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(54) Title: RADIATION THERAPY BIOMARKERS

(57) Abstract: Materials and methods related to using biomarkers for prediction of response to radiation therapy.



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RADIATION THERAPY BIOMARKERS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims benefit of priority from U.S. Provisional Application Serial No. 61/166,493, filed on April 3, 2009.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

This invention was made with government support under grant no. GM061388, awarded by the National Institute of General Medical Sciences. The government has certain rights in the invention.

TECHNICAL FIELD

This document relates to biomarkers for prediction of response to therapy, and more particularly to biomarkers that can be used to predict whether a subject will respond to radiation therapy.

BACKGROUND

Radiation is widely used to treat a variety of cancers. For some tumor types, radiation can be the most important element in therapy. Response to radiation varies widely, however. In addition, severe side effects (e.g., skin lesions, pulmonary fibrosis, or esophagitis, depending on the organ(s) being treated) can result from radiation treatment.

SUMMARY

This document is based in part on the discovery that single nucleotide polymorphisms (SNPs) may be useful as biomarkers to predict a subject's response to radiation therapy. Many factors can contribute to variation in response to radiation therapy, including genetic variation. A subject's response to radiation may be at least partially inherited. If a subject is determined to have biomarkers indicating that radiation treatment is likely to be effective, the treatment may be used. Conversely, if a subject's biomarker analysis indicates that radiation treatment is not likely to be effective, the

subject can be spared the potentially adverse side effects of radiation, and other avenues of treatment can be attempted.

In one aspect, this document features an *in vitro* method for predicting the effectiveness of radiation therapy in a subject, comprising (a) providing a biological sample from the subject; (b) assaying the biological sample to determine whether it comprises a radiation therapy signature; and (c) classifying the subject as having a greater likelihood of responding to radiation therapy if the signature is present in the biological sample, and classifying the subject as having a lesser likelihood of responding to radiation therapy if the signature is not present in the biological sample. The method can further comprise communicating to a medical professional information regarding whether or not the signature is present in the biological sample. The method can further comprise communicating to a medical professional information indicating that the presence of the signature correlates with effectiveness of radiation therapy. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs7000734, rs16885294, rs1561715, rs1610110, rs2859631, rs12569163, rs16889440, rs7554126, rs4742269, rs7591064, rs11250464, rs1853665, rs4392868, rs17598306, rs1471356, and rs4554799. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, and rs212551. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs1610110, rs1561715, rs1561714, rs4392868, rs7000734, and rs212551. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs6863920, rs6449478, rs2409791, rs4326096, rs206789, and rs286158. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs4463400, rs6578080, rs4397386, rs7387053, rs4487737, rs13275618, rs6578083, rs7814976, rs7841539, rs6578084, and rs9324519. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs12553351 and rs4742269. The radiation therapy signature can comprise rs1610110, rs1561715, or rs7000734.

In another aspect, this document features an *in vitro* method for determining a dose of radiation for administration to a subject, comprising (a) providing a biological

sample from the subject; (b) assaying the biological sample to determine whether it comprises a radiation therapy signature; and (c) determining that the dose is lower if the signature is present in the biological sample than if the signature is not present in the biological sample, and determining that the dose is higher if the signature is not present in the biological sample than if the signature is present in the biological sample. The method can comprise communicating to a medical professional information regarding whether or not the signature is present in the biological sample. The method can further comprise communicating to a medical professional information indicating that the presence of the signature correlates with a lower dose of radiation therapy. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs7000734, rs16885294, rs1561715, rs1610110, rs2859631, rs12569163, rs16889440, rs7554126, rs4742269, rs7591064, rs11250464, rs1853665, rs4392868, rs17598306, rs1471356, and rs4554799. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, and rs212551. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs1610110, rs1561715, rs1561714, rs4392868, rs7000734, and rs212551. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs6863920, rs6449478, rs2409791, rs4326096, rs206789, and rs286158. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs4463400, rs6578080, rs4397386, rs7387053, rs4487737, rs13275618, rs6578083, rs7814976, rs7841539, rs6578084, and rs9324519. The radiation therapy signature can comprise one or more markers selected from the group consisting of rs12553351 and rs4742269. The radiation therapy signature can comprise rs1610110, rs1561715, or rs7000734.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the

present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF DRAWINGS

FIG. 1 is a diagram of the human variation cell line model system described herein.

FIG. 2 is a plot of area under the curve (AUC) vs. SNPs based on p-value and chromosomal position. The y-axis gives the $-\log_{10}(\text{p-value})$ for the association, while the x-axis gives the relative chromosomal position for each SNP. Each dot represents an association identified. The analysis was conducted using a panel of 300 human lymphoblastoid cell lines (100 Caucasian American, 100 African American, and 100 Han-Chinese American cell lines), adjusted for ethnicity.

FIG. 3 is a plot of AUC vs. chromosome 8 SNPs based on p-value and chromosomal position. The y-axis gives the $-\log_{10}(\text{p-value})$ for the association, while the x-axis gives the relative position on chromosome 8 for each SNP. Each dot represents an association identified. The analysis was conducted using a panel of 100 human (Caucasian American) lymphoblastoid cell lines.

FIG. 4A is a graph plotting representative radiation cytotoxicity dose-response curves. Two cell lines from each of the three ethnic groups studied were selected to illustrate a range of radiation cytotoxicity “dose response” curves. Squares indicate African-Americans (AA), triangles Caucasian-Americans (CA) and circles Han Chinese-Americans (HCA). The x-axis indicates $\log_{10}$ (radiation dose) and the y-axis indicates the proportion of cell surviving after radiation exposure. FIG. 4B is a graph plotting the relationship of ethnic group to radiation AUC. FIG. 4C is a graph plotting the gender effect on radiation AUC. FIG. 4D is a graph plotting a frequency distribution histogram of $\ln$ AUC values for 277 cell lines.

FIG. 5A is a graph plotting genome-wide association of basal expression with radiation AUC for 277 cell lines. The y-axis represents the $-\log_{10}(\text{p value})$ for the association of individual expression array probe sets. Expression probe sets are plotted on the x-axis based on the chromosomal locations of their genes. If genes had more than one probe set, the one with the lowest p value was plotted. The horizontal line indicates a p value of 10^{-3} . FIG. 5B is a graph plotting genome-wide SNP association with radiation AUC for 277 cell lines. The y-axis represents $-\log_{10}(\text{p value})$ for the association of each SNP with radiation AUC. SNPs are plotted on the x-axis based on their chromosomal locations. The horizontal line indicates a p value of 10^{-4} . FIG. 5C is a graph plotting the most significant “locus” on chromosome 8 that was associated with radiation AUC. Diamonds indicate SNPs observed by genotyping, while triangles indicate imputed SNPs. The y-axis represents $-\log_{10}(\text{p value})$ for the association of each SNP with radiation AUC, and the x-axis represents the location of the SNP on chromosome 8.

FIG. 6 is a diagram depicting linkage disequilibrium analysis for 6 top SNPs on chromosome 8, locus “8C,” in AA and CA subjects.

FIG. 7 is a diagram of the strategy used to select genes for functional validation. Genome-wide association studies for radiation AUC were performed with 1.3 million SNPs or 54,000 expression probe sets. A SNP locus-Expression-AUC “integrated analysis” was performed using “loci” that contained at least 2 SNPs associated with radiation AUC with p values $<10^{-4}$, 54,000 expression probe sets and radiation AUC associations were used to identify SNPs associated with radiation AUC through their influence on gene expression (SNP-Expression p value $<10^{-4}$, Expression-AUC p value $<10^{-3}$). Finally, 23 candidate genes, including 1 from a SNP locus-AUC analysis, 12 from Expression-AUC analyses and 10 from SNP locus-Expression-AUC “integrated analyses”, were selected for functional validation studies performed with multiple cancer cell lines.

FIG. 8 presents data from siRNA screening of candidate genes by MTS assay in multiple cancer cell lines. Data are shown for five of the top 23 candidate genes, which were selected on the basis of “integrated analyses” and their potential biological implications, and were studied functionally in HupT3, MIA-PaCa2 and HeLa cancer cell lines by MTS assay after siRNA knockdown performed with two “unvalidated” or one

“validated” siRNA when available. Dark gray bars and squares indicate data for non-transfected cells; white bars and triangles indicate negative control siRNA; and striped bars, gray bars, and circles indicate data for specific siRNAs. If two siRNAs were available, “significance” was defined as a gene with a significant change in apparent AUC for both in comparison with control siRNA. FIG. 8A, Candidate gene symbols. FIG. 8B, QRT-PCR. The y-axis indicates relative gene expression after siRNA knockdown when compared with “all star negative” siRNA. FIG. 8C, MTS assays. The x-axis indicates the log₁₀ (radiation dose) and the y-axis indicates the proportion of cells surviving after exposure to radiation.

FIG. 9 presents data from siRNA screening of candidate genes by colony-forming assay performed with multiple cancer cell lines. Data for five of the 23 top candidate genes were selected for colony-forming assays using HupT3, MIA-PaCa2, HeLa and A549 cancer cell lines. QRT-PCR also was performed to determine knockdown efficiency. Dark gray bars and squares indicate data for non-transfected cells; white bars and triangles indicate negative control siRNA; and gray bars and circles indicate data for specific siRNAs. FIG. 9A, Candidate gene symbols. FIG. 9B, QRT-PCR to assess expression levels for each candidate gene after knockdown in each cell line. FIG. 9C, Colony-forming assays performed with HupT3, MIA-PaCa2, HeLa and A549 cancer cell lines. The x-axis indicates the log₁₀ (radiation dose), and the y-axis indicates colony-forming ability relative to control.

FIG. 10A is a pair of graphs plotting association of genotypes for two SNPs downstream of *DEPDC1B* with expression levels of *DEPDC1B* (left panel) and *BORA* (right panel) in 277 cell lines. FIG. 10B is a graph plotting the correlation of *DEPDC1B* and *BORA* log₂ expression in the 277 LCLs studied using microarray. The data are expressed as relative standard deviates (Z values). R represents the Pearson correlation coefficient. FIG. 10C is a pair of graphs plotting real time QRT-PCR to assess *BORA* expression levels after knockdown of *DEPDC1B* in HeLa (left panel) or HupT3 (right panel) cell lines. Cells were transfected with either negative control siRNA (grey) or specific siRNA for *DEPDC1B* (black). Controls (white) were untransfected cells. RNA was isolated 24 or 48 hours later to perform RT-PCR to determine *DEPDC1B* and *BORA* mRNA levels. Expression is expressed relative to levels after negative siRNA.

FIGS. 11A, 11B, and 11C are diagrams of the results of Ingenuity Pathway analyses. A total of 240 candidate genes, including 211 genes from either expression vs. AUC correlations (p value $<10^{-3}$) or from “integrated analyses” (SNP vs. Expression p value $<10^{-4}$, and Expression vs. AUC p value $<10^{-3}$), and 29 genes from 27 “loci” that were associated with radiation AUC, with each locus containing at least 2 SNPs within 50kb with p values $<10^{-4}$, were used in the network analyses.

DETAILED DESCRIPTION

Genotype-phenotype association studies

This document relates to results obtained using a panel of immortalized human lymphoblastoid cell lines obtained from healthy individuals of varying ethnicities. The panel can allow one to query genomic variation across the entire genome for the effects of inheritance on variation in response to drug or radiation therapy. Such a panel can be used for preclinical testing for common, functionally significant gene sequence variation that influences treatment phenotypes. For example, a cell line panel can be used to test individual responses to therapies such as radiation treatment, drugs (e.g., anti-cancer drugs and immunosuppressants), and drug metabolites. Further, pharmaceutical companies can test drugs on a cell line panel prior to clinical trials, and medical researchers can use such a cell line panel to determine genetic reasons for adverse reactions to therapies, or failure of a therapy to be efficacious.

Therapeutic response phenotypes can vary from life-threatening adverse reactions at one end of the spectrum to lack of the desired therapeutic efficacy at the other. Thus, a cell line panel such as that described herein can be used to define, prior to patient exposure, the possible effect of common DNA sequence variation on response to a particular therapy. For example, in depth resequencing data can be obtained in the cell lines for genes encoding proteins in known pathways for radiation effects (e.g., DNA damage, DNA repair, and cell cycle pathways), as well as drug metabolism, drug transport, and drug effects. In addition, genome-wide single nucleotide polymorphisms (SNPs) across the entire genome can be obtained for the individual cell lines for use in genome-wide association studies. Genotype-phenotype correlation analyses using SNPs and intragene haplotype (the combination of SNPs on a given allele) resulting from gene

resequencing and genome-wide SNPs can be performed to identify “therapogenomic” and pharmacogenomic candidate genes, both within traditional pharmacokinetic (PK) and pharmacodynamic (PD) pathways, as well as across the entire genome. Expression array data for every gene in the human genome encoding a protein, as well as exon array data and genome-wide gene copy number information also can be obtained for the cell lines.

Further, as future techniques for defining DNA sequence variation are developed, culminating in complete genomic sequence for each cell line, those techniques can be added to accumulate a dense array of information – in effect, a “data warehouse” – with respect to differences in DNA sequence and structure that can be correlated with variation in drug-related phenotypes. Those phenotypes may include variation in gene expression, variation in cytotoxicity, variation in apoptosis, variation in nucleic acid methylation, and variation in metabolites in response to varying levels of radiation or varying concentrations of drug, for example. All of this information can be used to perform both “pathway-based” and “genome-wide” genotype-phenotype correlations to identify genetic polymorphisms and/or haplotypes that can be used to develop hypotheses with the cell lines, which then can be tested functionally in the laboratory and also in the clinic, using patient DNA or tissue samples (see Figure 1). Therefore, the panel of cell lines described herein can be used to identify and characterize the effect of common variation in DNA sequence and structure in human populations on therapy response phenotypes that might be responsible for individual differences in adverse reactions to radiation therapy or in the efficacy of radiation therapy. It is noted that in addition to sequence information, data related to levels of metabolites, polypeptides, and mRNAs can be obtained from the panel of cell lines and correlated to individual variation in therapeutic effects.

Cells used in the model system described herein can be obtained commercially, for example, from the non-profit Coriell Institute for Medical Research (online at cimr.umdnj.edu). For example, the Human Variation Panel cell lines available from Coriell can be used. The Human Variation Panel includes immortalized lymphoblastoid cell lines collected from 100 African American (AA), 100 Caucasian American (CA), 100 Han-Chinese American (HCA) subjects and 23 CEPH (Utah family) cell lines. The panel used in the methods described herein can include any suitable number of individual

cell lines from any ethnic group. For example, the panel can include from 50 to 100 individual AA cell lines, from 50 to 100 CA cell lines, and/or from 50 to 100 HCA cell lines. DNA from the cell lines can be used for in-depth resequencing of genes of interest, and also to obtain genome-wide SNP data for use during genome-wide association studies. The advantage of this system is that the cells are “renewable” and broadly accessible to the general scientific community. In addition, these cell lines represent ethnically diverse population groups.

Modern genomic tools (e.g., genome-wide SNPs and in depth resequencing of functionally important genes) can be used with the cell line panel to identify genes that might be associated with therapeutic response phenotypes. Phenotypes correlated with this genetic variation can include, for example, expression array and metabolomic data, therapy-induced cytotoxicity, methylation status, copy number, and cell cycle effects. SNPs or genes showing significant association with these phenotypes then can be tested functionally and, eventually, clinically. In essence, each of the cell lines in the panel can be viewed as an individual “patient” with a unique genotype and a series of associated phenotypes that can be used for preclinical screening of candidate genes and SNPs. A tremendous advantage of this model system is the fact that high throughput genetic data for these cell lines can be added continuously. Therefore, unlike patient-based information, data for these cell lines can “accumulate” and be used for studies involving a variety of therapeutic response phenotypes and a virtually endless series of therapies or therapy candidates.

SNP and haplotype associations can be performed with cell-based phenotypes and/or with phenotypes related to the response to treatment of disease with particular therapies. Cell-based phenotypes include, for example, cytotoxicity, levels of intracellular metabolites, and gene expression before and after treatment in lymphoblastoid cells. Patient-related phenotypes include, for example, overall patient survival and/or time to progression after treatment, as well as therapy-related toxicity phenotypes, including neutrophil and platelet counts.

The association of each SNP with the quantitative phenotypes of metabolite concentration, cytotoxicity, and level of gene expression, as well as neutrophil and platelet counts can be evaluated with linear models in which genotypes for a SNP are

evaluated with two indicators as covariates. This provides a 2 degree-of-freedom (df) test for each SNP. To assess single SNP genotype associations with patient survival time and time to progression, the Kaplan-Meier method can be used to estimate survival curves for the different genotypes. The curves can be compared using log-rank tests. Survival time
5 as a function of genotype can be examined using the Cox proportional hazards model, and hazard ratios can be used to examine the survival rate by genotype (Cox (1972) *Journal of the Royal Statistical Society Series B*:187-220). Disease status, age at time of treatment, gender and duration of treatment can be included as covariates in the proportional hazards models.

10 In addition to the association of phenotypes with SNPs, their association with intragene haplotypes can be evaluated for candidate genes using a global test of association. Since haplotypes are not observed directly, unknown phase can be accounted for using the score statistics developed by Schaid *et al.* ((2002) *Am J Hum Genet* 70:425-34). To estimate the magnitude of effects from haplotypes found to be
15 significant using the score statistics, haplotype regression methods can be used. See, e.g., Lake *et al.* (2003) *Hum Hered* 55:56-65. Intragene haplotypes can be associated with clinical response using survival time and time to progression as phenotypes. All possible pairs of haplotypes can be evaluated for each patient, and the posterior probability can be associated with each haplotype using the EM algorithm, as implemented in the Splus
20 library *Haplostat* (Schaid *et al.*, *supra*). These posterior probabilities can be used to create expected design matrices to evaluate the association of haplotypes with survival time via the Cox model.

As used herein, a “radiation therapy signature” refers to a SNP profile where one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) of the SNPs listed
25 in the tables presented herein (e.g., Table 1, Table 6, Table 7, Table 8, or Table 9) are present in a mammal. In some cases, for example, a radiation therapy signature can be a profile where 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 percent of the SNPs listed in Table 1, Table 6, Table 7, Table 8, Table 9, or a combination thereof, are present in a mammal.

In addition to sequence information, data related to levels of one or more
30 metabolites, polypeptides, and/or RNAs (e.g., mRNAs) can be obtained from cell lines and correlated to drug responses. Cell lines can be characterized for any number of

SNPs, metabolites, polypeptides, and RNAs (e.g., at least 100, at least 1,000, at least 10,000, at least 20,000, at least 50,000, or at least 100,000 SNPs, metabolites, polypeptides, or RNAs). In some embodiments, a cell can be characterized for all known SNPs, and levels of all known metabolites, all known polypeptides, and/or all known mRNAs.

In some cases, information obtained for particular therapeutic agents can be extrapolated to other agents that have similar metabolic pathways. Further, information regarding the cellular response (e.g., apoptosis and metabolism) in various ethnic groups for various doses of particular agents can be obtained to determine whether higher or lower doses may be needed for efficacy and/or to avoid toxicity. For example, if it is determined that a particular ethnicity is likely to be more resistant to a therapeutic agent (e.g., radiation), a higher dose can be used, whereas if it is determined that a particular ethnicity is likely to be more responsive to the agent, a lower dose may be used. If it is determined that a particular ethnicity is more likely to experience adverse side effects in response to a therapeutic agent, a lower dose can be used, whereas if it is determined that a particular ethnicity is less likely to experience adverse side effects in response to the agent, a higher dose may be used.

Methods

This document provides methods for assessing a subject's likelihood of responding to radiation therapy, and/or for determining radiation dose levels. The methods provided herein can include, for example, testing a biological sample obtained from a subject to determine whether the sample contains one or more biomarkers indicating that the subject is likely to respond to radiation therapy, or to experience adverse side effects from radiation therapy. Such methods also can be used to, for example, determine whether a subject should be treated with a lower rather than a higher dose of radiation (e.g., if a biological sample from the subject contains a nucleotide polymorphism associated with responsiveness to radiation therapy or with adverse side effects to radiation therapy, it can be an indication that the subject should be treated with a lower dose of radiation than if the subject did not contain the polymorphism).

Any suitable biological sample can be used. A biological sample can be, for example, blood, serum, plasma, urine, cerebrospinal fluid, pleural fluid, sputum, peritoneal fluid, bladder washings, oral washings, tissue samples, touch preps, or fine-needle aspirates.

5 In some embodiments, a biomarker can be a nucleotide sequence variant (e.g., rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, or rs212551). Nucleotide sequence variants can be detected, for example, by sequencing exons, introns, 5' untranslated sequences, or 3' untranslated sequences, by performing allele-specific hybridization, allele-specific restriction digests, 10 mutation specific polymerase chain reactions (MSPCR), by single-stranded conformational polymorphism (SSCP) detection (Schafer *et al.* (1995) *Nat. Biotechnol.* 15:33-39), denaturing high performance liquid chromatography (DHPLC, Underhill *et al.* (1997) *Genome Res.* 7:996-1005), infrared matrix-assisted laser desorption/ionization (IR-MALDI) mass spectrometry (WO 99/57318), and combinations of such methods.

15 Genomic DNA generally is used in the analysis of nucleotide sequence variants, although mRNA also can be used. Genomic DNA is typically extracted from a biological sample such as a peripheral blood sample, but can be extracted from other biological samples, including tissues (e.g., mucosal scrapings of the lining of the mouth or from renal or hepatic tissue). Routine methods can be used to extract genomic DNA from a 20 blood or tissue sample, including, for example, phenol extraction. Alternatively, genomic DNA can be extracted with kits such as the QIAAMP[®] Tissue Kit (Qiagen, Chatsworth, CA) and the WIZARD[®] Genomic DNA purification kit (Promega).

An amplification step typically is performed before proceeding with the detection method. For example, exons or introns of a gene can be amplified and then directly 25 sequenced. Dye primer sequencing can be used to increase the accuracy of detecting heterozygous samples.

Allele specific hybridization is an example of a method that can be used to detect sequence variants, including complete haplotypes of a subject (e.g., a mammal such as a human). See, Stoneking *et al.* (1991) *Am. J. Hum. Genet.* 48:370-382; and Prince *et al.* 30 (2001) *Genome Res.* 11:152-162. In practice, samples of DNA or RNA from one or more mammals can be amplified using pairs of primers and the resulting amplification products

can be immobilized on a substrate (e.g., in discrete regions). Hybridization conditions are selected such that a nucleic acid probe can specifically bind to the sequence of interest, e.g., the variant nucleic acid sequence. Such hybridizations typically are performed under high stringency as some sequence variants include only a single
5 nucleotide difference. High stringency conditions can include the use of low ionic strength solutions and high temperatures for washing. For example, nucleic acid molecules can be hybridized at 42°C in 2X SSC (0.3M NaCl/0.03 M sodium citrate/0.1% sodium dodecyl sulfate (SDS) and washed in 0.1X SSC (0.015M NaCl/0.0015 M sodium citrate), 0.1% SDS at 65°C. Hybridization conditions can be adjusted to account for
10 unique features of the nucleic acid molecule, including length and sequence composition. Probes can be labeled (e.g., fluorescently) to facilitate detection. In some embodiments, one of the primers used in the amplification reaction is biotinylated (e.g., 5' end of reverse primer) and the resulting biotinylated amplification product is immobilized on an avidin or streptavidin coated substrate.

15 Allele-specific restriction digests can be performed in the following manner. For nucleotide sequence variants that introduce a restriction site, restriction digest with the particular restriction enzyme can differentiate the alleles. For sequence variants that do not alter a common restriction site, mutagenic primers can be designed that introduce a restriction site when the variant allele is present or when the wild type allele is present. A
20 portion of a nucleic acid can be amplified using the mutagenic primer and a wild type primer, followed by digest with the appropriate restriction endonuclease.

Certain variants, such as insertions or deletions of one or more nucleotides, change the size of the DNA fragment encompassing the variant. The insertion or deletion of nucleotides can be assessed by amplifying the region encompassing the variant and
25 determining the size of the amplified products in comparison with size standards. For example, a region of a gene can be amplified using a primer set from either side of the variant. One of the primers is typically labeled, for example, with a fluorescent moiety, to facilitate sizing. The amplified products can be electrophoresed through acrylamide gels with a set of size standards that are labeled with a fluorescent moiety that differs
30 from the primer.

PCR conditions and primers can be developed that amplify a product only when the variant allele is present or only when the wild type allele is present (MSPCR or allele-specific PCR). For example, patient DNA and a control can be amplified separately using either a wild type primer or a primer specific for the variant allele. Each set of reactions is then examined for the presence of amplification products using standard methods to visualize the DNA. For example, the reactions can be electrophoresed through an agarose gel and the DNA visualized by staining with ethidium bromide or other DNA intercalating dye. In DNA samples from heterozygous patients, reaction products would be detected in each reaction. Patient samples containing solely the wild type allele would have amplification products only in the reaction using the wild type primer. Similarly, patient samples containing solely the variant allele would have amplification products only in the reaction using the variant primer. Allele-specific PCR also can be performed using allele-specific primers that introduce priming sites for two universal energy-transfer-labeled primers (e.g., one primer labeled with a green dye such as fluorescein and one primer labeled with a red dye such as sulforhodamine). Amplification products can be analyzed for green and red fluorescence in a plate reader. See, Myakishev *et al.* (2001) *Genome* 11:163-169.

Mismatch cleavage methods also can be used to detect differing sequences by PCR amplification, followed by hybridization with the wild type sequence and cleavage at points of mismatch. Chemical reagents, such as carbodiimide or hydroxylamine and osmium tetroxide can be used to modify mismatched nucleotides to facilitate cleavage.

In some embodiments, a biomarker can be a variant polypeptide. Antibodies having specific binding affinity can be used to detect variant polypeptides. Variant polypeptides can be produced in various ways, including recombinantly, as known in the art. Host animals such as rabbits, chickens, mice, guinea pigs, and rats can be immunized by injection of a variant polypeptide. Various adjuvants that can be used to increase the immunological response depend on the host species and include Freund's adjuvant (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. Polyclonal antibodies are heterogeneous populations of antibody molecules that are contained in the sera of the immunized

animals. Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, can be prepared using a variant polypeptide and standard hybridoma technology. In particular, monoclonal antibodies can be obtained by any technique that provides for the production of antibody molecules by continuous cell lines in culture such as described by Kohler *et al.* (1975) *Nature* 256:495, the human B-cell hybridoma technique (Kosbor *et al.* (1983) *Immunology Today* 4:72; Cote *et al.* (1983) *Proc. Natl. Acad. Sci USA* 80:2026), and the EBV-hybridoma technique (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96 (1983). Such antibodies can be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. A hybridoma producing monoclonal antibodies can be cultivated *in vitro* or *in vivo*.

Antibody fragments that have specific binding affinity for a variant polypeptide can be generated using known techniques. For example, such fragments include but are not limited to F(ab')₂ fragments that can be produced by pepsin digestion of the antibody molecule, and Fab fragments that can be generated by reducing the disulfide bridges of F(ab')₂ fragments. Alternatively, Fab expression libraries can be constructed. See, for example, Huse *et al.* (1989) *Science* 246:1275. Once produced, antibodies or fragments thereof are tested for antigen recognition by standard immunoassay methods including ELISA techniques, radioimmunoassays and Western blotting. See, Short Protocols in Molecular Biology, Chapter 11, Green Publishing Associates and John Wiley & Sons, edited by Ausubel *et al.*, 1992.

In some embodiments, a biomarker can be a level of a nucleic acid (e.g., an RNA) polypeptide, or metabolite that is altered with respect to, for example, a control level of the nucleic acid, polypeptide, or metabolite. Levels of nucleic acids, polypeptides, and metabolites can be determined using any suitable methods, including those that are known in the art. These include, for example, antibody-based methods, reverse transcriptase PCR (RT-PCR) methods, and any other methods that can be used to measure the level of a nucleic acid, polypeptide, or metabolite in a biological sample.

The methods provided herein can be used to predict the effectiveness of radiation therapy or the likelihood of an adverse response to radiation therapy in a subject (e.g., a mammal such as a rat, a dog, or a human). For example, a method can include

determining whether a biological sample from a subject comprises one or more SNPs (e.g., rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, or rs212551), and classifying the subject as having a greater likelihood of responding to radiation therapy if the variant allele is present in the biological sample, and classifying the subject as having a lesser likelihood of responding to radiation therapy if the wild type allele is present in the biological sample. It is to be noted that although resistance to radiation therapy may indicate less disease response, it also may indicate protection against radiation damage. In addition, it is to be noted that allele frequencies will vary among ethnic groups. Thus, the markers disclosed herein may be useful to “individualize” this type of medical therapy.

The methods provided herein also can be used to determine a dose of radiation for administration to a subject. For example, using a method as described herein, it can be determined that a dose for a particular subject should be lower if a variant allele (e.g., rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, or rs212551) is present in a biological sample from the subject, and determining that the dose should be higher if the corresponding wild type allele is present in the biological sample.

The methods described herein can be carried out using a computer programmed to receive data (e.g., data from a chip containing a panel of SNPs, indicating whether a subject contains SNPs associated with sensitivity or resistance to radiation therapy). The computer can output for display information related to a subject’s biomarkers, and the likelihood that the subject will be sensitive or resistant to radiation therapy.

This document also provides methods and materials to assist medical or research professionals in determining whether or not a subject is likely to respond to or be adversely affected by radiation therapy. Medical professionals can be, for example, doctors, nurses, medical laboratory technologists, and pharmacists. Research professionals can be, for example, principle investigators, research technicians, postdoctoral trainees, and graduate students. A professional can be assisted by (1) determining whether a subject has one or more biomarkers associated with sensitivity or resistance to radiation therapy (e.g., the SNPs listed in Table 1), and (2) communicating information about the biomarkers to that professional.

In some embodiments, a method for assessing the likelihood that radiation therapy will be effective in a subject can include receiving a biological sample obtained from the subject, assaying the sample to determine whether it contains one or more particular variant alleles (e.g., rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, or rs212551), communicating to a medical professional information about whether the wild type or variant allele(s) are present in the sample, and, in some cases, before or after the first step, communicating to a medical professional information indicating that the presence of the variant allele(s) correlates with responsiveness to radiation therapy. Similarly, a method for determining a dose of radiation for administration to a subject can include receiving a biological sample obtained from a subject, assaying the sample to determine whether it contains one or more particular variant alleles (e.g., rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, or rs212551), communicating to a medical professional information about whether the wild type or variant allele(s) are present in the sample, and, in some cases, before or after the first step, communicating to a medical professional information indicating that the presence of the variant allele(s) correlates with a lower suggested dose.

After information regarding a subject's biomarkers is reported, a medical professional can take one or more actions that can affect patient care. For example, a medical professional can record the information in a subject's medical record. In some cases, a medical professional can record that the subject is likely or not likely to respond to radiation therapy, or otherwise transform the patient's medical record, to reflect the patient's medical condition. In some cases, a medical professional can review and evaluate a patient's medical record, and can assess multiple treatment strategies for clinical intervention of a patient's condition.

A medical professional can communicate information regarding biomarker analysis to a subject or a subject's family. In some cases, a medical professional can provide a subject and/or a subject's family with information regarding radiation therapy, including treatment options and potential side effects. In some cases, a medical professional can provide a copy of a subject's medical records to communicate information regarding biomarker analysis and/or disease states to a specialist.

A research professional can apply information regarding a subject's biomarkers to advance research into radiation toxicity. For example, a researcher can compile data on the presence of particular biomarkers (e.g., SNPs) with information regarding the efficacy of radiation therapy, or side effects associated with radiation therapy. In some cases, a research professional can obtain a subject's biomarker information to evaluate the subject's enrollment, or continued participation in a research study or clinical trial. In some cases, a research professional can communicate a subject's biomarker information to a medical professional, or can refer a subject to a medical professional for clinical assessment and/or treatment.

Any appropriate method can be used to communicate information to another person (e.g., a professional), and information can be communicated directly or indirectly. For example, a laboratory technician can input biomarker information into a computer-based record. In some cases, information can be communicated by making an physical alteration to medical or research records. For example, a medical professional can make a permanent notation or flag a medical record for communicating information to other medical professionals reviewing the record. Any type of communication can be used (e.g., mail, e-mail, telephone, and face-to-face interactions). Information also can be communicated to a professional by making that information electronically available to the professional. For example, information can be placed on a computer database such that a medical professional can access the information. In addition, information can be communicated to a hospital, clinic, or research facility serving as an agent for the professional.

Articles of Manufacture

This document also provides articles of manufacture that can include, for example, materials and reagents that can be used to determine whether a subject has a biomarker for predicting response to radiation therapy. An article of manufacture can include, for example, nucleic acids and/or polypeptides immobilized on a substrate (e.g., in discrete regions, with different populations of isolated nucleic acids or polypeptides immobilized in each discrete region). Suitable substrates can be of any shape or form and can be constructed from, for example, glass, silicon, metal, plastic, cellulose, or a

composite. For example, a suitable substrate can include a multiwell plate or membrane, a glass slide, a chip, or polystyrene or magnetic beads. Nucleic acid molecules or polypeptides can be synthesized *in situ*, immobilized directly on the substrate, or immobilized via a linker, including by covalent, ionic, or physical linkage. Linkers for
5 immobilizing nucleic acids and polypeptides, including reversible or cleavable linkers, are known in the art. See, for example, U.S. Patent No. 5,451,683 and WO98/20019. Immobilized nucleic acid molecules are typically about 20 nucleotides in length, but can vary from about 10 nucleotides to about 1000 nucleotides in length.

In practice, to detect a particular allele of a nucleic acid, for example, a sample of
10 DNA or RNA from a subject can be amplified, the amplification product hybridized to an article of manufacture containing populations of isolated nucleic acid molecules in discrete regions, and hybridization can be detected. Typically, the amplified product is labeled to facilitate detection of hybridization. See, for example, Hacia *et al.* (1996) *Nature Genet.* 14:441-447; and U.S. Patent Nos. 5,770,722 and 5,733,729.

15 The invention will be further described in the following example, which does not limit the scope of the invention described in the claims.

EXAMPLES

Example 1

20 Using an *in vitro* system, 300 “Human Variation Panel” lymphoblastoid cell lines were used to identify SNPs associated with radiation sensitivity. These 300 cell lines were obtained from the Coriell Institute supported by National Institute of General Medical Science (NIGMS). These EBV transformed lymphoblastoid cell lines were derived from
25 100 Caucasian-American, 100 African-American, and 100 Han-Chinese American subjects. Therefore, the cell lines have diverse genetic backgrounds across three ethnic groups. In addition, 1.3 million SNPs were obtained using two different platforms – the Affymetrix 6.0 SNP chip and the Illumina 550K and 510S Genechip – for each cell line. Since expression array data are available for all 300 cell lines, this system was ideal for generating and testing pharmacogenomic hypothesis.

30 To identify SNPs and/or genes that might be associated with radiation sensitivity, radiation cytotoxicity studies were performed with the 300 cell lines. Radiation doses

ranging from 2 to 10 Gray were used to treat each cell line for three days. Cell viability was assessed with a 96-well CellTiter-Blue Cell Viability Assay (Promega Corp.; Madison, WI), and the area under the curve (AUC) was calculated based on the dose-response curve for each cell line using the R package. The distribution of AUC across all three ethnicities was used as the radiation response phenotype shown in Figure 2. This genome-wide SNP association identified ten SNPs (Table 1) on chromosome 8q22 that were in linkage disequilibrium and were significantly associated with radiation sensitivity. The distribution of AUC chromosome 8 SNPs in the CA cell lines is shown in Figure 3. The “SNP signals” listed in Table 1 represent a “p value peak,” and SNPs with the lowest p values (i.e., the tops of the peaks in Figures 2 and 3) are particularly useful. The frequencies of these ten SNPs in each ethnicity are shown in Table 2.

The SNPs listed in Table 1 also were significantly associated with expression levels for 229 genes having p values less than 10^{-4} . These genes, which are listed in Table 3, are involved in DNA damage, DNA repair, and cell cycle pathways, and are biologically relevant to radiation treatment. Therefore, the ten SNPs identified in these studies may be useful biomarkers for prediction of response to radiation therapy.

Table 1

SNP	Polymorphism	P value
rs4392868	G/A	10^{-6}
rs297550	G/A	10^{-4}
rs1946944	A/C	10^{-4}
rs12548426	A/G	10^{-4}
rs1610110	C/T	10^{-7}
rs1561715	A/G	10^{-7}
rs1561714	A/C	10^{-5}
rs4734298	G/A	10^{-4}
rs7000734	C/T	10^{-7}
rs212551	G/A	10^{-5}

Table 2

	AA	HCA	CA
rs4392868			
A	0.91	0.02	0.21
G	0.08	0.98	0.79
rs297550			
G	0.96	0.99	0.84
A	0.04	0.01	0.16
rs1946944			
A	0.22	0.05	0.4
C	0.78	0.95	0.6
rs12548426			
A	0.79	0.93	0.58
G	0.21	0.07	0.42
rs1610110			
C	0.93	1	0.8
T	0.07	0	0.2
rs1561715			
A	0.93	1	0.8
G	0.07	0	0.2
rs1561714			
A	0.08	0	0.2
C	0.92	1	0.8
rs4734298			
G	0.8	0.93	0.6
A	0.2	0.07	0.4
rs7000734			
C	0.06	0	0.2
T	0.94	1	0.8
rs212551			
G	0.84	0.98	0.75
A	0.16	0.02	0.25

Table 3

A kinase (PRKA) anchor protein 13
Abelson helper integration site
acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
actin, gamma 1

Actinin, alpha 4
adenylate kinase 2
ADP-ribosylation factor related protein 2
ADP-ribosylhydrolase like 2
amyotrophic lateral sclerosis 4
ankyrin repeat domain 23
AP1 gamma subunit binding protein 1
arginase, type II
asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase)
ATPase family, AAA domain containing 2
ATPase, Ca ⁺⁺ transporting, cardiac muscle, fast twitch 1
ATPase, H ⁺ transporting, lysosomal V0 subunit a isoform 1
ATP-binding cassette, sub-family B (MDR/TAP), member 4
baculoviral IAP repeat-containing 5 (survivin)
baculoviral IAP repeat-containing 6 (apollon)
bolA-like 3 (E. coli)
Bromodomain containing 4
catenin (cadherin-associated protein), alpha-like 1
catenin (cadherin-associated protein), delta 1
CD44 antigen (homing function and Indian blood group system)
CDC28 protein kinase regulatory subunit 1B
CDC45 cell division cycle 45-like (S. cerevisiae)
CDNA clone IMAGE:30332316
CDNA FLJ31593 fis, clone NT2RI2002481
CDNA FLJ33139 fis, clone UTERU1000109
CDNA FLJ36209 fis, clone THYMU2000022
CDNA FLJ36837 fis, clone ASTRO2011422
CDNA FLJ38765 fis, clone KIDNE2014489
CDNA FLJ40647 fis, clone THYMU2017522
CDNA FLJ41675 fis, clone HCASM2002148
CDNA FLJ42561 fis, clone BRACE3006463
CDNA FLJ42786 fis, clone BRAWH3006761
CDNA FLJ46024 fis, clone SPLEN2022785
CDNA FLJ46713 fis, clone TRACH3016885
CDNA: FLJ23006 fis, clone LNG00414
cell division cycle 2, G1 to S and G2 to M
cell division cycle associated 2
cell division cycle associated 3
cell division cycle associated 7-like
CHK1 checkpoint homolog (S. pombe)

chondroitin sulfate glucuronyltransferase
chromodomain helicase DNA binding protein 9
chromosome 1 open reading frame 155
chromosome 1 open reading frame 183
chromosome 1 open reading frame 38
chromosome 10 open reading frame 84
Chromosome 14 open reading frame 32
chromosome 14 open reading frame 58
chromosome 16 open reading frame 51
chromosome 19 open reading frame 2
Chromosome 20 open reading frame 155
chromosome 20 open reading frame 30
chromosome 9 open reading frame 40
chymase 1, mast cell
Clone FLB8034 PRO2158
coenzyme Q3 homolog, methyltransferase (yeast) ; coenzyme Q3 homolog, methyltransferase (yeast)
coenzyme Q4 homolog (yeast)
Coiled-coil domain containing 18
COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)
core-binding factor, beta subunit
Cullin 4A
cyclin A2
cyclin B2
cyclin D2
cyclin-dependent kinase inhibitor 1A (p21, Cip1)
DAZ associated protein 1
dihydrouridine synthase 4-like (S. cerevisiae)
dilute suppressor
dynammin 3
E3 ubiquitin protein ligase, HECT domain containing, 1
EH-domain containing 1
ephrin-A1
Epidermal growth factor receptor pathway substrate 15
erythropoietin receptor
exosome component 8
family with sequence similarity 54, member A
family with sequence similarity 72, member A
F-box protein 5
FLJ20105 protein
FLJ39739 protein

Forkhead box O3A
Formin binding protein 1
Full length insert cDNA clone ZD50H02
G protein-coupled receptor 64
G protein-coupled receptor kinase interactor 2
gelsolin (amyloidosis, Finnish type)
general transcription factor IIIA
GRIP1 associated protein 1
hairy/enhancer-of-split related with YRPW motif 2
haloacid dehalogenase-like hydrolase domain containing 1A
heterogeneous nuclear ribonucleoprotein D-like
high-mobility group nucleosomal binding domain 2
histone 1, H2ai
Histone 1, H2bd
histone 1, H2be
histone 1, H2bf
histone 1, H2bi
histone 1, H2bk
Hypothetical LOC344887
Hypothetical protein BC009732
hypothetical protein FLJ10211
hypothetical protein FLJ10241
Hypothetical protein FLJ14082
hypothetical protein FLJ20534
Hypothetical protein FLJ25715
hypothetical protein FLJ38725
hypothetical protein LOC137886
Hypothetical protein LOC149478
hypothetical protein LOC284356
hypothetical protein LOC285954
hypothetical protein LOC286149
hypothetical protein MGC15875
hypothetical protein MGC20235
hypothetical protein MGC20235
Hypothetical protein MGC24039
hypothetical protein MGC5576
hypothetical protein PRO2852
inhibitor of growth family, member 2
insulin-like growth factor 2 receptor
interleukin 1, beta
isocitrate dehydrogenase 1 (NADP+), soluble

jagged 1 (Alagille syndrome)
KIAA0101
KIAA0319-like
KIAA0372
KIAA0922 protein
KIAA1659 protein
kinesin family member 1C
kinesin family member 2C
kinesin family member 9
L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain
lamin A/C
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
Leucine rich repeat (in FLII) interacting protein 2
leucine zipper protein 5
ligand of numb-protein X
lymphoblastic leukemia derived sequence 1
lysocardiolipin acyltransferase
major vault protein
Malate dehydrogenase 2, NAD (mitochondrial)
Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)
membrane-spanning 4-domains, subfamily A, member 7 ; membrane-spanning 4-domains, subfamily A, member 7
meningioma expressed antigen 5 (hyaluronidase)
mitogen-activated protein kinase kinase kinase 5
neurexin 3
nicastrin
nicotinamide nucleotide adenylyltransferase 2
N-myristoyltransferase 2
Nuclear receptor co-repressor 2
Nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
nucleophosmin (nucleolar phosphoprotein B23, numatrin)
nucleoporin 37kDa
NudC domain containing 2
PDZ binding kinase
peroxiredoxin 6
phosphoprotein enriched in astrocytes 15
pituitary tumor-transforming 3
pleckstrin homology-like domain, family A, member 3
polo-like kinase 4 (Drosophila)
primase, polypeptide 1, 49kDa
proline rich 6

Protein phosphatase 1, regulatory (inhibitor) subunit 16B
purinergic receptor P2X, ligand-gated ion channel, 4
RAB3 GTPase activating protein subunit 1 (catalytic)
RAB5B, member RAS oncogene family
radixin
RAS p21 protein activator 3
replication factor C (activator 1) 3, 38kDa
replication factor C (activator 1) 4, 37kDa
replication factor C (activator 1) 5, 36.5kDa
retinoblastoma-associated factor 600
Rho GTPase activating protein 19
ribonucleotide reductase M2 B (TP53 inducible)
ribosomal protein L10a
ribosomal protein S27-like
RIM binding protein 2
RNA binding motif protein 20
RNA methyltransferase like 1
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9
SH3-domain GRB2-like pseudogene 2
Sideroflexin 1
Similar to Hypothetical protein KIAA0563
Similar to Microneme antigen
Small nuclear ribonucleoprotein polypeptide N
solute carrier family 25, member 37
sperm associated antigen 5
spermatogenesis associated 18 homolog (rat)
ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
stathmin 1/oncoprotein 18
steroid sulfatase (microsomal), arylsulfatase C, isozyme S
syntaxin 16
syntaxin binding protein 4
TBC1 domain family, member 7
TBP-1 interacting protein
testes development-related NYD-SP21
thiamin pyrophosphokinase 1
timeless homolog (Drosophila)
timeless-interacting protein
TRAFs and NIK-associated protein
Transcribed locus, moderately similar to XP_517655.1 PREDICTED: similar to KIAA0825 protein [Pan troglodytes]

Transcribed locus, moderately similar to XP_519290.1 PREDICTED: reelin [Pan troglodytes]
Transcribed locus, weakly similar to NP_055301.1 neuronal thread protein AD7c-NTP [Homo sapiens]
Transcribed locus, weakly similar to NP_997349.1 FLJ46489 protein [Homo sapiens]
transgelin
transmembrane protein 48
transmembrane protein 76
trophoblast-derived noncoding RNA
TTK protein kinase
tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)
tyrosyl-DNA phosphodiesterase 1
U2-associated SR140 protein
ubiquitin protein ligase E3B
ubiquitin specific peptidase 1
Ubiquitin specific peptidase 13 (isopeptidase T-3)
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
UL16 binding protein 1
vaccinia related kinase 1
WD repeat domain 68
X Kell blood group precursor-related family, member 4
zinc binding alcohol dehydrogenase, domain containing 2
zinc finger protein 330
zinc finger protein 608
Zinc finger RNA binding protein
ZW10 interactor

Example 2

Further genome-wide basal gene expression profiles and genome-wide SNPs for
5 277 human lymphoblastoid cell lines (LCLs) were used to identify and functionally
validate SNPs/genes that might contribute to variation in radiation response. Basal gene
expression data was obtained for all 277 cell lines using Affymetrix U133 plus 2.0 Gene
Chips as well as genome-wide SNP data using Illumina HumanHap 550K and 510S
BeadChips together with publicly available Affymetrix SNP Array 6.0 SNP data,

resulting in a total of over 1.3 million SNPs per cell line. Radiation cytotoxicity assays were then performed with the same LCLs to obtain area under the radiation dose response curve (AUC) as an *in vitro* radiation response phenotype. A genome-wide association study was performed using the 1.3 million SNPs, basal gene expression array data and AUC as a radiation response phenotype. Twenty-seven “loci” were identified, defined as at least 2 SNPs within 50 kb having p values $<10^{-4}$ that were associated with radiation AUC. Genes also were identified with expression levels that were associated with radiation AUC with $p < 10^{-3}$. By then performing an “integrated analysis” of SNPs, gene expression and radiation AUC, a total of 23 candidate genes were selected to perform siRNA knockdown with multiple tumor cell lines, followed by MTS and colony-forming functional validation assays to identify genes that influenced radiation exposure sensitivity.

The series of experiments described below represents the application of genome-wide expression and SNP data from a cell line-based model system to identify genes associated with radiation sensitivity. Those genes, selected on the basis of their association with SNPs, with expression array data or the results of an “integrated analysis” using both SNP and expression array data, were then validated functionally. The p values used during the initial selection process were purposely not stringent since all candidate genes were going to be functionally validated. The functional validation involved siRNA gene knockdown performed with cancer cell lines, followed by MTS cytotoxicity and colony-forming assays. These studies were conducted to identify and functionally validate biomarkers for radiation response, and to identify novel mechanisms that might contribute to radiation sensitivity.

Materials and Methods

Cell lines: EBV-transformed LCLs from 93 African-American (AA), 89 Caucasian-American (CA), and 95 Han Chinese-American (HCA) unrelated healthy subjects (sample sets HD100AA, HD100CAU, HD100CHI) were purchased from the Coriell Cell Repository (Camden, NJ). These samples had been collected and anonymized by NIGMS. Human pancreatic cancer MIA-PaCa2 and HupT3 cell lines were gifts from Dr. Daniel D. Billadeau, Mayo Clinic. Human cervical cancer HeLa and

non-small cell lung cancer A549 cell lines were obtained from the ATCC (Manassas, VA).

LCLs were cultured in RPMI 1640 medium (Mediatech, Manassas, VA) supplemented with 15% heat-inactivated Fetal Bovine Serum (FBS) (Mediatech). HeLa and MIA-PaCa2 cell lines were cultured in DMEM medium containing 10% FBS. HupT3 and A549 cell lines were grown in RPMI 1640 medium with 10% FBS.

Cell proliferation assay: Cell proliferation assays were performed in triplicate at each radiation dose. Specifically, 100 μ l of cells (5×10^5 cells/ml) were plated into 96-well plates (Corning, Lowell, MA) Li et al. (2008) *Cancer Res.* 68:7050-7058, and were treated with ionizing radiation at 0, 0.156, 0.3125, 0.625, 1.25, 2.5, 5, 10 and 20 Gy using ^{137} Cesium gamma-rays (J. L. Shepherd and Associates Mark I Model 25 Irradiator, San Fernando, CA). After incubation for 3 days, 20 μ l of CellTiter 96 AQueous Non-Radioactive Cell Proliferation Assay solution (Promega Corporation, Madison, WI) was added to each well. Plates were read in a Safire2 plate reader (Tecan AG, Switzerland). Nineteen LCLs were selected randomly, and the MTS assay was repeated approximately one year after the initial assay. Cytotoxicity for human tumor cell lines was determined in a similar fashion except the cells were incubated overnight before radiation treatment at 0, 0.25, 0.5, 1, 2.5, 5, 10 and 20 Gy, followed by MTS and colony-forming assays.

Expression array assays: Total RNA was extracted from each of the cell lines using Qiagen RNeasy Mini kits (QIAGEN, Inc.). RNA quality was tested using an Agilent 2100 Bioanalyzer, followed by hybridization to Affymetrix U133 Plus 2.0 GeneChips. A total of 54,613 probe sets were used in the analyses. Expression array data were obtained for all of the cell lines, 174 of which had been used in previous studies (Li et al. (2008), *supra*; and Li et al. (2009) *PLoS One* 4:e7765).

Genome-wide SNP analysis: DNA from all of the LCLs was genotyped using Illumina HumanHap 550K and 510S BeadChips, which assayed 561,298 and 493,750 SNPs, respectively. Genotyping was performed in the Genotype Shared Resource (GSR) at the Mayo Clinic, Rochester, MN. Publicly available Affymetix SNP Array 6.0 Chip SNP data also was obtained for the same cell lines, which involved 643,600 SNPs unique to the Affymetrix SNP array. SNPs that deviated from Hardy-Weinberg Equilibrium (HWE, minimum exact test for HWE) (Wigginton et al. (2005) *Am. J. Hum. Genet.*

76:887-893) and the stratified test for HWE (Schaid et al. (2006) *Am. J. Hum. Genet.* 79:1071-1080) (p values <0.001); SNPs with call rates <95%; or SNPs with MAFs <5% were removed from the analysis.

Transient transfection and RNA interference: siRNAs for the candidate genes and
5 “all star negative control” siRNA were purchased from QIAGEN (Hiden, Germany). The human HeLa cervical cancer cell line and the human pancreatic cancer cell lines, MIA-PaCa2 and HupT3, were used for the siRNA knockdown experiments. Reverse transfection was performed in 96-well plates. About 3000-4000 cells were mixed with 0.1µl of LIPOFECTAMINE™ RNAiMAX reagent (Invitrogen, Carlsbad, CA) and 10
10 nM siRNA for these experiments.

Colony-forming assays: “All star negative control” and specific siRNAs were transfected into MIA-PaCa2, HupT3, HeLa and A459 cell lines. After 24 hours, about 400-1000 cells were plated in triplicate in 6-well plates. After exposure to radiation, cells were incubated for up to 7 days. Colonies in each well were fixed with methanol and
15 stained with crystal violet. All colonies were counted visually or by the use of Quantity One (Bio-Rad, Hercules, CA).

Real-time quantitative reverse transcription-PCR: Total RNA was isolated from cultured cells transfected with control or specific siRNAs with the Qiagen RNeasy kit (QIAGEN Inc. Valencia, CA), followed by QRT-PCR performed with the 1-step,
20 Brilliant SYBR Green QRT-PCR master mix kit (Stratagene, La Jolla, CA). Specifically, primers purchased from QIAGEN were used to perform QRT-PCR using the Stratagene Mx3005P™ Real-Time PCR detection system (Stratagene, La Jolla, CA). All experiments were performed in triplicate with β-actin as an internal control. Reverse transcribed Universal Human reference RNA (Stratagene) was used to generate a
25 standard curve. Control reactions lacked RNA template.

Statistical methods: The radiation cytotoxicity phenotype, AUC, was calculated based on a logistic model. Three different logistic functions (four parameter, three free parameters with a fixed asymptote at 0%, and three free parameters with a fixed asymptote at 100%) were used to fit the data with the R package “drc” (available online
30 at cran.r-project.org/doc/packages/drc.pdf). The best fit of the three logistic models with the lowest mean square error was used to determine the cytotoxicity AUC phenotype.

AUC was determined by numerically computing the area under the estimated dose-response curve, from dose 0 to 20 Gy. AUC values were then log transformed.

Expression array data were normalized on a log 2 scale using GCRMA (Wu et al. (2004) *J. Amer. Stat. Assoc.* 99:909-917). The normalized expression data and log transformed

AUC values were then regressed on gender. Because LCLs from multiple races/ethnic groups were used, before completing the genetic association analysis, population stratification was assessed and was adjusted using the method developed by Price et al. ((2006) *Nat. Genet.* 38:904-909). This approach uses an eigen analysis for detecting and adjusting for population stratification, in which the eigen analysis was performed within each of the three racial groups. Using the top five eigenvectors within each race, the individual genotypes were adjusted using the model $G_{ij} = \alpha_j + \gamma_{kj} + \varepsilon_{ij}$, with

G_{ij} representing the genotype for the *i*th cell line in racial group *j* (*j* = 1, 2, 3), α_j the race effect for race *j*, and γ_{kj} the *k*th eigenvector, *k* = 1, ..., 5, effect for race *j*. Similarly, for genetic analysis of SNPs with AUC or expression, the log transformed AUC values and normalized log2 expression values were also adjusted for race using the five eigenvectors, in addition to gender.

Association analyses of expression-AUC, expression-SNP and SNP-AUC were then completed using Pearson correlations and adjusted AUC, SNP and expression data. False Discovery q-values (Storey and Tibishirani (2003) *Proc. Natl. Acad. Sci. USA* 100:9440-9445) also were computed for each test. Pairwise LD was estimated using r-squared statistics and was displayed graphically using the Haploview software (Barrett et al. (2005) *Bioinformatics* 21:263-265). Genes and SNPs were annotated using NCBI Build 36.3. The pathway analysis was performed using Ingenuity Pathway Analysis (IPA; Ingenuity Systems, Redwood City, CA).

To integrate the genotype, expression, and drug cytotoxicity data, loci containing at least 2 SNPs associated with AUC with p values $<10^{-4}$ within 50kb of each other were first identified, followed by identification of all SNPs located within the specific loci with p values <0.001 . Next, a determination was made as to which expression probe sets were associated with these SNPs (p values $<10^{-4}$). Finally, to determine whether the expression probe sets associated with these SNPs were also associated with radiation

AUC values, expression probe sets associated with radiation AUC with a $p < 0.001$ were identified. A similar approach has been used successfully to detect novel candidate genes for functional follow-up (Li et al. (2009), *supra*).

For the most significant “locus” on chromosome 8, SNPs were imputed for a region 200Kb in length on either side of the most significant SNP. Imputation was performed using MACH 1.0 (Li and Abecasis (2006) *Am. J. Hum. Genet.* S79:2290), with HapMap data as the reference panel. Specifically, AA SNPs were imputed with CEPH and YRI data, CA with CEU, and HCA with CHB and JPT.

Results

Radiation cytotoxicity: Radiation cytotoxicity studies were performed to determine the range of variation in radiation AUC among the individual cell lines studied. Figure 4A shows representative radiation cytotoxicity data for a set of cell lines. AUC values differed significantly among the three racial groups studied, with cells from Han Chinese-American (HCA) subjects appearing to be more sensitive to radiation than were those of the cells from Caucasian-American (CA) subjects ($p=0.007$, Figure 4B). Gender did not have a significant effect on AUC ($p=0.125$, Figure 4C). The median AUC value for the 277 cell lines was 3.17, but the distribution was skewed. However, the distribution of values for the $\ln$ transformed AUC was nearly “normal,” with a mean value of 1.27 and a range ± 2 SD of the mean of 0.28 to 2.26, i.e., an 8-fold range (Figure 4D). A biological replication study also was performed for the cytotoxicity data. Specifically, cytotoxicity assays were repeated one year after the initial studies for 19 randomly selected cell lines. The results obtained at the two different times were significantly correlated ($R_p = 0.51$, $p=0.026$).

Correlation between expression and AUC: Correlation analyses were then performed for the association of expression array and radiation AUC data to identify genes with expression levels that might be associated with radiation AUC (Figure 5A). The association analysis identified 50 expression probe sets that were associated with radiation AUC with p values $< 10^{-4}$ (q values < 0.096), and 270 individual probe sets with p values $< 10^{-3}$ (q values < 0.182). These 270 expression probe sets represented 211 annotated genes, but only one of the probe sets remained significant after Bonferroni

correction ($p < 0.0002$). The top 20 probe sets are listed in Table 4, and the entire list of 270 expression probe sets is found in Table 5.

Table 4
Top 20 expression probe sets associated with radiation cytotoxicity (AUC values).

Probe ID	P value	Bonferroni p value	R value*	Q value	Chr	Gene Symbol	RefSeq ID
243826 at	1.97E-09	0.0001	0.351	9.68E-05	2	---	---
209605 at	1.96E-06	0.1073	-0.281	4.17E-02	22	TST	NM_003312
1554768 a at	3.63E-06	0.1981	-0.274	4.17E-02	14	MAD2L1	NM_002358
231149 s at	4.78E-06	0.2610	-0.271	4.17E-02	3	ULK4	NM_017886
210639 s at	5.35E-06	0.2920	-0.270	4.17E-02	6	ATG5	NM_004849
234863 x at	6.66E-06	0.3638	-0.267	4.17E-02	6	FBXO5	NM_001142522
204004 at	7.46E-06	0.4072	-0.266	4.17E-02	12	PAWR	NM_002583
238104 at	8.01E-06	0.4376	0.265	4.17E-02	23	---	---
207238 s at	8.81E-06	0.4809	-0.264	4.17E-02	1	PTPRC	NM_002838
201345 s at	8.90E-06	0.4863	-0.263	4.17E-02	5	UBE2D2	NM_003339
219869 s at	1.04E-05	0.5688	-0.262	4.17E-02	4	SLC39A8	NM_001135146
242364 x at	1.07E-05	0.5848	0.261	4.17E-02	17	LOC100131096	XM_001720907
204005 s at	1.10E-05	0.6034	-0.261	4.17E-02	12	PAWR	NM_002583
204887 s at	1.57E-05	0.8572	-0.256	5.51E-02	4	PLK4	NM_014264
214173 x at	1.83E-05	0.9986	-0.254	5.56E-02	19	C19orf2	NM_003796
201014 s at	1.90E-05	1.0000	-0.254	5.56E-02	4	PAICS	NM_001079524
227620 at	1.92E-05	1.0000	-0.254	5.56E-02	9	SLC44A1	NM_080546
227806 at	2.45E-05	1.0000	-0.251	6.69E-02	16	C16orf74	NM_206967
212896 at	2.60E-05	1.0000	-0.250	6.71E-02	5	SKIV2L2	NM_015360
225562 at	2.77E-05	1.0000	-0.249	6.81E-02	13	RASA3	NM_007368

*R values represent correlation coefficients for the association.

Table 5

The top 270 expression probe sets that were associated with radiation AUC with p values $< 10^{-3}$.

Probe ID	P value	Bonferroni p value	R value*	Q value	Chr	Gene Symbol [†]	RefSeq ID
243826 at	1.97E-09	0.0001	0.351	9.68E-05	2	---	---
209605 at	1.96E-06	0.1073	-0.281	4.17E-02	22	TST	NM_003312
1554768 a at	3.63E-06	0.1981	-0.274	4.17E-02	14	MAD2L1	NM_002358
231149 s at	4.78E-06	0.2610	-0.271	4.17E-02	3	ULK4	NM_017886
210639 s at	5.35E-06	0.2920	-0.270	4.17E-02	6	ATG5	NM_004849
234863 x at	6.66E-06	0.3638	-0.267	4.17E-02	6	FBXO5	NM_001142522
204004 at	7.46E-06	0.4072	-0.266	4.17E-02	12	PAWR	NM_002583
238104 at	8.01E-06	0.4376	0.265	4.17E-02	23	---	---
207238 s at	8.81E-06	0.4809	-0.264	4.17E-02	1	PTPRC	NM_002838
201345 s at	8.90E-06	0.4863	-0.263	4.17E-02	5	UBE2D2	NM_003339
219869 s at	1.04E-05	0.5688	-0.262	4.17E-02	4	SLC39A8	NM_001135146
242364 x at	1.07E-05	0.5848	0.261	4.17E-02	17	LOC100131096	XM_001720907
204005 s at	1.10E-05	0.6034	-0.261	4.17E-02	12	PAWR	NM_002583
204887 s at	1.57E-05	0.8572	-0.256	5.51E-02	4	PLK4	NM_014264
214173 x at	1.83E-05	0.9986	-0.254	5.56E-02	19	C19orf2	NM_003796
201014 s at	1.90E-05	1.0000	-0.254	5.56E-02	4	PAICS	NM_001079524
227620 at	1.92E-05	1.0000	-0.254	5.56E-02	9	SLC44A1	NM_080546
227806 at	2.45E-05	1.0000	-0.251	6.69E-02	16	C16orf74	NM_206967
212896 at	2.60E-05	1.0000	-0.250	6.71E-02	5	SKIV2L2	NM_015360
225562 at	2.77E-05	1.0000	-0.249	6.81E-02	13	RASA3	NM_007368
226223 at	2.91E-05	1.0000	-0.248	6.82E-02	20	---	---
1556932 at	3.77E-05	1.0000	0.245	8.30E-02	7	---	---
205071 x at	3.93E-05	1.0000	-0.244	8.30E-02	5	XRCC4	NM_003401
202708 s at	4.06E-05	1.0000	0.244	8.30E-02	1	HIST2H2BE	NM_003528
208382 s at	4.36E-05	1.0000	-0.243	8.31E-02	22	DMC1	NM_007068

202511 s at	4.54E-05	1.0000	-0.243	8.31E-02	6	ATG5	NM_004849
205240 at	4.57E-05	1.0000	-0.242	8.31E-02	1	GPSM2	NM_013296
212620 at	5.13E-05	1.0000	0.241	8.61E-02	15	ZNF609	NM_015042
220953 s at	5.40E-05	1.0000	-0.240	8.61E-02	5	MTMR12	NM_001040446
211363 s at	5.40E-05	1.0000	-0.240	8.61E-02	9	MTAP	NM_002451
216880 at	5.43E-05	1.0000	-0.240	8.61E-02	14	RAD51L1	NM_002877
1557984 s at	5.94E-05	1.0000	-0.239	8.93E-02	12	RPAP3	NM_024604
205716 at	6.01E-05	1.0000	-0.239	8.93E-02	7	SLC25A40	NM_018843
210570 x at	6.25E-05	1.0000	-0.238	8.93E-02	5	MAPK9	NM_001135044
206760 s at	6.79E-05	1.0000	0.237	8.93E-02	19	FCER2	NM_002002
212058 at	6.92E-05	1.0000	-0.237	8.93E-02	3	SR140	NM_001080415
204128 s at	7.02E-05	1.0000	-0.237	8.93E-02	13	RFC3	NM_002915
210972 x at	7.10E-05	1.0000	-0.236	8.93E-02	14	TRA@ /// TRAC /// TRAJ17 /// TRAV20	---
229053 at	7.25E-05	1.0000	0.236	8.93E-02	16	SYT17	NM_016524
204772 s at	7.27E-05	1.0000	-0.236	8.93E-02	9	TTF1	NM_007344
232270 at	8.19E-05	1.0000	0.234	9.55E-02	9	C9orf3	NM_032823
233655 s at	8.59E-05	1.0000	-0.234	9.55E-02	9	FAM29A	NM_017645
212588 at	8.78E-05	1.0000	-0.233	9.55E-02	1	PTPRC	NM_002838
216274 s at	8.79E-05	1.0000	-0.233	9.55E-02	15	SEC11A	NM_014300
209980 s at	9.06E-05	1.0000	-0.233	9.55E-02	17	SHMT1	NM_004169
216685 s at	9.19E-05	1.0000	-0.233	9.55E-02	9	MTAP	NM_002451
205159 at	9.41E-05	1.0000	-0.233	9.55E-02	22	CSF2RB	NM_000395
228374 at	9.73E-05	1.0000	-0.232	9.55E-02	10	C10orf28	NM_014472
204633 s at	9.78E-05	1.0000	-0.232	9.55E-02	14	RPS6KA5	NM_004755

1569607_s_at	9.89E-05	1.0000	0.232	9.55E-02	1	ANKRD20A1 /// ANKRD20A2 /// ANKRD20A3 /// ANKRD20A4 /// C21orf81 /// LOC100132733 /// LOC284232 /// LOC643187 /// LOC647595 /// LOC653436 /// LOC727770 /// LOC728783	NM_001012419
203768_s_at	1.01E-04	1.0000	-0.232	9.55E-02	23	STS	NM_000351
214540_at	1.01E-04	1.0000	0.232	9.55E-02	6	HIST1H2BO	NM_003527
200806_s_at	1.05E-04	1.0000	-0.231	9.59E-02	12	HSPD1	NM_002156
205429_s_at	1.06E-04	1.0000	-0.231	9.59E-02	7	MPP6	NM_016447
211902_x_at	1.08E-04	1.0000	-0.231	9.59E-02	14	TRA@	---
221504_s_at	1.11E-04	1.0000	0.230	9.59E-02	8	ATP6V1H	NM_015941
220721_at	1.12E-04	1.0000	-0.230	9.59E-02	19	ZNF614	NM_025040
204652_s_at	1.13E-04	1.0000	-0.230	9.59E-02	7	NRF1	NM_001040110
220390_at	1.16E-04	1.0000	0.230	9.69E-02	11	AGBL2	NM_024783
205981_s_at	1.20E-04	1.0000	-0.229	9.78E-02	4	ING2	NM_001564
219715_s_at	1.22E-04	1.0000	-0.229	9.78E-02	14	TDP1	NM_001008744
201688_s_at	1.24E-04	1.0000	-0.229	9.79E-02	8	TPD52	NM_001025252
210455_at	1.31E-04	1.0000	-0.228	1.01E-01	10	C10orf28	NM_014472
209724_s_at	1.34E-04	1.0000	-0.228	1.01E-01	18	ZFP161	NM_001143823
206759_at	1.34E-04	1.0000	0.228	1.01E-01	19	FCER2	NM_002002
226231_at	1.36E-04	1.0000	-0.227	1.01E-01	20	---	---
205124_at	1.38E-04	1.0000	0.227	1.01E-01	19	MEF2B	NM_001134794
1552634_a_at	1.51E-04	1.0000	-0.226	1.08E-01	19	ZNF101	NM_033204

209671	x at	1.52E-04	1.0000	-0.226	1.08E-01	14	TRA@ /// TRAC	---
201689	s at	1.55E-04	1.0000	-0.225	1.09E-01	8	TPD52	NM 001025252
220088	at	1.69E-04	1.0000	0.224	1.13E-01	19	C5AR1	NM 001736
1566001	at	1.70E-04	1.0000	0.224	1.13E-01	16	---	---
201946	s at	1.72E-04	1.0000	-0.224	1.13E-01	12	CCT2	NM 006431
209267	s at	1.72E-04	1.0000	-0.224	1.13E-01	4	SLC39A8	NM 001135146
218970	s at	1.73E-04	1.0000	-0.224	1.13E-01	10	CUTC	NM 015960
1555852	at	1.79E-04	1.0000	-0.223	1.15E-01	6	---	---
203524	s at	1.81E-04	1.0000	-0.223	1.15E-01	22	MPST	NM 001013436
201079	at	1.84E-04	1.0000	0.223	1.15E-01	15	SYNGR2	NM 004710
217640	x at	1.85E-04	1.0000	-0.223	1.15E-01	18	C18orf24	NM 001039535
1554883	a at	1.87E-04	1.0000	-0.223	1.15E-01	5	ERCC8	NM 000082
211088	s at	1.93E-04	1.0000	-0.222	1.17E-01	4	PLK4	NM 014264
203294	s at	1.96E-04	1.0000	-0.222	1.17E-01	18	LMAN1	NM 005570
213231	at	1.98E-04	1.0000	0.222	1.17E-01	19	DMWD	NM 004943
223495	at	2.09E-04	1.0000	0.221	1.19E-01	19	CCDC8	NM 032040
203218	at	2.10E-04	1.0000	-0.221	1.19E-01	5	MAPK9	NM 001135044
227261	at	2.12E-04	1.0000	-0.221	1.19E-01	13	KLF12	NM 007249
229285	at	2.13E-04	1.0000	-0.221	1.19E-01	1	RNASEL	NM 021133
206667	s at	2.15E-04	1.0000	-0.221	1.19E-01	5	SCAMP1	NM 004866
210813	s at	2.20E-04	1.0000	-0.220	1.19E-01	5	XRCC4	NM 003401
206617	s at	2.21E-04	1.0000	0.220	1.19E-01	23	RENBP	NM 002910
214335	at	2.21E-04	1.0000	0.220	1.19E-01	19	RPL18	NM 000979
202468	s at	2.24E-04	1.0000	-0.220	1.19E-01	9	CTNNA1	NM 003798
242843	at	2.29E-04	1.0000	-0.220	1.21E-01	1	BCAN	NM 021948
213498	at	2.40E-04	1.0000	0.219	1.24E-01	11	CREB3L1	NM 052854
206668	s at	2.44E-04	1.0000	-0.219	1.24E-01	5	SCAMP1	NM 004866
243399	at	2.47E-04	1.0000	0.219	1.24E-01	2	---	---
223207	x at	2.47E-04	1.0000	0.219	1.24E-01	9	PHPT1	NM 001135861
202180	s at	2.47E-04	1.0000	0.219	1.24E-01	16	MVP	NM 005115

233560	x at	2.54E-04	1.0000	-0.218	1.26E-01	20	MCM8	NM_032485
219286	s at	2.57E-04	1.0000	-0.218	1.26E-01	1	RBM15	NM_022768
219079	at	2.62E-04	1.0000	-0.218	1.26E-01	6	CYB5R4	NM_016230
202143	s at	2.62E-04	1.0000	-0.218	1.26E-01	2	COPS8	NM_006710
226826	at	2.64E-04	1.0000	-0.218	1.26E-01	5	---	---
1554543	at	2.79E-04	1.0000	0.217	1.32E-01	17	SPAG9	NM_001130528
209182	s at	2.89E-04	1.0000	0.216	1.33E-01	10	C10orf10	NM_007021
223171	at	2.89E-04	1.0000	-0.216	1.33E-01	18	DYM	NM_017653
200650	s at	2.89E-04	1.0000	-0.216	1.33E-01	1	LDHA	NM_001135239
201344	at	2.93E-04	1.0000	-0.216	1.33E-01	5	UBE2D2	NM_003339
238661	at	2.98E-04	1.0000	0.216	1.33E-01	8	LOC100130155	XM_001720201
237158	s at	3.01E-04	1.0000	-0.216	1.33E-01	12	MPHOSPH9	NM_022782
244398	x at	3.02E-04	1.0000	-0.216	1.33E-01	1	ZNF684	NM_152373
230134	s at	3.05E-04	1.0000	-0.215	1.33E-01	9	RC3H2	NM_001100588
221048	x at	3.08E-04	1.0000	-0.215	1.33E-01	17	C17orf80	NM_001100621
201691	s at	3.11E-04	1.0000	-0.215	1.33E-01	8	TPD52	NM_001025252
228485	s at	3.13E-04	1.0000	-0.215	1.33E-01	9	SLC44A1	NM_080546
225193	at	3.16E-04	1.0000	-0.215	1.33E-01	22	---	---
201641	at	3.19E-04	1.0000	0.215	1.33E-01	19	BST2	NM_004335
220794	at	3.21E-04	1.0000	0.215	1.33E-01	1	GREM2	NM_022469
220073	s at	3.22E-04	1.0000	0.215	1.33E-01	12	PLEKHG6	NM_018173
211080	s at	3.26E-04	1.0000	-0.214	1.33E-01	14	NEK2	NM_002497
218667	at	3.28E-04	1.0000	-0.214	1.33E-01	23	PJA1	NM_001032396
202089	s at	3.31E-04	1.0000	-0.214	1.33E-01	18	SLC39A6	NM_001099406
238977	at	3.39E-04	1.0000	-0.214	1.35E-01	2	MCM6	NM_005915
205722	s at	3.42E-04	1.0000	0.214	1.35E-01	8	GFRA2	NM_001495
221397	at	3.43E-04	1.0000	0.214	1.35E-01	12	TAS2R10	NM_023921
36888	at	3.50E-04	1.0000	-0.213	1.36E-01	19	KIAA0841	NM_015302
224076	s at	3.51E-04	1.0000	-0.213	1.36E-01	8	WHSC1L1	NM_017778
207079	s at	3.60E-04	1.0000	-0.213	1.38E-01	14	MED6	NM_005466

205891 at	3.65E-04	1.0000	0.213	1.39E-01	17	ADORA2B	NM_000676
238528 at	3.68E-04	1.0000	-0.213	1.39E-01	15	UBR1	NM_174916
223584 s at	3.74E-04	1.0000	-0.212	1.39E-01	7	KBTBD2	NM_015483
1562505 at	3.77E-04	1.0000	0.212	1.39E-01	20	---	---
225683 x at	3.81E-04	1.0000	0.212	1.39E-01	9	MAMDC4 /// PHPT1	NM_001135861
221195 at	3.84E-04	1.0000	-0.212	1.39E-01	17	RNFT1	NM_016125
1554474 a at	3.88E-04	1.0000	0.212	1.39E-01	6	MOXD1	NM_015529
1554397 s at	3.88E-04	1.0000	-0.212	1.39E-01	11	UEVLD	NM_001040697
219155 at	3.96E-04	1.0000	-0.211	1.39E-01	17	PITPNC1	NM_012417
1565269 s at	3.97E-04	1.0000	-0.211	1.39E-01	12	ATF1	NM_005171
225000 at	3.97E-04	1.0000	-0.211	1.39E-01	3	PRKAR2A	NM_004157
223585 x at	3.97E-04	1.0000	-0.211	1.39E-01	7	KBTBD2	NM_015483
222714 s at	4.07E-04	1.0000	-0.211	1.39E-01	8	LACTB2	NM_016027
202352 s at	4.08E-04	1.0000	-0.211	1.39E-01	17	PSMD12	NM_002816
220083 x at	4.10E-04	1.0000	-0.211	1.39E-01	1	UCHL5	NM_015984
234023 s at	4.13E-04	1.0000	-0.211	1.39E-01	13	CENPJ	NM_018451
224596 at	4.13E-04	1.0000	-0.211	1.39E-01	9	SLC44A1	NM_080546
1554271 a at	4.14E-04	1.0000	-0.211	1.39E-01	1	CENPL	NM_001127181
219501 at	4.18E-04	1.0000	0.211	1.40E-01	13	ENOX1	NM_001127615
218622 at	4.21E-04	1.0000	-0.210	1.40E-01	12	NUP37	NM_024057
230070 at	4.31E-04	1.0000	0.210	1.42E-01	11	CNIH2	NM_182553
218073 s at	4.33E-04	1.0000	-0.210	1.42E-01	1	TMEM48	NM_018087
209643 s at	4.42E-04	1.0000	0.210	1.43E-01	17	PLD2	NM_002663
215063 x at	4.42E-04	1.0000	0.210	1.43E-01	1	LRRC40	NM_017768
219030 at	4.54E-04	1.0000	-0.209	1.44E-01	2	TPRKB	NM_016058
203984 s at	4.54E-04	1.0000	-0.209	1.44E-01	1	CASP9	NM_001229
206935 at	4.55E-04	1.0000	0.209	1.44E-01	13	PCDH8	NM_002590
224984 at	4.66E-04	1.0000	0.209	1.47E-01	16	NFAT5	NM_001113178
231918 s at	4.80E-04	1.0000	-0.208	1.50E-01	5	GFM2	NM_032380

219292 at	4.85E-04	1.0000	-0.208	1.51E-01	8	THAP1	NM_018105
217801 at	4.92E-04	1.0000	0.208	1.52E-01	20	ATP5E	NM_001001977
216526 x at	4.99E-04	1.0000	0.208	1.52E-01	6	HLA-C	NM_002117
229173 at	5.00E-04	1.0000	-0.208	1.52E-01	2	KIAA1715	NM_030650
222387 s at	5.03E-04	1.0000	-0.208	1.52E-01	16	VPS35	NM_018206
226153 s at	5.05E-04	1.0000	-0.208	1.52E-01	15	CNOT6L	NM_144571
1552978 a at	5.11E-04	1.0000	-0.207	1.52E-01	5	SCAMP1	NM_004866
219126 at	5.14E-04	1.0000	-0.207	1.52E-01	6	PHF10	NM_018288
204417 at	5.22E-04	1.0000	-0.207	1.52E-01	14	GALC	NM_000153
206056 x at	5.33E-04	1.0000	0.207	1.52E-01	16	SPN	NM_001030288
219628 at	5.34E-04	1.0000	0.207	1.52E-01	3	ZMAT3	NM_022470
218967 s at	5.35E-04	1.0000	-0.207	1.52E-01	10	PTER	NM_001001484
227376 at	5.35E-04	1.0000	0.207	1.52E-01	7	GLI3	NM_000168
227447 at	5.37E-04	1.0000	-0.207	1.52E-01	5	SKIV2L2	NM_015360
201920 at	5.38E-04	1.0000	0.207	1.52E-01	2	SLC20A1	NM_005415
218603 at	5.39E-04	1.0000	-0.207	1.52E-01	6	HECA	NM_016217
203353 s at	5.39E-04	1.0000	-0.207	1.52E-01	18	MBD1	NM_002384
206030 at	5.43E-04	1.0000	0.207	1.52E-01	17	ASPA	NM_000049
204444 at	5.44E-04	1.0000	-0.207	1.52E-01	10	KIF11	NM_004523
241040 at	5.49E-04	1.0000	0.206	1.52E-01	8	---	---
1568949 at	5.54E-04	1.0000	-0.206	1.53E-01	17	PITPNC1	NM_012417
209583 s at	5.65E-04	1.0000	0.206	1.55E-01	3	CD200	NM_001004196
203856 at	5.68E-04	1.0000	-0.206	1.55E-01	14	VRK1	NM_003384
209016 s at	5.76E-04	1.0000	0.206	1.56E-01	12	KRT7	NM_005556
206220 s at	5.83E-04	1.0000	-0.205	1.56E-01	13	RASA3	NM_007368
1564962 at	5.86E-04	1.0000	-0.205	1.56E-01	7	ZNF92	NM_007139
226345 at	5.87E-04	1.0000	-0.205	1.56E-01	10	---	---
218584 at	5.88E-04	1.0000	0.205	1.56E-01	12	TCTN1	NM_001082537
213575 at	5.91E-04	1.0000	0.205	1.56E-01	7	TRA2A	NM_013293

225525_at	6.04E-04	1.0000	0.205	1.58E-01	22	CTA-221G9.4 /// LOC100131004	XM_001724436
202071_at	6.06E-04	1.0000	0.205	1.58E-01	20	SDC4	NM_002999
212552_at	6.10E-04	1.0000	-0.205	1.58E-01	2	HPCAL1	NM_002149
218875_s_at	6.19E-04	1.0000	-0.204	1.58E-01	6	FBXO5	NM_001142522
1554577_a_at	6.21E-04	1.0000	-0.204	1.58E-01	23	PSMD10	NM_002814
1562641_at	6.21E-04	1.0000	-0.204	1.58E-01	23	FAM122C	NM_138819
218634_at	6.21E-04	1.0000	0.204	1.58E-01	1	PHLDA3	NM_012396
219960_s_at	6.25E-04	1.0000	-0.204	1.58E-01	1	UCHL5	NM_015984
203767_s_at	6.29E-04	1.0000	-0.204	1.58E-01	23	STS	NM_000351
221698_s_at	6.37E-04	1.0000	0.204	1.59E-01	12	CLEC7A	NM_022570
212959_s_at	6.38E-04	1.0000	0.204	1.59E-01	12	GNPTAB	NM_024312
221743_at	6.45E-04	1.0000	0.204	1.59E-01	11	CUGBP1	NM_001025596
223785_at	6.49E-04	1.0000	-0.204	1.59E-01	15	FANCI	NM_001113378
225951_s_at	6.49E-04	1.0000	-0.204	1.59E-01	15	CHD2	NM_001042572
1554989_at	6.55E-04	1.0000	0.204	1.59E-01	14	KIAA0317	NM_001039479
231597_x_at	6.56E-04	1.0000	0.204	1.59E-01	NA	---	---
225455_at	6.58E-04	1.0000	-0.203	1.59E-01	1	TADA1L	NM_053053
211084_x_at	6.63E-04	1.0000	-0.203	1.59E-01	2	PRKD3	NM_005813
231878_at	6.69E-04	1.0000	-0.203	1.59E-01	16	C16orf53	NM_024516
222293_at	6.73E-04	1.0000	0.203	1.59E-01	19	CADM4	NM_145296
243721_at	6.73E-04	1.0000	0.203	1.59E-01	18	---	---
218957_s_at	6.75E-04	1.0000	-0.203	1.59E-01	11	PAAF1	NM_025155
231909_x_at	6.76E-04	1.0000	-0.203	1.59E-01	1	ODF2L	NM_001007022
1555762_s_at	6.79E-04	1.0000	-0.203	1.59E-01	1	RBM15	NM_022768
212587_s_at	6.84E-04	1.0000	-0.203	1.59E-01	1	PTPRC	NM_002838
33579_i_at	6.88E-04	1.0000	0.203	1.59E-01	22	GALR3	NM_003614
236228_at	6.93E-04	1.0000	0.203	1.59E-01	5	LOC100130744	XM_001720249
1559521_at	6.93E-04	1.0000	0.203	1.59E-01	21	---	---
218558_s_at	6.95E-04	1.0000	-0.203	1.59E-01	21	MRPL39	NM_017446

221094 s at	7.10E-04	1.0000	-0.202	1.61E-01	8	ELP3	NM_018091
235959 at	7.16E-04	1.0000	0.202	1.62E-01	1	---	---
242738 s at	7.37E-04	1.0000	0.202	1.64E-01	16	ZFH3	NM_006885
232937 at	7.39E-04	1.0000	0.202	1.64E-01	13	---	---
222777 s at	7.41E-04	1.0000	-0.202	1.64E-01	4	WHSC1	NM_001042424
228930 at	7.47E-04	1.0000	-0.201	1.64E-01	15	---	---
231873 at	7.51E-04	1.0000	0.201	1.64E-01	2	BMPR2	NM_001204
214168 s at	7.54E-04	1.0000	0.201	1.64E-01	15	TJP1	NM_003257
203770 s at	7.56E-04	1.0000	-0.201	1.64E-01	23	STS	NM_000351
219544 at	7.56E-04	1.0000	-0.201	1.64E-01	13	Bora	NM_024808
210416 s at	7.57E-04	1.0000	-0.201	1.64E-01	22	CHEK2	NM_001005735
200868 s at	7.61E-04	1.0000	-0.201	1.64E-01	20	RNF114	NM_018683
202142 at	7.65E-04	1.0000	-0.201	1.64E-01	2	COPS8	NM_006710
212124 at	7.67E-04	1.0000	-0.201	1.64E-01	10	ZMIZ1	NM_020338
1555830 s at	7.70E-04	1.0000	-0.201	1.64E-01	7	FAM62B	NM_020728
207738 s at	7.73E-04	1.0000	0.201	1.64E-01	2	NCKAP1	NM_013436
227803 at	7.90E-04	1.0000	0.201	1.67E-01	6	ENPP5	NM_021572
1555760 a at	8.02E-04	1.0000	-0.200	1.69E-01	22	RBM15	NM_022768
201690 s at	8.12E-04	1.0000	-0.200	1.69E-01	8	TPD52	NM_001025252
228378 at	8.16E-04	1.0000	-0.200	1.69E-01	12	C12orf29	NM_001009894
1564963 x at	8.22E-04	1.0000	-0.200	1.69E-01	7	ZNF92	NM_007139
224883 at	8.23E-04	1.0000	-0.200	1.69E-01	15	PLDN	NM_012388
239105 at	8.28E-04	1.0000	-0.200	1.69E-01	14	---	---
1561706 at	8.32E-04	1.0000	0.200	1.69E-01	NA	---	---
219812 at	8.37E-04	1.0000	-0.200	1.69E-01	7	PVRIG	NM_024070
1558794 at	8.40E-04	1.0000	0.200	1.69E-01	NA	LOC728190	NR_024397
209708 at	8.42E-04	1.0000	0.200	1.69E-01	6	MOXD1	NM_015529
233421 s at	8.44E-04	1.0000	-0.199	1.69E-01	1	NUP133	NM_018230
206039 at	8.46E-04	1.0000	-0.199	1.69E-01	23	RAB33A	NM_004794
232222 at	8.46E-04	1.0000	0.199	1.69E-01	18	C18orf49	---

226966 at	8.48E-04	1.0000	0.199	1.69E-01	12	PRPF40B	NM_001031698
209670 at	8.63E-04	1.0000	-0.199	1.70E-01	14	TRAC	---
231046 at	8.72E-04	1.0000	0.199	1.70E-01	5	---	---
220885 s at	8.75E-04	1.0000	-0.199	1.70E-01	13	CENPJ	NM_018451
1554493 s at	8.77E-04	1.0000	-0.199	1.70E-01	2	THADA	NM_001083953
223740 at	8.79E-04	1.0000	0.199	1.70E-01	6	RIPPLY2	NR_024277
1559059 s at	8.79E-04	1.0000	-0.199	1.70E-01	19	ZNF611	NM_030972
224699 s at	8.79E-04	1.0000	-0.199	1.70E-01	7	FAM62B	NM_020728
230974 at	8.81E-04	1.0000	-0.199	1.70E-01	16	DDX19B	NM_001014449
244470 at	8.88E-04	1.0000	0.199	1.70E-01	23	RNF12	NM_016120
203214 x at	8.92E-04	1.0000	-0.199	1.70E-01	10	CDC2	NM_001130829
231973 s at	8.93E-04	1.0000	-0.199	1.70E-01	2	ANAPC1	NM_022662
238190 at	8.94E-04	1.0000	-0.199	1.70E-01	16	TUFM	NM_003321
214521 at	9.00E-04	1.0000	0.198	1.71E-01	1	HES2	NM_019089
237221 at	9.11E-04	1.0000	0.198	1.72E-01	15	---	---
210559 s at	9.13E-04	1.0000	-0.198	1.72E-01	10	CDC2	NM_001130829
223010 s at	9.21E-04	1.0000	-0.198	1.73E-01	4	OCIAD1	NM_001079839
210742 at	9.50E-04	1.0000	0.198	1.77E-01	1	CDC14A	NM_003672
205393 s at	9.53E-04	1.0000	-0.197	1.77E-01	11	CHEK1	NM_001114121
223289 s at	9.56E-04	1.0000	-0.197	1.77E-01	4	USP38	NM_032557
217457 s at	9.71E-04	1.0000	-0.197	1.79E-01	4	RAP1GDS1	NM_001100426
215750 at	9.79E-04	1.0000	0.197	1.80E-01	22	KIAA1659	XM_001723799
205858 at	9.83E-04	1.0000	0.197	1.80E-01	17	NGFR	NM_002507
211318 s at	9.92E-04	1.0000	-0.197	1.81E-01	20	RAE1	NM_001015885
218295 s at	9.95E-04	1.0000	-0.197	1.81E-01	22	NUP50	NM_007172

* R values represent correlation coefficients for the association.

† Genes that were selected for siRNA screening are highlighted by shading.

Genome-wide SNP association with radiation AUC: An analysis of the association of genome-wide SNPs with radiation AUC also was performed (Figure 5B). A total of 561,298 SNPs on the Illumina 550K SNP array and 493,750 SNPs on the Illumina 510S SNP array had been genotyped using DNA from each of these 277 cell lines. In addition, the Affymetrix 6.0 SNP array data was publically available. Quality control (QC) was performed for all of these SNPs prior to performing the statistical analysis. Specifically, for data obtained with the Illumina 550K array, 12,261 SNPs were removed that had call rates <95%, 32,550 SNPs were removed with minor allele frequencies (MAFs) <5%, and 4,676 SNPs were removed that deviated from Hardy-Weinberg Equilibrium (HWE), using a stringent threshold of $p < 0.001$. Therefore, 511,811 Illumina 550K SNPs were used in the genome-wide SNP analysis. A similar approach was used for the QC analysis of SNPs on the Illumina 510S platform. After removing 10,353 SNPs with call rates <95%, 147,027 SNPs with a $MAF < 5\%$ and 3,805 SNPs that deviated from HWE ($p < 0.001$), a total of 332,565 Illumina 510S SNPs remained for analysis. For the publicly available Affymetrix 6.0 SNPs, SNPs that had already been genotyped using the Illumina platforms were first removed, resulting in 643,600 unique SNPs on the Affymetrix 6.0 SNP array for which the QC analysis was performed. After removing 26,140 SNPs with call rates <95%, 107,275 SNPs with a $MAF < 5\%$ and 5,763 that deviated from HWE ($p < 0.001$), 504,422 remained. Therefore, after combining data from the two platforms, 1,348,798 SNPs were available for use in the analysis (Figure 5B).

The p value for the most significant SNP, Affymetrix marker SNP_A-8538282 (rs7000734), was 3.82×10^{-7} ($r = 0.309$, $MAF = 0.081$). The top 16 SNPs, all with p values $< 10^{-5}$, are listed in Table 6, and the 1335 SNPs that had p values $< 10^{-3}$ are listed in Table 7. Of these, 151 SNPs were significantly associated with AUC, with p values $< 10^{-4}$. These 151 SNPs were located within or close to 99 unique genes on the basis of the annotation of genome build 36.3. Among the 151 top SNPs, 3 were within coding regions, 45 within introns, and 36 and 67 were within 5'- or 3'-UTR or flanking regions, respectively.

Table 6
The top 16 SNPs that were associated with radiation AUC with p values $<10^{-5}$.

SNP ID	P value	R value*	Q value	MAF	Chr	Position	Gene Symbol	Location	Location Relative to Gene (bp)
rs7000734	3.82E-07	0.309	0.259	0.081	8	96,196,206	PLEKHF2	5'-upstream	19,002
rs16885294	3.91E-07	0.310	0.259	0.071	6	54,373,355	TINAG	3'-downstream	10,483
rs1561715	9.58E-07	0.299	0.318	0.083	8	96,189,090	PLEKHF2	5'-upstream	26,118
rs1610110	9.58E-07	0.299	0.318	0.083	8	96,185,038	PLEKHF2	5'-upstream	30,170
rs2859631	1.20E-06	0.296	0.318	0.072	16	77,189,295	WWOX	intron	0
rs12569163	1.78E-06	0.292	0.394	0.118	1	239,945,170	WDR64	intron	0
rs16889440	2.14E-06	0.290	0.405	0.175	6	24,652,946	KIAA0319	3'-UTR	0
rs7554126	4.34E-06	0.287	0.667	0.297	1	239,953,804	WDR64	intron	0
rs4742269	4.73E-06	0.280	0.667	0.139	9	6,839,317	JMJD2C	intron	0
rs7591064	5.03E-06	0.279	0.667	0.110	2	49,031,105	FSHR	3'-downstream	12,051
rs11250464	5.61E-06	0.279	0.676	0.175	10	1,396,364	ADARB2	intron	0
rs1853665	6.87E-06	0.276	0.696	0.344	6	150,340,535	ULBP1	3'-downstream	3,996
rs4392868	8.24E-06	0.274	0.696	0.087	8	96,189,248	PLEKHF2	5'-upstream	25,960
rs17598306	8.60E-06	0.273	0.696	0.079	7	96,419,747	FLJ34048	3'-downstream	51,148
rs1471356	8.71E-06	0.273	0.696	0.230	14	97,373,084	LOC100132612	5'-upstream	86,450
rs4554799	9.00E-06	0.272	0.696	0.170	10	1,397,728	ADARB2	intron	0

*R values represent correlation coefficients for the association.

Table 7
Top 1335 SNPs associated with radiation AUC with p values $< 10^{-3}$.

SNP ID	P value	R value*	Q value	MAF	Chr	Position	Gene Symbol	Location	Location Relative to Gene (bp)
rs7000734	3.82E-07	0.309	0.259	0.081	8	96,196,206	PLEKHF2	5'-upstream	19,002
rs16885294	3.91E-07	0.310	0.259	0.071	6	54,373,355	TINAG	3'-downstream	10,483
rs1561715	9.58E-07	0.299	0.318	0.083	8	96,189,090	PLEKHF2	5'-upstream	26,118
rs1610110	9.58E-07	0.299	0.318	0.083	8	96,185,038	PLEKHF2	5'-upstream	30,170
rs2859631	1.20E-06	0.296	0.318	0.072	16	77,189,295	WVOX	intron	0
rs12569163	1.78E-06	0.292	0.394	0.118	1	239,945,170	WDR64	intron	0
rs16889440	2.14E-06	0.290	0.405	0.175	6	24,652,946	KIAA0319	3'-UTR	0
rs7554126	4.34E-06	0.287	0.667	0.297	1	239,953,804	WDR64	intron	0
rs4742269	4.73E-06	0.280	0.667	0.139	9	6,839,317	JMJD2C	intron	0
rs7591064	5.03E-06	0.279	0.667	0.110	2	49,031,105	FSHR	3'-downstream	12,051
rs11250464	5.61E-06	0.279	0.676	0.175	10	1,396,364	ADARB2	intron	0
rs1853665	6.87E-06	0.276	0.696	0.344	6	150,340,535	ULBP1	3'-downstream	3,996
rs4392868	8.24E-06	0.274	0.696	0.087	8	96,189,248	PLEKHF2	5'-upstream	25,960
rs17598306	8.60E-06	0.273	0.696	0.079	7	96,419,747	FLJ34048	3'-downstream	51,148
rs1471356	8.71E-06	0.273	0.696	0.230	14	97,373,084	LOC100132612	5'-upstream	86,450
rs4554799	9.00E-06	0.272	0.696	0.170	10	1,397,728	ADARB2	intron	0
rs2409791	1.09E-05	-0.270	0.696	0.280	5	59,920,074	DEPDC1B	3'-downstream	8,422
rs12657754	1.10E-05	0.270	0.696	0.221	5	3,875,893	IRX1	3'-downstream	221,376
rs7633553	1.17E-05	0.273	0.696	0.291	3	58,415,276	PDHB	5'-upstream	20,671
rs898387	1.24E-05	0.268	0.696	0.235	1	202,845,996	LRRN2	3'-downstream	6,928
rs6091189	1.27E-05	0.268	0.696	0.277	20	48,689,692	C20orf175	5'-upstream	2,859
rs1715958	1.28E-05	0.267	0.696	0.244	15	53,051,004	C15orf15	3'-downstream	209,800
rs10189510	1.30E-05	0.267	0.696	0.085	2	183,199,011	DNAJC10	5'-upstream	90,233
rs3777645	1.42E-05	0.267	0.696	0.100	6	54,309,669	TINAG	intron	0

rs10517564	1.44E-05	0.266	0.696	0.052	4	153,408,601	FBXW7	3'-downstream	53,259
rs631411	1.47E-05	0.266	0.696	0.299	9	199,325	C9orf66	3'-downstream	4,137
rs2498662	1.49E-05	0.266	0.696	0.065	6	139,467,599	HECA	5'-upstream	30,343
rs12553351	1.49E-05	0.265	0.696	0.117	9	6,828,348	JMJD2C	intron	0
rs12380100	1.55E-05	0.265	0.696	0.097	9	11,177,013	LOC646114	3'-downstream	146,728
rs869239	1.60E-05	0.265	0.696	0.495	4	183,690,033	ODZ3	intron	0
rs7676392	1.73E-05	0.264	0.696	0.281	4	183,613,233	ODZ3	intron	0
rs12705596	1.75E-05	0.263	0.696	0.161	7	108,893,619	LOC100128056	5'-upstream	372,799
rs10183821	1.81E-05	0.264	0.696	0.120	2	128,753,139	HS6ST1	intron	0
rs7901632	1.87E-05	0.262	0.696	0.072	10	80,382,672	ZMIZ1	5'-upstream	248,675
rs17598132	1.89E-05	0.263	0.696	0.076	7	96,417,275	FLJ34048	3'-downstream	53,620
rs7193297	1.97E-05	0.267	0.696	0.447	16	71,551,332	ZFHX3	missense	0
rs10515853	2.05E-05	0.261	0.696	0.051	5	162,588,458	MRP63P6	3'-downstream	189,268
rs1561714	2.14E-05	0.261	0.696	0.087	8	96,189,151	PLEKHF2	5'-upstream	26,057
rs942679	2.17E-05	0.261	0.696	0.213	1	154,617,690	RHBG	intron	0
rs12297511	2.20E-05	0.262	0.696	0.175	12	131,204,374	NOC4L	3'-downstream	1,435
rs10809359	2.22E-05	0.261	0.696	0.109	9	11,135,717	LOC646114	3'-downstream	105,432
rs10084239	2.31E-05	0.260	0.696	0.117	2	42,107,250	LOC91461	5'-upstream	22,007
rs17587765	2.33E-05	0.260	0.696	0.108	1	117,372,602	IGSF2	intron	0
rs672482	2.37E-05	0.259	0.696	0.092	1	143,543,612	TRNAQ-CUG	3'-downstream	7,181
rs13128522	2.38E-05	0.260	0.696	0.060	4	16,149,782	LDB2	intron	0
rs2249118	2.41E-05	-0.260	0.696	0.364	21	36,277,829	RPL23AP3	3'-downstream	32,264
rs10809395	2.50E-05	0.259	0.704	0.103	9	11,223,740	LOC646114	3'-downstream	193,455
rs2212916	2.80E-05	-0.257	0.711	0.366	21	36,281,638	RPL23AP3	3'-downstream	28,455
rs927984	2.81E-05	0.257	0.711	0.130	6	25,520,966	LRRC16A	intron	0
rs2826523	2.85E-05	0.258	0.711	0.068	21	21,100,816	PPIAP	5'-upstream	21,182
rs11731599	2.98E-05	0.257	0.711	0.489	4	183,691,126	ODZ3	intron	0
rs4314649	3.10E-05	0.257	0.711	0.242	8	35,052,669	LOC100133273	3'-downstream	200,898
rs894013	3.19E-05	0.261	0.711	0.472	3	4,353,142	SETMAR	3'-downstream	19,193

rs35018391	3.23E-05	0.255	0.711	0.049	4	181,217,870	hCG 2025798	3'-downstream	1,004,366
rs41333347	3.23E-05	0.255	0.711	0.049	4	181,227,186	hCG 2025798	3'-downstream	1,662,228
rs7680285	3.23E-05	0.255	0.711	0.049	4	181,228,438	hCG 2025798	3'-downstream	993,798
rs8089644	3.30E-05	0.255	0.711	0.099	18	2,942,642	LPIN2	intron	0
rs17657370	3.34E-05	0.255	0.711	0.078	7	96,444,428	FLJ34048	3'-downstream	26,467
rs2812604	3.40E-05	0.255	0.711	0.118	10	34,089,448	PAR3	3'-downstream	350,655
rs4326096	3.41E-05	-0.255	0.711	0.270	5	59,926,035	DEPDC1B	3'-downstream	2,461
rs6570180	3.45E-05	0.255	0.711	0.196	6	137,987,617	LOC391040	5'-upstream	73,852
rs29233661	3.46E-05	0.255	0.711	0.240	8	35,061,182	LOC100133273	3'-downstream	209,411
rs16988828	3.47E-05	-0.255	0.711	0.085	22	29,333,561	TCN2	intron	0
rs6079836	3.60E-05	-0.254	0.711	0.339	20	15,383,564	MACROD2	intron	0
rs6079839	3.60E-05	-0.254	0.711	0.339	20	15,384,282	MACROD2	intron	0
rs7990503	3.64E-05	0.254	0.711	0.195	13	79,518,643	LOC729485	3'-downstream	8,767
rs6873333	3.64E-05	0.254	0.711	0.072	5	155,195,850	LOC100131033	3'-downstream	342,496
rs2491142	3.66E-05	0.254	0.711	0.215	1	31,096,680	SDC3	3'-downstream	21,887
rs12376660	3.71E-05	0.254	0.711	0.089	9	11,175,487	LOC646114	3'-downstream	145,202
rs641372	3.75E-05	0.259	0.711	0.071	18	58,432,935	ZCCHC2	3'-downstream	36,137
rs2075243	3.91E-05	-0.254	0.725	0.327	12	15,552,430	PTPRO	intron	0
rs1994179	4.08E-05	0.253	0.725	0.259	14	96,989,660	LOC730217	5'-upstream	3,769
rs2862667	4.09E-05	0.252	0.725	0.266	11	43,099,468	LOC100128134	5'-upstream	44,525
rs807301	4.11E-05	0.252	0.725	0.051	6	119,969,706	LOC728727	intron	0
rs1650385	4.15E-05	0.252	0.725	0.437	5	174,991,457	HRH2	5'-upstream	50,861
rs6964059	4.15E-05	0.253	0.725	0.259	7	40,630,937	C7orf10	intron	0
rs898386	4.22E-05	0.253	0.727	0.229	1	202,846,320	LRRN2	3'-downstream	6,604
rs3924198	4.36E-05	0.252	0.727	0.399	3	545,612	LOC402123	3'-downstream	88,860
rs2837005	4.46E-05	0.251	0.727	0.318	21	39,691,677	LCA5L	3'-downstream	7,963
rs2045624	4.51E-05	0.251	0.727	0.258	1	202,851,008	LRRN2	3'-downstream	1,916
rs10490857	4.53E-05	0.251	0.727	0.051	3	6,934,982	GRM7	intron	0
rs4880503	4.54E-05	0.251	0.727	0.171	10	1,426,858	ADARB2	intron	0

rs11976501	4.59E-05	0.250	0.727	0.134	7	76,746,424	CCDC146	intron	0
rs4817696	4.61E-05	0.250	0.727	0.262	21	35,155,046	RUNX1	intron	0
rs8101536	4.79E-05	0.250	0.740	0.208	19	2,580,845	NG7	intron	0
rs12705601	4.80E-05	0.250	0.740	0.161	7	108,923,348	LOC100128056	5'-upstream	343,070
rs7309722	4.97E-05	-0.250	0.750	0.460	12	76,694,384	NAV3	5'-upstream	54,816
rs10516301	4.97E-05	0.250	0.750	0.072	4	16,143,251	LDB2	intron	0
rs4487737	5.14E-05	0.249	0.757	0.218	8	141,296,740	NIBP	intron	0
rs7387053	5.14E-05	0.249	0.757	0.218	8	141,295,342	NIBP	intron	0
rs2309691	5.36E-05	0.248	0.777	0.491	4	183,691,063	ODZ3	intron	0
rs17549345	5.39E-05	-0.248	0.777	0.336	3	88,163,269	CGGBP1	3'-downstream	20,521
rs27564	5.55E-05	-0.251	0.791	0.325	5	59,873,391	PART1	3'-downstream	20,403
rs206789	5.74E-05	-0.248	0.810	0.313	5	59,939,728	DEPDC1B	intron	0
rs1693219	5.89E-05	0.247	0.823	0.289	1	231,807,892	KCNK1	5'-upstream	8,481
rs11200175	6.20E-05	0.247	0.843	0.167	10	123,568,222	ATE1	intron	0
rs1693216	6.50E-05	0.247	0.843	0.286	1	231,808,517	KCNK1	5'-upstream	7,856
rs11559201	6.57E-05	0.245	0.843	0.141	8	99,075,924	MATN2	synonymous	0
rs11559202	6.57E-05	0.245	0.843	0.141	8	99,075,912	MATN2	synonymous	0
rs2981309	6.62E-05	0.249	0.843	0.241	8	35,048,829	LOC100133273	3'-downstream	197,058
rs13239088	6.64E-05	0.249	0.843	0.054	7	46,381,408	LOC730338	3'-downstream	313,968
rs12121447	6.73E-05	0.246	0.843	0.055	1	120,018,494	ZNF697	5'-upstream	26,581
rs4716858	6.74E-05	-0.245	0.843	0.468	7	157,461,158	PTPRN2	intron	0
rs688858	6.74E-05	-0.246	0.843	0.254	11	87,652,911	CTSC	3'-downstream	13,497
rs4570460	6.80E-05	0.245	0.843	0.058	1	200,955,651	JARID1B	3'-downstream	7,504
rs212551	6.85E-05	0.245	0.843	0.132	8	96,201,280	PLEKHF2	5'-upstream	13,928
rs10118338	6.89E-05	0.245	0.843	0.139	9	11,226,474	LOC646114	3'-downstream	196,189
rs2498090	6.97E-05	-0.245	0.843	0.194	23	89,016,027	LOC360018	5'-upstream	19,984
rs2243174	7.04E-05	0.244	0.843	0.444	1	205,078,108	IL19	intron	0
rs4948698	7.06E-05	0.245	0.843	0.062	10	42,859,465	RET	5'-upstream	33,058
rs2243188	7.11E-05	0.244	0.843	0.442	1	205,081,095	IL19	intron	0

rs13007983	7.12E-05	0.245	0.843	0.114	2	5,642,699	SOX11	5'-upstream	107,551
rs10900601	7.37E-05	0.244	0.845	0.227	1	202,838,673	LRRN2	3'-downstream	14,251
rs6578083	7.41E-05	-0.244	0.845	0.374	8	141,299,161	NIBP	intron	0
rs10240447	7.41E-05	0.244	0.845	0.495	7	157,460,585	PTPRN2	intron	0
rs11119670	7.45E-05	0.244	0.845	0.442	1	205,071,944	IL19	intron	0
rs12380191	7.47E-05	0.244	0.845	0.101	9	11,170,739	LOC646114	3'-downstream	140,454
rs10838023	7.64E-05	0.243	0.845	0.267	11	43,113,488	LOC100128134	5'-upstream	58,545
rs7378774	7.71E-05	0.245	0.845	0.064	5	155,221,392	LOC100131033	3'-downstream	368,038
rs12908333	7.72E-05	-0.243	0.845	0.298	15	32,219,109	C15orf29	3'-downstream	1,058
rs9520592	7.80E-05	0.243	0.845	0.215	13	107,268,488	FAM155A	intron	0
rs12705602	7.91E-05	0.243	0.845	0.166	7	108,929,460	LOC100128056	5'-upstream	336,958
rs4738839	8.01E-05	-0.243	0.845	0.227	8	61,960,444	CHD7	3'-downstream	18,425
rs7835942	8.01E-05	-0.243	0.845	0.227	8	61,960,345	CHD7	3'-downstream	18,326
rs535161	8.01E-05	0.243	0.845	0.148	11	78,322,944	ODZ4	5'-upstream	122,111
rs11788082	8.03E-05	0.243	0.845	0.150	9	11,208,170	LOC646114	3'-downstream	177,885
rs308731	8.21E-05	0.242	0.853	0.365	3	4,354,374	SETMAR	3'-downstream	20,425
rs12301261	8.36E-05	0.242	0.853	0.081	12	83,102,293	LOC100128335	3'-downstream	264,229
rs1518338	8.42E-05	0.242	0.853	0.288	3	117,912,015	LOC285194	5'-upstream	2,013
rs11102357	8.63E-05	0.242	0.853	0.471	1	112,277,072	KCND3	intron	0
rs4131469	8.86E-05	0.241	0.853	0.350	1	200,237,371	RNPEP	intron	0
rs4677119	8.96E-05	0.241	0.853	0.329	3	72,374,648	RYBP	3'-downstream	131,790
rs11888061	9.03E-05	0.241	0.853	0.199	2	66,217,781	LOC729348	5'-upstream	246,161
rs2309341	9.04E-05	-0.241	0.853	0.433	4	181,590,726	hCG 2025798	3'-downstream	631,510
rs1268087	9.14E-05	0.241	0.853	0.147	6	126,155,515	NCOA7	intron	0
rs4234440	9.23E-05	0.246	0.853	0.185	3	43,925,045	ABHD5	3'-downstream	189,749
rs12702213	9.29E-05	0.240	0.853	0.058	7	46,381,080	LOC730338	3'-downstream	314,296
rs165808	9.41E-05	0.240	0.853	0.155	22	15,707,595	ZNF402P	3'-downstream	10,431
rs10007934	9.47E-05	-0.240	0.853	0.087	4	138,044,051	PCDH18	3'-downstream	616,234
rs2735784	9.48E-05	0.240	0.853	0.375	1	200,243,103	ELF3	5'-upstream	593

rs10073856	9.49E-05	0.241	0.853	0.071	5	155,195,298	LOC100131033	3'-downstream	341,944
rs17139113	9.50E-05	0.240	0.853	0.094	16	5,995,338	A2BP1	5'-upstream	13,795
rs3088121	9.52E-05	0.241	0.853	0.105	8	99,117,225	MATN2	3'-UTR	0
rs1319550	9.56E-05	-0.240	0.853	0.475	2	80,253,062	CTNNA2	intron	0
rs7157518	9.58E-05	-0.240	0.853	0.374	14	74,900,170	LOC731223	3'-downstream	67,076
rs10770444	9.63E-05	0.240	0.853	0.243	12	8,341,081	LOC100130149	3'-downstream	22,953
rs9388949	9.76E-05	-0.240	0.853	0.484	6	132,319,155	CTGF	5'-upstream	4,944
rs2243193	9.77E-05	0.240	0.853	0.453	1	205,082,848	IL19	3'-UTR	0
rs1991676	9.83E-05	0.241	0.853	0.055	18	64,903,434	CCDC102B	3'-downstream	30,028
rs7751415	9.85E-05	0.241	0.853	0.147	6	87,098,629	LOC643926	5'-upstream	100,055
rs9852704	9.86E-05	-0.240	0.853	0.406	3	88,171,034	CGGBP1	3'-downstream	12,756
rs7379436	1.00E-04	0.239	0.853	0.074	5	155,158,726	LOC100131033	3'-downstream	305,372
rs12356119	1.02E-04	0.239	0.853	0.114	10	128,017,485	ADAM12	intron	0
rs4662786	1.02E-04	0.240	0.853	0.111	2	128,752,362	HS6ST1	intron	0
rs10959622	1.02E-04	0.239	0.853	0.099	9	11,201,722	LOC646114	3'-downstream	171,437
rs4397386	1.03E-04	0.242	0.853	0.214	8	141,294,034	NIBP	intron	0
rs10486811	1.03E-04	0.239	0.853	0.254	7	40,617,380	C7orf10	intron	0
rs1829346	1.04E-04	0.239	0.853	0.287	3	117,911,597	LOC285194	5'-upstream	2,431
rs1467166	1.04E-04	-0.239	0.853	0.424	11	36,432,948	FLJ14213	intron	0
rs9450667	1.04E-04	0.239	0.853	0.312	6	88,151,105	C6orf163	3'-downstream	19,205
rs10240312	1.04E-04	0.239	0.853	0.179	7	97,892,440	BAIAP2L1	5'-upstream	24,124
rs2090111	1.05E-04	0.239	0.853	0.217	4	6,149,700	JAKMIP1	intron	0
rs12881650	1.06E-04	0.239	0.853	0.175	14	69,805,287	ADAM21P	5'-upstream	21,016
rs9311337	1.06E-04	0.239	0.853	0.478	3	4,356,787	SUMF1	3'-downstream	21,043
rs10198712	1.07E-04	-0.238	0.853	0.477	2	80,252,590	CTNNA2	intron	0
rs884108	1.07E-04	0.241	0.853	0.180	1	202,857,860	LRRN2	intron	0
rs10996977	1.08E-04	0.238	0.857	0.065	10	67,640,579	CTNNA3	intron	0
rs2837006	1.10E-04	0.238	0.857	0.352	21	39,694,306	LCA5L	3'-downstream	5,334
rs8076804	1.10E-04	0.238	0.857	0.188	17	75,890,077	KIAA1618	intron	0

rs9856655	1.10E-04	0.238	0.857	0.067	3	6,917,072	GRM7	intron	0
rs6744963	1.12E-04	0.238	0.857	0.087	2	20,311,091	PUM2	3'-downstream	843
rs11952678	1.12E-04	-0.238	0.857	0.209	5	62,013,385	IPO11	3'-downstream	53,220
rs17149618	1.13E-04	0.238	0.857	0.105	8	9,140,544	PPP1R3B	5'-upstream	94,914
rs9467231	1.13E-04	0.238	0.857	0.188	6	24,667,566	KIAA0319	intron	0
rs1450705	1.14E-04	0.238	0.857	0.139	14	87,418,880	GALC	3'-downstream	50,231
rs11977013	1.15E-04	0.237	0.857	0.249	7	40,639,214	C7orf10	intron	0
rs297550	1.15E-04	0.237	0.857	0.063	8	96,170,970	LOC100130098	5'-upstream	15,945
rs165790	1.17E-04	0.238	0.857	0.150	22	15,720,906	ZNF402P	Unknown	--
rs7917910	1.18E-04	0.237	0.857	0.257	10	128,234,945	LOC728152	3'-downstream	28,706
rs7302505	1.18E-04	0.237	0.857	0.162	12	63,304,388	RASSF3	intron	0
rs1358531	1.19E-04	0.240	0.857	0.166	15	53,069,902	C15orf15	3'-downstream	190,902
rs11250461	1.19E-04	0.237	0.857	0.226	10	1,394,502	ADARB2	intron	0
rs4951088	1.20E-04	0.237	0.857	0.471	1	202,877,403	LRRN2	intron	0
rs41413447	1.20E-04	0.237	0.857	0.134	1	234,726,528	ENO1P	3'-downstream	11,621
rs10459842	1.21E-04	-0.238	0.857	0.456	16	6,673,694	A2BP1	intron	0
rs2568654	1.21E-04	0.237	0.857	0.280	7	13,727,929	LOC100131022	3'-downstream	132,576
rs11240239	1.22E-04	0.237	0.857	0.469	1	202,879,427	LRRN2	intron	0
rs1376519	1.22E-04	0.238	0.857	0.244	8	35,045,674	LOC100133273	3'-downstream	193,903
rs2490588	1.25E-04	0.236	0.857	0.276	9	78,077,812	LOC100133206	3'-downstream	13,418
rs17543709	1.26E-04	0.236	0.857	0.069	1	233,631,547	TBCE	intron	0
rs165698	1.27E-04	0.236	0.857	0.152	22	15,719,068	ZNF402P	Unknown	--
rs2988270	1.27E-04	0.236	0.857	0.112	1	50,428,660	ELAVL4	intron	0
rs6830998	1.28E-04	0.237	0.857	0.279	4	183,617,946	ODZ3	intron	0
rs384483	1.28E-04	0.238	0.857	0.127	5	122,289,472	SNX24	intron	0
rs2332277	1.33E-04	0.237	0.857	0.172	14	69,803,279	ADAM21P	5'-upstream	19,008
rs16994140	1.33E-04	0.236	0.857	0.092	4	37,687,960	TBC1D1	intron	0
rs10813853	1.33E-04	0.237	0.857	0.167	9	32,660,725	TAF1L	5'-upstream	35,058
rs286158	1.34E-04	-0.235	0.857	0.309	5	59,970,010	DEPDC1B	intron	0

rs2542443	1.34E-04	0.236	0.857	0.063	8	140,660,763	KCNK9	3'-downstream	33,223
rs11781720	1.34E-04	-0.235	0.857	0.327	8	4,038,118	CSMD1	intron	0
rs1773951	1.34E-04	0.235	0.857	0.070	1	231,802,262	KCNK1	5'-upstream	14,111
rs16843867	1.35E-04	0.235	0.857	0.065	1	197,053,576	MIRN181B1	3'-downstream	41,049
rs10419308	1.35E-04	0.235	0.857	0.143	19	60,431,625	TMEM86B	intron	0
rs11250496	1.38E-04	0.235	0.857	0.166	10	1,437,105	ADARB2	intron	0
rs10486799	1.38E-04	0.235	0.857	0.074	7	39,619,751	RALA	5'-upstream	9,936
rs1513412	1.39E-04	-0.235	0.857	0.379	3	147,081,068	LOC389156	5'-upstream	55,809
rs1698888	1.40E-04	0.235	0.857	0.356	11	19,285,798	LOC390102	5'-upstream	32,407
rs727695	1.42E-04	0.235	0.857	0.313	4	183,610,140	ODZ3	intron	0
rs6814420	1.42E-04	-0.235	0.857	0.251	4	165,350,800	ANP32C	5'-upstream	12,487
rs4659246	1.43E-04	0.234	0.857	0.101	1	120,224,228	ADAM30	3'-downstream	13,451
rs937131	1.44E-04	0.234	0.857	0.179	7	97,884,611	BAIAP2L1	5'-upstream	16,295
rs11822678	1.45E-04	0.234	0.857	0.087	11	21,169,711	NELL1	intron	0
rs4786910	1.45E-04	-0.234	0.857	0.365	16	6,674,599	A2BP1	intron	0
rs10095762	1.46E-04	0.236	0.857	0.291	8	129,567,766	PVT1	3'-downstream	385,085
rs9605252	1.46E-04	0.236	0.857	0.148	22	16,170,349	CECR1	5'-upstream	99,570
rs1038050	1.47E-04	0.234	0.857	0.291	9	1,704,233	SMARCA2	5'-upstream	301,109
rs262453	1.47E-04	-0.234	0.857	0.269	11	36,013,498	LDLRAD3	intron	0
rs10120246	1.47E-04	0.235	0.857	0.089	9	9,789,050	PTPRD	intron	0
rs17778445	1.48E-04	0.234	0.857	0.056	4	90,590,957	GPRIN3	5'-upstream	142,773
rs2290467	1.48E-04	0.234	0.857	0.108	8	99,109,330	MATN2	intron	0
rs1060681	1.49E-04	0.234	0.857	0.169	14	69,906,506	SYNJ2BP	3'-UTR	0
rs7852743	1.49E-04	0.237	0.857	0.350	9	132,855,205	LAMC3	5'-upstream	19,120
rs11206538	1.49E-04	0.233	0.857	0.406	1	55,488,000	LOC645506	3'-downstream	26,367
rs2836416	1.49E-04	0.233	0.857	0.170	21	38,755,361	ERG	intron	0
rs11628576	1.50E-04	-0.233	0.857	0.121	14	82,214,285	ENSAP2	3'-downstream	14,419
rs6793337	1.50E-04	0.235	0.857	0.234	3	189,475,302	LPP	intron	0
rs10803641	1.51E-04	0.234	0.857	0.190	2	236,038,499	CENTG2	5'-upstream	28,976

rs6853164	1.52E-04	0.233	0.857	0.477	4	74,370,644	ANKRD17	5'-upstream	27,278
rs7808549	1.54E-04	-0.237	0.857	0.300	7	103,370,996	RELN	intron	0
rs11822168	1.54E-04	0.233	0.857	0.256	11	105,136,013	GRIA4	intron	0
rs2887596	1.54E-04	-0.235	0.857	0.423	12	76,678,888	NAV3	5'-upstream	70,312
rs780266	1.55E-04	0.233	0.857	0.071	1	231,791,723	KCNK1	5'-upstream	24,650
rs936361	1.56E-04	0.233	0.857	0.347	3	88,410,116	LOC344653	5'-upstream	38,880
rs12830703	1.56E-04	0.235	0.857	0.055	12	18,061,759	RERGL	3'-downstream	63,311
rs1113599	1.56E-04	-0.233	0.857	0.457	12	76,699,323	NAV3	5'-upstream	49,877
rs10956429	1.57E-04	0.233	0.857	0.338	8	129,584,169	PVT1	3'-downstream	401,488
rs1030016	1.59E-04	0.233	0.857	0.191	7	38,406,097	AMPH	intron	0
rs8016862	1.59E-04	-0.233	0.857	0.429	14	26,656,409	RPS27AP4	3'-downstream	141,224
rs1015244	1.59E-04	-0.233	0.857	0.105	1	213,437,193	KCNK2	intron	0
rs10159003	1.60E-04	-0.233	0.857	0.097	1	213,440,307	KCNK2	intron	0
rs11240237	1.60E-04	0.232	0.857	0.475	1	202,879,141	LRRN2	intron	0
rs4951089	1.60E-04	0.232	0.857	0.475	1	202,877,521	LRRN2	intron	0
rs10157448	1.61E-04	-0.235	0.857	0.111	1	213,438,479	KCNK2	intron	0
rs7058743	1.61E-04	0.233	0.857	0.145	23	110,742,481	LOC643873	3'-downstream	5,789
rs16825358	1.62E-04	0.234	0.857	0.285	3	117,912,388	LOC285194	5'-upstream	1,640
rs7043006	1.62E-04	0.233	0.857	0.129	9	100,140,610	GABBR2	intron	0
rs12548426	1.62E-04	0.232	0.857	0.222	8	96,174,362	LOC100130098	5'-upstream	19,337
rs6905924	1.62E-04	0.234	0.857	0.226	6	22,763,578	LOC389370	intron	0
rs322608	1.63E-04	0.232	0.857	0.442	5	11,541,467	CTNND2	intron	0
rs6700381	1.63E-04	0.233	0.857	0.438	1	237,585,731	CHRM3	5'-upstream	273,265
rs2306774	1.65E-04	0.232	0.857	0.220	3	19,898,826	EFHB	intron	0
rs6426991	1.65E-04	0.232	0.857	0.214	1	164,553,110	LOC284685	5'-upstream	39,603
rs7911417	1.65E-04	-0.232	0.857	0.106	10	126,895,990	LOC642622	3'-downstream	9,917
rs6051490	1.65E-04	-0.232	0.857	0.475	20	293,864	NRSN2	3'-downstream	10,359
rs4657537	1.66E-04	0.235	0.857	0.422	1	164,534,672	LOC284685	5'-upstream	21,165
rs10221771	1.67E-04	0.232	0.857	0.231	2	236,034,695	CENTG2	5'-upstream	32,780

rs10508213	1.68E-04	-0.232	0.857	0.112	10	1,601,165	ADARB2	intron	0
rs2249971	1.69E-04	-0.232	0.857	0.352	21	36,284,531	RPL23AP3	3'-downstream	25,562
rs1648224	1.69E-04	0.232	0.857	0.372	11	19,269,478	LOC390102	5'-upstream	16,087
rs17171730	1.70E-04	0.232	0.857	0.264	7	40,558,272	C7orf10	intron	0
rs13138387	1.70E-04	0.232	0.857	0.065	4	16,142,474	LDB2	intron	0
rs7079372	1.74E-04	0.232	0.857	0.295	10	33,613,812	NRP1	intron	0
rs4691114	1.75E-04	-0.232	0.857	0.308	4	165,360,381	ANP32C	5'-upstream	22,068
rs1895373	1.76E-04	0.235	0.857	0.353	19	55,801,605	SYT3	3'-downstream	15,441
rs9974828	1.77E-04	0.231	0.857	0.348	21	39,693,915	LCA5L	3'-downstream	5,725
rs12659182	1.77E-04	0.231	0.857	0.094	5	8,570,119	LOC729506	5'-upstream	55,351
rs8083033	1.77E-04	0.231	0.857	0.125	18	17,973,918	LOC100128893	3'-downstream	26,939
rs26953	1.78E-04	-0.233	0.857	0.326	5	59,850,071	PART1	intron	0
rs524905	1.80E-04	0.231	0.857	0.155	5	152,862,559	GRIA1	intron	0
rs4707367	1.80E-04	-0.232	0.857	0.307	6	88,157,907	C6orf165	5'-upstream	16,533
rs2848848	1.80E-04	0.231	0.857	0.215	7	13,733,664	LOC100131022	3'-downstream	126,841
rs1516980	1.80E-04	0.231	0.857	0.332	8	129,587,463	PVT1	3'-downstream	404,782
rs12227066	1.80E-04	-0.231	0.857	0.336	12	76,749,241	NAV3	5'-UTR	0
rs26154	1.81E-04	0.232	0.857	0.442	5	11,546,913	CTNND2	intron	0
rs11955532	1.81E-04	-0.231	0.857	0.200	5	62,016,738	IPO11	3'-downstream	56,573
rs10850803	1.82E-04	0.231	0.857	0.117	12	116,166,212	NOS1	intron	0
rs11982022	1.82E-04	0.231	0.857	0.098	7	66,525,876	STAG3L4	3'-downstream	101,928
rs6858372	1.83E-04	-0.231	0.857	0.409	4	146,413,132	LOC100131639	5'-upstream	22,659
rs8016418	1.83E-04	0.230	0.857	0.170	14	69,868,042	C14orf112	intron	0
rs9864031	1.83E-04	-0.230	0.857	0.153	3	13,883,072	WNT7A	intron	0
rs17044859	1.84E-04	0.230	0.857	0.061	2	23,221,744	KLHL29	5'-upstream	237,459
rs11604121	1.84E-04	0.230	0.857	0.052	11	9,090,321	FLJ46111	3'-downstream	16,154
rs9895521	1.85E-04	-0.231	0.857	0.404	17	47,461,994	CA10	intron	0
rs10133631	1.88E-04	-0.230	0.857	0.421	14	95,089,084	GLRX5	3'-downstream	8,276
rs2835133	1.88E-04	0.231	0.857	0.289	21	36,055,327	RPS20P1	5'-upstream	35,893

rs17710575	1.88E-04	0.230	0.857	0.208	4	6,146,988	JAKMIP1	intron	0
rs6851839	1.88E-04	0.230	0.857	0.094	4	153,432,222	FBXW7	3'-downstream	29,638
rs1130790	1.88E-04	0.230	0.857	0.348	1	200,235,705	RNPEP	synonymous	0
rs1698889	1.89E-04	0.230	0.857	0.353	11	19,285,890	LOC390102	5'-upstream	32,499
rs17058081	1.89E-04	0.230	0.857	0.096	18	71,619,416	C18orf62	5'-upstream	350,839
rs10028068	1.89E-04	-0.230	0.857	0.426	4	66,479,717	LOC728048	5'-upstream	162,666
rs4951401	1.90E-04	0.230	0.857	0.184	1	202,804,271	MDM4	3'-downstream	17,922
rs11108379	1.90E-04	0.230	0.857	0.085	12	94,940,019	LTA4H	intron	0
rs17025033	1.90E-04	0.230	0.857	0.085	12	94,924,591	LTA4H	intron	0
rs12496773	1.93E-04	0.231	0.865	0.323	3	88,448,386	LOC344653	5'-upstream	610
rs1543780	1.94E-04	0.230	0.865	0.199	22	20,878,522	IGLVV-58	Unknown	--
rs4631019	1.94E-04	-0.230	0.865	0.489	4	148,586,417	LOC100130537	5'-upstream	19,464
rs9614763	1.95E-04	0.229	0.865	0.051	22	44,475,636	ATXN10	intron	0
rs12923661	1.96E-04	0.231	0.865	0.055	16	10,018,192	GRIN2A	intron	0
rs10898852	1.98E-04	-0.231	0.865	0.266	11	71,960,572	PDE2A	3'-downstream	4,261
rs17734670	1.98E-04	0.229	0.865	0.294	15	23,390,489	ATP10A	3'-downstream	84,463
rs2786723	1.99E-04	-0.230	0.865	0.230	1	197,787,994	LOC647202	3'-downstream	163,768
rs10051752	1.99E-04	-0.229	0.865	0.085	5	154,966,485	LOC100131033	3'-downstream	113,131
rs1523250	1.99E-04	0.230	0.865	0.080	8	3,789,239	CSMD1	intron	0
rs2772227	2.00E-04	0.229	0.865	0.152	1	202,882,023	LRRN2	intron	0
rs1929409	2.00E-04	0.229	0.865	0.245	9	11,942,643	LOC100049717	5'-upstream	334,680
rs6897849	2.00E-04	0.229	0.865	0.303	5	2,342,420	LOC100133292	3'-downstream	292,878
rs1105297	2.02E-04	-0.232	0.867	0.491	1	43,184,183	SLC2A1	intron	0
rs746168	2.03E-04	0.229	0.867	0.226	11	74,669,915	ARRB1	intron	0
rs10494959	2.04E-04	0.229	0.867	0.074	1	211,743,516	LOC643330	5'-upstream	28,312
rs165890	2.04E-04	0.229	0.867	0.188	22	15,708,627	ZNF402P	3'-downstream	9,399
rs165778	2.04E-04	0.229	0.867	0.174	22	15,699,156	CECR8	3'-downstream	8,931
rs4463400	2.06E-04	0.229	0.867	0.148	8	141,289,178	NIBP	intron	0
rs6784029	2.06E-04	0.229	0.867	0.217	3	189,462,427	LPP	intron	0

rs425545	2.07E-04	0.229	0.867	0.065	2	70,657,975	TGFA	5'-upstream	23,362
rs1877475	2.07E-04	0.229	0.867	0.184	13	95,335,275	UGCGL2	intron	0
rs9995176	2.07E-04	0.229	0.867	0.469	4	74,395,848	ANKRD17	5'-upstream	52,482
rs751210	2.08E-04	-0.229	0.867	0.482	1	43,183,446	SLC2A1	intron	0
rs718387	2.09E-04	0.232	0.870	0.337	21	36,049,947	RPS20P1	5'-upstream	30,513
rs4283786	2.11E-04	0.229	0.871	0.335	5	122,128,949	SNX2	5'-upstream	9,700
rs17031611	2.12E-04	0.229	0.871	0.196	2	66,216,728	LOC729348	5'-upstream	247,214
rs2776278	2.13E-04	-0.229	0.871	0.284	21	36,264,569	RPL23AP3	3'-downstream	45,524
rs6501930	2.13E-04	-0.229	0.871	0.138	17	72,520,666	MGAT5B	3'-downstream	62,600
rs2279120	2.13E-04	0.232	0.871	0.112	8	99,115,216	MATN2	intron	0
rs1450706	2.13E-04	0.229	0.871	0.140	14	87,418,971	GALC	3'-downstream	50,140
rs2348168	2.14E-04	-0.230	0.872	0.452	4	160,444,786	RAPGEF2	intron	0
rs11643459	2.15E-04	0.228	0.872	0.278	16	77,355,588	WVOX	intron	0
rs540375	2.16E-04	0.228	0.872	0.157	5	152,858,920	GRIA1	intron	0
rs2862465	2.22E-04	0.228	0.891	0.439	11	42,336,068	LOC387761	5'-upstream	103,940
rs2885552	2.23E-04	0.227	0.891	0.096	7	77,909,577	MAGI2	intron	0
rs8064932	2.23E-04	-0.228	0.891	0.167	17	65,095,146	MAP2K6	3'-downstream	45,081
rs17698900	2.23E-04	0.227	0.891	0.054	10	49,616,272	LOC100132924	3'-downstream	6,981
rs17616659	2.26E-04	-0.228	0.891	0.130	14	82,230,662	ENSAP2	5'-upstream	1,285
rs2631271	2.28E-04	-0.227	0.891	0.310	4	103,133,419	BANK1	intron	0
rs5945353	2.28E-04	0.228	0.891	0.101	23	152,720,129	PDZD4	3'-downstream	688
rs1949593	2.29E-04	-0.227	0.891	0.413	12	76,686,005	NAV3	5'-upstream	63,195
rs943560	2.31E-04	0.227	0.891	0.462	13	95,649,825	HS6ST3	intron	0
rs10030475	2.31E-04	0.227	0.891	0.350	4	70,842,360	CSN1S1	missense	0
rs12119699	2.31E-04	0.227	0.891	0.348	1	200,239,578	RNPEP	intron	0
rs2819358	2.31E-04	0.227	0.891	0.348	1	200,243,025	ELF3	5'-upstream	671
rs1329631	2.31E-04	0.227	0.891	0.307	1	202,883,013	LRRN2	intron	0
rs6756848	2.32E-04	0.227	0.891	0.191	2	66,215,108	LOC729348	5'-upstream	248,834
rs2043166	2.32E-04	0.230	0.891	0.074	18	64,902,308	CCDC102B	3'-downstream	28,902

rs37846	2.32E-04	0.227	0.891	0.168	16	3,318,451	ZNF75A	3'-downstream	9,876
rs10959554	2.33E-04	0.227	0.891	0.076	9	11,121,371	LOC646114	3'-downstream	91,086
rs4474187	2.33E-04	-0.227	0.891	0.188	23	89,042,895	LOC360018	3'-downstream	7,681
rs725224	2.33E-04	0.227	0.891	0.076	12	13,453,789	C12orf36	5'-upstream	32,877
rs9309382	2.34E-04	0.227	0.891	0.202	2	66,218,009	LOC729348	5'-upstream	245,933
rs9937123	2.35E-04	0.227	0.891	0.060	16	86,296,990	KLHDC4	3'-downstream	1,929
rs17131659	2.36E-04	0.227	0.891	0.388	1	84,631,560	UOX	intron	0
rs2981317	2.37E-04	0.227	0.891	0.200	8	35,069,374	LOC100133273	3'-downstream	217,603
rs10943011	2.37E-04	0.227	0.891	0.170	6	73,166,765	RIMS1	intron	0
rs11973006	2.38E-04	0.226	0.891	0.253	7	40,604,890	C7orf10	intron	0
rs7040113	2.38E-04	0.226	0.891	0.202	9	3,413,469	RFX3	intron	0
rs12114930	2.41E-04	0.226	0.900	0.430	8	102,621,763	GRHL2	intron	0
rs2717200	2.43E-04	0.232	0.902	0.247	4	112,745,218	LOC132719	5'-upstream	472,872
rs2329152	2.43E-04	0.226	0.902	0.238	13	79,509,454	LOC729479	3'-downstream	10,655
rs17058093	2.43E-04	0.227	0.902	0.083	18	71,620,850	C18orf62	5'-upstream	352,273
rs557874	2.45E-04	0.226	0.904	0.181	9	134,364,266	RP11-738I14.8	intron	0
rs5969778	2.46E-04	-0.227	0.906	0.409	23	16,808,998	RNU4P6	5'-upstream	5,634
rs9928219	2.47E-04	0.226	0.907	0.082	16	5,991,449	A2BP1	5'-upstream	17,684
rs17344511	2.48E-04	-0.226	0.907	0.094	1	165,421,751	LOC391130	5'-upstream	23,053
rs2480679	2.51E-04	0.226	0.919	0.179	1	165,674,141	CD247	intron	0
rs1878269	2.53E-04	0.226	0.923	0.119	3	56,454,506	ERC2	intron	0
rs12127605	2.55E-04	0.228	0.925	0.066	1	120,029,707	PHGDH	5'-upstream	26,326
rs17024410	2.56E-04	-0.226	0.926	0.100	1	213,439,776	KCNK2	intron	0
rs290255	2.58E-04	0.227	0.929	0.168	9	92,691,478	SYK	intron	0
rs10513226	2.58E-04	0.226	0.929	0.144	3	145,065,153	LOC257039	intron	0
rs2836257	2.58E-04	-0.227	0.929	0.419	21	38,557,419	LOC441964	intron	0
rs7720273	2.60E-04	-0.226	0.931	0.230	5	113,130,084	YTHDC2	3'-downstream	171,204
rs11006349	2.62E-04	-0.225	0.932	0.392	10	60,457,808	LOC644871	3'-downstream	108,580
rs10516939	2.63E-04	0.225	0.932	0.076	4	94,793,723	GRID2	intron	0

rs1435480	2.63E-04	0.225	0.932	0.076	4	94,769,500	GRID2	intron	0
rs1028182	2.65E-04	0.225	0.932	0.406	1	205,068,502	IL19	intron	0
rs10077572	2.66E-04	0.225	0.932	0.374	5	132,775,906	FSTL4	intron	0
rs780256	2.67E-04	0.225	0.932	0.288	1	231,809,726	KCNK1	5'-upstream	6,647
rs16993361	2.68E-04	0.225	0.932	0.255	22	43,834,071	PHF21B	5'-upstream	49,826
rs4725434	2.69E-04	-0.225	0.932	0.342	7	151,131,312	PRKAG2	intron	0
rs7038965	2.70E-04	0.225	0.932	0.099	9	111,004,281	EPB41L4B	intron	0
rs710310	2.70E-04	0.226	0.932	0.443	14	98,719,466	BCL11B	intron	0
rs1624327	2.71E-04	0.224	0.932	0.255	9	86,619,110	NTRK2	3'-UTR	0
rs13282927	2.71E-04	0.226	0.932	0.212	8	35,031,277	LOC100133273	3'-downstream	179,506
rs17078688	2.72E-04	0.225	0.932	0.054	6	117,394,116	RFXDC1	3'-downstream	34,109
rs841571	2.72E-04	-0.225	0.932	0.375	1	43,208,491	SLC2A1	5'-upstream	11,403
rs4936507	2.74E-04	0.224	0.932	0.067	11	119,439,773	TRIM29	3'-downstream	47,431
rs11823347	2.75E-04	0.225	0.932	0.084	11	21,170,916	NELL1	intron	0
rs11788925	2.76E-04	0.224	0.932	0.056	9	134,038,799	NTNG2	intron	0
rs953809	2.77E-04	0.225	0.932	0.177	1	165,670,249	CD247	intron	0
rs10506759	2.77E-04	-0.224	0.932	0.426	12	76,670,293	NAV3	5'-upstream	78,907
rs11665524	2.77E-04	0.224	0.932	0.088	18	2,968,535	LPIN2	intron	0
rs6778788	2.77E-04	0.229	0.932	0.321	3	88,422,500	LOC344653	5'-upstream	26,496
rs17714061	2.78E-04	0.224	0.932	0.076	7	39,613,030	RALA	5'-upstream	16,657
rs3114315	2.80E-04	-0.224	0.932	0.357	7	76,719,919	CCDC146	intron	0
rs12677635	2.80E-04	0.224	0.932	0.235	8	88,687,271	LOC642461	5'-upstream	4,113
rs17475516	2.82E-04	0.224	0.932	0.173	14	69,902,232	SYNJ2BP	3'-downstream	734
rs17125238	2.82E-04	-0.224	0.932	0.484	1	101,959,532	RP11-556K13.1	3'-downstream	47,413
rs7556071	2.83E-04	0.225	0.932	0.060	1	188,241,377	LOC647132	Unknown	--
rs11620973	2.84E-04	0.225	0.932	0.400	14	95,087,805	GLRX5	3'-downstream	6,997
rs17031608	2.85E-04	0.224	0.932	0.205	2	66,216,670	LOC729348	5'-upstream	247,272
rs3848333	2.85E-04	0.225	0.932	0.055	16	10,025,056	GRIN2A	intron	0
rs10982373	2.85E-04	0.224	0.932	0.411	9	116,503,083	LOC100129633	intron	0

rs13127174	2.86E-04	0.224	0.932	0.157	4	16,137,569	LDB2	intron	0
rs2816600	2.87E-04	0.224	0.932	0.139	1	43,039,717	CCDC23	3'-downstream	5,603
rs655741	2.87E-04	0.224	0.932	0.139	1	43,046,340	CCDC23	intron	0
rs6441728	2.87E-04	0.224	0.932	0.354	3	104,551,408	LOC644681	3'-downstream	188,760
rs10492841	2.87E-04	-0.224	0.932	0.342	16	6,679,934	A2BP1	intron	0
rs6990941	2.89E-04	-0.223	0.932	0.301	8	89,713,547	LOC100129100	3'-downstream	146,108
rs6965558	2.89E-04	0.228	0.932	0.352	7	1,518,964	INTS1	5'-upstream	5,765
rs6948724	2.90E-04	0.223	0.932	0.255	7	40,622,800	C7orf10	intron	0
rs4245739	2.90E-04	0.223	0.932	0.188	1	202,785,465	MDM4	3'-UTR	0
rs1654531	2.91E-04	0.225	0.932	0.241	19	56,167,461	KLK7	3'-downstream	4,080
rs12080720	2.92E-04	-0.224	0.932	0.462	1	115,823,107	LOC100132332	5'-upstream	85,419
rs10774976	2.93E-04	0.224	0.932	0.098	12	116,922,846	RFC5	5'-upstream	16,047
rs7430477	2.93E-04	0.224	0.932	0.447	3	38,740,494	SCN10A	intron	0
rs10841186	2.94E-04	0.224	0.932	0.249	12	8,345,682	LOC100130149	3'-downstream	27,554
rs2498667	2.95E-04	0.223	0.932	0.251	6	139,472,289	HECA	5'-upstream	25,653
rs7717457	2.95E-04	-0.223	0.932	0.310	5	40,923,538	C7	5'-upstream	21,818
rs6884002	2.96E-04	-0.223	0.932	0.099	5	154,872,015	LOC100131033	3'-downstream	18,661
rs957583	2.97E-04	0.223	0.932	0.120	23	108,979,979	LOC392520	5'-upstream	3,220
rs1400558	2.97E-04	-0.223	0.932	0.419	4	148,600,255	EDNRA	5'-upstream	21,320
rs1400560	2.97E-04	-0.223	0.932	0.419	4	148,599,582	EDNRA	5'-upstream	21,993
rs3826884	2.98E-04	0.223	0.932	0.139	19	60,429,993	TMEM86B	3'-UTR	0
rs717695	2.98E-04	-0.223	0.932	0.408	4	156,634,854	TRNAL-UAA	5'-upstream	30,352
rs11587357	3.00E-04	0.223	0.932	0.074	1	95,890,849	LOC729977	5'-upstream	334,442
rs11703864	3.00E-04	0.223	0.932	0.166	22	26,240,759	MIN1	3'-downstream	233,506
rs6962918	3.01E-04	0.223	0.932	0.126	7	36,081,241	PP13004	5'-upstream	3,978
rs17253026	3.01E-04	0.223	0.932	0.136	14	51,899,472	PTGER2	3'-downstream	34,398
rs11249617	3.01E-04	0.223	0.932	0.341	5	178,590,767	ADAMTS2	intron	0
rs6840083	3.01E-04	0.223	0.932	0.421	4	183,701,671	ODZ3	intron	0
rs1893636	3.04E-04	0.224	0.932	0.427	18	57,282,780	CDH20	5'-upstream	25,975

rs6804165	3.06E-04	0.223	0.932	0.107	3	11,016,808	SLC6A1	intron	0
rs7688236	3.06E-04	0.223	0.932	0.099	4	87,023,102	ARHGAP24	intron	0
rs10133760	3.06E-04	-0.223	0.932	0.388	14	95,088,964	GLRX5	3'-downstream	8,156
rs1712563	3.08E-04	0.222	0.932	0.352	3	108,135,110	LOC100128733	3'-downstream	84,301
rs10937476	3.08E-04	0.223	0.932	0.255	3	192,514,654	CCDC50	5'-upstream	14,914
rs7539399	3.08E-04	0.222	0.932	0.269	1	202,856,667	LRRN2	intron	0
rs16531	3.09E-04	0.223	0.932	0.252	17	34,603,181	CACNB1	intron	0
rs11848605	3.11E-04	0.224	0.932	0.241	14	43,266,962	ARHGAP16P	3'-downstream	131,674
rs39637	3.13E-04	0.222	0.932	0.253	3	22,842,432	LOC100129341	5'-upstream	78,195
rs7432616	3.13E-04	0.222	0.932	0.153	3	117,908,124	LOC285194	5'-upstream	5,904
rs7758611	3.14E-04	0.222	0.932	0.078	6	54,407,429	TINAG	3'-downstream	44,557
rs11849993	3.14E-04	0.223	0.932	0.243	14	43,268,583	ARHGAP16P	3'-downstream	133,295
rs28410948	3.15E-04	-0.222	0.932	0.469	1	19,061,043	ALDH4A1	3'-downstream	9,470
rs2503661	3.16E-04	0.222	0.932	0.222	6	92,817,083	LOC100129847	5'-upstream	234,231
rs2819360	3.17E-04	0.222	0.932	0.341	1	200,243,877	ELF3	5'-UTR	0
rs644809	3.18E-04	0.222	0.932	0.264	9	198,549	C9orf66	3'-downstream	4,913
rs2139108	3.18E-04	-0.222	0.932	0.267	16	78,827,814	LOC729847	intron	0
rs4697063	3.19E-04	0.222	0.932	0.359	4	24,147,671	DHX15	intron	0
rs2521676	3.19E-04	0.223	0.932	0.287	16	26,802,777	C16orf82	5'-upstream	182,752
rs6892211	3.19E-04	0.222	0.932	0.096	5	8,557,567	LOC729506	5'-upstream	42,799
rs4733581	3.20E-04	-0.222	0.932	0.371	8	129,016,957	PVT1	intron	0
rs7050429	3.20E-04	0.224	0.932	0.147	23	110,743,608	LOC643873	3'-downstream	4,662
rs10222063	3.21E-04	-0.222	0.932	0.310	21	41,216,672	DSCAM	5'-upstream	75,763
rs6869955	3.23E-04	0.222	0.932	0.099	5	55,400,449	ANKRD55	3'-downstream	30,815
rs9478311	3.23E-04	-0.222	0.932	0.413	6	150,328,828	ULBP1	intron	0
rs2501830	3.24E-04	0.222	0.932	0.119	23	108,965,630	LOC392520	5'-upstream	17,569
rs966951	3.24E-04	0.222	0.932	0.119	23	108,979,489	LOC392520	5'-upstream	3,710
rs2743218	3.24E-04	0.222	0.932	0.388	1	18,866,737	PAX7	intron	0
rs11025102	3.24E-04	0.222	0.932	0.332	11	19,307,344	LOC390102	5'-upstream	53,953

rs6449478	3.26E-04	-0.224	0.932	0.267	5	59,909,466	DEPDC1B	3'-downstream	19,030
rs2455377	3.26E-04	-0.222	0.932	0.484	5	55,956,448	LOC441073	5'-upstream	119,755
rs3915861	3.26E-04	0.222	0.932	0.368	9	78,082,346	LOC100133206	3'-downstream	8,884
rs16942674	3.27E-04	0.222	0.932	0.063	17	53,542,806	DYNLL2	3'-downstream	20,996
rs1872366	3.28E-04	0.225	0.932	0.169	12	30,580,467	IPO8	3'-downstream	92,722
rs2812617	3.29E-04	0.221	0.932	0.123	10	34,113,351	PAR3	3'-downstream	326,752
rs3910572	3.29E-04	-0.221	0.932	0.397	13	79,518,672	LOC729485	3'-downstream	8,738
rs812086	3.30E-04	0.222	0.932	0.353	11	19,279,293	LOC390102	5'-upstream	25,902
rs6578080	3.31E-04	0.222	0.932	0.228	8	141,291,830	NIBP	intron	0
rs6489900	3.31E-04	-0.222	0.932	0.357	12	112,439,970	LHX5	5'-upstream	45,710
rs7061836	3.32E-04	0.221	0.932	0.152	23	110,733,178	LOC643873	3'-downstream	15,092
rs1376071	3.35E-04	-0.221	0.932	0.422	15	35,027,798	MEIS2	intron	0
rs17151081	3.35E-04	0.222	0.932	0.101	7	76,755,796	CCDC146	intron	0
rs6979107	3.36E-04	-0.223	0.932	0.147	7	64,508,216	ZNF92	3'-downstream	4,783
rs1220854	3.36E-04	0.222	0.932	0.498	4	70,846,893	CSN2	3'-downstream	8,671
rs12621560	3.36E-04	0.222	0.932	0.478	2	74,787,875	SEMA4F	3'-downstream	25,182
rs2243668	3.37E-04	0.221	0.932	0.157	10	33,603,899	NRP1	intron	0
rs7100693	3.37E-04	0.221	0.932	0.063	10	64,590,594	JMJD1C	3'-downstream	6,397
rs6567819	3.44E-04	0.221	0.932	0.119	23	108,991,343	LOC392520	3'-downstream	7,539
rs283128	3.46E-04	0.221	0.932	0.464	5	32,102,829	PDZD2	intron	0
rs10962837	3.46E-04	-0.221	0.932	0.312	9	1,704,649	SMARCA2	5'-upstream	300,693
rs881790	3.46E-04	0.221	0.932	0.195	4	16,147,055	LDB2	intron	0
rs4455605	3.47E-04	0.221	0.932	0.265	5	40,184,520	LOC285634	5'-upstream	391,073
rs1946944	3.47E-04	0.221	0.932	0.218	8	96,171,901	LOC100130098	5'-upstream	16,876
rs4734298	3.47E-04	0.221	0.932	0.218	8	96,170,962	LOC100130098	5'-upstream	15,937
rs10124468	3.48E-04	0.221	0.932	0.115	9	11,235,830	LOC646114	3'-downstream	205,545
rs17060993	3.48E-04	0.221	0.932	0.058	8	26,978,029	LOC100132229	5'-upstream	52,134
rs11696891	3.48E-04	-0.221	0.932	0.422	20	54,876,477	PTMAP6	5'-upstream	166,484
rs994772	3.49E-04	0.225	0.932	0.143	4	100,546,687	ADH7	3'-downstream	5,754

rs1469095	3.49E-04	-0.221	0.932	0.293	5	62,019,604	IPO11	3'-downstream	59,439
rs2777508	3.49E-04	0.223	0.932	0.119	10	34,112,449	PAR3	3'-downstream	327,654
rs8053650	3.50E-04	-0.220	0.932	0.222	16	11,450,946	LOC400499	intron	0
rs10805350	3.50E-04	0.222	0.932	0.313	4	16,140,499	LDB2	intron	0
rs4845144	3.50E-04	0.222	0.932	0.458	1	205,083,271	IL19	3'-downstream	324
rs1755938	3.51E-04	0.220	0.932	0.182	9	92,684,769	SYK	intron	0
rs10833372	3.51E-04	0.221	0.932	0.478	11	20,628,328	SLC6A5	intron	0
rs1477357	3.51E-04	-0.220	0.932	0.206	5	62,003,267	IPO11	3'-downstream	43,102
rs12494229	3.52E-04	0.221	0.932	0.317	3	190,356,633	LOC100132319	5'-upstream	5,014
rs649870	3.52E-04	-0.220	0.932	0.469	11	118,476,461	DPAGT1	intron	0
rs17616768	3.52E-04	-0.220	0.932	0.130	14	82,235,273	ENSAP2	5'-upstream	5,896
rs12581982	3.53E-04	0.221	0.932	0.076	12	13,452,773	C12orf36	5'-upstream	31,861
rs6492840	3.53E-04	0.220	0.932	0.464	13	95,637,435	HS6ST3	intron	0
rs2305089	3.54E-04	-0.222	0.932	0.418	6	166,499,260	T	missense	0
rs6678565	3.54E-04	-0.220	0.932	0.087	1	213,429,084	KCNK2	intron	0
rs7657364	3.55E-04	0.220	0.932	0.419	4	24,181,029	DHX15	intron	0
rs11135305	3.56E-04	0.220	0.932	0.065	5	163,529,934	LOC391844	5'-upstream	402,292
rs6500550	3.57E-04	0.221	0.932	0.486	16	3,686,242	TRAP1	intron	0
rs6907305	3.57E-04	0.220	0.932	0.121	6	21,505,616	CDKAL1	3'-downstream	165,873
rs12606882	3.57E-04	0.221	0.932	0.404	18	27,743,193	KIAA1012	intron	0
rs4634366	3.59E-04	-0.222	0.932	0.272	5	169,523,385	KRT18P41	5'-upstream	14,507
rs7939727	3.59E-04	0.220	0.932	0.061	11	11,734,325	USP47	5'-upstream	85,221
rs7397057	3.59E-04	-0.220	0.932	0.422	12	131,201,474	NOC4L	intron	0
rs17379645	3.60E-04	0.221	0.932	0.058	1	162,614,736	LOC729952	3'-downstream	20,655
rs11252650	3.61E-04	0.222	0.932	0.097	10	4,704,053	LOC338588	3'-downstream	9,442
rs1155097	3.63E-04	0.220	0.932	0.233	4	156,634,165	TRNAL-UAA	5'-upstream	29,663
rs10518301	3.64E-04	-0.220	0.932	0.339	4	120,454,573	FABP2	3'-downstream	3,280
rs290226	3.65E-04	0.220	0.932	0.178	9	92,677,103	SYK	intron	0
rs6578084	3.66E-04	-0.220	0.932	0.366	8	141,311,849	NIBP	intron	0

rs10494457	3.66E-04	0.220	0.932	0.254	1	164,528,747	LOC284685	5'-upstream	15,240
rs7552585	3.67E-04	-0.220	0.932	0.097	1	203,675,794	MIRN135B	3'-downstream	8,259
rs1861595	3.67E-04	-0.220	0.932	0.395	12	15,552,491	PTPRO	intron	0
rs2631246	3.67E-04	0.220	0.932	0.356	4	103,098,344	BANK1	intron	0
rs12650712	3.68E-04	0.220	0.932	0.159	4	165,672,051	LOC100133261	5'-upstream	65,239
rs3091377	3.68E-04	-0.220	0.932	0.101	22	38,527,581	ENTHD1	intron	0
rs2835680	3.69E-04	0.220	0.932	0.415	21	37,526,440	DSCR3	intron	0
rs16878245	3.69E-04	-0.220	0.932	0.137	4	10,730,190	LOC643446	5'-upstream	241,891
rs9806917	3.71E-04	0.220	0.936	0.054	16	23,298,357	SCNN1B	intron	0
rs16907672	3.72E-04	0.220	0.936	0.089	11	21,184,140	NELL1	intron	0
rs10965572	3.73E-04	0.219	0.936	0.191	9	23,032,805	LOC646609	3'-downstream	294,529
rs9651539	3.73E-04	-0.219	0.936	0.341	10	13,519,502	C10orf30	3'-downstream	988
rs12581742	3.75E-04	0.220	0.938	0.074	12	13,453,060	C12orf36	5'-upstream	32,148
rs2842721	3.76E-04	0.220	0.939	0.396	1	205,254,830	C1orf116	3'-downstream	3,659
rs13114034	3.80E-04	0.219	0.944	0.076	4	6,575,335	PPP2R2C	5'-upstream	50,108
rs17397811	3.81E-04	0.220	0.944	0.373	8	102,618,040	GRHL2	intron	0
rs1552290	3.81E-04	-0.219	0.944	0.179	1	101,873,811	RP11-556K13.1	3'-downstream	133,134
rs3848332	3.81E-04	0.220	0.944	0.058	16	10,025,038	GRIN2A	intron	0
rs2467383	3.82E-04	0.219	0.944	0.278	11	34,153,060	ABTB2	intron	0
rs6918518	3.83E-04	-0.222	0.944	0.487	6	158,850,684	TULP4	3'-UTR	0
rs2922388	3.84E-04	-0.222	0.944	0.101	8	137,005,767	KHDRBS3	3'-downstream	276,736
rs11627491	3.85E-04	-0.220	0.944	0.113	14	82,278,510	LOC730105	3'-downstream	46,045
rs2969778	3.86E-04	0.219	0.944	0.164	2	47,759,696	LOC285053	3'-downstream	11,587
rs12546486	3.86E-04	0.219	0.944	0.327	8	95,195,882	CDH17	3'-downstream	12,684
rs856119	3.86E-04	0.220	0.944	0.195	1	157,166,371	PYHIN1	5'-upstream	1,595
rs7690945	3.86E-04	-0.221	0.944	0.425	4	155,213,440	DCHS2	3'-downstream	161,698
rs10509583	3.88E-04	0.219	0.944	0.097	10	91,634,406	hCG 2024094	3'-downstream	46,965
rs12932835	3.90E-04	0.219	0.944	0.058	16	10,019,526	GRIN2A	intron	0
rs1046623	3.92E-04	0.219	0.944	0.372	16	83,157,772	COTL1	3'-UTR	0

rs1328379	3.95E-04	0.219	0.944	0.170	6	165,923,631	PDE10A	intron	0
rs12291695	3.95E-04	-0.219	0.944	0.317	11	12,752,238	TEAD1	intron	0
rs9324519	3.96E-04	-0.219	0.944	0.375	8	141,312,047	NIBP	intron	0
rs5888	3.97E-04	0.221	0.944	0.304	12	123,850,701	SCARB1	synonymous	0
rs2883036	3.99E-04	-0.221	0.944	0.361	1	205,091,385	IL19	3'-downstream	8,438
rs1426227	3.99E-04	0.219	0.944	0.107	18	2,157,478	LOC100128360	5'-upstream	235,792
rs11643910	3.99E-04	0.218	0.944	0.065	16	80,997,215	CDH13	5'-upstream	220,864
rs1032915	4.02E-04	0.218	0.944	0.397	18	73,608,817	BDP1P	5'-upstream	330,525
rs2381623	4.02E-04	-0.218	0.944	0.339	9	7,502,409	LOC158345	5'-upstream	34,028
rs12331227	4.02E-04	-0.221	0.944	0.463	4	30,827,466	LOC645716	3'-downstream	5,071
rs870522	4.02E-04	0.218	0.944	0.363	14	51,028,639	FRMD6	intron	0
rs12154459	4.02E-04	0.219	0.944	0.316	7	145,885,441	CNTNAP2	intron	0
rs1528474	4.03E-04	0.218	0.944	0.150	15	53,130,237	C15orf15	3'-downstream	130,567
rs1699195	4.04E-04	0.218	0.944	0.072	1	211,596,070	LOC643330	3'-downstream	72,604
rs1455096	4.04E-04	0.218	0.944	0.287	6	67,460,312	NUFIP1P	5'-upstream	598,780
rs895851	4.04E-04	-0.218	0.944	0.110	8	137,012,462	KHDRBS3	3'-downstream	283,431
rs16944718	4.04E-04	-0.219	0.944	0.133	17	11,274,781	FLJ45455	intron	0
rs16952353	4.05E-04	0.219	0.944	0.112	17	2,588,038	LOC100128142	5'-upstream	2,849
rs999787	4.06E-04	0.219	0.944	0.158	15	53,079,743	C15orf15	3'-downstream	181,061
rs1379694	4.06E-04	0.219	0.944	0.346	3	88,448,629	LOC344653	5'-upstream	367
rs431791	4.07E-04	0.218	0.944	0.179	9	135,841,095	VAV2	intron	0
rs1413730	4.07E-04	0.218	0.944	0.065	6	117,389,088	RFXDC1	3'-downstream	29,081
rs9979015	4.09E-04	0.218	0.944	0.278	21	35,157,438	RUNX1	intron	0
rs9866355	4.09E-04	0.218	0.944	0.356	3	117,909,276	LOC285194	5'-upstream	4,752
rs3886706	4.09E-04	0.218	0.944	0.491	1	111,590,302	CHI3L2	3'-downstream	2,717
rs17047903	4.12E-04	0.218	0.944	0.428	3	68,785,403	PSMC1P	3'-downstream	16,220
rs302828	4.12E-04	-0.219	0.944	0.117	19	61,102,152	NLRP13	intron	0
rs10499617	4.16E-04	0.219	0.944	0.049	7	40,749,097	C7orf10	intron	0
rs4733583	4.16E-04	-0.218	0.944	0.379	8	129,017,407	PVT1	intron	0

rs11731134	4.17E-04	-0.218	0.944	0.491	4	148,599,064	EDNRA	5'-upstream	22,511
rs4835405	4.17E-04	-0.218	0.944	0.491	4	148,598,134	EDNRA	5'-upstream	23,441
rs10117265	4.18E-04	0.218	0.944	0.110	9	100,135,923	GABBR2	intron	0
rs4384204	4.18E-04	-0.219	0.944	0.345	1	213,478,228	KCNK2	3'-downstream	1,169
rs12678629	4.19E-04	0.218	0.944	0.215	8	35,025,990	LOC100133273	3'-downstream	174,219
rs7547418	4.19E-04	0.218	0.944	0.233	1	164,542,624	LOC284685	5'-upstream	29,117
rs4953672	4.20E-04	-0.220	0.944	0.482	2	42,953,942	LOC100128048	5'-upstream	45,681
rs10900418	4.20E-04	0.218	0.944	0.309	1	202,880,789	LRRN2	intron	0
rs7920683	4.21E-04	0.218	0.944	0.435	10	20,429,242	PLXDC2	intron	0
rs7157515	4.21E-04	0.218	0.944	0.128	14	53,558,366	LOC645560	5'-upstream	29,903
rs6901033	4.21E-04	0.218	0.944	0.061	6	117,373,420	RFXDC1	3'-downstream	13,413
rs7765150	4.25E-04	0.217	0.944	0.056	6	50,271,304	DEFB112	5'-upstream	146,981
rs12810670	4.26E-04	-0.219	0.944	0.278	12	76,732,425	NAV3	5'-upstream	16,775
rs9550637	4.27E-04	-0.218	0.944	0.442	13	19,810,527	CRYL1	3'-downstream	65,279
rs11722847	4.28E-04	-0.218	0.944	0.339	4	120,452,569	FABP2	3'-downstream	5,284
rs2197164	4.29E-04	0.217	0.944	0.065	18	65,279,551	DOK6	intron	0
rs6578233	4.32E-04	-0.218	0.944	0.221	8	136,447,775	LOC286094	3'-downstream	69,795
rs247325	4.33E-04	0.218	0.944	0.276	12	14,812,901	HIST4H4	3'-downstream	2,020
rs784235	4.34E-04	-0.217	0.944	0.112	18	51,574,142	LOC100132501	3'-downstream	25,133
rs871503	4.36E-04	0.217	0.944	0.330	5	173,534,310	HMP19	3'-downstream	65,522
rs4739519	4.36E-04	0.217	0.944	0.347	8	37,532,017	LOC100128034	intron	0
rs6005031	4.40E-04	0.217	0.944	0.309	22	25,095,167	SEZ6L	intron	0
rs2387137	4.40E-04	0.217	0.944	0.375	19	55,829,472	SYT3	intron	0
rs2564942	4.41E-04	-0.217	0.944	0.430	3	53,114,546	RFT1	intron	0
rs2559658	4.42E-04	0.217	0.944	0.088	10	79,415,275	POLR3A	intron	0
rs17678419	4.44E-04	0.217	0.944	0.054	12	113,486,329	LOC652191	3'-downstream	14,280
rs7866090	4.45E-04	0.217	0.944	0.103	9	11,130,883	LOC646114	3'-downstream	100,598
rs10075142	4.46E-04	0.217	0.944	0.074	5	73,962,740	ENC1	intron	0
rs1393155	4.47E-04	-0.222	0.944	0.319	5	40,925,894	C7	5'-upstream	19,462

rs9992415	4.48E-04	-0.217	0.944	0.460	4	30,827,933	LOC645716	3'-downstream	5,538
rs7775551	4.48E-04	0.217	0.944	0.162	6	17,155,652	FLJ23152	5'-upstream	80,496
rs11190790	4.49E-04	-0.217	0.944	0.294	10	102,762,273	PDZD7	3'-downstream	4,806
rs9405834	4.50E-04	0.220	0.944	0.325	6	5,402,826	FARS2	intron	0
rs10125981	4.52E-04	0.217	0.944	0.465	9	101,735,129	STX17	intron	0
rs2839025	4.53E-04	0.216	0.944	0.458	21	46,112,881	PCBP3	intron	0
rs633959	4.54E-04	-0.217	0.944	0.388	23	120,477,514	LOC158714	5'-upstream	310,479
rs17138853	4.54E-04	0.216	0.944	0.076	5	115,450,634	COMMD10	intron	0
rs1333165	4.55E-04	0.217	0.944	0.359	13	64,944,921	STARP1	5'-upstream	161,834
rs6958942	4.55E-04	0.217	0.944	0.114	7	76,755,130	CCDC146	intron	0
rs3831958	4.55E-04	0.216	0.944	0.171	1	165,666,815	CD247	3'-UTR	0
rs13066320	4.55E-04	0.216	0.944	0.209	3	117,888,889	LOC285194	5'-upstream	25,139
rs10500136	4.58E-04	0.216	0.944	0.166	7	142,724,366	CLCN1	intron	0
rs17397776	4.58E-04	0.216	0.944	0.319	8	102,617,910	GRHL2	intron	0
rs16948648	4.58E-04	0.216	0.944	0.433	17	45,510,770	ITGA3	intron	0
rs3755913	4.59E-04	-0.216	0.944	0.137	4	81,324,786	PRDM8	5'-upstream	662
rs824725	4.60E-04	0.218	0.944	0.107	12	40,772,739	GLT8D3	intron	0
rs1286147	4.60E-04	0.217	0.944	0.261	14	90,537,320	RPS6KA5	intron	0
rs2718016	4.60E-04	0.217	0.944	0.162	7	36,051,448	LOC100129326	Unknown	--
rs9518363	4.62E-04	0.216	0.944	0.408	13	100,733,288	NALCN	intron	0
rs12632003	4.65E-04	0.216	0.944	0.303	3	72,371,435	RYBP	3'-downstream	135,003
rs6688859	4.65E-04	0.216	0.944	0.229	1	113,577,284	LOC643441	5'-upstream	26,886
rs12284447	4.66E-04	-0.216	0.944	0.097	11	4,507,612	OR52M2P	5'-upstream	13,782
rs12347985	4.66E-04	0.216	0.944	0.203	9	3,392,590	RFX3	intron	0
rs1414402	4.66E-04	0.216	0.944	0.458	9	132,911,893	LAMC3	intron	0
rs10899613	4.67E-04	0.218	0.944	0.328	11	69,570,122	LOC100127946	3'-downstream	29,518
rs6968662	4.67E-04	0.216	0.944	0.060	7	22,487,980	MGC87042	3'-downstream	4,967
rs1603165	4.68E-04	0.217	0.944	0.158	4	135,308,676	PABPC4L	3'-downstream	28,262
rs11786195	4.68E-04	0.216	0.944	0.204	8	35,020,843	LOC100133273	3'-downstream	169,072

rs9323262	4.69E-04	0.216	0.944	0.274	14	53,863,964	CDKN3	5'-upstream	69,512
rs10849083	4.69E-04	-0.217	0.944	0.185	12	4,512,833	C12orf4	intron	0
rs919676	4.70E-04	0.217	0.944	0.297	1	164,534,461	LOC284685	5'-upstream	20,954
rs11022188	4.70E-04	0.216	0.944	0.129	11	12,105,328	MICAL2	intron	0
rs35749343	4.71E-04	0.216	0.944	0.056	17	39,942,006	GPATCH8	5'-upstream	5,678
rs6474174	4.71E-04	0.217	0.944	0.078	8	39,718,465	ADAM2	3'-downstream	1,946
rs17046758	4.74E-04	-0.216	0.944	0.085	4	166,716,836	LOC402191	5'-upstream	25,192
rs6489016	4.74E-04	0.216	0.944	0.428	12	124,862,044	TMEM132B	3'-downstream	152,502
rs7846979	4.75E-04	0.216	0.944	0.424	9	116,472,765	LOC100129633	intron	0
rs10886992	4.76E-04	0.216	0.944	0.316	10	123,572,169	ATE1	intron	0
rs246274	4.77E-04	0.216	0.944	0.125	5	122,308,702	SNX24	intron	0
rs647535	4.78E-04	0.217	0.944	0.418	18	57,295,795	CDH20	5'-upstream	12,960
rs6669771	4.78E-04	-0.218	0.944	0.064	1	114,421,345	SYT6	3'-downstream	12,092
rs12145049	4.79E-04	0.215	0.944	0.114	1	202,044,364	ZC3H11A	intron	0
rs6817351	4.79E-04	0.215	0.944	0.085	4	94,761,025	GRID2	intron	0
rs6842880	4.79E-04	0.215	0.944	0.085	4	94,761,175	GRID2	intron	0
rs7945719	4.79E-04	-0.217	0.944	0.323	11	12,705,396	TEAD1	intron	0
rs12331869	4.80E-04	0.216	0.944	0.215	4	55,706,906	KDR	5'-upstream	20,387
rs12962880	4.80E-04	-0.217	0.944	0.097	18	45,714,978	MYO5B	intron	0
rs7814976	4.80E-04	-0.221	0.944	0.334	8	141,306,070	NIBP	intron	0
rs1873418	4.80E-04	0.215	0.944	0.087	3	195,146,719	LOC100128023	3'-downstream	46,724
rs12889132	4.80E-04	0.215	0.944	0.076	14	51,826,994	LOC100131689	3'-downstream	1,177
rs366178	4.80E-04	-0.215	0.944	0.462	8	8,808,564	MFHAS1	5'-upstream	20,023
rs400404	4.80E-04	-0.215	0.944	0.462	8	8,807,864	MFHAS1	5'-upstream	19,323
rs6788478	4.81E-04	0.217	0.944	0.354	3	104,561,945	LOC644681	3'-downstream	178,223
rs17095581	4.81E-04	0.215	0.944	0.056	14	97,098,999	LOC730217	intron	0
rs10468282	4.81E-04	0.215	0.944	0.135	16	53,547,149	LOC100132339	5'-upstream	15,852
rs8054030	4.81E-04	0.215	0.944	0.135	16	53,545,075	LOC100132339	5'-upstream	13,778
rs2140501	4.82E-04	0.215	0.944	0.164	2	167,911,362	hCG 1660379	intron	0

rs1627784	4.82E-04	0.215	0.944	0.338	9	86,618,686	NTRK2	3'-UTR	0
rs17138063	4.82E-04	0.216	0.944	0.181	17	32,264,382	LOC727862	3'-downstream	28,667
rs2044002	4.85E-04	-0.215	0.944	0.399	10	55,708,837	PCDH15	intron	0
rs9691998	4.86E-04	0.215	0.944	0.166	7	77,986,916	MAGI2	intron	0
rs2016644	4.86E-04	0.216	0.944	0.087	7	96,433,985	FLJ34048	3'-downstream	36,910
rs10515468	4.87E-04	0.217	0.944	0.044	5	134,572,389	H2AFY	3'-downstream	125,581
rs4129316	4.88E-04	0.218	0.944	0.172	18	20,937,539	ZNF521	intron	0
rs6490281	4.88E-04	0.215	0.944	0.392	12	118,937,209	CCDC64	intron	0
rs2110586	4.88E-04	0.215	0.944	0.099	19	17,818,309	JAK3	intron	0
rs4645284	4.91E-04	-0.215	0.944	0.469	4	118,614,104	NT5C3P1	3'-downstream	101,283
rs838623	4.92E-04	0.215	0.944	0.148	3	144,671,616	SLC9A9	intron	0
rs3740873	4.92E-04	-0.216	0.944	0.495	11	20,626,016	SLC6A5	intron	0
rs2047422	4.93E-04	0.215	0.944	0.350	1	55,484,555	LOC645506	3'-downstream	22,922
rs7142654	4.94E-04	0.215	0.944	0.087	14	88,473,343	TRNAA-AGC	5'-upstream	41,852
rs7257500	4.95E-04	0.215	0.944	0.193	19	2,570,143	GNP7	intron	0
rs7182363	4.95E-04	-0.215	0.944	0.184	15	68,295,072	TLE3	5'-upstream	117,762
rs2836994	4.95E-04	0.216	0.944	0.311	21	39,669,876	WRB	5'-upstream	4,264
rs2815832	4.95E-04	0.215	0.944	0.168	1	202,883,863	LRRN2	intron	0
rs17734826	4.96E-04	0.216	0.944	0.071	12	113,473,404	LOC652191	3'-downstream	1,355
rs33219	4.96E-04	0.218	0.944	0.165	12	30,960,265	TSPAN11	5'-upstream	10,840
rs10202724	4.97E-04	0.216	0.944	0.364	2	222,880,471	LOC440934	5'-upstream	9,168
rs13222164	4.97E-04	0.215	0.944	0.150	7	108,885,600	LOC100128056	5'-upstream	380,818
rs6432096	4.97E-04	0.215	0.944	0.383	2	10,478,834	HPCAL1	intron	0
rs2581829	4.98E-04	-0.215	0.944	0.430	3	53,108,566	RFT1	intron	0
rs10790715	4.99E-04	0.215	0.944	0.161	11	124,298,892	HEPACAM	missense	0
rs488787	5.00E-04	0.215	0.944	0.293	9	202,908	C9orf66	3'-downstream	554
rs7234341	5.00E-04	0.215	0.944	0.404	18	27,768,263	KIAA1012	intron	0
rs7234798	5.00E-04	0.215	0.944	0.404	18	27,731,401	KIAA1012	intron	0
rs838636	5.00E-04	0.215	0.944	0.146	3	144,681,492	SLC9A9	intron	0

rs838637	5.00E-04	0.215	0.944	0.146	3	144,681,741	SLC9A9	intron	0
rs9525149	5.00E-04	0.215	0.944	0.491	13	95,653,783	HS6ST3	intron	0
rs640520	5.01E-04	-0.215	0.944	0.234	11	87,646,776	CTSC	3'-downstream	19,632
rs17139455	5.03E-04	0.215	0.944	0.078	5	115,668,006	COMMD10	3'-downstream	11,126
rs17139495	5.03E-04	0.215	0.944	0.078	5	115,684,720	COMMD10	3'-downstream	27,840
rs838622	5.03E-04	0.215	0.944	0.149	3	144,671,246	SLC9A9	intron	0
rs9549100	5.03E-04	0.215	0.944	0.177	13	39,666,838	FOXO1	3'-downstream	360,963
rs7248157	5.04E-04	0.215	0.944	0.107	19	41,026,442	NPHS1	intron	0
rs6917844	5.04E-04	0.215	0.944	0.182	6	165,928,377	PDE10A	intron	0
rs2836431	5.05E-04	0.215	0.944	0.113	21	38,771,787	ERG	intron	0
rs134784	5.05E-04	-0.215	0.944	0.224	22	25,982,075	LOC100130624	5'-upstream	368,531
rs11033637	5.06E-04	-0.215	0.944	0.464	11	36,436,365	FLJ14213	intron	0
rs1256066	5.07E-04	0.215	0.944	0.193	14	63,768,644	ESR2	intron	0
rs11700554	5.08E-04	-0.215	0.944	0.435	21	46,203,918	PCBP3	3'-downstream	17,123
rs7102231	5.09E-04	0.215	0.944	0.127	11	3,359,053	LOC650368	intron	0
rs7966890	5.09E-04	0.217	0.944	0.338	12	82,112,052	LOC401725	3'-downstream	41,952
rs4786181	5.09E-04	-0.215	0.944	0.399	16	7,535,679	A2BP1	intron	0
rs9635917	5.09E-04	0.214	0.944	0.363	18	27,760,837	KIAA1012	intron	0
rs1246386	5.10E-04	0.214	0.944	0.469	1	84,639,736	DNASE2B	intron	0
rs1645519	5.10E-04	-0.216	0.944	0.267	5	40,913,936	CARD6	3'-downstream	22,723
rs5957355	5.10E-04	0.214	0.944	0.213	23	119,338,041	FAM70A	5'-upstream	8,622
rs6433815	5.11E-04	-0.214	0.944	0.368	2	180,517,361	KIAA1604	3'-downstream	488
rs17655198	5.15E-04	0.214	0.944	0.181	8	139,244,364	FAM135B	intron	0
rs11726299	5.15E-04	-0.214	0.944	0.190	4	183,556,319	ODZ3	intron	0
rs2930579	5.16E-04	0.214	0.944	0.238	15	23,392,329	ATP10A	3'-downstream	82,623
rs11004392	5.17E-04	0.220	0.944	0.091	10	56,002,909	PCDH15	intron	0
rs1227777	5.17E-04	0.214	0.944	0.097	11	21,891,492	TMEM16E	5'-upstream	279,806
rs10584	5.17E-04	-0.215	0.944	0.469	15	88,129,555	ANPEP	3'-UTR	0
rs16847359	5.18E-04	0.214	0.944	0.056	2	163,379,281	KCNH7	intron	0

rs10735299	5.18E-04	0.214	0.944	0.058	12	76,695,128	NAV3	5'-upstream	54,072
rs2249599	5.19E-04	-0.215	0.944	0.251	21	36,281,873	RPL23AP3	3'-downstream	28,220
rs2535358	5.19E-04	0.215	0.944	0.413	18	57,293,930	CDH20	5'-upstream	14,825
rs363624	5.20E-04	0.214	0.944	0.487	2	74,784,350	SEMA4F	3'-downstream	21,657
rs323719	5.22E-04	0.214	0.944	0.132	1	43,043,515	CCDC23	3'-downstream	1,805
rs4140770	5.22E-04	0.214	0.944	0.267	7	55,108,970	EGFR	intron	0
rs3927807	5.23E-04	-0.216	0.944	0.311	11	66,755,431	FBXL11	intron	0
rs12712919	5.24E-04	0.214	0.944	0.381	2	44,629,187	C2orf34	intron	0
rs139915	5.26E-04	-0.214	0.944	0.395	22	39,050,909	TNRC6B	3'-UTR	0
rs4799933	5.26E-04	-0.214	0.944	0.141	18	33,322,457	BRUNOL4	intron	0
rs3114316	5.27E-04	-0.214	0.944	0.341	7	76,720,858	CCDC146	intron	0
rs17783784	5.27E-04	-0.214	0.944	0.154	7	64,539,287	ZNF92	3'-downstream	35,854
rs1994474	5.30E-04	0.214	0.944	0.397	12	26,838,121	ITPR2	intron	0
rs4461463	5.30E-04	0.214	0.944	0.054	3	152,201,282	CLRN1	5'-upstream	27,806
rs966957	5.31E-04	0.214	0.944	0.305	17	47,543,904	CA10	intron	0
rs12921960	5.32E-04	0.214	0.944	0.209	16	6,639,750	A2BP1	intron	0
rs7695937	5.32E-04	-0.214	0.944	0.284	4	7,584,470	SORCS2	intron	0
rs7026133	5.32E-04	0.214	0.944	0.130	9	32,409,461	ACO1	intron	0
rs658312	5.33E-04	0.215	0.944	0.163	11	78,308,368	ODZ4	5'-upstream	107,535
rs271970	5.33E-04	0.214	0.944	0.373	20	57,469,557	LOC645605	intron	0
rs11771918	5.34E-04	-0.214	0.944	0.153	7	64,538,847	ZNF92	3'-downstream	35,414
rs2729076	5.35E-04	0.214	0.944	0.413	3	491,255	CHL1	3'-downstream	65,157
rs3114314	5.36E-04	-0.215	0.944	0.338	7	76,719,565	CCDC146	intron	0
rs2837002	5.36E-04	0.214	0.944	0.308	21	39,685,856	WRB	intron	0
rs10124457	5.36E-04	0.214	0.944	0.400	9	2,338,820	SMARCA2	3'-downstream	155,196
rs2226567	5.37E-04	0.214	0.944	0.179	11	105,186,923	GRIA4	intron	0
rs12612483	5.37E-04	0.214	0.944	0.193	2	122,770,055	LOC728241	3'-downstream	91,149
rs1808458	5.39E-04	0.214	0.944	0.054	2	118,595,723	INSIG2	3'-downstream	11,656
rs6948900	5.40E-04	0.214	0.944	0.289	7	40,585,520	C7orf10	intron	0

rs10088287	5.40E-04	0.216	0.944	0.068	8	39,718,049	ADAM2	3'-downstream	2,362
rs11146187	5.41E-04	0.214	0.944	0.144	10	133,771,375	JAKMIP3	intron	0
rs2143361	5.41E-04	0.214	0.944	0.402	6	9,278,882	LOC389365	3'-downstream	79,742
rs7749385	5.42E-04	0.214	0.944	0.346	6	141,350,701	LOC729076	5'-upstream	498,334
rs7090540	5.43E-04	-0.215	0.944	0.062	10	20,958,985	NEBL	3'-downstream	151,108
rs3776362	5.43E-04	0.214	0.944	0.080	5	142,379,050	ARHGAP26	intron	0
rs3934816	5.44E-04	0.213	0.944	0.399	11	11,488,807	GALNTL4	intron	0
rs857395	5.46E-04	0.214	0.944	0.433	10	55,759,269	PCDH15	intron	0
rs4606763	5.46E-04	-0.213	0.944	0.220	17	6,017,765	LOC100132641	3'-downstream	41,585
rs4357753	5.47E-04	-0.213	0.944	0.141	12	111,225,092	C12orf51	intron	0
rs2331548	5.47E-04	0.213	0.944	0.101	4	170,199,179	CBR4	5'-upstream	31,182
rs294782	5.48E-04	-0.214	0.944	0.467	3	22,858,039	LOC100129341	5'-upstream	62,588
rs2651460	5.48E-04	0.215	0.944	0.319	8	97,706,848	SDC2	3'-downstream	13,635
rs7931660	5.49E-04	0.215	0.944	0.116	11	3,356,910	ZNF195	5'-UTR	0
rs9577858	5.51E-04	0.213	0.944	0.359	13	112,549,621	ATP11A	intron	0
rs6930152	5.52E-04	0.214	0.944	0.082	6	15,830,078	DTNBP1	5'-upstream	58,828
rs4252718	5.53E-04	0.213	0.944	0.482	1	202,778,818	MDM4	intron	0
rs11081718	5.55E-04	0.213	0.944	0.404	18	27,670,175	KIAA1012	intron	0
rs10954975	5.56E-04	0.213	0.944	0.217	8	35,019,032	LOC100133273	3'-downstream	167,261
rs6887101	5.59E-04	0.213	0.944	0.335	5	122,137,106	SNX2	5'-upstream	1,543
rs1542188	5.60E-04	0.213	0.944	0.128	11	3,081,011	OSBPL5	intron	0
rs9418078	5.60E-04	0.213	0.944	0.168	10	34,077,361	PARD3	3'-downstream	362,742
rs2131858	5.62E-04	0.213	0.944	0.350	8	104,397,766	FZD6	intron	0
rs2276433	5.63E-04	0.213	0.944	0.480	11	20,630,443	SLC6A5	synonymous	0
rs1935704	5.63E-04	0.213	0.944	0.184	6	112,828,477	LOC643859	5'-upstream	33,138
rs12039454	5.64E-04	0.213	0.944	0.484	1	202,809,203	MDM4	3'-downstream	22,854
rs2369244	5.64E-04	0.213	0.944	0.484	1	202,781,922	MDM4	intron	0
rs17758104	5.65E-04	0.213	0.944	0.052	12	106,551,651	BTBD11	intron	0
rs10902900	5.67E-04	0.213	0.944	0.199	10	124,954,909	LOC100131719	3'-downstream	14,586

rs4702401	5.68E-04	-0.216	0.944	0.319	5	6,961,507	POLS	3'-downstream	151,346
rs9423652	5.69E-04	0.213	0.944	0.078	10	5,590,140	CALML3	3'-downstream	31,915
rs12143625	5.70E-04	-0.213	0.944	0.347	1	213,458,463	KCNK2	intron	0
rs1471173	5.70E-04	0.213	0.944	0.134	4	170,199,727	CBR4	5'-upstream	31,730
rs4845804	5.73E-04	-0.213	0.944	0.353	1	5,568,030	NPHP4	3'-downstream	277,427
rs9905727	5.73E-04	0.216	0.944	0.194	17	75,887,409	KIAA1618	intron	0
rs1108734	5.73E-04	0.213	0.944	0.112	1	43,050,829	CCDC23	intron	0
rs11210721	5.73E-04	0.213	0.944	0.112	1	43,044,833	CCDC23	3'-downstream	487
rs10039039	5.76E-04	-0.216	0.944	0.091	5	169,847,542	KCNIP1	intron	0
rs13185531	5.77E-04	0.212	0.944	0.137	5	40,179,748	LOC285634	5'-upstream	386,301
rs11785367	5.77E-04	0.212	0.944	0.083	8	51,974,064	LOC100128686	3'-downstream	38,889
rs2290854	5.77E-04	0.212	0.944	0.478	1	202,782,648	MDM4	intron	0
rs4951389	5.77E-04	0.212	0.944	0.478	1	202,742,457	TRNAK-UUU	3'-downstream	324
rs2812599	5.78E-04	0.212	0.944	0.191	10	34,080,299	PARD3	3'-downstream	359,804
rs1361697	5.78E-04	0.212	0.944	0.134	6	22,676,513	HDGFL1	5'-upstream	1,144
rs6942987	5.78E-04	0.212	0.944	0.101	7	50,996,595	COBL	3'-downstream	54,809
rs7337058	5.78E-04	0.213	0.944	0.360	13	112,550,584	ATP11A	intron	0
rs1019287	5.79E-04	0.212	0.944	0.202	7	38,427,071	AMPH	intron	0
rs6427140	5.81E-04	0.214	0.944	0.432	1	166,885,640	DPT	3'-downstream	45,690
rs7841539	5.82E-04	-0.212	0.944	0.496	8	141,308,196	NIBP	intron	0
rs10516562	5.82E-04	0.212	0.944	0.076	4	111,525,712	LOC100133103	3'-downstream	14,666
rs1240375	5.83E-04	0.214	0.944	0.254	10	88,723,172	KIAA1975	intron	0
rs13061155	5.83E-04	0.212	0.944	0.417	3	60,244,988	FHIT	intron	0
rs5003114	5.83E-04	-0.213	0.944	0.198	1	166,727,502	LOC730016	5'-upstream	40,429
rs6530113	5.84E-04	-0.213	0.944	0.185	23	7,705,276	VCX	5'-upstream	65,027
rs7713342	5.86E-04	0.213	0.944	0.133	5	40,144,931	LOC285634	5'-upstream	351,484
rs12895027	5.89E-04	0.213	0.944	0.055	14	51,812,394	PTGDR	3'-UTR	0
rs13239901	5.90E-04	0.213	0.944	0.232	7	108,935,937	LOC100128056	5'-upstream	330,481
rs2078395	5.90E-04	0.213	0.944	0.443	4	181,140,358	hCG 2025798	3'-downstream	1,081,878

rs1237375	5.91E-04	-0.217	0.944	0.500	4	70,846,395	CSN1S1	intron	0
rs30045	5.92E-04	0.212	0.944	0.127	5	122,299,518	SNX24	intron	0
rs10245778	5.97E-04	0.212	0.944	0.097	7	142,460,269	OR6V1	missense	0
rs12668105	5.97E-04	0.212	0.944	0.097	7	142,470,988	OR6W1P	Unknown	--
rs11126440	5.98E-04	0.212	0.944	0.486	2	74,782,998	SEMA4F	3'-downstream	20,305
rs363620	5.98E-04	0.212	0.944	0.486	2	74,781,858	SEMA4F	3'-downstream	19,165
rs2392518	5.98E-04	0.214	0.944	0.366	7	37,800,734	GPR141	3'-downstream	53,296
rs12541355	5.99E-04	-0.213	0.944	0.176	8	8,486,098	CLDN23	5'-upstream	110,978
rs7707152	6.00E-04	-0.212	0.944	0.191	5	112,004,964	APC	5'-upstream	96,519
rs11831152	6.01E-04	0.212	0.944	0.081	12	130,300,928	LOC116437	3'-downstream	42,704
rs4878782	6.03E-04	0.213	0.944	0.203	9	38,293,243	ALDH1B1	5'-upstream	89,459
rs2836999	6.03E-04	0.212	0.944	0.316	21	39,683,415	WRB	intron	0
rs2817738	6.04E-04	0.212	0.944	0.426	6	24,899,079	GMNN	3'-downstream	4,822
rs378437	6.05E-04	0.212	0.944	0.103	1	55,782,058	LOC645538	3'-downstream	175,023
rs6869344	6.07E-04	0.213	0.944	0.053	5	59,642,077	LOC653198	intron	0
rs1496412	6.07E-04	-0.212	0.944	0.317	5	6,986,887	POLS	3'-downstream	176,726
rs4673021	6.08E-04	0.212	0.944	0.209	2	223,013,767	SGPP2	intron	0
rs4908425	6.09E-04	0.212	0.944	0.129	1	6,823,605	CAMTA1	intron	0
rs12154354	6.09E-04	-0.212	0.944	0.149	7	64,540,471	ZNF92	3'-downstream	37,038
rs4501594	6.10E-04	0.212	0.944	0.238	8	88,681,411	LOC642461	Unknown	--
rs2972588	6.11E-04	0.212	0.944	0.105	19	8,814,922	MBD3L1	missense	0
rs7149245	6.12E-04	0.212	0.944	0.260	14	53,863,105	CDKN3	5'-upstream	70,371
rs17091512	6.13E-04	0.211	0.944	0.060	14	56,013,748	C14orf101	5'-upstream	102,516
rs2101018	6.14E-04	0.211	0.944	0.199	4	136,714,417	LOC100132574	5'-upstream	6,655
rs1327634	6.14E-04	0.211	0.944	0.489	13	95,659,303	HS6ST3	intron	0
rs2213325	6.15E-04	0.212	0.944	0.147	22	32,804,560	LARGE	5'-upstream	158,150
rs6743895	6.15E-04	0.211	0.944	0.090	2	56,106,433	MIRN216B	5'-upstream	24,999
rs555864	6.18E-04	0.211	0.944	0.052	5	178,745,813	ADAMTS2	5'-upstream	40,878
rs2461935	6.19E-04	0.211	0.944	0.426	10	20,447,496	PLXDC2	intron	0

rs2021306	6.19E-04	0.212	0.944	0.165	9	14,355,307	NFIB	5'-upstream	51,362
rs4786182	6.19E-04	-0.212	0.944	0.313	16	7,535,702	A2BP1	intron	0
rs1341936	6.20E-04	-0.212	0.944	0.253	23	93,118,684	LOC100127890	5'-upstream	156,422
rs11949163	6.20E-04	0.212	0.944	0.143	5	40,210,503	LOC285634	5'-upstream	417,056
rs2837007	6.21E-04	0.211	0.944	0.347	21	39,694,354	LCA5L	3'-downstream	5,286
rs2814609	6.22E-04	0.211	0.944	0.108	1	189,872,382	RGS18	5'-upstream	521,833
rs4918047	6.24E-04	0.211	0.944	0.081	10	105,512,330	SH3PXD2A	intron	0
rs2839034	6.25E-04	-0.212	0.944	0.411	21	46,121,013	PCBP3	intron	0
rs7895784	6.25E-04	0.211	0.944	0.471	10	18,912,878	NSUN6	intron	0
rs12624214	6.25E-04	0.211	0.944	0.128	2	124,348,173	LOC100131284	3'-downstream	111,052
rs4951409	6.26E-04	0.211	0.944	0.475	1	202,827,613	LRRN2	3'-downstream	25,311
rs7532236	6.26E-04	0.211	0.944	0.475	1	202,828,240	LRRN2	3'-downstream	24,684
rs10489218	6.27E-04	0.212	0.944	0.458	1	166,883,302	DPT	3'-downstream	48,028
rs1501254	6.27E-04	-0.212	0.944	0.445	17	47,435,164	CA10	intron	0
rs11240764	6.28E-04	0.211	0.944	0.475	1	202,835,999	LRRN2	3'-downstream	16,925
rs10506537	6.30E-04	0.211	0.944	0.150	12	63,317,157	RASSF3	intron	0
rs6983491	6.30E-04	0.211	0.944	0.052	8	74,338,532	LOC100130301	intron	0
rs2296948	6.31E-04	0.211	0.944	0.415	9	116,473,506	LOC100129633	intron	0
rs5752014	6.31E-04	-0.211	0.944	0.375	22	23,617,889	SGSM1	intron	0
rs9695517	6.31E-04	0.211	0.944	0.430	9	116,479,676	LOC100129633	intron	0
rs6853611	6.31E-04	0.211	0.944	0.480	4	70,951,620	HTN1	intron	0
rs2812669	6.33E-04	0.211	0.944	0.168	10	34,076,104	PARD3	3'-downstream	363,999
rs6882373	6.37E-04	0.211	0.944	0.081	5	14,531,601	TRIO	intron	0
rs352517	6.37E-04	0.211	0.944	0.267	6	69,250,301	LOC728052	3'-downstream	150,609
rs7117175	6.37E-04	0.211	0.944	0.130	11	3,078,716	OSBPL5	intron	0
rs7680113	6.38E-04	0.211	0.944	0.284	4	188,911,848	LOC644325	5'-upstream	5,495
rs7994097	6.40E-04	0.211	0.944	0.177	13	19,831,064	CRYL1	3'-downstream	44,742
rs459552	6.40E-04	0.211	0.944	0.114	5	112,204,655	APC	missense	0
rs478859	6.41E-04	-0.211	0.944	0.363	1	100,568,708	LOC646970	3'-downstream	564

rs587058	6.41E-04	-0.211	0.944	0.363	1	100,568,472	LOC646970	3'-downstream	800
rs11242152	6.41E-04	0.211	0.944	0.344	5	132,770,349	FSTL4	intron	0
rs6576425	6.41E-04	-0.212	0.944	0.438	15	23,254,330	UBE3A	5'-upstream	19,109
rs2291787	6.42E-04	0.213	0.944	0.496	8	86,428,972	CA1	intron	0
rs2073925	6.43E-04	-0.211	0.944	0.263	9	135,027,080	GBGT1	intron	0
rs246285	6.44E-04	0.216	0.944	0.179	5	122,272,867	SNX24	intron	0
rs1775416	6.44E-04	-0.211	0.944	0.424	1	5,568,851	NPHP4	3'-downstream	276,606
rs7280598	6.44E-04	-0.211	0.944	0.285	21	36,295,016	RPL23AP3	3'-downstream	15,077
rs183108	6.44E-04	0.211	0.944	0.082	6	54,418,757	CLNS1B	3'-downstream	38,420
rs1369802	6.44E-04	0.211	0.944	0.158	4	28,856,822	LOC100131674	3'-downstream	57,831
rs869546	6.47E-04	-0.211	0.944	0.110	3	190,999,791	TP63	intron	0
rs10225135	6.48E-04	0.211	0.944	0.264	7	107,965,198	PNPLA8	5'-upstream	11,324
rs7144713	6.48E-04	-0.212	0.944	0.130	14	56,969,647	NAT12	3'-downstream	22,011
rs11040173	6.48E-04	0.214	0.944	0.227	11	5,965,954	OR52L1	5'-upstream	1,218
rs16851729	6.48E-04	-0.211	0.944	0.094	3	130,061,684	LOC653712	3'-downstream	1,357
rs7044279	6.49E-04	0.212	0.944	0.084	9	111,009,022	EPB41L4B	intron	0
rs9297854	6.49E-04	-0.211	0.944	0.426	8	133,724,160	LRRC6	intron	0
rs6716756	6.49E-04	0.211	0.944	0.125	2	102,667,630	SLC9A2	intron	0
rs34823274	6.51E-04	-0.211	0.944	0.118	4	14,805,437	LOC100129903	intron	0
rs7009336	6.51E-04	0.210	0.944	0.478	8	91,453,737	TMEM64	3'-downstream	251,041
rs3828558	6.51E-04	0.210	0.944	0.251	4	24,143,785	DHX15	intron	0
rs11668269	6.52E-04	0.212	0.944	0.434	19	22,305,800	LOC100130518	3'-downstream	13,982
rs1269683	6.53E-04	0.210	0.944	0.072	7	107,710,367	NRCAM	intron	0
rs6672295	6.53E-04	0.211	0.944	0.162	1	50,487,276	ELAVL4	3'-downstream	47,628
rs17171172	6.53E-04	0.210	0.944	0.222	7	37,839,175	TXNDC3	5'-upstream	15,549
rs4776290	6.55E-04	0.211	0.944	0.433	15	64,279,015	MEGF11	intron	0
rs6594018	6.56E-04	0.210	0.944	0.478	1	202,834,775	LRRN2	3'-downstream	18,149
rs1460040	6.56E-04	0.210	0.944	0.116	5	122,133,131	SNX2	5'-upstream	5,518
rs1383415	6.56E-04	-0.210	0.944	0.368	2	180,565,958	KIAA1604	intron	0

rs12208513	6.58E-04	0.210	0.944	0.063	6	154,942,722	LOC646269	3'-downstream	2,801
rs7049523	6.58E-04	0.211	0.944	0.092	23	110,697,230	LOC643873	3'-downstream	51,040
rs7162388	6.59E-04	0.210	0.944	0.090	15	59,117,034	RORA	intron	0
rs2984610	6.60E-04	0.212	0.944	0.060	1	167,195,740	LOC391132	3'-downstream	20,884
rs6785072	6.61E-04	-0.210	0.944	0.464	3	198,552,075	DLG1	5'-upstream	42,231
rs994377	6.62E-04	0.210	0.944	0.278	6	67,448,299	NUFIP1P	5'-upstream	586,767
rs2406623	6.63E-04	0.211	0.944	0.116	4	153,403,766	FBXW7	3'-downstream	58,094
rs9833267	6.63E-04	0.211	0.944	0.353	3	104,553,964	LOC644681	3'-downstream	186,204
rs4739296	6.64E-04	0.210	0.944	0.215	8	35,073,349	LOC100133273	3'-downstream	221,578
rs12509760	6.64E-04	0.210	0.944	0.357	4	24,163,182	DHX15	intron	0
rs6103592	6.67E-04	-0.210	0.944	0.101	20	42,124,801	TOX2	intron	0
rs3902916	6.68E-04	0.211	0.944	0.284	4	188,907,021	LOC644325	5'-upstream	668
rs175154	6.68E-04	0.210	0.944	0.183	22	15,706,668	ZNF402P	3'-downstream	11,358
rs2387653	6.69E-04	0.212	0.944	0.130	10	1,397,826	ADARB2	intron	0
rs6977083	6.69E-04	0.210	0.944	0.412	7	70,893,394	CALN1	intron	0
rs17724918	6.70E-04	-0.210	0.944	0.129	14	57,193,866	LOC401777	3'-downstream	26,706
rs7626560	6.72E-04	0.210	0.944	0.101	3	12,450,088	PPARG	intron	0
rs2251741	6.74E-04	0.210	0.944	0.449	8	95,227,558	CDH17	synonymous	0
rs12109819	6.76E-04	-0.210	0.944	0.460	5	32,103,783	PDZD2	intron	0
rs11640308	6.77E-04	0.210	0.944	0.129	16	55,497,470	SLC12A3	intron	0
rs2111211	6.78E-04	0.210	0.944	0.314	12	107,563,998	CORO1C	3'-UTR	0
rs17632029	6.81E-04	0.212	0.944	0.072	10	14,008,131	FRMD4A	intron	0
rs13263539	6.81E-04	0.210	0.944	0.292	8	102,613,455	GRHL2	intron	0
rs10906218	6.82E-04	0.211	0.944	0.103	10	12,837,291	CAMK1D	intron	0
rs6421114	6.82E-04	0.212	0.944	0.172	23	113,479,287	LOC100131029	5'-upstream	50,581
rs9495256	6.82E-04	0.210	0.944	0.165	6	139,161,606	CCDC28A	3'-downstream	5,457
rs9954037	6.82E-04	-0.213	0.944	0.131	18	57,564,436	RNF152	3'-downstream	68,848
rs3744950	6.83E-04	-0.210	0.944	0.408	18	59,073,256	BCL2	intron	0
rs12656478	6.83E-04	0.210	0.944	0.078	5	123,769,231	ZNF608	3'-downstream	231,278

rs10760699	6.84E-04	0.210	0.944	0.464	9	101,707,078	LOC441461	intron	0
rs1962051	6.84E-04	0.210	0.944	0.464	9	101,709,698	STX17	intron	0
rs4965473	6.84E-04	0.210	0.944	0.067	15	97,679,431	LRR28	intron	0
rs4867950	6.85E-04	-0.210	0.944	0.345	5	169,593,380	LOC133874	intron	0
rs2186184	6.85E-04	-0.210	0.944	0.409	1	90,070,893	LRR8D	intron	0
rs9516644	6.86E-04	0.210	0.944	0.489	13	95,680,681	HS6ST3	intron	0
rs2291239	6.88E-04	0.210	0.944	0.262	18	27,698,809	KIAA1012	intron	0
rs11611384	6.88E-04	0.210	0.944	0.171	12	113,454,146	LOC652191	5'-upstream	17,697
rs6679717	6.89E-04	0.212	0.944	0.480	1	202,827,300	LRRN2	3'-downstream	25,624
rs1092656	6.92E-04	-0.213	0.944	0.319	6	113,679,429	LOC643884	3'-downstream	27,462
rs10260248	6.95E-04	0.209	0.944	0.083	7	142,629,853	TAS2R40	missense	0
rs2581790	6.96E-04	0.209	0.944	0.359	3	53,076,820	LOC553148	5'-upstream	2,579
rs2258497	6.96E-04	0.209	0.944	0.181	1	165,674,697	CD247	intron	0
rs2744603	6.96E-04	0.209	0.944	0.267	6	24,645,844	KIAA0319	3'-downstream	6,467
rs17741796	6.96E-04	0.210	0.944	0.256	18	27,663,317	KIAA1012	3'-UTR	0
rs7199337	6.97E-04	0.211	0.944	0.318	16	77,356,261	WVOX	intron	0
rs10447342	6.97E-04	0.209	0.944	0.049	6	92,809,429	LOC100129847	5'-upstream	226,577
rs2900886	6.98E-04	0.209	0.944	0.067	1	167,182,814	LOC391132	3'-downstream	7,958
rs2984605	6.98E-04	0.209	0.944	0.067	1	167,194,079	LOC391132	3'-downstream	19,223
rs2984608	6.98E-04	0.209	0.944	0.067	1	167,195,678	LOC391132	3'-downstream	20,822
rs2984609	6.98E-04	0.209	0.944	0.067	1	167,195,711	LOC391132	3'-downstream	20,855
rs2984612	6.98E-04	0.209	0.944	0.067	1	167,199,277	LOC391132	3'-downstream	24,421
rs3735478	6.99E-04	-0.209	0.944	0.166	7	44,766,701	ZMIZ2	missense	0
rs552760	6.99E-04	0.210	0.944	0.174	1	205,099,462	IL20	5'-upstream	6,315
rs11823077	6.99E-04	-0.210	0.944	0.096	11	4,505,525	OR52M2P	5'-upstream	11,695
rs6986126	7.01E-04	0.210	0.944	0.105	8	14,335,688	SGCZ	intron	0
rs7961254	7.01E-04	0.209	0.944	0.058	12	95,913,090	NEDD1	3'-downstream	42,918
rs4505038	7.02E-04	0.211	0.944	0.327	11	45,891,273	PEX16	intron	0
rs7704817	7.04E-04	-0.210	0.944	0.223	5	154,968,300	LOC100131033	3'-downstream	114,946

rs9896168	7.04E-04	-0.209	0.944	0.431	17	47,453,436	CA10	intron	0
rs12767108	7.04E-04	0.209	0.944	0.123	10	72,784,238	SLC29A3	intron	0
rs12428610	7.04E-04	0.210	0.944	0.491	13	95,663,351	HS6ST3	intron	0
rs1250220	7.04E-04	-0.210	0.944	0.368	2	216,028,295	FN1	5'-upstream	19,259
rs4954723	7.05E-04	-0.209	0.944	0.273	2	139,285,272	NXPH2	5'-upstream	30,991
rs1938969	7.05E-04	0.210	0.944	0.254	11	105,143,204	GRIA4	intron	0
rs5761495	7.06E-04	0.213	0.944	0.360	22	25,089,278	SEZ6L	intron	0
rs5769445	7.06E-04	0.210	0.944	0.191	22	47,964,086	LOC643653	3'-downstream	31,701
rs2836248	7.06E-04	-0.210	0.944	0.465	21	38,551,067	LOC441964	intron	0
rs7406705	7.07E-04	0.210	0.944	0.306	17	77,222,329	TSPAN10	intron	0
rs10494791	7.09E-04	0.214	0.944	0.066	1	197,626,453	LOC647202	3'-downstream	2,227
rs7813136	7.09E-04	-0.210	0.944	0.218	8	136,444,840	LOC286094	3'-downstream	66,860
rs17599976	7.09E-04	0.209	0.944	0.112	17	72,352,169	MGAT5B	5'-upstream	24,224
rs12247156	7.11E-04	-0.209	0.944	0.155	10	34,675,535	PARD3	intron	0
rs2673942	7.12E-04	-0.209	0.944	0.149	1	233,060,091	PP2672	5'-upstream	97,869
rs16973748	7.12E-04	0.211	0.944	0.172	16	85,387,316	LOC729979	3'-downstream	58,383
rs17416875	7.14E-04	0.209	0.944	0.060	7	39,662,643	RALA	intron	0
rs3779203	7.14E-04	0.209	0.944	0.060	7	39,703,321	RALA	intron	0
rs8090593	7.14E-04	0.209	0.944	0.356	18	69,667,938	FBXO15	3'-downstream	223,647
rs11754612	7.14E-04	0.209	0.944	0.052	6	35,584,540	TULP1	intron	0
rs2032319	7.16E-04	-0.209	0.944	0.283	21	36,295,592	RPL23AP3	3'-downstream	14,501
rs560642	7.17E-04	0.209	0.944	0.319	12	24,338,715	SOX5	intron	0
rs2304733	7.18E-04	0.209	0.944	0.489	11	12,860,019	TEAD1	synonymous	0
rs1975174	7.18E-04	0.210	0.944	0.398	19	22,307,091	LOC100130518	3'-downstream	15,273
rs2834652	7.20E-04	0.209	0.944	0.199	21	35,151,507	RUNX1	intron	0
rs6986563	7.21E-04	-0.209	0.944	0.199	8	101,677,135	SNX31	intron	0
rs12495344	7.22E-04	0.209	0.944	0.177	3	192,516,457	CCDC50	5'-upstream	13,111
rs17386017	7.22E-04	0.209	0.944	0.132	1	43,069,669	ERMAP	intron	0
rs7198511	7.22E-04	0.209	0.944	0.287	16	77,355,868	WWOX	intron	0

rs4075410	7.22E-04	0.209	0.944	0.446	8	144,300,478	LY6H	3'-downstream	10,228
rs6015519	7.23E-04	-0.209	0.944	0.264	20	57,532,222	LOC645605	5'-upstream	28,985
rs2514788	7.23E-04	0.209	0.944	0.453	8	95,212,920	CDH17	intron	0
rs655205	7.25E-04	0.209	0.944	0.478	1	189,766,343	RGS18	5'-upstream	627,872
rs10483200	7.25E-04	-0.209	0.944	0.097	22	38,565,782	ENTHD1	intron	0
rs1469569	7.28E-04	-0.209	0.944	0.421	3	88,158,887	CGGBP1	3'-downstream	24,903
rs7516412	7.28E-04	-0.209	0.944	0.305	1	200,242,824	ELF3	5'-upstream	872
rs788460	7.29E-04	0.210	0.944	0.209	12	28,041,539	PTHLH	5'-upstream	25,356
rs6100472	7.29E-04	0.209	0.944	0.359	20	57,523,252	LOC645605	5'-upstream	20,015
rs17025231	7.31E-04	-0.209	0.944	0.166	2	101,043,095	TBC1D8	intron	0
rs9893317	7.32E-04	0.209	0.944	0.299	17	47,547,164	CA10	intron	0
rs6427139	7.32E-04	0.210	0.944	0.442	1	166,879,549	DPT	3'-downstream	51,781
rs1918981	7.34E-04	-0.209	0.944	0.184	23	7,702,055	VCX	5'-upstream	68,248
rs5980147	7.34E-04	-0.209	0.944	0.184	23	7,701,717	VCX	5'-upstream	68,586
rs6863920	7.37E-04	-0.209	0.944	0.304	5	59,898,210	DEPDC1B	3'-downstream	30,286
rs11100879	7.37E-04	0.208	0.944	0.173	4	146,579,862	LOC100132841	5'-upstream	16,745
rs7588830	7.38E-04	0.208	0.944	0.464	2	215,985,917	FN1	intron	0
rs17049639	7.38E-04	0.209	0.944	0.200	3	8,858,603	RAD18	3'-downstream	37,957
rs12223997	7.38E-04	0.208	0.944	0.374	11	7,570,138	PPFIBP2	intron	0
rs6862076	7.39E-04	-0.209	0.944	0.435	5	32,105,667	PDZD2	intron	0
rs5949475	7.43E-04	-0.210	0.944	0.070	23	93,699,769	LOC780816	3'-downstream	78,290
rs12517436	7.44E-04	0.208	0.944	0.052	5	3,867,700	IRX1	3'-downstream	213,183
rs2635462	7.45E-04	-0.208	0.944	0.276	6	152,558,808	SYNE1	intron	0
rs1297214	7.46E-04	0.209	0.944	0.132	21	15,253,724	NRIP1	3'-downstream	1,703
rs12819780	7.47E-04	0.208	0.944	0.265	12	29,659,102	TMTC1	intron	0
rs11796119	7.47E-04	-0.208	0.944	0.217	23	9,996,515	WWC3	intron	0
rs266585	7.47E-04	-0.208	0.944	0.134	5	64,364,371	SDCCAG10	3'-downstream	14,025
rs11965065	7.48E-04	0.209	0.944	0.051	6	15,838,249	DTNBP1	5'-upstream	66,999
rs12789020	7.48E-04	0.208	0.944	0.103	11	21,902,827	TMEM16E	5'-upstream	268,471

rs1861594	7.48E-04	-0.208	0.944	0.397	12	15,552,237	PTPRO	intron	0
rs16893606	7.49E-04	0.208	0.944	0.173	4	16,146,608	LDB2	intron	0
rs4330653	7.49E-04	0.208	0.944	0.079	8	10,483,001	RPIL1	3'-downstream	18,268
rs1342782	7.50E-04	0.208	0.944	0.426	1	90,908,805	BARHL2	3'-downstream	41,362
rs12814885	7.52E-04	0.209	0.944	0.089	12	7,396,641	CD163L1	3'-downstream	2,182
rs1520459	7.52E-04	0.213	0.944	0.425	15	44,730,699	SQRDL	3'-downstream	959,928
rs6848945	7.53E-04	0.208	0.944	0.103	4	30,258,917	PCDH7	5'-upstream	72,218
rs2047324	7.54E-04	-0.208	0.944	0.327	5	6,958,147	POLS	3'-downstream	147,986
rs517480	7.54E-04	-0.208	0.944	0.285	11	113,588,679	ZBTB16	intron	0
rs17056169	7.57E-04	0.208	0.944	0.072	9	72,806,374	TRPM3	intron	0
rs926571	7.57E-04	-0.209	0.944	0.301	6	22,781,432	LOC389370	intron	0
rs8047997	7.58E-04	-0.208	0.944	0.484	16	1,253,302	TPSD1	3'-downstream	4,807
rs4758198	7.58E-04	0.209	0.944	0.365	11	7,556,800	PPFIBP2	intron	0
rs41535144	7.60E-04	0.208	0.944	0.129	14	53,626,570	LOC645560	5'-upstream	98,107
rs4909741	7.60E-04	0.208	0.944	0.197	8	139,253,233	FAM135B	intron	0
rs7750712	7.61E-04	0.208	0.944	0.134	6	22,673,295	HDGFL1	5'-upstream	4,362
rs17066591	7.61E-04	-0.208	0.944	0.354	5	165,645,102	LOC441114	5'-upstream	96,686
rs9912487	7.62E-04	0.213	0.944	0.182	17	52,863,276	MSI2	intron	0
rs30038	7.63E-04	0.209	0.944	0.126	5	122,305,261	SNX24	intron	0
rs7221855	7.64E-04	0.208	0.944	0.310	17	72,176,449	MXRA7	3'-downstream	6,955
rs1563828	7.65E-04	0.208	0.944	0.484	1	202,783,200	MDM4	intron	0
rs6676563	7.67E-04	0.208	0.944	0.440	1	55,425,571	USP24	intron	0
rs7536204	7.67E-04	0.208	0.944	0.440	1	55,439,065	USP24	intron	0
rs6992422	7.67E-04	0.208	0.944	0.365	8	5,054,945	LOC648237	5'-upstream	81,705
rs3747961	7.68E-04	0.209	0.944	0.092	1	94,231,009	ABCA4	3'-UTR	0
rs1462839	7.70E-04	0.208	0.944	0.128	10	67,626,355	CTNNA3	intron	0
rs16907660	7.70E-04	0.208	0.944	0.092	11	21,172,953	NELL1	intron	0
rs9828276	7.70E-04	0.208	0.944	0.361	3	144,723,903	SLC9A9	intron	0
rs7607788	7.71E-04	0.208	0.944	0.209	2	236,020,154	CENTG2	5'-upstream	47,321

rs10503974	7.71E-04	0.208	0.944	0.218	8	35,018,934	LOC100133273	3'-downstream	167,163
rs17030975	7.71E-04	0.208	0.944	0.329	3	53,743,245	CACNA1D	intron	0
rs1795846	7.74E-04	0.208	0.944	0.444	12	53,175,347	LOC100130272	intron	0
rs1992044	7.75E-04	0.208	0.944	0.141	8	59,003,462	FAM110B	5'-upstream	66,205
rs1992045	7.75E-04	0.208	0.944	0.141	8	59,003,478	FAM110B	5'-upstream	66,189
rs9650192	7.75E-04	0.208	0.944	0.141	8	59,004,444	FAM110B	5'-upstream	65,223
rs8007000	7.75E-04	0.208	0.944	0.130	14	53,616,199	LOC645560	5'-upstream	87,736
rs6095882	7.75E-04	0.208	0.944	0.060	20	48,409,292	TRNAL-AAG	5'-upstream	23,462
rs10094861	7.76E-04	0.208	0.944	0.192	8	1,254,336	C8orf68	3'-downstream	179,152
rs12956309	7.77E-04	0.208	0.944	0.227	18	5,752,597	LOC645355	intron	0
rs10098626	7.78E-04	0.208	0.944	0.442	8	35,008,456	LOC100133273	3'-downstream	156,685
rs10900596	7.79E-04	0.208	0.944	0.477	1	202,789,080	MDM4	3'-downstream	2,731
rs595578	7.79E-04	-0.208	0.944	0.098	18	75,554,323	CTDP1	intron	0
rs12776025	7.80E-04	0.209	0.944	0.168	10	27,279,372	LOC100131912	5'-upstream	6,019
rs10519649	7.80E-04	0.208	0.944	0.419	4	143,674,003	INPP4B	intron	0
rs11765212	7.80E-04	0.207	0.944	0.076	7	70,053,725	AUTS2	3'-downstream	157,935
rs4758930	7.80E-04	-0.207	0.944	0.085	12	132,088,232	ZNF26	intron	0
rs12450865	7.80E-04	-0.207	0.944	0.403	17	47,525,332	CA10	intron	0
rs661322	7.81E-04	0.209	0.944	0.482	1	189,778,133	RGS18	5'-upstream	616,082
rs7488840	7.82E-04	0.208	0.944	0.102	12	7,394,106	CD163L1	3'-downstream	4,717
rs10900799	7.84E-04	-0.207	0.944	0.327	5	130,567,627	LYRM7	3'-UTR	0
rs10870249	7.84E-04	0.207	0.944	0.144	10	133,767,689	JAKMIP3	5'-upstream	614
rs2040622	7.86E-04	-0.207	0.944	0.161	17	65,096,191	MAP2K6	3'-downstream	46,126
rs7161490	7.86E-04	0.207	0.944	0.105	14	95,083,965	GLRX5	3'-downstream	3,157
rs2279700	7.87E-04	0.207	0.944	0.444	8	86,398,102	CA13	3'-downstream	14,548
rs6530110	7.90E-04	-0.208	0.944	0.184	23	7,704,976	VCX	5'-upstream	65,327
rs11608789	7.92E-04	0.207	0.944	0.085	12	106,998,822	LOC100129448	intron	0
rs4252685	7.92E-04	0.208	0.944	0.482	1	202,763,479	MDM4	intron	0
rs17147844	7.92E-04	0.207	0.944	0.074	4	70,813,132	CSN1S1	5'-upstream	18,256

rs4951393	7.92E-04	0.210	0.944	0.487	1	202,756,180	MDM4	intron	0
rs4984643	7.93E-04	0.209	0.944	0.403	16	1,279,756	LOC650474	Unknown	--
rs2185416	7.93E-04	0.210	0.944	0.178	10	72,796,733	SLC29A3	3'-downstream	3,580
rs9447086	7.93E-04	-0.208	0.944	0.135	6	74,741,057	CD109	3'-downstream	146,296
rs4353793	7.93E-04	0.208	0.944	0.056	3	1,756,437	LOC391504	5'-upstream	143,508
rs7334785	7.94E-04	0.207	0.944	0.215	13	39,669,985	FOXO1	3'-downstream	357,816
rs250851	7.94E-04	0.208	0.944	0.355	5	132,783,374	FSTL4	intron	0
rs619491	7.97E-04	-0.209	0.944	0.305	5	40,920,837	C7	5'-upstream	24,519
rs11762157	7.98E-04	0.207	0.944	0.394	7	17,066,715	LOC100131425	3'-downstream	171,675
rs7526462	7.98E-04	0.208	0.944	0.065	1	167,176,576	LOC391132	3'-downstream	1,720
rs1420741	7.98E-04	0.207	0.944	0.063	12	106,545,252	BTBD11	intron	0
rs10927390	7.98E-04	0.208	0.944	0.315	1	243,320,667	EFCAB2	3'-downstream	2,906
rs6785333	8.00E-04	-0.209	0.944	0.414	3	88,168,323	CGGBP1	3'-downstream	15,467
rs1439566	8.01E-04	0.208	0.944	0.192	5	124,577,237	LOC644659	Unknown	--
rs2718019	8.05E-04	0.207	0.944	0.177	7	36,047,961	LOC100129326	Unknown	--
rs11027159	8.05E-04	-0.207	0.944	0.384	11	23,318,586	LOC100131557	3'-downstream	29,676
rs11151507	8.05E-04	0.207	0.944	0.162	18	65,277,685	DOK6	intron	0
rs10251707	8.06E-04	0.207	0.944	0.222	7	40,664,407	C7orf10	intron	0
rs1339408	8.06E-04	-0.207	0.944	0.087	1	213,432,681	KCNK2	intron	0
rs6780419	8.07E-04	0.208	0.944	0.474	3	191,539,016	CLDN1	5'-upstream	16,107
rs4304370	8.07E-04	-0.207	0.944	0.301	9	1,725,187	SMARCA2	5'-upstream	280,155
rs6488556	8.07E-04	0.207	0.944	0.256	12	12,818,994	MIRN613	3'-downstream	10,050
rs7390284	8.07E-04	0.207	0.944	0.359	9	18,379,998	ADAMTSL1	5'-upstream	84,106
rs11052699	8.07E-04	0.207	0.944	0.092	12	7,395,698	CD163L1	3'-downstream	3,125
rs6517434	8.07E-04	0.207	0.944	0.090	21	38,109,926	KCNJ6	intron	0
rs41434745	8.08E-04	-0.207	0.944	0.397	1	205,098,415	IL20	5'-upstream	7,362
rs26147	8.08E-04	0.211	0.944	0.396	5	11,535,412	CTNND2	intron	0
rs2132482	8.08E-04	0.207	0.944	0.065	11	43,231,114	LOC399881	3'-downstream	8,516
rs636811	8.09E-04	0.207	0.944	0.090	1	231,815,644	KCNK1	5'-upstream	729

rs7677823	8.10E-04	-0.207	0.944	0.458	4	160,416,083	RAPGEF2	intron	0
rs9910052	8.10E-04	0.207	0.944	0.323	17	72,180,396	MXRA7	3'-downstream	3,008
rs17423995	8.11E-04	0.207	0.944	0.051	4	37,416,631	RELL1	5'-upstream	52,237
rs2969208	8.12E-04	-0.207	0.944	0.116	17	11,279,499	FLJ45455	intron	0
rs9525158	8.12E-04	0.207	0.944	0.489	13	95,675,242	HS6ST3	intron	0
rs332433	8.13E-04	-0.207	0.944	0.235	11	36,677,824	C11orf74	3'-downstream	40,431
rs332434	8.13E-04	-0.207	0.944	0.235	11	36,677,733	C11orf74	3'-downstream	40,340
rs11055065	8.13E-04	0.210	0.944	0.224	12	12,825,721	APOLD1	5'-upstream	4,161
rs10900594	8.14E-04	0.207	0.944	0.478	1	202,736,752	TRNAK-UUU	5'-upstream	5,526
rs1265181	8.16E-04	0.207	0.944	0.123	6	31,263,764	HCG27	5'-upstream	9,814
rs776858	8.16E-04	0.207	0.944	0.495	4	70,860,054	CSN2	intron	0
rs6713893	8.18E-04	0.207	0.944	0.119	2	2,649,185	MYT1L	5'-upstream	335,133
rs13028443	8.19E-04	0.207	0.944	0.460	2	63,457,221	LOC51057	intron	0
rs993794	8.19E-04	-0.207	0.944	0.159	10	108,081,693	LOC100132397	5'-upstream	200,523
rs1884452	8.21E-04	0.209	0.944	0.048	23	145,413,585	LOC100128690	5'-upstream	22,445
rs11651547	8.21E-04	0.207	0.944	0.119	17	39,376,774	PYY	3'-downstream	8,858
rs1418561	8.22E-04	0.209	0.944	0.182	6	112,809,914	LOC643859	5'-upstream	14,575
rs185009	8.24E-04	0.207	0.944	0.126	5	122,301,666	SNX24	intron	0
rs246287	8.24E-04	0.207	0.944	0.126	5	122,273,325	SNX24	intron	0
rs246317	8.24E-04	0.207	0.944	0.126	5	122,337,759	SNX24	intron	0
rs246322	8.24E-04	0.207	0.944	0.126	5	122,335,168	SNX24	intron	0
rs30029	8.24E-04	0.207	0.944	0.126	5	122,311,069	SNX24	intron	0
rs30039	8.24E-04	0.207	0.944	0.126	5	122,305,078	SNX24	intron	0
rs30049	8.24E-04	0.207	0.944	0.126	5	122,333,996	SNX24	intron	0
rs431878	8.24E-04	0.207	0.944	0.126	5	122,289,690	SNX24	intron	0
rs1927807	8.25E-04	0.207	0.944	0.487	13	95,672,758	HS6ST3	intron	0
rs11248542	8.25E-04	0.207	0.944	0.129	10	125,218,584	GPR26	5'-upstream	197,277
rs1496533	8.25E-04	0.207	0.944	0.496	8	86,420,726	CA1	3'-downstream	6,983
rs701556	8.28E-04	-0.206	0.944	0.238	13	102,406,882	LOC121952	3'-downstream	59,838

rs1391240	8.28E-04	-0.208	0.944	0.498	6	164,885,480	LOC728275	3'-downstream	206,903
rs10985459	8.28E-04	-0.208	0.944	0.166	9	123,743,153	TTL11	3'-downstream	47,857
rs2850377	8.29E-04	0.206	0.944	0.338	4	103,131,182	BANK1	intron	0
rs2850378	8.29E-04	0.206	0.944	0.338	4	103,134,990	BANK1	intron	0
rs10485526	8.30E-04	-0.206	0.944	0.361	20	15,383,203	MACROD2	intron	0
rs11015427	8.30E-04	0.206	0.944	0.173	10	27,291,815	LOC100131912	5'-upstream	18,462
rs11015433	8.30E-04	0.206	0.944	0.173	10	27,296,142	LOC100131912	5'-upstream	22,789
rs6488592	8.32E-04	0.206	0.944	0.121	12	7,739,894	GDF3	5'-upstream	267
rs9292290	8.33E-04	-0.207	0.944	0.149	5	28,755,133	LOC729862	5'-upstream	206,329
rs7332561	8.34E-04	0.208	0.944	0.201	13	28,860,516	KIAA0774	intron	0
rs4659221	8.35E-04	-0.206	0.944	0.274	1	119,969,876	LOC100130667	intron	0
rs10503973	8.36E-04	0.207	0.944	0.219	8	35,018,804	LOC100133273	3'-downstream	167,033
rs10993511	8.37E-04	0.206	0.944	0.078	9	92,259,202	LOC340515	3'-downstream	5,332
rs12022129	8.37E-04	0.206	0.944	0.394	1	205,069,997	IL19	intron	0
rs2124761	8.39E-04	0.207	0.944	0.053	11	100,441,556	PGR	intron	0
rs4964848	8.39E-04	0.207	0.944	0.199	12	128,198,132	TMEM132D	intron	0
rs6745008	8.41E-04	-0.206	0.944	0.233	2	230,069,842	DNER	intron	0
rs363625	8.41E-04	0.206	0.944	0.489	2	74,784,407	SEMA4F	3'-downstream	21,714
rs17154379	8.42E-04	-0.207	0.944	0.185	8	8,506,621	CLDN23	5'-upstream	90,455
rs3015224	8.43E-04	-0.206	0.944	0.309	9	71,918,208	MAMDC2	intron	0
rs6436753	8.44E-04	-0.206	0.944	0.222	2	228,703,258	SPHKAP	intron	0
rs2717329	8.44E-04	0.207	0.944	0.471	7	19,029,300	HDAC9	3'-downstream	25,782
rs13275618	8.46E-04	-0.207	0.944	0.382	8	141,298,387	NIBP	intron	0
rs2837008	8.49E-04	0.206	0.944	0.305	21	39,695,357	LCA5L	3'-downstream	4,283
rs9392684	8.49E-04	0.208	0.944	0.434	6	5,371,264	FARS2	intron	0
rs7545496	8.50E-04	-0.206	0.944	0.087	1	190,777,580	RGS1	5'-upstream	33,900
rs897405	8.52E-04	0.206	0.944	0.338	6	68,867,259	LOC100128293	3'-downstream	165,964
rs10831908	8.53E-04	-0.208	0.944	0.291	11	12,768,995	TEAD1	intron	0
rs2581830	8.53E-04	-0.207	0.944	0.429	3	53,109,138	RFT1	intron	0

rs12701867	8.54E-04	-0.208	0.944	0.114	7	41,197,194	C7orf10	3'-downstream	330,312
rs13428208	8.54E-04	0.206	0.944	0.051	2	128,744,772	HS6ST1	intron	0
rs17814562	8.55E-04	0.206	0.944	0.054	12	106,553,998	BTBD11	intron	0
rs12417886	8.59E-04	-0.206	0.944	0.291	11	12,768,307	TEAD1	intron	0
rs12607786	8.59E-04	0.206	0.944	0.264	18	27,672,175	KIAA1012	intron	0
rs437168	8.60E-04	0.206	0.944	0.225	19	41,026,259	NPHS1	synonymous	0
rs1392934	8.64E-04	-0.206	0.944	0.417	17	47,425,763	CA10	intron	0
rs11674390	8.64E-04	0.206	0.944	0.074	2	45,258,664	SIX2	5'-upstream	168,638
rs4758578	8.64E-04	0.206	0.944	0.078	11	3,354,643	ZNF195	intron	0
rs2663989	8.67E-04	0.206	0.944	0.143	15	42,325,952	CASC4	5'-upstream	42,269
rs828560	8.69E-04	0.206	0.944	0.374	6	165,929,442	PDE10A	intron	0
rs4909747	8.69E-04	0.206	0.944	0.191	8	139,260,139	FAM135B	intron	0
rs6682208	8.70E-04	0.206	0.944	0.478	1	202,832,806	LRRN2	3'-downstream	20,118
rs2252505	8.73E-04	-0.206	0.944	0.400	5	10,292,278	LOC134145	synonymous	0
rs875521	8.73E-04	0.206	0.944	0.219	3	124,992,028	MYLK	intron	0
rs11629141	8.75E-04	0.206	0.944	0.125	14	96,597,819	LOC730133	3'-downstream	116,339
rs3820439	8.77E-04	-0.206	0.944	0.319	1	200,240,188	RNPEP	missense	0
rs17023187	8.77E-04	0.206	0.944	0.045	4	148,542,379	LOC100130537	3'-downstream	24,197
rs6460688	8.78E-04	0.207	0.944	0.431	7	70,893,725	CALN1	intron	0
rs1981828	8.80E-04	-0.205	0.944	0.388	19	38,468,052	CEBPA	3'-downstream	14,724
rs17742014	8.80E-04	0.205	0.944	0.262	18	27,728,798	KIAA1012	intron	0
rs1494826	8.80E-04	0.207	0.944	0.134	5	116,553,682	LOC728342	5'-upstream	225,422
rs7120935	8.81E-04	0.208	0.944	0.270	11	21,036,518	NELL1	intron	0
rs4951407	8.84E-04	0.206	0.944	0.489	1	202,824,693	LRRN2	3'-downstream	28,231
rs560279	8.84E-04	0.205	0.944	0.352	11	121,528,721	MIRNLET7A2	5'-upstream	6,210
rs10954881	8.85E-04	0.205	0.944	0.406	8	30,134,238	DCTN6	intron	0
rs3935679	8.86E-04	0.205	0.944	0.334	5	97,504,067	PSME2P1	5'-upstream	70,679
rs12882488	8.87E-04	0.205	0.944	0.079	14	94,950,974	C14orf49	3'-downstream	2,610
rs16865402	8.89E-04	0.205	0.944	0.081	3	191,536,737	CLDN1	5'-upstream	13,828

rs6789805	8.89E-04	0.205	0.944	0.081	3	191,537,787	CLDN1	5'-upstream	14,878
rs6801146	8.89E-04	0.205	0.944	0.081	3	191,537,856	CLDN1	5'-upstream	14,947
rs17152434	8.89E-04	0.208	0.944	0.199	5	124,579,475	LOC644659	Unknown	--
rs9590371	8.90E-04	-0.209	0.944	0.356	13	95,658,077	HS6ST3	intron	0
rs6969427	8.91E-04	0.208	0.944	0.333	7	152,673,499	FLJ42291	3'-downstream	40,448
rs12815715	8.92E-04	0.206	0.944	0.093	12	7,380,620	ACSM4	3'-downstream	8,384
rs10808355	8.92E-04	0.205	0.944	0.412	8	98,455,047	TSPYL5	5'-upstream	95,695
rs10868721	8.93E-04	0.207	0.944	0.062	9	89,974,849	LOC389768	5'-upstream	6,279
rs1882055	8.94E-04	0.205	0.944	0.153	7	36,062,475	LOC100129326	Unknown	--
rs10205005	8.94E-04	0.205	0.944	0.132	2	42,102,217	LOC91461	5'-upstream	27,040
rs9599779	8.94E-04	0.208	0.944	0.246	13	70,578,186	DACH1	3'-downstream	331,913
rs4451621	8.94E-04	0.205	0.944	0.412	10	12,471,373	CAMK1D	intron	0
rs3217916	8.95E-04	0.206	0.944	0.397	12	4,278,934	CCND2	intron	0
rs2535357	8.95E-04	0.205	0.944	0.431	18	57,293,491	CDH20	5'-upstream	15,264
rs6560606	8.96E-04	0.205	0.944	0.236	9	79,352,869	GNAI4	intron	0
rs11997340	8.97E-04	-0.206	0.944	0.388	8	3,822,506	CSMD1	intron	0
rs6770415	8.98E-04	-0.205	0.944	0.255	3	13,242,771	NUP210	3'-downstream	89,966
rs4304369	8.98E-04	-0.207	0.944	0.335	9	1,725,113	SMARCA2	5'-upstream	280,229
rs10900597	8.99E-04	0.205	0.944	0.500	1	202,789,112	MDM4	3'-downstream	2,763
rs13152233	9.01E-04	0.205	0.944	0.072	4	143,296,300	INPP4B	intron	0
rs8070612	9.01E-04	0.205	0.944	0.056	17	18,840,335	SLC5A10	intron	0
rs12474898	9.01E-04	0.205	0.944	0.199	2	236,032,106	CENTG2	5'-upstream	35,369
rs7279643	9.02E-04	-0.205	0.944	0.424	21	46,200,229	PCBP3	3'-downstream	13,434
rs6959836	9.04E-04	-0.205	0.944	0.112	7	5,065,893	RBAK	intron	0
rs12702227	9.04E-04	0.205	0.944	0.052	7	46,519,896	LOC730338	3'-downstream	175,480
rs12702228	9.04E-04	0.205	0.944	0.052	7	46,522,406	LOC730338	3'-downstream	172,970
rs1265178	9.06E-04	0.205	0.944	0.120	6	31,269,208	HCG27	5'-upstream	4,370
rs920499	9.09E-04	-0.205	0.944	0.366	14	104,437,544	KIAA0284	3'-downstream	3,412
rs5985614	9.09E-04	0.205	0.944	0.235	23	110,696,134	LOC643873	3'-downstream	52,136

rs1684149	9.11E-04	0.205	0.944	0.187	12	32,162,607	BICD1	intron	0
rs17708126	9.11E-04	0.205	0.944	0.056	7	14,221,389	DGKB	intron	0
rs2018445	9.12E-04	0.211	0.944	0.268	11	43,117,351	LOC100128134	5'-upstream	62,408
rs1798	9.12E-04	0.205	0.944	0.195	1	205,082,748	IL19	3'-UTR	0
rs7524812	9.12E-04	0.205	0.944	0.081	1	97,342,695	DPYD	intron	0
rs12672751	9.12E-04	-0.208	0.944	0.341	7	133,745,915	AKR1B1	3'-downstream	31,732
rs9302094	9.13E-04	-0.207	0.944	0.371	13	95,650,741	HS6ST3	intron	0
rs8076286	9.14E-04	-0.205	0.944	0.431	17	47,451,755	CA10	intron	0
rs3775763	9.14E-04	0.206	0.944	0.482	4	70,929,238	HTN3	intron	0
rs2804875	9.14E-04	-0.205	0.944	0.242	10	33,883,553	NRP1	5'-upstream	219,714
rs4556834	9.15E-04	0.205	0.944	0.300	17	47,549,854	CA10	intron	0
rs11023907	9.16E-04	0.209	0.944	0.152	11	16,281,025	SOX6	intron	0
rs2974000	9.18E-04	0.206	0.944	0.191	5	119,230,346	LOC348958	3'-downstream	184,639
rs7307293	9.18E-04	0.205	0.944	0.094	12	67,114,413	LOC729376	intron	0
rs9323880	9.18E-04	-0.205	0.944	0.271	14	92,199,563	RIN3	intron	0
rs10022167	9.19E-04	0.206	0.944	0.460	4	74,497,673	ALB	intron	0
rs6896653	9.20E-04	0.206	0.944	0.164	5	107,732,780	FBXL17	intron	0
rs1727387	9.20E-04	0.205	0.944	0.079	12	118,356,085	CCDC60	intron	0
rs831571	9.20E-04	0.205	0.944	0.253	3	64,023,337	PRICKLE2	3'-downstream	31,250
rs1235399	9.20E-04	0.208	0.944	0.074	5	136,761,637	SPOCK1	intron	0
rs1428280	9.20E-04	0.205	0.944	0.067	5	13,640,660	LOC391738	3'-downstream	50,364
rs9542594	9.22E-04	0.205	0.944	0.206	13	70,617,166	DACH1	3'-downstream	292,933
rs17540362	9.23E-04	-0.205	0.944	0.112	7	11,263,913	PHF14	3'-downstream	88,143
rs5751080	9.23E-04	-0.205	0.944	0.493	22	40,066,213	ZC3H7B	intron	0
rs12955535	9.23E-04	0.205	0.944	0.090	18	74,145,153	LOC100132713	5'-upstream	214,048
rs896088	9.25E-04	0.205	0.944	0.419	5	165,875,957	LOC441114	3'-downstream	133,588
rs447278	9.27E-04	0.205	0.944	0.406	6	5,398,289	FARS2	intron	0
rs7773352	9.29E-04	0.205	0.944	0.273	6	108,423,962	LOC642741	3'-downstream	8,220
rs1887309	9.30E-04	-0.205	0.944	0.431	9	136,448,063	RXRA	intron	0

rs7283239	9.32E-04	0.205	0.944	0.070	21	21,062,388	PPIAP	5'-upstream	59,610
rs361488	9.32E-04	0.205	0.944	0.487	7	141,727,289	TRBV8-1	Unknown	--
rs10508612	9.32E-04	0.206	0.944	0.440	10	20,425,576	PLXDC2	intron	0
rs7256207	9.33E-04	0.205	0.944	0.149	19	33,539,522	LOC727780	5'-upstream	43,275
rs838600	9.33E-04	-0.205	0.944	0.496	3	144,698,162	SLC9A9	intron	0
rs11002468	9.35E-04	0.208	0.944	0.307	10	79,682,057	LOC100132987	5'-upstream	154,250
rs10921053	9.35E-04	0.204	0.944	0.215	1	190,234,692	RGS18	5'-upstream	159,523
rs674424	9.35E-04	0.204	0.944	0.146	11	118,535,962	ABCG4	intron	0
rs9447089	9.36E-04	-0.204	0.944	0.139	6	74,751,120	CD109	3'-downstream	156,359
rs2290	9.39E-04	0.204	0.944	0.056	4	121,875,517	PRDM5	intron	0
rs2409758	9.41E-04	0.205	0.944	0.380	21	36,412,525	LOC100133286	intron	0
rs10019178	9.42E-04	-0.204	0.944	0.424	4	16,139,177	LDB2	intron	0
rs7050164	9.42E-04	-0.204	0.944	0.159	23	7,668,041	VCX	5'-upstream	102,262
rs12740426	9.42E-04	-0.204	0.944	0.482	1	6,237,066	GPR153	intron	0
rs4375446	9.43E-04	-0.204	0.944	0.314	11	66,667,402	FBXL11	intron	0
rs2581806	9.44E-04	0.204	0.944	0.338	3	53,038,400	SFMBT1	intron	0
rs1778913	9.44E-04	0.205	0.944	0.266	9	86,625,557	NTRK2	intron	0
rs2854541	9.44E-04	0.204	0.944	0.486	7	141,726,054	TRBV8-1	Unknown	--
rs12007499	9.44E-04	0.205	0.944	0.173	23	23,157,121	LOC653707	3'-downstream	30,532
rs4948700	9.45E-04	0.204	0.944	0.206	10	42,869,213	RET	5'-upstream	23,310
rs17711345	9.45E-04	-0.205	0.944	0.170	7	64,543,602	ZNF92	3'-downstream	40,169
rs9849264	9.45E-04	-0.205	0.944	0.409	3	126,651,497	SNX4	intron	0
rs2784846	9.47E-04	0.204	0.944	0.164	10	86,264,851	KIAA1128	3'-UTR	0
rs13065032	9.47E-04	-0.204	0.944	0.083	3	129,993,284	RAB7A	intron	0
rs354113	9.47E-04	-0.205	0.944	0.174	12	30,425,805	IPO8	3'-downstream	247,384
rs7943820	9.48E-04	0.204	0.944	0.280	11	107,894,495	EXPH5	intron	0
rs10749486	9.48E-04	0.204	0.944	0.141	10	86,101,607	KIAA1128	intron	0
rs1209475	9.48E-04	0.204	0.944	0.141	10	86,248,339	KIAA1128	intron	0
rs4261230	9.48E-04	0.204	0.944	0.141	10	86,109,189	KIAA1128	intron	0

rs11584409	9.49E-04	0.204	0.944	0.058	1	95,957,886	LOC729977	5'-upstream	401,479
rs10243011	9.49E-04	-0.205	0.944	0.170	7	121,070,149	tcag7.23	5'-upstream	118,405
rs4845143	9.49E-04	0.209	0.944	0.379	1	205,069,942	IL19	intron	0
rs10493976	9.49E-04	0.204	0.944	0.181	1	102,036,497	OLFM3	3'-downstream	4,221
rs10249085	9.50E-04	-0.204	0.944	0.370	7	34,842,539	NPSR1	intron	0
rs3924091	9.52E-04	0.205	0.944	0.283	4	188,905,046	LOC644325	Unknown	--
rs12028349	9.52E-04	0.204	0.944	0.309	1	75,293,188	LHX8	5'-upstream	73,519
rs10861956	9.53E-04	0.204	0.944	0.296	12	107,578,604	CORO1C	intron	0
rs7300726	9.53E-04	0.204	0.944	0.296	12	107,577,991	CORO1C	intron	0
rs2405747	9.53E-04	0.204	0.944	0.054	2	128,748,295	HS6ST1	intron	0
rs6717511	9.53E-04	0.204	0.944	0.054	2	128,747,543	HS6ST1	intron	0
rs7229568	9.54E-04	0.204	0.944	0.184	18	4,814,081	PPIAP14	3'-downstream	178,430
rs17152492	9.54E-04	0.204	0.944	0.090	8	10,705,344	PINX1	intron	0
rs3752558	9.55E-04	0.204	0.944	0.108	20	41,621,277	SGK2	intron	0
rs6929812	9.56E-04	-0.205	0.944	0.473	6	27,492,499	MCFD2L	3'-downstream	8,745
rs2835623	9.58E-04	0.204	0.944	0.146	21	37,433,401	TTC3	intron	0
rs165190	9.60E-04	-0.204	0.944	0.391	5	139,126,284	PSD2	5'-upstream	29,306
rs11012265	9.60E-04	-0.204	0.944	0.289	10	21,010,483	NEBL	3'-downstream	99,610
rs11929275	9.60E-04	0.206	0.944	0.082	3	72,807,027	SHQ1	3'-downstream	74,091
rs981213	9.61E-04	0.204	0.944	0.341	12	77,115,380	NAV3	intron	0
rs11038044	9.62E-04	0.204	0.944	0.083	11	44,497,871	LOC646535	3'-downstream	20,034
rs1485803	9.62E-04	-0.206	0.944	0.385	18	22,880,887	CHST9	intron	0
rs12614728	9.62E-04	-0.204	0.944	0.237	2	76,502,501	LOC647275	5'-upstream	162,970
rs202124	9.63E-04	0.205	0.944	0.265	17	47,342,798	CA10	intron	0
rs748353	9.64E-04	0.204	0.944	0.183	11	105,164,699	GRIA4	intron	0
rs1250249	9.64E-04	0.204	0.944	0.464	2	215,995,521	FN1	intron	0
rs922140	9.65E-04	0.204	0.944	0.316	5	122,116,789	SNX2	5'-upstream	21,860
rs10268122	9.65E-04	-0.204	0.944	0.108	7	5,066,937	RBAK	intron	0
rs1989614	9.68E-04	-0.204	0.944	0.421	2	80,259,773	CTNNA2	intron	0

rs4878192	9.68E-04	0.205	0.944	0.222	9	38,288,804	ALDH1B1	5'-upstream	93,898
rs4395807	9.69E-04	0.204	0.944	0.106	7	142,457,413	OR6V1	5'-upstream	2,147
rs16912758	9.69E-04	0.204	0.944	0.114	10	60,300,047	BICC1	3'-downstream	41,196
rs12204014	9.70E-04	0.204	0.944	0.341	6	67,456,669	NUFIP1P	5'-upstream	595,137
rs4105713	9.71E-04	0.205	0.944	0.425	12	118,937,703	CCDC64	intron	0
rs16834635	9.71E-04	-0.204	0.944	0.112	1	163,006,475	PBX1	intron	0
rs2816567	9.71E-04	0.204	0.944	0.237	6	87,065,440	LOC643916	5'-upstream	84,418
rs10494980	9.72E-04	0.204	0.944	0.144	1	212,725,200	PTPN14	intron	0
rs10839797	9.73E-04	0.204	0.944	0.442	11	7,502,978	PPFIBP2	intron	0
rs444386	9.76E-04	0.205	0.944	0.215	10	90,518,158	LIPN	intron	0
rs4252725	9.77E-04	0.205	0.944	0.476	1	202,779,879	MDM4	intron	0
rs9868005	9.78E-04	0.204	0.944	0.433	3	64,607,454	ADAMTS9	intron	0
rs9383810	9.78E-04	0.204	0.944	0.081	6	156,895,326	ARID1B	5'-upstream	245,452
rs6913087	9.79E-04	0.204	0.944	0.208	6	54,245,008	C6orf142	3'-downstream	5,971
rs9687159	9.80E-04	-0.204	0.944	0.243	5	15,077,237	LOC402198	3'-downstream	19,353
rs2426278	9.81E-04	0.204	0.944	0.094	20	49,236,052	RPSAP1	5'-upstream	54,341
rs12197200	9.81E-04	0.204	0.944	0.054	6	163,503,111	PACRG	intron	0
rs6965133	9.81E-04	-0.204	0.944	0.232	7	103,368,862	RELN	intron	0
rs4806332	9.82E-04	0.204	0.944	0.173	19	33,548,847	LOC727780	5'-upstream	52,600
rs1019286	9.84E-04	0.204	0.944	0.188	7	38,426,876	AMPH	intron	0
rs6520403	9.85E-04	-0.205	0.944	0.208	23	48,927,746	PRICKLE3	intron	0
rs17025652	9.85E-04	0.204	0.944	0.365	3	88,441,414	LOC344653	5'-upstream	7,582
rs8139876	9.85E-04	0.204	0.944	0.109	22	20,865,973	IGLVV-58	Unknown	--
rs4146616	9.85E-04	0.205	0.944	0.051	10	67,550,131	CTNNA3	intron	0
rs4767867	9.85E-04	0.204	0.944	0.412	12	118,906,208	CCDC64	5'-upstream	5,823
rs1280374	9.86E-04	-0.204	0.944	0.173	15	55,542,924	CGNL1	intron	0
rs2073505	9.87E-04	0.205	0.944	0.100	4	3,414,301	HGFAC	synonymous	0
rs12410848	9.89E-04	0.204	0.944	0.306	1	111,636,507	CHIA	intron	0
rs9562045	9.89E-04	0.204	0.944	0.466	13	95,638,906	HS6ST3	intron	0

rs34922583	9.90E-04	0.203	0.944	0.139	5	40,169,516	LOC285634	5'-upstream	376,069
rs12890069	9.90E-04	0.204	0.944	0.073	14	51,827,323	LOC100131689	3'-downstream	1,506
rs5023021	9.91E-04	0.204	0.944	0.120	9	11,094,151	LOC646114	3'-downstream	63,866
rs17134115	9.93E-04	0.204	0.944	0.091	7	51,008,773	COBL	3'-downstream	42,631
rs13021679	9.93E-04	0.203	0.944	0.446	2	215,984,620	FN1	intron	0
rs10962894	9.93E-04	-0.205	0.944	0.297	9	1,716,601	SMARCA2	5'-upstream	288,741

* R values represent correlation coefficients for the association.

“Integrated analyses” of SNPs with both expression array and cytotoxicity data were started with the 1335 SNPs that had p values $<10^{-3}$. When the locations of these 1335 SNPs were determined, 27 regions were identified that each contained at least 2 SNPs with p values $<10^{-4}$ within 50 kb (a total of 175 SNPs). For purposes of this analysis, each of these regions was defined as a “locus” or a “SNP peak region.” All 27 of these loci, and the SNPs within each locus, are listed in Table 8. These “loci” were the focus of the integrated analyses. The most significant locus, locus 8C, mapped to chromosome 8 (Figure 5C and Table 8). This region had 6 SNPs within 50kb with p values $<10^{-4}$, including the SNP with the lowest p value (3.82×10^{-7}). The gene closest to this region encoded *PLEKHF2*. All 6 of the SNPs were in tight linkage disequilibrium (LD), with R^2 values that ranged from 0.7 to 1.0 in CAs, with slightly lower values in the AA subjects (Figure 6). The allele frequencies for these SNPs also were higher in CA and AA subjects than in HCA subjects. SNPs not on the genotyping platforms that were located 200kb up or downstream of SNP_A-8538282, the most significant SNP on chromosome 8 (see Figure 5C) also were imputed. That area contained 222 “observed SNPs” that were on the combined Illumina and Affymetrix platforms, plus 104 SNPs that were imputed (Figure 5C).

Table 8
The 27 "loci" associated with radiation AUC

Locus	SNP ID	P value	R value*	Q value	MAF	Chr	Position	GeneSymbol [†]	Location	Location Relative To Gene (bp)
1A	rs1130790	1.88E-04	0.230	0.857	0.348	1	200,235,705	RNPEP	exon	0
	rs4131469	8.86E-05	0.241	0.853	0.350	1	200,237,371	RNPEP	intron	0
	rs12119699	2.31E-04	0.227	0.891	0.348	1	200,239,578	RNPEP	intron	0
	rs3820439	8.77E-04	-0.206	0.944	0.319	1	200,240,188	RNPEP	exon	0
	rs7516412	7.28E-04	-0.209	0.944	0.305	1	200,242,824	ELF3	5'-upstream	872
	rs2819358	2.31E-04	0.227	0.891	0.348	1	200,243,025	ELF3	5'-upstream	671
	rs2735784	9.48E-05	0.240	0.853	0.375	1	200,243,103	ELF3	5'-upstream	593
	rs2819360	3.17E-04	0.222	0.932	0.341	1	200,243,877	ELF3	5'-UTR	0
1B	rs4951407	8.84E-04	0.206	0.944	0.489	1	202,824,693	LRRN2	3'-downstream	28,231
	rs6679717	6.89E-04	0.212	0.944	0.480	1	202,827,300	LRRN2	3'-downstream	25,624
	rs4951409	6.26E-04	0.211	0.944	0.475	1	202,827,613	LRRN2	3'-downstream	25,311
	rs7532236	6.26E-04	0.211	0.944	0.475	1	202,828,240	LRRN2	3'-downstream	24,684
	rs6682208	8.70E-04	0.206	0.944	0.478	1	202,832,806	LRRN2	3'-downstream	20,118
	rs6594018	6.56E-04	0.210	0.944	0.478	1	202,834,775	LRRN2	3'-downstream	18,149
	rs11240764	6.28E-04	0.211	0.944	0.475	1	202,835,999	LRRN2	3'-downstream	16,925
	rs10900601	7.37E-05	0.244	0.845	0.227	1	202,838,673	LRRN2	3'-downstream	14,251
	rs898387	1.24E-05	0.268	0.696	0.235	1	202,845,996	LRRN2	3'-downstream	6,928
	rs898386	4.22E-05	0.253	0.727	0.229	1	202,846,320	LRRN2	3'-downstream	6,604
	rs2045624	4.51E-05	0.251	0.727	0.258	1	202,851,008	LRRN2	3'-downstream	1,916
	rs7539399	3.08E-04	0.222	0.932	0.269	1	202,856,667	LRRN2	intron	0
	rs884108	1.07E-04	0.241	0.853	0.180	1	202,857,860	LRRN2	intron	0
	rs4951088	1.20E-04	0.237	0.857	0.471	1	202,877,403	LRRN2	intron	0
	rs4951089	1.60E-04	0.232	0.857	0.475	1	202,877,521	LRRN2	intron	0
	rs11240237	1.60E-04	0.232	0.857	0.475	1	202,879,141	LRRN2	intron	0
	rs11240239	1.22E-04	0.237	0.857	0.469	1	202,879,427	LRRN2	intron	0

	rs109000418	4.20E-04	0.218	0.944	0.309	1	202,880,789	LRRN2	intron	0
	rs2772227	2.00E-04	0.229	0.865	0.152	1	202,882,023	LRRN2	intron	0
	rs1329631	2.31E-04	0.227	0.891	0.307	1	202,883,013	LRRN2	intron	0
	rs2815832	4.95E-04	0.215	0.944	0.168	1	202,883,863	LRRN2	intron	0
1C	rs1028182	2.65E-04	0.225	0.932	0.406	1	205,068,502	IL19	intron	0
	rs4845143	9.49E-04	0.209	0.944	0.379	1	205,069,942	IL19	intron	0
	rs12022129	8.37E-04	0.206	0.944	0.394	1	205,069,997	IL19	intron	0
	rs11119670	7.45E-05	0.244	0.845	0.442	1	205,071,944	IL19	intron	0
	rs2243174	7.04E-05	0.244	0.843	0.444	1	205,078,108	IL19	intron	0
	rs2243188	7.11E-05	0.244	0.843	0.442	1	205,081,095	IL19	intron	0
	rs1798	9.12E-04	0.205	0.944	0.195	1	205,082,748	IL19	3'-UTR	0
	rs2243193	9.77E-05	0.240	0.853	0.453	1	205,082,848	IL19	3'-UTR	0
	rs4845144	3.50E-04	0.222	0.932	0.458	1	205,083,271	IL19	3'-downstream	324
	rs2883036	3.99E-04	-0.221	0.944	0.361	1	205,091,385	IL19	3'-downstream	8,438
1D	rs780266	1.55E-04	0.233	0.857	0.071	1	231,791,723	KCNK1	5'-upstream	24,650
	rs1773951	1.34E-04	0.235	0.857	0.070	1	231,802,262	KCNK1	5'-upstream	14,111
	rs1693219	5.89E-05	0.247	0.823	0.289	1	231,807,892	KCNK1	5'-upstream	8,481
	rs1693216	6.50E-05	0.247	0.843	0.286	1	231,808,517	KCNK1	5'-upstream	7,856
	rs780256	2.67E-04	0.225	0.932	0.288	1	231,809,726	KCNK1	5'-upstream	6,647
	rs636811	8.09E-04	0.207	0.944	0.090	1	231,815,644	KCNK1	5'-upstream	729
1E	rs12569163	1.78E-06	0.292	0.394	0.118	1	239,945,170	WDR64	intron	0
	rs7554126	4.34E-06	0.287	0.667	0.297	1	239,953,804	WDR64	intron	0
3A	rs894013	3.19E-05	0.261	0.711	0.472	3	4,353,142	SETMAR	3'-downstream	19,193
	rs308731	8.21E-05	0.242	0.853	0.365	3	4,354,374	SETMAR	3'-downstream	20,425
3B	rs1469569	7.28E-04	-0.209	0.944	0.421	3	88,158,887	CGGBP1	3'-downstream	24,903
	rs17549345	5.39E-05	-0.248	0.777	0.336	3	88,163,269	CGGBP1	3'-downstream	20,521
	rs6785333	8.00E-04	-0.209	0.944	0.414	3	88,168,323	CGGBP1	3'-downstream	15,467

	rs9852704	9.86E-05	-0.240	0.853	0.406	3	88,171,034	CGGBP1	3'-downstream	12,756
4A	rs13127174	2.86E-04	0.224	0.932	0.157	4	16,137,569	LDB2	intron	0
	rs10019178	9.42E-04	-0.204	0.944	0.424	4	16,139,177	LDB2	intron	0
	rs10805350	3.50E-04	0.222	0.932	0.313	4	16,140,499	LDB2	intron	0
	rs13138387	1.70E-04	0.232	0.857	0.065	4	16,142,474	LDB2	intron	0
	rs10516301	4.97E-05	0.250	0.750	0.072	4	16,143,251	LDB2	intron	0
	rs16893606	7.49E-04	0.208	0.944	0.173	4	16,146,608	LDB2	intron	0
	rs881790	3.46E-04	0.221	0.932	0.195	4	16,147,055	LDB2	intron	0
	rs13128522	2.38E-05	0.260	0.696	0.060	4	16,149,782	LDB2	intron	0
4B	rs2078395	5.90E-04	0.213	0.944	0.443	4	181,140,358	hCG_2025798	3'-downstream	1,081,878
	rs35018391	3.23E-05	0.255	0.711	0.049	4	181,217,870	hCG_2025798	3'-downstream	1,004,366
	rs41333347	3.23E-05	0.255	0.711	0.049	4	181,227,186	hCG_2025798	3'-downstream	995,050
	rs7680285	3.23E-05	0.255	0.711	0.049	4	181,228,438	hCG_2025798	3'-downstream	993,798
	rs2309341	9.04E-05	-0.241	0.853	0.433	4	181,590,726	hCG_2025798	3'-downstream	631,510
4C	rs11726299	5.15E-04	-0.214	0.944	0.190	4	183,556,319	ODZ3	intron	0
	rs727695	1.42E-04	0.235	0.857	0.313	4	183,610,140	ODZ3	intron	0
	rs7676392	1.73E-05	0.264	0.696	0.281	4	183,613,233	ODZ3	intron	0
	rs6830998	1.28E-04	0.237	0.857	0.279	4	183,617,946	ODZ3	intron	0
	rs869239	1.60E-05	0.265	0.696	0.495	4	183,690,033	ODZ3	intron	0
	rs2309691	5.36E-05	0.248	0.777	0.491	4	183,691,063	ODZ3	intron	0
	rs11731599	2.98E-05	0.257	0.711	0.489	4	183,691,126	ODZ3	intron	0
	rs6840083	3.01E-04	0.223	0.932	0.421	4	183,701,671	ODZ3	intron	0
5A	rs26953	1.78E-04	-0.233	0.857	0.326	5	59,850,071	PART1	intron	0
	rs27564	5.55E-05	-0.251	0.791	0.325	5	59,873,391	PART1	3'-downstream	20,403
	rs6863920	7.37E-04	-0.209	0.944	0.304	5	59,898,210	DEPDC1B	3'-downstream	30,286
	rs6449478	3.26E-04	-0.224	0.932	0.267	5	59,909,466	DEPDC1B	3'-downstream	19,030
	rs2409791	1.09E-05	-0.270	0.696	0.280	5	59,920,074	DEPDC1B	3'-downstream	8,422
	rs4326096	3.41E-05	-0.255	0.711	0.270	5	59,926,035	DEPDC1B	3'-downstream	2,461

	rs206789	5.74E-05	-0.248	0.810	0.313	5	59,939,728	DEPDCIB	intron	0
	rs286158	1.34E-04	-0.235	0.857	0.309	5	59,970,010	DEPDCIB	intron	0
5B	rs6884002	2.96E-04	-0.223	0.932	0.099	5	154,872,015	LOC100131033	3'-downstream	18,661
	rs10051752	1.99E-04	-0.229	0.865	0.085	5	154,966,485	LOC100131033	3'-downstream	113,131
	rs7704817	7.04E-04	-0.210	0.944	0.223	5	154,968,300	LOC100131033	3'-downstream	114,946
	rs7379436	1.00E-04	0.239	0.853	0.074	5	155,158,726	LOC100131033	3'-downstream	305,372
	rs10073856	9.49E-05	0.241	0.853	0.071	5	155,195,298	LOC100131033	3'-downstream	341,944
	rs6873333	3.64E-05	0.254	0.711	0.072	5	155,195,850	LOC100131033	3'-downstream	342,496
	rs7378774	7.71E-05	0.245	0.845	0.064	5	155,221,392	LOC100131033	3'-downstream	368,038
7A	rs12702213	9.29E-05	0.240	0.853	0.058	7	46,381,080	LOC730338	3'-downstream	314,296
	rs13239088	6.64E-05	0.249	0.843	0.054	7	46,381,408	LOC730338	3'-downstream	313,968
	rs12702227	9.04E-04	0.205	0.944	0.052	7	46,519,896	LOC730338	3'-downstream	175,480
	rs12702228	9.04E-04	0.205	0.944	0.052	7	46,522,406	LOC730338	3'-downstream	172,970
7B	rs17598132	1.89E-05	0.263	0.696	0.076	7	96,417,275	FLJ34048	3'-downstream	53,620
	rs17598306	8.60E-06	0.273	0.696	0.079	7	96,419,747	FLJ34048	3'-downstream	51,148
	rs2016644	4.86E-04	0.216	0.944	0.087	7	96,433,985	FLJ34048	3'-downstream	36,910
	rs17657370	3.34E-05	0.255	0.711	0.078	7	96,444,428	FLJ34048	3'-downstream	26,467
7C	rs13222164	4.97E-04	0.215	0.944	0.150	7	108,885,600	LOC100128056	5'-upstream	380,818
	rs12705596	1.75E-05	0.263	0.696	0.161	7	108,893,619	LOC100128056	5'-upstream	372,799
	rs12705601	4.80E-05	0.250	0.740	0.161	7	108,923,348	LOC100128056	5'-upstream	343,070
	rs12705602	7.91E-05	0.243	0.845	0.166	7	108,929,460	LOC100128056	5'-upstream	336,958
	rs13239901	5.90E-04	0.213	0.944	0.232	7	108,935,937	LOC100128056	5'-upstream	330,481
7D	rs10240447	7.41E-05	0.244	0.845	0.495	7	157,460,585	PTPRN2	intron	0
	rs4716858	6.74E-05	-0.245	0.843	0.468	7	157,461,158	PTPRN2	intron	0
8A	rs10098626	7.78E-04	0.208	0.944	0.442	8	35,008,456	LOC100133273	3'-downstream	156,685
	rs10503973	8.36E-04	0.207	0.944	0.219	8	35,018,804	LOC100133273	3'-downstream	167,033

	rs10503974	7.71E-04	0.208	0.944	0.218	8	35,018,934	LOC100133273	3'-downstream	167,163
	rs10954975	5.56E-04	0.213	0.944	0.217	8	35,019,032	LOC100133273	3'-downstream	167,261
	rs11786195	4.68E-04	0.216	0.944	0.204	8	35,020,843	LOC100133273	3'-downstream	169,072
	rs12678629	4.19E-04	0.218	0.944	0.215	8	35,025,990	LOC100133273	3'-downstream	174,219
	rs13282927	2.71E-04	0.226	0.932	0.212	8	35,031,277	LOC100133273	3'-downstream	179,506
	rs1376519	1.22E-04	0.238	0.857	0.244	8	35,045,674	LOC100133273	3'-downstream	193,903
	rs2981309	6.62E-05	0.249	0.843	0.241	8	35,048,829	LOC100133273	3'-downstream	197,058
	rs4314649	3.10E-05	0.257	0.711	0.242	8	35,052,669	LOC100133273	3'-downstream	200,898
	rs2923661	3.46E-05	0.255	0.711	0.240	8	35,061,182	LOC100133273	3'-downstream	209,411
	rs2981317	2.37E-04	0.227	0.891	0.200	8	35,069,374	LOC100133273	3'-downstream	217,603
	rs4739296	6.64E-04	0.210	0.944	0.215	8	35,073,349	LOC100133273	3'-downstream	221,578
8B	rs7835942	8.01E-05	-0.243	0.845	0.227	8	61,960,345	CHD7	3'-downstream	18,326
	rs4738839	8.01E-05	-0.243	0.845	0.227	8	61,960,444	CHD7	3'-downstream	18,425
8C	rs1610110	9.58E-07	0.299	0.318	0.083	8	96,185,038	PLEKHF2	5'-upstream	30,170
	rs1561715	9.58E-07	0.299	0.318	0.083	8	96,189,090	PLEKHF2	5'-upstream	26,118
	rs1561714	2.14E-05	0.261	0.696	0.087	8	96,189,151	PLEKHF2	5'-upstream	26,057
	rs4392868	8.24E-06	0.274	0.696	0.087	8	96,189,248	PLEKHF2	5'-upstream	25,960
	rs7000734	3.82E-07	0.309	0.259	0.081	8	96,196,206	PLEKHF2	5'-upstream	19,002
	rs212551	6.85E-05	0.245	0.843	0.132	8	96,201,280	PLEKHF2	5'-upstream	13,928
8D	rs11559202	6.57E-05	0.245	0.843	0.141	8	99,075,912	MATN2	exon	0
	rs11559201	6.57E-05	0.245	0.843	0.141	8	99,075,924	MATN2	exon	0
	rs2290467	1.48E-04	0.234	0.857	0.108	8	99,109,330	MATN2	intron	0
	rs2279120	2.13E-04	0.232	0.871	0.112	8	99,115,216	MATN2	intron	0
	rs3088121	9.52E-05	0.241	0.853	0.105	8	99,117,225	MATN2	3'-UTR	0
8E	rs4463400	2.06E-04	0.229	0.867	0.148	8	141,289,178	NIBP	intron	0
	rs6578080	3.31E-04	0.222	0.932	0.228	8	141,291,830	NIBP	intron	0
	rs4397386	1.03E-04	0.242	0.853	0.214	8	141,294,034	NIBP	intron	0
	rs7387053	5.14E-05	0.249	0.757	0.218	8	141,295,342	NIBP	intron	0

	rs4487737	5.14E-05	0.249	0.757	0.218	8	141,296,740	NIBP	intron	0
	rs13275618	8.46E-04	-0.207	0.944	0.382	8	141,298,387	NIBP	intron	0
	rs6578083	7.41E-05	-0.244	0.845	0.374	8	141,299,161	NIBP	intron	0
	rs7814976	4.80E-04	-0.221	0.944	0.334	8	141,306,070	NIBP	intron	0
	rs7841539	5.82E-04	-0.212	0.944	0.496	8	141,308,196	NIBP	intron	0
	rs6578084	3.66E-04	-0.220	0.932	0.366	8	141,311,849	NIBP	intron	0
	rs9324519	3.96E-04	-0.219	0.944	0.375	8	141,312,047	NIBP	intron	0
9A	rs12553351	1.49E-05	0.265	0.696	0.117	9	6,828,348	JMJD2C	intron	0
	rs4742269	4.73E-06	0.280	0.667	0.139	9	6,839,317	JMJD2C	intron	0
9B	rs5023021	9.91E-04	0.204	0.944	0.120	9	11,094,151	LOC646114	3'-downstream	63,866
	rs10959554	2.33E-04	0.227	0.891	0.076	9	11,121,371	LOC646114	3'-downstream	91,086
	rs7866090	4.45E-04	0.217	0.944	0.103	9	11,130,883	LOC646114	3'-downstream	100,598
	rs10809359	2.22E-05	0.261	0.696	0.109	9	11,135,717	LOC646114	3'-downstream	105,432
	rs12380191	7.47E-05	0.244	0.845	0.101	9	11,170,739	LOC646114	3'-downstream	140,454
	rs12376660	3.71E-05	0.254	0.711	0.089	9	11,175,487	LOC646114	3'-downstream	145,202
	rs12380100	1.55E-05	0.265	0.696	0.097	9	11,177,013	LOC646114	3'-downstream	146,728
	rs10959622	1.02E-04	0.239	0.853	0.099	9	11,201,722	LOC646114	3'-downstream	171,437
	rs11788082	8.03E-05	0.243	0.845	0.150	9	11,208,170	LOC646114	3'-downstream	177,885
	rs10809395	2.50E-05	0.259	0.704	0.103	9	11,223,740	LOC646114	3'-downstream	193,455
	rs10118338	6.89E-05	0.245	0.843	0.139	9	11,226,474	LOC646114	3'-downstream	196,189
	rs10124468	3.48E-04	0.221	0.932	0.115	9	11,235,830	LOC646114	3'-downstream	205,545
10A	rs11250461	1.19E-04	0.237	0.857	0.226	10	1,394,502	ADARB2	intron	0
	rs11250464	5.61E-06	0.279	0.676	0.175	10	1,396,364	ADARB2	intron	0
	rs4554799	9.00E-06	0.272	0.696	0.170	10	1,397,728	ADARB2	intron	0
	rs2387653	6.69E-04	0.212	0.944	0.130	10	1,397,826	ADARB2	intron	0
	rs4880503	4.54E-05	0.251	0.727	0.171	10	1,426,858	ADARB2	intron	0
	rs11250496	1.38E-04	0.235	0.857	0.166	10	1,437,105	ADARB2	intron	0
	rs10508213	1.68E-04	-0.232	0.857	0.112	10	1,601,165	ADARB2	intron	0

11A	rs2862667	4.09E-05	0.252	0.725	0.266	11	43,099,468	LOC100128134	5'-upstream	44,525
	rs10838023	7.64E-05	0.243	0.845	0.267	11	43,113,488	LOC100128134	5'-upstream	58,545
	rs2018445	9.12E-04	0.211	0.944	0.268	11	43,117,351	LOC100128134	5'-upstream	62,408
20A	rs10485526	8.30E-04	-0.206	0.944	0.361	20	15,383,203	MACROD2	intron	0
	rs6079836	3.60E-05	-0.254	0.711	0.339	20	15,383,564	MACROD2	intron	0
	rs6079839	3.60E-05	-0.254	0.711	0.339	20	15,384,282	MACROD2	intron	0
21A	rs2776278	2.13E-04	-0.229	0.871	0.284	21	36,264,569	RPL23AP3	3'-downstream	45,524
	rs2249118	2.41E-05	-0.260	0.696	0.364	21	36,277,829	RPL23AP3	3'-downstream	32,264
	rs2212916	2.80E-05	-0.257	0.711	0.366	21	36,281,638	RPL23AP3	3'-downstream	28,455
	rs2249599	5.19E-04	-0.215	0.944	0.251	21	36,281,873	RPL23AP3	3'-downstream	28,220
	rs2249971	1.69E-04	-0.232	0.857	0.352	21	36,284,531	RPL23AP3	3'-downstream	25,562
	rs7280598	6.44E-04	-0.211	0.944	0.285	21	36,295,016	RPL23AP3	3'-downstream	15,077
	rs2032319	7.16E-04	-0.209	0.944	0.283	21	36,295,592	RPL23AP3	3'-downstream	14,501

*R values represent correlation coefficients for the association.

† Genes selected for siRNA screening are highlighted by shading.

“Integrated” SNP, basal expression and radiation AUC analyses: The effect of genetic variation on radiation-induced cytotoxicity may result, in part, from the regulation of gene expression. Post radiation gene expression is known to be influenced by DNA sequence variation (Correa and Cheung (2004) *Am. J. Hum. Genet.* 75:885-890; and Smirnov et al. (2009) *Nature* 459:587-591. However, few studies have focused on basal gene expression levels and their possible relationship to radiation response, i.e., on information that might be used to predict response. Therefore, an “integrated analysis” that included data for SNPs, basal expression, and radiation AUC also was performed. Specifically, 175 SNPs were identified with p values $<10^{-3}$ that mapped to the 27 identified “loci” (Table 8), and then data for the 54,000 basal expression array probe sets on the Affymetrix U133 Plus 2.0 platform were used to identify SNPs within those loci that might be associated with basal gene expression, in either a cis or trans fashion.

Specifically, 2,432 SNP-expression associations were observed for the 175 SNPs with p values $<10^{-4}$. These 2,432 expression probe sets were correlated with radiation AUC, and probe sets with p values $<10^{-3}$ for association with radiation AUC were identified. A less stringent p value cutoff was selected for this final step to capture as much information as possible, with the understanding that many of the associations would be false-positives. This “integrated analysis,” moving from “loci” to SNPs to expression, identified 50 unique SNPs located in 14 of the 27 loci that were significantly associated with data for 47 probe sets that represented 39 unique annotated genes, i.e., basal expression of these genes was associated with radiation AUC with $p < 10^{-3}$ (Table 9). None of the SNPs were in cis-regulatory regions, defined as 5Mb on either side of the gene identified. These 50 unique SNPs mapped to 8 different chromosomes, with at least 2 SNPs on each of those chromosomes. The four most significant “loci” or “SNP peak regions” mapped to chromosomes 1, 4, 5 and 8, respectively, and contained the *LRRN2*, *IL19*, *KCNK1*, *LDB2*, *hCG_2025798*, *DEPDC1B*, *LOC100131033* and *PLEKHF2* genes (Table 9). The SNPs near *PLEKHF2* within the “locus” on chromosome 8 (Figure 5C) were particularly striking since they were associated with variation in the expression of six annotated genes, and variation in the expression of those genes was, in turn, significantly associated with radiation AUC. The chromosome 1 locus contained the largest number of SNPs (19) that were associated with radiation AUC, with p values that

ranged from 10^{-3} to 10^{-4} . Those 19 SNPs were significantly associated with the expression of 12 annotated genes that were also significantly associated with radiation AUC with p values that ranged from 10^{-3} to 10^{-4} . Six annotated genes were associated with the locus on chromosome 8 that contained the most significant 6 linked SNPs (p values $<10^{-4}$), and those 6 genes were significantly associated with radiation AUC, with p values $<10^{-3}$. The chromosome 4 and 5 loci included 7 and 6 SNPs, respectively, that were associated with radiation AUC with p values that ranged from 10^{-3} to 10^{-4} , and those SNPs were associated with the expression of 11 and 4 unique annotated genes, respectively, with p values that ranged from 10^{-4} to 10^{-7} . Expression levels for those 15 genes also were associated with radiation AUC, with p values $<10^{-3}$.

Tables 9A, 9B, and 9C

“Integrated analyses” with the top expression probe sets that were associated with SNPs within “loci” and with radiation AUC (SNP vs Expression p-value $<10^{-4}$, and Expression vs AUC p-value $<10^{-3}$).

9A	SNP				
	SNP ID	MAF	Chr	Position	Closest gene [†]
1	rs13128522	0.060	4	16,149,782	LDB2
2	rs10516301	0.072	4	16,143,251	LDB2
3	rs13128522	0.060	4	16,149,782	LDB2
4	rs13138387	0.065	4	16,142,474	LDB2
5	rs13128522	0.060	4	16,149,782	LDB2
6	rs4742269	0.139	9	6,839,317	IMJD2C
7	rs12702213	0.058	7	46,381,080	LOC730338
8	rs13239088	0.054	7	46,381,408	LOC730338
9	rs6873333	0.072	5	155,195,850	LOC100131033
10	rs7378774	0.064	5	155,221,392	LOC100131033
11	rs10073856	0.071	5	155,195,298	LOC100131033
12	rs780266	0.071	1	231,791,723	KCNK1
13	rs1773951	0.070	1	231,802,262	KCNK1
14	rs10516301	0.072	4	16,143,251	LDB2
15	rs10805350	0.313	4	16,140,499	LDB2
16	rs13128522	0.060	4	16,149,782	LDB2
17	rs13138387	0.065	4	16,142,474	LDB2
18	rs898386	0.229	1	202,846,320	LRRN2
19	rs7539399	0.269	1	202,856,667	LRRN2
20	rs898387	0.235	1	202,845,996	LRRN2
21	rs898386	0.229	1	202,846,320	LRRN2

22	rs898387	0.235	1	202,845,996	LRRN2
23	rs1561715	0.083	8	96,189,090	PLEKHF2
24	rs1610110	0.083	8	96,185,038	PLEKHF2
25	rs7000734	0.081	8	96,196,206	PLEKHF2
26	rs4392868	0.087	8	96,189,248	PLEKHF2
27	rs13128522	0.060	4	16,149,782	LDB2
28	rs2883036	0.361	1	205,091,385	IL19
29	rs6873333	0.072	5	155,195,850	LOC100131033
30	rs7379436	0.074	5	155,158,726	LOC100131033
31	rs7378774	0.064	5	155,221,392	LOC100131033
32	rs10073856	0.071	5	155,195,298	LOC100131033
33	rs1561714	0.087	8	96,189,151	PLEKHF2
34	rs1561715	0.083	8	96,189,090	PLEKHF2
35	rs1610110	0.083	8	96,185,038	PLEKHF2
36	rs7000734	0.081	8	96,196,206	PLEKHF2
37	rs212551	0.132	8	96,201,280	PLEKHF2
38	rs4392868	0.087	8	96,189,248	PLEKHF2
39	rs13138387	0.065	4	16,142,474	LDB2
40	rs4951407	0.489	1	202,824,693	LRRN2
41	rs2212916	0.366	21	36,281,638	RPL23AP3
42	rs780256	0.288	1	231,809,726	KCNK1
43	rs1693219	0.289	1	231,807,892	KCNK1
44	rs1693216	0.286	1	231,808,517	KCNK1
45	rs2249971	0.352	21	36,284,531	RPL23AP3
46	rs212551	0.132	8	96,201,280	PLEKHF2
47	rs7680285	0.049	4	181,228,438	hCG_2025798
48	rs35018391	0.049	4	181,217,870	hCG_2025798
49	rs41333347	0.049	4	181,227,186	hCG_2025798
50	rs780266	0.071	1	231,791,723	KCNK1
51	rs1773951	0.070	1	231,802,262	KCNK1
52	rs884108	0.180	1	202,857,860	LRRN2
53	rs11240237	0.475	1	202,879,141	LRRN2
54	rs11240239	0.469	1	202,879,427	LRRN2
55	rs4951089	0.475	1	202,877,521	LRRN2
56	rs4951088	0.471	1	202,877,403	LRRN2
57	rs11250496	0.166	10	1,437,105	ADARB2
58	rs212551	0.132	8	96,201,280	PLEKHF2
59	rs13128522	0.060	4	16,149,782	LDB2
60	rs10516301	0.072	4	16,143,251	LDB2
61	rs13128522	0.060	4	16,149,782	LDB2
62	rs13138387	0.065	4	16,142,474	LDB2
63	rs17657370	0.078	7	96,444,428	FLJ34048
64	rs17598132	0.076	7	96,417,275	FLJ34048
65	rs898386	0.229	1	202,846,320	LRRN2
66	rs780266	0.071	1	231,791,723	KCNK1

67	rs1773951	0.070	1	231,802,262	KCNK1
68	rs10508213	0.112	10	1,601,165	ADARB2
69	rs898386	0.229	1	202,846,320	LRRN2
70	rs898387	0.235	1	202,845,996	LRRN2
71	rs1561715	0.083	8	96,189,090	PLEKHF2
72	rs1610110	0.083	8	96,185,038	PLEKHF2
73	rs7000734	0.081	8	96,196,206	PLEKHF2
74	rs212551	0.132	8	96,201,280	PLEKHF2
75	rs4392868	0.087	8	96,189,248	PLEKHF2
76	rs13128522	0.060	4	16,149,782	LDB2
77	rs6873333	0.072	5	155,195,850	LOC100131033
78	rs7379436	0.074	5	155,158,726	LOC100131033
79	rs7378774	0.064	5	155,221,392	LOC100131033
80	rs10073856	0.071	5	155,195,298	LOC100131033
81	rs10516301	0.072	4	16,143,251	LDB2
82	rs13128522	0.060	4	16,149,782	LDB2
83	rs13138387	0.065	4	16,142,474	LDB2
84	rs13138387	0.065	4	16,142,474	LDB2
85	rs780266	0.071	1	231,791,723	KCNK1
86	rs1773951	0.070	1	231,802,262	KCNK1
87	rs1561715	0.083	8	96,189,090	PLEKHF2
88	rs1610110	0.083	8	96,185,038	PLEKHF2
89	rs7000734	0.081	8	96,196,206	PLEKHF2
90	rs10516301	0.072	4	16,143,251	LDB2
91	rs884108	0.180	1	202,857,860	LRRN2
92	rs10516301	0.072	4	16,143,251	LDB2
93	rs13128522	0.060	4	16,149,782	LDB2
94	rs2243188	0.442	1	205,081,095	IL19
95	rs4845144	0.458	1	205,083,271	IL19
96	rs2243174	0.444	1	205,078,108	IL19
97	rs11119670	0.442	1	205,071,944	IL19
98	rs4326096	0.270	5	59,926,035	DEPDC1B
99	rs2409791	0.280	5	59,920,074	DEPDC1B
100	rs13138387	0.065	4	16,142,474	LDB2
101	rs10959554	0.076	9	11,121,371	LOC646114
102	rs11250464	0.175	10	1,396,364	ADARB2
103	rs2387653	0.130	10	1,397,826	ADARB2
104	rs780266	0.071	1	231,791,723	KCNK1
105	rs1773951	0.070	1	231,802,262	KCNK1
106	rs1561715	0.083	8	96,189,090	PLEKHF2
107	rs1610110	0.083	8	96,185,038	PLEKHF2
108	rs7000734	0.081	8	96,196,206	PLEKHF2
109	rs4392868	0.087	8	96,189,248	PLEKHF2

9B	Probe set		
ID	Probe	Chr	Gene Symbol
1	204004_at	12	PAWR
2	207238_s_at	1	PTPRC
3	207238_s_at	1	PTPRC
4	207238_s_at	1	PTPRC
5	204005_s_at	12	PAWR
6	214173_x_at	19	C19orf2
7	227806_at	16	C16orf74
8	227806_at	16	C16orf74
9	220953_s_at	5	MTMR12
10	220953_s_at	5	MTMR12
11	220953_s_at	5	MTMR12
12	1557984_s_at	12	RPAP3
13	1557984_s_at	12	RPAP3
14	212588_at	1	PTPRC
15	212588_at	1	PTPRC
16	212588_at	1	PTPRC
17	212588_at	1	PTPRC
18	216685_s_at	9	MTAP
19	216685_s_at	9	MTAP
20	216685_s_at	9	MTAP
21	204652_s_at	7	NRF1
22	204652_s_at	7	NRF1
23	205981_s_at	4	ING2
24	205981_s_at	4	ING2
25	205981_s_at	4	ING2
26	205981_s_at	4	ING2
27	226231_at	20	---
28	1566001_at	16	---
29	201946_s_at	12	CCT2
30	201946_s_at	12	CCT2
31	201946_s_at	12	CCT2
32	201946_s_at	12	CCT2
33	1555852_at	6	---
34	1555852_at	6	---
35	1555852_at	6	---
36	1555852_at	6	---
37	1555852_at	6	---

38	1555852 at	6	---
39	203524 s at	22	MPST
40	203218 at	5	MAPK9
41	213498 at	11	CREB3L1
42	202180 s at	16	MVP
43	202180 s at	16	MVP
44	202180 s at	16	MVP
45	202180 s at	16	MVP
46	202180 s at	16	MVP
47	200650 s at	1	LDHA
48	200650 s at	1	LDHA
49	200650 s at	1	LDHA
50	207079 s at	14	MED6
51	207079 s at	14	MED6
52	222714 s at	8	LACTB2
53	222714 s at	8	LACTB2
54	222714 s at	8	LACTB2
55	222714 s at	8	LACTB2
56	222714 s at	8	LACTB2
57	224596 at	9	SLC44A1
58	1554271 a at	1	CENPL
59	219501 at	13	ENOX1
60	206935 at	13	PCDH8
61	206935 at	13	PCDH8
62	206935 at	13	PCDH8
63	206935 at	13	PCDH8
64	206935 at	13	PCDH8
65	229173 at	2	KIAA1715
66	222387 s at	16	VPS35
67	222387 s at	16	VPS35
68	203353 s at	18	MBD1
69	204444 at	10	KIF11
70	204444 at	10	KIF11
71	203856 at	14	VRK1
72	203856 at	14	VRK1
73	203856 at	14	VRK1
74	203856 at	14	VRK1
75	203856 at	14	VRK1
76	209016 s at	12	KRT7
77	206220 s at	13	RASA3
78	206220 s at	13	RASA3
79	206220 s at	13	RASA3
80	206220 s at	13	RASA3
81	218584 at	12	TCTN1
82	218584 at	12	TCTN1

83	218584 at	12	TCTN1
84	225525 at	22	CTA-221G9.4 /// LOC100131004
85	1554577 a at	23	PSMD10
86	1554577 a at	23	PSMD10
87	218634 at	1	PHLDA3
88	218634 at	1	PHLDA3
89	218634 at	1	PHLDA3
90	221698 s at	12	CLEC7A
91	243721 at	18	---
92	212587 s at	1	PTPRC
93	212587 s at	1	PTPRC
94	235959 at	1	---
95	235959 at	1	---
96	235959 at	1	---
97	235959 at	1	---
98	219544 at	13	BORA
99	219544 at	13	BORA
100	212124 at	10	ZMIZ1
101	1558794 at	10	LOC728190
102	209670 at	14	TRAC
103	209670 at	14	TRAC
104	1554493 s at	2	THADA
105	1554493 s at	2	THADA
106	215750 at	22	KIAA1659
107	215750 at	22	KIAA1659
108	215750 at	22	KIAA1659
109	215750 at	22	KIAA1659

9C	GWAS					
ID	R value* (SNP vs Exp)	P value (SNP vs Exp)	R value (SNP vs AUC)	P Value (SNP vs AUC)	R value (EXP vs AUC)	P value (EXP vs AUC)
1	-0.251	3.53E-05	0.260	2.38E-05	-0.266	7.46E-06
2	-0.275	5.16E-06	0.250	4.97E-05	-0.264	8.81E-06
3	-0.288	1.74E-06	0.260	2.38E-05	-0.264	8.81E-06
4	-0.277	4.31E-06	0.232	1.70E-04	-0.264	8.81E-06
5	-0.276	5.00E-06	0.260	2.38E-05	-0.261	1.10E-05
6	-0.238	8.37E-05	0.280	4.73E-06	-0.254	1.83E-05
7	-0.250	3.48E-05	0.240	9.29E-05	-0.251	2.45E-05
8	-0.245	6.52E-05	0.249	6.64E-05	-0.251	2.45E-05
9	-0.242	6.14E-05	0.254	3.64E-05	-0.240	5.40E-05
10	-0.254	2.96E-05	0.245	7.71E-05	-0.240	5.40E-05
11	-0.247	4.40E-05	0.241	9.49E-05	-0.240	5.40E-05

12	-0.252	3.13E-05	0.233	1.55E-04	-0.239	5.94E-05
13	-0.252	2.91E-05	0.235	1.34E-04	-0.239	5.94E-05
14	-0.308	2.86E-07	0.250	4.97E-05	-0.233	8.78E-05
15	-0.253	3.14E-05	0.222	3.50E-04	-0.233	8.78E-05
16	-0.333	2.65E-08	0.260	2.38E-05	-0.233	8.78E-05
17	-0.294	9.98E-07	0.232	1.70E-04	-0.233	8.78E-05
18	-0.257	2.14E-05	0.253	4.22E-05	-0.233	9.19E-05
19	-0.242	6.39E-05	0.222	3.08E-04	-0.233	9.19E-05
20	-0.259	1.75E-05	0.268	1.24E-05	-0.233	9.19E-05
21	-0.278	4.32E-06	0.253	4.22E-05	-0.230	1.13E-04
22	-0.266	1.04E-05	0.268	1.24E-05	-0.230	1.13E-04
23	-0.248	4.09E-05	0.299	9.58E-07	-0.229	1.20E-04
24	-0.248	4.09E-05	0.299	9.58E-07	-0.229	1.20E-04
25	-0.239	7.62E-05	0.309	3.82E-07	-0.229	1.20E-04
26	-0.248	4.08E-05	0.274	8.24E-06	-0.229	1.20E-04
27	-0.271	7.48E-06	0.260	2.38E-05	-0.227	1.36E-04
28	-0.260	2.07E-05	-0.221	3.99E-04	0.224	1.70E-04
29	-0.284	2.35E-06	0.254	3.64E-05	-0.224	1.72E-04
30	-0.246	4.56E-05	0.239	1.00E-04	-0.224	1.72E-04
31	-0.283	3.10E-06	0.245	7.71E-05	-0.224	1.72E-04
32	-0.290	1.49E-06	0.241	9.49E-05	-0.224	1.72E-04
33	-0.295	8.57E-07	0.261	2.14E-05	-0.223	1.79E-04
34	-0.322	7.04E-08	0.299	9.58E-07	-0.223	1.79E-04
35	-0.322	7.04E-08	0.299	9.58E-07	-0.223	1.79E-04
36	-0.302	4.57E-07	0.309	3.82E-07	-0.223	1.79E-04
37	-0.239	7.95E-05	0.245	6.85E-05	-0.223	1.79E-04
38	-0.312	2.01E-07	0.274	8.24E-06	-0.223	1.79E-04
39	-0.252	2.93E-05	0.232	1.70E-04	-0.223	1.81E-04
40	-0.239	8.10E-05	0.206	8.84E-04	-0.221	2.10E-04
41	-0.237	8.99E-05	-0.257	2.80E-05	0.219	2.40E-04
42	0.261	1.54E-05	0.225	2.67E-04	0.219	2.47E-04
43	0.247	4.47E-05	0.247	5.89E-05	0.219	2.47E-04
44	0.253	3.15E-05	0.247	6.50E-05	0.219	2.47E-04
45	-0.241	6.89E-05	-0.232	1.69E-04	0.219	2.47E-04
46	0.258	1.87E-05	0.245	6.85E-05	0.219	2.47E-04
47	-0.242	6.36E-05	0.255	3.23E-05	-0.216	2.89E-04
48	-0.242	6.36E-05	0.255	3.23E-05	-0.216	2.89E-04
49	-0.242	6.36E-05	0.255	3.23E-05	-0.216	2.89E-04
50	-0.246	5.00E-05	0.233	1.55E-04	-0.213	3.60E-04
51	-0.242	6.23E-05	0.235	1.34E-04	-0.213	3.60E-04
52	-0.240	8.32E-05	0.241	1.07E-04	-0.211	4.07E-04
53	-0.242	6.33E-05	0.232	1.60E-04	-0.211	4.07E-04
54	-0.238	8.54E-05	0.237	1.22E-04	-0.211	4.07E-04
55	-0.252	2.94E-05	0.232	1.60E-04	-0.211	4.07E-04
56	-0.242	6.12E-05	0.237	1.20E-04	-0.211	4.07E-04

57	-0.254	2.65E-05	0.235	1.38E-04	-0.211	4.13E-04
58	-0.239	7.84E-05	0.245	6.85E-05	-0.211	4.14E-04
59	0.246	5.11E-05	0.260	2.38E-05	0.211	4.18E-04
60	0.276	4.76E-06	0.250	4.97E-05	0.209	4.55E-04
61	0.271	7.23E-06	0.260	2.38E-05	0.209	4.55E-04
62	0.245	4.92E-05	0.232	1.70E-04	0.209	4.55E-04
63	0.239	7.84E-05	0.255	3.34E-05	0.209	4.55E-04
64	0.245	5.33E-05	0.263	1.89E-05	0.209	4.55E-04
65	-0.245	5.33E-05	0.253	4.22E-05	-0.208	5.00E-04
66	-0.243	5.96E-05	0.233	1.55E-04	-0.208	5.03E-04
67	-0.242	6.21E-05	0.235	1.34E-04	-0.208	5.03E-04
68	0.238	8.11E-05	-0.232	1.68E-04	-0.207	5.39E-04
69	-0.243	6.10E-05	0.253	4.22E-05	-0.207	5.44E-04
70	-0.236	9.50E-05	0.268	1.24E-05	-0.207	5.44E-04
71	-0.256	2.17E-05	0.299	9.58E-07	-0.206	5.68E-04
72	-0.256	2.17E-05	0.299	9.58E-07	-0.206	5.68E-04
73	-0.257	2.00E-05	0.309	3.82E-07	-0.206	5.68E-04
74	-0.280	3.27E-06	0.245	6.85E-05	-0.206	5.68E-04
75	-0.246	4.98E-05	0.274	8.24E-06	-0.206	5.68E-04
76	0.302	5.15E-07	0.260	2.38E-05	0.206	5.76E-04
77	-0.268	8.39E-06	0.254	3.64E-05	-0.205	5.83E-04
78	-0.241	6.83E-05	0.239	1.00E-04	-0.205	5.83E-04
79	-0.289	1.81E-06	0.245	7.71E-05	-0.205	5.83E-04
80	-0.264	1.28E-05	0.241	9.49E-05	-0.205	5.83E-04
81	0.312	1.98E-07	0.250	4.97E-05	0.205	5.88E-04
82	0.307	3.22E-07	0.260	2.38E-05	0.205	5.88E-04
83	0.246	4.84E-05	0.232	1.70E-04	0.205	5.88E-04
84	0.266	1.03E-05	0.232	1.70E-04	0.205	6.04E-04
85	-0.242	6.35E-05	0.233	1.55E-04	-0.204	6.21E-04
86	-0.247	4.22E-05	0.235	1.34E-04	-0.204	6.21E-04
87	0.237	9.02E-05	0.299	9.58E-07	0.204	6.21E-04
88	0.237	9.02E-05	0.299	9.58E-07	0.204	6.21E-04
89	0.241	6.88E-05	0.309	3.82E-07	0.204	6.21E-04
90	0.287	1.82E-06	0.250	4.97E-05	0.204	6.37E-04
91	0.250	4.19E-05	0.241	1.07E-04	0.203	6.73E-04
92	-0.248	4.31E-05	0.250	4.97E-05	-0.203	6.84E-04
93	-0.257	2.13E-05	0.260	2.38E-05	-0.203	6.84E-04
94	0.258	1.94E-05	0.244	7.11E-05	0.202	7.16E-04
95	0.240	8.31E-05	0.222	3.50E-04	0.202	7.16E-04
96	0.239	7.90E-05	0.244	7.04E-05	0.202	7.16E-04
97	0.239	8.17E-05	0.244	7.45E-05	0.202	7.16E-04
98	0.236	9.97E-05	-0.255	3.41E-05	-0.201	7.56E-04
99	0.245	4.86E-05	-0.270	1.09E-05	-0.201	7.56E-04
100	-0.244	5.55E-05	0.232	1.70E-04	-0.201	7.67E-04
101	0.241	7.10E-05	0.227	2.33E-04	0.200	8.40E-04

102	-0.241	7.38E-05	0.279	5.61E-06	-0.199	8.63E-04
103	-0.265	1.24E-05	0.212	6.69E-04	-0.199	8.63E-04
104	-0.246	4.77E-05	0.233	1.55E-04	-0.199	8.77E-04
105	-0.249	3.84E-05	0.235	1.34E-04	-0.199	8.77E-04
106	0.263	1.31E-05	0.299	9.58E-07	0.197	9.79E-04
107	0.263	1.31E-05	0.299	9.58E-07	0.197	9.79E-04
108	0.259	1.71E-05	0.309	3.82E-07	0.197	9.79E-04
109	0.250	3.73E-05	0.274	8.24E-06	0.197	9.79E-04

*R values represent correlation coefficients for each association.

†Genes selected for siRNA screening are highlighted by shading.

Functional validation of candidate genes in tumor cell lines: The initial

association experiments were performed with human LCLs. Since non-genetic factors might confound the results of these association studies, and since gene regulation is tissue specific Dimas et al. (2009) *Science* 325:1246-1250, studies were done with human tumor cell lines. Specifically, two pancreatic cancer cell lines (MIA-PaCa2; p53 mutant and HupT3; p53 mutant), and one cervical cancer cell line (HeLa; p53 wild type (WT)), were used to functionally validate association results obtained with LCLs. These functional experiments involved siRNA knockdown followed by MTS cytotoxicity assays and, subsequently, colony-forming assays. These three cancer cell lines were selected because of their relative sensitivity to radiation after testing with MTS assays.

Based on the analysis of the 54,000 basal expression probe sets, 1.3 million SNPs and radiation AUC data, as well as an evaluation of their biological function, 23 candidate genes identified as described herein were selected for siRNA screening with the tumor cell lines. These genes were chosen based on the following criteria: genes with at least one expression array probe set that had a p value $<10^{-3}$ for association with radiation AUC; genes containing SNPs found within a “locus” associated with radiation AUC ($p < 10^{-4}$); or genes for which expression was associated with both AUC and SNPs ($p < 10^{-3}$ for AUC and $p < 10^{-4}$ for SNPs, i.e., the “integrated analysis”). In addition, the genes had to be expressed in the lymphoblastoid cell lines (expression level >50 after GCRMA normalization) and could not previously have been implicated in radiation sensitivity. Application of this approach resulted in the selection of 10 genes that were identified during the “integrated” analyses; 1 gene was selected based on the SNP-AUC

analysis, and 12 genes were selected on the basis of the expression-AUC analysis. This overall selection strategy is depicted graphically in Figure 7.

For functional validation, either two unvalidated siRNAs or one validated siRNA (based on QIAGEN data) were used to knockdown each of the 23 candidate genes. If two siRNAs were available, “significance” was defined as a gene with a significant change in apparent AUC for both siRNAs in comparison with a control siRNA. MTS assays were performed with all three tumor cell lines for all 23 of the genes selected for study. Knockdown of 7 genes had a significant effect on radiation sensitivity in one cell line, 3 genes were positive for two cell lines and knockdown of 2 genes significantly altered radiation sensitivity in all three cell lines (Table 10 and Figure 8). Five genes were then selected for further study for which knockdown with specific siRNAs significantly altered radiation sensitivity in at least 2 cancer cell lines, specifically *BORA* (*C13orf34*), *MAD2L1*, *PLK4*, *TPD52*, and *TTF1* (Table 10, Figure 8). *DEPDC1B* also was included, even though this gene only showed an effect of knockdown on radiation sensitivity in HeLa cells, since two SNPs located 2.5 and 8.4kb downstream of this gene (rs4326096 and rs2409791) were significantly correlated with the expression of *BORA* ($p=9.97 \times 10^{-5}$ and 4.86×10^{-5} , respectively), a gene that displayed a functional effect on radiation-induced cytotoxicity in all three cancer cell lines (Figure 8, Table 10). The two SNPs were highly linked ($r^2 > 0.9$).

As the next step in the analysis, and to further confirm results obtained with the MTS assay, performed colony-forming assays were performed for these same six genes in the MIA-PaCa2, HupT3 and HeLa cells used to perform the MTS assays. A lung cancer cell line (A459) also was used, since radiation is commonly used to treat lung cancer. As shown graphically in Figure 9, knockdown of *BORA*, *DEPDC1B* and *TPD52* desensitized all four cell lines to radiation treatment. *MAD2L1* knockdown had a significant impact on radiation effect in HeLa and HupT3, but not in the A549 cell line. However, knockdown of *MAD2L1* resulted in lack of colony formation in MIA-PaCa2 cells in the absence of radiation treatment, indicating that this gene might be essential for cell proliferation. Knockdown of *PLK4* only desensitized radiation response in HupT3 cells, consistent with the MTS assay results, and *TTF1* knockdown did not alter radiation sensitivity in any of the four cell lines.

Since the rs4326096 and rs2409791 SNPs were close to *DEPDC1B* and also were associated with *BORA* expression, and since *BORA* knockdown altered radiation sensitivity with both MTS and colony-forming assays, studies were conducted to determine whether the influence of these two SNPs on *BORA* expression might be mediated through the regulation of *DEPDC1B* expression. An association analysis was performed for these SNPs using microarray data for *DEPDC1B*, and the result showed that both SNPs were also highly associated with *DEPDC1B* gene expression level (Figure 10A). Furthermore, expression levels for *BORA* and *DEPDC1B* were significantly and positively correlated (Fig. 10B, $R_p=0.516$, $p<0.0001$), a relationship consistent with the results of the siRNA knockdown experiments. Finally to further characterize the relationship between *DEPDC1B* and *BORA*, siRNA knockdown of *DEPDC1B* was performed, followed by determination of *BORA* expression in HeLa and HupT3 cell lines (Figure 10C), two cell lines that showed significant effects on radiation sensitivity after knockdown of both genes (Figure 8). The results for HeLa cells showed that 24 hours after the knockdown of *DEPDC1B*, *BORA* expression decreased dramatically, while in HupT3 cells this effect was most prominent 48 hours after *DEPDC1B* knockdown.

Table 10: Candidate genes selected for siRNA screening

ID	Gene Symbol	Basis for Selection*			MTS Assay [†]			Colony-forming Assay [‡]			
		Exp. vs. AUC [¶]	SNP vs. AUC [§]	Integrated Analysis [‡]	HupT3	HeLa	MIAPaCa2	HupT3	HeLa	A549	MIAPaCa2
1	<i>BORA (C13orf34)</i>	Yes	---	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	<i>C19orf2</i>	Yes	---	Yes	---	Yes	---	NP	NP	NP	NP
3	<i>CENPL</i>	Yes	---	Yes	---	---	Yes	NP	NP	NP	NP
4	<i>CTNNA1</i>	Yes	---	---	---	---	---	NP	NP	NP	NP
5	<i>DEPDC1B</i>	---	Yes	Yes	---	Yes	---	Yes	Yes	Yes	Yes
6	<i>FAM62B</i>	Yes	---	---	---	Yes	---	NP	NP	NP	NP
7	<i>JMJD2C</i>	---	Yes	Yes	---	---	---	NP	NP	NP	NP
8	<i>KBTBD2</i>	Yes	---	---	---	---	---	NP	NP	NP	NP
9	<i>LDHA</i>	Yes	---	Yes	---	---	---	NP	NP	NP	NP
10	<i>MAD2L1</i>	Yes	---	---	Yes	Yes	Yes	Yes	Yes	---	NC
11	<i>MTMRI2</i>	Yes	---	Yes	---	---	---	NP	NP	NP	NP
12	<i>NIBP (TRAPPC9)</i>	---	Yes	---	---	---	---	NP	NP	NP	NP
13	<i>NRF1</i>	Yes	---	Yes	Yes	---	---	NP	NP	NP	NP
14	<i>PAWR</i>	Yes	---	Yes	---	---	---	NP	NP	NP	NP
15	<i>PLK4</i>	Yes	---	---	Yes	Yes	---	Yes	---	---	---
16	<i>SR140</i>	Yes	---	---	---	---	---	NP	NP	NP	NP
17	<i>STS</i>	Yes	---	---	---	---	---	NP	NP	NP	NP
18	<i>TDP1</i>	Yes	---	---	---	---	---	NP	NP	NP	NP
19	<i>TMEM48</i>	Yes	---	---	---	Yes	---	NP	NP	NP	NP
20	<i>TPD52</i>	Yes	---	---	Yes	Yes	---	Yes	Yes	Yes	Yes
21	<i>TTF1</i>	Yes	---	---	Yes	Yes	---	---	---	---	---
22	<i>UBE2D2</i>	Yes	---	---	---	Yes	---	NP	NP	NP	NP
23	<i>PLEKHF2</i>	---	Yes	Yes	---	---	---	NP	NP	NP	NP

* “Yes” indicates individual candidate genes with the p value listed

† “Yes” indicates knockdown of the gene altered radiation cytotoxicity (AUC values) when compared with control siRNA

‡ P<10⁻³; § P<10⁻⁴; ¶ SNP vs Exp P<10⁻⁴ and Exp vs AUC P<10⁻³

“NP” = not performed; “NC” = no colonies formed for that cell line after knockdown with a specific siRNA

The analyses of SNP, basal gene expression, and radiation cytotoxicity (AUC) data yielded a total of 240 candidate genes, including 211 identified as a result of either expression vs AUC associations ($p < 10^{-3}$) or an “integrated analysis” that included SNP expression and radiation AUC data. In addition, 29 genes also were identified based on the association of SNPs with AUC ($p < 10^{-4}$). When Ingenuity Pathway analysis was performed for these 240 genes, the top three networks all involved “cell death” and centered around NF κ B, PI3K/Akt and p38MAPK/ERK as “network hubs” (Figures 11A-11C). Many candidate genes identified during these studies have been reported to have altered levels of expression in response to radiation exposure in the NCI-60 cell lines or in lymphoblastoid cell lines, especially p53 dependent genes such as *CDC2*, *PHLDA3* and *PTPRC* (Amundson et al. (1999) *Oncogene* 18:3666-3672; Amundson et al. (2005) *Oncogene* 24:4572-4579; Amundson et al. (2008) *Cancer Res.* 68:415-424; Amundson et al. (2003) *Mol. Cancer Res.* 1:445-452; and Jen and Cheung (2005) *Cancer Res.* 65:7666-7673). In addition, genes such as *MEF2B*, *NRF1*, *PHPT1*, *ZMAT3*, *CHEK1*, and *GALR3* that are up- or down-regulated by ionizing radiation exposure, also were found to be associated with radiation AUC (Amundson et al. (2004) *Cancer Res.* 64:6368-6371; Dressman et al. (2007) *PLoS Med.* 4:e106; Jen and Cheung, *supra*; Paul and Amundson (2008) *Int. J. Radiat. Oncol. Biol. Phys.* 71:1236-1244; Rzeszowska-Wolny et al. (2009) *DNA Repair (Amst)* 8:732-738; and Westbury et al. (2009) *J. Pathol.* 219:131-140. The correlation between basal gene expression and radiation cytotoxicity was of greater interest, however, because basal gene expression may eventually be more useful to help predict radiation sensitivity and resistance, while change in gene expression in response to radiation might be more closely related to downstream signaling events.

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An *in vitro* method for predicting the effectiveness of radiation therapy in a subject, said method comprising:

- (a) providing a biological sample from the subject;
- (b) assaying the biological sample to determine whether it comprises a radiation therapy signature; and
- (c) classifying the subject as having a greater likelihood of responding to radiation therapy if the signature is present in the biological sample, and classifying the subject as having a lesser likelihood of responding to radiation therapy if the signature is not present in the biological sample.

2. The method of claim 1, further comprising communicating to a medical professional information regarding whether or not the signature is present in the biological sample.

3. The method of claim 2, further comprising communicating to a medical professional information indicating that the presence of the signature correlates with effectiveness of radiation therapy.

4. The method of claim 1, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs7000734, rs16885294, rs1561715, rs1610110, rs2859631, rs12569163, rs16889440, rs7554126, rs4742269, rs7591064, rs11250464, rs1853665, rs4392868, rs17598306, rs1471356, and rs4554799.

5. The method of claim 1, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, and rs212551.

6. The method of claim 1, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs1610110, rs1561715, rs1561714, rs4392868, rs7000734, and rs212551.

7. The method of claim 1, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs6863920, rs6449478, rs2409791, rs4326096, rs206789, and rs286158.
8. The method of claim 1, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs4463400, rs6578080, rs4397386, rs7387053, rs4487737, rs13275618, rs6578083, rs7814976, rs7841539, rs6578084, and rs9324519.
9. The method of claim 1, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs12553351 and rs4742269.
10. The method of claim 1, wherein said radiation therapy signature comprises rs1610110.
11. The method of claim 1, wherein said radiation therapy signature comprises rs1561715.
12. The method of claim 1, wherein said radiation therapy signature comprises rs7000734.
13. An *in vitro* method for determining a dose of radiation for administration to a subject, said method comprising:
 - (a) providing a biological sample from the subject;
 - (b) assaying the biological sample to determine whether it comprises a radiation therapy signature; and
 - (c) determining that the dose is lower if the signature is present in the biological sample than if the signature is not present in the biological sample, and determining that the dose is higher if the signature is not present in the biological sample than if the signature is present in the biological sample.
14. The method of claim 13, further comprising communicating to a medical professional information regarding whether or not the signature is present in the biological sample.

15. The method of claim 14, further comprising communicating to a medical professional information indicating that the presence of the signature correlates with a lower dose of radiation therapy.

16. The method of claim 13, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs7000734, rs16885294, rs1561715, rs1610110, rs2859631, rs12569163, rs16889440, rs7554126, rs4742269, rs7591064, rs11250464, rs1853665, rs4392868, rs17598306, rs1471356, and rs4554799.

17. The method of claim 13, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs4392868, rs297550, rs1946944, rs12548426, rs1610110, rs1561715, rs1561714, rs4734298, rs7000734, and rs212551.

18. The method of claim 13, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs1610110, rs1561715, rs1561714, rs4392868, rs7000734, and rs212551.

19. The method of claim 13, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs6863920, rs6449478, rs2409791, rs4326096, rs206789, and rs286158.

20. The method of claim 13, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs4463400, rs6578080, rs4397386, rs7387053, rs4487737, rs13275618, rs6578083, rs7814976, rs7841539, rs6578084, and rs9324519.

21. The method of claim 13, wherein said radiation therapy signature comprises one or more markers selected from the group consisting of rs12553351 and rs4742269.

22. The method of claim 13, wherein said radiation therapy signature comprises rs1610110.

23. The method of claim 13, wherein said radiation therapy signature comprises rs1561715.

24. The method of claim 13, wherein said radiation therapy signature comprises
rs7000734.

Figure 1

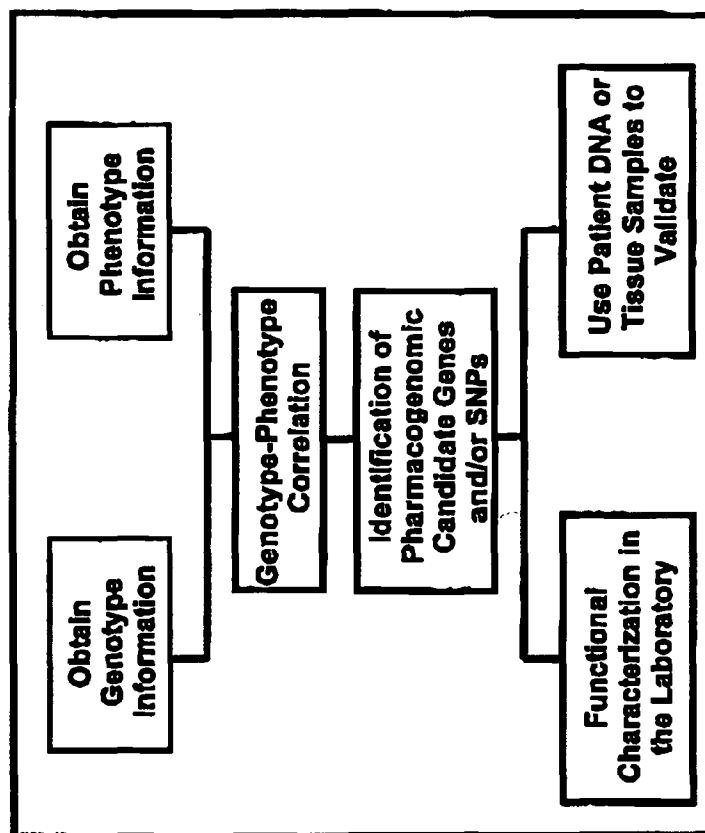


Figure 2

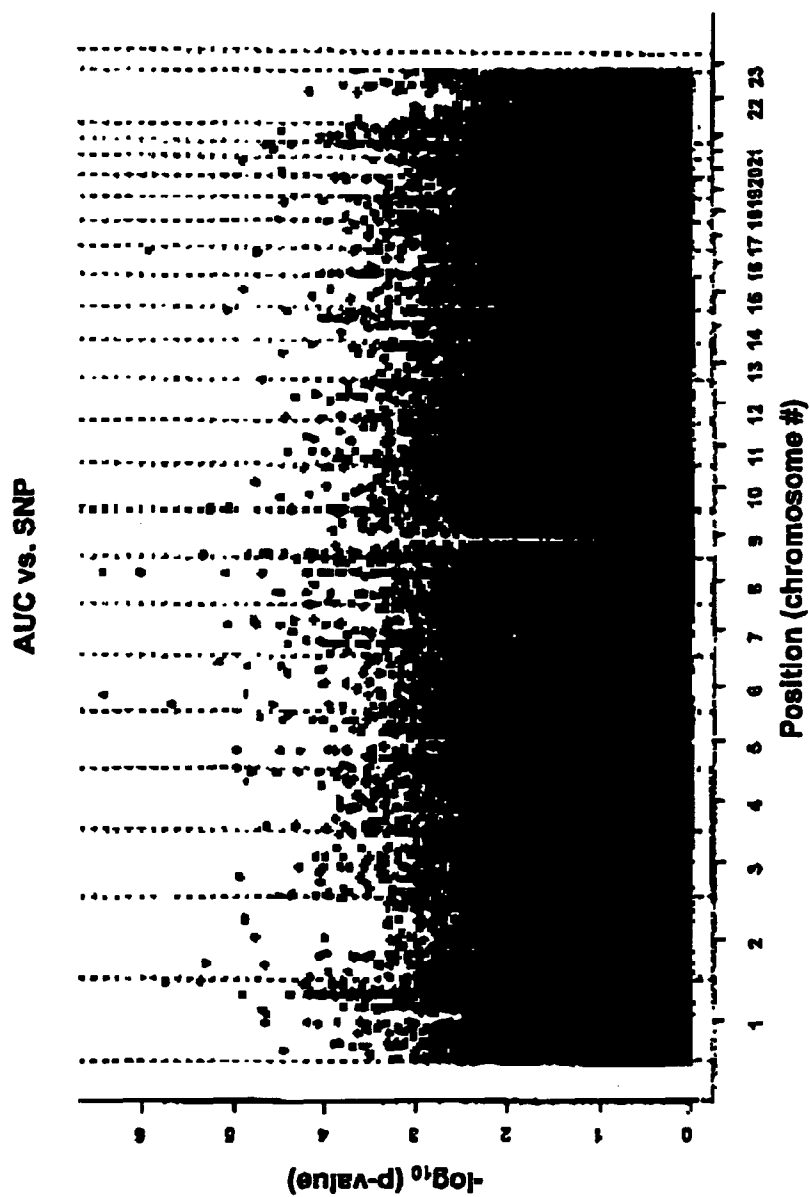


Figure 3

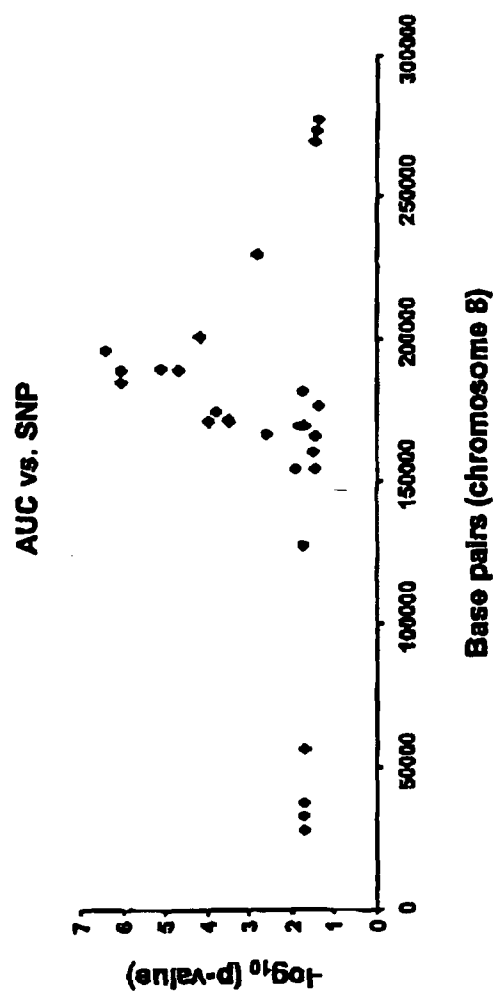


Figure 4

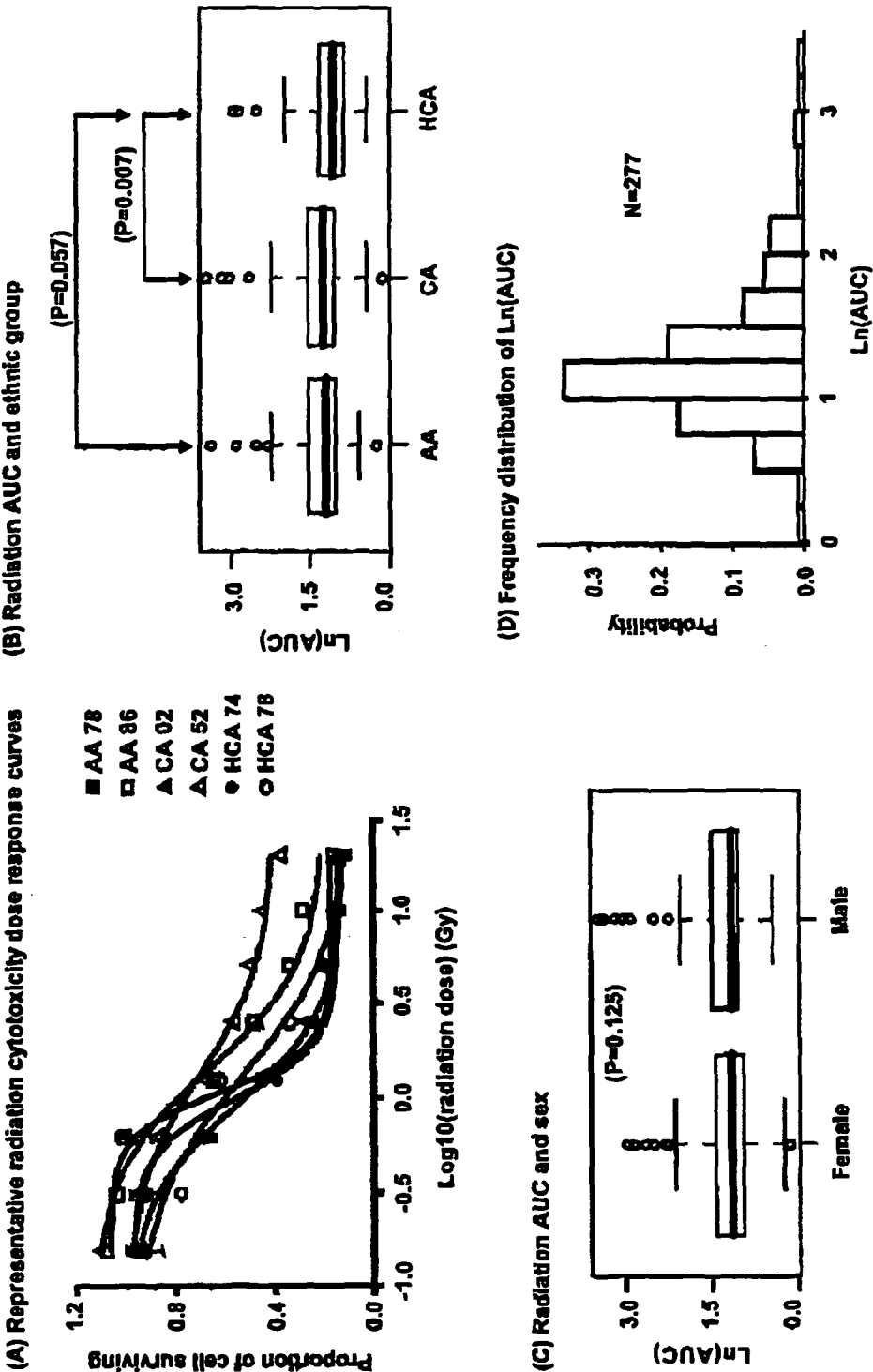
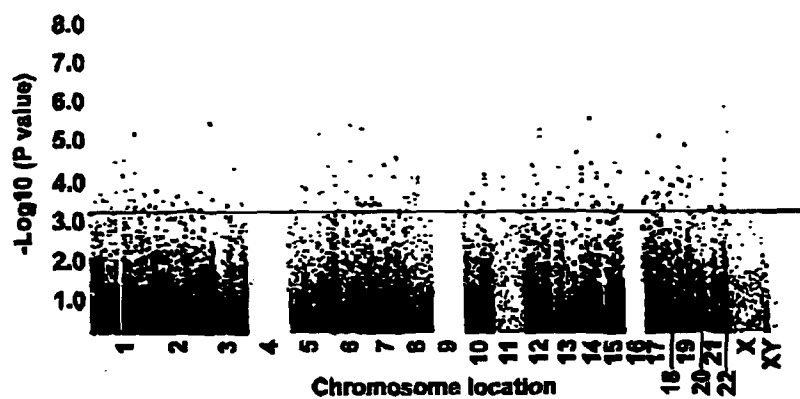
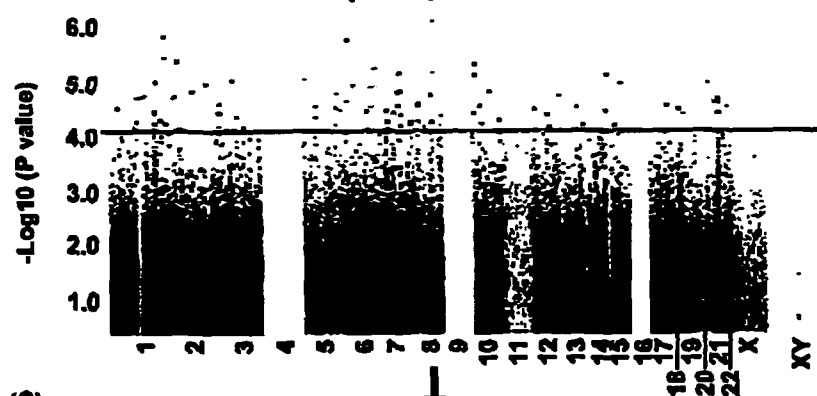


Figure 5

(A) Association of basal expression with radiation AUC



(B) Association of genome-wide SNPs with radiation AUC



(C)

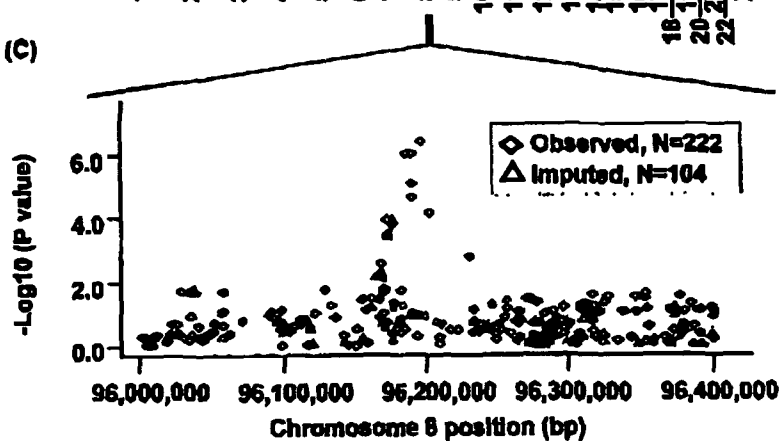


Figure 6

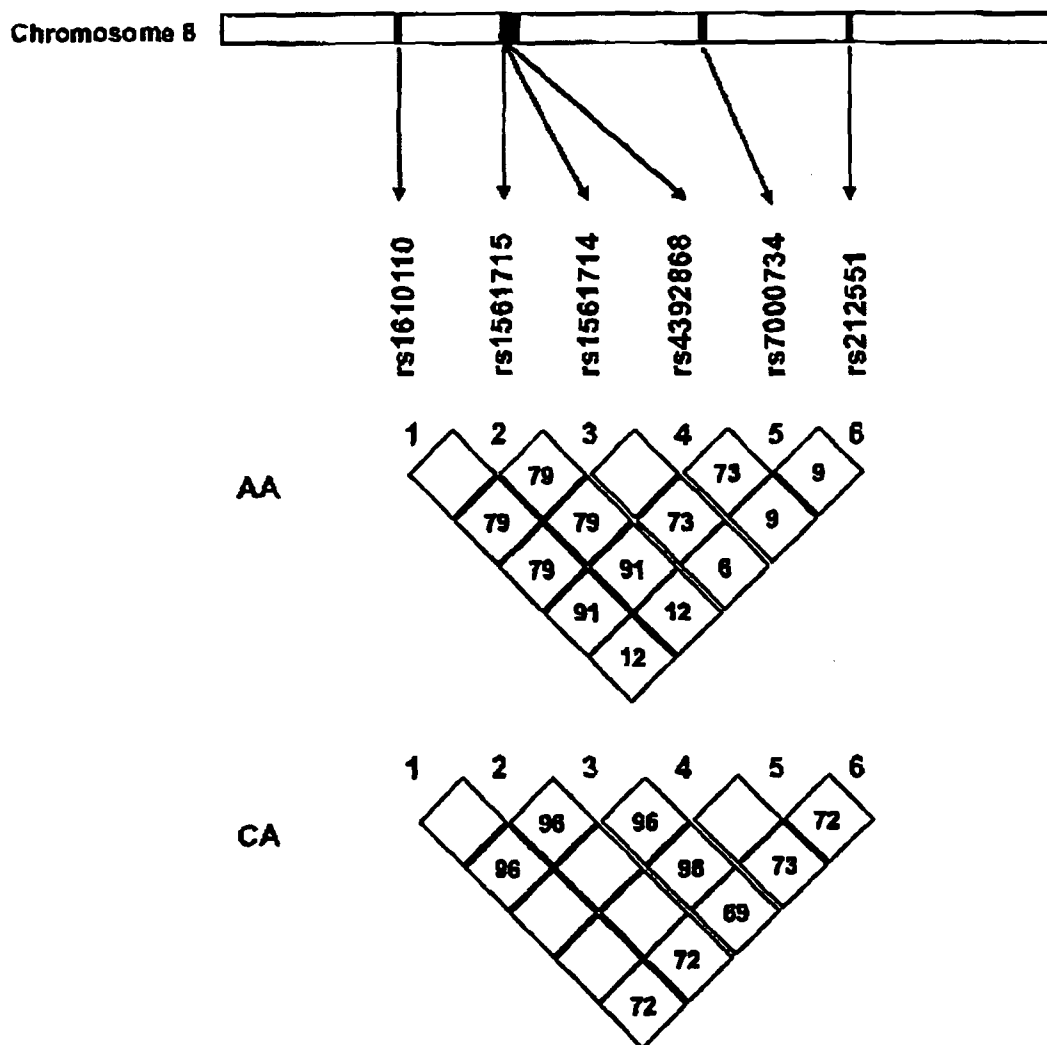


Figure 7

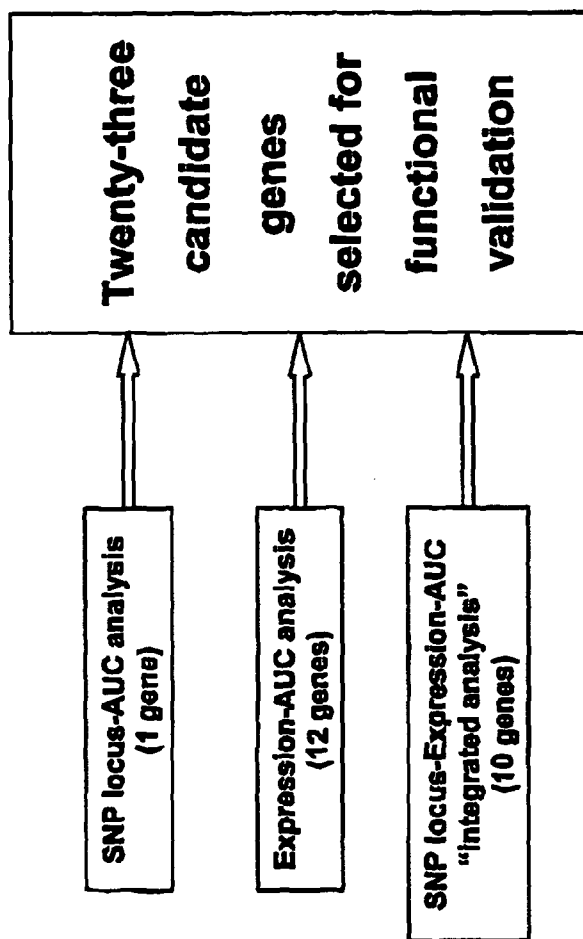


Figure 8

(A) Gene symbol

(B) QRT-PCR

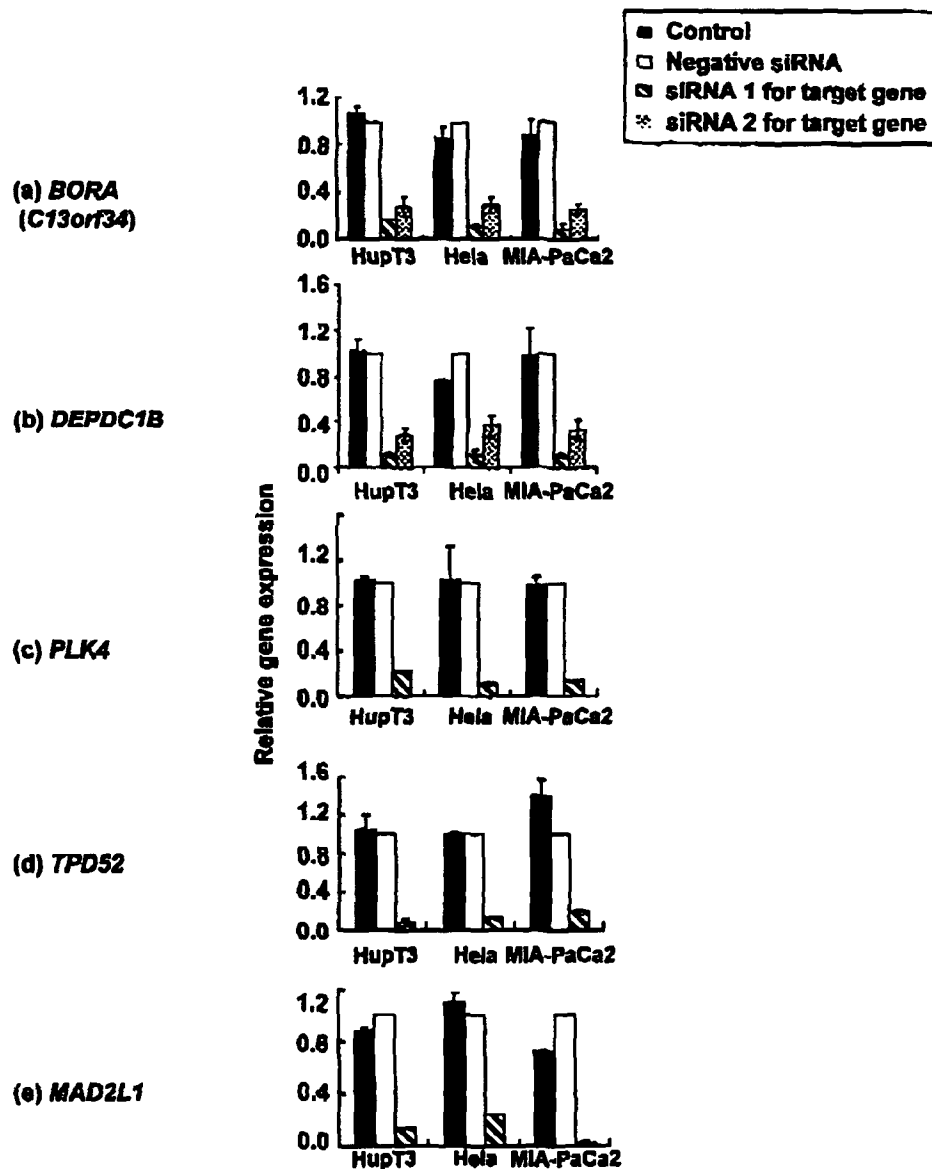


Figure 8C

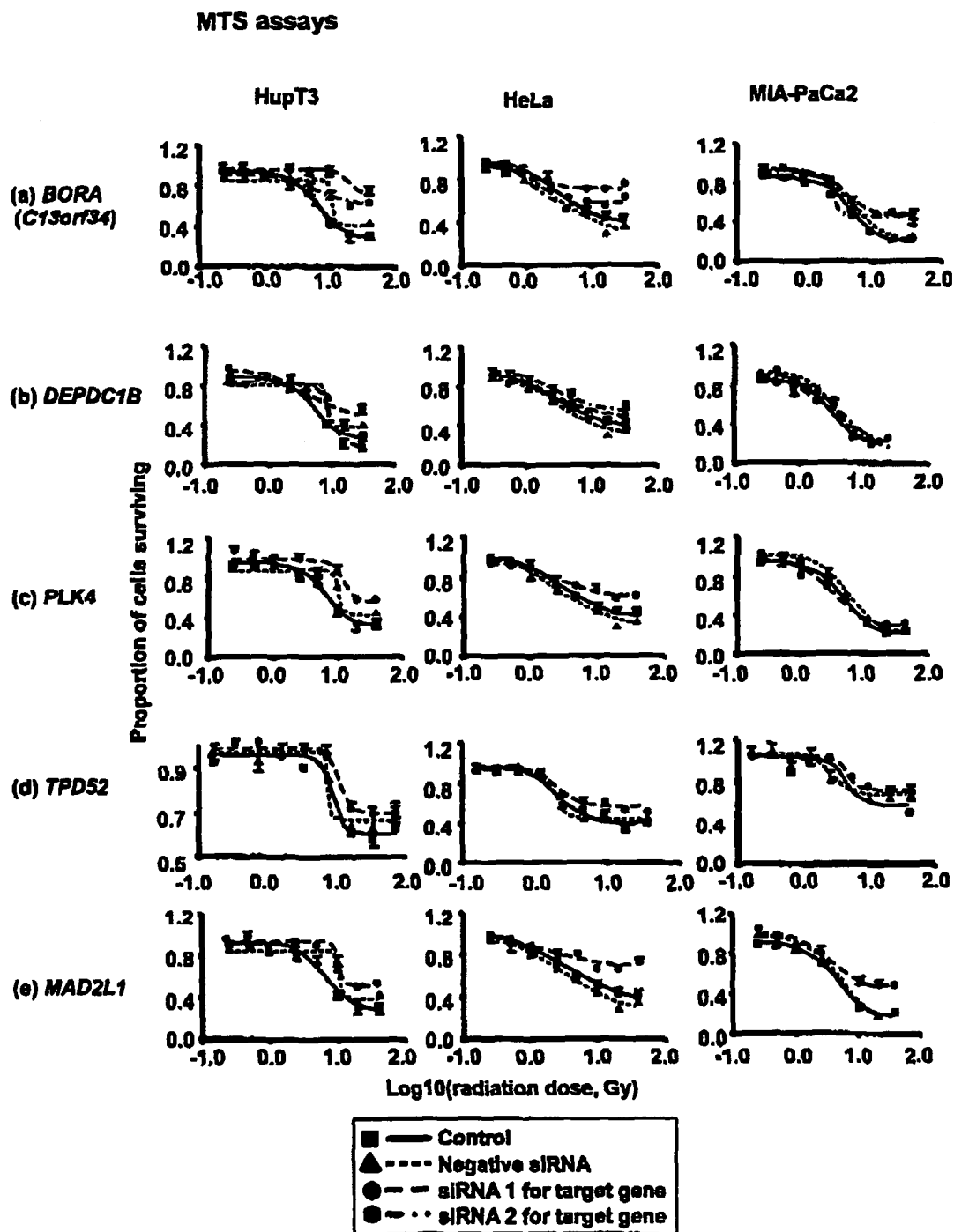


Figure 9

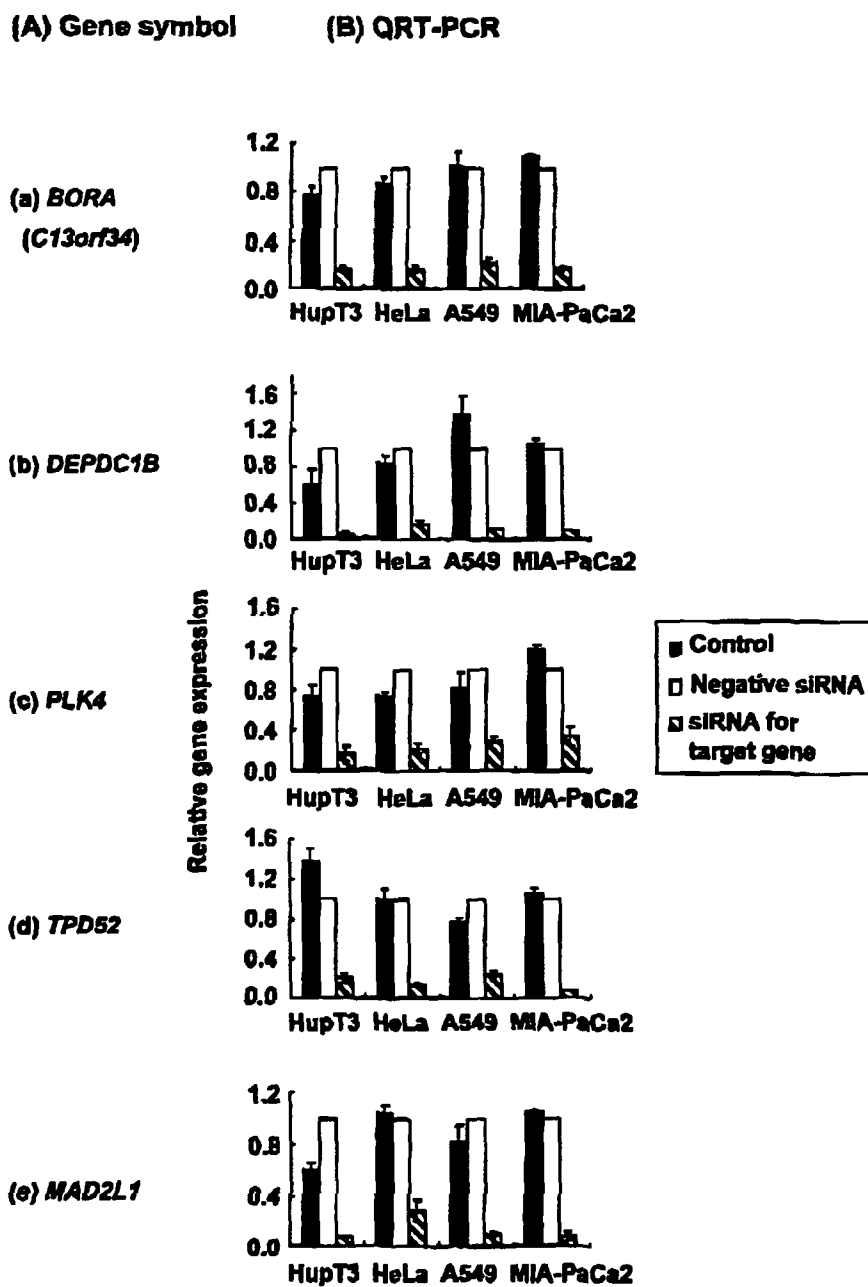


Figure 9C

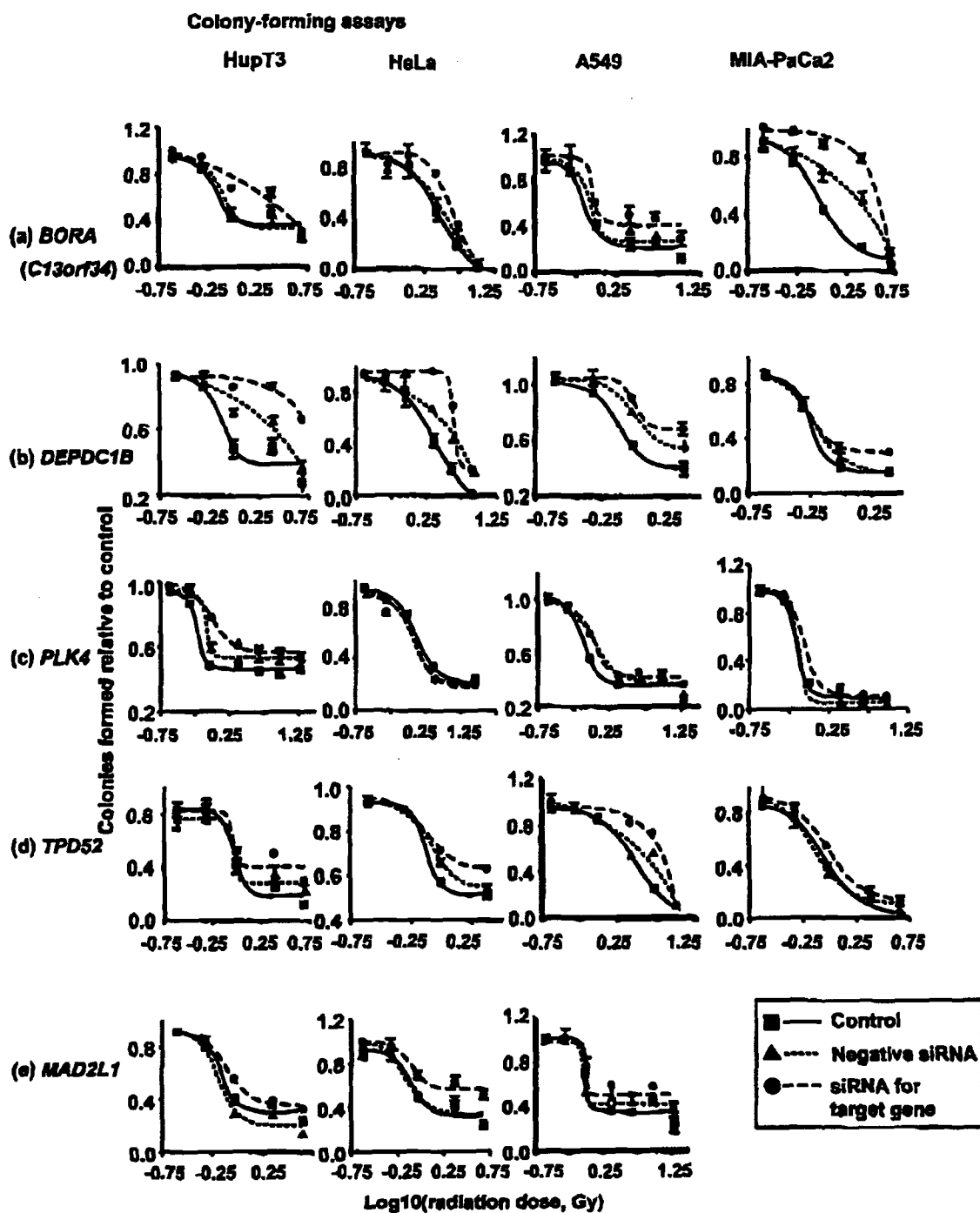


Figure 10A

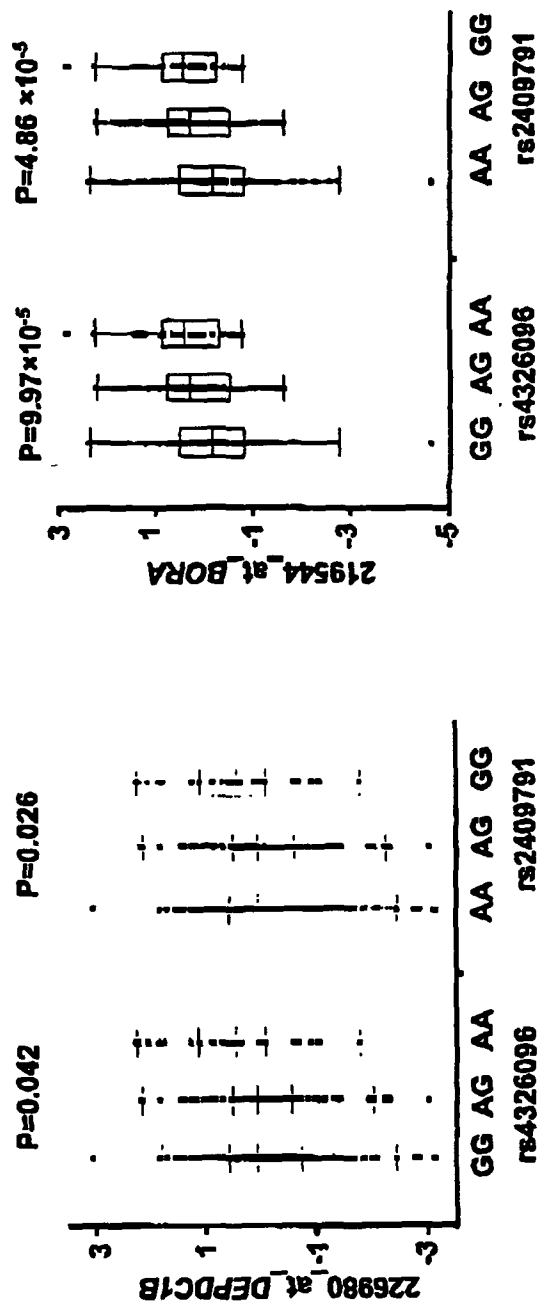


Figure 10B

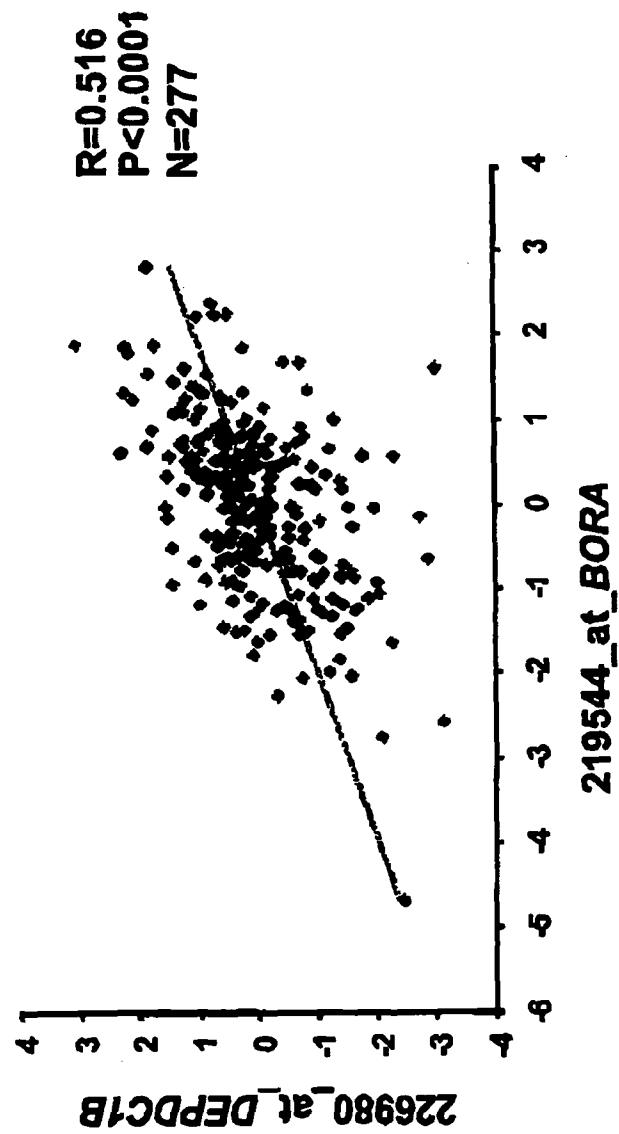


Figure 10C

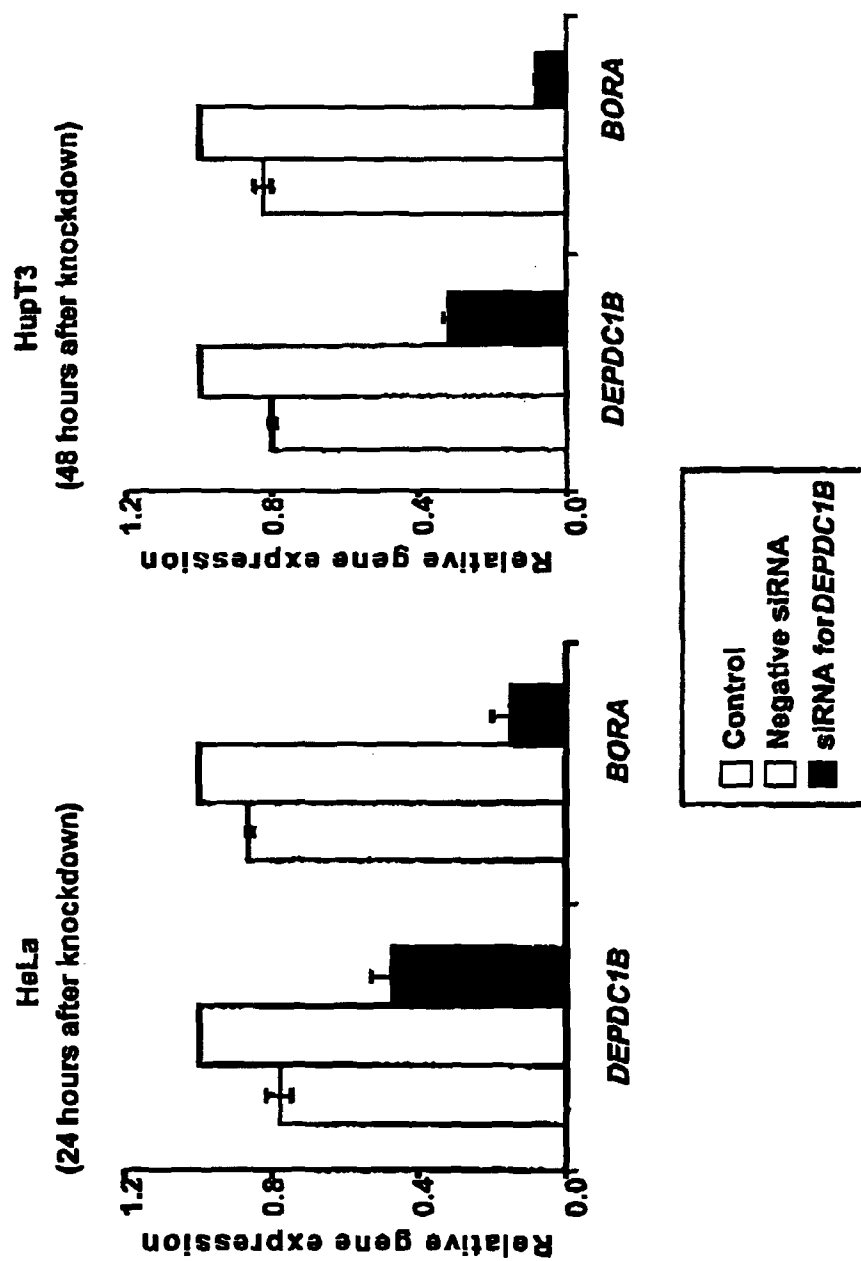


Figure 11B

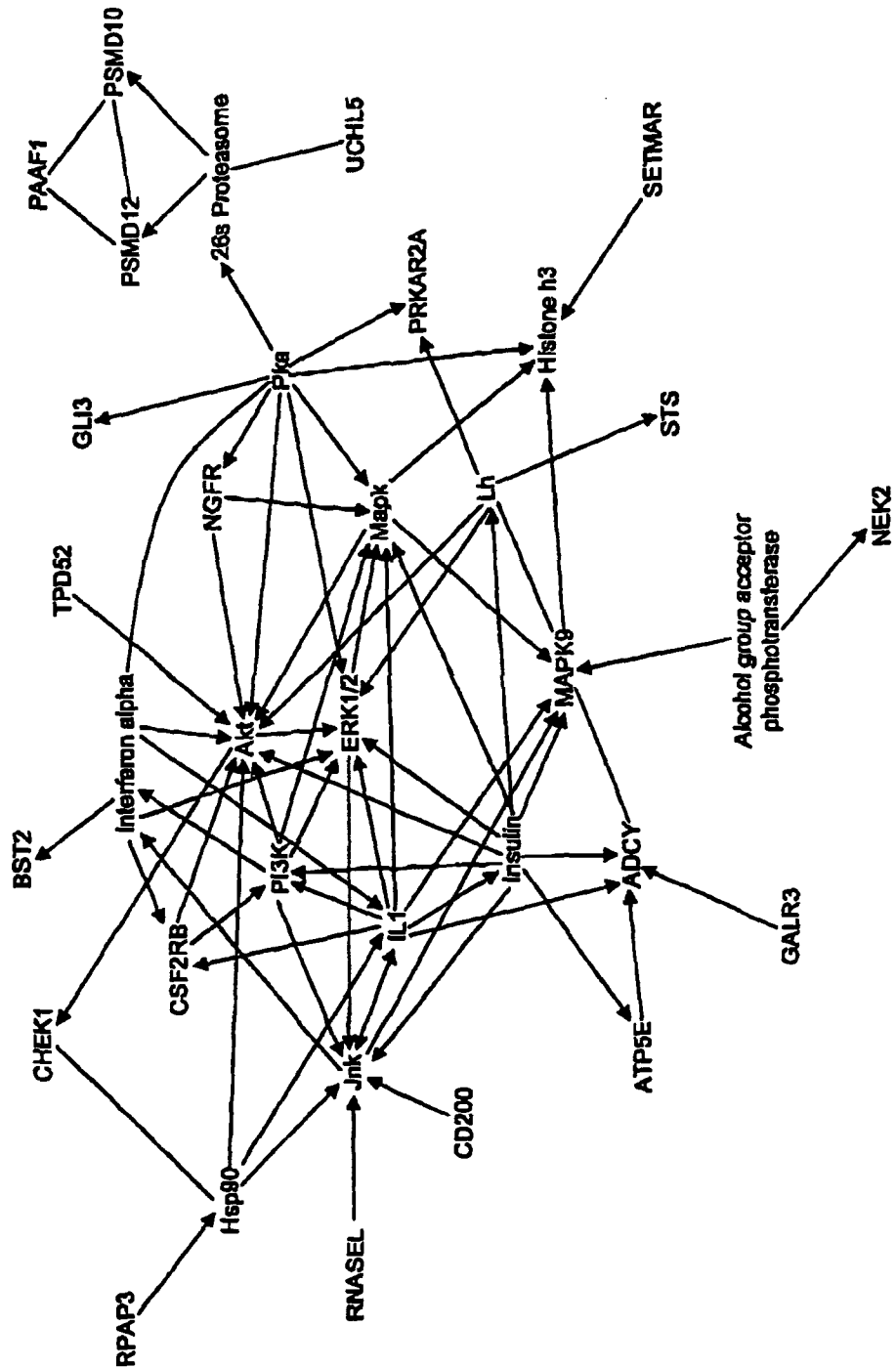


Figure 11C

