161912	T	C	0.2992	-0.0010	0.9990	0.9994
7	7_130627014_G_T	130627014	130942255	rs12533596	T	G	0.2236	-0.0067	0.9933	0.9970
7	7_130656911_C_T	130656911	130972152	rs12706954	T	C	0.3734	-0.0045	0.9955	0.9966
7	7_130657509_C_G	130657509	130972750	rs205733	G	C	0.5361	0.0087	1.0087	1.0094
7	7_130666992_C_C	130666992	130982233	rs5887486	CA	C	0.3634	-0.0019	0.9981	0.9986

7	7_130667258_G_A	130667258	130982499	rs4141794	A	G	0.3684	-0.0062	0.9938	0.9955
7	7_130667323_A_C	130667323	130982564	rs205752	C	A	0.5683	0.0025	1.0025	1.0028
7	7_130668383_T_C	130668383	130983624	rs6973318	C	T	0.6341	0.0012	1.0012	1.0015
7	7_130674481_G_A	130674481	130989722	rs68056147	A	G	0.2971	0.0101	1.0102	1.0060
7	7_130688577_G_A	130688577	131003818	rs983173	A	G	0.5633	-0.0086	0.9914	0.9904
7	7_130984689_G_A	130984689	131299930	rs7812294	A	G	0.1644	-0.0029	0.9971	0.9990
7	7_131009008_G_C	131009008	131324249	rs10233294	C	G	0.0526	-0.0231	0.9772	0.9976
7	7_131349841_AT_A	131349841	131665082	7:131349841_AT_A	A	AT	0.6715	-0.0062	0.9938	0.9917
7	7_135015546_C_T	135015546	135330794	rs12532231	T	C	0.1995	0.0007	1.0007	1.0003
7	7_135358202_A_G	135358202	135673454	rs79580568	G	A	0.1280	-0.0181	0.9821	0.9954
7	7_135843296_C_T	135843296	136158548	rs55875516	T	C	0.2567	0.0077	1.0077	1.0040
7	7_135853583_G_A	135853583	136168835	rs756421	A	G	0.4022	0.0028	1.0028	1.0023
7	7_139835660_C_T	139835660	140135860	rs79485117	T	C	0.0882	-0.0181	0.9821	0.9968
7	7_139943702_CT_C	139943702	140243902	rs201664599	C	CT	0.5381	0.0167	1.0168	1.0182
7	7_139943889_A_G	139943889	140244089	rs2003526	G	A	0.5509	0.0000	1.0000	1.0000
7	7_139946053_A_G	139946053	140246253	rs13225058	G	A	0.3330	0.0099	1.0099	1.0066
7	7_139950193_A_A	139950193	140250393	rs71170962	AT	A	0.2221	0.0048	1.0048	1.0021
7	7_139954640_C_A	139954640	140254840	rs12703654	A	C	0.4571	0.0046	1.0046	1.0042
7	7_142355935_A_C	142355935	142648438	rs2226970	C	A	0.3990	-0.0053	0.9947	0.9958
7	7_144048902_G_T	144048902	144351809	rs62485509	T	G	0.2284	-0.0219	0.9783	0.9901
7	7_144074929_G_A	144074929	144377836	rs720475	A	G	0.2520	0.0000	1.0000	1.0000
7	7_144079218_G_A	144079218	144382125	rs1635083	A	G	0.8585	-0.0019	0.9981	0.9967
7	7_144149298_A_G	144149298	144452205	rs117837628	G	A	0.0158	-0.0158	0.9843	0.9995
7	7_144331267_G_A	144331267	144634174	rs78749260	A	G	0.0206	0.0048	1.0048	1.0002
7	7_144906844_G_A	144906844	145209751	rs7791708	A	G	0.6742	-0.0066	0.9934	0.9911

7	7_148739428_A_G	148739428	149042336	rs10808055	G	A	0.9370	-0.0097	0.9903	0.9820
7	7_150121933_G_A	150121933	150424845	rs10268592	A	G	0.7453	-0.0057	0.9943	0.9915
7	7_150542611_A_A T	150542611	150845523	rs150149364	AT	A	0.1198	-0.0035	0.9965	0.9992
7	7_150542646_G_A	150542646	150845558	rs6977381	A	G	0.5538	-0.0022	0.9978	0.9976
7	7_150542711_G_A	150542711	150845623	rs6977416	A	G	0.3542	-0.0035	0.9965	0.9975
7	7_151092104_CTG C	151092104	151395018	rs754370996	C	CTG	0.6263	-0.0002	0.9998	0.9997
7	7_151092578_A_A GG	151092578	151395492	rs200990584	AGG	A	0.7033	-0.0015	0.9985	0.9979
7	7_151538608_G_T	151538608	151841522	rs62638844	T	G	0.7029	-0.0069	0.9931	0.9904
7	7_152174826_G_C	152174826	152477741	rs11765960	C	G	0.6782	0.0057	1.0057	1.0078
7	7_152336554_A_A AAAT	152336554	152639469	rs372925374	AAAAT	A	0.6708	0.0041	1.0041	1.0055
7	7_152676742_TA_T	152676742	152979657	7:152676742_ TA_T	T	TA	0.0247	0.0226	1.0229	1.0011
7	7_152697402_T_A	152697402	153000317	rs114108757	A	T	0.0454	0.0019	1.0019	1.0002
7	7_154995361_G_A	154995361	155203651	rs114735553	A	G	0.0430	0.0235	1.0238	1.0020
7	7_155527763_T_C	155527763	155735069	rs61071575	C	T	0.0470	-0.0156	0.9845	0.9985
7	7_155734665_A_G	155734665	155941971	rs4716944	G	A	0.5497	-0.0083	0.9917	0.9909
7	7_155737385_C_T	155737385	155944691	rs12698353	T	C	0.4532	-0.0007	0.9993	0.9994
7	7_155740535_T_A	155740535	155947841	rs11764203	A	T	0.4545	-0.0004	0.9996	0.9996
8	8_156768_G_A	156768	206768	rs10086982	A	G	0.2619	0.0000	1.0000	1.0000
8	8_163366_T_C	163366	213366	rs34810249	C	T	0.2384	0.0065	1.0065	1.0031
8	8_174546_G_A	174546	224546	rs2906324	A	G	0.2294	0.0000	1.0000	1.0000
8	8_182807_A_G	182807	232807	rs2286137	G	A	0.3447	0.0080	1.0080	1.0055
8	8_185668_C_T	185668	235668	rs10093989	T	C	0.1778	0.0000	1.0000	1.0000
8	8_235700_C_T	235700	285700	rs6558572	T	C	0.3152	0.0087	1.0087	1.0055

8	8_1169041_C_T	1169041	1219041	rs147988121	T	C	0.0123	-0.0305	0.9700	0.9993
8	8_4140685_G_T	4140685	4283163	rs2680602	T	G	0.0465	0.0020	1.0020	1.0002
8	8_4261060_A_T	4261060	4403538	rs13267484	T	A	0.2565	0.0018	1.0018	1.0009
8	8_4293754_A_G	4293754	4436232	rs73178944	G	A	0.0793	0.0224	1.0227	1.0036
8	8_5422803_G_T	5422803	5565281	rs7015839	T	G	0.0109	-0.0466	0.9545	0.9990
8	8_5645808_C_G	5645808	5788286	rs7463406	G	C	0.7231	-0.0047	0.9953	0.9932
8	8_5683118_G_A	5683118	5825596	rs12678253	A	G	0.3175	0.0085	1.0085	1.0054
8	8_5973923_A_G	5973923	6116401	rs11786309	G	A	0.0186	0.0321	1.0326	1.0012
8	8_6743729_G_C	6743729	6886207	rs10110272	C	G	0.0970	-0.0200	0.9802	0.9962
8	8_8270294_T_G	8270294	8412784	rs6601697	G	T	0.6394	-0.0097	0.9903	0.9877
8	8_8287139_G_A	8287139	8429629	rs73496865	A	G	0.5280	-0.0016	0.9984	0.9983
8	8_10445702_G_A	10445702	10588192	rs12543042	A	G	0.1970	-0.0025	0.9975	0.9990
8	8_10465942_T_A	10465942	10608432	rs28446662	A	T	0.2215	-0.0071	0.9929	0.9969
8	8_11094473_C_T	11094473	11236964	rs11250124	T	C	0.0110	-0.0206	0.9796	0.9996
8	8_11368283_CAAA T_C	11368283	11510774	8:11368283_C AAAT_C	C	CAAAT	0.5945	-0.0020	0.9980	0.9976
8	8_11485820_C_T	11485820	11628311	rs7837995	T	C	0.4589	-0.0068	0.9932	0.9938
8	8_11495497_T_A	11495497	11637988		A	T	0.4038	-0.0020	0.9980	0.9984
8	8_13687830_G_A	13687830	13830321	rs10283191	A	G	0.2909	0.0037	1.0037	1.0022
8	8_15657837_G_C	15657837	15800328	rs2604384	C	G	0.4819	-0.0042	0.9958	0.9960
8	8_16080739_T_C	16080739	16223230	rs7819754	C	T	0.7365	0.0006	1.0006	1.0009
8	8_16087631_C_T	16087631	16230122	rs10101109	T	C	0.6993	0.0052	1.0052	1.0073
8	8_16087729_G_A	16087729	16230220	rs10100384	A	G	0.6307	0.0008	1.0008	1.0010
8	8_16125987_T_C	16125987	16268478	rs1480147	C	T	0.3135	-0.0032	0.9968	0.9980
8	8_16418358_T_C	16418358	16560849	rs17123231	C	T	0.0562	0.0143	1.0144	1.0016
8	8_16418370_A_G	16418370	16560861	rs10094727	G	A	0.9161	-0.0021	0.9979	0.9962
8	8_17051352_C_T	17051352	17193843	rs36026940	T	C	0.0681	0.0004	1.0004	1.0001

8	8_17083095_T_C	17083095	17225586	rs73198600	C	T	0.0525	-0.0076	0.9924	0.9992
8	8_17531802_T_G	17531802	17674293	rs28679501	G	T	0.6962	0.0042	1.0042	1.0059
8	8_17787610_CT_C	17787610	17930101	8:17787610_C T_C	C	CT	0.6230	-0.0091	0.9909	0.9887
8	8_17848555_AT_A	17848555	17991046		ATT	AT	0.1317	0.0026	1.0026	1.0007
8	8_17872760_T_TA	17872760	18015251		TA	T	0.6157	-0.0014	0.9986	0.9983
8	8_18056532_C_CT	18056532	18199023	rs35361039	CT	C	0.0413	0.0153	1.0154	1.0013
8	8_19685909_G_T	19685909	19828398	rs7017697	T	G	0.6686	-0.0029	0.9971	0.9961
8	8_21760026_A_G	21760026	21902515	rs7017582	G	A	0.8838	0.0076	1.0076	1.0135
8	8_21773384_C_T	21773384	21915873	rs11783414	T	C	0.5060	-0.0026	0.9974	0.9974
8	8_23024091_A_G	23024091	23166578	rs111135706	G	A	0.6959	-0.0099	0.9901	0.9863
8	8_23377604_A_C	23377604	23520091	rs36104352	C	A	0.1114	-0.0113	0.9888	0.9975
8	8_23447496_A_G	23447496	23589983	rs1028016	G	A	0.6487	-0.0038	0.9962	0.9951
8	8_23465063_C_A	23465063	23607550	rs13264439	A	C	0.4385	-0.0095	0.9905	0.9917
8	8_23654713_G_A	23654713	23797200	rs182563	A	G	0.3615	0.0000	1.0000	1.0000
8	8_23663653_C_A	23663653	23806140	rs310295	A	C	0.4032	0.0031	1.0031	1.0025
8	8_23668492_T_TTA	23668492	23810979	rs141496299	TTA	T	0.3131	0.0098	1.0098	1.0062
8	8_25399102_C_T	25399102	25541586	rs7387502	T	C	0.2489	-0.0160	0.9841	0.9921
8	8_25831778_C_T	25831778	25974262	rs13256025	T	C	0.2047	0.0035	1.0035	1.0014
8	8_25936499_A_G	25936499	26078983	rs138748843	G	A	0.0224	0.0199	1.0201	1.0009
8	8_27424542_CAAA AAA_C	27424542	27567025	rs758758659	C	CAAAAA A	0.2934	-0.0008	0.9992	0.9995
8	8_27425564_T_TA	27425564	27568047	rs554790141	TA	T	0.3320	-0.0006	0.9994	0.9996
8	8_27475320_T_G	27475320	27617803	rs504038	G	T	0.6103	-0.0031	0.9969	0.9962
8	8_28612960_T_C	28612960	28755443	rs73235028	C	T	0.0531	0.0000	1.0000	1.0000
8	8_29416526_T_G	29416526	29559009	rs6986919	G	T	0.7546	0.0038	1.0038	1.0058

8	8_29502631_G_A	29502631	29645115	rs12680857	A	G	0.5874	-0.0090	0.9910	0.9895
8	8_29509616_A_C	29509616	29652100	rs9693444	C	A	0.6756	-0.0321	0.9684	0.9578
8	8_29520078_G_T	29520078	29662562	rs6981127	T	G	0.6470	-0.0003	0.9997	0.9996
8	8_29735604_C_T	29735604	29878088	rs16876096	T	C	0.1654	0.0091	1.0091	1.0030
8	8_30165116_T_C	30165116	30307600	rs10097469	C	T	0.0814	-0.0117	0.9884	0.9981
8	8_30210274_T_C	30210274	30352758	rs4349946	C	T	0.6697	-0.0096	0.9904	0.9872
8	8_31842475_C_T	31842475	31984959	rs13255716	T	C	0.6789	0.0079	1.0079	1.0108
8	8_32015145_G_A	32015145	32157629	rs1994058	A	G	0.8913	-0.0179	0.9823	0.9686
8	8_34123592_C_T	34123592	34266074	rs7840552	T	C	0.0198	-0.0188	0.9814	0.9993
8	8_34297670_A_T	34297670	34440152	rs558139335	T	A	0.0250	-0.0235	0.9768	0.9988
8	8_34955466_G_C	34955466	35097948	rs17337391	C	G	0.0257	-0.0015	0.9985	0.9999
8	8_36829456_C_CT AAA	36829456	36971938	rs61146997	CTAAA	C	0.2043	0.0000	1.0000	1.0000
8	8_36858483_A_G	36858483	37000965	rs13365225	G	A	0.1820	-0.0504	0.9508	0.9822
8	8_38565629_T_C	38565629	38708111	rs10481324	C	T	0.3509	0.0074	1.0074	1.0052
8	8_39609628_T_C	39609628	39752109	rs151305136	C	T	0.0217	-0.0396	0.9612	0.9983
8	8_39923349_C_A	39923349	40065830	rs116220892	A	C	0.0161	-0.0258	0.9745	0.9992
8	8_40179383_C_T	40179383	40321864	rs4146443	T	C	0.3020	0.0053	1.0053	1.0032
8	8_42637683_A_C	42637683	42782540	rs7825261	C	A	0.1982	-0.0077	0.9923	0.9970
8	8_51573102_AG_A	51573102	50660542	rs763199418	A	AG	0.2025	0.0053	1.0053	1.0022
8	8_51743692_GTT_ GT	51743692	50831132		GT	GTT	0.1943	0.0069	1.0069	1.0027
8	8_51788340_G_GA AACAAAC	51788340	50875780		GAAACAA AC	G	0.1918	0.0040	1.0040	1.0015
8	8_51983919_C_T	51983919	51071359	rs7824633	T	C	0.1133	0.0000	1.0000	1.0000
8	8_58757924_T_C	58757924	57845365	rs2217891	C	T	0.3577	0.0056	1.0056	1.0040
8	8_62103694_C_T	62103694	61191135	rs145226881	T	C	0.0235	-0.0243	0.9760	0.9989

8	8_65248253_T_G	65248253	64335696	rs7824601	G	T	0.2946	-0.0050	0.9950	0.9971
8	8_69403589_C_G	69403589	68491354	rs55775457	G	C	0.0283	-0.0308	0.9697	0.9983
8	8_69688844_G_A	69688844	68776609	rs7833861	A	G	0.4535	-0.0017	0.9983	0.9985
8	8_74645139_C_T	74645139	73732904	rs77875439	T	C	0.1292	-0.0048	0.9952	0.9988
8	8_75857876_G_C	75857876	74945641	rs11786917	C	G	0.3156	0.0001	1.0001	1.0001
8	8_76230943_A_G	76230943	75318708	rs1511243	G	A	0.8282	0.0549	1.0564	1.0957
8	8_76297613_C_A	76297613	75385378	rs66854431	A	C	0.0960	0.0093	1.0093	1.0018
8	8_76315325_C_T	76315325	75403090	rs72658076	T	C	0.2185	0.0028	1.0028	1.0012
8	8_76317377_G_A	76317377	75405142	rs2980236	A	G	0.5427	0.0000	1.0000	1.0000
8	8_76330610_G_A	76330610	75418375	rs6993283	A	G	0.2790	0.0000	1.0000	1.0000
8	8_76333056_C_T	76333056	75420821	rs72658084	T	C	0.0878	0.0577	1.0594	1.0105
8	8_76356580_T_A	76356580	75444345	rs830787	A	T	0.5301	-0.0072	0.9928	0.9924
8	8_76373469_C_T	76373469	75461234	rs2672860	T	C	0.3348	-0.0010	0.9990	0.9993
8	8_76416112_C_T	76416112	75503877	rs2926589	T	C	0.0603	0.0097	1.0097	1.0012
8	8_76419496_CT_C	76419496	75507261	rs763756695	C	CT	0.3757	-0.0155	0.9846	0.9885
8	8_76442665_T_TA	76442665	75530430	rs34475936	TA	T	0.4106	-0.0004	0.9996	0.9997
8	8_76475304_T_C	76475304	75563069	rs2941476	C	T	0.1916	-0.0043	0.9957	0.9984
8	8_76502796_A_G	76502796	75590561	rs2977973	G	A	0.1160	0.0021	1.0021	1.0005
8	8_76538833_G_A	76538833	75626598	rs200255906	A	G	0.0819	0.0076	1.0076	1.0013
8	8_76900329_T_A	76900329	75988094	rs12682248	A	T	0.7404	0.0003	1.0003	1.0004
8	8_76910809_A_G	76910809	75998574	rs62517886	G	A	0.0617	-0.0078	0.9922	0.9990
8	8_77222075_C_G	77222075	76309840	rs7461846	G	C	0.4219	-0.0004	0.9996	0.9997
8	8_77920482_G_A	77920482	77008246	rs7843788	A	G	0.5692	-0.0102	0.9899	0.9885
8	8_78194627_C_CA ATGATAAAT	78194627	77282391	rs5892590	CAATGAT AAAT	C	0.7218	-0.0063	0.9937	0.9910
8	8_81359895_G_T	81359895	80447660	rs10095089	T	G	0.1766	0.0118	1.0119	1.0042

8	8_81407157_CAAA	81407157	80494922	8:81407157_C AAA_C	C	CAAA	0.2504	0.0000	1.0000	1.0000
8	8_81543123_A_T	81543123	80630888	rs7833340	T	A	0.0686	-0.0218	0.9784	0.9970
8	8_81738475_G_C	81738475	80826240	rs13272724	C	G	0.2257	0.0011	1.0011	1.0005
8	8_81846059_C_A	81846059	80933824	rs4739773	A	C	0.6759	-0.0089	0.9911	0.9881
8	8_82226077_G_A	82226077	81313842	rs74696448	A	G	0.0508	0.0024	1.0024	1.0002
8	8_87932278_A_G	87932278	86920050	rs144776497	G	A	0.0163	0.0028	1.0028	1.0001
8	8_87933880_C_T	87933880	86921652	rs7387763	T	C	0.3788	-0.0023	0.9977	0.9983
8	8_87953354_G_A	87953354	86941126	rs13248262	A	G	0.5093	0.0057	1.0057	1.0058
8	8_94438986_C_T	94438986	93426758	rs117879122	T	C	0.0289	-0.0128	0.9873	0.9993
8	8_95847833_C_CT	95847833	94835605	rs543122431	CT	C	0.2380	-0.0068	0.9932	0.9968
8	8_95909498_T_C	95909498	94897270	rs16917117	C	T	0.1841	-0.0052	0.9948	0.9981
8	8_96024387_T_A	96024387	95012159	rs62523112	A	T	0.0529	0.0122	1.0123	1.0013
8	8_99022175_C_T	99022175	98009947	rs117612714	T	C	0.0415	-0.0185	0.9817	0.9985
8	8_99411087_T_C	99411087	98398859	rs9297284	C	T	0.1745	-0.0206	0.9796	0.9929
8	8_99545465_C_T	99545465	98533237	rs13270534	T	C	0.3658	-0.0021	0.9979	0.9985
8	8_99553840_A_T	99553840	98541612	rs10108828	T	A	0.4334	-0.0002	0.9998	0.9998
8	8_99943768_C_T	99943768	98931540	rs111593659	T	C	0.0110	0.0327	1.0332	1.0007
8	8_101225241_CCC GCGGCCT_CCCGG GCTCCGCGCCT	101225241	100213013		CCCGGG CCTCCGC GGCCT	CCCGGG GCCT	0.5168	0.0042	1.0042	1.0044
8	8_101394894_G_A	101394894	100382666	rs17424879	A	G	0.0572	0.0095	1.0095	1.0011
8	8_102410989_A_C	102410989	101398761	rs62516992	C	A	0.1356	0.0000	1.0000	1.0000
8	8_102475114_G_A	102475114	101462886	rs1264590	A	G	0.7583	-0.0071	0.9929	0.9893
8	8_102482149_C_T	102482149	101469921	rs16867729	T	C	0.0256	0.0232	1.0235	1.0012
8	8_102483100_T_C	102483100	101470872	rs62517052	C	T	0.0967	0.0062	1.0062	1.0012
8	8_102499101_T_C	102499101	101486873	rs509357	C	T	0.6749	-0.0023	0.9977	0.9969

8	8_102502448_A_G	102502448	101490220	rs570630	G	A	0.2694	0.0009	1.0009	1.0005
8	8_102636399_TCA CAGTA_T	102636399	101624171	8:102636399_ TCACAGTA_T	T	TCACAG TA	0.0282	-0.0002	0.9998	1.0000
8	8_103750362_A_T	103750362	102738134	rs62524036	T	A	0.0887	-0.0044	0.9956	0.9992
8	8_104278384_T_C	104278384	103266156	rs80346003	C	T	0.1214	0.0065	1.0065	1.0016
8	8_106310917_C_T	106310917	105298689	rs62525396	T	C	0.2612	0.0000	1.0000	1.0000
8	8_106321126_G_C	106321126	105308898	rs74339976	C	G	0.5092	0.0031	1.0031	1.0032
8	8_106340292_T_C	106340292	105328064	rs41324545	C	T	0.2417	0.0057	1.0057	1.0028
8	8_106349980_G_G	106349980	105337752	rs5893739	GT	G	0.6510	0.0000	1.0000	1.0000
8	8_106358620_A_T	106358620	105346392	rs12546444	T	A	0.1003	-0.0263	0.9740	0.9948
8	8_106385049_A_G	106385049	105372821	rs17283482	G	A	0.1628	0.0000	1.0000	1.0000
8	8_106393022_TTA_ T	106393022	105380794	8:106393022_ TTA_T	T	TTA	0.5416	0.0043	1.0043	1.0047
8	8_107067404_CT_C TT	107067404	106055176	rs768648054	CTT	CT	0.2454	0.0115	1.0116	1.0057
8	8_107075960_A_G	107075960	106063732	rs1540419	G	A	0.2578	0.0055	1.0055	1.0028
8	8_110884805_CTCT T_C	110884805	109872576	8:110884805_ CTCTT_C	C	CTCTT	0.0248	-0.0308	0.9697	0.9985
8	8_111297253_TA_T	111297253	110285024	8:111297253_ TA_T	T	TA	0.6847	0.0043	1.0043	1.0059
8	8_113683162_C_T	113683162	112670933	rs6469434	T	C	0.1969	-0.0047	0.9953	0.9982
8	8_115343864_CAT ATAG_CATATAGAT ATAG	115343864	114331635	rs149695242	CATATAG ATATAG	CATATA G	0.1716	-0.0051	0.9949	0.9983
8	8_116679547_A_G	116679547	115667320	rs13277568	G	A	0.3695	-0.0095	0.9905	0.9930
8	8_116934978_G_C	116934978	115922753	rs6996098	C	G	0.8369	0.0029	1.0029	1.0049
8	8_117016733_CAA	117016733	116004508	rs751476560	C	CAAA	0.5897	0.0000	1.0000	1.0000

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8	8_124757130_A_G	124757130	123744890	rs10105069	G	A	0.8856	0.0000	1.0000	1.0000
8	8_124757661_C_T	124757661	123745421	rs17350191	T	C	0.3338	0.0093	1.0093	1.0062
8	8_125586636_A_G	125586636	124574395	rs4286935	G	A	0.1429	-0.0057	0.9943	0.9984
8	8_125599071_T_C	125599071	124586830	rs17372817	C	T	0.1240	-0.0154	0.9847	0.9962
8	8_127923940_A_G	127923940	126911695	rs71520605	G	A	0.0252	0.0028	1.0028	1.0001
8	8_128208454_G_A	128208454	127196209	rs7819779	A	G	0.2785	-0.0053	0.9947	0.9971
8	8_128213561_C_C	128213561	127201316	rs35961416	CA	C	0.4153	-0.0187	0.9815	0.9847
8	8_128260769_TTTT A_T	128260769	127248524	rs759883143	T	TTTTA	0.0149	0.0244	1.0247	1.0007
8	8_128305596_G_C	128305596	127293351	rs283717	C	G	0.1521	0.0005	1.0005	1.0002
8	8_128336236_A_G	128336236	127323991	rs11775799	G	A	0.4302	-0.0053	0.9947	0.9955
8	8_128351442_A_C	128351442	127339197	rs56898669	C	A	0.3949	0.0000	1.0000	1.0000
8	8_128352730_C_T	128352730	127340485	rs10087810	T	C	0.5744	0.0000	1.0000	1.0000
8	8_128355940_G_A	128355940	127343694	rs76102714	A	G	0.5324	0.0000	1.0000	1.0000
8	8_128366477_G_G AA	128366477	127354231	rs71566627	GAA	G	0.3242	-0.0179	0.9823	0.9885
8	8_128368513_C_T	128368513	127356267	rs9693995	T	C	0.5615	-0.0046	0.9954	0.9949
8	8_128370949_C_G	128370949	127358703	rs12550713	G	C	0.4020	0.0421	1.0430	1.0349
8	8_128372172_A_G	128372172	127359926	rs10096351	G	A	0.5446	0.0123	1.0124	1.0135
8	8_128378025_C_T	128378025	127365779	rs9693143	T	C	0.4257	-0.0171	0.9830	0.9856
8	8_128383415_C_T	128383415	127371169	rs117952826	T	C	0.0266	0.0142	1.0143	1.0008
8	8_128386556_A_G	128386556	127374310	rs2121631	G	A	0.7179	0.0000	1.0000	1.0000
8	8_128391537_G_C	128391537	127379292	rs750816	C	G	0.1974	0.0000	1.0000	1.0000
8	8_128399222_GA_ G	128399222	127386977		G	GA	0.1850	0.0000	1.0000	1.0000
8	8_128595821_G_C	128595821	127583576	rs76671734	C	G	0.1734	-0.0072	0.9928	0.9975
8	8_128638040_A_G	128638040	127625795	rs62515760	G	A	0.0584	0.0032	1.0032	1.0004

8	8_128689325_T_C	128689325	127677080	rs7833090	C	T	0.2555	-0.0164	0.9837	0.9917
8	8_129170126_C_G	129170126	128157880	rs2608029	G	C	0.3372	0.0000	1.0000	1.0000
8	8_129184555_G_A	129184555	128172309	rs12542202	A	G	0.1571	0.0183	1.0185	1.0058
8	8_129191563_A_TTTT	129191563	128179317	rs149396369	A	ATTTT TT	0.5278	0.0000	1.0000	1.0000
8	8_129204262_T_C	129204262	128192016	rs7017073	C	T	0.2155	0.0134	1.0135	1.0058
8	8_129205103_G_A	129205103	128192857	rs72722767	A	G	0.2977	0.0054	1.0054	1.0032
8	8_129229645_A_G	129229645	128217399	rs7829149	G	A	0.3107	0.0000	1.0000	1.0000
8	8_129489903_C_CT	129489903	128477657	rs34358875	CTT	C	0.8614	-0.0144	0.9857	0.9755
8	8_131968469_T_C	131968469	130956223	rs6988340	C	T	0.9270	-0.0195	0.9807	0.9645
8	8_132006257_A_C	132006257	130994011	rs12676386	C	A	0.0246	0.0183	1.0185	1.0009
8	8_132124207_G_A	132124207	131111960	rs78580956	A	G	0.0449	0.0022	1.0022	1.0002
8	8_134224717_C_T	134224717	133212474	rs7824539	T	C	0.1015	0.0000	1.0000	1.0000
8	8_134393849_C_T	134393849	133381606	rs117057283	T	C	0.0123	0.0201	1.0203	1.0005
8	8_134415857_C_T	134415857	133403614	rs79792639	T	C	0.0482	0.0044	1.0044	1.0004
8	8_135117638_TTG_T	135117638	134105395	8:135117638_ TTG_T	T	TTG	0.4317	-0.0114	0.9887	0.9902
8	8_135551130_G_A	135551130	134538887		AA	G	0.4066	-0.0037	0.9963	0.9970
8	8_139234794_T_C	139234794	138222551	rs78827478	C	T	0.1290	0.0002	1.0002	1.0001
8	8_139236107_C_A	139236107	138223864	rs60498507	A	C	0.1119	0.0172	1.0173	1.0039
8	8_140464740_T_A	140464740	139452497	rs2447563	A	T	0.9010	0.0154	1.0155	1.0282
8	8_140990881_G_A	140990881	139980672	rs13279341	A	G	0.1398	-0.0095	0.9905	0.9974
8	8_143669254_A_G	143669254	142587893	rs7830152	G	A	0.3390	-0.0141	0.9860	0.9905
8	8_143670711_GGT GT_G	143670711	142589350	8:143670711_ GGTGT_G	G	GGTGT	0.2001	-0.0088	0.9912	0.9965
8	8_144750677_T_C	144750677	143668507	rs117423761	C	T	0.0256	0.0122	1.0123	1.0006

9	9_1035756_A_AAA AAAC	1035756	1035756	rs150549203	AAAAAAC	A	0.1705	0.0038	1.0038	1.0013
9	9_1696976_T_C	1696976	1696976	rs7039610	C	T	0.3452	-0.0014	0.9986	0.9990
9	9_2124140_C_T	2124140	2124140	rs10811481	T	C	0.1416	0.0047	1.0047	1.0013
9	9_4094321_G_A	4094321	4094321	rs564275	A	G	0.5667	0.0042	1.0042	1.0048
9	9_4167470_G_C	4167470	4167470	rs10758562	C	G	0.2643	0.0092	1.0092	1.0049
9	9_5595577_C_G	5595577	5595577	rs117152319	G	C	0.0159	0.0165	1.0166	1.0005
9	9_5917799_G_A	5917799	5917799	rs10815309	A	G	0.1987	0.0027	1.0027	1.0011
9	9_6002135_T_C	6002135	6002135	rs10815338	C	T	0.2149	0.0046	1.0046	1.0020
9	9_6135481_T_C	6135481	6135481	rs113396459	C	T	0.0187	-0.0238	0.9765	0.9991
9	9_6185360_T_C	6185360	6185360	rs13291323	C	T	0.0586	0.0046	1.0046	1.0005
9	9_6445966_TC_T	6445966	6445966	rs144889864	T	TC	0.4814	0.0069	1.0069	1.0067
9	9_6867766_T_C	6867766	6867766	rs12002100	C	T	0.2785	0.0000	1.0000	1.0000
9	9_6880263_A_G	6880263	6880263	rs10975870	G	A	0.2855	0.0117	1.0118	1.0067
9	9_8147463_A_G	8147463	8147463	rs73640585	G	A	0.1313	-0.0123	0.9878	0.9968
9	9_8287456_G_C	8287456	8287456	rs141167506	C	G	0.0118	-0.0200	0.9802	0.9995
9	9_8415317_T_C	8415317	8415317	rs61454491	C	T	0.0290	0.0368	1.0375	1.0022
9	9_8545593_G_A	8545593	8545593	rs76007978	A	G	0.0126	-0.0595	0.9422	0.9985
9	9_9017452_G_A	9017452	9017452	rs140019155	A	G	0.0413	-0.0006	0.9994	1.0000
9	9_10270636_A_G	10270636	10270636	rs1322155	G	A	0.6771	-0.0066	0.9934	0.9911
9	9_11896699_A_G	11896699	11896699	rs12553199	G	A	0.0297	0.0078	1.0078	1.0005
9	9_12021101_A_G	12021101	12021101	rs75934379	G	A	0.0195	-0.0045	0.9955	0.9998
9	9_12141554_G_A	12141554	12141554	rs78752415	A	G	0.0169	-0.0400	0.9608	0.9987
9	9_13488564_C_G	13488564	13488564	rs7856695	G	C	0.4329	0.0004	1.0004	1.0003
9	9_13592493_A_T	13592493	13592493	rs5009186	T	A	0.7545	0.0049	1.0049	1.0074
9	9_13942940_G_A	13942940	13942940	rs77457752	A	G	0.1303	-0.0225	0.9778	0.9942
9	9_14021151_T_C	14021151	14021152	rs35473056	C	T	0.1442	0.0121	1.0122	1.0035

9	9_14021276_G_C	14021276	14021277	rs77875888	C	G	0.0658	-0.0002	0.9998	1.0000
9	9_15044787_C_T	15044787	15044789	rs72715698	T	C	0.0475	0.0065	1.0065	1.0006
9	9_16046463_A_G	16046463	16046465	rs3008694	G	A	0.2861	0.0132	1.0133	1.0076
9	9_16093549_G_T	16093549	16093551	rs62552203	T	G	0.1760	-0.0045	0.9955	0.9984
9	9_16337782_T_C	16337782	16337784	rs10962385	C	T	0.2976	0.0042	1.0042	1.0025
9	9_16838211_A_G	16838211	16838213	rs4995398	G	A	0.2828	-0.0010	0.9990	0.9994
9	9_16841628_A_G	16841628	16841630	rs10810643	G	A	0.2293	-0.0037	0.9963	0.9983
9	9_16844142_G_GT	16844142	16844144	rs5896709	GT	G	0.2208	-0.0117	0.9884	0.9949
9	9_18817372_C_T	18817372	18817374	rs7873880	T	C	0.6976	-0.0056	0.9944	0.9922
9	9_20812064_G_A	20812064	20812065	rs74354652	A	G	0.0152	-0.0385	0.9622	0.9989
9	9_21631421_A_G	21631421	21631422	rs117276645	G	A	0.0221	-0.0257	0.9746	0.9989
9	9_21950780_A_T	21950780	21950781	rs112109214	T	A	0.0237	-0.0011	0.9989	0.9999
9	9_21964882_CAAA A_C	21964882	21964883	rs745322029	C	CAAAA	0.3184	0.0281	1.0285	1.0182
9	9_22003223_C_T	22003223	22003224	rs3217992	T	C	0.3813	-0.0133	0.9868	0.9900
9	9_22005330_T_G	22005330	22005331	rs3217986	G	T	0.0813	0.0014	1.0014	1.0002
9	9_22011083_G_C	22011083	22011084	rs76959412	C	G	0.0166	0.0350	1.0356	1.0012
9	9_22041998_C_G	22041998	22041999	rs17694493	G	C	0.1393	0.0013	1.0013	1.0004
9	9_26040096_G_A	26040096	26040098	rs35323787	A	G	0.0464	0.0277	1.0281	1.0026
9	9_29638167_G_T	29638167	29638169	rs546929	T	G	0.0872	0.0033	1.0033	1.0006
9	9_29849357_G_C	29849357	29849359	rs115652823	C	G	0.0115	0.0004	1.0004	1.0000
9	9_32455674_A_G	32455674	32455676	rs1133071	G	A	0.3118	-0.0093	0.9907	0.9942
9	9_32523737_T_C	32523737	32523739	rs11795343	C	T	0.4051	0.0000	1.0000	1.0000
9	9_34108800_T_A	34108800	34108802	rs10738923	A	T	0.7218	-0.0020	0.9980	0.9971
9	9_34130435_G_A	34130435	34130437	rs61237993	A	G	0.1289	0.0023	1.0023	1.0006
9	9_36209082_G_A	36209082	36209085	rs62541769	A	G	0.0523	-0.0121	0.9880	0.9987
9	9_36921921_C_A	36921921	36921924	rs4880037	A	C	0.7525	0.0000	1.0000	1.0000

9	9_36928288_T_C	36928288	36928291	rs4880038	C	T	0.5349	0.0096	1.0096	1.0103
9	9_36931653_C_G	36931653	36931656	rs4369064	G	C	0.2502	-0.0006	0.9994	0.9997
9	9_36951035_A_G	36951035	36951038	rs10511936	G	A	0.2432	-0.0034	0.9966	0.9983
9	9_36974535_G_A	36974535	36974538	rs58210769	A	G	0.2266	-0.0040	0.9960	0.9982
9	9_71922028_C_T	71922028	69307112	rs117355427	T	C	0.0268	-0.0260	0.9743	0.9986
9	9_72519703_G_A	72519703	69904787	rs11140844	A	G	0.7393	0.0049	1.0049	1.0073
9	9_73394053_C_G	73394053	70779137	rs1328145	G	C	0.9425	-0.0082	0.9918	0.9847
9	9_73874330_G_A	73874330	71259414	rs149472628	A	G	0.0397	0.0080	1.0080	1.0006
9	9_73910400_A_G	73910400	71295484	rs72733896	G	A	0.0554	0.0139	1.0140	1.0016
9	9_74794895_G_T	74794895	72179979	rs10869141	T	G	0.2132	-0.0087	0.9913	0.9963
9	9_74910180_C_A	74910180	72295264	rs12238801	A	C	0.1740	0.0096	1.0096	1.0034
9	9_77752967_A_G	77752967	75138051	rs1009282	G	A	0.5733	0.0108	1.0109	1.0125
9	9_78308301_G_A	78308301	75693385	rs7032375	A	G	0.1046	0.0228	1.0231	1.0048
9	9_78910108_A_G	78910108	76295192	rs13283901	G	A	0.4401	-0.0021	0.9979	0.9982
9	9_78934242_A_T	78934242	76319326	rs56383794	T	A	0.1247	0.0026	1.0026	1.0006
9	9_78969417_C_T	78969417	76354501	rs72745133	T	C	0.2807	0.0005	1.0005	1.0003
9	9_78971232_G_A	78971232	76356316	rs10869765	A	G	0.5413	-0.0063	0.9937	0.9932
9	9_80148344_C_A	80148344	77533428	rs13287722	A	C	0.1472	-0.0005	0.9995	0.9999
9	9_80151268_T_G	80151268	77536352	rs10869939	G	T	0.2444	-0.0093	0.9907	0.9955
9	9_80716880_A_C	80716880	78101964	rs4877178	C	A	0.4793	-0.0040	0.9960	0.9962
9	9_82584696_GA_G	82584696	79969781	9:82584696_G_A_G	G	GA	0.0325	-0.0150	0.9851	0.9990
9	9_85950924_C_T	85950924	83336009	rs72618135	T	C	0.0923	0.0139	1.0140	1.0026
9	9_86065360_T_C	86065360	83450445	rs28719707	C	T	0.0807	-0.0011	0.9989	0.9998
9	9_87736422_G_A	87736422	85121507	rs11140866	A	G	0.4293	0.0033	1.0033	1.0028
9	9_87782211_T_C	87782211	85167296	rs665889	C	T	0.5094	0.0131	1.0132	1.0135
9	9_87889877_TC_T	87889877	85274962	9:87889877_T	T	TC	0.0302	0.0110	1.0111	1.0007

9	9_88011274_C_G	88011274	85396359	C_T	G	C	0.0875	0.0000	1.0000	1.0000
9	9_89438251_A_G	89438251	86823336	rs28657389	G	A	0.3477	0.0025	1.0025	1.0017
9	9_89440695_C_T	89440695	86825780	rs7847644	T	C	0.3995	0.0012	1.0012	1.0010
9	9_90274681_C_A	90274681	87659766	rs10868490	A	C	0.1114	0.0039	1.0039	1.0009
9	9_92263290_CAA_C	92263290	89648375	rs6560013	C	CAA	0.1546	-0.0092	0.9908	0.9972
9	9_92848755_A_G	92848755	90086473	9:92263290_C_AA_C	G	A	0.4743	0.0000	1.0000	1.0000
9	9_94229859_T_C	94229859	91467577	rs11792411	C	T	0.0148	0.0064	1.0064	1.0002
9	9_94260641_T_C	94260641	91498359	rs117362578	C	T	0.0149	0.0149	1.0150	1.0004
9	9_94260650_G_A	94260650	91498368	rs149668079	A	G	0.0447	0.0140	1.0141	1.0013
9	9_95751862_A_G	95751862	92989580	rs57587931	G	A	0.5401	-0.0043	0.9957	0.9954
9	9_97770605_C_A	97770605	95008323	rs4744162	A	C	0.0145	-0.0506	0.9507	0.9986
9	9_98022968_T_A	98022968	95260686	rs7862618	A	T	0.4322	0.0039	1.0039	1.0034
9	9_98329088_C_T	98329088	95566806	rs7021497	T	C	0.0853	0.0044	1.0044	1.0008
9	9_98362587_T_C	98362587	95600305	rs28675274	C	T	0.0940	0.0238	1.0241	1.0045
9	9_98474673_T_A	98474673	95712391	rs10120432	A	T	0.1234	0.0095	1.0095	1.0024
9	9_100806287_CTT_C	100806287	98044005	rs60806471	C	CTT	0.2575	0.0028	1.0028	1.0014
9	9_107013881_C_T	107013881	104251600	rs762895782	T	C	0.5306	-0.0046	0.9954	0.9951
9	9_107100197_G_G	107100197	104337916	rs4743702	GTT	G	0.0268	0.0248	1.0251	1.0013
9	9_107637306_A_G	107637306	104875025	rs59237458	G	A	0.4372	0.0000	1.0000	1.0000
9	9_107872109_C_G	107872109	105109828	rs55659643	G	C	0.0131	0.0032	1.0032	1.0001
9	9_107958636_C_G	107958636	105196355	rs327970	G	C	0.1796	0.0059	1.0059	1.0021
9	9_107979858_A_C	107979858	105217577	rs399707	C	A	0.1784	0.0036	1.0036	1.0013
9	9_110275369_T_C	110275369	107513088	rs149346572	C	T	0.0179	0.0175	1.0177	1.0006

9	9_110275852_A_T	110275852	107513571	rs10816524	T	A	0.0725	0.0227	1.0230	1.0033
9	9_110300994_A_G	110300994	107538713	rs4979065	G	A	0.4992	0.0034	1.0034	1.0034
9	9_110303463_A_G	110303463	107541182	rs2185857	G	A	0.2716	0.0005	1.0005	1.0003
9	9_110303808_TAA_T	110303808	107541527	9:110303808_TAA_T	T	TAA	0.2065	0.0461	1.0472	1.0196
9	9_110304319_A_T	110304319	107542038	rs3956	T	A	0.1044	0.0050	1.0050	1.0010
9	9_110305205_CT_C	110305205	107542924	9:110305205_CT_C	C	CT	0.2667	0.0000	1.0000	1.0000
9	9_110429664_A_G	110429664	107667383	rs77233150	G	A	0.0574	-0.0096	0.9904	0.9989
9	9_110458648_A_C	110458648	107696367	rs10123702	C	A	0.1482	-0.0082	0.9918	0.9976
9	9_110462837_G_A	110462837	107700556	rs4979255	A	G	0.1678	-0.0002	0.9998	0.9999
9	9_110479474_T_A	110479474	107717193	rs59221680	A	T	0.3645	-0.0027	0.9973	0.9980
9	9_110484484_T_C	110484484	107722203	rs11792761	C	T	0.2913	-0.0030	0.9970	0.9983
9	9_110484770_T_C	110484770	107722489	rs1962079	C	T	0.4170	-0.0032	0.9968	0.9973
9	9_110773040_C_T	110773040	108010759	rs60778117	T	C	0.1826	0.0000	1.0000	1.0000
9	9_110821050_C_T	110821050	108058769	rs10979183	T	C	0.4054	0.0058	1.0058	1.0047
9	9_110837073_A_G	110837073	108074792	rs10816625	G	A	0.0630	0.0720	1.0747	1.0094
9	9_110837176_C_T	110837176	108074895	rs13294895	T	C	0.1750	0.0368	1.0375	1.0132
9	9_110849525_G_T	110849525	108087244	rs7848334	T	G	0.5977	0.0067	1.0067	1.0081
9	9_110869006_A_A_TATAT	110869006	108106726	rs10644017	ATATAT	A	0.4163	0.0071	1.0071	1.0059
9	9_110882390_T_C	110882390	108120110	rs667052	C	T	0.4689	0.0000	1.0000	1.0000
9	9_110885479_C_T	110885479	108123199	rs630965	T	C	0.6222	0.0634	1.0655	1.0831
9	9_110902100_T_C	110902100	108139820	rs575270	C	T	0.5870	0.0021	1.0021	1.0025
9	9_110919211_C_T	110919211	108156931	rs189368445	T	C	0.0264	-0.0147	0.9854	0.9992
9	9_110920305_G_A	110920305	108158025	rs7850979	A	G	0.3122	0.0016	1.0016	1.0010
9	9_110921715_G_A	110921715	108159435	rs10119131	A	G	0.2387	0.0000	1.0000	1.0000

9	9_110925407_C_A	110925407	108163127	rs630611	A	C	0.6230	0.0000	1.0000	1.0000	1.0000
9	9_110988346_A_G	110988346	108226066	rs7043432	G	A	0.2052	0.0040	1.0040	1.0040	1.0016
9	9_111059697_T_C	111059697	108297417	rs55638805	C	T	0.1357	0.0012	1.0012	1.0012	1.0003
9	9_111329010_A_G	111329010	108566730	rs10125630	G	A	0.1935	0.0002	1.0002	1.0002	1.0001
9	9_111859015_C_T	111859015	109096735	rs142211233	T	C	0.0101	-0.0130	0.9871	0.9871	0.9997
9	9_111927669_C_T	111927669	109165389	rs62576372	T	C	0.0256	-0.0303	0.9702	0.9702	0.9985
9	9_112053123_T_C	112053123	109290843	rs55700539	C	T	0.1575	-0.0011	0.9989	0.9989	0.9997
9	9_112606832_A_G	112606832	109844552	rs11789107	G	A	0.1196	0.0032	1.0032	1.0032	1.0008
9	9_112607249_A_G	112607249	109844969	rs78904538	G	A	0.1643	0.0025	1.0025	1.0025	1.0008
9	9_114700288_G_A	114700288	111938008	rs79312461	A	G	0.0351	-0.0152	0.9849	0.9849	0.9989
9	9_114965309_C_CT	114965309	112203029	rs35116137	CT	C	0.4294	0.0012	1.0012	1.0012	1.0010
9	9_115202610_G_A	115202610	112440330	rs10123584	A	G	0.7014	0.0000	1.0000	1.0000	1.0000
9	9_115737007_G_A	115737007	112974727	rs12377906	A	G	0.2157	-0.0004	0.9996	0.9996	0.9998
9	9_115737606_A_T	115737606	112975326	rs4979199	T	A	0.2706	-0.0056	0.9944	0.9944	0.9970
9	9_116188725_G_T	116188725	113426445	rs7870912	T	G	0.1881	-0.0091	0.9909	0.9909	0.9966
9	9_117802247_T_A	117802247	115039968	rs10982505	A	T	0.0464	0.0043	1.0043	1.0043	1.0004
9	9_118408986_G_C	118408986	115646707	rs62575330	C	G	0.0759	0.0052	1.0052	1.0052	1.0008
9	9_119153708_C_T	119153708	116391429	rs74363364	T	C	0.0598	0.0002	1.0002	1.0002	1.0000
9	9_119254872_C_T	119254872	116492593	rs13296745	T	C	0.2291	-0.0023	0.9977	0.9977	0.9989
9	9_119308184_G_T	119308184	116545905	rs7029693	T	G	0.3643	-0.0078	0.9922	0.9922	0.9943
9	9_119313486_A_G	119313486	116551207	rs1895062	G	A	0.4087	-0.0145	0.9856	0.9856	0.9883
9	9_119487573_A_T	119487573	116725294	rs894206	T	A	0.2536	-0.0001	0.9999	0.9999	0.9999
9	9_119863594_C_A	119863594	117101315	rs79282494	A	C	0.2170	0.0000	1.0000	1.0000	1.0000
9	9_123311473_C_T	123311473	120549195	rs77565290	T	C	0.0651	0.0145	1.0146	1.0146	1.0019
9	9_123651703_CA_C	123651703	120889425	9:123651703_CA_C	C	CA	0.5931	-0.0052	0.9948	0.9948	0.9939
9	9_123896570_TA_T	123896570	121134292	rs200665428	T	TA	0.6521	-0.0083	0.9917	0.9917	0.9892

9	9_124330970_T_C	124330970	121568691	rs10985320	C	T	0.1644	0.0046	1.0046	1.0015
9	9_126741702_A_G	126741702	123979423	rs116991872	G	A	0.0178	0.0277	1.0281	1.0010
9	9_126837432_G_A	126837432	124075153	rs10986200	A	G	0.0603	0.0035	1.0035	1.0004
9	9_129346682_T_C	129346682	126584403	rs6478744	C	T	0.3584	-0.0002	0.9998	0.9999
9	9_129399562_A_G	129399562	126637283	rs62578132	G	A	0.0857	0.0013	1.0013	1.0002
9	9_129402567_G_A	129402567	126640288	rs12342373	A	G	0.0927	0.0026	1.0026	1.0005
9	9_129409062_C_A	129409062	126646783	rs4837102	A	C	0.0436	-0.0065	0.9935	0.9994
9	9_129424719_A_G	129424719	126662440	rs3861871	G	A	0.4577	-0.0157	0.9844	0.9858
9	9_129426469_G_T	129426469	126664190	rs10429515	T	G	0.1074	-0.0125	0.9876	0.9973
9	9_129687836_GAA_G	129687836	126925557	9:129687836_GAA_G	G	GAA	0.4405	-0.0004	0.9996	0.9996
9	9_130164993_C_T	130164993	127402714	rs1138739	T	C	0.2263	-0.0026	0.9974	0.9988
9	9_130488607_G_A	130488607	127726328	rs142193455	A	G	0.0163	-0.0148	0.9853	0.9995
9	9_131217803_A_G	131217803	128455524	rs55969420	G	A	0.1025	-0.0061	0.9939	0.9988
9	9_133069741_C_A	133069741	130307462	rs143378550	A	C	0.0264	0.0422	1.0431	1.0023
9	9_133888994_T_C	133888994	131013607	rs115491381	C	T	0.0707	0.0068	1.0068	1.0010
9	9_135871155_T_C	135871155	132995768	rs3011266	C	T	0.7426	-0.0027	0.9973	0.9960
9	9_136146597_C_T	136146597	133271182	rs550057	T	C	0.2727	0.0078	1.0078	1.0043
9	9_136149830_G_A	136149830	133274414	rs532436	A	G	0.2038	0.0001	1.0001	1.0000
9	9_136336804_C_T	136336804	133471682	rs41307428	T	C	0.0456	-0.0136	0.9865	0.9988
9	9_136350150_T_C	136350150	133485028	rs3094324	C	T	0.7391	-0.0097	0.9903	0.9858
9	9_136361351_TTGT_G_TTG	136361351	133496229	9:136361351_TTG_T	TTG	TTGTG	0.4886	-0.0022	0.9978	0.9979
9	9_138532484_T_A	138532484	135640638	rs62577654	A	T	0.0535	0.0379	1.0386	1.0041
9	9_140488857_C_G	140488857	137594405	9:140488857_C_G	G	C	0.3502	-0.0064	0.9936	0.9955
10	10_2135126_T_C	2135126	2092932	rs11594194	C	T	0.2071	0.0000	1.0000	1.0000

10	10_5401308_T_C	5401308	5359345	rs7081234	C	T	0.5155	0.0035	1.0035	1.0036
10	10_5760276_C_T	5760276	5718313	rs35585360	T	C	0.4766	-0.0015	0.9985	0.9986
10	10_5794652_A_G	5794652	5752689	rs55910451	G	A	0.2137	0.0112	1.0113	1.0048
10	10_5871493_T_G	5871493	5829530	rs12763451	G	T	0.4373	-0.0069	0.9931	0.9940
10	10_5872086_C_T	5872086	5830123	rs112168619	T	C	0.2031	0.0063	1.0063	1.0026
10	10_5942711_G_A	5942711	5900748	rs34825212	A	G	0.1397	-0.0085	0.9915	0.9976
10	10_6151327_C_A	6151327	6109364	rs7916878	A	C	0.5254	0.0048	1.0048	1.0051
10	10_8215279_C_A	8215279	8173316	rs67549624	A	C	0.3135	0.0026	1.0026	1.0016
10	10_8357966_T_C	8357966	8316003	rs1819622	C	T	0.6198	-0.0077	0.9923	0.9905
10	10_8437546_G_A	8437546	8395583	rs2787136	A	G	0.5271	0.0009	1.0009	1.0009
10	10_8697128_G_A	8697128	8655165	rs74433033	A	G	0.0354	0.0101	1.0102	1.0007
10	10_9101963_T_TAT ATATATATAC	9101963	9060000	rs796812026	TATATAT ATATAC	T	0.6538	-0.0029	0.9971	0.9962
10	10_9107670_G_A	9107670	9065707	rs34724453	A	G	0.1169	0.0205	1.0207	1.0048
10	10_9203158_GTT_ GT	9203158	9161195		GT	GTT	0.4642	0.0003	1.0003	1.0003
10	10_11186952_C_G	11186952	11144989	rs7919542	G	C	0.1130	0.0041	1.0041	1.0009
10	10_11198434_G_C	11198434	11156471	rs666871	C	G	0.2607	0.0097	1.0097	1.0051
10	10_11242078_TGA GAA_T	11242078	11200115	10:11242078_ TGAGAA_T	T	TGAGAA	0.0375	0.0121	1.0122	1.0009
10	10_13560152_A_G	13560152	13518152	rs118012425	G	A	0.0141	0.0657	1.0679	1.0019
10	10_13907236_T_C	13907236	13865236	rs10906522	C	T	0.4691	0.0123	1.0124	1.0116
10	10_13917699_C_T	13917699	13875699	rs11258686	T	C	0.3629	-0.0007	0.9993	0.9995
10	10_13947651_T_C	13947651	13905651	rs12776420	C	T	0.3592	-0.0020	0.9980	0.9986
10	10_14289822_G_A	14289822	14247823	rs146106883	A	G	0.0101	0.0440	1.0450	1.0009
10	10_14332199_G_A	14332199	14290200	rs148393137	A	G	0.0276	0.0299	1.0304	1.0017
10	10_17605117_A_G	17605117	17563118	rs2186113	G	A	0.5546	-0.0048	0.9952	0.9947

10	10_19552471_C_T	19552471	19263542	rs12356390	T	C	0.1461	-0.0117	0.9884	0.9966
10	10_20077518_G_A	20077518	19788589	rs77016942	A	G	0.0192	-0.0199	0.9803	0.9992
10	10_20390278_G_A	20390278	20101349	rs7068493	A	G	0.0283	-0.0104	0.9897	0.9994
10	10_21772735_CA_C	21772735	21483806	10:21772735_CA_C	C	CA	0.3823	0.0000	1.0000	1.0000
10	10_21811487_G_A	21811487	21522558	rs11012730	A	G	0.3781	0.0000	1.0000	1.0000
10	10_21824727_G_A	21824727	21535798	rs10828249	A	G	0.3615	0.0234	1.0237	1.0172
10	10_22032942_A_G	22032942	21744013	rs7072776	G	A	0.7085	-0.0010	0.9990	0.9986
10	10_22037809_A_G	22037809	21748880	rs6482190	G	A	0.7107	-0.0026	0.9974	0.9963
10	10_22043407_A_G	22043407	21754478	rs17409138	G	A	0.1913	0.0000	1.0000	1.0000
10	10_22216608_T_C	22216608	21927679	rs72797470	C	T	0.0211	0.0378	1.0385	1.0016
10	10_22233099_G_G	22233099	21944170	rs11411342	GT	G	0.6056	0.0000	1.0000	1.0000
10	10_22294687_C_G	22294687	22005758	rs7069830	G	C	0.6923	0.0000	1.0000	1.0000
10	10_22432882_C_T	22432882	22143953	rs56346589	T	C	0.0194	0.0073	1.0073	1.0003
10	10_22477776_ACC_A	22477776	22188847	rs762131501	A	ACC	0.0202	0.0637	1.0658	1.0027
10	10_22487991_T_C	22487991	22199062	rs72812786	C	T	0.0187	0.0081	1.0081	1.0003
10	10_22718486_G_T	22718486	22429557	rs75723675	T	G	0.0528	0.0050	1.0050	1.0005
10	10_22861490_A_C	22861490	22572561	rs10764337	C	A	0.9370	0.0056	1.0056	1.0106
10	10_22862487_C_A	22862487	22573558	rs11013052	A	C	0.3118	0.0036	1.0036	1.0023
10	10_22863028_CAA_A_C	22863028	22574099	10:22863028_CAAA_C	C	CAAA	0.9453	0.0000	1.0000	1.0000
10	10_22863425_A_G	22863425	22574496	rs12260388	G	A	0.9613	0.0256	1.0259	1.0505
10	10_22915624_T_C	22915624	22626695	rs1359642	C	T	0.1594	-0.0062	0.9938	0.9980
10	10_23336057_T_C	23336057	23047128	rs10764375	C	T	0.9664	0.0405	1.0413	1.0815
10	10_23728182_T_C	23728182	23439253	rs7093562	C	T	0.0114	0.0132	1.0133	1.0003

10	10_23947566_A_G	23947566	23658637	rs2150798	G	A	0.0126	0.0101	1.0102	1.0003
10	10_26164083_A_G	26164083	25875154	rs2367985	G	A	0.5630	0.0071	1.0071	1.0080
10	10_26687402_C_T	26687402	26398473	rs17528774	T	C	0.6450	0.0101	1.0102	1.0131
10	10_27479070_C_T	27479070	27190141	rs788211	T	C	0.1911	-0.0078	0.9922	0.9970
10	10_28119997_G_A	28119997	27831068	rs61843170	A	G	0.0412	-0.0323	0.9682	0.9974
10	10_31043077_G_A	31043077	30754148	rs11008223	A	G	0.4930	0.0088	1.0088	1.0087
10	10_31057888_C_G	31057888	30768959	rs11008239	G	C	0.4008	0.0009	1.0009	1.0007
10	10_32094576_TCA_T	32094576	31805648	10:32094576_TCA_T	T	TCA	0.4725	-0.0029	0.9971	0.9973
10	10_32270666_G_G	32270666	31981738	rs35103129	GA	G	0.4520	0.0026	1.0026	1.0024
10	10_32287347_CT_C	32287347	31998419	10:32287347_CT_C	C	CT	0.7028	0.0030	1.0030	1.0042
10	10_32678141_C_T	32678141	32389213	rs7070638	T	C	0.2348	0.0052	1.0052	1.0025
10	10_32908838_CTTT_TTTTTT_C	32908838	32619910	10:32908838_CTTT_TTTTTT_C	C	CTTTT TTTTT	0.8629	0.0110	1.0111	1.0192
10	10_33089200_A_T	33089200	32800272	rs2095555	T	A	0.1626	-0.0001	0.9999	1.0000
10	10_33724400_A_C	33724400	33435472	rs60101430	C	A	0.0153	0.0026	1.0026	1.0001
10	10_33764406_G_A	33764406	33475478	rs12247780	A	G	0.0685	0.0087	1.0087	1.0012
10	10_35214293_A_G	35214293	34925365	rs10827464	G	A	0.2665	0.0089	1.0089	1.0048
10	10_37390610_C_A	37390610	37101682	rs1200921	A	C	0.4628	-0.0043	0.9957	0.9960
10	10_37661344_T_A	37661344	37372416	rs1938420	A	T	0.6124	-0.0013	0.9987	0.9984
10	10_38530780_T_TA	38530780	38241852	rs199668839	TA	T	0.0633	0.0004	1.0004	1.0001
10	10_38634076_T_TA	38634076	38345148	rs369577778	TA	T	0.4240	0.0146	1.0147	1.0125
10	10_39100944_C_T	39100944	38807813	rs201983031	T	C	0.0772	0.0171	1.0172	1.0027
10	10_43073537_GAC_G	43073537	42578089	10:43073537_GAC_G	G	GAC	0.7593	0.0068	1.0068	1.0104

10	10_44285159_T_C	44285159	43789711	rs1998748	C	T	0.0953	-0.0076	0.9924	0.9986
10	10_45524771_T_C	45524771	45029323	rs10900158	C	T	0.7143	-0.0113	0.9888	0.9840
10	10_45545941_C_G	45545941	45050493	rs2311846	G	C	0.7628	-0.0067	0.9933	0.9898
10	10_45642534_G_A	45642534	45147086	rs1339746	A	G	0.9356	-0.0137	0.9864	0.9747
10	10_45912771_T_G	45912771	45417323	rs11239524	G	T	0.1541	0.0050	1.0050	1.0015
10	10_49594141_C_A	49594141	48386098	rs56278337	A	C	0.1065	0.0017	1.0017	1.0004
10	10_49717579_C_T	49717579	48509536	rs72785120	T	C	0.1533	0.0118	1.0119	1.0036
10	10_50450147_T_G	50450147	49242102	rs143362844	G	T	0.0112	0.0529	1.0543	1.0012
10	10_51602606_C_A	51602606	45993229	rs75914490	A	C	0.2758	-0.0098	0.9902	0.9946
10	10_52696552_T_A	52696552	50936792	rs74572072	A	T	0.0181	-0.0358	0.9648	0.9987
10	10_53676045_T_C	53676045	51916285	rs4935290	C	T	0.6715	-0.0076	0.9924	0.9899
10	10_53692969_C_T	53692969	51933209	rs7920008	T	C	0.4080	-0.0001	0.9999	0.9999
10	10_53773995_G_A	53773995	52014235	rs4495849	A	G	0.1970	-0.0068	0.9932	0.9973
10	10_55033677_G_T	55033677	53273917	rs142145443	T	G	0.0156	-0.0147	0.9854	0.9995
10	10_56741909_G_T	56741909	54982149	rs2222872	T	G	0.4688	0.0000	1.0000	1.0000
10	10_59111940_T_G	59111940	57352180	rs1904757	G	T	0.1653	-0.0031	0.9969	0.9990
10	10_61394137_G_A	61394137	59634379	rs11599171	A	G	0.2403	0.0091	1.0091	1.0044
10	10_61399990_T_C	61399990	59640232	rs2893807	C	T	0.2745	0.0000	1.0000	1.0000
10	10_62099814_C_T	62099814	60340056	rs10821732	T	C	0.0129	-0.0209	0.9793	0.9995
10	10_63192414_TA_AA	63192414	61432656		AA	TA	0.7840	0.0094	1.0094	1.0149
10	10_63417282_C_T	63417282	61657524	rs55645517	T	C	0.0788	-0.0061	0.9939	0.9990
10	10_63425659_AAT_A	63425659	61665901	10:63425659_AAT_A	A	AAT	0.4267	0.0049	1.0049	1.0042
10	10_63476983_T_C	63476983	61717225	rs17281372	C	T	0.4134	0.0000	1.0000	1.0000
10	10_63617615_A_G	63617615	61857856	rs74847539	G	A	0.0431	0.0035	1.0035	1.0003
10	10_63871993_T_A	63871993	62112234	rs57591366	A	T	0.3785	0.0000	1.0000	1.0000

10	10_64219094_T_C	64219094	62459335	rs78021475	C	T	0.0124	0.0102	1.0103	1.0003
10	10_64257828_T_C	64257828	62498069	rs10509168	C	T	0.5227	0.0174	1.0176	1.0184
10	10_64263402_C_G	64263402	62503643	rs4746409	G	C	0.5052	-0.0055	0.9945	0.9945
10	10_64268764_T_C	64268764	62509005	rs10995182	C	T	0.1335	-0.0114	0.9887	0.9970
10	10_64293571_AAA GG_A	64293571	62533812	rs764349609	A	AAAGG	0.3392	0.0088	1.0088	1.0060
10	10_64299890_A_G	64299890	62540131	rs10995201	G	A	0.1603	-0.0819	0.9214	0.9750
10	10_64309151_C_C AT	64309151	62549392	rs10638039	CAT	C	0.3933	0.0043	1.0043	1.0034
10	10_64414265_C_T	64414265	62654505	rs34632941	T	C	0.0752	-0.0031	0.9969	0.9995
10	10_64440842_T_C	64440842	62681082	rs16917616	C	T	0.0105	0.0000	1.0000	1.0000
10	10_64562524_G_A	64562524	62802764	rs7905654	A	G	0.1184	-0.0036	0.9964	0.9991
10	10_64578483_C_T	64578483	62818723	rs61865884	T	C	0.0700	-0.0164	0.9837	0.9977
10	10_64582482_T_C	64582482	62822722	rs61865900	C	T	0.0617	-0.0107	0.9894	0.9987
10	10_64611042_A_G	64611042	62851282	rs117807754	G	A	0.0246	0.0171	1.0172	1.0008
10	10_64763893_G_A	64763893	63004133	rs11595405	A	G	0.4803	0.0016	1.0016	1.0015
10	10_64802682_GA_ G	64802682	63042922	rs35598651	G	GA	0.3303	0.0076	1.0076	1.0050
10	10_64817375_C_T	64817375	63057615	rs34942900	T	C	0.0374	0.0000	1.0000	1.0000
10	10_64819996_G_T	64819996	63060236	rs6479868	T	G	0.1958	0.0090	1.0090	1.0035
10	10_65224458_CA_ C	65224458	63464698	10:65224458_ CA_C	C	CA	0.5455	-0.0014	0.9986	0.9985
10	10_67686579_T_C	67686579	65926821	rs12251157	C	T	0.0389	-0.0081	0.9919	0.9994
10	10_68380961_A_G	68380961	66621203	rs144769797	G	A	0.0223	-0.0317	0.9688	0.9986
10	10_71078937_A_G	71078937	69319181	rs75634211	G	A	0.0280	-0.0018	0.9982	0.9999
10	10_71147630_A_A T	71147630	69387874	rs11424399	AT	A	0.4766	0.0022	1.0022	1.0021
10	10_71152091_T_C	71152091	69392335	rs2278745	C	T	0.5242	0.0030	1.0030	1.0032

10	10_71333897_C_T	71333897	69574141	rs12785008	T	C	0.1740	-0.0026	0.9974	0.9991
10	10_71335574_C_T	71335574	69575818	rs111833376	T	C	0.3179	-0.0164	0.9837	0.9897
10	10_72765137_G_A	72765137	71005380	rs75693169	A	G	0.0495	0.0280	1.0284	1.0028
10	10_73649779_C_T	73649779	71890021	rs7915996	T	C	0.1882	0.0058	1.0058	1.0022
10	10_75383954_G_T	75383954	73624196	rs556862051	T	G	0.0410	-0.0120	0.9881	0.9990
10	10_75400405_A_T	75400405	73640647	rs11000726	T	A	0.1177	-0.0126	0.9875	0.9971
10	10_80290002_G_A	80290002	78530245	rs117315821	A	G	0.0261	-0.0503	0.9509	0.9974
10	10_80322047_ACA GTGCTGTCT_A	80322047	78562290	10:80322047_– ACAGTGTCTGT CT_A	A	ACAGTG CTGTCT	0.0431	-0.0037	0.9963	0.9997
10	10_80830292_T_C	80830292	79070535	rs2485698	C	T	0.9249	0.0000	1.0000	1.0000
10	10_80833595_C_C AG	80833595	79073838	rs34518733	CAG	C	0.4438	0.0000	1.0000	1.0000
10	10_80835868_G_A	80835868	79076111	rs10824713	A	G	0.5805	0.0000	1.0000	1.0000
10	10_80836590_C_T	80836590	79076833	rs1658329	T	C	0.6233	-0.0098	0.9902	0.9879
10	10_80842416_T_C	80842416	79082659	rs704009	C	T	0.7779	0.0000	1.0000	1.0000
10	10_80847150_C_T	80847150	79087393	rs1250002	T	C	0.1828	-0.0037	0.9963	0.9987
10	10_80851257_G_T	80851257	79091500	rs719338	T	G	0.6172	-0.0305	0.9700	0.9633
10	10_80852892_AAC AC_A	80852892	79093135	10:80852892_– AACAC_A	A	AACAC	0.4946	-0.0145	0.9856	0.9858
10	10_80855650_G_A	80855650	79095893	rs11002811	A	G	0.1567	0.0063	1.0063	1.0020
10	10_80870324_G_C	80870324	79110567	rs7914988	C	G	0.5861	0.0039	1.0039	1.0046
10	10_80882589_A_G	80882589	79122832	rs1658322	G	A	0.4397	0.0008	1.0008	1.0007
10	10_80883311_T_C	80883311	79123554	rs1866157	C	T	0.1927	0.0124	1.0125	1.0048
10	10_80886726_A_G	80886726	79126969	rs4980029	G	A	0.1631	0.0303	1.0308	1.0101
10	10_80926036_T_C	80926036	79166279	rs703994	C	T	0.5562	0.0020	1.0020	1.0022
10	10_84397685_AT_– A	84397685	82637929	rs201016760	A	AT	0.6268	-0.0003	0.9997	0.9996

10	10_85694849_G_C	85694849	83935093	rs7099146	C	G	0.1752	0.0089	1.0089	1.0031
10	10_88440446_CA_C	88440446	86680689	rs753019787	C	CA	0.2154	0.0070	1.0070	1.0030
10	10_88832746_C_T	88832746	87072989	rs9421579	T	C	0.0908	0.0021	1.0021	1.0004
10	10_90112623_C_G	90112623	88352866	rs1086833	G	C	0.2542	-0.0007	0.9993	0.9996
10	10_90151393_T_A	90151393	88391636	rs1774973	A	T	0.4614	-0.0009	0.9991	0.9992
10	10_90198801_A_G	90198801	88439044	rs17426488	G	A	0.2552	-0.0086	0.9914	0.9956
10	10_91784322_C_T	91784322	90024565	rs11185975	T	C	0.2349	0.0012	1.0012	1.0006
10	10_91824299_A_C	91824299	90064542	rs7900020	C	A	0.2291	0.0054	1.0054	1.0025
10	10_92537170_G_A	92537170	90777413	rs12416468	A	G	0.0655	-0.0138	0.9863	0.9982
10	10_92559908_G_T	92559908	90800151	rs7916403	T	G	0.4358	-0.0035	0.9965	0.9970
10	10_92604139_G_A	92604139	90844382	rs7084468	A	G	0.1668	-0.0036	0.9964	0.9988
10	10_92803107_G_A	92803107	91043350	rs117414562	A	G	0.0463	0.0035	1.0035	1.0003
10	10_93569805_A_G	93569805	91810048	rs79611925	G	A	0.0273	-0.0083	0.9917	0.9995
10	10_93932286_A_G	93932286	92172529	rs72807246	G	A	0.1415	-0.0057	0.9943	0.9984
10	10_95292187_CAA_C	95292187	93532430	10:95292187_CAA_C	C	CAA	0.8234	-0.0187	0.9815	0.9697
10	10_95725628_C_T	95725628	93965871	rs10882371	T	C	0.7145	0.0065	1.0065	1.0093
10	10_97810637_T_C	97810637	96050880	rs880518	C	T	0.0138	0.0000	1.0000	1.0000
10	10_101130302_A_T	101130302	99370545	rs1892511	T	A	0.8815	0.0101	1.0102	1.0180
10	10_102936499_C_G	102936499	101176742	rs10883594	G	C	0.1116	-0.0139	0.9862	0.9969
10	10_104168611_G_T	104168611	102408854	rs148440547	T	G	0.0675	0.0052	1.0052	1.0007
10	10_106354417_C_T	106354417	104594659	rs11192129	T	C	0.1396	0.0024	1.0024	1.0007
10	10_106385271_G_T	106385271	104625513	rs1577222	T	G	0.6041	-0.0011	0.9989	0.9987
10	10_107275646_T_T	107275646	105515888	rs201520282	TAC	T	0.1334	-0.0116	0.9885	0.9969

10	10_119262365_A_G	119262365	117502854	rs2901157	G	A	0.1147	-0.0078	0.9922	0.9982
10	10_119679243_T_C	119679243	117919732	rs12242896	C	T	0.0677	-0.0141	0.9860	0.9981
10	10_120541197_C_T	120541197	118781685	rs962890	T	C	0.7345	-0.0012	0.9988	0.9982
10	10_120822033_T_G	120822033	119062521	rs2152240	G	T	0.4115	-0.0031	0.9969	0.9975
10	10_120851811_T_C	120851811	119092299	rs2420491	C	T	0.5933	0.0043	1.0043	1.0051
10	10_121381615_A_G	121381615	119622103	rs196310	G	A	0.4770	0.0039	1.0039	1.0037
10	10_121405714_G_A	121405714	119646202	rs7083324	A	G	0.2455	0.0043	1.0043	1.0021
10	10_122230768_A_G	122230768	120471256	rs142147598	G	A	0.0278	-0.0408	0.9600	0.9978
10	10_122752466_A_T	122752466	120992953	rs12359502	T	A	0.3175	-0.0022	0.9978	0.9986
10	10_122755774_G_A	122755774	120996261	rs11199696	A	G	0.2253	0.0024	1.0024	1.0011
10	10_122802462_A_C	122802462	121042949	rs748476	C	A	0.1778	0.0149	1.0150	1.0053
10	10_122837858_T_C	122837858	121078345	rs732640	C	T	0.2555	-0.0109	0.9892	0.9945
10	10_123094959_G_A	123094959	121335445	10:123094959_GAA_G	G	GAA	0.2921	0.0000	1.0000	1.0000
10	10_123095209_G_A	123095209	121335695	rs9421410	A	G	0.3269	-0.0273	0.9731	0.9825
10	10_123153472_A_G	123153472	121393958	rs2420928	G	A	0.4207	0.0084	1.0084	1.0071
10	10_123155416_C_T	123155416	121395902	rs4751835	T	C	0.3647	0.0016	1.0016	1.0012
10	10_123240645_C_T	123240645	121481131	rs3135821	T	C	0.0999	-0.0084	0.9916	0.9983
10	10_123320793_C_T	123320793	121561279	rs145549294	T	C	0.0142	0.0000	1.0000	1.0000
10	10_123331690_A_T	123331690	121572176	rs4752569	T	A	0.4860	0.0000	1.0000	1.0000
10	10_123340311_C_T	123340311	121580797	rs2981578	T	C	0.5295	-0.0223	0.9779	0.9768

10	10_123340431_GC_G	123340431	121580917	10:123340431_GC_G	G	GC	0.5963	-0.1732	0.8410	0.8193
10	10_123343909_T_G	123343909	121584395	rs1696840	G	T	0.3860	0.0000	1.0000	1.0000
10	10_123346116_G_A	123346116	121586602	rs2981575	A	G	0.6067	-0.0137	0.9864	0.9836
10	10_123349324_A_T	123349324	121589810	rs45631563	T	A	0.0484	-0.0880	0.9158	0.9919
10	10_123356175_A_T	123356175	121596661	rs2936871	T	A	0.8416	-0.0065	0.9935	0.9891
10	10_123484962_G_A	123484962	121725447	rs12771557	A	G	0.3796	-0.0001	0.9999	0.9999
10	10_123788291_G_C	123788291	122028776	rs61679579	C	G	0.5760	0.0000	1.0000	1.0000
10	10_123800974_C_T	123800974	122041459	rs2459078	T	C	0.6139	0.0000	1.0000	1.0000
10	10_127258691_G_A	127258691	125570122	rs7084502	A	G	0.4132	0.0077	1.0077	1.0064
10	10_127981161_T_C	127981161	126292592	rs4962336	C	T	0.3085	0.0092	1.0092	1.0057
10	10_129233816_T_G	129233816	127435552	rs11816982	G	T	0.1199	-0.0048	0.9952	0.9989
10	10_129248015_G_C	129248015	127449751	rs55798271	C	G	0.1009	0.0027	1.0027	1.0005
10	10_133833155_T_G	133833155	132019651	rs117413668	G	T	0.0967	0.0044	1.0044	1.0009
10	10_133947465_C_A	133947465	132133961	rs78501832	A	C	0.0719	-0.0089	0.9911	0.9987
10	10_134561926_C_T	134561926	132748422	rs11146497	T	C	0.0725	-0.0103	0.9898	0.9985
11	11_322722_C_T	322722	322722	rs10794307	T	C	0.3530	-0.0008	0.9992	0.9994
11	11_418735_G_A	418735	418735	rs12792208	A	G	0.0202	0.0039	1.0039	1.0002
11	11_428489_T_C	428489	428489	rs10794324	C	T	0.7746	-0.0174	0.9828	0.9735
11	11_433617_T_C	433617	433617	rs7394715	C	T	0.7969	-0.0025	0.9975	0.9960
11	11_445331_C_T	445331	445331	rs71487288	T	C	0.1448	-0.0103	0.9898	0.9970

11	11_701616_A_G	701616	701616	rs7112603	G	A	0.9095	0.0042	1.0042	1.0077
11	11_803017_A_G	803017	803017	rs6597981	G	A	0.5167	0.0192	1.0194	1.0201
11	11_835407_C_T	835407	835407	rs7126859	T	C	0.5106	0.0074	1.0074	1.0076
11	11_1091080_G_A	1091080	1093142	rs41414549	A	G	0.0359	0.0047	1.0047	1.0003
11	11_1876228_C_T	1876228	1854998	rs11602798	T	C	0.2643	0.0000	1.0000	1.0000
11	11_1891284_T_A	1891284	1870054	rs688601	A	T	0.5486	-0.0215	0.9787	0.9768
11	11_1895708_C_A	1895708	1874478	rs4980386	A	C	0.3924	-0.0031	0.9969	0.9976
11	11_1900765_C_T	1900765	1879535	rs11041615	T	C	0.1752	-0.0072	0.9928	0.9975
11	11_1902097_C_T	1902097	1880867	rs4980383	T	C	0.4404	0.0077	1.0077	1.0068
11	11_1902475_G_A	1902475	1881245	rs620315	A	G	0.3842	-0.0160	0.9841	0.9878
11	11_1905292_T_C	1905292	1884062	rs661348	C	T	0.4361	-0.0055	0.9945	0.9952
11	11_1948186_T_C	1948186	1926956	rs7125631	C	T	0.3530	0.0056	1.0056	1.0040
11	11_1951960_G_C	1951960	1930730	rs10466507	C	G	0.1542	0.0000	1.0000	1.0000
11	11_1975106_T_C	1975106	1953876	rs757409	C	T	0.2939	0.0000	1.0000	1.0000
11	11_1979118_C_G	1979118	1957888	rs217213	G	C	0.4215	-0.0031	0.9969	0.9974
11	11_1979223_G_C	1979223	1957993	rs2063550	C	G	0.5189	0.0031	1.0031	1.0032
11	11_1997572_- _GTCC	1997572	1976342	rs112088979	GTCC	G	0.4328	0.0008	1.0008	1.0007
11	11_2016908_G_A	2016908	1995678	rs217727	A	G	0.1926	-0.0041	0.9959	0.9984
11	11_2024544_G_A	2024544	2003314	rs4930103	A	G	0.5249	0.0059	1.0059	1.0062
11	11_2223850_G_C	2223850	2202620	rs10840550	C	G	0.5600	0.0043	1.0043	1.0048
11	11_2332694_A_G	2332694	2311464	rs80120162	G	A	0.0477	0.0185	1.0187	1.0018
11	11_2354538_T_C	2354538	2333308	rs567031996	C	T	0.0410	0.0004	1.0004	1.0000
11	11_2390064_G_A	2390064	2368834	rs77369403	A	G	0.0401	0.0028	1.0028	1.0002
11	11_2830946_CG_C	2830946	2809716	rs775385647	C	CG	0.0920	-0.0080	0.9920	0.9985
11	11_2894562_C_A	2894562	2873332	rs111875758	A	C	0.0222	-0.0256	0.9747	0.9989
11	11_3215893_G_T	3215893	3194663	rs72848229	T	G	0.0606	0.0249	1.0252	1.0031

11	11_3223621_G_A	3223621	3202391	rs72848239	A	G	0.0383	0.0072	1.0072	1.0006
11	11_5768236_C_G	5768236	5747006	rs36173363	G	C	0.0977	0.0009	1.0009	1.0002
11	11_6255984_C_T	6255984	6234754	rs12274456	T	C	0.2463	0.0088	1.0088	1.0044
11	11_9726369_T_C	9726369	9704822	rs34043654	C	T	0.3496	-0.0083	0.9917	0.9942
11	11_9936951_G_A	9936951	9915404	rs4910077	A	G	0.2951	0.0038	1.0038	1.0022
11	11_10147968_T_C	10147968	10126421	rs12363292	C	T	0.2240	-0.0131	0.9870	0.9942
11	11_10472239_A_G	10472239	10450692	rs61891367	G	A	0.1757	-0.0132	0.9869	0.9954
11	11_10540013_CTG_AA_C	10540013	10518466	11:10540013_CTGAA_C	C	CTGAA	0.3415	-0.0090	0.9910	0.9939
11	11_11498224_G_C	11498224	11476677	rs34203081	C	G	0.0678	0.0062	1.0062	1.0008
11	11_11596321_-CT	11596321	11574774	rs11386655	CT	C	0.6763	0.0002	1.0002	1.0003
11	11_11671547_TA_T	11671547	11650000	11:11671547_TA_T	T	TA	0.0544	-0.0160	0.9841	0.9983
11	11_14014644_TTA_T	14014644	13993097	rs781998923	T	TTA	0.1185	0.0106	1.0107	1.0025
11	11_15333431_C_T	15333431	15311885	rs2350987	T	C	0.4678	-0.0092	0.9908	0.9915
11	11_16593142_C_A	16593142	16571595	rs72859467	A	C	0.1514	0.0003	1.0003	1.0001
11	11_16644500_G_A	16644500	16622953	rs72861246	A	G	0.0823	0.0046	1.0046	1.0008
11	11_17455371_G_A	17455371	17433824	rs4148617	A	G	0.2455	-0.0079	0.9921	0.9961
11	11_17462858_T_C	17462858	17441311	rs8733314	C	T	0.2083	-0.0062	0.9938	0.9974
11	11_18403867_A_G	18403867	18382320	rs10766474	G	A	0.5474	0.0010	1.0010	1.0011
11	11_18664241_T_G	18664241	18642694	rs10832963	G	T	0.7293	0.0203	1.0205	1.0301
11	11_18666897_C_T	18666897	18645350	rs72882183	T	C	0.0647	-0.0063	0.9937	0.9992
11	11_18687025_G_A	18687025	18665478	rs12787397	A	G	0.2940	0.0024	1.0024	1.0014
11	11_22610647_T_C	22610647	22589101	rs11026677	C	T	0.1902	-0.0001	0.9999	1.0000
11	11_24366115_T_C	24366115	24344569	rs6484042	C	T	0.1730	-0.0036	0.9964	0.9988
11	11_25390994_A_T	25390994	25369448	rs7934880	T	A	0.1136	-0.0014	0.9986	0.9997

11	11_25391785_C_T	25391785	25370239	rs7935930	T	C	0.1165	-0.0031	0.9969	0.9993
11	11_25408575_T_C	25408575	25387029	rs78467396	C	T	0.0138	-0.0218	0.9784	0.9994
11	11_25518333_T_G	25518333	25496787	rs79087301	G	T	0.1468	-0.0033	0.9967	0.9990
11	11_25614733_ATA TACT_A	25614733	25593187	rs776163159	A	ATATAC T	0.1625	-0.0058	0.9942	0.9981
11	11_25624927_- _CTATA	25624927	25603381	rs374893599	CTATA	C	0.1220	-0.0003	0.9997	0.9999
11	11_27085203_CA_ C	27085203	27063656	11:27085203_ CA_C	C	CA	0.4195	0.0038	1.0038	1.0032
11	11_27428264_C_A	27428264	27406717	rs12787344	A	C	0.2200	0.0000	1.0000	1.0000
11	11_31589116_G_A	31589116	31567569	rs80001711	A	G	0.0640	-0.0118	0.9883	0.9985
11	11_31605896_A_T	31605896	31584349	rs11031419	T	A	0.0341	-0.0005	0.9995	1.0000
11	11_34728612_TC_T	34728612	34707065	11:34728612_ TC_T	T	TC	0.1918	0.0068	1.0068	1.0026
11	11_35331642_G_A	35331642	35310095	rs3903687	A	G	0.6171	-0.0018	0.9982	0.9978
11	11_35487857_T_C	35487857	35466309	rs11602786	C	T	0.1579	0.0091	1.0091	1.0029
11	11_35841576_T_C	35841576	35820026	rs10501143	C	T	0.1913	-0.0146	0.9855	0.9945
11	11_35890696_C_T	35890696	35869146	rs7131104	T	C	0.1630	0.0000	1.0000	1.0000
11	11_42841708_C_T	42841708	42820158	rs10768892	T	C	0.5972	0.0000	1.0000	1.0000
11	11_42844441_C_T	42844441	42822891	rs4472923	T	C	0.3279	-0.0133	0.9868	0.9914
11	11_44169325_- _CTTTT	44169325	44147775	rs374108596	CTTTT	C	0.8577	0.0113	1.0114	1.0196
11	11_44368892_G_A	44368892	44347342	rs10838267	A	G	0.5495	0.0105	1.0106	1.0116
11	11_46318032_C_G	46318032	46296481	rs77047825	G	C	0.0659	-0.0235	0.9768	0.9969
11	11_46350213_AG_ A	46350213	46328663	rs773391321	A	AG	0.1407	0.0077	1.0077	1.0022
11	11_47377283_A_G	47377283	47355732	rs71475909	G	A	0.3615	0.0000	1.0000	1.0000
11	11_47980568_T_G	47980568	47959016	rs7939345	G	T	0.7916	0.0017	1.0017	1.0027

11	11_48113430_A_C	48113430	48091878	rs12576134	C	A	0.1613	-0.0056	0.9944	0.9982
11	11_55279127_TTC_T	55279127	55511651	11:55279127_TTC_T	T	TTC	0.2956	-0.0041	0.9959	0.9976
11	11_55303837_A_G	55303837	55536361	rs58194256	G	A	0.1183	-0.0057	0.9943	0.9987
11	11_61819018_T_G	61819018	62051546	rs6591691	G	T	0.2886	0.0000	1.0000	1.0000
11	11_61880295_C_CT	61880295	62112823	rs11408362	CT	C	0.3829	0.0042	1.0042	1.0032
11	11_61895444_A_G	61895444	62127972	rs79215615	G	A	0.3351	-0.0047	0.9953	0.9969
11	11_61937658_C_T	61937658	62170186	rs7127472	T	C	0.2100	0.0025	1.0025	1.0011
11	11_61960809_C_A	61960809	62193337	rs7951859	A	C	0.7410	-0.0054	0.9946	0.9920
11	11_61974845_G_G	61974845	62207373	rs536206626	GA	G	0.3371	-0.0018	0.9982	0.9988
11	11_62183438_A_G	62183438	62415966	rs2509971	G	A	0.8543	0.0001	1.0001	1.0002
11	11_62183838_C_T	62183838	62416366	rs3758962	T	C	0.1652	-0.0086	0.9914	0.9972
11	11_62187269_G_A	62187269	62419797	rs12270961	A	G	0.1976	-0.0071	0.9929	0.9972
11	11_62679450_A_G	62679450	62911978	rs118112787	G	A	0.0310	0.0017	1.0017	1.0001
11	11_62772106_G_A	62772106	63004634	rs7113486	A	G	0.0509	0.0249	1.0252	1.0026
11	11_64618768_T_C	64618768	64851296	rs10897532	C	T	0.7060	-0.0068	0.9932	0.9905
11	11_65553492_C_A	65553492	65786021	rs12287832	A	C	0.1867	0.0164	1.0165	1.0062
11	11_65572431_G_A	65572431	65804960	rs10896047	A	G	0.4886	-0.0220	0.9782	0.9789
11	11_65601650_G_C	65601650	65834179	rs548082010	C	G	0.4937	0.0000	1.0000	1.0000
11	11_65637273_A_G	65637273	65869802	rs501630	G	A	0.5556	0.0000	1.0000	1.0000
11	11_66337388_CA_C	66337388	66569917	11:66337388_CA_C	C	CA	0.3372	0.0149	1.0150	1.0101
11	11_66694971_T_C	66694971	66927500	rs141065168	C	T	0.0867	-0.0023	0.9977	0.9996
11	11_66751902_G_A	66751902	66984431	rs60197393	A	G	0.0543	-0.0124	0.9877	0.9987
11	11_66825559_T_C	66825559	67058088	rs58876856	C	T	0.0853	-0.0086	0.9914	0.9985
11	11_68959319_T_C	68959319	69191851	rs12800787	C	T	0.2972	0.0013	1.0013	1.0008

11	11_69289737_C_T	69289737	69474969	rs72927565	T	C	0.1282	0.0067	1.0067	1.0017
11	11_69322445_A_T	69322445	69507677	rs7952215	T	A	0.1035	-0.0125	0.9876	0.9974
11	11_69330983_G_A	69330983	69516215	rs661204	A	G	0.1250	0.0760	1.0790	1.0198
11	11_69331418_C_T	69331418	69516650	rs78540526	T	C	0.0753	0.1358	1.1455	1.0220
11	11_69332712_C_T	69332712	69517944	rs657315	T	C	0.2157	0.0000	1.0000	1.0000
11	11_69334716_T_A	69334716	69519948	rs4608107	A	T	0.1627	-0.0105	0.9896	0.9966
11	11_69343815_C_T	69343815	69529047	rs75296154	T	C	0.0423	0.0199	1.0201	1.0017
11	11_69352436_T_A	69352436	69537668	rs650524	A	T	0.8684	0.0052	1.0052	1.0091
11	11_69475386_C_T	69475386	69660618	rs147070975	T	C	0.0460	0.0057	1.0057	1.0005
11	11_69561529_A_G	69561529	69746761	rs9665984	G	A	0.6989	0.0070	1.0070	1.0098
11	11_69865341_GA_G	69865341	70019235	11:69865341_GA_G	G	GA	0.7463	0.0024	1.0024	1.0036
11	11_72687549_G_T	72687549	72976504	rs573529	T	G	0.9898	0.0305	1.0310	1.0622
11	11_73101250_T_G	73101250	73390205	rs56411180	G	T	0.2363	0.0024	1.0024	1.0011
11	11_73186685_T_TA	73186685	73475640	rs141436441	TA	T	0.1038	0.0101	1.0102	1.0021
11	11_73348752_T_G	73348752	73637707	rs11235828	G	T	0.5592	-0.0038	0.9962	0.9958
11	11_74042329_T_C	74042329	74331284	rs11236059	C	T	0.6350	-0.0088	0.9912	0.9889
11	11_81598184_C_G	81598184	81887142	rs12418804	G	C	0.0690	0.0125	1.0126	1.0017
11	11_82445154_T_C	82445154	82734112	rs34030508	C	T	0.3603	-0.0051	0.9949	0.9963
11	11_86277652_C_CC	86277652	86566610	rs10636674	CCA	C	0.2577	0.0096	1.0096	1.0050
11	11_87588165_C_A	87588165	87877273	rs117766181	A	C	0.0312	-0.0066	0.9934	0.9996
11	11_91461188_A_G	91461188	91728022	rs794409	G	A	0.8227	0.0102	1.0103	1.0169
11	11_91711270_C_G	91711270	91978104	rs12295844	G	C	0.0702	0.0067	1.0067	1.0009
11	11_91717620_T_C	91717620	91984454	rs74735677	C	T	0.0254	0.0093	1.0093	1.0005
11	11_95526086_T_TA	95526086	95792922	rs35157937	TA	T	0.4061	-0.0121	0.9880	0.9903
11	11_95884017_G_A	95884017	96150853	rs511141	A	G	0.3610	-0.0129	0.9872	0.9908

11	11_97355695_T_G	97355695	97484695	rs10895838	G	T	0.6098	0.0015	1.0015	1.0018
11	11_97380744_A_A TT	97380744	97509744	rs139559507	ATT	A	0.1318	-0.0142	0.9859	0.9963
11	11_97403126_T_C	97403126	97532126	rs60829647	C	T	0.1818	-0.0121	0.9880	0.9956
11	11_97414086_C_T	97414086	97543086	rs111239357	T	C	0.1173	-0.0019	0.9981	0.9996
11	11_100885969_A_ G	100885969	101015238	rs10895042	G	A	0.1584	0.0151	1.0152	1.0048
11	11_103614438_T_ G	103614438	103743710	rs7125780	G	T	0.6572	0.0000	1.0000	1.0000
11	11_103647409_CT_ C	103647409	103776681	11:103647409 _CT_C	C	CT	0.5503	0.0088	1.0088	1.0098
11	11_103872193_T_C	103872193	104001465	rs61904889	C	T	0.0685	-0.0040	0.9960	0.9995
11	11_106494949_C_T	106494949	106624223	rs72983856	T	C	0.1586	-0.0070	0.9930	0.9978
11	11_107903818_A_ G	107903818	108033092	rs36034326	G	A	0.0147	0.0000	1.0000	1.0000
11	11_107965390_A_ G	107965390	108094663	rs71488291	G	A	0.0449	0.0000	1.0000	1.0000
11	11_108267402_C_C A	108267402	108396675	rs199504893	CA	C	0.4173	0.0000	1.0000	1.0000
11	11_108267561_A_ AAAT	108267561	108396834	rs553909636	AAAAT	A	0.5482	0.0000	1.0000	1.0000
11	11_108406943_G_ A	108406943	108536216	rs117706999	A	G	0.0243	0.0000	1.0000	1.0000
11	11_108431166_C_T	108431166	108560439	rs78142456	T	C	0.0130	0.0000	1.0000	1.0000
11	11_11117137_A_T	11117137	111246412	rs12803934	T	A	0.2323	-0.0112	0.9889	0.9948
11	11_111120698_C_T	111120698	111249973	rs10891239	T	C	0.2794	0.0044	1.0044	1.0025
11	11_111170540_A_ G	111170540	111299815	rs10891246	G	A	0.7194	0.0000	1.0000	1.0000
11	11_111188216_A_T	111188216	111317491	rs138219610	T	A	0.0213	-0.0052	0.9948	0.9998

11	11_111195925_G_A	111195925	111325200	rs78790112	A	G	0.0621	-0.0113	0.9888	0.9986
11	11_111220796_A_T	111220796	111350071	rs78904682	T	A	0.0219	-0.0042	0.9958	0.9998
11	11_111415800_T_T	111415800	111545075	rs34170562	TA	T	0.3780	-0.0088	0.9912	0.9934
11	11_111468326_C_T	111468326	111597602	rs145056657	T	C	0.0110	-0.0218	0.9784	0.9995
11	11_111696440_T_C	111696440	111825716	rs610437	C	T	0.6221	0.0000	1.0000	1.0000
11	11_111742493_CAAA_CAAAAA	111742493	111871769		CAAAAA	CAAAA	0.3621	0.0113	1.0114	1.0082
11	11_112392948_C_T	112392948	112522225	rs11214235	T	C	0.0467	-0.0034	0.9966	0.9997
11	11_113506860_C_T	113506860	113636138	rs10891576	T	C	0.8149	0.0026	1.0026	1.0042
11	11_113536710_G_A	113536710	113665988	rs10789956	A	G	0.7967	0.0024	1.0024	1.0038
11	11_113679119_C_T	113679119	113808397	rs2465647	T	C	0.8197	0.0041	1.0041	1.0067
11	11_113700546_CAAA_C	113700546	113829824	rs780916647	C	CA	0.6977	0.0008	1.0008	1.0011
11	11_113807181_G_A	113807181	113936459	rs11214775	A	G	0.2937	-0.0044	0.9956	0.9974
11	11_113814744_CT_C	113814744	113944022	11:113814744_CT_C	C	CT	0.3475	-0.0077	0.9923	0.9947
11	11_114130424_AA_CT_A	114130424	114259702	rs773108752	A	AACT	0.2377	0.0033	1.0033	1.0016
11	11_114162880_T_C	114162880	114292158	rs73566515	C	T	0.0110	-0.0160	0.9841	0.9997
11	11_115044211_C_T	115044211	115173491	rs4450197	T	C	0.9716	0.0026	1.0026	1.0051
11	11_115434178_T_TTTG	115434178	115563460	rs35864364	TTTTG	T	0.6001	0.0108	1.0109	1.0131
11	11_115447170_A_G	115447170	115576452	rs2446889	G	A	0.8291	0.0019	1.0019	1.0032
11	11_116684562_C_	116684562	116813846	rs2727791	G	C	0.5259	-0.0005	0.9995	0.9995

	G					T	C				-0.0084	0.9916	0.9981
11	11_116724232_C_T	116724232	116853516	rs888246		T	C			0.1131	-0.0084	0.9916	0.9981
11	11_116727936_A_T	116727936	116857220	rs625145		T	A			0.2046	-0.0076	0.9924	0.9969
11	11_116883543_G_ GTT	116883543	117012827	rs529358042		GTT	G			0.0475	0.0166	1.0167	1.0016
11	11_117074299_I_C	117074299	117203583	rs2269397		C	T			0.0935	0.0071	1.0071	1.0013
11	11_118568715_C_C A	118568715	118698006	rs558343369		CA	C			0.2214	-0.0119	0.9882	0.9948
11	11_120205001_G_ GT	120205001	120334292	rs34108129		GT	G			0.3948	0.0068	1.0068	1.0054
11	11_122966626_A_ G	122966626	123095918	rs7121616		G	A			0.2922	-0.0150	0.9851	0.9913
11	11_123014229_C_C G	123014229	123143521	rs571232271		CG	C			0.1556	-0.0047	0.9953	0.9985
11	11_123053078_T_C 11_123136459_G_ A	123053078 123136459	123182370 123265751	rs7113140 rs145464316		C A	T G			0.5648 0.0176	-0.0019 -0.0159	0.9981 0.9842	0.9979 0.9994
11	11_123910023_A_ G	123910023	124039316	rs17128251		G	A			0.7284	-0.0037	0.9963	0.9946
11	11_125291621_A_ G	125291621	125421725	rs608529		G	A			0.1470	0.0008	1.0008	1.0002
11	11_125573435_CTT C	125573435	125703540	rs113811036		C	CTT			0.1911	-0.0057	0.9943	0.9978
11	11_125880063_C_T 11_129216251_A_ G	125880063 129216251	126010168 129346356	rs55905554 rs111738532		T G	C A			0.1789 0.0174	0.0114 0.0058	1.0115 1.0058	1.0041 1.0002
11	11_129243417_T_ G	129243417	129373522	rs7939702		G	T			0.8620	-0.0105	0.9896	0.9821
11	11_129248862_G_ A	129248862	129378967	rs6590383		A	G			0.8258	-0.0087	0.9913	0.9857

12	12_1045023_AAAA T_A	1045023	935857	12:1045023_A AAAT_A	A	AAAAT	0.7525	0.0097	1.0097	1.0147
12	12_1593428_A_G	1593428	1484262	rs61912164	G	A	0.0440	-0.0098	0.9902	0.9991
12	12_2294263_A_G	2294263	2185097	rs758171	G	A	0.3750	0.0005	1.0005	1.0004
12	12_2340798_A_C	2340798	2231632	rs34382810	C	A	0.4235	0.0085	1.0085	1.0072
12	12_5638925_G_GG ACCTCCACCAGA	5638925	5529759	rs149293159	GGACCTC CCACCAG A	G	0.2378	0.0101	1.0102	1.0048
12	12_5665330_A_T	5665330	5556164	rs11063753	T	A	0.2427	0.0012	1.0012	1.0006
12	12_6294636_A_G	6294636	6185470	rs80286123	G	A	0.5265	0.0020	1.0020	1.0021
12	12_12008900_G_T	12008900	11855966	rs80046954	T	G	0.0524	-0.0045	0.9955	0.9995
12	12_12044393_T_TT A	12044393	11891459	rs71435871	TTA	T	0.3140	-0.0023	0.9977	0.9986
12	12_12575921_T_TA	12575921	12422987	rs113936393	TA	T	0.2064	0.0005	1.0005	1.0002
12	12_12710877_G_T	12710877	12557943	rs74945783	T	G	0.0807	0.0259	1.0262	1.0042
12	12_12871099_T_G	12871099	12718165	rs2066827	G	T	0.2387	-0.0015	0.9985	0.9993
12	12_13144492_C_T	13144492	12991558	rs11834741	T	C	0.0615	-0.0031	0.9969	0.9996
12	12_13191493_C_C AA	13191493	13038559	rs3080953	CAA	C	0.7517	0.0002	1.0002	1.0003
12	12_13270924_T_C	13270924	13117990	rs10845705	C	T	0.2541	-0.0062	0.9938	0.9969
12	12_13337385_G_A	13337385	13184451	rs6488595	A	G	0.8931	-0.0139	0.9862	0.9755
12	12_13360231_G_A	13360231	13207297	rs74063269	A	G	0.1112	0.0003	1.0003	1.0001
12	12_14408554_G_C	14408554	14255620	rs75905550	C	G	0.1956	0.0159	1.0160	1.0063
12	12_14413931_G_C	14413931	14260997	rs12422552	C	G	0.2619	0.0093	1.0093	1.0049
12	12_14730966_T_A	14730966	14578032	rs78973331	A	T	0.1545	0.0034	1.0034	1.0011
12	12_15308279_G_A	15308279	15155345	rs67581511	A	G	0.2423	0.0074	1.0074	1.0036
12	12_17591303_A_G	17591303	17438369	rs1163944	G	A	0.7418	0.0014	1.0014	1.0021
12	12_18250884_G_T	18250884	18097950	rs111219473	T	G	0.1234	0.0159	1.0160	1.0040

12	12_18398806_T_C	18398806	18245872	rs10505814	C	T	0.7008	0.0057	1.0057	1.0080
12	12_18459387_C_T	18459387	18306453	rs12582971	T	C	0.1331	-0.0037	0.9963	0.9990
12	12_20645903_G_T	20645903	20492969	rs7295612	T	G	0.6845	0.0011	1.0011	1.0015
12	12_20650951_C_T	20650951	20498017	rs7484304	T	C	0.2491	-0.0105	0.9896	0.9948
12	12_20650985_C_T	20650985	20498051	rs7131827	T	C	0.3039	0.0050	1.0050	1.0030
12	12_25189664_TTTG	25189664	25036730	rs757757128	T	TTTG	0.0313	-0.0249	0.9754	0.9985
12	12_28045047_A_G	28045047	27892114	rs111798596	G	A	0.0233	-0.0140	0.9861	0.9994
12	12_28139846_T_C	28139846	27986913	rs805510	C	T	0.8782	0.0302	1.0307	1.0546
12	12_28149568_C_T	28149568	27996635	rs788458	T	C	0.1170	-0.0094	0.9906	0.9978
12	12_28151609_A_C	28151609	27998676	rs812020	C	A	0.2759	-0.0167	0.9834	0.9909
12	12_28152993_G_A	28152993	28000060	rs805583	A	G	0.3033	-0.0027	0.9973	0.9984
12	12_28157711_G_A	28157711	28004778	rs11049266	A	G	0.0151	0.0000	1.0000	1.0000
12	12_28174817_C_T	28174817	28021884	rs7297051	T	C	0.2421	-0.0506	0.9507	0.9762
12	12_28183286_A_G	28183286	28030353	rs7976725	G	A	0.2321	-0.0029	0.9971	0.9987
12	12_28221970_T_A	28221970	28069037	rs6487658	A	T	0.4614	-0.0044	0.9956	0.9960
12	12_28258195_G_T	28258195	28105262	rs185286466	T	G	0.0189	0.0077	1.0077	1.0003
12	12_28304439_T_C	28304439	28151506	rs1600346	C	T	0.3603	-0.0227	0.9776	0.9839
12	12_28347382_C_T	28347382	28194449	rs11049431	T	C	0.2153	-0.0021	0.9979	0.9991
12	12_29000608_C_T	29000608	28847675	rs5018009	T	C	0.8697	0.0031	1.0031	1.0054
12	12_29140260_G_A	29140260	28987327	rs1027113	A	G	0.9126	0.0357	1.0363	1.0674
12	12_29229856_G_A	29229856	29076923	rs10771479	A	G	0.8569	-0.0028	0.9972	0.9952
12	12_29352686_G_A	29352686	29199753	rs10743648	A	G	0.8415	-0.0034	0.9966	0.9943
12	12_29489004_A_G	29489004	29336071	rs77301656	G	A	0.0483	-0.0228	0.9775	0.9978
12	12_29634797_T_A	29634797	29481864	rs35049626	A	T	0.0319	-0.0080	0.9920	0.9995
12	12_29964996_T_C	29964996	29812063	rs566253232	C	T	0.0233	-0.0059	0.9941	0.9997
12	12_31276226_G_A	31276226	31123292	rs7133957	A	G	0.1029	-0.0121	0.9880	0.9975

12	12_31522408_A_C	31522408	31369474	rs708205	C	A		0.3605	0.0049	1.0049	1.0035
12	12_31763639_G_A	31763639	31610705	rs7310240	A	G		0.5441	-0.0057	0.9943	0.9938
12	12_32362886_G_A	32362886	32209952	rs3850981	A	G		0.0799	-0.0130	0.9871	0.9979
12	12_32843389_G_C	32843389	32690455	rs73082818	C	G		0.0215	-0.0195	0.9807	0.9992
12	12_42498057_A_T	42498057	42104255	rs34619182	T	A		0.1824	0.0041	1.0041	1.0015
12	12_42528698_T_G	42528698	42134896	rs3852593	G	T		0.3560	0.0059	1.0059	1.0042
12	12_46522194_A_A	46522194	46128411		AGTATTC TATG	A		0.2437	-0.0016	0.9984	0.9992
12	12_48251076_C_T	48251076	47857293	rs12721367	T	C		0.0227	0.0139	1.0140	1.0006
12	12_49123316_C_C	49123316	48729533	rs149424542	CA	C		0.2958	0.0079	1.0079	1.0047
12	12_50006464_A_C	50006464	49612681	rs117792145	C	A		0.0108	0.0174	1.0176	1.0004
12	12_53931047_TTCT CCATG_T	53931047	53537263	12_53931047_ TTCTCCATG_T	T	TTCTCC ATG		0.0240	0.0132	1.0133	1.0006
12	12_54958164_C_G	54958164	54564380	rs7953703	G	C		0.2905	0.0022	1.0022	1.0013
12	12_54967901_C_T	54967901	54574117	rs3782411	T	C		0.3142	0.0036	1.0036	1.0023
12	12_55047126_G_A	55047126	54653342	rs11171005	A	G		0.2241	-0.0016	0.9984	0.9993
12	12_56438149_T_TG	56438149	56044365	rs59385427	TG	T		0.9371	-0.0066	0.9934	0.9877
12	12_56493822_A_C	56493822	56100038	rs2292238	C	A		0.4123	-0.0076	0.9924	0.9938
12	12_57146069_T_G	57146069	56752285	rs22777339	G	T		0.1037	-0.0212	0.9790	0.9957
12	12_57836098_A_G	57836098	57442315	rs2943692	G	A		0.2404	-0.0086	0.9914	0.9959
12	12_57847938_G_A	57847938	57454155	rs703845	A	G		0.2773	-0.0052	0.9948	0.9971
12	12_57887130_ATA TATAT_A	57887130	57493347	rs756746321	A	ATATAT AT		0.1301	-0.0047	0.9953	0.9988
12	12_58091039_T_G	58091039	57697256	rs17455486	G	T		0.0291	-0.0106	0.9895	0.9994
12	12_58274737_G_T	58274737	57880954	rs147072673	T	G		0.0132	0.0240	1.0243	1.0006
12	12_58912426_C_T	58912426	58518643	rs79808633	T	C		0.0251	-0.0097	0.9903	0.9995

12	12_64105782_TA_T AA	64105782	63712002		TAA	TA	0.1771	0.0031	1.0031	1.0011
12	12_64318956_C_A	64318956	63925176	rs61933130	A	C	0.0358	-0.0280	0.9724	0.9980
12	12_64428763_T_G	64428763	64034983	rs73130130	G	T	0.2550	0.0085	1.0085	1.0044
12	12_64531763_A_T	64531763	64137983	rs12831194	T	A	0.5177	-0.0020	0.9980	0.9979
12	12_68002302_G_C	68002302	67608522	rs11176802	C	G	0.1429	0.0062	1.0062	1.0018
12	12_68112905_A_G	68112905	67719125	rs9652024	G	A	0.6277	-0.0079	0.9921	0.9901
12	12_68199301_A_G	68199301	67805521	rs116654690	G	A	0.0224	-0.0442	0.9568	0.9981
12	12_68554461_A_G	68554461	68160681	rs2069732	G	A	0.0367	-0.0098	0.9902	0.9993
12	12_69100408_C_T	69100408	68706628	rs2546522	T	C	0.2749	-0.0081	0.9919	0.9956
12	12_69363979_C_T	69363979	68970199	rs117531987	T	C	0.0290	0.0048	1.0048	1.0003
12	12_69418116_A_G	69418116	69024336	rs55836995	G	A	0.0909	-0.0082	0.9918	0.9985
12	12_69551106_T_C	69551106	69157326	rs78574703	C	T	0.0575	0.0120	1.0121	1.0014
12	12_69553408_A_C	69553408	69159628	rs61926895	C	A	0.0988	0.0030	1.0030	1.0006
12	12_69676379_TTA_ T	69676379	69282599	12:69676379_ TTA_T	T	TTA	0.6234	0.0074	1.0074	1.0093
12	12_69823491_T_G	69823491	69429711	rs17106576	G	T	0.2477	0.0018	1.0018	1.0009
12	12_70088344_T_C	70088344	69694564	rs75229567	C	T	0.0530	-0.0050	0.9950	0.9995
12	12_70798355_A_T	70798355	70404575	rs2870876	T	A	0.1810	0.0145	1.0146	1.0053
12	12_70809003_C_G	70809003	70415223	rs28672988	G	C	0.2422	0.0012	1.0012	1.0006
12	12_72324371_G_C	72324371	71930591	rs4131347	C	G	0.2225	-0.0073	0.9927	0.9968
12	12_72391545_GA_ G	72391545	71997765	12:72391545_ GA_G	G	GA	0.2647	0.0000	1.0000	1.0000
12	12_77429681_TA_T	77429681	77035901	12:77429681_ TA_T	T	TA	0.5275	0.0085	1.0085	1.0090
12	12_77445728_T_A	77445728	77051948	rs74650509	A	T	0.1068	0.0020	1.0020	1.0004
12	12_80441323_A_G	80441323	80047543	rs59956390	G	A	0.0245	-0.0125	0.9876	0.9994

12	12_82472014_T_A	82472014	82078235	rs7979964	A	T	0.5239	0.0013	1.0013	1.0014
12	12_83064195_G_G A	83064195	82670416	rs111622698	GA	G	0.0992	0.0115	1.0116	1.0023
12	12_83085107_A_A T	83085107	82691328	rs111797688	AT	A	0.1178	0.0050	1.0050	1.0012
12	12_83105773_T_C	83105773	82711994	rs7134766	C	T	0.8773	-0.0106	0.9895	0.9816
12	12_84692840_G_G TA	84692840	84299061	rs10677679	GTA	G	0.2820	0.0028	1.0028	1.0016
12	12_85004551_C_T	85004551	84610772	rs10862899	T	C	0.4955	0.0086	1.0086	1.0086
12	12_85009437_T_C	85009437	84615658	rs202049448	C	T	0.3360	-0.0069	0.9931	0.9954
12	12_85019560_G_A	85019560	84625781	rs73365443	A	G	0.1936	-0.0008	0.9992	0.9997
12	12_85024975_G_A	85024975	84631196	rs11116506	A	G	0.1721	-0.0001	0.9999	1.0000
12	12_87480758_ATCT _A	87480758	87086981	12:87480758_ ATCT_A	A	ATCT	0.1753	-0.0069	0.9931	0.9976
12	12_88165225_T_C	88165225	87771448	rs77205452	C	T	0.0225	-0.0076	0.9924	0.9997
12	12_88253612_AAA AATAGACCTTCCAA AT_A	88253612	87859835	rs774846867	A	AAAAAT AGACCT TCCAAA T	0.6417	0.0000	1.0000	1.0000
12	12_92251023_A_G	92251023	91857247	rs67075180	G	A	0.0302	0.0188	1.0190	1.0011
12	12_92948635_T_C	92948635	92554859	rs116937902	C	T	0.0145	-0.0067	0.9933	0.9998
12	12_93190239_T_TT A	93190239	92796463	rs144029000	TTA	T	0.4649	-0.0016	0.9984	0.9985
12	12_93478349_A_C	93478349	93084573	rs142852759	C	A	0.0181	-0.0088	0.9912	0.9997
12	12_93958657_A_G	93958657	93564881	rs10859531	G	A	0.1047	0.0044	1.0044	1.0009
12	12_94661453_A_G	94661453	94267677	rs61708525	G	A	0.2937	0.0047	1.0047	1.0028
12	12_94661511_T_G	94661511	94267735	rs56725874	G	T	0.1144	0.0006	1.0006	1.0001
12	12_94672888_G_A	94672888	94279112	rs832504	A	G	0.8467	-0.0045	0.9955	0.9924

12	12_95407517_C_T	95407517	95013741	rs138868138	T	C	0.0205	-0.0208	0.9794	0.9992
12	12_95906139_C_T	95906139	95512363	rs71458596	T	C	0.0267	-0.0102	0.9899	0.9995
12	12_96021033_T_C	96021033	95627257	rs2367556	C	T	0.5086	-0.0010	0.9990	0.9990
12	12_96022099_G_C	96022099	95628323	rs12307566	C	G	0.5710	-0.0069	0.9931	0.9922
12	12_96027467_C_T	96027467	95633691	rs11836367	T	C	0.3436	-0.0329	0.9676	0.9779
12	12_96027759_A_G	96027759	95633983	rs17356907	G	A	0.2963	-0.0267	0.9737	0.9844
12	12_96028525_A_G	96028525	95634749	rs1833472	G	A	0.9296	-0.0056	0.9944	0.9896
12	12_96141866_A_G	96141866	95748088	rs117374882	G	A	0.1717	-0.0012	0.9988	0.9996
12	12_96243051_G_A	96243051	95849273	rs76415780	A	G	0.0498	0.0112	1.0113	1.0011
12	12_97221040_G_A	97221040	96827262	rs62644119	A	G	0.7167	0.0043	1.0043	1.0062
12	12_97283972_T_C	97283972	96890194	rs918105	C	T	0.4619	0.0053	1.0053	1.0049
12	12_97606385_C_T	97606385	97212607	rs6538789	T	C	0.0297	-0.0147	0.9854	0.9991
12	12_103097070_A_G	103097070	102703292	rs7306173	G	A	0.1148	0.0140	1.0141	1.0032
12	12_103101412_T_C	103101412	102707634	rs1463770	C	T	0.7164	-0.0057	0.9943	0.9919
12	12_105978901_C_T	105978901	105585123	rs11112601	T	C	0.0303	0.0131	1.0132	1.0008
12	12_106022283_A_AGGGT	106022283	105628505	rs200487971	AGGGGT	A	0.5686	0.0030	1.0030	1.0034
12	12_106421904_C_T	106421904	106028126	rs76487198	T	C	0.1013	-0.0014	0.9986	0.9997
12	12_108098065_G_C	108098065	107704288	rs67446565	C	G	0.1602	-0.0056	0.9944	0.9982
12	12_109905720_G_A	109905720	109467915	rs9943764	A	G	0.1806	-0.0073	0.9927	0.9974
12	12_111189543_T_G	111189543	110751738	rs10161511	G	T	0.7724	-0.0017	0.9983	0.9974
12	12_111288843_T_C	111288843	110851039	rs10219717	C	T	0.6135	0.0013	1.0013	1.0016
12	12_111349849_A_G	111349849	110912045	rs11065766	G	A	0.3151	0.0027	1.0027	1.0017

12	12_111427783_GT_G	111427783	110989979	12:111427783_GT_G	G	GT	0.6130	0.0034	1.0034	1.0042
12	12_111600134_G_T	111600134	111162330	rs11065822	T	G	0.3715	-0.0188	0.9814	0.9862
12	12_111712755_CA_C	111712755	111274951	rs771598754	C	CA	0.2212	0.0003	1.0003	1.0001
12	12_111826477_A_AAAATT	111826477	111388673	rs111338191	AAAATT	A	0.5074	0.0053	1.0053	1.0054
12	12_113028429_G_A	113028429	112590625	rs67436553	A	G	0.0239	0.0018	1.0018	1.0001
12	12_113032969_TA_T	113032969	112595165	12:113032969_TA_T	T	TA	0.5827	0.0016	1.0016	1.0019
12	12_114108404_T_C	114108404	113670599	rs535239	C	T	0.0184	0.0019	1.0019	1.0001
12	12_115092018_A_T	115092018	114654213	rs35383422	T	A	0.2493	0.0000	1.0000	1.0000
12	12_115108136_T_C	115108136	114670331	rs1061657	C	T	0.2615	0.0026	1.0026	1.0014
12	12_115109223_C_G	115109223	114671418	rs3741698	G	C	0.2829	0.0219	1.0221	1.0126
12	12_115364215_A_G	115364215	114926410	rs75843093	G	A	0.0372	0.0062	1.0062	1.0005
12	12_115370514_CA_C	115370514	114932709	12:115370514_CA_C	C	CA	0.7071	-0.0013	0.9987	0.9982
12	12_115374162_G_A	115374162	114936357	rs2891538	A	G	0.4143	-0.0043	0.9957	0.9964
12	12_115478150_G_A	115478150	115040345	rs355515	A	G	0.0559	-0.0252	0.9751	0.9972
12	12_115558444_G_C	115558444	115120639	rs7970854	C	G	0.3370	0.0000	1.0000	1.0000
12	12_115570046_G_A	115570046	115132241	rs35426	A	G	0.5793	0.0045	1.0045	1.0052

12	12_11583800_G_A	115583800	115145995	rs35423	A	G	0.5037	0.0000	1.0000	1.0000
12	12_115710648_G_A	115710648	115272843	rs1155698	A	G	0.6599	0.0000	1.0000	1.0000
12	12_115775595_C_T	115775595	115337790	rs74959053	T	C	0.1050	0.0135	1.0136	1.0029
12	12_115789327_T_C	115789327	115351522	rs4767312	C	T	0.1432	0.0000	1.0000	1.0000
12	12_115796577_A_G	115796577	115358772	rs11067551	G	A	0.1959	-0.0235	0.9768	0.9909
12	12_115831911_G_GA	115831911	115394106	12:115831911_GA_G	G	GA	0.1628	0.0000	1.0000	1.0000
12	12_115834946_C_G	115834946	115397141	rs2133317	G	C	0.3827	-0.0046	0.9954	0.9965
12	12_115835836_T_C	115835836	115398031	rs2454399	C	T	0.4171	-0.0458	0.9552	0.9630
12	12_115837032_T_A	115837032	115399227		TA	T	0.3914	-0.0083	0.9917	0.9935
12	12_115838544_T_A	115838544	115400739	rs10466929	A	T	0.4886	0.0010	1.0010	1.0010
12	12_115852376_A_C	115852376	115414571	rs7979538	C	A	0.2902	0.0047	1.0047	1.0027
12	12_115916851_C_C	115916851	115479046	rs576675881	CA	C	0.0645	-0.0074	0.9926	0.9990
12	12_115935967_C_T	115935967	115498162	rs57863152	T	C	0.0444	0.0000	1.0000	1.0000
12	12_115937885_T_C	115937885	115500080	rs66707136	C	T	0.0518	-0.0213	0.9789	0.9978
12	12_116017035_A_G	116017035	115579230	rs7953921	G	A	0.5045	0.0008	1.0008	1.0008
12	12_116347863_A_G	116347863	115910058	rs12296461	G	A	0.4791	-0.0048	0.9952	0.9954
12	12_116757287_A_T	116757287	116319482	rs4767396	T	A	0.3410	-0.0133	0.9868	0.9910
12	12_117068276_C_G	117068276	116630471	rs12814231	G	C	0.3478	0.0035	1.0035	1.0024
12	12_117071777_C_T	117071777	116633972	rs12823501	T	C	0.4735	0.0011	1.0011	1.0010

12	12_120793690_G_GAA	120793690	120355887	rs56655594	GGAA	G	0.1619	0.0009	1.0009	1.0003
12	12_120832146_C_T	120832146	120394343	rs206966	T	C	0.1593	0.0216	1.0218	1.0070
12	12_121416622_C_G	121416622	120978819	rs1169289	G	C	0.4556	-0.0078	0.9922	0.9929
12	12_121450384_G_C	121450384	121012581	rs2254971	C	G	0.3843	-0.0019	0.9981	0.9985
12	12_122717710_C_A	122717710	122233163	rs117523992	A	C	0.0253	-0.0066	0.9934	0.9997
12	12_123430082_C_T	123430082	122945535	rs12815479	T	C	0.0840	-0.0109	0.9892	0.9982
12	12_123896851_G_A	123896851	123412304	rs28624763	A	G	0.0301	-0.0245	0.9758	0.9985
12	12_125674073_T_T	125674073	125189527		TG	T	0.3895	-0.0011	0.9989	0.9991
12	12_127144291_A_G	127144291	126659745	rs7138452	G	A	0.7640	0.0064	1.0064	1.0098
12	12_129209173_T_G	129209173	128724628	rs61669394	G	T	0.0181	0.0280	1.0284	1.0010
12	12_130476989_C_G	130476989	129992444	rs117236628	G	C	0.0200	-0.0223	0.9779	0.9991
13	13_19536600_A_C	19536600	18962460	rs11617737	C	A	0.4332	-0.0025	0.9975	0.9978
13	13_21019209_C_G	21019209	20445070	rs73160875	G	C	0.0155	0.0338	1.0344	1.0011
13	13_23625664_G_A	23625664	23051525	rs7986188	A	G	0.6557	0.0010	1.0010	1.0013
13	13_24281011_T_C	24281011	23706872	rs4770478	C	T	0.1748	0.0006	1.0006	1.0002
13	13_24298749_CA_C	24298749	23724610	13:24298749_CA_C	C	CA	0.1624	0.0001	1.0001	1.0000
13	13_24341843_G_A	24341843	23767704	rs9510851	A	G	0.1703	0.0112	1.0113	1.0038
13	13_24971857_C_T	24971857	24397719	rs55813922	T	C	0.1334	0.0123	1.0124	1.0033
13	13_24976086_T_C	24976086	24401948	rs7321198	C	T	0.5663	0.0028	1.0028	1.0032
13	13_24984540_AC_T	24984540	24410402		TC	AC	0.3572	-0.0046	0.9954	0.9967

13	C	13_25018249_C_T	25018249	24444111	rs143552353	T	C	0.0339	-0.0020	0.9980	0.9999
13		13_30107388_T_C	30107388	29533251	rs3783256	C	T	0.6418	-0.0062	0.9938	0.9921
13		13_30118193_C_T	30118193	29544056	rs9578107	T	C	0.0971	0.0095	1.0095	1.0019
13	A	13_32704954_AT_	32704954	32130817	13:32704954_	A	AT	0.3699	0.0029	1.0029	1.0021
13		13_32755706_C_T	32755706	32181569	rs2520691	T	C	0.1984	-0.0017	0.9983	0.9993
13		13_32773204_C_T	32773204	32199067	rs73169113	T	C	0.1829	0.0125	1.0126	1.0046
13		13_32798235_T_TA	32798235	32224098	rs5802638	TA	T	0.5514	0.0017	1.0017	1.0019
13		13_32972626_A_T	32972626	32398489	rs11571833	T	A	0.0079	0.1809	1.1983	1.0031
13		13_33170934_A_G	33170934	32596797	rs9535012	G	A	0.1065	0.0000	1.0000	1.0000
13		13_34752214_T_A	34752214	34178077	rs9598722	A	T	0.4438	-0.0026	0.9974	0.9977
13	A	13_34784728_AT_	34784728	34210591	13:34784728_	A	AT	0.4373	0.0074	1.0074	1.0065
13		13_36071786_T_C	36071786	35497649	rs1381476	C	T	0.6499	-0.0100	0.9900	0.9871
13		13_36072172_G_A	36072172	35498035	rs1466402	A	G	0.9553	-0.0140	0.9861	0.9736
13		13_36133143_T_A	36133143	35559006	rs73171571	A	T	0.0240	0.0029	1.0029	1.0001
13		13_36521433_T_G	36521433	35947296	rs1936004	G	T	0.6645	-0.0029	0.9971	0.9962
13		13_37897575_G_A	37897575	37323438	rs2209245	A	G	0.8802	-0.0004	0.9996	0.9993
13		13_39337618_C_G	39337618	38763481	rs55864343	G	C	0.7249	0.0065	1.0065	1.0095
13		13_40088007_G_A	40088007	39513870	rs7981122	A	G	0.2279	0.0030	1.0030	1.0014
13		13_40339158_C_T	40339158	39765021	rs73179574	T	C	0.0674	0.0006	1.0006	1.0001
13		13_40355430_G_A	40355430	39781293	rs73179582	A	G	0.0529	0.0144	1.0145	1.0015
13		13_40658787_C_T	40658787	40084650	rs1414932	T	C	0.5009	0.0071	1.0071	1.0072
13		13_40772172_T_C	40772172	40198035	rs61954176	C	T	0.2187	0.0024	1.0024	1.0011
13		13_40808620_G_A	40808620	40234483	rs4943745	A	G	0.7499	-0.0030	0.9970	0.9955
13		13_40815320_G_A	40815320	40241183	rs11147786	A	G	0.0647	0.0062	1.0062	1.0008

13	13_40824180_C_T	40824180	40250043	rs11840120	T	C	0.1530	0.0095	1.0095	1.0029
13	13_41891170_C_T	41891170	41317034	rs7319540	T	C	0.0742	-0.0117	0.9884	0.9983
13	13_41981801_AT_A	41981801	41407665	13_41981801_AT_A	A	AT	0.0657	-0.0001	0.9999	1.0000
13	13_41988053_C_A	41988053	41413917	rs4427698	A	C	0.1760	-0.0096	0.9904	0.9966
13	13_43501356_A_G	43501356	42927220	rs9315973	G	A	0.8303	0.0251	1.0254	1.0427
13	13_43522038_G_A	43522038	42947902	rs12427475	A	G	0.0608	0.0000	1.0000	1.0000
13	13_48352745_G_A	48352745	47778610	rs149670665	A	G	0.0200	-0.0007	0.9993	1.0000
13	13_51085041_G_A	51085041	50510905	rs9562985	A	G	0.2441	-0.0095	0.9905	0.9954
13	13_57924666_G_C	57924666	57350532	rs78449128	C	G	0.0180	-0.0272	0.9732	0.9990
13	13_57984399_G_A	57984399	57410265	rs78263459	A	G	0.0322	-0.0263	0.9740	0.9983
13	13_58257265_A_G	58257265	57683131	rs9597587	G	A	0.2958	-0.0062	0.9938	0.9963
13	13_58463779_C_T	58463779	57889645	rs34667220	T	C	0.2481	0.0073	1.0073	1.0036
13	13_58713360_C_G	58713360	58139226	rs3012850	G	C	0.2380	0.0028	1.0028	1.0013
13	13_61217736_C_T	61217736	60643602	rs61968726	T	C	0.0124	0.0227	1.0230	1.0006
13	13_69370155_T_G	69370155	68796023	rs117211244	G	T	0.0443	0.0059	1.0059	1.0005
13	13_70007016_C_T	70007016	69432884	rs353836	T	C	0.5833	0.0000	1.0000	1.0000
13	13_70205508_T_G	70205508	69631376	rs117950521	G	T	0.0528	0.0000	1.0000	1.0000
13	13_73806982_T_C	73806982	73232845	rs12870942	C	T	0.3153	0.0108	1.0109	1.0069
13	13_73818924_A_A	73818924	73244787	rs111683019	AT	A	0.4544	0.0000	1.0000	1.0000
13	13_73960952_A_G	73960952	73386815	rs2181965	G	A	0.7618	0.0138	1.0139	1.0213
13	13_73967507_T_C	73967507	73393370	rs4885096	C	T	0.6870	0.0081	1.0081	1.0112
13	13_78996578_C_T	78996578	78422443	rs61964767	T	C	0.0313	-0.0164	0.9837	0.9990
13	13_80391295_A_C	80391295	79817160	rs4386023	C	A	0.4948	-0.0030	0.9970	0.9970
13	13_85861553_T_G	85861553	85287418	rs9566061	G	T	0.0353	-0.0053	0.9947	0.9996
13	13_88381395_C_T	88381395	87729140	rs117480076	T	C	0.0188	-0.0018	0.9982	0.9999

13	13_90611517_A_G	90611517	89959263	rs12050059	G	A	0.2091	-0.0187	0.9815	0.9923
13	13_91434105_G_C	91434105	90781851	rs56375900	C	G	0.1741	0.0064	1.0064	1.0022
13	13_91939972_CAA AT_C	91939972	91287718	rs375709528	C	CAAAT	0.4593	-0.0103	0.9898	0.9906
13	13_92457036_T_C	92457036	91804782	rs1854971	C	T	0.5565	0.0110	1.0111	1.0123
13	13_92792534_C_T	92792534	92140281	rs17188390	T	C	0.1587	-0.0065	0.9935	0.9979
13	13_93663234_T_C	93663234	93010981	rs76619105	C	T	0.0459	-0.0012	0.9988	0.9999
13	13_93897052_T_G	93897052	93244799	rs60426741	G	T	0.0754	-0.0097	0.9903	0.9985
13	13_97886728_T_C	97886728	97234474	rs9516878	C	T	0.7067	0.0036	1.0036	1.0051
13	13_98815232_C_T	98815232	98162978	rs72653394	T	C	0.0666	0.0156	1.0157	1.0021
13	13_99068255_T_C	99068255	98416001	rs12429460	C	T	0.1370	-0.0044	0.9956	0.9988
13	13_99429807_C_T	99429807	98777553	rs9557057	T	C	0.3229	-0.0037	0.9963	0.9976
13	13_100648099_A_	100648099	99995845	rs1347190	G	A	0.4435	-0.0035	0.9965	0.9969
13	13_100693650_TA_	100693650	100041396		T	TA	0.5201	-0.0089	0.9911	0.9908
13	13_103141574_G_	103141574	102489224	rs10508088	A	G	0.0528	-0.0030	0.9970	0.9997
13	13_103155752_A_C	103155752	102503402	rs78529221	C	A	0.0752	-0.0024	0.9976	0.9996
13	13_103424321_T_C	103424321	102771971	rs151250473	C	T	0.0131	-0.0137	0.9864	0.9996
13	13_104277179_A_	104277179	103624829	rs7320001	G	A	0.0473	0.0032	1.0032	1.0003
13	13_105115053_C_A	105115053	104462703	rs73594938	A	C	0.0154	-0.0407	0.9601	0.9988
13	13_106422213_G_	106422213	105769864	rs1576158	A	G	0.6553	0.0041	1.0041	1.0054
13	13_107577537_A_	107577537	106925189	rs9555296	G	A	0.2937	0.0064	1.0064	1.0038
13	13_107680606_G_	107680606	107028258	rs12877195	A	G	0.0577	-0.0006	0.9994	0.9999

13	13_108669929_A_G	108669929	108017581	rs12875908	G	A	0.5196	0.0030	1.0030	1.0031
13	13_110629518_C_G	110629518	109977171	rs7334266	G	C	0.2438	0.0096	1.0096	1.0047
13	13_110651131_C_T	110651131	109998784	rs11069818	T	C	0.4934	0.0008	1.0008	1.0008
13	13_110857823_C_T	110857823	110205476	rs482757	T	C	0.6356	0.0124	1.0125	1.0159
13	13_111592904_G_A	111592904	110940557	rs60926826	A	G	0.1410	-0.0006	0.9994	0.9998
13	13_111649724_T_C	111649724	110997377	rs61968960	C	T	0.1654	-0.0072	0.9928	0.9976
13	13_112077465_C_G	112077465	111425118	rs2528773	G	C	0.5521	0.0074	1.0074	1.0082
13	13_114323997_T_C	114323997	113669682	rs9796234	C	T	0.5006	0.0072	1.0072	1.0072
13	13_114433140_G_A	114433140	113730167	rs36149740	A	G	0.4614	-0.0001	0.9999	0.9999
13	13_114632156_T_C	114632156	113929183	rs9604487	C	T	0.0450	-0.0146	0.9855	0.9987
14	14_23317825_A_G	23317825	22848616	rs17882077	G	A	0.3725	0.0070	1.0070	1.0052
14	14_24730100_A_C	24730100	24260894	rs7151201	C	A	0.1879	0.0032	1.0032	1.0012
14	14_24735624_A_G	24735624	24266418	rs2877612	G	A	0.2328	0.0065	1.0065	1.0030
14	14_24736027_G_A	24736027	24266821	rs14193	A	G	0.3619	0.0025	1.0025	1.0018
14	14_25555593_C_T	25555593	25086387	rs4494455	T	C	0.3012	-0.0076	0.9924	0.9954
14	14_25630912_G_A	25630912	25161706	rs17109642	A	G	0.1904	0.0100	1.0101	1.0038
14	14_25655764_A_G	25655764	25186558	rs11159142	G	A	0.6991	0.0036	1.0036	1.0050
14	14_25695907_A_G	25695907	25226701	rs17212065	G	A	0.1092	0.0055	1.0055	1.0012
14	14_25875224_T_G	25875224	25406018	rs72688549	G	T	0.1497	0.0040	1.0040	1.0012
14	14_27865166_A_G	27865166	27395960	rs8021545	G	A	0.0912	-0.0160	0.9841	0.9971
14	14_32012593_G_A	32012593	31543387	rs8016747	A	G	0.7366	-0.0095	0.9905	0.9861
14	14_32310803_T_C	32310803	31841597	rs7158089	C	T	0.3163	0.0048	1.0048	1.0030
14	14_32596649_T_C	32596649	32127443	rs140783387	C	T	0.0887	0.0230	1.0233	1.0041

14	14_32900776_C_A	32900776	32431570	rs71419908	A	C	0.4487	0.0020	1.0020	1.0018
14	14_32987758_A_G	32987758	32518552	rs148987100	G	A	0.2279	-0.0128	0.9873	0.9942
14	14_33046471_T_G	33046471	32577265	rs768787	G	T	0.6510	0.0081	1.0081	1.0106
14	14_35260354_A_A AAGAG	35260354	34791148		AAAAGAG	A	0.1359	0.0000	1.0000	1.0000
14	14_35323160_T_C	35323160	34853954	rs10129577	C	T	0.1015	-0.0076	0.9924	0.9985
14	14_35359783_C_T	35359783	34890577	rs59307778	T	C	0.3970	0.0062	1.0062	1.0049
14	14_35412105_G_G A	35412105	34942899	rs542632225	GA	G	0.3003	-0.0039	0.9961	0.9977
14	14_35422811_C_T	35422811	34953605	rs75759052	T	C	0.2217	-0.0015	0.9985	0.9993
14	14_35582138_A_G	35582138	35112932	rs12879871	G	A	0.3869	-0.0103	0.9898	0.9921
14	14_37122790_A_G	37122790	36653585	rs1018464	G	A	0.2478	-0.0069	0.9931	0.9966
14	14_37123250_A_C	37123250	36654045	rs1018466	C	A	0.5321	-0.0068	0.9932	0.9928
14	14_37128564_C_A	37128564	36659359	rs34914085	A	C	0.2122	-0.0356	0.9650	0.9852
14	14_37129341_A_C	37129341	36660136	rs2073242	C	A	0.6189	0.0000	1.0000	1.0000
14	14_37228504_C_T	37228504	36759299	rs2253012	T	C	0.4434	0.0152	1.0153	1.0136
14	14_37268797_G_A	37268797	36799592	rs848092	A	G	0.3396	-0.0035	0.9965	0.9976
14	14_37481041_G_A	37481041	37011836	rs17767511	A	G	0.1012	-0.0074	0.9926	0.9985
14	14_37660202_G_A	37660202	37190997	rs117137044	A	G	0.1075	-0.0128	0.9873	0.9973
14	14_38142026_ATT_ A	38142026	37672821	rs774465251	A	ATT	0.2735	0.0104	1.0105	1.0057
14	14_38208687_G_C	38208687	37739482	rs2415410	C	G	0.6884	-0.0030	0.9970	0.9959
14	14_38848824_T_A	38848824	38379620	rs1168548	A	T	0.2795	-0.0003	0.9997	0.9998
14	14_38849500_A_G	38849500	38380296	rs8023173	G	A	0.3203	0.0000	1.0000	1.0000
14	14_38996181_TCAT TTAAGCCTTC_T	38996181	38526977	14:38996181_ TCATTAAAGC CTTC_T	T	TCATT AAAGCC TTC	0.0239	-0.0113	0.9888	0.9995
14	14_38996493_G_A	38996493	38527289	rs75951442	A	G	0.0353	-0.0002	0.9998	1.0000

14	14_39414930_C_T	39414930	38945726	rs1951221	T	C	0.8803	-0.0114	0.9887	0.9801
14	14_39416898_C_T	39416898	38947694	rs2025063	T	C	0.5403	-0.0024	0.9976	0.9974
14	14_39674203_C_A	39674203	39204999	rs10149495	A	C	0.1213	-0.0015	0.9985	0.9996
14	14_40925291_G_A	40925291	40456087	rs78979382	A	G	0.0369	0.0137	1.0138	1.0010
14	14_40955886_CT_C	40955886	40486682	14:40955886_ CT_C	C	CT	0.0369	0.0170	1.0171	1.0013
14	14_42183290_AT_A	42183290	41714087	14:42183290_ AT_A	A	AT	0.0243	-0.0270	0.9734	0.9987
14	14_45043928_C_T	45043928	44574725	rs10152023	T	C	0.5769	-0.0069	0.9931	0.9921
14	14_45397355_A_C	45397355	44928152	rs79851852	C	A	0.0211	0.0000	1.0000	1.0000
14	14_49274078_C_G	49274078	48804875	rs2416185	G	C	0.0825	0.0000	1.0000	1.0000
14	14_50520602_C_T	50520602	50053884	rs7156043	T	C	0.1140	-0.0086	0.9914	0.9980
14	14_52123148_C_T	52123148	51656430	rs1966185	T	C	0.9492	0.0204	1.0206	1.0395
14	14_52282868_CGG TGAGCGT_C	52282868	51816150	rs771414926	C	CGGTGA GCGT	0.5632	-0.0034	0.9966	0.9962
14	14_53696414_A_T	53696414	53229696	rs7401132	T	A	0.2721	-0.0088	0.9912	0.9952
14	14_53711660_T_C	53711660	53244942	rs12891259	C	T	0.1043	0.0059	1.0059	1.0012
14	14_53890820_T_C	53890820	53424102	rs7151904	C	T	0.8285	0.0011	1.0011	1.0018
14	14_54017042_G_A	54017042	53550324	rs79974315	A	G	0.0609	0.0196	1.0198	1.0024
14	14_58810321_C_T	58810321	58343603	rs61974494	T	C	0.0206	0.0000	1.0000	1.0000
14	14_59100519_C_C AA	59100519	58633801	rs529583772	CAA	C	0.6868	-0.0071	0.9929	0.9903
14	14_59108678_T_C	59108678	58641960	rs167481	C	T	0.7415	-0.0021	0.9979	0.9969
14	14_59121567_CA_C	59121567	58654849	rs569494089	C	CA	0.3847	-0.0009	0.9991	0.9993
14	14_60505617_G_T	60505617	60038899	rs192657698	T	G	0.0172	-0.0127	0.9874	0.9996
14	14_62389498_T_C	62389498	61922780	rs150761741	C	T	0.0120	0.0051	1.0051	1.0001
14	14_62588317_G_A	62588317	62121599	rs74506686	A	G	0.1656	0.0161	1.0162	1.0054

14	14_63173004_C_G	63173004	62706286	rs1889370	G	C	0.5119	0.0015	1.0015	1.0015
14	14_63177144_T_C	63177144	62710426	rs8669834	C	T	0.4175	-0.0024	0.9976	0.9980
14	14_63181859_A_C	63181859	62715141	rs1027171	C	A	0.4284	0.0069	1.0069	1.0059
14	14_63207288_T_C	63207288	62740570	rs10133621	C	T	0.5549	0.0021	1.0021	1.0023
14	14_63681322_C_T	63681322	63214604	rs4899110	T	C	0.5989	0.0000	1.0000	1.0000
14	14_65655124_G_A	65655124	65188406	rs55839896	A	G	0.1735	-0.0088	0.9912	0.9970
14	14_68423215_G_A	68423215	67956498	rs28649231	A	G	0.1932	0.0000	1.0000	1.0000
14	14_68583829_A_C	68583829	68117112	rs378408	C	A	0.1749	0.0000	1.0000	1.0000
14	14_68589677_A_A	68589677	68122960	rs145099242	AAC	A	0.1583	0.0000	1.0000	1.0000
14	14_68650809_CAA_C	68650809	68184092	14:68650809_CAA_C	C	CAA	0.8293	-0.0130	0.9871	0.9787
14	14_68660428_T_C	68660428	68193711	rs2588809	C	T	0.8345	-0.0063	0.9937	0.9895
14	14_68723484_C_G	68723484	68256767	rs3784095	G	C	0.2487	0.0000	1.0000	1.0000
14	14_68968551_C_G	68968551	68501834	rs2525511	G	C	0.6754	-0.0006	0.9994	0.9992
14	14_68974410_A_G	68974410	68507693	rs739874	G	A	0.2631	-0.0138	0.9863	0.9928
14	14_68975374_C_T	68975374	68508657	rs2842346	T	C	0.2412	0.0000	1.0000	1.0000
14	14_68979835_T_C	68979835	68513118	rs11624333	C	T	0.2581	-0.0272	0.9732	0.9862
14	14_69005614_G_A	69005614	68538897	rs34636650	A	G	0.2628	-0.0106	0.9895	0.9945
14	14_69026379_G_A	69026379	68559662	rs11844632	A	G	0.2728	-0.0118	0.9883	0.9936
14	14_69035425_G_A	69035425	68568708	rs8007194	A	G	0.4698	-0.0034	0.9966	0.9968
14	14_69047006_C_T	69047006	68580289	rs74933543	T	C	0.2968	-0.0098	0.9902	0.9942
14	14_69098816_G_T	69098816	68632099	rs7153037	T	G	0.1531	0.0026	1.0026	1.0008
14	14_69114465_T_G	69114465	68647748	rs61987115	G	T	0.1330	-0.0042	0.9958	0.9989
14	14_69312861_T_C	69312861	68846144	rs8012068	C	T	0.0910	-0.0107	0.9894	0.9981
14	14_69314579_A_T	69314579	68847862	rs79514844	T	A	0.6310	0.0020	1.0020	1.0025
14	14_69449755_A_C	69449755	68983038	rs78009683	C	A	0.2295	-0.0079	0.9921	0.9964

14	14_73281244_G_C	73281244	72814536	rs4479167	C	G	0.9397	0.0009	1.0009	1.0017
14	14_76784399_T_G	76784399	76318056	rs34966488	G	T	0.6594	-0.0060	0.9940	0.9921
14	14_76803463_G_A	76803463	76337120	rs11623829	A	G	0.3982	-0.0001	0.9999	0.9999
14	14_77130070_A_G	77130070	76663727	rs4903445	G	A	0.1640	-0.0108	0.9893	0.9965
14	14_77474707_C_T	77474707	77008364	rs1558858	T	C	0.9828	-0.0246	0.9757	0.9528
14	14_77545648_T_C	77545648	77079305	rs12897324	C	T	0.5692	-0.0006	0.9994	0.9993
14	14_77547212_C_T	77547212	77080869	rs10873302	T	C	0.2834	-0.0081	0.9919	0.9954
14	14_77733856_C_G	77733856	77267513	rs28988624	G	C	0.0241	-0.0343	0.9663	0.9984
14	14_78445003_G_C	78445003	77978660	rs11625014	C	G	0.7618	-0.0059	0.9941	0.9911
14	14_78506992_A_G	78506992	78040649	rs1955577	G	A	0.6700	-0.0024	0.9976	0.9968
14	14_81488416_C_T	81488416	81022072	rs35789100	T	C	0.1163	-0.0006	0.9994	0.9999
14	14_81743718_C_T	81743718	81277374	rs34323725	T	C	0.1042	0.0087	1.0087	1.0018
14	14_83131247_C_T	83131247	82664903	rs17616180	T	C	0.3169	-0.0040	0.9960	0.9975
14	14_83187970_A_C	83187970	82721626	rs1370761	C	A	0.2330	-0.0150	0.9851	0.9931
14	14_84156160_C_T	84156160	83689816	rs116988070	T	C	0.0550	-0.0027	0.9973	0.9997
14	14_84253506_A_G	84253506	83787162	rs76569814	G	A	0.2805	-0.0052	0.9948	0.9971
14	14_84262197_T_A	84262197	83795853	rs12895560	A	T	0.3417	-0.0004	0.9996	0.9997
14	14_84262786_T_A	84262786	83796442	rs8021562	A	T	0.4746	-0.0017	0.9983	0.9984
14	14_84938169_C_T	84938169	84471825	rs72687274	T	C	0.0444	-0.0081	0.9919	0.9993
14	14_85106220_CTCC CAT_GTCCCAT	85106220	84639876	rs138543705	GTCCCAT	CTCCA T	0.0159	-0.0498	0.9514	0.9985
14	14_85678604_C_T	85678604	85212260	rs4467007	T	C	0.5580	0.0054	1.0054	1.0061
14	14_85682017_G_T	85682017	85215673	rs1667521	T	G	0.7368	0.0042	1.0042	1.0062
14	14_88180858_C_T	88180858	87714514	rs1959718	T	C	0.9349	0.0066	1.0066	1.0124
14	14_89885100_CCT_ C	89885100	89418756	14:89885100_ CCT_C	C	CCT	0.1574	-0.0118	0.9883	0.9963
14	14_91574779_G_A	91574779	91108435	rs140850061	A	G	0.0187	0.0007	1.0007	1.0000

14	14_91734164_T_G	91734164	91267820	rs12895175	G	T	0.2424	0.0000	1.0000	1.0000
14	14_91751788_TC_T	91751788	91285444	14:91751788_ TC_T	T	TC	0.6934	0.0212	1.0214	1.0299
14	14_91757542_T_C	91757542	91291198	rs3825658	C	T	0.1193	0.0000	1.0000	1.0000
14	14_91841069_A_G	91841069	91374725	rs941764	G	A	0.3444	0.0214	1.0216	1.0150
14	14_91845133_A_G	91845133	91378789	rs1046311	G	A	0.1781	0.0072	1.0072	1.0026
14	14_91848177_A_A AAC	91848177	91381833	rs113889692	AAAC	A	0.7571	-0.0002	0.9998	0.9997
14	14_91880062_G_A	91880062	91413718	rs17804398	A	G	0.2452	-0.0007	0.9993	0.9997
14	14_91888924_T_TA	91888924	91422580	rs150658557	TA	T	0.1986	-0.0083	0.9917	0.9967
14	14_92011796_TTTT C_T	92011796	91545452	14:92011796_ TTTT_C	T	TTTT	0.2549	-0.0040	0.9960	0.9980
14	14_92032916_C_T	92032916	91566572	rs117534345	T	C	0.0134	-0.0274	0.9730	0.9993
14	14_92996181_G_A	92996181	92529837	rs8019318	A	G	0.4094	0.0102	1.0103	1.0084
14	14_93004912_G_A	93004912	92538568	rs8015844	A	G	0.4104	0.0026	1.0026	1.0021
14	14_93005020_C_G	93005020	92538676	rs74645156	G	C	0.1513	-0.0105	0.9896	0.9968
14	14_93035214_T_C	93035214	92568869	rs2104240	C	T	0.0658	0.0042	1.0042	1.0006
14	14_93070286_C_T	93070286	92603941	rs78440108	T	C	0.1709	-0.0004	0.9996	0.9999
14	14_93078646_CAG _C	93078646	92612301	rs758966327	C	CAG	0.2563	-0.0058	0.9942	0.9970
14	14_93104072_T_C	93104072	92637727	rs11627032	C	T	0.2530	-0.0147	0.9854	0.9926
14	14_93132299_G_C	93132299	92665954	rs12895078	C	G	0.4609	-0.0038	0.9962	0.9965
14	14_93232421_T_A	93232421	92766076	rs144169808	A	T	0.1589	0.0118	1.0119	1.0038
14	14_93263033_C_T	93263033	92796688	rs12437409	T	C	0.5827	0.0016	1.0016	1.0019
14	14_95789794_T_C	95789794	95323457	rs68179258	C	T	0.2397	0.0106	1.0107	1.0051
14	14_99690907_C_A	99690907	99224570	rs807736	A	C	0.8433	0.0048	1.0048	1.0081
14	14_100257281_A_ G	100257281	99790944	rs7154519	G	A	0.3971	0.0019	1.0019	1.0015

14	14_101303361_C_T	101303361	100837024	rs8019930	T	C	0.3692	-0.0079	0.9921	0.9942
14	14_101311729_C_T	101311729	100845392	rs56363527	T	C	0.3268	-0.0031	0.9969	0.9980
14	14_101318311_C_G	101318311	100851974	rs2295389	G	C	0.3639	-0.0025	0.9975	0.9982
14	14_102628910_TTC_T	102628910	102162573	14_102628910_TTCTC_T	T	TTCTC	0.0453	0.0099	1.0099	1.0009
14	14_103238221_G_A	103238221	102771884	rs72702772	A	G	0.2035	-0.0086	0.9914	0.9965
14	14_103381882_C_T	103381882	102915545	rs72704741	T	C	0.1737	-0.0058	0.9942	0.9980
14	14_104374675_G_T	104374675	103908338		T	G	0.0171	0.0044	1.0044	1.0002
14	14_104837529_T_C	104837529	104371192	rs61577366	C	T	0.3982	-0.0099	0.9901	0.9922
14	14_105154105_A_G	105154105	104687768	rs3809456	G	A	0.5121	0.0044	1.0044	1.0045
14	14_105213978_T_G	105213978	104747641	rs4983544	G	T	0.4588	0.0154	1.0155	1.0143
14	14_105320853_C_T	105320853	104854516	rs148957187	T	C	0.5973	-0.0030	0.9970	0.9964
15	15_22944416_T_A	22944416	22928652	rs28439038	A	T	0.2763	0.0127	1.0128	1.0071
15	15_25498397_A_G	25498397	25253250	rs6576416	G	A	0.5524	0.0028	1.0028	1.0031
15	15_25978812_G_A	25978812	25733665	rs61998562	A	G	0.3916	0.0104	1.0105	1.0082
15	15_26015425_C_G	26015425	25770278	rs28627117	G	C	0.2125	0.0049	1.0049	1.0021
15	15_30211357_T_C	30211357	29919154	rs1719339	C	T	0.0265	0.0303	1.0308	1.0016
15	15_30906165_T_C	30906165	30613962	rs200113015	C	T	0.2334	0.0000	1.0000	1.0000
15	15_30913755_A_T	30913755	30621552	rs62018335	T	A	0.2680	0.0126	1.0127	1.0068
15	15_31802360_G_A	31802360	31510157	rs12441163	A	G	0.1404	-0.0105	0.9896	0.9971
15	15_31808639_C_T	31808639	31516436	rs4779888	T	C	0.2795	-0.0008	0.9992	0.9996
15	15_32191559_T_C	32191559	31899356	rs117164250	C	T	0.0565	-0.0156	0.9845	0.9983
15	15_32941233_A_C	32941233	32649032	rs113137317	C	A	0.0238	0.0446	1.0456	1.0022

15	15_35753643_A_G	35753643	35461442	rs16961010	G	A	0.0857	0.0069	1.0069	1.0012
15	15_37466649_G_A	37466649	37174448	rs12911895	A	G	0.0769	0.0077	1.0077	1.0012
15	15_38125629_G_T	38125629	37833428	rs12907082	T	G	0.3992	-0.0040	0.9960	0.9968
15	15_38156880_G_A	38156880	37864679	rs35103746	A	G	0.1290	-0.0044	0.9956	0.9989
15	15_38329343_G_A	38329343	38037142	rs6495940	A	G	0.8894	0.0051	1.0051	1.0091
15	15_40130800_A_A GAT	40130800	39838599	rs573759836	AGAT	A	0.0178	-0.0149	0.9852	0.9995
15	15_40889198_CAA _C	40889198	40597000	rs774126232	C	CAA	0.7748	0.0114	1.0115	1.0178
15	15_40905557_T_C	40905557	40613359	rs17747351	C	T	0.1316	-0.0023	0.9977	0.9994
15	15_40992997_CA _C	40992997	40700799	15:40992997_ CA_C	C	CA	0.1325	-0.0020	0.9980	0.9995
15	15_41097573_CAA AAAAA_C	41097573	40805375	15:41097573_ CAAAAAAA_C	C	CAAAAA AAA	0.3868	0.0011	1.0011	1.0009
15	15_43534967_A_G	43534967	43242769	rs11855754	G	A	0.0990	-0.0100	0.9900	0.9980
15	15_43535096_A_G	43535096	43242898	rs525403	G	A	0.7070	0.0018	1.0018	1.0025
15	15_44216559_C_CT	44216559	43924361	rs5812256	CT	C	0.3255	-0.0109	0.9892	0.9930
15	15_44438763_T_C	44438763	44146565	rs2615272	C	T	0.9671	0.0171	1.0172	1.0336
15	15_44474906_T_C	44474906	44182708	rs2256928	C	T	0.1506	-0.0003	0.9997	0.9999
15	15_44497361_A_A G	44497361	44205163	rs796947891	AG	A	0.0638	0.0000	1.0000	1.0000
15	15_44514657_T_A	44514657	44222459	rs2464693	A	T	0.5896	0.0021	1.0021	1.0025
15	15_45488821_C_T	45488821	45196623	rs62026664	T	C	0.3464	0.0054	1.0054	1.0038
15	15_45513647_G_A	45513647	45221449	rs10851421	A	G	0.3071	0.0021	1.0021	1.0013
15	15_46680811_C_A	46680811	46388613	rs187010898	A	C	0.0115	-0.0125	0.9876	0.9997
15	15_46788586_C_T	46788586	46496388	rs147041270	T	C	0.0131	-0.0754	0.9274	0.9981
15	15_47059047_CT_C	47059047	46766849	rs773759620	C	CT	0.6689	-0.0001	0.9999	0.9999

15	15_47675569_G_A	47675569	47383372	rs281264	A	G	0.6481	-0.0028	0.9972	0.9964
15	15_47685504_T_C	47685504	47393307	rs281297	C	T	0.3794	0.0051	1.0051	1.0039
15	15_47686081_C_T	47686081	47393884	rs281299	T	C	0.6170	0.0024	1.0024	1.0030
15	15_47686590_C_T	47686590	47394393	rs11070582	T	C	0.1343	0.0047	1.0047	1.0013
15	15_47702127_T_C	47702127	47409930	rs2433020	C	T	0.5264	0.0051	1.0051	1.0054
15	15_47716150_A_G	47716150	47423953	rs11632616	G	A	0.3103	0.0065	1.0065	1.0041
15	15_50342912_A_G	50342912	50050715	rs138654651	G	A	0.0109	0.0000	1.0000	1.0000
15	15_50663903_G_A	50663903	50371706	rs34565064	A	G	0.3554	-0.0046	0.9954	0.9967
15	15_50667009_G_A	50667009	50374812	rs12905736	A	G	0.2801	-0.0021	0.9979	0.9988
15	15_50672808_C_G	50672808	50380611	rs4775879	G	C	0.5622	-0.0016	0.9984	0.9982
15	15_50673281_T_C	50673281	50381084	rs34174311	C	T	0.3492	-0.0047	0.9953	0.9967
15	15_50694608_C_A	50694608	50402411	rs11070772	A	C	0.3876	0.0048	1.0048	1.0037
15	15_51383131_G_G	51383131	51090934	rs60211045	GA	G	0.3980	-0.0020	0.9980	0.9984
15	15_51493515_CT_C	51493515	51201318	15:51493515_CT_C	C	CT	0.8054	0.0069	1.0069	1.0112
15	15_51498587_G_T	51498587	51206390	rs6493485	T	G	0.8241	0.0060	1.0060	1.0099
15	15_51498708_A_G	51498708	51206511	rs6493486	G	A	0.7334	0.0020	1.0020	1.0029
15	15_51527398_A_G	51527398	51235201	rs3784308	G	A	0.0428	0.0085	1.0085	1.0007
15	15_52384414_C_T	52384414	52092217	rs113379345	T	C	0.0820	-0.0160	0.9841	0.9974
15	15_54640812_G_A	54640812	54348614	rs62012035	A	G	0.0413	0.0168	1.0169	1.0014
15	15_55609126_G_A	55609126	55316928	rs116918550	A	G	0.0161	-0.0161	0.9840	0.9995
15	15_55626817_C_T	55626817	55334619	rs4774764	T	C	0.2288	0.0083	1.0083	1.0038
15	15_56073123_A_G	56073123	55780925	rs149316549	G	A	0.1592	-0.0004	0.9996	0.9999
15	15_56090609_C_T	56090609	55798411	rs17238405	T	C	0.3252	-0.0071	0.9929	0.9954
15	15_56114197_G_A	56114197	55821999	rs34555597	A	G	0.2014	0.0050	1.0050	1.0020
15	15_56283412_C_T	56283412	55991214	rs17238531	T	C	0.0158	0.0196	1.0198	1.0006

15	15_57671246_T_G	57671246	57379048	rs1664471	G	T	0.6118	0.0004	1.0004	1.0005
15	15_57999304_G_C	57999304	57707106	rs11858659	C	G	0.0596	-0.0199	0.9803	0.9977
15	15_59280279_G_A	59280279	58988080	rs12905422	A	G	0.2189	-0.0012	0.9988	0.9995
15	15_59393174_T_G	59393174	59100975	rs59025291	G	T	0.0760	-0.0228	0.9775	0.9966
15	15_60342686_T_G	60342686	60050487	rs2899654	G	T	0.0121	-0.0448	0.9562	0.9989
15	15_62808539_C_T	62808539	62516340	rs956006	T	C	0.3342	0.0092	1.0092	1.0062
15	15_63351451_C_T	63351451	63059252	rs78809927	T	C	0.0136	-0.0299	0.9705	0.9992
15	15_63742901_A_G	63742901	63450702	rs12907670	G	A	0.8421	0.0102	1.0103	1.0173
15	15_63758647_C_T	63758647	63466448	rs4984247	T	C	0.1359	-0.0044	0.9956	0.9988
15	15_63810625_G_C	63810625	63518426	rs72750932	C	G	0.1445	0.0103	1.0104	1.0030
15	15_64369496_CAA CAA_CAAACAAACA A	64369496	64077297		CAACAAA ACAA	CAACAA	0.6938	0.0118	1.0119	1.0165
15	15_65010075_G_A	65010075	64717876	rs16948203	A	G	0.0654	-0.0027	0.9973	0.9996
15	15_66570312_GA_ G	66570312	66277974		G	GA	0.3334	0.0024	1.0024	1.0016
15	15_66802208_T_G	66802208	66509870	rs12905354	G	T	0.3353	0.0084	1.0084	1.0057
15	15_66861719_G_A	66861719	66569381	rs8038632	A	G	0.6668	-0.0041	0.9959	0.9946
15	15_66891819_G_A	66891819	66599481	rs144711219	A	G	0.0293	-0.0193	0.9809	0.9989
15	15_67457698_A_G	67457698	67165360	rs35874463	G	A	0.0496	0.0173	1.0175	1.0017
15	15_67762759_G_A	67762759	67470421	rs150073640	A	G	0.0159	0.0303	1.0308	1.0010
15	15_69965730_G_A	69965730	69673391	rs59384564	A	G	0.2322	0.0000	1.0000	1.0000
15	15_74487024_A_G	74487024	74194683	rs58138979	G	A	0.1055	0.0179	1.0181	1.0038
15	15_75059627_A_G	75059627	74767286	rs12903541	G	A	0.6503	0.0044	1.0044	1.0057
15	15_75145098_T_C	75145098	74852757	rs936230	C	T	0.6997	0.0081	1.0081	1.0114
15	15_75750383_T_C	75750383	75458042	rs8035987	C	T	0.2604	-0.0168	0.9833	0.9913
15	15_75932777_C_T	75932777	75640436	rs11072553	T	C	0.2480	-0.0027	0.9973	0.9987

15	15_86140791_G_A	86140791	85597560	rs17633749	A	G	0.3429	0.0000	1.0000	1.0000
15	15_86298852_A_G	86298852	85755621	rs2542606	G	A	0.5896	0.0089	1.0089	1.0106
15	15_86300805_T_TT CC	86300805	85757574	rs547514224	TTCC	T	0.3141	-0.0024	0.9976	0.9985
15	15_86832749_G_A	86832749	86289518	rs12904524	A	G	0.2828	-0.0061	0.9939	0.9966
15	15_86840700_C_T	86840700	86297469	rs8038617	T	C	0.3452	-0.0018	0.9982	0.9988
15	15_88502947_C_T	88502947	87959716	rs76289332	T	C	0.0512	0.0069	1.0069	1.0007
15	15_90054067_T_C	90054067	89510836	rs2119009	C	T	0.0710	0.0175	1.0177	1.0025
15	15_90095006_G_A	90095006	89551775	rs138481434	A	G	0.0238	0.0116	1.0117	1.0006
15	15_90122062_T_C	90122062	89578831	rs118118631	C	T	0.0797	0.0044	1.0044	1.0007
15	15_90768959_A_C	90768959	90225727	rs908044	C	A	0.3416	-0.0024	0.9976	0.9984
15	15_91426560_G_A	91426560	90883330	rs4702	A	G	0.5581	-0.0092	0.9908	0.9898
15	15_91512267_G_T	91512267	90969037	rs2290202	T	G	0.1353	-0.0220	0.9782	0.9941
15	15_94513089_C_G	94513089	93969860	rs74630476	G	C	0.0140	0.0331	1.0337	1.0009
15	15_94534591_G_A	94534591	93991362	rs2009580	A	G	0.5807	-0.0112	0.9889	0.9871
15	15_94550152_A_G	94550152	94006923	rs11074245	G	A	0.4716	-0.0012	0.9988	0.9989
15	15_95675091_T_G	95675091	95131862	rs28675767	G	T	0.1211	-0.0074	0.9926	0.9982
15	15_97887273_G_T	97887273	97344043	rs62025230	T	G	0.1526	0.0000	1.0000	1.0000
15	15_97944913_G_A	97944913	97401683	rs7181086	A	G	0.6006	0.0099	1.0099	1.0120
15	15_99610212_G_A	99610212	99066983	rs34097694	A	G	0.1882	0.0151	1.0152	1.0057
15	15_100572999_G_ A	100572999	100032794	rs79270656	A	G	0.0858	0.0062	1.0062	1.0011
15	15_100891226_C_T	100891226	100351021	rs74917211	T	C	0.0319	-0.0113	0.9888	0.9993
15	15_100905819_A_C	100905819	100365614	rs144767203	C	A	0.1100	-0.0145	0.9856	0.9968
15	15_101087943_G_ A	101087943	100547738	rs4965671	A	G	0.8706	0.0018	1.0018	1.0031
15	15_101140715_G_ A	101140715	100600510	rs76361074	A	G	0.0632	-0.0166	0.9835	0.9979

15	15_101158823_G_T	101158823	100618618	rs12907972	T	G	0.3695	-0.0010	0.9990	0.9993
16	16_1407441_A_G	1407441	1357440	rs6600137	G	A	0.8928	-0.0017	0.9983	0.9970
16	16_3980445_T_C	3980445	3930444	rs8049367	C	T	0.3914	0.0036	1.0036	1.0028
16	16_4008542_CAAA_AA_C	4008542	3958541	16:4008542_C AAAAA_C	C	CAAAAA	0.8213	0.0000	1.0000	1.0000
16	16_4008901_C_G	4008901	3958900	rs7199977	G	C	0.7785	0.0000	1.0000	1.0000
16	16_4015316_A_G	4015316	3965315	rs1045475	G	A	0.8238	0.0094	1.0094	1.0156
16	16_4034640_G_C	4034640	3984639	rs61124411	C	G	0.1029	-0.0065	0.9935	0.9987
16	16_4064637_G_C	4064637	4014636	rs62036957	C	G	0.9198	0.0057	1.0057	1.0105
16	16_4071508_G_A	4071508	4021507	rs4785949	A	G	0.0168	-0.0188	0.9814	0.9994
16	16_4106788_C_A	4106788	4056787	rs11076805	A	C	0.2643	0.0000	1.0000	1.0000
16	16_4108158_TA_T	4108158	4058157	16:4108158_T A_T	T	TA	0.5053	0.0070	1.0070	1.0071
16	16_4133076_C_A	4133076	4083075	rs7193552	A	C	0.4968	0.0046	1.0046	1.0046
16	16_4161270_TG_T	4161270	4111269	16:4161270_T G_T	T	TG	0.1104	0.0000	1.0000	1.0000
16	16_4171880_A_G	4171880	4121879	rs6500580	G	A	0.5202	0.0018	1.0018	1.0019
16	16_4182495_C_G	4182495	4132494	rs231611	G	C	0.4471	0.0000	1.0000	1.0000
16	16_4250892_A_C	4250892	4200891	rs879150	C	A	0.8543	0.0060	1.0060	1.0103
16	16_4958716_A_AT	4958716	4908715	rs143780013	AT	A	0.2036	-0.0022	0.9978	0.9991
16	16_5432429_T_C	5432429	5382428	rs568903	C	T	0.5663	-0.0037	0.9963	0.9958
16	16_5460523_T_C	5460523	5410522	rs561856	C	T	0.6247	-0.0058	0.9942	0.9928
16	16_5710377_A_G	5710377	5660376	rs12598977	G	A	0.1120	-0.0044	0.9956	0.9990
16	16_5725267_T_A	5725267	5675266	rs2079740	A	T	0.1220	-0.0015	0.9985	0.9996
16	16_6963972_C_G	6963972	6913971	rs12709163	G	C	0.7835	0.0136	1.0137	1.0216
16	16_6971642_ATAT_AT_A	6971642	6921641	rs869118530	A	ATATAT	0.7591	0.0026	1.0026	1.0040

16	16_6980296_T_C	6980296	6930295	rs4786951	C	T	0.5977	0.0003	1.0003	1.0004
16	16_6980653_C_T	6980653	6930652	rs117771295	T	C	0.1106	0.0066	1.0066	1.0015
16	16_7590853_C_G	7590853	7540851	rs12934004	G	C	0.7156	-0.0026	0.9974	0.9963
16	16_7596179_A_G	7596179	7546177	rs12928189	G	A	0.7460	-0.0029	0.9971	0.9957
16	16_7893537_T_C	7893537	7843535	rs7198296	C	T	0.1396	0.0136	1.0137	1.0038
16	16_8772835_G_C	8772835	8678978	rs150465260	C	G	0.0138	0.0282	1.0286	1.0008
16	16_10706580_G_A	10706580	10612723	rs34872983	A	G	0.0695	-0.0262	0.9741	0.9964
16	16_11190930_T_C	11190930	11097073	rs11649025	C	T	0.1088	-0.0261	0.9742	0.9944
16	16_11439679_C_G	11439679	11345822	rs9187738	G	C	0.5100	0.0014	1.0014	1.0014
16	16_13625515_G_A	13625515	13531658	rs11864841	A	G	0.0688	0.0125	1.0126	1.0017
16	16_19334821_C_T	19334821	19323499	rs8059096	T	C	0.1012	-0.0143	0.9858	0.9971
16	16_19505813_T_A	19505813	19494491	rs2353696	A	T	0.7385	0.0000	1.0000	1.0000
16	16_23007047_G_T	23007047	22995726	rs75753503	T	G	0.0236	0.0329	1.0334	1.0016
16	16_23009777_A_C	23009777	22998456	rs10459775	C	A	0.6944	-0.0063	0.9937	0.9913
16	16_24116697_A_T	24116697	24105376	rs9746011	T	A	0.1490	-0.0008	0.9992	0.9998
16	16_24117477_C_T	24117477	24106156	rs2470688	T	C	0.5360	0.0033	1.0033	1.0035
16	16_24124184_G_A	24124184	24112863	rs11646540	A	G	0.0502	-0.0220	0.9782	0.9978
16	16_25347678_G_A	25347678	25336357	rs2112816	A	G	0.8529	0.0059	1.0059	1.0101
16	16_26730593_A_G	26730593	26719272	rs80216903	G	A	0.0361	0.0094	1.0094	1.0007
16	16_26737749_TC_T	26737749	26726428	16:26737749_ TC_T	T	TC	0.2995	-0.0025	0.9975	0.9985
16	16_26740721_G_A	26740721	26729400	rs321460	A	G	0.7547	-0.0069	0.9931	0.9896
16	16_48923223_C_G	48923223	48889312	rs10521172	G	C	0.0511	0.0054	1.0054	1.0006
16	16_48954205_T_C	48954205	48920294	rs16946656	C	T	0.0388	0.0000	1.0000	1.0000
16	16_49929346_A_G	49929346	49895435	rs62029447	G	A	0.0946	-0.0041	0.9959	0.9992
16	16_50493430_A_G	50493430	50459519	rs4785426	G	A	0.7513	0.0074	1.0074	1.0112
16	16_50612108_A_G	50612108	50578197	rs80279569	G	A	0.0203	0.0257	1.0260	1.0011

16	16_50912801_G_T	50912801	50878890	rs16949000	T	G	0.1983	0.0055	1.0055	1.0022
16	16_51689434_G_A	51689434	51655523	rs73593554	A	G	0.1051	-0.0015	0.9985	0.9997
16	16_51692074_C_T	51692074	51658163	rs8053944	T	C	0.2283	-0.0005	0.9995	0.9998
16	16_51737524_A_G	51737524	51703613	rs112648548	G	A	0.1441	-0.0088	0.9912	0.9975
16	16_51752251_T_A	51752251	51718340	rs1381452	A	T	0.7274	0.0095	1.0095	1.0139
16	16_51754407_C_T	51754407	51720496	rs7190518	T	C	0.0774	-0.0057	0.9943	0.9991
16	16_51976568_A_G	51976568	51942656	rs12932954	G	A	0.2484	-0.0012	0.9988	0.9994
16	16_52415071_G_A	52415071	52381159	rs140770615	A	G	0.0538	-0.0017	0.9983	0.9998
16	16_52535810_T_C	52535810	52501898	rs4784220	C	T	0.3666	0.0000	1.0000	1.0000
16	16_52538825_C_A	52538825	52504913	rs35668161	A	C	0.2562	0.1017	1.1071	1.0556
16	16_52573732_C_T	52573732	52539820	rs34928352	T	C	0.0245	-0.0102	0.9899	0.9995
16	16_52586477_A_G	52586477	52552565	rs3803661	G	A	0.7310	0.0000	1.0000	1.0000
16	16_52599188_C_T	52599188	52565276	rs4784227	T	C	0.2406	0.0860	1.0898	1.0437
16	16_53167951_A_G	53167951	53134039	rs117216872	G	A	0.0337	-0.0085	0.9915	0.9994
16	16_53795665_CAA CT_C	53795665	53761753	rs759431941	C	CAACT	0.1766	0.0043	1.0043	1.0015
16	16_53797908_C_G	53797908	53763996	rs7206790	G	C	0.4793	-0.0001	0.9999	0.9999
16	16_53798622_G_T	53798622	53764710	rs8047587	T	G	0.4539	-0.0127	0.9874	0.9886
16	16_53809123_C_T	53809123	53775211	rs55872725	T	C	0.4201	-0.0353	0.9653	0.9711
16	16_53850170_A_G	53850170	53816258	rs1421090	G	A	0.2604	0.0000	1.0000	1.0000
16	16_53861139_C_T	53861139	53827227	rs6499648	T	C	0.7604	0.0000	1.0000	1.0000
16	16_53861592_G_A	53861592	53827680	rs7184573	A	G	0.3663	-0.0186	0.9816	0.9865
16	16_53865368_A_A G	53865368	53831456	rs34853502	AG	A	0.7189	-0.0145	0.9856	0.9794
16	16_53871626_C CTG	53871626	53837714	16:53871626_ CTG_C	C	CTG	0.1564	-0.0020	0.9980	0.9994
16	16_54114262_T_C	54114262	54080350	rs11646290	C	T	0.3275	0.0109	1.0110	1.0072

16	16_54679668_G_C	54679668	54645756	rs7205346	C	G	0.5980	0.0047	1.0047	1.0056
16	16_54679720_CTTT_C	54679720	54645808	16:54679720_CTTT_C	C	CTTT	0.1587	0.0012	1.0012	1.0004
16	16_54682064_G_A	54682064	54648152	rs28539243	A	G	0.4850	0.0218	1.0220	1.0215
16	16_54683802_T_C	54683802	54649890	rs3893264	C	T	0.1948	0.0009	1.0009	1.0004
16	16_56379792_C_T	56379792	56345880	rs3790110	T	C	0.5968	-0.0073	0.9927	0.9913
16	16_56379937_C_T	56379937	56346025	rs13337678	T	C	0.5599	0.0000	1.0000	1.0000
16	16_56437872_T_A	56437872	56403960	rs2432542	A	T	0.5165	-0.0008	0.9992	0.9992
16	16_57673762_G_A	57673762	57639850	rs1975630	A	G	0.5416	-0.0043	0.9957	0.9954
16	16_61911209_T_TA	61911209	61877305	rs576519137	TA	T	0.2284	0.0000	1.0000	1.0000
16	16_61919615_CA_C	61919615	61885711	16:61919615_CA_C	C	CA	0.4080	0.0098	1.0098	1.0081
16	16_63026665_G_A	63026665	62992761	rs567866625	A	G	0.0128	0.0391	1.0399	1.0010
16	16_63250011_T_C	63250011	63216107	rs12597559	C	T	0.4320	0.0133	1.0134	1.0116
16	16_63360933_A_G	63360933	63327029	rs117910740	G	A	0.0120	0.0175	1.0177	1.0004
16	16_63401800_T_C	63401800	63367896	rs143470	C	T	0.4395	0.0018	1.0018	1.0016
16	16_63446812_C_T	63446812	63412908	rs7189722	T	C	0.3580	0.0021	1.0021	1.0015
16	16_65310299_A_G	65310299	65276396	rs147958546	G	A	0.0512	0.0027	1.0027	1.0003
16	16_65430352_C_T	65430352	65396449	rs76021007	T	C	0.0759	0.0067	1.0067	1.0010
16	16_67003618_C_T	67003618	66969715	rs61743167	T	C	0.0219	-0.0091	0.9909	0.9996
16	16_67181999_A_G	67181999	67148096	rs9033	G	A	0.4512	0.0101	1.0102	1.0092
16	16_71388416_G_A	71388416	71354513	rs142248381	A	G	0.0161	-0.0183	0.9819	0.9994
16	16_71438287_A_C	71438287	71404384	rs8051854	C	A	0.3630	0.0096	1.0096	1.0070
16	16_71513034_C_A	71513034	71479131	rs2288486	A	C	0.5383	-0.0073	0.9927	0.9922
16	16_71830922_T_C	71830922	71797019	rs61451008	C	T	0.4986	-0.0092	0.9908	0.9909
16	16_72047385_A_G	72047385	72013486	rs138910759	G	A	0.0184	-0.0182	0.9820	0.9993
16	16_73048109_G_C	73048109	73014210	rs12325298	C	G	0.4705	-0.0105	0.9896	0.9902

16	16_75526936_C_A	75526936	75493038	rs2550901	A	C	0.0206	0.0337	1.0343	1.0014
16	16_78864207_T_TT A	78864207	78830310	rs3085447	TTA	T	0.3175	0.0005	1.0005	1.0003
16	16_79223834_G_A	79223834	79189937	rs7186097	A	G	0.3076	-0.0055	0.9945	0.9966
16	16_79238563_A_C	79238563	79204666	rs71398138	C	A	0.1492	-0.0012	0.9988	0.9996
16	16_79330312_C_T	79330312	79296415	rs77471625	T	C	0.0547	-0.0239	0.9764	0.9974
16	16_79362587_A_T	79362587	79328690	rs17724699	T	A	0.0455	-0.0044	0.9956	0.9996
16	16_79816295_A_TTT TTT_A	79816295	79782398	rs143581936	A	ATTTTT T	0.6870	0.0037	1.0037	1.0051
16	16_80648296_A_G	80648296	80614399	rs7500067	G	A	0.2303	0.0542	1.0557	1.0258
16	16_80652246_G_C	80652246	80618349	rs11645914	C	G	0.1885	0.0001	1.0001	1.0000
16	16_80656966_G_T	80656966	80623069	rs9927571	T	G	0.2444	0.0027	1.0027	1.0013
16	16_80849567_T_C	80849567	80815670	rs12448585	C	T	0.1875	-0.0035	0.9965	0.9987
16	16_81809272_T_C	81809272	81775667	rs78266002	C	T	0.0279	0.0270	1.0274	1.0015
16	16_82079091_G_A	82079091	82045486	rs6564961	A	G	0.6080	-0.0105	0.9896	0.9873
16	16_82111279_C_A	82111279	82077674	rs67777781	A	C	0.3644	0.0016	1.0016	1.0012
16	16_82712315_A_G	82712315	82678710	rs10514555	G	A	0.1043	0.0036	1.0036	1.0008
16	16_82862855_C_T	82862855	82829250	rs2549157	T	C	0.3159	0.0000	1.0000	1.0000
16	16_82927367_A_G	82927367	82893762	rs1862681	G	A	0.3684	0.0000	1.0000	1.0000
16	16_84285777_T_C	84285777	84252171	rs390112	C	T	0.6256	0.0032	1.0032	1.0040
16	16_85144693_C_A	85144693	851111087	rs8060060	A	C	0.4520	0.0000	1.0000	1.0000
16	16_85145977_T_C	85145977	85112371	rs9931038	C	T	0.4856	0.0000	1.0000	1.0000
16	16_85828183_T_C	85828183	85794577	rs56306388	C	T	0.1097	0.0000	1.0000	1.0000
16	16_85876104_A_G	85876104	85842498	rs9674291	G	A	0.1449	0.0139	1.0140	1.0041
16	16_87044630_T_C	87044630	87011024	rs2313582	C	T	0.3038	-0.0041	0.9959	0.9975
16	16_87046969_T_C	87046969	87013363	rs71390870	C	T	0.1719	0.0000	1.0000	1.0000
16	16_87053923_A_C	87053923	87020317	rs929859	C	A	0.1869	-0.0076	0.9924	0.9972

16	16_87058866_T_C	87058866	87025260	rs12445782	C	T	0.2068	0.0000	1.0000	1.0000
16	16_87069983_G_T	87069983	87036377	rs3901356	T	G	0.2335	0.0000	1.0000	1.0000
16	16_87086492_T_C	87086492	87052886	rs12449271	C	T	0.2586	-0.0073	0.9927	0.9962
16	16_87135504_G_A	87135504	87101898	rs1559336	A	G	0.2406	-0.0078	0.9922	0.9963
16	16_88619156_G_A	88619156	88552748	rs72807472	A	G	0.0133	0.0227	1.0230	1.0006
16	16_88822095_C_G	88822095	88755687	rs4782346	G	C	0.3302	-0.0109	0.9892	0.9929
16	16_89802396_G_T	89802396	89735988	rs7202427	T	G	0.2681	0.0028	1.0028	1.0015
16	16_89850170_C_T	89850170	89783762	rs17226274	T	C	0.0877	0.0003	1.0003	1.0001
16	16_89850776_CA_C	89850776	89784368	16:89850776_CA_C	C	CA	0.3322	-0.0056	0.9944	0.9963
16	16_89981345_TTG_T	89981345	89914937		T	TTG	0.0916	0.0170	1.0171	1.0031
16	16_89986608_A_G	89986608	89920200	rs2228478	G	A	0.1048	0.0019	1.0019	1.0004
17	17_1902751_AAC_A	1902751	1999457	17:1902751_AAC_A	A	AAC	0.6720	-0.0123	0.9878	0.9836
17	17_2099183_C_T	2099183	2195889	rs16952006	T	C	0.1079	-0.0137	0.9864	0.9971
17	17_2217876_CAA_C	2217876	2314582	17:2217876_CAA_C	C	CAA	0.5766	-0.0016	0.9984	0.9982
17	17_3419690_A_G	3419690	3516396	rs8082339	G	A	0.9854	-0.0294	0.9710	0.9437
17	17_4696873_C_A	4696873	4793578	rs12937934	A	C	0.6872	-0.0127	0.9874	0.9827
17	17_4963726_CT_C	4963726	5060431	17:4963726_CT_C	C	CT	0.6003	-0.0034	0.9966	0.9959
17	17_6332522_C_T	6332522	6429202	rs140991377	T	C	0.0204	0.0072	1.0072	1.0003
17	17_6498498_C_T	6498498	6595178	rs4796339	T	C	0.5713	-0.0088	0.9912	0.9900
17	17_7166932_T_TG	7166932	7263613	rs201780804	TG	T	0.6330	0.0111	1.0112	1.0142
17	17_7206781_G_A	7206781	7303462	rs62059194	A	G	0.4402	0.0024	1.0024	1.0021
17	17_7358000_C_G	7358000	7454681	rs4796418	G	C	0.1481	0.0069	1.0069	1.0021

17	17_8907415_A_C	8907415	9004098	rs11868829	C	A	0.3252	0.0039	1.0039	1.0025
17	17_8944220_C_T	8944220	9040903	rs117766280	T	C	0.0143	0.0537	1.0552	1.0016
17	17_11717399_G_T	11717399	11814082	rs11078033	T	G	0.4080	0.0087	1.0087	1.0071
17	17_17766877_CT_C	17766877	17863563	rs537436727	C	CT	0.6128	-0.0036	0.9964	0.9956
17	17_17878524_CTT_C	17878524	17975210	rs117878524_CTT_C	C	CTT	0.3275	0.0096	1.0096	1.0063
17	17_18227272_T_C	18227272	18323958	rs921985	C	T	0.6274	0.0062	1.0062	1.0078
17	17_25767765_T_C	25767765	27440739	rs117920301	C	T	0.5192	-0.0021	0.9979	0.9978
17	17_26351978_G_A	26351978	28024952	rs77038763	A	G	0.0248	0.0337	1.0343	1.0017
17	17_27771132_G_G	27771132	29444114	rs569046653	GA	G	0.3291	0.0096	1.0096	1.0064
17	17_28653780_C_T	28653780	30326762	rs60450790	T	C	0.0627	-0.0026	0.9974	0.9997
17	17_28867862_G_C	28867862	30540844	rs9911207	C	G	0.0704	-0.0148	0.9853	0.9979
17	17_29163591_T_A	29163591	30836573	rs117662433	A	T	0.0387	-0.0159	0.9842	0.9988
17	17_29168077_G_T	29168077	30841059	rs79461387	T	G	0.2613	-0.0242	0.9761	0.9875
17	17_29271319_A_T	29271319	30944301	rs6505220	T	A	0.4505	0.0100	1.0101	1.0091
17	17_29325023_G_C	29325023	30998005	rs12453269	C	G	0.2326	0.0000	1.0000	1.0000
17	17_29848534_C_T	29848534	31521516	rs11653842	T	C	0.0554	-0.0016	0.9984	0.9998
17	17_32542662_G_A	32542662	34215643	rs28843509	A	G	0.2229	-0.0066	0.9934	0.9971
17	17_32622343_G_A	32622343	34295324	rs201838321	A	G	0.1166	0.0161	1.0162	1.0038
17	17_37949924_A_G	37949924	39793671	rs17676191	G	A	0.0979	-0.0079	0.9921	0.9985
17	17_38105334_C_T	38105334	39949081	rs7217240	T	C	0.2278	-0.0002	0.9998	0.9999
17	17_38124892_C_A	38124892	39968639	rs59843584	A	C	0.2307	-0.0020	0.9980	0.9991
17	17_38149033_G_A	38149033	39992780	rs11652139	A	G	0.6017	-0.0026	0.9974	0.9969
17	17_38211557_GT_G	38211557	40055304	rs776336978	G	GT	0.0796	-0.0006	0.9994	0.9999
17	17_38238725_C_T	38238725	40082472	rs113855596	T	C	0.3348	0.0011	1.0011	1.0007

17	17_38251385_A_A T	38251385	40095132	rs141144358	AT	A	0.3417	0.0094	1.0094	1.0065
17	17_39178958_T_A	39178958	41022706	rs146491350	A	T	0.0705	0.0140	1.0141	1.0020
17	17_39215439_G_A	39215439	41059187	rs113045371	A	G	0.1329	0.0063	1.0063	1.0017
17	17_39251123_T_C	39251123	41094871	rs150537328	C	T	0.0682	0.0151	1.0152	1.0021
17	17_39272523_A_G	39272523	41116271	rs111447797	G	A	0.2635	0.0044	1.0044	1.0023
17	17_39305956_G_A	39305956	41149704	rs1497383	A	G	0.4865	0.0011	1.0011	1.0011
17	17_39449318_T_C	39449318	41293066	rs191981806	C	T	0.0291	0.0000	1.0000	1.0000
17	17_40114587_G_A	40114587	41962569	rs9899099	A	G	0.1020	0.0000	1.0000	1.0000
17	17_40127060_T_C	40127060	41975042	rs111296	C	T	0.0570	0.0000	1.0000	1.0000
17	17_40485239_G_T	40485239	42333221	rs17881320	T	G	0.0874	-0.0067	0.9933	0.9988
17	17_40534672_C_CT	40534672	42382654	rs541465138	CT	C	0.0948	-0.0027	0.9973	0.9995
17	17_40569439_T_C	40569439	42417421	rs12938957	C	T	0.2155	0.0053	1.0053	1.0023
17	17_40574052_C_A	40574052	42422034	rs9909335	A	C	0.0862	0.0000	1.0000	1.0000
17	17_40599241_CA_C	40599241	42447223	17:40599241_CA_C	C	CA	0.7133	-0.0071	0.9929	0.9899
17	17_40744470_G_A	40744470	42592452	rs149370081	A	G	0.0124	0.0559	1.0575	1.0014
17	17_40756882_C_T	40756882	42604864	rs76189032	T	C	0.0722	0.0040	1.0040	1.0006
17	17_40867365_C_G	40867365	42715347	rs115818584	G	C	0.0149	0.0173	1.0175	1.0005
17	17_40893920_G_C	40893920	42741902	rs113025290	C	G	0.0652	0.0049	1.0049	1.0006
17	17_42362104_A_G	42362104	44284736	rs7213794	G	A	0.5371	-0.0031	0.9969	0.9967
17	17_43212339_C_CT	43212339	45134972	rs545502941	CT	C	0.2284	0.0122	1.0123	1.0056
17	17_43811260_G_A	43811260	45733894	rs1880753	A	G	0.5450	0.0000	1.0000	1.0000
17	17_43929696_T_C	43929696	45852330	rs9890016	C	T	0.0773	0.0067	1.0067	1.0010
17	17_44067847_G_T	44067847	45990481	rs2435213	T	G	0.1953	0.0075	1.0075	1.0029
17	17_44252468_G_A	44252468	46175102	rs2532263	A	G	0.1877	-0.0075	0.9925	0.9972
17	17_44283858_G_A	44283858	46206492	rs2668667	A	G	0.1895	-0.0162	0.9839	0.9939

17	17_44877342_C_T	44877342	46799976	rs116332759	T	C	0.0143	-0.0072	0.9928	0.9998
17	17_45385526_A_A AATAATAATAATAA TAAT	45385526	47308160	rs368542936	AAATAAT AATAATA ATAAT	A	0.4583	0.0047	1.0047	1.0043
17	17_45912302_C_T	45912302	47834936	rs11079797	T	C	0.1592	0.0008	1.0008	1.0003
17	17_46051911_G_A	46051911	47974545	rs886444	A	G	0.4015	0.0015	1.0015	1.0012
17	17_47286962_C_T	47286962	49209600	rs22333359	T	C	0.1005	0.0110	1.0111	1.0022
17	17_47316758_C_T	47316758	49239396	rs112075909	T	C	0.1032	0.0072	1.0072	1.0015
17	17_47793042_G_A	47793042	49715680	rs2017835	A	G	0.5735	0.0054	1.0054	1.0062
17	17_48244531_C_G	48244531	50167170	rs12939159	G	C	0.1274	-0.0031	0.9969	0.9992
17	17_48251875_G_G T	48251875	50174514	rs200753576	GT	G	0.2058	0.0025	1.0025	1.0010
17	17_49430739_T_C	49430739	51353378	rs138253853	C	T	0.0179	0.0073	1.0073	1.0003
17	17_49609158_C_T	49609158	51531797	rs11867780	T	C	0.3025	-0.0077	0.9923	0.9954
17	17_49828922_C_T	49828922	51751562	rs1263945	T	C	0.4834	-0.0082	0.9918	0.9921
17	17_52947714_T_G	52947714	54870353	rs4436838	G	T	0.2662	-0.0086	0.9914	0.9954
17	17_52975265_C_G	52975265	54897904	rs72840963	G	C	0.1924	-0.0007	0.9993	0.9997
17	17_53116708_T_TA	53116708	55039347	rs11463240	TA	T	0.7073	0.0000	1.0000	1.0000
17	17_53209774_A_C	53209774	55132413	rs2787486	C	A	0.3023	-0.0361	0.9645	0.9787
17	17_53214654_C_T	53214654	55137293	rs244315	T	C	0.2795	-0.0213	0.9789	0.9883
17	17_53306601_C_T	53306601	55229240	rs10515091	T	C	0.2360	-0.0031	0.9969	0.9985
17	17_53324637_G_A	53324637	55247276	rs1106351	A	G	0.1643	0.0058	1.0058	1.0019
17	17_54154040_T_C	54154040	56076679	rs2877726	C	T	0.6450	-0.0113	0.9888	0.9856
17	17_54336709_G_A	54336709	56259348	rs17821183	A	G	0.0536	0.0107	1.0108	1.0012
17	17_55451218_G_C	55451218	57373857	rs17221133	C	G	0.0525	0.0037	1.0037	1.0004
17	17_56494343_G_C	56494343	58416982	rs12950320	C	G	0.2290	-0.0116	0.9885	0.9947

17	17_57561718_CAA_C	57561718	59484357	17:57561718_CAA_C	C	CAA	0.0343	-0.0207	0.9795	0.9986
17	17_57870240_T_A	57870240	59792879	rs34678827	A	T	0.7974	-0.0003	0.9997	0.9995
17	17_57929319_T_C	57929319	59851958	rs1292068	C	T	0.3023	-0.0046	0.9954	0.9972
17	17_58051316_G_A	58051316	59973955	rs4968402	A	G	0.8424	-0.0029	0.9971	0.9951
17	17_59547250_C_T	59547250	61469889	rs3785830	T	C	0.1062	0.0147	1.0148	1.0031
17	17_59765855_C_A	59765855	61688494	rs188327672	A	C	0.0314	-0.0107	0.9894	0.9993
17	17_59963779_A_C	59963779	61886418	rs4968455	C	A	0.1646	0.0126	1.0127	1.0042
17	17_64886173_C_G	64886173	66890056	rs11079671	G	C	0.3071	-0.0044	0.9956	0.9973
17	17_65261171_AAA TAAT_A	65261171	67265055	17:65261171_AAA AAATAAT_A	A	AAATAA T	0.5142	-0.0065	0.9935	0.9933
17	17_65367292_T_C	65367292	67371176	rs6504501	C	T	0.2431	0.0125	1.0126	1.0061
17	17_66553479_T_C	66553479	68557338	rs11655740	C	T	0.0301	-0.0027	0.9973	0.9998
17	17_66626373_A_C	66626373	68630232	rs11077678	C	A	0.4830	-0.0050	0.9950	0.9952
17	17_66804173_G_A	66804173	68808032	rs2053585	A	G	0.6688	-0.0033	0.9967	0.9956
17	17_66900804_C_T	66900804	68904663	rs36059695	T	C	0.0336	-0.0135	0.9866	0.9991
17	17_68080125_G_C	68080125	70083984	rs8075605	C	G	0.7594	0.0066	1.0066	1.0101
17	17_69085396_G_T	69085396	71089255	rs8065642	T	G	0.4126	-0.0037	0.9963	0.9970
17	17_70004689_T_C	70004689	72008548	rs2160441	C	T	0.5843	0.0051	1.0051	1.0060
17	17_70106428_T_C	70106428	72110287	rs1477066	C	T	0.6338	0.0077	1.0077	1.0098
17	17_70161079_G_A	70161079	72164938	rs11650866	A	G	0.1026	-0.0059	0.9941	0.9988
17	17_70502866_T_C	70502866	72506726	rs9893321	C	T	0.0674	-0.0005	0.9995	0.9999
17	17_70535819_A_A C	70535819	72539679	rs150766779	AC	A	0.0655	0.0000	1.0000	1.0000
17	17_70605514_G_A	70605514	72609375	rs11651456	A	G	0.3628	0.0013	1.0013	1.0009
17	17_72570682_A_G	72570682	74574543	rs2655606	G	A	0.6700	0.0098	1.0098	1.0132

17	17_72774778_C_TTT	72774778	74778639	17:72774778_CTTT_C	C	CTTT	0.5737	0.0083	1.0083	1.0096
17	17_75581812_C_T	75581812	77585730	rs11871602	T	C	0.0880	0.0000	1.0000	1.0000
17	17_76224762_T_A	76224762	78228681	rs744960	A	T	0.0822	-0.0189	0.9813	0.9969
17	17_76247543_C_T	76247543	78251462	rs11888431	T	C	0.5183	-0.0067	0.9933	0.9931
17	17_76371592_A_G	76371592	78375511	rs12601655	G	A	0.2020	0.0040	1.0040	1.0016
17	17_76386412_A_G	76386412	78390331	rs7503405	G	A	0.8805	-0.0037	0.9963	0.9935
17	17_76492576_G_A	76492576	78496494	rs11657288	A	G	0.4078	0.0000	1.0000	1.0000
17	17_77781725_A_G	77781725	79807926	rs745570	G	A	0.5038	-0.0122	0.9879	0.9878
17	17_77784268_T_C	77784268	79810469	rs2587505	C	T	0.4117	-0.0057	0.9943	0.9953
17	17_77795012_C_T	77795012	79821213	rs8080723	T	C	0.0871	-0.0094	0.9906	0.9984
17	17_77804840_C_T	77804840	79831041	rs9747992	T	C	0.0898	0.0000	1.0000	1.0000
17	17_77888930_A_G	77888930	79915131	rs1663186	G	A	0.0619	-0.0166	0.9835	0.9980
17	17_78038139_C_T	78038139	80064340	rs56071031	T	C	0.1032	0.0215	1.0217	1.0045
17	17_78255053_T_C	78255053	80281254	rs62635847	C	T	0.3990	-0.0053	0.9947	0.9958
17	17_80553220_C_G	80553220	82595344	rs11078002	G	C	0.7343	-0.0057	0.9943	0.9917
17	17_80555477_T_C	80555477	82597601	rs62079673	C	T	0.5987	-0.0046	0.9954	0.9945
17	17_80840588_A_G	80840588	82882712	rs9747095	G	A	0.4039	0.0029	1.0029	1.0023
17	17_80865406_G_C	80865406	82907530	rs2085615	C	G	0.3624	0.0003	1.0003	1.0002
17	17_80895487_AG_A	80895487	82937611	17:80895487_AG_A	A	AG	0.0687	0.0069	1.0069	1.0010
17	17_80904310_C_T	80904310	82946434	rs898097	T	C	0.6529	0.0057	1.0057	1.0075
18	18_809911_G_A	809911	809910	rs9952321	A	G	0.0980	0.0043	1.0043	1.0008
18	18_862734_T_C	862734	862733	rs72871016	C	T	0.0997	0.0111	1.0112	1.0022
18	18_1197256_A_C	1197256	1197255	rs34516086	C	A	0.0242	-0.0138	0.9863	0.9993
18	18_1630070_A_C	1630070	1630069	rs61229115	C	A	0.4179	0.0063	1.0063	1.0053
18	18_4293666_A_G	4293666	4293666	rs619143	G	A	0.6030	0.0000	1.0000	1.0000

18	18_7177489_C_T	7177489	7177491	rs9950440	T	C	0.1516	-0.0154	0.9847	0.9954
18	18_8952017_G_A	8952017	8952019	rs62085542	A	G	0.0924	-0.0211	0.9791	0.9961
18	18_8986040_G_A	8986040	8986042	rs57259999	A	G	0.2050	0.0027	1.0027	1.0011
18	18_8989816_C_T	8989816	8989818	rs12966593	T	C	0.1030	-0.0030	0.9970	0.9994
18	18_9002582_G_A	9002582	9002584	rs965848	A	G	0.4379	0.0072	1.0072	1.0063
18	18_9008345_A_G	9008345	9008347	rs35743226	G	A	0.1243	-0.0001	0.9999	1.0000
18	18_9484523_A_AT	9484523	9484525		AT	A	0.7180	0.0050	1.0050	1.0072
18	18_9531069_C_T	9531069	9531071	rs7226980	T	C	0.2016	0.0072	1.0072	1.0029
18	18_11066412_G_A	11066412	11066413	rs76722466	A	G	0.0102	-0.0224	0.9778	0.9995
18	18_11696613_C_T	11696613	11696614	rs16976596	T	C	0.1379	-0.0082	0.9918	0.9977
18	18_11750822_T_C	11750822	11750823	rs1005270	C	T	0.1598	0.0000	1.0000	1.0000
18	18_11757627_C_G	11757627	11757628	rs6505672	G	C	0.0309	-0.0112	0.9889	0.9993
18	18_11771248_A_G	11771248	11771249	rs78297897	G	A	0.1212	-0.0026	0.9974	0.9994
18	18_11807889_G_A	11807889	11807890	rs73946348	A	G	0.0849	0.0000	1.0000	1.0000
18	18_12937444_G_C	12937444	12937445	rs55796886	C	G	0.0287	-0.0193	0.9809	0.9989
18	18_12956438_G_A	12956438	12956439	rs61480660	A	G	0.2243	-0.0103	0.9898	0.9954
18	18_20634253_C_T	20634253	23054290	rs11665269	T	C	0.6403	-0.0260	0.9743	0.9674
18	18_22117430_G_A	22117430	24537466	rs8093079	A	G	0.1839	0.0109	1.0110	1.0040
18	18_23164099_C_G	23164099	25584135	rs983864	G	C	0.4430	0.0013	1.0013	1.0012
18	18_23500096_T_C	23500096	25920132	rs7228892	C	T	0.6270	0.0031	1.0031	1.0039
18	18_23520441_T_A	23520441	25940477	rs4800697	A	T	0.5411	0.0095	1.0095	1.0104
18	18_24067931_A_G	24067931	26487967	rs2155759	G	A	0.5712	-0.0086	0.9914	0.9902
18	18_24110979_G_A	24110979	26531015	rs62087056	A	G	0.1506	0.0117	1.0118	1.0035
18	18_24125857_T_C	24125857	26545893	rs1111207	C	T	0.4214	0.0070	1.0070	1.0059
18	18_24156018_C_T	24156018	26576054	rs7240205	T	C	0.6096	-0.0005	0.9995	0.9994
18	18_24249279_G_A	24249279	26669315	rs7228610	A	G	0.6184	-0.0032	0.9968	0.9961
18	18_24250541_G_C	24250541	26670577	rs78888860	C	G	0.0358	0.0124	1.0125	1.0009

18	18_24319537_A_G	24319537	26739573	rs582356	G	A	0.4067	-0.0046	0.9954	0.9963
18	18_24321813_C_G	24321813	26741849	rs659378	G	C	0.5983	-0.0037	0.9963	0.9956
18	18_24327257_A_G	24327257	26747293	rs139376186	G	A	0.0359	-0.0029	0.9971	0.9998
18	18_24337424_C_G	24337424	26757460	rs527616	G	C	0.6205	0.0193	1.0195	1.0243
18	18_24453528_T_G	24453528	26873564	rs12969503	G	T	0.3019	0.0000	1.0000	1.0000
18	18_24497839_A_A	24497839	26917875		ATT	A	0.1133	0.0006	1.0006	1.0001
18	18_24516214_C_T	24516214	26936250	rs10502480	T	C	0.1925	-0.0044	0.9956	0.9983
18	18_24518050_AT_A	24518050	26938086	18:24518050_AT_A	A	AT	0.2773	-0.0195	0.9807	0.9893
18	18_24524941_A_T	24524941	26944977	rs12954099	T	A	0.2080	-0.0018	0.9982	0.9993
18	18_24532012_G_A	24532012	26952048	rs335920	A	G	0.4333	-0.0097	0.9903	0.9917
18	18_24575223_TA_T	24575223	26995259	18:24575223_TA_T	T	TA	0.1534	-0.0017	0.9983	0.9995
18	18_24580869_C_T	24580869	27000905	rs74689581	T	C	0.0830	0.0041	1.0041	1.0007
18	18_24592146_C_T	24592146	27012182	rs1785519	T	C	0.4375	-0.0072	0.9928	0.9937
18	18_24632639_G_A	24632639	27052675	rs4800783	A	G	0.7864	-0.0016	0.9984	0.9975
18	18_24979859_TAC	24979859	27399895	18:24979859_TAC	T	TACAC	0.4407	0.0066	1.0066	1.0058
18	18_25215126_A_G	25215126	27635162	rs62080926	G	A	0.4110	-0.0010	0.9990	0.9992
18	18_25400338_GT_G	25400338	27820374	rs200577232	G	GT	0.6588	0.0000	1.0000	1.0000
18	18_25401204_AT_A	25401204	27821240	18:25401204_AT_A	A	AT	0.6968	0.0071	1.0071	1.0100
18	18_25407918_A_A	25407918	27827954	rs36088218	AT	A	0.5683	0.0000	1.0000	1.0000
18	18_25444712_A_G	25444712	27864748	rs3924216	G	A	0.7271	0.0131	1.0132	1.0193
18	18_25458783_A_G	25458783	27878819	rs12386074	G	A	0.3590	0.0000	1.0000	1.0000

18	18_25460298_C_T	25460298	27880334	rs35149382	T	C	0.2476	0.0000	1.0000	1.0000
18	18_28936833_A_G	28936833	31356870	rs10502568	G	A	0.1432	-0.0087	0.9913	0.9975
18	18_29138749_G_A	29138749	31558786	rs1791202	A	G	0.2257	0.0111	1.0112	1.0050
18	18_29981526_G_A	29981526	32401563	rs72931898	A	G	0.0474	-0.0654	0.9367	0.9940
18	18_31713658_A_G	31713658	34133694	rs139406178	G	A	0.0181	-0.0056	0.9944	0.9998
18	18_31768835_T_C	31768835	34188871	rs80264215	C	T	0.0260	0.0042	1.0042	1.0002
18	18_32606939_C_G	32606939	35026975	rs72950602	G	C	0.1732	-0.0034	0.9966	0.9988
18	18_32633575_G_G	32633575	35053611	rs147017679	GT	G	0.0657	-0.0323	0.9682	0.9958
18	18_32925069_AC_A	32925069	35345105	18:32925069_AC_A	A	AC	0.0555	-0.0066	0.9934	0.9993
18	18_33355868_T_G	33355868	35775904	rs72878547	G	T	0.0441	-0.0194	0.9808	0.9983
18	18_33766007_G_C	33766007	36186044	rs607856	C	G	0.4912	0.0000	1.0000	1.0000
18	18_38314044_A_T	38314044	40734080	rs6507380	T	A	0.1582	-0.0097	0.9903	0.9969
18	18_38534727_T_C	38534727	40954763	rs521589	C	T	0.8374	0.0076	1.0076	1.0128
18	18_42371193_G_A	42371193	44791228	rs113636799	A	G	0.0166	0.0000	1.0000	1.0000
18	18_42374231_G_G TTTGAAAAAA	42374231	44794266	rs147804054	GTTTGAA AAAAA	G	0.0686	-0.0078	0.9922	0.9989
18	18_42411803_G_C	42411803	44831838	rs9954058	C	G	0.0717	-0.0407	0.9601	0.9943
18	18_42880242_A_G	42880242	45300277	rs12456097	G	A	0.3301	-0.0076	0.9924	0.9950
18	18_42888797_T_C	42888797	45308832	rs9952980	C	T	0.3519	-0.0235	0.9768	0.9837
18	18_42974182_A_G	42974182	45394217	rs1362838	G	A	0.5465	0.0032	1.0032	1.0035
18	18_45044188_A_C	45044188	47517817	rs4939795	C	A	0.2754	0.0024	1.0024	1.0013
18	18_45055714_ATG TGTG_A	45055714	47529343	18:45055714_ATG ATGTGTG_A	A	ATGTGT G	0.4258	0.0069	1.0069	1.0059
18	18_45642989_T_C	45642989	48116618	rs4479321	C	T	0.6957	-0.0061	0.9939	0.9916
18	18_46451146_G_A	46451146	48924776	rs12956924	A	G	0.3241	-0.0075	0.9925	0.9952

18	18_46453681_A_A T	46453681	48927311	rs557304297	AT	A	0.4350	-0.0009	0.9991	0.9992
18	18_46458227_A_C	46458227	48931857	rs9946510	C	A	0.3034	0.0022	1.0022	1.0013
18	18_48157969_G_C	48157969	50631599	rs8091238	C	G	0.6052	-0.0089	0.9911	0.9893
18	18_48490805_G_A	48490805	50964435	rs646736	A	G	0.0205	0.0266	1.0270	1.0011
18	18_50371995_A_C	50371995	52845625	rs117929956	C	A	0.0303	0.0013	1.0013	1.0001
18	18_50436732_A_T	50436732	52910362	rs75666527	T	A	0.0398	0.0085	1.0085	1.0007
18	18_50681175_G_T	50681175	53154805	rs117276949	T	G	0.0247	0.0082	1.0082	1.0004
18	18_51766607_A_T	51766607	54240237	rs60287506	T	A	0.2291	-0.0003	0.9997	0.9999
18	18_51847180_AT_ A	51847180	54320810	18:51847180_ AT_A	A	AT	0.2389	-0.0069	0.9931	0.9967
18	18_53605004_G_C	53605004	55937773	rs80129237	C	G	0.0172	-0.0236	0.9767	0.9992
18	18_54060289_T_C	54060289	56393058	rs302039	C	T	0.3670	0.0003	1.0003	1.0002
18	18_54200266_T_C	54200266	56533035	rs663220	C	T	0.3957	0.0066	1.0066	1.0052
18	18_55404115_C_T	55404115	57736883	rs9676158	T	C	0.0671	-0.0126	0.9875	0.9983
18	18_56058384_A_C	56058384	58391152	rs8098126	C	A	0.5435	-0.0102	0.9899	0.9890
18	18_56061323_A_G	56061323	58394091	rs8086848	G	A	0.5736	-0.0044	0.9956	0.9950
18	18_56958687_C_T	56958687	59291455	rs8082941	T	C	0.3554	0.0041	1.0041	1.0029
18	18_57056766_G_T	57056766	59389534	rs8087926	T	G	0.4013	0.0000	1.0000	1.0000
18	18_57898005_AT_ ATT	57898005	60230772	rs35407057	ATT	AT	0.2624	-0.0007	0.9993	0.9996
18	18_60047489_G_A	60047489	62380256	rs9948182	A	G	0.3344	-0.0045	0.9955	0.9970
18	18_60296752_C_T	60296752	62629519	rs668519	T	C	0.8361	0.0007	1.0007	1.0012
18	18_60393565_T_G	60393565	62726332	rs189749253	G	T	0.0540	-0.0189	0.9813	0.9980
18	18_60826343_G_A	60826343	63159110	rs4940572	A	G	0.1475	0.0077	1.0077	1.0023
18	18_60835170_A_T	60835170	63167937	rs8094630	T	A	0.1506	0.0053	1.0053	1.0016
18	18_60845291_T_C	60845291	63178058	rs4940575	C	T	0.1644	0.0035	1.0035	1.0012

18	18_66888054_A_G	66888054	69220817	rs17080623	G	A	0.2338	0.0074	1.0074	1.0035
18	18_66888819_T_C	66888819	69221582	rs615767	C	T	0.6311	-0.0043	0.9957	0.9946
18	18_66889796_C_G	66889796	69222559	rs8093619	G	C	0.0513	0.0162	1.0163	1.0017
18	18_74194978_T_C	74194978	76483022	rs78380260	C	T	0.1186	-0.0179	0.9823	0.9958
18	18_74197470_T_C	74197470	76485514	rs58045795	C	T	0.6370	0.0014	1.0014	1.0018
18	18_74199721_C_T	74199721	76487765	rs10460104	T	C	0.1152	-0.0071	0.9929	0.9984
18	18_74967894_T_C	74967894	77255938	rs9959924	C	T	0.0760	0.0088	1.0088	1.0013
18	18_75006480_A_G	75006480	77294524	rs11659581	G	A	0.0786	0.0034	1.0034	1.0005
18	18_75105794_C_T	75105794	77393838	rs78446678	T	C	0.0332	-0.0337	0.9669	0.9978
18	18_75618836_G_A	75618836	77906880	rs76184407	A	G	0.0225	-0.0245	0.9758	0.9989
18	18_75912922_A_G	75912922	78152922	rs4798896	G	A	0.3497	-0.0131	0.9870	0.9909
18	18_76342086_A_G	76342086	78582086	rs75819391	G	A	0.0192	-0.0081	0.9919	0.9997
19	19_1396952_T_C	1396952	1396953	rs2666813	C	T	0.0369	-0.0335	0.9671	0.9976
19	19_2211050_C_T	2211050	2211051	rs2301800	T	C	0.4279	0.0164	1.0165	1.0142
19	19_4920414_A_G	4920414	4920402	rs12972366	G	A	0.2567	-0.0043	0.9957	0.9978
19	19_4922095_A_G	4922095	4922083	rs2656922	G	A	0.2365	-0.0056	0.9944	0.9974
19	19_4939092_A_AT	4939092	4939080	rs71170881	AT	A	0.2354	-0.0003	0.9997	0.9999
19	19_5836856_AAAA T_A	5836856	5836845	19:5836856_A AAAT_A	A	AAAAT	0.2760	-0.0052	0.9948	0.9971
19	19_5840619_C_T	5840619	5840608	rs708686	T	C	0.3104	-0.0026	0.9974	0.9984
19	19_8367525_G_C	8367525	8302641	rs2227288	C	G	0.1209	0.0027	1.0027	1.0007
19	19_9060605_G_A	9060605	8949929	rs2194168	A	G	0.8888	-0.0111	0.9890	0.9805
19	19_11342703_A_G	11342703	11232027	rs12979813	G	A	0.1832	-0.0018	0.9982	0.9993
19	19_12069444_T_G	12069444	11958629	rs279273	G	T	0.0806	0.0222	1.0224	1.0036
19	19_13070749_G_T	13070749	12959935	rs12984830	T	G	0.6454	-0.0018	0.9982	0.9977
19	19_13094298_C_T	13094298	12983484	rs7409148	T	C	0.8202	-0.0037	0.9963	0.9940
19	19_13158277_T_C	13158277	13047463	rs78269692	C	T	0.0510	0.0386	1.0394	1.0040

19	19_13171576_T_TG	13171576	13060762	rs35712689	TG	T	0.0606	-0.0091	0.9909	0.9989
19	19_13208001_GTTT_GTTTT	13208001	13097187		GTTTT	GTTT	0.0323	-0.0001	0.9999	1.0000
19	19_13249921_G_T	13249921	13139107	rs117922601	T	G	0.0513	0.0056	1.0056	1.0006
19	19_13954571_G_A	13954571	13843757	rs2594714	A	G	0.2285	-0.0027	0.9973	0.9988
19	19_13956663_T_G	13956663	13845849	rs4271693	G	T	0.2547	0.0000	1.0000	1.0000
19	19_13959052_C_CC CG	13959052	13848238	rs5827214	CCCG	C	0.2543	0.0000	1.0000	1.0000
19	19_14629171_C_T	14629171	14518359	rs34966794	T	C	0.0820	-0.0042	0.9958	0.9993
19	19_17117341_GA_G	17117341	17006531	19:17117341_GA_G	G	GA	0.1921	-0.0039	0.9961	0.9985
19	19_17120477_G_A	17120477	17009667	rs113926826	A	G	0.0958	-0.0045	0.9955	0.9991
19	19_17148096_C_T	17148096	17037286	rs755088	T	C	0.3747	0.0041	1.0041	1.0031
19	19_17210615_G_A	17210615	17099805	rs7249698	A	G	0.3677	-0.0073	0.9927	0.9947
19	19_17332663_A_C	17332663	17221854	rs7253172	C	A	0.3572	0.0000	1.0000	1.0000
19	19_17383602_C_T	17383602	17272793	rs62126227	T	C	0.4212	-0.0002	0.9998	0.9998
19	19_17393925_C_A	17393925	17283116	rs56069439	A	C	0.2958	0.0121	1.0122	1.0072
19	19_17397501_T_G	17397501	17286692	rs1465582	G	T	0.3998	-0.0097	0.9903	0.9923
19	19_17404269_GGG GCGGGGGT_G	17404269	17293460	19:17404269_GGGCGGGG GT_G	G	GGGC GGGG T	0.5129	0.0000	1.0000	1.0000
19	19_17913671_T_A	17913671	17802862	rs424788	A	T	0.2346	-0.0007	0.9993	0.9997
19	19_18217776_ATTT TTTTTTTTTTT_A	18217776	18106966	19:18217776_ATTT TTTTTTTTTTT_A	A	ATTTTT TTTTTT TTT	0.4258	0.0115	1.0116	1.0099
19	19_18569492_C_T	18569492	18458682	rs10164323	T	C	0.3481	-0.0491	0.9521	0.9669
19	19_18589943_C_T	18589943	18479133	rs11670056	T	C	0.0823	0.0000	1.0000	1.0000
19	19_18637610_C_T	18637610	18526800	rs4808814	T	C	0.3254	-0.0012	0.9988	0.9992

19	19_18695690_C_T	18695690	18584880	rs144474740	T	C	0.0681	0.0000	1.0000	1.0000
19	19_19347367_G_A	19347367	19236558	rs77927505	A	G	0.0630	0.0054	1.0054	1.0007
19	19_19347538_CTT_C	19347538	19236729	19:19347538_CTT_C	C	CTT	0.0369	0.0168	1.0169	1.0013
19	19_19517054_C_C_GGGCG	19517054	19406245	rs140702307	CGGGCG	C	0.3537	0.0017	1.0017	1.0012
19	19_19577215_C_G	19577215	19466406	rs4808961	G	C	0.3673	0.0189	1.0191	1.0141
19	19_19765269_G_C	19765269	19654460	rs892036	C	G	0.7114	0.0103	1.0104	1.0148
19	19_19856490_G_A	19856490	19745681	rs8099910	A	G	0.3558	-0.0032	0.9968	0.9977
19	19_21439532_G_A	21439532	21256730	rs76145660	A	G	0.0165	0.0253	1.0256	1.0008
19	19_29565686_C_G	29565686	29074779	rs71363948	G	C	0.0166	-0.0068	0.9932	0.9998
19	19_30230785_A_T	30230785	29739878	rs12976223	T	A	0.6343	-0.0098	0.9902	0.9877
19	19_30273316_G_A	30273316	29782409	rs73552114	A	G	0.0433	-0.0054	0.9946	0.9995
19	19_30344206_CT_C	30344206	29853299	19:30344206_CT_C	C	CT	0.2769	0.0016	1.0016	1.0009
19	19_30350666_T_C	30350666	29859759	rs17599667	C	T	0.2766	0.0000	1.0000	1.0000
19	19_30365074_C_A	30365074	29874167	rs62104509	A	C	0.2816	0.0000	1.0000	1.0000
19	19_33521150_A_G	33521150	33030244	rs73039428	G	A	0.0608	0.0139	1.0140	1.0017
19	19_34208223_A_G	34208223	33717318	rs157726	G	A	0.5528	0.0034	1.0034	1.0038
19	19_35099785_T_G	35099785	34608880	rs78034480	G	T	0.0263	0.0097	1.0097	1.0005
19	19_36001912_T_C	36001912	35511010	rs75264675	C	T	0.0217	0.0077	1.0077	1.0003
19	19_37833311_ATTT_TTT_A	37833311	37342409	rs756411001	A	ATTTTT	0.2660	0.0018	1.0018	1.0010
19	19_38336063_C_C_A	38336063	37845423	rs572041567	CA	C	0.2859	0.0047	1.0047	1.0027
19	19_38399256_GT_G	38399256	37908616	19:38399256_GT_G	G	GT	0.1790	0.0054	1.0054	1.0019
19	19_38704921_A_C	38704921	38214281	rs12610840	C	A	0.2005	0.0010	1.0010	1.0004

19	19_38705656_A_A G	38705656	38215016	rs200548028	AG	A	0.1891	0.0050	1.0050	1.0019
19	19_39459994_G_A	39459994	38969354	rs4803141	A	G	0.3635	-0.0072	0.9928	0.9948
19	19_41564691_TA_T	41564691	41058786	19:41564691_ TA_T	T	TA	0.0318	0.0158	1.0159	1.0010
19	19_42345760_C_C	42345760	41841665	rs587607752	CA	C	0.4612	-0.0073	0.9927	0.9933
19	19_43204784_A_G	43204784	42700632	rs1807350	G	A	0.0795	0.0030	1.0030	1.0005
19	19_43979589_G_T	43979589	43475437	rs1055099	T	G	0.4155	-0.0064	0.9936	0.9947
19	19_43986874_G_C	43986874	43482722	rs143888974	C	G	0.0555	-0.0102	0.9899	0.9989
19	19_44283031_T_C	44283031	43778879	rs56681946	C	T	0.3519	0.0289	1.0293	1.0207
19	19_44283447_C_T	44283447	43779295	rs12609846	T	C	0.5667	-0.0034	0.9966	0.9962
19	19_44284315_C_G	44284315	43780163	rs12461670	G	C	0.1461	-0.0031	0.9969	0.9991
19	19_44374631_A_G	44374631	43870479	rs11673020	G	A	0.5150	-0.0104	0.9897	0.9894
19	19_44377614_G_A	44377614	43873462	rs76483217	A	G	0.0218	0.0000	1.0000	1.0000
19	19_44427764_G_T	44427764	43923612	rs450880	T	G	0.1704	-0.0100	0.9900	0.9966
19	19_44481934_A_G	44481934	43977782	rs79428339	G	A	0.0182	0.0000	1.0000	1.0000
19	19_45134682_A_C	45134682	44631381	rs62119267	C	A	0.0187	0.0034	1.0034	1.0001
19	19_45191450_GTTT TC_G	45191450	44688178	19:45191450_ GTTTC_G	G	GTTTC	0.1169	-0.0184	0.9818	0.9957
19	19_45198477_C_T	45198477	44695207	rs10422568	T	C	0.0432	0.0196	1.0198	1.0017
19	19_45475713_A_G	45475713	44972456	rs204482	G	A	0.4095	0.0028	1.0028	1.0023
19	19_46134289_G_C	46134289	45631031	rs57724625	C	G	0.2434	0.0002	1.0002	1.0001
19	19_46164766_G_A	46164766	45661508	rs74174203	A	G	0.5407	0.0000	1.0000	1.0000
19	19_46166073_T_C	46166073	45662815	rs4399645	C	T	0.6074	-0.0096	0.9904	0.9884
19	19_46182741_G_G	46182741	45679483	rs572702775	GA	G	0.2722	-0.0062	0.9938	0.9966
19	19_46183586_C_T	46183586	45680328	rs61373376	T	C	0.1691	0.0042	1.0042	1.0014

19	19_46199363_G_A	46199363	45696105	rs74889068	A	G		0.1550	0.0018	1.0018	1.0006
19	19_46238239_C_T	46238239	45734981	rs62111736	T	C		0.0140	-0.0265	0.9738	0.9993
19	19_46274624_G_A	46274624	45771366	rs146680240	A	G		0.0155	0.0416	1.0425	1.0013
19	19_47298001_T_C	47298001	46794744	rs57753335	C	T		0.2228	-0.0120	0.9881	0.9947
19	19_49634592_ATTT_A	49634592	49131335	rs763666162	A	ATTT		0.6530	0.0028	1.0028	1.0037
19	19_49784891_A_G	49784891	49281634	rs354002	G	A		0.5218	0.0035	1.0035	1.0037
19	19_54421924_G_A	54421924	53918670	rs28462357	A	G		0.0149	0.0301	1.0306	1.0009
19	19_54654779_C_T	54654779	54151042	rs36660	T	C		0.2813	-0.0027	0.9973	0.9985
19	19_54665970_C_T	54665970	54162234	rs36655	T	C		0.3269	-0.0086	0.9914	0.9944
19	19_54672776_CT_C	54672776	54169029	19:54672776_CT_C	C	CT		0.3141	-0.0028	0.9972	0.9982
19	19_55816678_C_T	55816678	55305310	rs1172821	T	C		0.3626	-0.0060	0.9940	0.9957
19	19_55837531_G_A	55837531	55326163	rs2384686	A	G		0.3524	-0.0074	0.9926	0.9948
19	19_56060541_C_G	56060541	55549175	rs7247512	G	C		0.1831	-0.0097	0.9903	0.9965
20	20_1932164_G_A	1932164	1951518	rs6105964	A	G		0.1038	-0.0036	0.9964	0.9993
20	20_3679816_G_A	3679816	3699169	rs45587432	A	G		0.0279	-0.0316	0.9689	0.9983
20	20_5746348_A_G	5746348	5765702	rs6107689	G	A		0.3868	-0.0129	0.9872	0.9901
20	20_5762289_A_AT	5762289	5781643	rs147459548	AT	A		0.2528	-0.0026	0.9974	0.9987
20	20_5948227_G_A	5948227	5967581	rs16991615	A	G		0.0628	0.0233	1.0236	1.0030
20	20_6046437_A_T	6046437	6065791	rs745296	T	A		0.5945	0.0011	1.0011	1.0013
20	20_6047152_T_C	6047152	6066506	rs1884650	C	T		0.3136	0.0039	1.0039	1.0025
20	20_6059635_T_C	6059635	6078988	rs2236147	C	T		0.2043	0.0052	1.0052	1.0021
20	20_6427312_C_A	6427312	6446665	rs74460586	A	C		0.0115	-0.0139	0.9862	0.9997
20	20_6670853_C_T	6670853	6690206	rs2876050	T	C		0.5484	0.0012	1.0012	1.0013
20	20_6821115_C_T	6821115	6840468	rs1392626	T	C		0.0914	0.0150	1.0151	1.0028
20	20_7876255_A_G	7876255	7895608	rs6117980	G	A		0.7022	0.0051	1.0051	1.0072

20	20_10652959_G_A	10652959	10672311	rs2235810	A	G	0.1140	-0.0018	0.9982	0.9996
20	20_11177529_G_A	11177529	11196881	rs2207412	A	G	0.4969	0.0007	1.0007	1.0007
20	20_11186652_C_T	11186652	11206004	rs6078099	T	C	0.3669	0.0089	1.0089	1.0066
20	20_11379842_T_C	11379842	11399194	rs1154723	C	T	0.9483	0.0365	1.0372	1.0718
20	20_11414962_CA_C	11414962	11434314		C	CA	0.0913	0.0000	1.0000	1.0000
20	20_11461558_A_G	11461558	11480910	rs6078210	G	A	0.7071	0.0000	1.0000	1.0000
20	20_11502618_A_A	11502618	11521970	rs141526427	AAC	A	0.2463	-0.0080	0.9920	0.9961
20	20_11530650_G_A	11530650	11550002	rs2423573	A	G	0.2664	-0.0033	0.9967	0.9982
20	20_11612323_A_T	11612323	11631675	rs75314238	T	A	0.0583	-0.0058	0.9942	0.9993
20	20_13825007_AGT GT_A	13825007	13844361	20:13825007_AGTGT_A	A	AGTGT	0.7515	0.0078	1.0078	1.0118
20	20_16625607_T_A	16625607	16644962	rs967603	A	T	0.2126	0.0066	1.0066	1.0028
20	20_16626691_G_C	16626691	16646046	rs2184501	C	G	0.1367	0.0017	1.0017	1.0005
20	20_16741090_C_G	16741090	16760445	rs4814552	G	C	0.4183	-0.0007	0.9993	0.9994
20	20_19186447_G_C	19186447	19205803	rs78309861	C	G	0.0239	-0.0115	0.9886	0.9995
20	20_19199808_A_C	19199808	19219164	rs149337215	C	A	0.0248	-0.0313	0.9692	0.9985
20	20_19239386_A_G	19239386	19258742	rs6035268	G	A	0.5804	0.0090	1.0090	1.0105
20	20_19547213_C_T	19547213	19566569	rs2328411	T	C	0.7711	-0.0154	0.9847	0.9766
20	20_19721433_G_A	19721433	19740789	rs56236053	A	G	0.3377	0.0046	1.0046	1.0031
20	20_19743404_A_T	19743404	19762760	rs6081740	T	A	0.4312	0.0008	1.0008	1.0007
20	20_20570540_A_T	20570540	20589896	rs6075678	T	A	0.0422	0.0010	1.0010	1.0001
20	20_20703519_A_A	20703519	20722876	rs373593768	AAAT	A	0.0385	0.0215	1.0217	1.0017
20	20_20895989_T_C	20895989	20915346	rs117558716	C	T	0.0132	-0.0170	0.9831	0.9996
20	20_30437522_A_G	30437522	31849719	rs3746599	G	A	0.4158	-0.0059	0.9941	0.9951

20	20_31984124_G_A	31984124	33396318	rs6059298	A	G	0.1677	-0.0072	0.9928	0.9976
20	20_32381337_A_G	32381337	33793531	rs2747567	G	A	0.5880	-0.0028	0.9972	0.9967
20	20_32468680_CT_C	32468680	33880874	20:32468680_CT_C	C	CT	0.1395	-0.0025	0.9975	0.9993
20	20_34472105_C_T	34472105	35884183	rs3787173	T	C	0.0996	0.0145	1.0146	1.0029
20	20_39522409_T_C	39522409	40893769	rs6124289	C	T	0.4092	0.0036	1.0036	1.0030
20	20_40014674_G_A	40014674	41386034	rs4810315	A	G	0.3348	0.0013	1.0013	1.0009
20	20_40014981_TTG	40014981	41386341	20:40014981_TTG_T	T	TTGGG	0.1565	-0.0065	0.9935	0.9980
20	20_41613706_C_G	41613706	42985066	rs6030585	G	C	0.7928	0.0102	1.0103	1.0163
20	20_43374159_AGG	43374159	44745518	20:43374159_AGG_A	A	AGGAG	0.0337	0.0019	1.0019	1.0001
20	20_43374227_C_A	43374227	44745586	rs6031778	A	C	0.0297	0.0056	1.0056	1.0003
20	20_44220832_G_A	44220832	45592193	rs6130867	A	G	0.0640	0.0230	1.0233	1.0030
20	20_47078957_A_G	47078957	48450711	rs926693	G	A	0.4750	0.0035	1.0035	1.0033
20	20_48946692_A_G	48946692	50330155	rs12479601	G	A	0.1787	0.0095	1.0095	1.0034
20	20_49002504_G_T	49002504	50385967	rs113609374	T	G	0.0256	0.0006	1.0006	1.0000
20	20_49023796_C_A	49023796	50407259	rs6063510	A	C	0.7557	0.0000	1.0000	1.0000
20	20_49031318_G_T	49031318	50414781	rs6020487	T	G	0.2672	0.0046	1.0046	1.0025
20	20_49058736_C_T	49058736	50442199	rs6095944	T	C	0.4503	0.0000	1.0000	1.0000
20	20_49061380_TA_T	49061380	50444843	20:49061380_TA_T	T	TA	0.4591	-0.0023	0.9977	0.9979
20	20_49072666_G_A	49072666	50456129	rs118137582	A	G	0.0613	0.0085	1.0085	1.0010
20	20_49240476_C_T	49240476	50623939	rs2426172	T	C	0.0340	0.0126	1.0127	1.0009
20	20_49392744_C_T	49392744	50776207	rs151002938	T	C	0.0477	0.0000	1.0000	1.0000
20	20_49394206_TC_T	49394206	50777669	20:49394206_TC_T	T	TC	0.0158	-0.0162	0.9839	0.9995
20	20_49428692_T_C	49428692	50812155	rs62202841	C	T	0.2844	-0.0062	0.9938	0.9965

20	20_50788244_T_G	50788244	52171705	rs1964133	G	T	0.5109	-0.0003	0.9997	0.9997
20	20_51200352_T_G	51200352	52583813	rs17733099	G	T	0.1805	-0.0008	0.9992	0.9997
20	20_52296849_G_A	52296849	53680310	rs13039563	A	G	0.2400	0.0204	1.0206	1.0099
20	20_52298228_G_A	52298228	53681689	rs6097525	A	G	0.3126	0.0000	1.0000	1.0000
20	20_52298514_A_G	52298514	53681975	rs13039994	G	A	0.2366	0.0000	1.0000	1.0000
20	20_52300359_C_T	52300359	53683820	rs6126919	T	C	0.4305	-0.0014	0.9986	0.9988
20	20_52573971_T_G	52573971	53957432	rs35575210	G	T	0.1807	0.0209	1.0211	1.0076
20	20_53229113_C_A	53229113	54612574	rs35338030	A	C	0.1845	-0.0090	0.9910	0.9967
20	20_54963164_C_CC ATGTGGGTTTATAA ATGTGAATGAGATT ACAGATTATTCAAAT TAGACAAGACCAAC CTG	54963164	56388108	20:54963164_ C_CCATGTGG GTTTATAAATG TGAATGAGAT TACAGATTATT CAATTTAGACA AGACCAACCT G	CCATGTG GGTTTAT AAATGTG AATGAGA TTACAGA TTATTCA ATTTAGA CAAGACC AACCTG	C	0.0147	0.0056	1.0056	1.0002
	20_58247236_T_C	58247236	59672181	rs860973	C	T	0.8214	-0.0062	0.9938	0.9899
20	20_58248796_G_C	58248796	59673741	rs73140881	C	G	0.1653	0.0035	1.0035	1.0012
20	20_59044356_G_A	59044356	60469298	rs348798	A	G	0.6481	0.0093	1.0093	1.0121
20	20_59056866_T_C	59056866	60481808	rs348787	C	T	0.5891	0.0036	1.0036	1.0043
20	20_59363112_A_G	59363112	60788056	rs2426921	G	A	0.3715	0.0090	1.0090	1.0067
20	20_61373122_G_A	61373122	62741770	rs117647014	A	G	0.0286	0.0046	1.0046	1.0003
20	20_62692060_A_C	62692060	64060707	rs6090040	C	A	0.5150	0.0015	1.0015	1.0015
20	20_62856686_A_G	62856686	64225333	rs2320360	G	A	0.2700	0.0063	1.0063	1.0034
20	20_62877959_C_T	62877959	64246606	rs2427628	T	C	0.1520	0.0106	1.0107	1.0032
21	21_16227626_A_G	16227626	14855305	rs7278690	G	A	0.9220	-0.0071	0.9929	0.9870
21	21_16234888_C_G	16234888	14862567	rs976051	G	C	0.8337	-0.0008	0.9992	0.9987

21	21_16353809_A_C	16353809	14981488	rs17274750	C	A	0.0984	0.0245	1.0248	1.0049
21	21_16364756_T_G	16364756	14992435	rs2822999	G	T	0.1732	0.0098	1.0098	1.0034
21	21_16432738_T_C	16432738	15060417	rs62221393	C	T	0.2007	0.0106	1.0107	1.0043
21	21_16455526_T_C	16455526	15083205	rs2142364	C	T	0.8670	-0.0004	0.9996	0.9993
21	21_16461783_G_A	16461783	15089462	rs2823046	A	G	0.2714	-0.0045	0.9955	0.9976
21	21_16462541_C_G	16462541	15090220	rs2823049	G	C	0.4752	-0.0003	0.9997	0.9997
21	21_16481934_G_A	16481934	15109613	rs34336435	A	G	0.1673	0.0030	1.0030	1.0010
21	21_16517891_G_C	16517891	15145570	rs2049880	C	G	0.2190	0.0000	1.0000	1.0000
21	21_16520878_A_G	16520878	15148557	rs2823094	G	A	0.0712	0.0091	1.0091	1.0013
21	21_16520935_A_T	16520935	15148614	rs2896680	T	A	0.2633	-0.0007	0.9993	0.9996
21	21_16522082_A_G	16522082	15149761	rs2823096	G	A	0.1860	-0.0296	0.9708	0.9892
21	21_16546125_G_T	16546125	15173805	rs12483016	T	G	0.2240	-0.0012	0.9988	0.9995
21	21_16547435_A_G	16547435	15175115	rs11909473	G	A	0.2945	0.0000	1.0000	1.0000
21	21_16563309_G_A	16563309	15190989	rs2823128	A	G	0.3244	-0.0055	0.9945	0.9964
21	21_16566350_A_G	16566350	15194030	rs2823130	G	A	0.0873	0.0117	1.0118	1.0021
21	21_16574455_C_A	16574455	15202135	rs2403907	A	C	0.3167	-0.0279	0.9725	0.9826
21	21_16609549_C_CT	16609549	15237229	rs34690096	CT	C	0.5758	0.0000	1.0000	1.0000
21	21_16645377_C_A	16645377	15273058	rs35965339	A	C	0.0662	0.0014	1.0014	1.0002
21	21_18744081_A_C	18744081	17371762	rs11908794	C	A	0.5505	0.0030	1.0030	1.0033
21	21_18764525_A_G	18764525	17392206	rs13051956	G	A	0.5409	0.0031	1.0031	1.0034
21	21_19797287_C_T	19797287	18424970	rs4818409	T	C	0.4563	-0.0055	0.9945	0.9950
21	21_20202110_T_C	20202110	18829792	rs8130151	C	T	0.0544	0.0000	1.0000	1.0000
21	21_20656535_AT_A	20656535	19284218	21_20656535_AT_A	A	AT	0.6869	0.0040	1.0040	1.0055
21	21_20680408_T_G	20680408	19308091	rs9983076	G	T	0.7202	0.0044	1.0044	1.0064
21	21_21275203_A_C	21275203	19902889	rs62222014	C	A	0.0389	-0.0169	0.9832	0.9987
21	21_25798887_A_G	25798887	24426573	rs1119269	G	A	0.2401	0.0053	1.0053	1.0026

21	21_25823497_G_T	25823497	24451183	rs59551976	T	G	0.2513	0.0023	1.0023	1.0012
21	21_25892954_G_A	25892954	24520640	rs62215720	A	G	0.2994	0.0045	1.0045	1.0027
21	21_26008883_TTAT ATA_T	26008883	24636569	21:26008883- TTATATA_T	T	TTATAT A	0.8764	-0.0018	0.9982	0.9969
21	21_26933938_A_T	26933938	25561626	rs79507471	T	A	0.0337	-0.0153	0.9848	0.9990
21	21_27152333_TTC_ T	27152333	25780022	21:27152333- TTC_T	T	TTC	0.0330	-0.0002	0.9998	1.0000
21	21_28258281_T_G	28258281	26885962	rs988609	G	T	0.0985	0.0153	1.0154	1.0030
21	21_33340086_C_T	33340086	31967774	rs2833586	T	C	0.1009	-0.0122	0.9879	0.9976
21	21_33427423_G_A	33427423	32055110	rs57217265	A	G	0.0777	0.0000	1.0000	1.0000
21	21_33428993_G_C	33428993	32056680	rs11909436	C	G	0.1275	-0.0139	0.9862	0.9965
21	21_33492560_T_C	33492560	32120248	rs2833661	C	T	0.7813	0.0008	1.0008	1.0013
21	21_33501003_T_C	33501003	32128692	rs13049602	C	T	0.7854	0.0082	1.0082	1.0130
21	21_33876502_T_C	33876502	32504192	rs7275591	C	T	0.1805	0.0000	1.0000	1.0000
21	21_33914960_C_T	33914960	32542650	rs2833872	T	C	0.2097	0.0149	1.0150	1.0063
21	21_33941082_G_C	33941082	32568772	rs844989	C	G	0.2326	0.0012	1.0012	1.0006
21	21_34251327_C_T	34251327	32879019	rs2833983	T	C	0.4091	0.0036	1.0036	1.0030
21	21_35815455_A_C	35815455	34443157	rs58060663	C	A	0.0373	0.0085	1.0085	1.0006
21	21_36080290_C_T	36080290	34707992	rs6517254	T	C	0.3724	-0.0026	0.9974	0.9981
21	21_36253194_T_A	36253194	34880897	rs2298354	A	T	0.2505	0.0037	1.0037	1.0019
21	21_38622181_A_G	38622181	37249880	rs147700715	G	A	0.0178	0.0130	1.0131	1.0005
21	21_38642243_C_T	38642243	37269942	rs117110236	T	C	0.0214	0.0197	1.0199	1.0009
21	21_38784359_A_C	38784359	37412057	rs13052173	C	A	0.0666	-0.0144	0.9857	0.9981
21	21_40709960_C_T	40709960	39338034	rs1963676	T	C	0.5774	-0.0046	0.9954	0.9947
21	21_42191862_A_G	42191862	40819936	rs2837838	G	A	0.9293	-0.0158	0.9843	0.9711
21	21_44472345_G_A	44472345	43052235	rs57063354	A	G	0.0376	0.0124	1.0125	1.0009
21	21_44475877_C_T	44475877	43055767	rs8132811	T	C	0.2049	0.0025	1.0025	1.0010

21	21_44477543_G_C	44477543	43057433	rs234702	C	G		0.9190	-0.0110	0.9891	0.9800
21	21_45467448_C_T	45467448	44047567	rs9974857	T	C		0.0550	-0.0197	0.9805	0.9979
21	21_45740823_A_G	45740823	44320940	rs3827256	G	A		0.6519	-0.0028	0.9972	0.9964
21	21_47718961_CT_C	47718961	46299047	21_47718961_CT_C	C	CT		0.8400	-0.0022	0.9978	0.9963
21	21_47762932_G_A	47762932	46343018	rs4818836	A	G		0.0355	0.0314	1.0319	1.0023
21	21_47982363_G_A	47982363	46562450	rs2070430	A	G		0.4970	0.0057	1.0057	1.0057
22	22_19151419_G_A	19151419	19163906	rs66493436	A	G		0.2310	-0.0061	0.9939	0.9972
22	22_19619489_CCT_C	19619489	19631966	22_19619489_CCT_C	C	CCT		0.0322	0.0122	1.0123	1.0008
22	22_19765322_C_T	19765322	19777799	rs4819521	T	C		0.4444	-0.0076	0.9924	0.9933
22	22_19766107_G_A	19766107	19778584	rs41297994	A	G		0.1812	-0.0023	0.9977	0.9992
22	22_19766137_C_T	19766137	19778614	rs9798754	T	C		0.3798	-0.0035	0.9965	0.9973
22	22_28341053_C_T	28341053	27945065	rs9985181	T	C		0.1698	0.0064	1.0064	1.0022
22	22_29077631_C_C	29077631	28681643	rs34661406	CA	C		0.0230	0.0000	1.0000	1.0000
22	22_29121087_A_G	29121087	28725099	rs17879961	G	A		0.0054	0.0861	1.0899	1.0010
22	22_29135543_G_A	29135543	28739555	rs5997390	A	G		0.0870	0.0255	1.0258	1.0045
22	22_29157487_G_A	29157487	28761499	rs6005864	A	G		0.4206	0.0044	1.0044	1.0037
22	22_29167536_CT_C	29167536	28771548	rs773867741	C	CT		0.2511	0.0001	1.0001	1.0001
22	22_29203724_C_T	29203724	28807736	rs34134147	T	C		0.0209	0.0539	1.0554	1.0023
22	22_29272637_C_T	29272637	28876649	rs62235753	T	C		0.0177	0.0455	1.0466	1.0017
22	22_29305061_G_T	29305061	28909073	rs7364229	T	G		0.2022	0.0028	1.0028	1.0011
22	22_29375026_C_T	29375026	28979038	rs10854810	T	C		0.3024	-0.0020	0.9980	0.9988
22	22_29406219_A_T	29406219	29010231	rs13054095	T	A		0.0224	0.0000	1.0000	1.0000
22	22_29529148_A_G	29529148	29133160	rs5997447	G	A		0.0470	0.0000	1.0000	1.0000
22	22_29551872_A_G	29551872	29155884	rs132289	G	A		0.9846	-0.1118	0.8942	0.8026

22	22_29669648_G_C	29669648	29273659	rs4820803	C	G	0.1712	-0.0014	0.9986	0.9995
22	22_30160747_C_T	30160747	29764758	rs8142292	T	C	0.0400	-0.0208	0.9794	0.9984
22	22_30161801_A_G	30161801	29765812	rs5997518	G	A	0.0554	0.0014	1.0014	1.0002
22	22_30868599_G_A	30868599	30472612	rs11705494	A	G	0.0824	-0.0033	0.9967	0.9995
22	22_32732644_A_G	32732644	32336657	rs61693297	G	A	0.1994	-0.0142	0.9859	0.9944
22	22_32771017_G_T	32771017	32375030	rs5754049	T	G	0.2577	-0.0048	0.9952	0.9975
22	22_33168255_T_C	33168255	32772269	rs76307741	C	T	0.0352	-0.0159	0.9842	0.9989
22	22_34514287_T_C	34514287	34118298	rs9609951	C	T	0.0363	-0.0312	0.9693	0.9978
22	22_37369880_G_A	37369880	36973839	rs2251446	A	G	0.4241	0.0081	1.0081	1.0069
22	22_37750349_T_C	37750349	37354309	rs2899289	C	T	0.6411	-0.0069	0.9931	0.9912
22	22_37751638_CA_C	37751638	37355598	22:37751638_CA_C	C	CA	0.4035	-0.0005	0.9995	0.9996
22	22_37770357_A_G	37770357	37374317	rs7292751	G	A	0.3783	0.0017	1.0017	1.0013
22	22_37771158_G_A	37771158	37375118	rs2071857	A	G	0.4266	0.0026	1.0026	1.0022
22	22_38195596_G_A	38195596	37799589	rs8140423	A	G	0.2200	-0.0024	0.9976	0.9989
22	22_38200124_C_T	38200124	37804117	rs11703407	T	C	0.3184	0.0000	1.0000	1.0000
22	22_38426471_G_G	38426471	38030464	rs5845363	GC	G	0.1820	0.0020	1.0020	1.0007
22	22_38568833_C_G	38568833	38172826	rs738321	G	C	0.3805	-0.0125	0.9876	0.9906
22	22_38583315_AAAAG_AAAAGAAAG	38583315	38187308	AAAAGAAAG	AG	AAAAG	0.2805	-0.0071	0.9929	0.9960
22	22_38605067_T_G	38605067	38209060	rs11705176	G	T	0.3078	0.0000	1.0000	1.0000
22	22_38613851_AAAAG_A	38613851	38217844	22:38613851_AAAAG_A	A	AAAAG	0.3425	0.0000	1.0000	1.0000
22	22_38757568_AAAATAAAATAAT_A	38757568	38361563	22:38757568_AAAATAAAATAATAAAAT_A	A	AAAATAAAATAATAAT	0.3887	0.0044	1.0044	1.0034

22	22_39194068_C_T	39194068	38798063	rs9619765	T	C	0.0348	-0.0284	0.9720	0.9981
22	22_39286208_A_T	39286208	38890203	rs132502	T	A	0.3899	-0.0007	0.9993	0.9995
22	22_39343916_T_A	39343916	38947911	rs5750715	A	T	0.2541	0.0076	1.0076	1.0039
22	22_39524131_G_A	39524131	39128126	rs139376	A	G	0.5276	0.0033	1.0033	1.0035
22	22_39626375_A_C	39626375	39230370	rs4821874	C	A	0.7286	-0.0047	0.9953	0.9932
22	22_40121441_C_T	40121441	39725436	rs10427962	T	C	0.0821	-0.0047	0.9953	0.9992
22	22_40242010_C_A	40242010	39846005	rs78943183	A	C	0.0319	-0.0158	0.9843	0.9990
22	22_40476546_A_G	40476546	40080542	rs118176772	G	A	0.0261	0.0267	1.0271	1.0014
22	22_40496066_TTTT TATTA_T	40496066	40100062	22:40496066_ TTTTTATTA_T	T	TTTTAT TA	0.2343	0.0000	1.0000	1.0000
22	22_40810946_T_C	40810946	40414942	rs729982	C	T	0.1310	0.0109	1.0110	1.0029
22	22_40904707_CT_C	40904707	40508703	22:40904707_ CT_C	C	CT	0.1099	0.0624	1.0644	1.0142
22	22_40930212_C_T	40930212	40534208	rs2413624	T	C	0.6352	-0.0088	0.9912	0.9889
22	22_41049402_G_T	41049402	40653398	rs56051217	T	G	0.1000	0.0020	1.0020	1.0004
22	22_41059547_C_C A	41059547	40663543	rs562341638	CA	C	0.1951	0.0064	1.0064	1.0025
22	22_41062415_CA_ C	41062415	40666411	22:41062415_ CA_C	C	CA	0.2277	0.0000	1.0000	1.0000
22	22_43110115_A_G	43110115	42714109	rs5758891	G	A	0.5772	0.0022	1.0022	1.0025
22	22_43178526_A_C	43178526	42782520	rs552455424	C	A	0.0264	0.0106	1.0107	1.0006
22	22_43433100_C_T	43433100	43037094	rs9611990	T	C	0.1144	-0.0176	0.9826	0.9960
22	22_43468665_G_T	43468665	43072659	rs28599928	T	G	0.1097	-0.0073	0.9927	0.9984
22	22_43560309_AAC ACAC_A	43560309	43164303	22:43560309_ AACACAC_A	A	AACACA C	0.4483	-0.0024	0.9976	0.9979
22	22_44598088_A_G	44598088	44202208	rs139164	G	A	0.9292	-0.0057	0.9943	0.9895
22	22_45276346_C_T	45276346	44880466	rs17542188	T	C	0.4064	-0.0048	0.9952	0.9961

22	22_45295419_G_C	45295419	44899539	rs4823408	C	G	0.4000	0.0023	1.0023	1.0018
22	22_45301457_C_T	45301457	44905577	rs5766175	T	C	0.3688	0.0002	1.0002	1.0001
22	22_45321906_C_CC TGTTGGTGGGAAAGG CCCACACAGCACGG CCCTGTGGTGGATT CCAGGGGAAGTGG GTT	45321906	44926026	22:45321906_ C CCTGTGGTG GGAAGGCCCA CACAGCACGG CCCTGTGGTG GATTCCCAGG GAAGTGGGTT	CCTGTGG TGGGAAG GCCACA CAGCACG GCCCTGT GGTGGAT TCCCAGG GAAGTGG GTT	C	0.3696	0.0000	1.0000	1.0000
22	22_46156825_G_C	46156825	45760945	rs4823322	C	G	0.4169	-0.0040	0.9960	0.9967
22	22_46160624_G_A	46160624	45764744	rs138203	A	G	0.7477	-0.0047	0.9953	0.9930
22	22_46175966_CT_C	46175966	45780086	22:46175966_ CT_C	C	CT	0.8215	-0.0023	0.9977	0.9962
22	22_46274072_A_G	46274072	45878192	rs77848624	G	A	0.1622	0.0064	1.0064	1.0021
22	22_46283297_G_A	46283297	45887417	rs28512361	A	G	0.1117	0.0310	1.0315	1.0070
22	22_46320819_T_C	46320819	45924939	rs28548232	C	T	0.1307	0.0032	1.0032	1.0008
22	22_49094148_T_C	49094148	48698336	rs56307769	C	T	0.5791	-0.0042	0.9958	0.9952
22	22_49096694_C_T	49096694	48700882	rs130129	T	C	0.3437	-0.0012	0.9988	0.9992
22	22_49312374_A_C	49312374	48916562	rs13055787	C	A	0.9377	-0.0083	0.9917	0.9846
22	22_50602304_T_A	50602304	50163875	rs200311816	A	T	0.0299	0.0050	1.0050	1.0003

Genetic Risk Score

An individual's "polygenic risk score" can be defined as the weighted sum of the individuals' genotypes at multiple genetic loci. In other words, they are the linear combinations of the risk alleles across a set of candidate SNPs. For example, a PRS for individual i can be calculated as:

$$PRS_i = \beta_1 x_{i1} + \beta_2 x_{i2} + \dots + \beta_j x_{ij} + \dots + \beta_p x_{ip}, \quad (1)$$

where $x_{ij} \in \{0,1,2\}$ are risk allele counts and β_j are the weights for SNP $j = 1; \dots; p$.

The PRS can also be represented as: $PRS = \sum (\text{No of Risk Alleles} \times \beta$
coefficient).

In one embodiment, the key steps to construct a polygenic risk score (PRS) are to determine which SNPs to include and how to weight their effects. In one embodiment, the maxCT and SCT methods (Privé et al., 2019) are used. These methods are based on clumping and thresholding. The aim of clumping and thresholding is to remove correlated SNPs while keeping the most important SNPs in the PRS. In order to do this, the values of a range of hyperparameters including the correlation threshold (r^2), the clumping window size (kb) and the p-value significance threshold (p) are decided. Different selection of these hyperparameters values would in general give a different section of SNPs to include. For the weights, the reported GWAS coefficients (i.e., regression coefficients or log odds ratios) from external published GWAS can be used. The core idea of the maxCT and SCT procedures is to select a set of different hyperparameters values and compute a PRS for each combination of these values.

This will usually create a large number of PRSs, for example, around 100,000 vectors of PRSs for a typical GWAS. After constructing these PRSs, there are two approaches to create the final PRS. In maxCT, the PRS that has the strongest predictive performance (e.g., largest AUC) are selected as the final PRS. In SCT, the PRSs by a penalized logistic regression model, for example, the popular lasso procedure are combined. Since the outcome of SCT will be a linear combination of PRSs, where each PRS is again a linear combination of variants, the final PRS still has the form of (1), which means the effect sizes of SNPs can be obtained and used for prediction.

In an preferred example, a log-additive risk model can then be used to define three genotypes AA, AB, and BB for a single SNP having relative risk values of 1, OR, and OR^2 , under a rare disease model, where OR is the previously reported disease odds ratio for the high-risk allele, B, vs the low-risk allele, A. If the B allele has frequency (p), then these genotypes have population frequencies of $(1 - p)^2$, $2p(1 - p)$, and p^2 ,

assuming Hardy–Weinberg equilibrium. The genotype relative risk values for each SNP can then be scaled so that based on these frequencies the average relative risk in the population is 1. Specifically, given the unscaled population average relative risk:

$$(\mu) = (1 - p)^2 + 2p(1 - p)OR + p^2OR^2$$

- 5 Adjusted risk values $1/\mu$, OR/μ , and OR^2/μ are used for AA, AB, and BB genotypes. Missing genotypes are assigned a relative risk of 1. The following formula can be used to define the genetic risk:

SNP₁ x SNP₂ x SNP₃ x SNP₄ x SNP₅ x SNP₆ x SNP₇ x SNP₈, etc.

Similar calculations can be performed for non-SNP polymorphisms.

- 10 An alternate method for calculating the composite SNP risk is described in Mavaddat et al. (2015). In this example, the following formula is used;

$$PRS = \beta_1 x_1 + \beta_2 x_2 + \dots \beta_n x_n$$

- where β_k is the per-allele log odds ratio (OR) for breast cancer associated with the
15 minor allele for SNP k , and x_k the number of alleles for the same SNP (0, 1 or 2), n is the total number of SNPs and PRS is the polygenic risk score (which can also be referred to as composite SNP risk).

It is envisaged that the “risk” of a human subject for developing breast cancer can be provided as a relative risk (or risk ratio) or an absolute risk as required.

- 20 In an embodiment, the genetic risk assessment obtains the “relative risk” of a human subject for developing breast cancer. Relative risk (or risk ratio), measured as the incidence of a disease in individuals with a particular characteristic (or exposure) divided by the incidence of the disease in individuals without the characteristic, indicates whether that particular exposure increases or decreases risk. Relative risk is
25 helpful to identify characteristics that are associated with a disease, but by itself is not particularly helpful in guiding screening decisions because the frequency of the risk (incidence) is cancelled out.

- In another embodiment, the genetic risk assessment obtains the “absolute risk” of a human subject for developing breast cancer. Absolute risk is the numerical
30 probability of a human subject developing breast cancer within a specified period (e.g. 5, 10, 15, 20 or more years). It reflects a human subject’s risk of developing breast cancer insofar as it does not consider various risk factors in isolation.

Breast Cancer Risk Assessment

In an embodiment, when using the % breast density as the mammographic density score a risk (Breast Cancer Risk (BRISK)) score is determined using;

$$5 \quad brisk1_N = \frac{(cumul1_b_N - cumul1_b)}{(1 - cumul1_b)}$$

where:

N is the number of years of risk to calculate,

10 $incid_b$ is the ethnicity specific cumulative breast cancer incidence up to current age, and

$incid_bN$ is the ethnicity specific cumulative breast cancer incidence up to current age plus N years.

In another embodiment, % breast density as the mammographic density score is used to estimate lifetime risk (Breast Cancer Risk (BRISK)) score using;

$$15 \quad brisk1_rem_life = \frac{(cumul1_full_life - cumul1_b)}{(1 - cumul1_b)}$$

where:

20 $incid_b$ is the ethnicity specific cumulative breast cancer incidence up to current age, and

$incid_full_life$ is the ethnicity specific cumulative breast cancer incidence up to 90 years (i.e. full-lifetime risk).

In an embodiment,

$$25 \quad \begin{aligned} cumul1_b &= 1 - e^{-risk_mod1 \times incid_b} \\ cumul1_b_N &= 1 - e^{-risk_mod1 \times incid_b_N} \\ cumul1_full_life &= 1 - e^{-risk_mod1 \times incid_full_life} \end{aligned}$$

Furthermore,

$$30 \quad \begin{aligned} lnrisk1 &= \ln(PRS) \times \beta_{PRS} \\ &+ (\text{sqrt}(\text{percent_density}) - \text{sqrt}(\text{meanDENS})) \times \beta_{DENS} \\ &+ \ln(fh_risk_1) \\ &+ \ln(fh_risk_2) \\ 35 \quad &+ \text{intercept}_{PRE} + ((\ln(bmi/5) - \ln(\text{meanBMI}/5)) \times \beta_{PRE}) \text{ if pre-menopausal} \end{aligned}$$

+ intercept_{POST} + ((ln(bmi/5) – ln(mean_{BMI}/5)) × β_{POST}) if post-menopausal

then:

$$\text{risk_mod l} = e^{\ln \text{risk l}}$$

5

where:

β_{PRS} is the natural logarithm of the relative risk associated with a one-unit increase in the PRS (such as the β_{PRS} is between 0.93 and 1.13, or between 0.98 and 1.08, or is 1.03);

10 mean_{DENS} = the mean percent density in the population in which the test is used (such as the mean_{DENS} is between 15.14 and 19.14, or between 16.14 and 18.14, or is 17.14);

β_{DENS} is the natural logarithm of the relative risk associated with a one-unit increase in the square root of percent density (such as the β_{DENS} is between 0.02 and 0.22, or between 0.07 and 0.17 or is 0.12);

15 intercept_{PRE} is the equation intercept for pre-menopausal women (such as the intercept_{PRE} is between -0.01 and -0.07, or between -0.03 and -0.05 or is -0.04);

intercept_{POST} is the equation intercept for post-menopausal women (such as the intercept_{POST} is between 0.02 and 0.07, or between 0.04 and 0.06, or is 0.05);

20 mean_{BMI} is the mean body mass index (kg/m²) in the population in which the test is used (such as the mean_{BMI} is between 23.27 and 27.27, or between 24.27 and 26.27, or is 25.27);

β_{PRE} is the natural logarithm of the relative risk associated with being pre-menopausal (such as the β_{PRE} is between -0.15 and -0.55, or between -0.25 and -0.45 or is -0.35); and

25 β_{POST} is the natural logarithm of the relative risk associated with being post-menopausal (such as the β_{POST} is between 0.68 and 1.08, or between 0.78 and .098 or is 0.88).

30 In an embodiment, β_{PRS} = 1.03, mean_{DENS} = 17.14, β_{DENS} = 0.12, intercept_{PRE} = -0.04, intercept_{POST} = 0.05, mean_{BMI} = 25.27, β_{PRE} = -0.35 and β_{POST} = 0.88.

In an embodiment, when using the BI-RADS category as the mammographic density score a risk (Breast Cancer Risk (BRISK)) score is determined using;

N-year risk

$$35 \quad \text{brisk2_N} = \frac{(\text{cumul2_b_N} - \text{cumul2_b})}{(1 - \text{cumul2_b})}$$

240

where:

N is the number of years of risk to calculate,

incid_b is the ethnicity specific cumulative breast cancer incidence up to current age, and

5 incid_bN is the ethnicity specific cumulative breast cancer incidence up to current age plus N years.

In another embodiment, BI-RADS category as the mammographic density score is used to estimate a lifetime risk (Breast Cancer Risk (BRISK)) score using;

$$10 \quad \text{brisk2_rem_life} = \frac{(\text{cumul2_full_life} - \text{cumul2_b})}{(1 - \text{cumul2_b})}$$

where:

incid_b is the ethnicity specific cumulative breast cancer incidence up to current age, and

15 incid_full_life is the ethnicity specific cumulative breast cancer incidence up to 90 years (i.e. full-lifetime risk).

In an embodiment,

$$20 \quad \begin{aligned} \text{cumul2_b} &= 1 - e^{-\text{risk_mod2} \times \text{incid_b}} \\ \text{cumul2_b_N} &= 1 - e^{-\text{risk_mod2} \times \text{incid_b_N}} \\ \text{cumul2_full_life} &= 1 - e^{-\text{risk_mod2} \times \text{incid_full_life}} \end{aligned}$$

Furthermore,

$$25 \quad \begin{aligned} \text{lnrisk2} &= \ln(\text{PRS}) \times \beta_{\text{PRS}} \\ &+ X \text{ if BI-RADS category is A or B} \\ &+ Y \text{ if BI-RADS category is C or D} \\ &+ \ln(\text{fh_risk_1}) \\ &+ \ln(\text{fh_risk_2}) \\ 30 \quad &+ \text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}}) \text{ if pre-menopausal} \\ &+ \text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}}) \text{ if post-} \\ &\text{menopausal} \end{aligned}$$

then:

$$35 \quad \text{risk_mod2} = e^{\text{lnrisk2}}$$

where:

X is between -0.05 and -0.25, or between -0.1 and -0.2 or is -0.15;

Y is between 0.14 and 0.34, or between 0.19 and 0.29, or is 0.24;

β_{PRS} is the natural logarithm of the relative risk associated with a one-unit increase in the PRS (such as the β_{PRS} is between 0.93 and 1.13, or between 0.98 and
5 1.08, or is 1.03);

intercept_{PRE} is the equation intercept for pre-menopausal women (such as the intercept_{PRE} is between -0.01 and -0.07, or between -0.03 and -0.05 or is -0.04);

intercept_{POST} is the equation intercept for post-menopausal women (such as the intercept_{POST} is between 0.02 and 0.07, or between 0.04 and 0.06, or is 0.05);

10 mean_{BMI} is the mean body mass index (kg/m²) in the population in which the test is used (such as the mean_{BMI} is between 23.27 and 27.27, or between 24.27 and 26.27, or is 25.27);

β_{PRE} is the natural logarithm of the relative risk associated with being pre-menopausal (such as the β_{PRE} is between -0.15 and -0.55, or between -0.25 and -0.45 or
15 is -0.35); and

β_{POST} is the natural logarithm of the relative risk associated with being post-menopausal (such as the β_{POST} is between 0.68 and 1.08, or between 0.78 and .098 or is 0.88).

In an embodiment, $X = -0.15$, $Y = 0.24$, $\beta_{PRS} = 1.03$, $\text{intercept}_{PRE} = -0.04$,
20 $\text{intercept}_{POST} = 0.05$, $\text{mean}_{BMI} = 25.27$, $\beta_{PRE} = -0.35$ and $\beta_{POST} = 0.88$.

In an embodiment, one or more threshold value(s) are set for determining a particular action such as the need for routine diagnostic testing or preventative therapy. For example, a score determined using a method of the invention is compared to a pre-determined threshold, and if the score is higher than the threshold a recommendation is
25 made to take the pre-determined action. Methods of setting such thresholds have now become widely used in the art and are described in, for example, US 20140018258. For example, at present The American Society of Clinical Oncology recommends that Tamoxifen be offered for the chemoprevention of breast cancer for women who have a 5-year risk exceeding >1.66 or ≥ 1.67 , the United States Preventive Services Task Force
30 recommends that Tamoxifen be offered for the chemoprevention of breast cancer for women who have a 5-year risk exceeding 3.00%, and The National Comprehensive Cancer Network recommends that increased screening, including the option of annual MRIs be offered to women who have a lifetime risk of breast cancer exceeding 20.0%.

Treatment

After performing the methods of the present disclosure treatment may be prescribed or administered to the subject.

Accordingly, in an embodiment, the methods of the present disclosure relate to
5 an anti-cancer therapy for use in preventing or reducing the risk of breast cancer in a human subject at risk thereof.

One of skill in the art will appreciate that breast cancer is a heterogeneous disease with distinct clinical outcomes (Sorlie et al., 2001). For example, it is discussed in the art that breast cancer may be oestrogen receptor positive or oestrogen
10 receptor negative. In one embodiment, it is not envisaged that the methods of the present disclosure be limited to assessing the risk of developing a particular type or subtype of breast cancer. For example, it is envisaged that the methods of the present disclosure can be used to assess the risk of developing oestrogen receptor positive or oestrogen receptor negative breast cancer. In another embodiment, the methods of the
15 present disclosure are used to assess the risk of developing oestrogen receptor positive breast cancer. In another embodiment, the methods of the present disclosure are used to assess the risk of developing oestrogen receptor negative breast cancer. In another embodiment, the methods of the present disclosure are used to assess the risk of developing metastatic breast cancer. In an example, a therapy that inhibits oestrogen is
20 prescribed or administered to the subject.

In another example, a chemopreventative is prescribed or administered to the subject. There are two main classes of drugs currently utilized for breast cancer chemoprevention:

(1) Selective Estrogen Receptor Modulators (SERMs) which block oestrogen
25 molecules from binding to their associated cellular receptor. This class of drugs includes for example Tamoxifen and Raloxifene.

(2) Aromatase Inhibitors which inhibit the conversion of androgens into oestrogens by the aromatase enzyme by reducing the production of oestrogens. This class of drugs includes for example Exemestane, Letrozole, Anastrozole,
30 Vorozole, Formestane, Fadrozole.

In an example, a SERM or an aromatase inhibitor is prescribed or administered to the subject.

In an example, Tamoxifen, Raloxifene, Exemestane, Letrozole, Anastrozole, Vorozole, Formestane or Fadrozole is prescribed or administered to a subject.

35 In an embodiment, the methods of the present disclosure are used to assess the risk of a human female subject for developing breast cancer and administering a

treatment appropriate for the risk of developing breast cancer. For example, when performing the methods of the present disclosure indicates a high risk of breast cancer an aggressive chemopreventative treatment regimen can be established. In contrast, when performing the methods of the present disclosure indicates a moderate risk of breast cancer a less aggressive chemopreventative treatment regimen can be established. Alternatively, when performing the methods of the present disclosure indicates a low risk of breast cancer a chemopreventative treatment regimen need not be established. It is envisaged that the methods of the present disclosure can be performed over time so that the treatment regimen can be modified in accordance with the subject's risk of developing breast cancer.

Marker Detection Strategies

Amplification primers for amplifying markers (e.g., marker loci) and suitable probes to detect such markers or to genotype a sample with respect to multiple marker alleles, can be used in the disclosure. For example, primer selection for long-range PCR is described in US 10/042,406 and US 10/236,480; for short-range PCR, US 10/341,832 provides guidance with respect to primer selection. Also, there are publicly available programs such as "Oligo" available for primer design. With such available primer selection and design software, the publicly available human genome sequence and the polymorphism locations, one of skill can construct primers to amplify the polymorphisms to practice the disclosure. Further, it will be appreciated that the precise probe to be used for detection of a nucleic acid comprising a polymorphism (e.g., an amplicon comprising the polymorphism) can vary, e.g., any probe that can identify the region of a marker amplicon to be detected can be used in conjunction with the present disclosure. Further, the configuration of the detection probes can, of course, vary. Thus, the disclosure is not limited to the sequences recited herein.

Indeed, it will be appreciated that amplification is not a requirement for marker detection, for example one can directly detect unamplified genomic DNA simply by performing a Southern blot on a sample of genomic DNA.

Typically, molecular markers are detected by any established method available in the art, including, without limitation, allele specific hybridization (ASH), detection of extension, array hybridization (optionally including ASH), or other methods for detecting polymorphisms, amplified fragment length polymorphism (AFLP) detection, amplified variable sequence detection, randomly amplified polymorphic DNA (RAPD) detection, restriction fragment length polymorphism (RFLP) detection, self-sustained

sequence replication detection, simple sequence repeat (SSR) detection, and single-strand conformation polymorphisms (SSCP) detection.

As the skilled person will appreciate, the sequence of the genomic region to which these oligonucleotides hybridize can be used to design primers which are longer
5 at the 5' and/or 3' end, possibly shorter at the 5' and/or 3' (as long as the truncated version can still be used for amplification), which have one or a few nucleotide differences (but nonetheless can still be used for amplification), or which share no sequence similarity with those provided but which are designed based on genomic sequences close to where the specifically provided oligonucleotides hybridize and
10 which can still be used for amplification.

In some embodiments, the primers are radiolabelled, or labelled by any suitable means (e.g., using a non-radioactive fluorescent tag), to allow for rapid visualization of differently sized amplicons following an amplification reaction without any additional labelling step or visualization step. In some embodiments, the primers are not labelled,
15 and the amplicons are visualized following their size resolution, e.g., following agarose or acrylamide gel electrophoresis. In some embodiments, ethidium bromide staining of the PCR amplicons following size resolution allows visualization of the different size amplicons.

It is not intended that the primers be limited to generating an amplicon of any
20 particular size. For example, the primers used to amplify the marker loci and alleles herein are not limited to amplifying the entire region of the relevant locus, or any subregion thereof. The primers can generate an amplicon of any suitable length for detection. In some embodiments, marker amplification produces an amplicon at least 20 nucleotides in length, or alternatively, at least 50 nucleotides in length, or
25 alternatively, at least 100 nucleotides in length, or alternatively, at least 200 nucleotides in length. Amplicons of any size can be detected using the various technologies described herein. Differences in base composition or size can be detected by conventional methods such as electrophoresis.

Some techniques for detecting genetic markers utilize hybridization of a probe
30 nucleic acid to nucleic acids corresponding to the genetic marker (e.g., amplified nucleic acids produced using genomic DNA as a template). Hybridization formats, including, but not limited to: solution phase, solid phase, mixed phase, or in situ hybridization assays are useful for allele detection. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in*
35 *Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes* Elsevier, New York, as well as in Sambrook et al. (supra).

PCR detection using dual-labelled fluorogenic oligonucleotide probes, commonly referred to as "TaqMan™" probes, can also be performed according to the present disclosure. These probes are composed of short (e.g., 20-25 base) oligodeoxynucleotides that are labelled with two different fluorescent dyes. On the 5' terminus of each probe is a reporter dye, and on the 3' terminus of each probe a quenching dye is found. The oligonucleotide probe sequence is complementary to an internal target sequence present in a PCR amplicon. When the probe is intact, energy transfer occurs between the two fluorophores and emission from the reporter is quenched by the quencher by FRET. During the extension phase of PCR, the probe is cleaved by 5' nuclease activity of the polymerase used in the reaction, thereby releasing the reporter from the oligonucleotide-quencher and producing an increase in reporter emission intensity. Accordingly, TaqMan™ probes are oligonucleotides that have a label and a quencher, where the label is released during amplification by the exonuclease action of the polymerase used in amplification. This provides a real time measure of amplification during synthesis. A variety of TaqMan™ reagents are commercially available, e.g., from Applied Biosystems (Division Headquarters in Foster City, Calif.) as well as from a variety of specialty vendors such as Biosearch Technologies (e.g., black hole quencher probes). Further details regarding dual-label probe strategies can be found, e.g., in WO 92/02638.

Other similar methods include e.g. fluorescence resonance energy transfer between two adjacently hybridized probes, e.g., using the "LightCycler®" format described in US 6,174,670.

Array-based detection can be performed using commercially available arrays, e.g., from Affymetrix (Santa Clara, Calif.) or other manufacturers. Reviews regarding the operation of nucleic acid arrays include Sapolsky et al. (1999); Lockhart (1998); Fodor (1997a); Fodor (1997b) and Chee et al. (1996). Array based detection is one preferred method for identification markers of the disclosure in samples, due to the inherently high-throughput nature of array based detection.

The nucleic acid sample to be analysed is isolated, amplified and, typically, labelled with biotin and/or a fluorescent reporter group. The labelled nucleic acid sample is then incubated with the array using a fluidics station and hybridization oven. The array can be washed and or stained or counter-stained, as appropriate to the detection method. After hybridization, washing and staining, the array is inserted into a scanner, where patterns of hybridization are detected. The hybridization data are collected as light emitted from the fluorescent reporter groups already incorporated into the labelled nucleic acid, which is now bound to the probe array. Probes that most

clearly match the labelled nucleic acid produce stronger signals than those that have mismatches. Since the sequence and position of each probe on the array are known, by complementarity, the identity of the nucleic acid sample applied to the probe array can be identified.

5 Markers and polymorphisms can also be detected using DNA sequencing. DNA sequencing methods are well known in the art and can be found for example in Ausubel et al, eds., *Short Protocols in Molecular Biology*, 3rd ed., Wiley, (1995) and Sambrook et al, *Molecular Cloning*, 2nd ed., Chap. 13, Cold Spring Harbor Laboratory Press, (1989). Sequencing can be carried out by any suitable method, for example, dideoxy
10 sequencing, chemical sequencing, or variations thereof.

Suitable sequencing methods also include Second Generation, Third Generation, or Fourth Generation sequencing technologies, all referred to herein as “next generation sequencing”, including, but not limited to, pyrosequencing, sequencing-by-ligation, single molecule sequencing, sequence-by-synthesis (SBS),
15 massive parallel clonal, massive parallel single molecule SBS, massive parallel single molecule real-time, massive parallel single molecule real-time nanopore technology, etc. A review of some such technologies can be found in (Morozova and Marra, 2008), herein incorporated by reference. Accordingly, in some embodiments, performing a genetic risk assessment as described herein involves detecting the at least two
20 polymorphisms by DNA sequencing. In an embodiment, the at least two polymorphisms are detected by next generation sequencing.

Next generation sequencing (NGS) methods share the common feature of massively parallel, high-throughput strategies, with the goal of lower costs in comparison to older sequencing methods (see, Voelkerding et al., 2009; MacLean et al.,
25 2009).

A number of such DNA sequencing techniques are known in the art, including fluorescence-based sequencing methodologies (Birren et al., 1997). In some embodiments, automated sequencing techniques are used. In some embodiments, parallel sequencing of partitioned amplicons is used (WO2006084132). In some
30 embodiments, DNA sequencing is achieved by parallel oligonucleotide extension (See, e.g., US 5,750,341 and US 6,306,597). Additional examples of sequencing techniques include the Church polony technology (Mitra et al., 2003; Shendure et al., 2005; US 6,432,36; US 6,485,944; US 6,511,803), the 454 picotiter pyrosequencing technology (Margulies et al., 2005; US 20050130173), the Solexa single base addition technology
35 (Bennett et al., 2005; US 6,787,308; US 6,833,246), the Lynx massively parallel

signature sequencing technology (Brenner et al., 2000; US 5,695,934; US 5,714,330), and the Adessi PCR colony technology (Adessi et al., 2000).

Computer Implemented Method

5 It is envisaged that the methods of the present disclosure may be implemented by a system such as a computer implemented method. For example, the system may be a computer system comprising one or a plurality of processors which may operate together (referred to for convenience as “processor”) connected to a memory. The memory may be a non-transitory computer readable medium, such as a hard drive, a
10 solid state disk, CD-ROM or the cloud. Software, that is executable instructions or program code, such as program code grouped into code modules, may be stored on the memory, and may, when executed by the processor, cause the computer system to perform functions such as determining that a task is to be performed to assist a user to determine the risk of a human female subject for developing breast cancer; receiving
15 data indicating the first clinical risk assessment, the second clinical risk assessment, and the genetic risk assessment of the female subject developing breast cancer, wherein the genetic risk was derived by detecting at least two polymorphisms known to be associated with breast cancer; processing the data to combine the first clinical risk assessment, the second clinical risk assessment, and the genetic risk assessment to
20 obtain the risk of a human female subject for developing breast cancer; outputting the risk of a human female subject for developing breast cancer.

For example, the memory may comprise program code, which when executed by the processor causes the system to determine at least two polymorphisms known to be associated with breast cancer; process the data to combine the first clinical risk
25 assessment, the second clinical risk assessment, and the genetic risk assessment to obtain the risk of a human female subject for developing breast cancer; report the risk of a human female subject for developing breast cancer.

In another embodiment, the system may be coupled to a user interface to enable the system to receive information from a user and/or to output or display information.
30 For example, the user interface may comprise a graphical user interface, a voice user interface or a touchscreen.

In an embodiment, the program code may cause the system to determine the “Breast Cancer Risk” (BRISK).

In an embodiment, the system may be configured to communicate with at least
35 one remote device or server across a communications network such as a wireless communications network. For example, the system may be configured to receive

information from the device or server across the communications network and to transmit information to the same or a different device or server across the communications network. In other embodiments, the system may be isolated from direct user interaction.

5 In another embodiment, performing the methods of the present disclosure to assess the risk of a human female subject for developing breast cancer, enables establishment of a diagnostic or prognostic rule based on the the first clinical risk assessment, the second clinical risk assessment and the genetic risk assessment of the female subject developing breast cancer.

10 In an embodiment, the threshold level of risk is the level recommended by the American Cancer Society (ACS) guidelines for screening breast MRIc and mammography. In this example, the threshold level is preferably greater than about (20% lifetime risk).

In another embodiment, the threshold level of risk is the level recommended
15 American Society of Clinical Oncology for offering an oestrogen receptor therapy to reduce a subject's risk.

In another embodiment, the diagnostic or prognostic rule is based on the application of a statistical and machine learning algorithm. Such an algorithm uses relationships between a population of polymorphisms and disease status observed in
20 training data (with known disease status) to infer relationships which are then used to determine the risk of a human female subject for developing breast cancer in subjects with an unknown risk. An algorithm is employed which provides an risk of a human female subject developing breast cancer. The algorithm performs a multivariate or univariate analysis function.

25

EXAMPLES

EXAMPLE 1 - Breast Cancer Risk (BRISK) Scores Using Mammographic Density Score

First calculate a risk modifier score (risk_mod1) for each woman:

30

$$\begin{aligned} \lnrisk1 &= \ln(PRS) \times \beta_{PRS} \\ &+ (\text{sqrt}(\text{percent_density}) - \text{sqrt}(\text{meanDENS})) \times \beta_{DENS} \\ &+ \ln(fh_risk_1) \\ &+ \ln(fh_risk_2) \\ 35 &+ \text{intercept}_{PRE} + ((\ln(bmi/5) - \ln(\text{mean}_{BMI}/5)) \times \beta_{PRE}) \text{ if pre-menopausal} \\ &+ \text{intercept}_{POST} + ((\ln(bmi/5) - \ln(\text{mean}_{BMI}/5)) \times \beta_{POST}) \text{ if post-} \\ &\text{menopausal} \end{aligned}$$

then:

$$\text{risk_mod1} = e^{\ln \text{risk1}}$$

where:

- 5 fh_risk_1 and fh_risk_2 are obtained from Tables 1 and 2 respectively,
 β_{PRS} is the natural logarithm of the relative risk associated with a one-unit increase in the PRS ($\beta_{\text{PRS}} = 1.03$),
 $\text{mean}_{\text{DENS}}$ is the mean percent density in the population in which the test is used ($\text{mean}_{\text{DENS}} = 17.14$),
 10 β_{DENS} is the natural logarithm of the relative risk associated with a one-unit increase in the square root of percent density ($\beta_{\text{DENS}} = 0.12$),
 $\text{intercept}_{\text{PRE}}$ is the equation intercept for pre-menopausal women ($\text{intercept}_{\text{PRE}} = -0.04$),
 $\text{intercept}_{\text{POST}}$ is the equation intercept for post-menopausal women ($\text{intercept}_{\text{POST}}$
 15 $= 0.05$),
 mean_{BMI} is the mean body mass index (kg/m²) in the population in which the test is used ($\text{mean}_{\text{BMI}} = 25.27$),
 β_{PRE} is the natural logarithm of the relative risk associated with being pre-menopausal ($\beta_{\text{PRE}} = -0.35$), and
 20 β_{POST} is the natural logarithm of the relative risk associated with being post-menopausal ($\beta_{\text{POST}} = 0.88$).

Next, calculate cumulative risks as follows:

$$\begin{aligned} 25 \quad \text{cumul1_b} &= 1 - e^{-\text{risk_mod1} \times \text{incid_b}} \\ \text{cumul1_b_N} &= 1 - e^{-\text{risk_mod1} \times \text{incid_b_N}} \\ \text{cumul1_full_life} &= 1 - e^{-\text{risk_mod1} \times \text{incid_full_life}} \end{aligned}$$

- Where incid_b, incid_b_N and incid_full_life are derived from publically available
 30 country- and ethnicity-specific population-based breast cancer incidence data (such as provided in Tables 3 to 7).

Then calculate the two BRISK scores as follows:

- 35 5-year risk

$$\text{brisk1_N} = \frac{(\text{cumul1_b_N} - \text{cumul1_b})}{(1 - \text{cumul1_b})}$$

Remaining lifetime risk (to age 90 years)

$$brisk1_rem_life = \frac{(cumul1_full_life - cumul1_b)}{(1 - cumul1_b)}$$

5 Where:

N is the number of years of risk to calculate,

incid_b is the ethnicity-specific cumulative breast cancer incidence up to current age,

10 incid_bN is the ethnicity-specific cumulative breast cancer incidence up to current age plus N years, and

incid_full_life is the ethnicity-specific cumulative breast cancer incidence up to 90 years (i.e. full-lifetime risk).

EXAMPLE 2 - Breast Cancer Risk (BRISK) Scores Using BI-RADS

15 First calculate a risk modifier score (risk_mod2) for each woman:

$$\begin{aligned} \lnrisk2 = & \ln(PRS) \times \beta_{PRS} \\ & + -0.15 \text{ if BI-RADS category is A or B} \\ & + 0.24 \text{ if BI-RADS category is C or D} \\ 20 & + \ln(fh_risk_1) \\ & + \ln(fh_risk_2) \\ & + intercept_{PRE} + ((\ln(bmi/5) - \ln(mean_{BMI}/5)) \times \beta_{PRE}) \text{ if pre-menopausal} \\ & + intercept_{POST} + ((\ln(bmi/5) - \ln(mean_{BMI}/5)) \times \beta_{POST}) \text{ if post-} \\ & \text{menopausal} \end{aligned}$$

25 then:

$$risk_mod2 = e^{\lnrisk2}$$

where

fh_risk_1 and fh_risk_2 are obtained from Tables 1 and 2 respectively,

30 β_{PRS} is the natural logarithm of the relative risk associated with a one-unit increase in the PRS ($\beta_{PRS} = 1.03$),

intercept_{PRE} is the equation intercept for pre-menopausal women (intercept_{PRE} = -0.04),

intercept_{POST} is the equation intercept for post-menopausal women (intercept_{POST} = 0.05),

mean_{BMI} is the mean body mass index (kg/m²) in the population in which the test is used (mean_{BMI} = 25.27),

β_{PRE} is the natural logarithm of the relative risk associated with being pre-menopausal ($\beta_{\text{PRE}} = -0.35$),

5 β_{POST} is the natural logarithm of the relative risk associated with being post-menopausal ($\beta_{\text{POST}} = 0.88$).

Next, calculate cumulative risks as follows:

$$\begin{aligned} 10 \quad \text{cumul2_b} &= 1 - e^{-\text{risk_mod2} \times \text{incid_b}} \\ \text{cumul2_b_N} &= 1 - e^{-\text{risk_mod2} \times \text{incid_b_N}} \\ \text{cumul2_full_life} &= 1 - e^{-\text{risk_mod2} \times \text{incid_full_life}} \end{aligned}$$

Where incid_b, incid_b_N and incid_full_life are derived from publically available
15 country- and ethnicity-specific population-based breast cancer incidence data (such as provided in Tables 3 to 7).

Then calculate the two BRISK scores as follows:

20 5-year risk

$$\text{brisk2_N} = \frac{(\text{cumul2_b_N} - \text{cumul2_b})}{(1 - \text{cumul2_b})}$$

Remaining lifetime risk (to age 85 years)

$$\text{brisk2_rem_life} = \frac{(\text{cumul2_full_life} - \text{cumul2_b})}{(1 - \text{cumul2_b})}$$

25

Where:

N is the number of years of risk to calculate,

incid_b is the ethnicity-specific cumulative breast cancer incidence up to current age,

30 incid_b_N is the ethnicity-specific cumulative breast cancer incidence up to current age plus N years, and

incid_full_life is the ethnicity-specific cumulative breast cancer incidence up to 90 years (i.e. full-lifetime risk).

35

EXAMPLE 3 – Test Performance

The inventors tested the performance of the risk model using 200,559 eligible female participants of the UK Biobank prospective cohort study. Participants were female, genetically Caucasian and aged 40 to 69 years at baseline assessment date. It is
5 noteworthy, that the dataset did not contain mammographic density and only incomplete family history data. Therefore, the discriminatory accuracy will be even better than that portrayed in this example.

The inventors tested the discriminatory accuracy of three versions of the risk model: incorporating a polygenic risk score comprising 77, 313, or 3,820 SNPs (Tables
10 11, 18 and 19). The results are provided in Table 19.

Table 19. Area under the receiver operating characteristic curve (AUC) and 95% confidence interval (CI) for various polygenic risk scores incorporated into the model.

Risk Algorithm	AUC	(95% CI)
BRISK+77 SNPs 5-year risk	0.628	(0.620, 0.636)
BRISK+77 SNPs full lifetime risk	0.623	(0.615, 0.632)
BRISK+313 SNPs 5-year risk	0.648	(0.639, 0.656)
BRISK+313 SNPs full lifetime risk	0.643	(0.635, 0.651)
BRISK+3820 SNPs 5-year risk	0.650	(0.641, 0.658)
BRISK+3820 SNPs full lifetime risk	0.646	(0.639, 0.654)

15 The inventors assessed calibration using logistic regression of the logit of the risk score to estimate the intercept and the slope (β coefficient). An intercept close to 0 indicates good calibration, while an intercept of less than 0 indicates overall overestimation and an intercept of greater than 0 indicated overall underestimation of
20 risk.

In terms of the dispersion of the risk score, a slope of close to 1 indicates good estimation across the spectrum of risk. A slope of less than 1 means that the predicted probabilities do not vary enough (i.e. underestimation of true high risk and overestimation of true low risk). Conversely, a slope of greater than one means that the
25 predicted probabilities vary too much (i.e. underestimation of true low risk and overestimation of true high risk).

Table 20 and Figure 1 show the calibration analysis for the three risk models.

Table 20. Slope and intercept values of the calibration plots for each of the risk models.

Risk Algorithm	Slope	Intercept
Brisk + 77 SNPs	1.000	0.068
Brisk + 313 SNPs	1.026	0.081
Brisk + 3,820 SNPs	0.813	0.104

5

The present application claims priority from AU 2021903955 filed 7 December 2021, the entire contents of which are incorporated herein by reference.

It will be appreciated by persons skilled in the art that numerous variations
10 and/or modifications may be made to the invention as shown in the specific
embodiments without departing from the spirit or scope of the invention as broadly
described. The present embodiments are, therefore, to be considered in all respects as
illustrative and not restrictive.

All publications discussed and/or referenced herein are incorporated herein in
15 their entirety.

Any discussion of documents, acts, materials, devices, articles or the like which
has been included in the present specification is solely for the purpose of providing a
context for the present invention. It is not to be taken as an admission that any or all of
these matters form part of the prior art base or were common general knowledge in the
20 field relevant to the present invention as it existed before the priority date of each claim
of this application.

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CLAIMS

1. A computer-implemented method for assessing the risk of a human female subject developing breast cancer, the method comprising:
 - 5 determining a genetic risk score based on genetic data derived from a biological sample taken from the female subject;
 - determining a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;
 - determining a first-degree family history risk score and a second-degree family
 - 10 history risk score based on family history data of the female subject;
 - determining a body mass index risk score based on the body mass index and menopause status of the subject;
 - calculating a risk modifier score, the risk modifier score being a function of the polygenetic risk score, mammographic density risk score, first-degree family history
 - 15 risk score, second-degree family history risk score and body mass index risk score;
 - calculating at least two cumulative risk scores of the female subject developing breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer incidence value based on the subjects age and ethnicity, and
 - 20 calculating the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.
2. The method of claim 1, wherein the genetic risk score is determined by $\ln(\text{PRS}) \times \beta_{\text{PRS}}$, where the PRS is the polygenic risk score that represents the female subject's
- 25 genetic predisposition to breast cancer, and β_{PRS} is the natural logarithm of the relative risk associated with a one-unit increase in $\ln(\text{PRS})$.
3. The method of claim 1 or claim 2, wherein the genetic risk score is determined using at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least
- 30 313, at least 350, at least 400, at least 450, at least 500, at least 550, at least 600, at least 650, at least 700, at least 750, at least 800, at least 825, at least 850, at least 3,820 or all of the polymorphism provided in one or more of Tables 8 to 18, or a polymorphism in linkage disequilibrium with one or more thereof.
- 35 4. The method according to any one of claims 1 to 3, wherein the genetic risk score is determined using the 313 polymorphism of Table 17.

5. The method according to any one of claims 1 to 3, wherein the genetic risk score is determined using the 3,820 polymorphisms of Table 18.
- 5 6. The method according to any one of claims 1 to 5, wherein the first-degree family history risk score (fh_risk_1) is based on the subjects age and the number and youngest age affected of the subjects first-degree relatives with invasive breast cancer.
7. The method of claim 6, wherein the first-degree family history risk score is
10 $\ln(\text{fh_risk_1})$.
8. The method according to any one of claims 1 to 7, wherein the second-degree family history risk score (fh_risk_2) is based on the subjects age and the subject's number of second-degree relatives with invasive breast cancer.
- 15 9. The method of claim 8, wherein the second-degree family history risk score is $\ln(\text{fh_risk_2})$.
10. The method according to any one of claims 1 to 9, wherein the body mass index risk score is determined using $\text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}})$ if pre-menopausal, or $\text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}})$ if post-menopausal, where mean_{BMI} is the mean body mass index in the population in which the test is used, $\text{intercept}_{\text{PRE}}$ is the equation intercept for pre-menopausal women and $\text{intercept}_{\text{POST}}$ is the equation intercept for post-menopausal women.
- 25 11. The method according to any one of claims 1 to 9, wherein the mammographic density risk score is determined using $(\text{sqrt}(\text{percent_density}) - \text{sqrt}(\text{mean}_{\text{DENS}})) \times \beta_{\text{DENS}}$, where $\text{mean}_{\text{DENS}}$ is the mean percent density in the population in which the test is used, and β_{DENS} is the natural logarithm of the relative risk associated with a one-unit increase in the square root of percent density.
- 30 12. The method according to any one of claims 1 to 11, wherein the risk modifier score (risk_mod1) is determined using:
- $$\begin{aligned} \ln \text{risk1} &= \ln(\text{PRS}) \times \beta_{\text{PRS}} \\ 35 &+ (\text{sqrt}(\text{percent_density}) - \text{sqrt}(\text{mean}_{\text{DENS}})) \times \beta_{\text{DENS}} \\ &+ \ln(\text{fh_risk_1}) \end{aligned}$$

258

$$\begin{aligned}
& + \ln(fh_risk_2) \\
& + intercept_{PRE} + ((\ln(bmi/5) - \ln(mean_{BMI}/5)) \times \beta_{PRE}) \text{ if pre-menopausal} \\
& + intercept_{POST} + ((\ln(bmi/5) - \ln(mean_{BMI}/5)) \times \beta_{POST}) \text{ if post-menopausal}
\end{aligned}$$

5 then:

$$risk_mod1 = e^{lnrisk1}$$

13. The method of claim 12, wherein the at least two cumulative risk scores are
 10 selected from:

$$\begin{aligned}
cumul1_b &= 1 - e^{-risk_mod1 \times incid_b} \\
cumul1_b_N &= 1 - e^{-risk_mod1 \times incid_b_N} \\
cumul1_full_life &= 1 - e^{-risk_mod1 \times incid_full_life}
\end{aligned}$$

15 where:

N is the number of years of risk to calculate

incid_b = is the ethnicity-specific cumulative breast cancer incidence up to
 current age,

20 incid_bN = is the ethnicity-specific cumulative breast cancer incidence up to
 current age plus 5N years, and

incid_full_life is the ethnicity-specific cumulative breast cancer incidence up to
 90 years.

14. The method of claim 12, wherein the breast cancer risk score is determined
 25 using either of:

$$brisk1_N = \frac{(cumul1_b_N - cumul1_b)}{(1 - cumul1_b)}$$

or

30

$$brisk1_rem_life = \frac{(cumul1_full_life - cumul1_b)}{(1 - cumul1_b)}$$

15. The method according to any one of claims 1 to 9, wherein the mammographic
 density risk score is a BI-RADS category.

16. The method according to any one of claims 1 to 9 or 15, wherein the risk modifier score (risk_mod2) is determined using:

$$\begin{aligned}
 \text{lnrisk1} &= \ln(\text{PRS}) \times \beta_{\text{PRS}} \\
 5 \quad &+ X \text{ if BI-RADS category is A or B} \\
 &+ Y \text{ if BI-RADS category is C or D} \\
 &+ \ln(\text{fh_risk_1}) \\
 &+ \ln(\text{fh_risk_2}) \\
 &+ \text{intercept}_{\text{PRE}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{PRE}}) \text{ if pre-menopausal} \\
 10 \quad &+ \text{intercept}_{\text{POST}} + ((\ln(\text{bmi}/5) - \ln(\text{mean}_{\text{BMI}}/5)) \times \beta_{\text{POST}}) \text{ if post-menopausal}
 \end{aligned}$$

wherein, X is between -0.05 and -0.25, and Y is between 0.14 and 0.34,

then:

$$\begin{aligned}
 15 \quad &\text{risk_mod2} = e^{\text{lnrisk2}}.
 \end{aligned}$$

17. The method of claim 16, wherein the at least two cumulative risk scores are selected from:

$$\begin{aligned}
 20 \quad &\text{cumul2_b} = 1 - e^{-\text{risk_mod2} \times \text{incid_b}} \\
 &\text{cumul2_b_N} = 1 - e^{-\text{risk_mod2} \times \text{incid_b_N}} \\
 &\text{cumul2_full_life} = 1 - e^{-\text{risk_mod2} \times \text{incid_full_life}}
 \end{aligned}$$

where:

- 25 N is the number of years of risk to calculate,
 incid_b is the ethnicity-specific cumulative breast cancer incidence up to current age,
 incid_b_N5 is the ethnicity-specific cumulative breast cancer incidence up to current age plus 5N years, and
 30 incid_full_life is the ethnicity-specific cumulative breast cancer incidence up to 90 years (i.e. full-lifetime risk).

18. The method of claim 12, wherein the breast cancer risk score is determined using either of:

35

$$brisk2_N = \frac{(cumul2_b_N - cumul2_b)}{(1 - cumul2_b)}$$

or

$$brisk2_rem_life = \frac{(cumul2_full_life - cumul2_b)}{(1 - cumul2_b)}$$

19. The method according to any one of claims 1 to 18 which further comprises comparing the score to a pre-determined threshold.
20. The method according to any one of claims 1 to 19 which further comprises outputting the breast cancer risk score.
21. A computer-implemented method for assessing the risk of a human female subject developing breast cancer, the method comprising:
 - 15 determining a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;
 - determining a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;
 - determining a body mass index risk score based on the body mass index and
 - 20 menopause status of the subject;
 - calculating a risk modifier score, the risk modifier score being a function of the mammographic density risk score, first-degree family history risk score, second-degree family history risk score and body mass index risk score;
 - calculating at least two cumulative risk scores of the female subject developing
 - 25 breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer incidence value based on the subjects age and ethnicity, and
 - calculating the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.
 - 30
22. A computer readable storage medium storing executable code, wherein when a processor executes the code, the processor is cause to perform the method of any one of claims 1 to 21.

23. A device for assessing the risk of a human female subject developing breast cancer, the device comprising:

a processor; and

a memory device storing executable code, the memory being accessible to the

5 processor;

wherein when caused to execute the executable code stored in the memory device, the processor is caused to:

determine a genetic risk score based on genetic data derived from a biological sample taken from the female subject;

10 determine a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;

determine a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;

15 determine a body mass index risk score based on the body mass index and menopause status of the subject;

calculate a risk modifier score, the risk modifier score being a function of the polygenetic risk score, mammographic density risk score, first-degree family history risk score, second-degree family history risk score and body mass index risk score

20 calculate at least two cumulative risk scores of the female subject developing breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer incidence value based on the subjects age and ethnicity, and

calculate the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.

25

24. A device for assessing the risk of a human female subject developing breast cancer, the device comprising:

a processor; and

a memory device storing executable code, the memory being accessible to the

30 processor;

wherein when caused to execute the executable code stored in the memory device, the processor is caused to:

determine a mammographic density risk score based on data derived from a clinical assessment of the mammographic density of the female subject;

35 determine a first-degree family history risk score and a second-degree family history risk score based on family history data of the female subject;

determine a body mass index risk score based on the body mass index and menopause status of the subject;

calculate a risk modifier score, the risk modifier score being a function of the mammographic density risk score, first-degree family history risk score, second-degree
5 family history risk score and body mass index risk score

calculate at least two cumulative risk scores of the female subject developing breast cancer to her current age, to the next N years and/or full lifetime, the cumulative risk being a function of the risk modifier score and a cumulative breast cancer incidence value based on the subjects age and ethnicity, and

10 calculate the female subject's absolute risk of breast cancer in the next N years, and/or in the subjects full lifetime, using the cumulative risk scores.

25. The device of claim 23 or claim 24, further comprising a display component, wherein the processor is further caused to display the breast cancer risk score of the
15 female subject for developing breast cancer on the display component.

26. The device according to any one of claims 23 to 25, further comprising a communications module, wherein the processor is further caused to communicate the breast cancer risk score of the female subject for developing breast cancer to an
20 external device via the communications module.

27. A method for assessing the risk of a human female subject for developing breast cancer comprising:

i) determining the age, ethnicity, family history of breast cancer incorporating
25 number of first-degree relatives who have had breast cancer, the age of the youngest first-degree relative at diagnosis with breast cancer, the number of second-degree relatives who have had breast cancer, country of residence, mammographic breast density, body mass index (BMI) and menopausal status,

ii) determining the genotype of the human female subject at 50 or more
30 polymorphic loci associated with a risk of a human female subject for developing breast cancer,

iii) determining a breast cancer risk score based on i) and ii).

28. A method for assessing the risk of a human female subject for developing breast
35 cancer comprising:

i) determining the age, ethnicity, family history of breast cancer incorporating number of first-degree relatives who have had breast cancer, the age of the youngest first-degree relative at diagnosis with breast cancer, the number of second-degree relatives who have had breast cancer, country of residence, mammographic breast
5 density, body mass index (BMI) and menopausal status,

ii) determining a breast cancer risk score based on i).

29. The method according to any one of claims 1 to 21, 27 or 28, wherein the results of the assessment indicate that the female should be subjected to more frequent
10 screening and/or prophylactic anti-breast cancer therapy.

30. The method according to any one of claims 1 to 21, or 27 or 29, wherein if it is determined that the subject has a risk of developing breast cancer, the subject is more likely to be responsive to oestrogen inhibition therapy than non-responsive.
15

31. The method according to any one of claims 1 to 21 or 27 to 30, wherein the breast cancer is oestrogen receptor positive or oestrogen receptor negative.

32. A method for determining the need for routine diagnostic testing of a human
20 female subject for breast cancer comprising assessing the risk of the subject for developing breast cancer using the method according to any one of claims 1 to 21 or 27 to 31.

33. The method of claim 32, wherein an risk score greater than about 20% lifetime
25 risk indicates that the subject should be enrolled in a screening breast MRI and mammography program.

34. A method of screening for breast cancer in a human female subject, the method comprising assessing the risk of the subject for developing breast cancer using the
30 method according to any one of claims 1 to 21 or 27 to 31, and routinely screening for breast cancer in the subject if they are assessed as having a risk for developing breast cancer.

35. A method for determining the need of a human female subject for prophylactic
35 anti-breast cancer therapy comprising assessing the risk of the subject for developing breast cancer using the method according to any one of claims 1 to 21 or 27 to 31.

36. The method of claim 35, wherein an risk score greater than about 1.66% 5-year risk indicates that oestrogen receptor antagonist therapy should be offered to the subject.

5

37. A method for preventing breast cancer in a human female subject, the method comprising assessing the risk of the subject for developing breast cancer using the method according to any one of claims 1 to 21 or 27 to 31, and administering an anti-breast cancer therapy to the subject if they are assessed as having a risk for developing

10

38. The method of claim 37, wherein the therapy inhibits oestrogen.

39. An anti-breast cancer therapy for use in preventing breast cancer in a human

15

31.

40. A method for stratifying a group of human female subjects for a clinical trial of a candidate therapy, the method comprising assessing the individual risk of the subjects for developing breast cancer using the method according to any one of claims 1 to 21 or 27 to 31, and using the results of the assessment to select subjects more likely to be responsive to the therapy.

20

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