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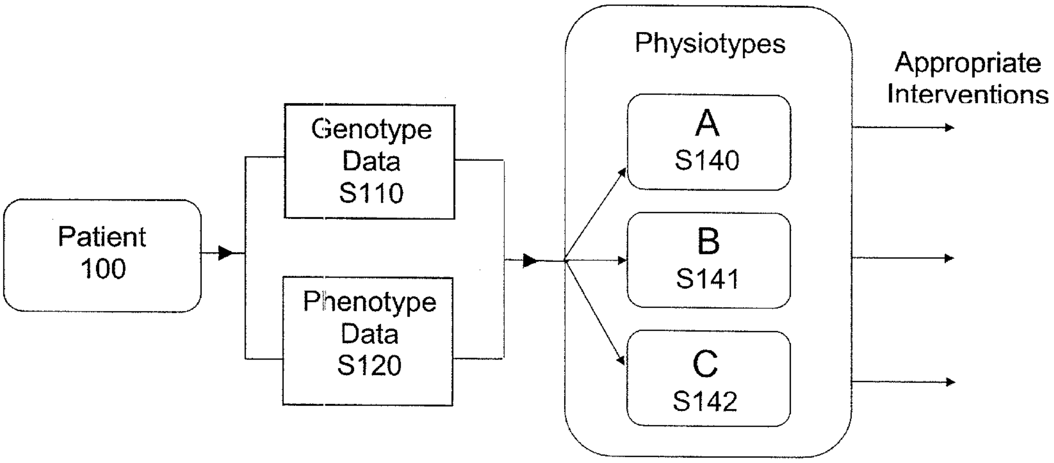
(54) Title: A PHYSIOGENOMIC METHOD FOR PREDICTING CLINICAL OUTCOMES OF TREATMENTS IN PATIENTS



(57) Abstract: A physiogenomic-based method for predicting the outcome of treatment regimens in human patients based upon association screening to identify genetic markers and related physiological characteristics that influence the disease status of a patient, the progression to disease and response to the treatment. By repeating the analysis quantitatively for each of multiple treatment regimens, a profile can be created for each patient to determine which of several treatment regimens are best suited to the patient's clinical needs.

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A Physiogenomic Method For Predicting Clinical Outcomes of Treatments in Patients

Field of the Invention

[0001] In general, the field of the invention is physiogenomics. More specifically, the invention comprises a physiotype method for predicting the results of treatment regimens in a patient.

Background

[0002] Although clinically highly relevant, physiology has remained a systems and macroscopic embodiment of scientific thought separate from the molecular basis of genetics. The physiogenomics method of the present invention bridges the gap between the systems approach and the genomic approach by using human variability in physiological processes, either in health or disease, to drive their understanding at the genome level. Physiogenomics is particularly relevant to the phenotypes of complex diseases and the clustering of phenotypes into domains according to measurement technique, ranging from functional imaging and clinical scales to protein serology and gene expression.

[0003] Physiogenomics integrates genotypes, phenotypes and population analysis of functional variability among individuals. In physiogenomics, allelic genetic markers (single nucleotide polymorphisms or "SNPs", haplotypes, insertion/deletions, tandem repeats) are analyzed to discover statistical associations to physiological characteristics in populations of individuals either at baseline or after they have been similarly exposed or challenged to environmental triggers. These environmental challenges span the gamut from exercise and diet to drugs and toxins, and from extremes of temperature, pressure and altitude to radiation. In the case of complex diseases we are likely to find both baseline characteristics and response phenotypes to as yet undetermined environmental triggers. Variability in a genomic marker among individuals that tracks with the variability in physiological characteristics establishes associations and mechanistic links with specific genes.

[0004] Physiogenomics is a medical application of engineering sensitivity analysis [see, e.g., G. Ruano, A. Windemuth, and T. Holford: "Physiogenomics: Integrating systems engineering and nanotechnology for personalized health", The Biomedical Engineering Handbook, 3rd Edition, CRC Press 2006; T.R. Holford, A. Windemuth, and G. Ruano, "Personalizing public health", Personalized Medicine, 2(3), 2005; and A. Saltelli, K. Chan, and E. M. Scott "Sensitivity Analysis", John Wiley and Sons, Chichester, 2000]. Sensitivity analysis is the study about the relations between the input and the output of a model and the analysis utilizing systems theory, of how variation of the input leads to changes in the output quantities. Physiogenomics integrates systems engineering with molecular probes stemming from genomic markers available from industrial technologies. Physiogenomics utilizes as input the variability in genes and relates the genetic variability to variability in the physiological characteristics, which is the output. As a non-limiting example, the genetic variability may be measured by the frequency of single nucleotide polymorphisms (SNPs). With physiogenomics, ensembles of 10^5 to 10^6 SNP markers can be integrated with population analysis of functional variability among individuals similarly treated [T.R. Holford, A. Windemuth, and G. Ruano, "Personalizing public health", Personalized Medicine, 2(3), 2005]. Variability in SNP frequency among individuals, which tracks with variability in physiological characteristics, establishes genetic associations and mechanistic links with specific genes.

[0005] The physiogenomic method of the invention marks the entry of genomics into systems biology and requires novel analytical platforms to integrate the data and derive the most robust associations. Once physiological systems are under scrutiny, the industrial tools of high-throughput genomics do not suffice, as fundamentals processes such as signal amplification, functional reserve and feedback loops of homeostasis must be incorporated.

[0006] The inventive physiogenomics method includes marker discovery and model building. Each of these interrelated components will be described in a generic fashion. Reduction to practice of the generic physiogenomic invention will then be demonstrated by our experimental data in the Examples section.

Summary of the Invention

[0007] One aspect of this invention is to provide a physiogenomics method for predicting whether a particular treatment regimen will produce a beneficial effect on a patient. The method comprises (a) selecting a plurality of genetic markers based on an analysis of the entire human genome or a fraction thereof; (b) identifying significant covariates among demographic data and the other phenotypes using mathematical modeling, preferably by linear regression and R^2 analysis or more preferably by principal component analysis; (c) performing for each selected genetic marker an unadjusted association test using genetic data; (d) using permutation testing to obtain a non-parametric and marker complexity probability ("p") value for identifying significant markers, wherein the significance is shown by $p<0.10$, more preferably $p<0.05$, and even more preferably $p<0.01$; (e) constructing a physiogenomic model by linear regression analyses and model parameterization for the dependence of said patient's response to treatment with respect to said markers, wherein said physiogenomic model has $p<0.10$, more preferably $p<0.05$, and even more preferably $p<0.01$; and (f) identifying one or more genes not associated with a particular outcome in said patient to serve as a physiogenomic control.

[0008] Another aspect of this invention is to provide a method for treating an individual suffering from a disease or disorder. This method includes the steps of (1) preparing a physiogenomics database that contains a plurality of physiotypes, (2) obtaining genotype and phenotype data of the individual; (3) comparing the genotype data of the individual with said physiotypes in said physiogenomics database; and (4) recommending a treatment regimen based on said comparison.

[0009] In an example of the utility of the invention, apolipoprotein E (APOE) haplotypes are used to predict the outcome of exercise training on serum lipid profiles, such as low density lipoprotein cholesterol (LDL-C), high density lipoprotein cholesterol (HDL-C) and lipoprotein particle size distributions.

[0010] In another example of the utility of the invention, apolipoprotein A1 (APOA1) genotypes are used to predict the outcome of exercise training on serum lipid profiles, such as LDL-C, HDL-C and lipoprotein particle size distributions.

[0011] In still another example of the utility of the invention, genotypes for cholesterol ester transfer protein (CETP), angiotensin converting enzyme (ACE), lipoprotein lipase (LPL), hepatic lipase (LIPC), and peroxisome proliferator-activated receptor-alpha (PPARA) are provided.

[0012] In still another embodiment of the invention, cardiovascular inflammatory markers in blood are associated with exercise training, with genetic probes being derived from candidate genes relevant to energy production, inflammation, muscle structure, mitochondrial oxygen consumption, blood pressure, lipid metabolism, and behavior, as well as transcription factors potentially influencing multiple physiological axes.

[0013] In yet another embodiment of the invention, phenotypes related to plasma concentrations of interleukins and growth factors and cellular expression of ligand receptors are added to the analysis.

[0014] In still another embodiment of the invention, a physiogenomic profile is created for a patient by combining the genomic data for the patient with the patient's clinical and physiological data for each possible treatment modality, said profile serving to provide a logical basis for selecting the most efficacious treatment(s) for the patient.

Brief Description of the Drawings

[0015] Figure 1: A schematic diagram of the physiogenomic method according to the invention.

[0016] Figure 2: Figure 2a shows the response distribution corresponding to serum creatine kinase (CK) activity as the result of statin treatment for the individuals in a reference population whose genetic data was used to form a physiogenomic database. More specifically, Figure 2a shows a 40 SNP ensemble (represented as one per row) for 40 individuals (represented as one per column) in a reference population. Each square is a genotype for a person for one of the SNPs in the ensemble. The color coding is as follows: Black-homozygous, Gray-heterozygous genotypes. Individuals 233 through 149 (20 people) are on the left of the figure and are representative of the bottom quartile of response rankings. Individuals 110 through 70 (20 people) are on the right of the figure and are representative of the upper quartile of response rankings. Figure 2b shows a percentile ranking of a test individual C1's predicted physical response against the distribution of SNP marker ensembles of the reference population which constitute the distribution curve.

[0017] Figure 3: The trend in required sample size to detect a 0.5 standard deviation effect by number of comparisons and carrier prevalence along with the estimate using this approximation.

[0018] Figure 4: A detailed representation of the genetic association tests for 10 SNPs. The overall distribution of log(CK) is shown along with the individual genotypes and a LOESS fit of the allele frequency as a function of log(CK).

Detailed Description of the Preferred Embodiments

[0019] A physiogenomic method for predicting whether or not a particular treatment regimen will have a beneficial outcome in a patient has been invented. The physiogenomic aspect of the method consists of determining genetic markers that are associated with beneficial effects of a particular treatment regimen, and then selecting patients for treatment who present with the beneficial genotype. The physiotype aspect of the method consists of establishing a treatment profile for the patient by combining the aforementioned genomic data with physiological and clinical data for the same patient for each of a set of possible treatments for the patient's medical condition, so as to customize interventions for the patient.

[0020] The following definitions will be used in the specification and claims:

1. Correlations or other statistical measures of relatedness between genotypes and physiologic parameters are as used by one of ordinary skill in this art.
2. As use herein, "polymorphism" refers to DNA sequence variations in the cellular genomes of animals, preferably mammals. Such variations include mutations, single nucleotide changes, insertions and deletions. Single nucleotide polymorphism ("SNP") refers to those differences among samples of DNA in which a single nucleotide pair has been substituted by another.
3. As used herein, "variants" is synonymous with polymorphism.

4. As used herein, "phenotype" refers to any observable or otherwise measurable physiological, morphological, biological, biochemical or clinical characteristic of an organism. The point of genetic studies is to detect consistent relationships between phenotypes and DNA sequence variation (genotypes).
5. As used herein, "genotype" refers to the genetic composition of an organism. More specifically, "genotyping" as used herein refers to the analysis of DNA in a sample obtained from a subject to determine the DNA sequence in one or more specific regions of the genome, for example, at a gene that influences a disease or drug response.
6. As used herein, "genetic marker" refers to the partial or complete sequence of an inherited segment of DNA constitutional to an individual. The DNA segment may include a SNP, a part of a gene, an entire gene, several genes or a region devoid of genes
7. As used herein, the term "associated with" in connection with a relationship between a genetic marker (SNP, haplotype, insertion/deletion, tandem repeat) and a phenotype refers to a statistically significant dependence of marker frequency with respect to a quantitative scale or qualitative gradation of the phenotype.
8. As used herein, a "gene" is a sequence of DNA present in a cell that directs the expression of biochemicals, i.e., proteins, through, most commonly, a complementary RNA.
9. "BMI" refers to body mass index.

[0021] This invention provides methods for determining physiotypes acquired from physiogenomic data and using the physiotypes to select which treatment or treatments would be most efficacious for a patient suffering from a disease or a disorder. Physiotypes are useful for describing an ensemble of genetic markers and an interpretative algorithm used as a medical device or platform to predict an individual's physiological response to a treatment. The use of physiotypes for studying environmental interactions for the prevention and treatment of disease is attractive, for several reasons. For example, because the determination of a physiotype involves, in part, a determination of a genotype component that does not change as a result of environmental stimuli, the contribution of the genotype component is not confounded with environmental stimuli. Furthermore, some genotypes associated with a phenotype can act as a surrogate marker for the phenotype, which can be useful when measurement of the phenotype is difficult, expensive, or confounded by environmental conditions. Additionally, the cost of developing robust, reliable physiotypes has decreased with the decreasing cost associated with new automated genotyping technologies, which have allowed for economic determination of multiple genotypes from different genes coding for proteins in interacting pathways.

[0022] Figure 1 shows a schematic diagram of the method according to the invention. The inventive method uses genotype data S110 and phenotype data S120 of patient 100 as inputs for physiogenomic analysis S130, which establishes physiotypes A, B, and C (corresponding to reference numerals S140, S141, and S142 in Figure 1, respectively). In determining which interventions would be appropriate, it is often useful to calculate a patient's predicted physiological response using the physiological responses of the reference population whose genetic data forms the physiogenomic database. By way of example, Figure 2a shows genetic data of a reference population consisting of 40 individuals. As shown in Figure 2b, the predicted physiological response of a test individual C1 can be graphically displayed, on a percentile basis, by comparing the genetic data of C1 against the genetic marker ensembles of the reference population, illustrated as a distribution curve.

[0023] These physiotypes taken together constitute a physiogenomics database to which a physician could refer in order to determine an efficacious, personalized treatment protocol for a patient. A physician with genetic and clinical information about a particular patient could determine which interventions would be appropriate, by comparing the patient data with the physiotypes in the physiogenomic database.

[0024] As used herein, the term "interventions" refers to any type of treatment, non-limiting examples of which include dietary changes or restrictions, drug therapy, exercise, or even specific combinations of such treatments. Generally, the number of interventions will be sufficient such that the probability that the patient will respond poorly to all of the interventions will be quite small. For example, in a scenario where there are three possible interventions, the probability that the patient's response will be in the bottom 25% for all three treatments is $(1/4)^3 = 1/64$ or about 1.5%.

Development of Physiotypes

[0025] Physiotypes may be developed from genotypes from various genes and genomic regions. As set forth below, in preferred embodiments, the physiotypes are developed using either (1) hypothesis free association screening, or (2) hypothesis-led association screening. In either method of screening, genetic markers are correlated with phenotypes that may be determined from clinical studies. However, this invention also recognizes that sometimes genetic effects are not direct, and that it is advantageous to use endophenotypes in the development of physiotypes. As used herein, "endophenotypes" are observable intermediate phenotypes that can be measured to provide additional information about the association between an individual's genes and his response. Non-limiting examples of endophenotypes contemplated by the invention include mRNA expression levels, functional brain imaging data, and blood levels of cells, proteins, lipids, and metabolites. The use of endophenotypes to break down genetic/physiological associations into intermediate levels is advantageous for several reasons. First, each individual interaction is more direct, and therefore stronger (i.e., less diluted by confounding variables) and easier to detect. Second, there may be multiple associations on each level contributing to the overall association, providing a degree of redundancy such that the overall association can still be found, even if some of the components are missed. Third, the structure of the intermediate associations provides a significant amount of information about the underlying mechanism that gives rise to the association.

A. Determination of Markers by Hypothesis Free Association Screening

Array Design and Fabrication

[0026] With the rapid development array technology for SNP analysis, it has now become possible to use a "hypothesis free association screening" approach to determine the genotype component of a physiotype. In this context, the term "hypothesis free association screening" refers to a method of genetic screening that involves screening the entire human genome, rather than a subset of the genome based on a pre-conceived "hypothesis" of which genes would be relevant. This method offers the possibility of discovering new, previously unknown correlations between genotypes and phenotypes.

[0027] The genetic screening contemplated by the invention for hypothesis testing is not particularly limited, and may involve any DNA screening platform that has sufficiently high throughput density and is sensitive to one or more genetic markers, non-limiting examples of which include SNPs, haplotypes, insertions/deletions, and tandem repeats. By way of example, the array may be a fixed array, wherein SNP specific reagents are deposited on a substrate using photolithographic techniques similar to that commonly used in the semiconductor industry. Alternatively, the exemplary array may be a random array, wherein the location of the SNP specific reagents is not predetermined but random, and the identity of reagents is identified by use of various markers. For example, a SNP specific random array may be a microbead array, wherein various SNP specific reagents are chemically linked to microscopic beads (e.g., 2 microns or less) that also have covalently attached fluorescent identifier molecules. Typically, in such bead-based arrays, the beads are immobilized to a surface prior to detection. (See, e.g., U.S. Patent Nos. 6,327,410; 6,429,027; and 6,797,524, all of which are hereby incorporated by reference in their entirety.)

[0028] In a particularly preferred embodiment of the invention, the DNA array platform involves attaching oligonucleotide probes 10-20 nm long onto the surface of microbeads with an average diameter of about 2 microns. The beads are divided into different subpopulations, wherein each bead in a given subpopulation has a different SNP specific oligonucleotided (typically about 50 bases in length) which is designed to hybridize specifically to a specific spot on the genome adjacent to the SNP. Allele specific extension with labeled oligonucleotides is used to confer a fluorescent signal to only those beads that carry a matching probe for a given allele. Furthermore, the individual subpopulations are marked by subpopulation-specific markers.

[0029] In addition to the fixed and random arrays described above, this invention also contemplates the use of a "liquid arrays", which do not require the immobilization of beads, but instead use a microfluidic device similar to a flow cytometer to identify and to read the signal from the microscopic beads while they are suspended in liquid. While current liquid arrays are suitable for small arrays only (e.g., analyzing 100 SNPs in parallel), the rapid advances in liquid array technology suggest that liquid array technology holds promise for large scale genetic analysis.

Determination of Array Size

[0030] While microarray technology, such as the bead-based microarray technology described above, can be used to produce thousands of biomarkers for subject, it is widely recognized that Type I error rates (i.e., the error rate resulting from false positives that exist when a test incorrectly reports that it has found a result when none really exists) from studies of numerous markers can become unacceptably high, producing false discoveries that arise from multiple comparisons. Accordingly, sample size must be increased to take into account these multiple comparisons. One aspect of this invention is the recognition that the logarithmic dependence of sample size on marker number makes it possible to analyze a large number of markers with only a modest increase in the number of people in the test population. For example, using a typical expression for calculating sample size, *n*, as well as an approximation to the error function yields a good approximation to sample size calculation with a Bonferroni adjustment, where the significance level is α / c (α = significance level, and c = number of SNPs

$$n = \frac{\left(z_\alpha \sigma_0 + z_\beta \sigma_1\right)^2}{p\left(1-p\right)\Delta^2} + \frac{2\left(1+\left(z_\beta / \sqrt{0.5 \ln c_{\max} - 2\ln\alpha}\right)\right)\sigma_0^2}{p\left(1-p\right)\Delta^2} \cdot \ln c$$

where σ_0^2 and σ_1^2 are variances of response under null and alternative hypotheses, β = Type II error (a Type II error, also called a false negative, exists when a test incorrectly reports that a result was not detected, when it was really present), $z_{.}$ = standard normal deviate, p = carrier proportion (under Hardy-Weinberg equilibrium, $p = 1-\left(1-\phi\right)^2$ where ϕ = allele frequency), and Δ = effect size. Thus, the increased sample size required to study 10 genes (using the Bonferroni adjustment) instead of one is the same as that required to study 100 genes instead of 10. Thus, huge gains in efficiency may be realized with a modest increase in sample size. Figure 3 shows the trend in required sample size to detect 0.5 standard deviation effect by number of comparisons and carrier prevalence along with the estimate using this approximation.

For example, when the carrier prevalence is 20%, the total sample size required for a single gene is 263, which increases to 412 for 10 genes and 561 for 100 genes. Thus, if one were to consider the entire human genome (about 100,000 genes), the required sample size is only 1009, about four times as large for a single gene study.

[0031] By way of example, Table 1 lists a few strong associations reported in the literature, along with the sample sizes needed to detect each of them as significant (alpha = 0.05, power = 80%), while correcting for 100,000 markers testing using the Bonferroni correction. All of the markers listed would be detected as significant in a genome wide study of 400 subjects, In particular, the angiotensin converting enzyme would be significant at N=100.

Table 1: Selection of strong associations reported in the literature. The minimum sample size (Nwg) required to detect the association in a whole genome association study of 100,000 markers is given for each.

Marker			N		Effect		
Gene	Allele	Freq	tot	carr	Absolute	SD	Nwg
Apolioprotein E	*2 hom	0.0081	14	4	-53 mg/dl apo B in VLDL	3.15	412
Apolioprotein A1	-75 G/A	0.3	75	22	7.9 mg/dl HDL	0.7	324
Hepatic Lipase	514 C/T	0.015	133	2	28 mg/dl HDL-C	2.8	283
Apolioprotein E	*4	0.31	260	81	0.93 mg/L CRP	0.86	207
Adipocyte-derived leucine aminopeptidase	Arg527	0.4	40	16	13.4 g/m^2 dLVMI	0.85	190
Angiotensin converting enzyme	250 bp Ins/del	0.17	80	14	100 µg/l ACEser	1.5	101

[0032] While the Bonferroni method provides a conservative estimate of the required sample size, this invention also contemplates other methods of determining sample size, such as the false discovery rate (see. e.g., A Reinere, et al. "Identifying differentially expressed genes using false discovery rate controlling procedures", Bioinformatics 2003, 19:368-375; Y. Benjamin et al, "Controlling the false discovery rate: a practical and powerful approach to multiple testing"; Journal of the Royal Statistical Society, Series B 1995; 57:289-300; Y. Benjamin et al., "On adaptive control of the false discovery rate in multiple testing with independent statistics"; Journal of Educational and Behavior Statistics 2000; 25:60-83.)

B. Determining physiogenomic markers by hypothesis-led association screening

Association Screening

[0033] In addition to hypothesis free testing, this invention also contemplates identifying physiogenomic markers by association screening. The purpose of association screening is to identify any of a large set of genetic markers (SNPs, haplotypes, insertion/deletions, tandem repeats) associated with physiological characteristics, i.e., factors that have an influence on the disease status of the patient, the progression to disease or the response to treatment. In certain preferred embodiments of the invention, association screening uses DNA screening technology (such as the fixed or random array technology described above) in order to determine the relevant genetic markers. However, unlike the hypothesis free association screening approach, the hypothesis-led association screening approach does not examine the entire human genome, but instead uses only a subset of genome as candidate genes. Typically, candidate genes have been already reported in the literature. For example, in certain preferred embodiments, the genetic markers of interest are SNPs, and the array is constructed using SNPs that are reported in the SNP Knowledge resource database, a user-friendly source for SNP annotation that represents a compendium of information derived from dbSNP, ENSEMBL, HapMap.Org, and Illumina's database. Useful factors to consider in the designing an array include Minor Allele Frequencies (MAF) information, validation status, genome coordinates, and locations within genes (intron, exon, splice site, promoter)

Association Testing

[0034] One of the challenges in data analysis is spotting the trends in the data when the amount of data is extremely large. This is particularly true in physiogenomic studies, where the entire genome may be investigated (e.g., by hypothesis free discovery) or a large set of genetic markers has been pre-selected (e.g., by hypothesis-led association screening) One aspect of this invention is the recognition that (1) it is advantageous to log transform clinically derived data (such as the serum concentration of a particular substance) in order to derive an approximately normally distributed variable, and (2) that an association can be visualized by plotting a locally smoothed function of the genetic marker data (e.g., the SNP frequency) against such log transformed data. In one particularly preferred embodiment, the locally smoothed function of the genetic data is obtained by using LOESS (LOcally-wEighted Scatter plot Smooth) smoothing. LOESS is a method to smooth data using a locally weighted linear regression [e.g., see W.S. Cleveland, "Robust locally weighted regression and smoothing scatterplots", J. Am. Stat. Assoc. 74, 829-836 (1979); W.S. Cleveland et al, "Locally weighted regression: an approach to regression analysis by local fitting, J. Am.Stat. Assoc. 83, 596-610 (1988)]. At each point on the LOESS curve, a quadratic polynomial is fitted to the data in the vicinity of that point. The data are weighted such that they contribute less if they are further away, according to the tricubic function

$$w_i = \left(1 - \left|\frac{x - x_i}{d(x)}\right|^3\right)^3$$

where x is the abscissa of the point to be estimated, the x_i are data points in the vicinity, and $d(x)$ is the maximum distance of x to the x_i.

[0035] The LOESS curve generated for a particular set of data that has been plotted as the genetic marker frequency versus the log transformed clinical data is useful because it shows the localized frequency of the least common allele for sectors of the distribution. For genetic markers with strong association, the marker frequency is significantly different between the high end and the low end of the distribution. Conversely, if a marker is neutral, the LOESS curve is essentially flat, because the marker frequency will be independent of the log transformed clinical data. By way of example, Figure 4 shows a detailed representation of the genetic association tests for 10 different SNPs, and their relationship to creatine kinase (CK) levels. The overall distribution of log(CK) is shown along with the individual genotypes and a LOESS fit of the allele frequency as a function of log(CK). The bell curve shows the actual distribution of CK activity phenotype in a clinical database. The LOESS curve shows the localized frequency of the least common allele for sectors of the distribution. For SNPs with a strong association, the marker frequency is significantly different between the high end and the low end of the distribution. Conversely, if a marker is neutral, the frequency is independent on the CK activity and the LOESS curve is essentially flat. For example, the first figure of the panel shows the LOESS curve for SNP rs12695902 which is located in the gene for angiotensin II receptor, type 1 (AGTR1). The frequency of the minor allele is almost zero in subjects with low CK activity, whereas it approaches 50% at the high end of CK activity. This is indicative of a strong association between the marker and CK activity.

[0036] In certain embodiments, the association between each genetic marker and the outcome, whether derived from hypothesis-free discovery or by hypothesis-led association screening, is tested using logistic regression models, controlling for the other genetic markers that have been found to be relevant. The magnitude of these associations is measured with the odds ratio, and the statistical significance of these associations is determined by constructing 95% confidence intervals. Multivariate analyses are used which include all genetic markers that have been found to be important based on univariate analyses. Because the number of possible comparisons can become very large in analyses that evaluate the combined effects of two or more genes, the results include a random permutation test for the null hypothesis of no effect for two through five combinations of genes. This test is performed by randomly assigning phenotypes to each individual in the study. Random associations of phenotypes and genotypes of the invidividuals are implied by the null distribution of no genetic effect. A test statistic can be calculated that corresponds to the null hypothesis of the random combination effects of genotypes and phenotypes. Repeating this process 1000 times provides an empirical estimate of the distribution for the test statistic, and hence a p-value that takes into account the process that gave rise to the multiple comparisons.

[0037] A single association test will proceed in 3 steps:

(Step 1) Covariates

[0038] The purpose of this step is to identify significant covariates among demographic data and the other phenotypes and delineate correlated phenotypes by principal component analysis. Covariates are determined by generating a covariance matrix for all markers and selecting each significantly correlated markers for use as a covariate in the association test of each marker. Serological markers and baseline outcomes are tested using linear regression.

(Step 2) Associations

The purpose of this step is to perform an unadjusted association test, linear regression for serum levels and baselines). Tests should be performed on each marker, and markers that clear a significance threshold of $p < 0.05$ are selected for permutation testing.

(Step 3) Multiple comparison corrections

[0039] In this step, a non-parametric and marker complexity adjusted p-value are generated by permutation testing. This procedure is important because the p-value is used for identifying a few significant markers out of the large number of candidates. Model-based p-values are unsuitable for such selection, because the multiple testing of every potential serological marker and every polymorphic marker will be likely to yield some results that appear to be statistically significant even though they occurred by chance alone. If not corrected, such differences will lead to spurious markers being picked as the most significant. A correction will be made by permutation testing, i.e., the same tests will be performed on a large number of data sets that differ from the original by having the response variable permuted at random with respect to the marker, thereby providing a non parametric estimate of the null distribution of the test statistics. The ranking of the non-permuted test result in the distribution of permuted test results will provide a non-parametric and statistically rigorous estimate of the false positive rate for this marker. For permutation testing, a large number *(e.g.,* 1000) of permutated data sets are generated, and each candidate marker is retested on each of those sets. A p-value is assigned according to the ranking of the original test result within the control results. A marker is selected for model building when the original test ranks, for example, within the top 50 of the 1000 ($p<0.05$).

(Step 4) Genomic controls and negative results

[0040] Each gene not associated with a particular outcome effectively serves as a negative control, and demonstrates neutral segregation of non-related markers. The negative controls altogether constitute a "genomic control" for the positive associations where segregation of alleles tracks segregation of outcomes. By requiring the representation of the least common allele for each gene to be at least 10% of the population, one can rule out associations clearly driven by statistical outliers. Negative results are thus particularly useful in physiogenomics. To the extent that specific candidate genes are not linked to phenotypes, one can still gain mechanistic understanding of complex systems, especially for segregating the influences of the various candidate genes among the various phenotypes.

B. Construction of physiogenomic models

(Step 1) Model building

[0041] The next stage in the inventive method is physiogenomic modeling. Once the associated markers have been determined, a model is built for the dependence of response on the genetic markers. In the first phase, linear regression models of the following form are preferably used:

$$R = R_o + \sum_i \alpha_i M_i + \sum_i \beta_i D_i + \varepsilon$$

where R is the respective phenotype variable (e.g., BMI), M_i represents the marker variables, D_i are demographic covariates, and ε is the residual unexplained variation. The model parameters that are to be estimated from the data are R_0, α_i and β_i.

(Step 2) Model parameters

[0042] The models built in the previous step will include parameters based on the data. The maximum likelihood method is preferably used, as this is a well-established method for obtaining optimal estimates of parameters.

[0043] In addition to optimizing the parameters, model refinement may be performed. In the first phase linear regression model, this consists of considering a set of simplified models by eliminating each variable in turn and re-optimizing the likelihood function. The ratio between the two maximum likelihoods of the original compared to the simplified model then provides a significance measure for the contribution of each variable to the model.

(Step 3) Model validation

[0044] A cross-validation approach is used to evaluate the performance of models by separating the data used for parameterization (training set) from the data used for testing (test set). A model to be evaluated is readjusted with parameters derived using all data except for one patient. The likelihood of the outcome for this patient is calculated using the outcome distribution from the model. The procedure is repeated for each patient, and the product of all likelihoods is computed. The resulting likelihood is compared with the likelihood of the data under the null model (no markers, predicted distribution equal to general distribution). If the likelihood ratio is $p < 0.05$, the model should be evaluated as providing a significant improvement of the null model. If this threshold is not reached, the model is not sufficiently supported by the data, which could mean either that there is not enough data, or that the model does not reflect actual dependencies between the variables.

[0045] Physiotypes for various treatments are used for decision support in a menu driven format (see Example 6, below). For achieving a desired therapeutic outcome for a given patient, physiotypes for each of the various treatment alternatives (exercise, drugs, and diet) are applied to predict quantitatively the patient's response for each. To derive the physiotypes, physiological and clinical data gathered by the physician and genomic data from several genetic markers, are combined to produce an intervention profile menu. Predictions made by the physiotype will rank the best alternatives among the menu options to achieve a desired goal. As more options are built into the menu, the greater the chance that all patients will be served with increased precision of intervention and with optimal outcome.

[0046] As long as the appropriate physiogenomics research has been performed for each intervention in the menu, an individual's physiotypes would evaluate all possibilities for optimized healthcare. The clinician can query for simple indexes such as raising HDL, or lowering triglycerides or compounded indexes such as LDL/HDL ratios or simultaneous elevation of HDL and reduction of TG. Physiotypes are derived for each intervention to predict a single effect or combined outcomes, and the same decision-making process can proceed seamlessly.

[0047] Models can be created by the method of the invention that predict various lipid, inflammatory and anthropometric responses to diet, exercise and drugs.

[0048] The baseline physiological and clinical level is measured for several phenotypes ranging from serology, physical exam, imaging, endocrinology for genomic/proteomics markers. The response of each individual for the phenotypes is then acquired after the exposure. Physiogenomics utilizes variability in response in the cohort to derive the predictors of response. After the physiotypes have been established for each given intervention, they can be applied to predict the response of a new individual to the intervention.

[0049] The medical utility of the invention will depend on the range of options it can customize. Within each of the major treatment modes (exercise, drug and diet), alternatives should be available to achieve specified goals. For example, consider dietary intervention to raise HDL in a patient with metabolic syndrome, and a decision on whether to proceed with a low fat or low carbohydrate diet. With physiotypes discovered each for low fat and low carbohydrate diets, predictions can be drawn for an individual's response to either. The person's genetic markers would be entered into the physiotypes, and the best diet based on the physiotype's prediction can be identified for the individual. Physiotypes can be generated, not only for various kinds of diet, but also for various kinds of exercise and drug treatments. The menu of possible interventions is thus broadened. The physiotype yielding the best outcome for a given desired effect guides the mode of intervention from an increasingly diversified menu, thus allowing enhanced personalization and customization of treatment.

[0050] It is within the scope of the present invention to produce for a given patient in permanent printed form a record of the prognostic results of his/her physiogenomic analyses disclosed above. This profile will become part of the patient's records. The printed form may be produced by any means, including a computer-generated printout.

[0051] We have applied the physiogenomic prognostic method described above to several treatment regimens, including those described below in the Examples section. Examples are designed to illustrate the inventive method, and should not be interpreted as limiting the scope of the invention.

EXAMPLES

Example 1

Determination of Sample Size

[0052] In order to determine the sample size requirements for a study, preliminary data is obtained and the percent change in BMI with treatment is assessed. For example, the standard deviation for percent change in BMI among the subjects was 5%. Table 2 shows the total sample size required, compared against the physiogenomic prevalence to detect a given percent change in BMI using a 5% two-tailed test with 80% power. This demonstrates that a study with 150 subjects should have sufficient power to detect a mean difference of 2.5% BMI if the genetic prevalence is between 25% and 75% of the population and 3.0% if between 10% and 90%.

Table 2: Sample size required by percent change in BMI for 5% significance level and 80% power at genetic marker frequencies between 25% and 75% in the sample population

Percent BMI Change	Sample Size
2.5	150
3.0	100
4.0	60
5.0	40

Example 2

Phvsiogenomics of Exercise

[0053] The inventive method was tested by examining the effects of exercise on lipid profiles, as a function of the genotypes of seven marker biochemicals that are known to be involved in lipid metabolism and serum lipid levels. We correlated the exercise responses as measured by various outcomes with the variability of the selected candidate genes. The candidate genes were selected according to known mechanisms of cholesterol homeostasis and the exercise response. The candidate genes and the candidate genotypes are shown in Table 3. The genes and their abbreviations are: apolipoprotein E *(APOE),* apolipoprotein A1 *(APOA1),* cholesterol ester transfer protein *(CETP),* angiotensin converting enzyme *(ACE),* lipoprotein lipase *(LPL),* hepatic lipase *(LIPC),* and peroxisome proliferator-activated receptor-alpha *(PPARA).* Other genes analyzed were ATP-binding cassette, sub-family G (WHITE), member 5 (sterolin 1) *(ABCG5)* and cholesterol 7-alpha hydroxylase gene *(CYP7).*

Table 3

Genes	**Candidate Genetic Markers**	**References**
APOE	Haplotype *E2, E3, E4*	Thompson PD, et al., *Metabolism* 53: 193-202 (2004)
APOA1	SNP *-75G/A*	Marin, C et al., *Am. J. Clin. Nutr.* 76: 319 (2002)
CETP	SNP *-629 C/A*	Tai, ES et al., *Clin. Genet.* 63: 19 (2003)
LPL	SNP *-93 T/G* S447X (CtoG)	Corella et al., *J. Lipid Res.* 43: 416-427 (2002)
LIPC	SNP *-514 C/T*	Ordovas, JM et al., *Circulation* 106: 2315 (2002)
ACE	Insertion/Deletion *I/D 287*	Rankinen T, et al., J. *Appl. Physiol.* 88: 1029-1035 (2000)
PPARA	SNP *Leu162Val*	Tai, ES et al. Clin. Genet. 63:19 (2003)

[0054] A preferred method for obtaining additional genotypes is the BeadStation 500GX system (Illumina, Inc., 9885 Towne Creek Center Drive, San Diego, CA 02121). This is an integrated system that supports highly parallel SNP genotyping and RNA profiling applications on a single, high-performance platform that delivers a scalable range of sample throughput.

Example 3

Exercise Physiogenomics Incorporating APOE Genetic markers

[0055] The following experiments explored the inventive concept that APOE variability is related to lipid changes with exercise training. To this end, three equal cohorts with subjects having the most common APOE haplotype pairs in the general population, APOE 2/3, 3/3, and 3/4, were recruited. To control for this design characteristic, APOE haplotype was utilized as covariate for the analysis of the other genetic markers, and was found not to be associated, thus demonstrating that none of the other genetic markers were in physical linkage with APOE and assorted randomly in the three cohorts. Variability in each gene was measured by a genetic polymorphism with a frequency of at least 10%. Such sampling establishes three groups of individuals for each gene: homozygous for either allele or heterozygous.

Table 4

Physiogenomics data analysis and screening for associations of gene marker and phenotypes

Lipids							**Physiological**			
A	*B*	*C*	*D*	*E*	*F*	*G*	*H*	*I*	*J*	**Phenotype**
4	0	3	23	2	5	1	27	30	0	APOE
4	3	1	5	3	16	17	25	23	3	PPARA
0	3	4	6	0	27	0	7	3	11	LIPC
0	0	3	0	3	2	4	1	5	16	LPL
21	32	21	0	1	2	11	2	3	6	APOA1
9	5	0	0	23	5	3	9	12	11	CETP
4	6	5	2	1	1	0	3	1	2	ACE
1	2	0	1	5	8	9	1	0	0	ABCG5
2	2	3	4	6	0	4	0	2	2	CYP7

Table 5

Summary of highest ranked association results from Table 4

Column	Gene	Phenotype	Adj P	In Count	Out Count
B	APOA1	*CHGSMHDL*	32	22	53
I	APOE	*VMAXLCHG*	30	42	77
H	APOE	*VMXMLCHG*	27	42	77

F	LIPC	*CHGAPOB*	27	6	83
H	PPARA	*VMXMLCHG*	25	11	89
D	APOE	*CHGL2M*	23	40	66
I	PPARA	*VMAXLCHG*	23	11	89
E	CETP	*CHGLDLSZ*	23	44	25
C	APOA1	*CHGH345*	21	22	53
A	APOA1	*CHGV56*	21	22	53
G	PPARA	*CHGHLA*	17	11	86
F	PPARA	*CHGAPOB*	16	11	90
J	LPL	*CHGBMI*	16	18	64

The code letters and names for the phenotypes in Tables 4 and 5 are defined as:

A CHGV56 = change in VLDL subpopulations V5 and V6 (i.e., largest VLDL particles)
B CHGSMHDL=Change in small HDL
C CHGH345=change in large HDL cholesterol
D CHGL2M=change in medium LDL particle concentration
E CHGLDLSZ=change in LDL diameter (this is the mean for entire LDL population)
F CHGAPOB=change in apo B
G CHGHLA=change in hepatic lipase activity
H VMXMLCHG=change in VO2 max, mL 02 per kg BW per minute
I VMAXLCHG=change in VO2 max, Liters per minute
J CHGBM1 =change in Body Mass Index (BMI)

[0056] The basis of the statistical analysis in physiogenomics is a parallel search for associations between multiple phenotypes and genetic markers for several candidate genes. The summary in Table 3 depicts the data set gathered from the initial application to exercise physiogenomics. In the top panel, each column represents a single phenotype measurement. Each row represents alleles for a given gene, and quantitatively render associations of specific alleles to the variability in the phenotype. The various numbers in the table refer to the negative logarithms of p value times 10. These p values are adjusted for multiple comparisons using the non parametric permutation test described earlier. For example, 30 refers to a p value of <0.001. Because of the large numbers of genes and outcomes that can be found, an interactive program can be prepared that can be used to search a large table with a structure similar to that shown in Table 4. As already noted, the p-value displayed in a cell is generated under the assumption of a linear trend for the effect of an intervention.

[0057] The platform allows visual recognition of highly significant association domains. There are also clearly negative fields. The same gene is associated to some phenotypes but not to others Similarly, a given phenotype may have associations to some genes, but not others. Each negative result lends power to the positive associations. Had the populations related to a phenotype being stratified based on confounder founder effects, most genes would have had specific founder alleles overrepresented in that population, and associated with similarly stratified founder phenotypes.

[0058] Table 5 above provides information on the association grid. The table lists in order of significance the "hits" of positive association between a gene alleles and a phenotype. The top ranking associations refer to APOA1 and CHGSMH, change in cholesterol, small HDL sub-fraction change (adjusted p of 32 or $p<10-^{3.2}$). Noteworthy also are high ranking associations of APOE to VMAXLCHG, change in maximum oxygen consumption (adjusted p of 30 or $p<10^{-3}$) and to CHGL2M (adjusted p of 23 or $p<10^{-2.3}$). The "lnCount" represents individuals with the associated allele, and the "OutCount", individuals without. The counts among various phenotypes may be different depending on measurement sampling during the study. Well represented distributions among the "in" and "out" groups to assure that a given association is not being driven by outliers. In the case of rare side effects, the outliers actually represent the susceptible population associated with a lower frequency predictive marker.

[0059] The initial analysis yielded several associations.

- Changes in serum lipids were related to APOE haplotype. Specifically, changes in the ratios of lower density lipoprotein to HDL, were greater in the APOE haplotype 3/3 subjects than in those subjects with haplotypes 2/3 and 3/4. This demonstrates that the lipid response to an environmental challenge, exercise training, is influenced by APOE haplotype.
- Despite the more favorable lipid response to exercise training, the increase in exercise performance was less in the APOE haplotype 3/3 subjects than in the other two genetic groups. This is a novel observation, but suggests that genes related to lipid metabolism affect the increase in exercise performance with exercise training. These results are consistent with animal studies showing reduced exercise capacity and muscle amyloid accumulation in APOE-deficient mice.
- The response of the LDL and HDL lipid subfractions to exercise also varied by APOE haplotype. Reductions in small dense LDL, an atherogenic particle, were greatest in APOE haplotype 3/3 subjects.
- APOA1 genotypes correlate with a switch of small to large HDL particles in some individuals and of large to small HDL particles in others. The direction of the switch in a given individual correlates with APOA1 genotype.

[0060] Small dense LDL particles are atherogenic. Therefore lipoprotein particle subpopulations were analyzed in 106 subjects. Exercise decreased small LDL particle concentration by -13.7 ± ±5.1 mg/dL selectively in those with the APOE *3/3* haplotypes, compared to increases of +5.6 ± 5.2, and +12.6 ± 5.6 mg/dL, respectively, in those with *2/3* and *3/4* haplotypes. Surprisingly, maximal oxygen uptake, the best marker of aerobic fitness, increased 9-10% for the entire cohort, but only 5% in the *3/3* subjects vs. 13% in the *2/3* and *3/4* groups. This difference in the response of exercise performance to exercise training was significantly different among the haplotypes ($p<0.01$ for changes). Thus, subjects with APOE *3/3* haplotypes, the most common APOE haplotype in the general population, experienced greater improvement in clinically relevant lipid parameters compared to subjects with APOE haplotypes *2/3* and *3/4,* despite smaller improvements in cardiorespiratory fitness.

Example 4

Exercise Phvsiogenomics incorporating APOA1 genetic markers

[0061] APOA1 is necessary for nascent HDL generation. Tables 3 and 4 above also demonstrate APOA1 genetic association to Cholesterol (CH) values (LDL, HDL and their sub-fractions). The APOA1 gene has a well-characterized SNP in its promoter, namely, -75 *G/A*. The data demonstrates that this variant was highly predictive of changes in the concentrations of small and large HDL particles with exercise training. Exercise markedly affects HDL fractions, eliciting a transition from small to large HDL in some individuals and the opposite in others. The presence of the A allele was associated with increased small HDL by 4.7 mg/dL with exercise and decreased large HDL. In contrast, the *G/G* genotype was associated with increased large HDL concentration by 1.8 mg/dL and decreased small HDL particles. APOA1 appears to be involved in the switch in particle size in response to exercise and the -75A allele of APOA1 is a potential predictor of the polarity of the HDL fraction switch in response to exercise. When translated into a DNA diagnostic, would be useful for the individualization of exercise programs to effect desired changes in lipid profiles of individuals.

Example 5

Results of Model Building

[0062] To illustrate the creation of predictive models that are the central part of physiogenomics, a data set was explored to find optimally predictive linear regression models for small LDL particle concentration and small HDL particle concentration. These two response variables have the strongest genetic component observed herein.

[0063] The objective of these analyses is to search for genetic markers that modify the effect produced by a particular type of intervention, which epidemiologists refer to as an effect modifier. These are be parameterized in our models as gene-intervention interactions. For example, if M_i is a 0 or 1 indicator of the presence of at least one recessive allele of gene i, and X_j represents the level of intervention, then the entire contribution to the outcome will be given by the contribution of not only the gene and intervention main effects, but their interaction, as well, i.e., $M_i\alpha_i + X_j\beta_j + M_iX_j(\alpha\beta)_{ij}$. Under this model, when the allele is absent (M_i=0), the effect of a unit change in the intervention is described by the slope, β_j, but when the allele is present (M_i=1), the effect of a unit change in the intervention is $\beta_j + (\alpha\beta)_{ij}$. Thus, the gene-intervention interaction parameter, $(\alpha\beta)_{ij}$, represents the difference in the effect of the intervention seen when the allele is present.

[0064] In the usual modeling framework, the response is assumed to be a continuous variable in which the error distribution is normal with mean 0 and a constant variance. However, it is not uncommon for the outcomes to have an alternative distribution that may be skewed, such as the gamma, or it may even be categorical. In these circumstances, one can make use of a generalized linear model, which includes a component of the model that is linear, referred to as the linear predictor, thus enabling one to still consider the concept of a gene-intervention interaction, as described earlier. The advantage of this broader framework is that it allows for considerable flexibility in formulating the model through the specification of the link function that described the relationship between the mean and the linear predictor, and it also provides considerable flexibility in the specification of the error distribution, as well (McCullagh P, et al. Generalized Linear Models. London: Chapman and Hall, 1989, which is incorporated herein by reference).

[0065] To this point, an analysis has been developed in which the effect of the intervention is assumed to be linear, but in practice the effect may take place until a threshold is past, or it may even change directions. Thus, an important component of one's exploration of the intervention effect on a particular response may involve the form for the relationship. In this case one can make use of generalized additive models (GAMs, Hastie et *al. Stat. Sci.* 1 :297 (1986)) in which the contribution of the marker and intervention is given by $M_i\alpha_i + \beta(X_j) + M_i\beta_\alpha(X_j)$. In this case, the effect when the allele is absent (M_i=0) is $\beta(X_j)$ which is an unspecified function of the level of the intervention. In subject in which the allele is present (M_i=1), the effect is given by the function $\beta(X_j) + M_i\beta_\alpha(X_j)$). In practice, these functions may be estimated through the use of cubic regression splines (Durrelman, S *et al., Stat. Med.* 8:551 (1989), which is incorporated herein by reference).

[0066] Predictive models may be sought by starting out with a hypothesis (which may be the null model of no marker dependence) and then adding each one out of a specified set of markers to the model in turn. The marker that most improves the p-value of the model is kept, and the process is repeated with the remaining set of markers until the model can no longer be improved by adding a marker. The p-value of a model is defined as the probability of observing a data set as consistent with the model as the actual data when in fact the null-model holds. The resulting model is then checked for any markers with coefficients that are not significantly (at $p<0.05$) different from zero. Such markers are removed from the model.

[0067] For predicting small LDL-C change *(CHGL1S)* in response to exercise, we started out with the null model, and considered the three categories of variables in Table 6. We arrived at an optimized model, specified in Table 6, containing three markers: baseline small LDL *(L1S.1)*, pre-exercise triglycerides *(TGPRE),* and two APOE haplotypes *(APOE GENE).* The model explains 47% of the observed variance for small LDL-C change *(CHGL1S)* in response to exercise and has a p-value of 4×10^{-13}. The p-values for the components are 5×10^{-14} for *L1S.1*, 8×10^{-9} for *TGPRE,* 3×10^{-3} for $APOE\ GENE_1$, and 6×10^{-2} for $APOE\ GENE_2$. The correlation between the response predicted by the model vs. the observed response for all subjects can be depicted graphically.

Table 6

Predictors of Response to Diet. Exercise and Drugs

Genetic	*Physiological*	*Demographic*
Genotype alpha (gene A)	Baseline Factor 1	Gender
Genotype beta (gene B)	Baseline Factor 2	Heredity
Genotype gamma (gene C)	Baseline Factor 3	Age

Table 7

Most predictive linear model of small LDL change due to exercise

CHGL1S ~ L 1S.1 + TGPRE + APOE GENE

[1] Explains: 46.6 %

[1] P-value: 4.23e-013

	Value	StdErr	t value	Pr(>|t|)
Intercept	-	4.1346	-0.6069	5.4530e-001
L1S.1	-	0.0832	-8.7388	5.3291e-014
TGPRE	0.19923	0.0316	6.2901	8.2059e-009
$APOEGENE_1$	-	2.7148	-3.0293	3.1126e-003
$APOEGENE_2$	3.14274	1.6655 10	1.88700	6.2038e-002

[0068] For predicting small HDL-C change (*CHGSMHDL*) in response to exercise, the initial hypothesis was that the response depends on APOA1 genotype, as discovered in the physiogenomics analysis. We also considered the three categories of variables in Table 6, and constructed an optimized model, specified in Table 8, The model contains three markers: two APOA1 genotypes *(APOA1.1)*, the pre-exercise small HDL cholesterol concentration *(SM HDL.1),* and the baseline ratio of fat mass to body mass *(PERFAT.1).* This model explained 43% of the observed variance for small HDL-C change *(CHGSMHDL)* in response to exercise and had a p-value of 7×10^{-8}. The p-values for the components are 9×10^{-3} and 9×10^{-1} for APOA1 genotypes *(APOA1.11* and *APOA1.12),* 1×10^{-6} for *SM HDL.1,* and 3×10^{-2} for *PERFAT.1.* The correlation between the response predicted by the model vs. the observed response for all subjects can be depicted graphically.

Table 8

Most predictive linear model of small HDL change due to exercise

CHGSMHDL ~ APOA1.1 + SM HDL.1 + PERFAT.1

[1] Explains: 42.7 %

[1] P-value: 6.9e-008

	Value	StdErr	t value	Pr(>|t|)
Intercept	4.72843	2.140831	2.20869	3.0520e-002
APOA1.11	2.00143	0.745134	2.68599	9.0513e-003
APOA1.12	0.14581	1.035824	0.14077	8.8846e-001
SMHDL.1	-0.48786	0.092239	-5.28914	1.3722e-006
PERFAT.1	0.18331	0.085013	2.15632	3.45479e-002

Example 6

Exercise and markers of inflammation

[0069] The above-described analyses permits the extension of the present examples to additional genes and outcomes. For example, inflammatory markers and their relationship to atherosclerosis are an area of intense interest in clinical medicine. The ability to measure changes in inflammatory markers with exercise training and related genes provides a unique opportunity to examine genes determining the interplay of exercise response and inflammation. The gene probes are derived from candidate genes relevant to energy generation, inflammation, muscle structure, mitochondria, oxygen consumption, blood pressure, lipid metabolism, and behavior, as well as transcription factors potentially influencing multiple physiological axes. The method utilizes blood plasma and DNA from each patient to measure the appropriate genotypes and inflammatory markers in blood.

[0070] The inflammatory markers will introduce proteomics to the physiogenomic study of exercise. By profiling at high sensitivity the plasma concentrations of various interleukins, growth factors, and the cellular expression of various receptors, phenotypic components can be added to the analysis. In addition, peripheral white cell monitoring can be included in protocols to demonstrate reporter gene array expression levels. It will also be possible to introduce phenotypic morphometric markers to introduce further bridges between genotype and outcome.

[0071] Table 9 provides an example of personalized healthcare by customizing treatment intervention. In the table, the choices are to recommend a given kind of exercise, drug or diet regimen. If one of the options is high scoring, it can be used on its own. Thus in the example, diet is high scoring in the first patient, a drug in the second, and exercise in the fourth. If the options are midrange, they can be used in combination, as is the case in the third patient, where exercise and diet will each have a positive effect but unlikely to be sufficient independently. If none of the options is high or at least mid-scoring, the physiotype analysis suggests that the patient requires another option not yet in the menu. As more options are built into the menu, the greater the chance that all patients will be served at increased precision of intervention and with optimal outcome.

Table 9

Personalized Healthcare by Customizing Intervention

Interventions

Physiotype Scores

Patient No.	Exercise	Drugs	Diet
1	3	4	7
2	4	9	5
3	4	2	5
4	8	2	3

Example 7

Construction of a physiogenomics array using hypothesis-led association screening

[0072] In this example, a physiogenomics array consisting of 384 SNPs from 215 genes known to be relevant to certain physiological processes has been designed and tested. The array has been tested on 2000 different samples from different clinical studies for validation of the gene and SNP selection process. After identifying candidate genes through an intensive review of the literature, as well as public databases (dbSNP, ensembl) for validated SNPs with known heterozygosities (HET) for mixed or Caucasian populations. The low HET limit was set to 10% to ensure a sufficient representation of the respective SNP. The high HET limit was set at 30% under the assumption that alleles with a close to even distribution are more likely to be neutral (i.e., not associated with a phenotype). The number of SNPs per gene was based on the length of the gene: < 25kb = 1SNP, 25 to 100kb=2SNPs, >100kb = 3 SNPs. The reference numbers of the identified SNPs were evaluated by Illumina using the electronic OligoDesigner software package, and only SNPs with a score higher than 0.6 were used for the gene array.

[0073] Furthermore, the OligoDesigner algorithm uses information from a variety of sources to derive a numerical value intended to score the likelihood of a given assay being developed on the Illumina platform. Some of the criteria used to calculate this value include (1) the presence of adjacent SNPs in the DNA sequence, (2) proximity to the repetitive elements, (3) uniqueness of oligo target sequences, (4) melting temperatures of any oligos selected for the assay, and (5) whether there is any complementation in the 3' regions of the assay oligos. The result of this informatics process is a score between 0 and 1 with assays scoring 0 being disallowed.

[0074] While it is often advantageous to construct a physiogenomics array using all 384 SNPs in Table 10, this invention is not limited to such an embodiment. In other embodiments, a physiogenomics array is constructed that contains at least about 10 SNPs taken from Table 10, more preferably at least about 20 SNPs, even more preferably at least about 50 SNPs, even more preferably at least about 100 SNPs, even more preferably at least about 200 SNPs, even more preferably, at least about 300 SNPs.

[0075] The 480 samples in this example were run in five different batches of 96 samples each. The DNA was quantitated and normalized using the picogreen quantitation assay. Genotyping was performed strictly according to Illumina protocols, using a Senstrix Array Matrix and the Illumina Beadstation 500. Data were analyzed using GenCall version 6.0.7, and reports were prepared with GTS Reports version 4.1.2.0. Table 10 shows a comprehensive listing of all the SNPs on the array with an indication of the quality of data achieved. Furthermore, a numerical measure of quality is given as the sum over all 5 arrays of the 10% percentile of the GenCall scores, as reported by the Locus report of the GTS Reports. In addition, the following was defined as the quality control (QC) criteria for any given assay: (1) Fail if the p-value of the chi-squared test for Hardy-Weinberg equilibrium is less than 0.02; (2) Fail if the 10% GC score is less than 0.3; (3) Fail if the GenTrain score is less than 0.4; (4) Fail if the minor allele frequency is zero; (5) Fail if the number of calls is less than 80% of the number of samples. For each SNP assay, the number of runs in which the assay passed these quality control requirements is listed in Table 10, and the results are summarized in Table 11. There is a clear bimodal distribution, with 18% of the assays which never worked, and 36% of the assays that worked in 3 runs. We considered assays that never worked or only worked once as failures, resulting in 99 failed assays for an assay conversion rate of 73%.

Table 10: List of the 384 SNPs in the physiogenomics array. CEU, HCB, JPT, and YRI stand for the allele frequencies in the central European, Han Chinese, Tokyo Japanese and Yoruban African populations according to the HapMap database. GenScore lists the 10th percentile GenScores added up for all 5 runs. Good Runs is the number of runs in which the genotype data passed quality control. MAF is the minor allele frequency as observed in our research samples.

Gene	Symbol	SNP	CEU	HCB	JPT	YRI	Gen-Score	Sequence Context	MAF
apolipoprotein L, 1	APOL1	rs136163	0.73	0.85	0.9	1	2.18	ACTGCTCTCTAGTTGGAAAGA[A/C]GAAAGGATAAGGTTGGAGGA (SEQ ID NO. 1)	16.1%
selectin P (granule membrane protein 140kDa, antigen CD62)	SELP	rs6136	0.1	0.07	0	0	2.99	CAAGAGAATGGCCACTGGTCA[A/C]CTACCGTGCCAACCTGCCAA (SEQ ID NO. 2)	10.2%
cytochrome P450, family 2, subfamily C, polypeptide 19	CYP2C19	rs10509676	0.15	0.26	0.28	0.14	2.49	CTTTACAACAGGCATAAATTA[A/T]TTCTTCAGAGAAGTTCAATT (SEQ ID NO. 3)	14.1%
lipase, hepatic	LIPC	rs6078	0	0.03	0.08	0	3.10	TCCCCTCCTCAGGTGGACGGC[A/G]TGCTAGAAAACTGGATCTGG (SEQ ID NO. 4)	5.2%
kinase insert domain receptor (a type III receptor tyrosine kinase)	KDR	rs2125489	0.15	0.01	0.01	0	3.46	GCAGATGTCTTTGTAAAACTC[A/G]TCTCTTTATTCTGGAAATTA (SEQ ID NO. 5)	12.8%
leptin receptor	LEPR	rs1171276	0.13	0.04	0.02	0.55	2.61	AGTTTCATGTACATTAAATAT[A/G]AATTTCTTTTGGCTGGAAAT (SEQ ID NO. 6)	25.3%
adenosine A2b receptor	ADORA2B	rs758857	0.83	0.68	0.63	0.18	2.65	CCTTACTCAGAGTCTCTCTGC[A/G]CCCAGTGTGCTAGCCTTGTG (SEQ ID NO. 7)	22.9%
solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	SLC6A3	rs3756450	0.16	0.44	0.44	0.5	2.88	CCTAAATGCCAAGTCGGCTTT[A/G]TTATCATTGTGGTTGCTGCT (SEQ ID NO. 8)	13.5%
apoptosis, caspase activation inhibitor	AVEN	rs2702285	0.86	0.53	0.47	0.07	3.09	AGCTTTCAAATGTCATGCATT[A/G]TGTGGCAGGAGTAGGTTTTA (SEQ ID NO. 9)	25.3%
dystrobrevin binding protein 1	DTNBP1	rs1040410	0.08	0.07	0.09	0.23	2.54	AAGAGTCCATTCAAAAGGGTT[A/G]TACAGACAGAAAACCAGTGG (SEQ ID NO. 10)	9.9%
glycogen synthase 2 (liver)	GYS2	rs10505873	0.63	0.79	0.91	0.38	2.88	TGCTCAGCCTTCTTCAATGAC[A/G]GTGTTTTGCTATTGTCTCTA (SEQ ID NO. 11)	44.8%
phosphoinositide-3-kinase, class 2, gamma polypeptide	PIK3C2G	rs11044082	0.14	0.27	0.28	0.31	3.11	TTGTTTTTCAAGTTTTGATTT[A/C]TCTGCTAAAATTCAGACCTG (SEQ ID NO. 12)	20.6%
dopamine beta-hydroxylase (dopamine beta-monooxygenase)	DBH	rs1611115	0.83	0.78	0.84	0.88	3.29	CTCTCCCTCCTGTCCTCTCCC[A/G]CAAGTAGACTGAGGGCAGCT (SEQ ID NO. 13)	20.6%
cytochrome P450, family 2, subfamily C, polypeptide 9	CYP2C9	rs1799853	0	0	0	0	0.10	AGCGGGCTTCCTCTTGAACAC[A/G]GTCCTCAATGCTCCTCTTCC (SEQ ID NO. 14)	13.0%
chemokine (C-C motif) ligand 2	CCL2	rs3760396	0.26	0.11	0.06	0	1.65	GACAGAGAGAGGACCCAAGCA[C/G]GCAACTAGTTGGAGGACTTG (SEQ ID NO. 15)	22.7%

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corticotropin releasing hormone receptor 2	CRHR2	rs2240403					3.11	TTTCAACTCCTTCCTGCAGTC[A/G]TTCCAGGTGGGGCCTGTGAC (SEQ ID NO. 16)	7.0%
dopamine receptor D1 interacting protein	DRD1IP	rs2298122	0.81	0.94	0.86	0.35	3.52	CTCCCCTCTCAGTTCAGGGCT[A/C]TCTTGGGTCCCTGCCAGCTG (SEQ ID NO. 17)	23.4%
Tyrosine hydroxylase	TH	rs6578993	0.91	0.9	0.77	0.93	2.92	CCCTCATCTGAAACAAGAACT[A/G]GAGGCCTGGGCTGCTCCTCC (SEQ ID NO. 18)	15.1%
cholesteryl ester transfer protein, plasma	CETP	rs711752	0.5	0.4	0.4	0.22	2.52	TTCAAGGTCAAGTTCTTTGGT[A/G]AGAAGGTCCTAGCTGCATTG (SEQ ID NO. 19)	40.9%
lipase, endothelial	LIPG	rs4245232	0.81	0.54	0.42	1	2.52	TAAAAAACTAAAGCCCGCCTG[A/C]GTCTTGTTAATGAATGATAG (SEQ ID NO. 20)	20.3%
peroxisome proliferative activated receptor, alpha	PPARA	rs5766741	0.29	0.22	0.13	0.22	3.03	GCATAAAGGAAGAAACCATCA[A/G]ATGGTTCAGAATTGGTAAGA (SEQ ID NO. 21)	28.6%
apolipoprotein A-IV	APOA4	rs5092					2.72	CAGTGCTGACCAGGTGGCCAC[A/G]GTGATGTGGGACTACTTCAG (SEQ ID NO. 22)	19.5%
phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	rs7556371	0.74	0.7	0.72	0.33	2.69	CCGTGCTCTTAACCATCTGCC[A/G]AACTTGCACTGCCAGTCATT (SEQ ID NO. 23)	27.6%
scavenger receptor class B, member 2	SCARB2	rs3853188	0.05	0.18	0.3	0.13	2.83	TTCACATACTGGGGAGTTCAG[A/C]ATAGTAATGTTTTTGGAAAA (SEQ ID NO. 24)	9.6%
interleukin 10	IL10	rs1800871	0.83	0.26	0.31	0.54	2.95	AGCAAACTGAGGCACAGAGAT[A/G]TTACATCACCTGTACAAGGG (SEQ ID NO. 25)	27.6%
cytochrome P450, family 2, subfamily D, polypeptide 6	CYP2D6	rs1058167	0.32			0.9	2.33	CCAGCCAGCGCTGGGATGTGC[A/G]GGAGGACGGGGACAGCATTC (SEQ ID NO. 26)	35.2%
transforming growth factor, beta 1 (Camurati-Engelmann disease)	TGFB1	rs1800471					2.26	TACTGGTGCTGACGCCTGGCC[C/G]GCCGGCCGCGGGACTATCCA (SEQ ID NO. 27)	11.7%
cytochrome P450, family 3, subfamily A, polypeptide 4	CYP3A4	rs2242480	0.08	0.26	0.25	0.89	3.02	ACCCAATAAGGTGAGTGGATG[A/G]TACATGGAGAAGGAGGGAGG (SEQ ID NO. 28)	15.4%
insulin receptor	INSR	rs4804103	0.21	0.14	0.14	0.45	2.79	TCCTGTGAGAGAGTTGAGAGC[A/G]ATAATTTTAGGGTGGTTATT (SEQ ID NO. 29)	18.5%
histamine receptor H3	HRH3	rs1614845	0.78	0.92	0.99	0.96	2.88	AAGCTGCTGTAAATGGAGGCT[A/G]CCTAGAGAGGAGAGGGCCTG (SEQ ID NO. 30)	18.8%
Notch homolog 4 (Drosophila)	NOTCH4	rs204987	0.98	1	1	1	3.03	GGAGAGAGCAGCCCCTCAAAC[A/G]CAGCCCCTGGGCAAGGAGAC (SEQ ID NO. 31)	2.9%
v-akt murine thymoma viral oncogene homolog 2	AKT2	rs7247515	0.08	0.1	0.06	0.3	2.94	CTAGCACATCTCTTGCCCGAG[A/G]GCCTCAGCGCTTGCTGTCGC (SEQ ID NO. 32)	10.7%
acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	ACAT2	rs2146162	0.18	0.4	0.41	0.15	2.82	AAACTAGGAATTACATGGTAA[A/G]TTGAAAGAGGAAGTTAGGGG (SEQ ID NO. 33)	18.0%
cytochrome P450, family 3, subfamily A, polypeptide 5	CYP3A5	rs776746	0.06	0.33	0.25	0.85	2.22	AAAGAGCTCTTTTGTCTTTCA[A/G]TATCTCTTCCCTGTTTGGAC (SEQ ID NO. 34)	12.5%

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lipoprotein lipase	LPL	rs264	0.14	0.24	0.23	0.08	3.10	TCTCTTGAAGGTGGGTGGGCC[A/G]CTACCACCAAGAATATCTCC (SEQ ID NO. 35)	16.4%
guanine nucleotide binding protein (G protein), beta polypeptide 3	GNB3	rs6489738					3.02	GCCACTGAGGGAGAAGGCCAC[A/G]GACGTGATGCCGCAGATGAT (SEQ ID NO. 36)	36.5%
choline acetyltransferase	CHAT	rs3810947	0.06	0.68	0.52	0.58	3.18	ATCTTTTAGAGTCCGACCTCT[A/G]GAAATGTGTGTATGATGTGA (SEQ ID NO. 37)	8.9%
solute carrier organic anion transporter family, member 1B1	SLCO1B1	rs4149056	0.16	0.16	0.1	0.01	2.85	CGAAGCATATTACCCATGAAC[A/G]CATATATCCACATGTATGAC (SEQ ID NO. 38)	15.4%
phosphoinositide-3-kinase, class 2, gamma polypeptide	PIK3C2G	rs11043982	0.08	0	0	0	3.01	TGCAAAGTTCTGTGACAATAC[A/G]TACTCGGGCTAGAGGTGACT (SEQ ID NO. 39)	8.1%
ATP-binding cassette, sub-family C (CFTR/MRP), member 8	ABCC8	rs916829	0.88	0.86	0.94	0.99	2.96	CGGGGCTGGCTCTCATTGCTG[A/G]CCTTCACTGTGCACTGTGAG (SEQ ID NO. 40)	14.3%
fatty acid synthase	FASN	rs2228309	0.55	0.17	0.15	0.5	2.76	GGTGTTGGGCTTCAGCAGGAC[A/G]TTGATGCCCCCCACGATGGC (SEQ ID NO. 41)	45.1%
transcriptional adaptor 2 (ADA2 homolog, yeast)-like	TADA2L	rs7211875	0.85	0.75	0.75	0.93	2.00	CACTGTACTTACTGCTAAAGG[A/G]ACCCAAACGGTCCATTCCCT (SEQ ID NO. 42)	34.6%
solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	SLC6A4	rs140700	0.1	0.06	0.1	0.04	2.13	ATCTTTCTGCCACACCACCTC[A/G]CCCTCCTTTCTCAAGGTCTT (SEQ ID NO. 43)	8.9%
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	rs8110695	0.17	0.38	0.39	0.55	2.88	AAACTGAGTCCCAGAAGGATT[A/T]AGTCAGTTACCCAAGTTGTT (SEQ ID NO. 44)	24.5%
lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	LIPA	rs1556478	0.25	0.86	0.69	0.26	3.38	CACGGAGACTTATGCACCAGA[A/G]TGAAATGCTGAGATGTTCTT (SEQ ID NO. 45)	33.3%
adrenergic, alpha-1A-, receptor	ADRA1A	rs7816340	0.85	1	1	1	2.77	GTCAAGGGTATAACACCTTAG[A/G]GTATAATTTGTTACAGTGTT (SEQ ID NO. 46)	18.0%
tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	rs235249	0.25	0.24	0.18	0.26	1.82	TGCATGAGTGTGTCCGTGTCC[A/G]TGGGGGTGATTGTGGGTAAG (SEQ ID NO. 47)	26.0%
phosphoinositide-3-kinase, class 3	PIK3C3	rs7229485	0.01	0	0	0.21	2.81	AGAATTTGTATCTCACACCAA[A/G]TAATTTTTAAAAAGGTCATT (SEQ ID NO. 48)	0.8%
adenosine A1 receptor	ADORA1	rs3766560	0.19	0.08	0.24	0.53	2.76	ATGATGTGTGTGGGGGAGGAA[A/G]AAGCTTATCAAATCAAAGCC (SEQ ID NO. 49)	17.4%
phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	rs1877394	0.02	0.12	0.1	0.05	3.19	AGTTTGAGACGTGGGTGAAAC[A/G]TAGGTGGAAAAGTCCAGCAA (SEQ ID NO. 50)	2.1%
apolipoprotein A-IV	APOA4	rs675					3.22	GAGAAAGAGAGCCAGGACAAG[A/T]CTCTCTCCCTCCCTGAGCTG (SEQ ID NO. 51)	18.8%
corticotropin releasing hormone receptor 1	CRHR1	rs4792887	0.07	0	0	0.3	2.64	CTCTCCAGTGTGGCCAAGATC[A/G]AAGATGTACCTGGTGACCCC (SEQ ID NO. 52)	9.6%

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similar to apoptosis inhibitor 5; fibroblast growth factor 2-interacting factor 2; API5-like 1	LOC441514	rs5950584	1	1	1	0.58	2.56	CTATCCTCAAATGCTATATAA[A/C]CCAACTGGTGGAAAAAAATT (SEQ ID NO. 53)	4.2%
cholesteryl ester transfer protein, plasma	CETP	rs3764261	0.37	0.17	0.21	0.26	2.95	AGTGAATGAGATAGCAGACAA[A/C]CCAGATGCCTACCGACAGGT (SEQ ID NO. 54)	32.3%
adrenergic, beta-1-, receptor	ADRB1	rs1801252		0	0	0.01	0.23	TTGCTGCCTCCCGCCAGCGAA[A/G]GCCCCGAGCCGCTGTCTCAG (SEQ ID NO. 55)	25.5%
cytochrome P450, family 2, subfamily C, polypeptide 19	CYP2C19	rs4986894	0.16	0.26	0.28	0.14	2.63	GTGTGTGCCTCTTTGATGGAT[A/G]AAGTGGCCAATCACCTAGGC (SEQ ID NO. 56)	15.1%
insulin receptor	INSR	rs891087	0.08	0.07	0.07	0.26	3.06	GCAGGTCTCCACACACCTGCC[A/G]TCCAGGTAGAAGTTGCGGCA (SEQ ID NO. 57)	8.9%
phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	rs2230461					3.16	TGAATGGCTGAATTATGATAT[A/G]TACATTCCTGATCTTCCTCG (SEQ ID NO. 58)	10.2%
pyruvate kinase, liver and RBC	PKLR	rs3762272					3.11	AACAAAGATTCTCCTTTCCTC[A/G]TTCACCACTTTCTTGCTGTT (SEQ ID NO. 59)	4.2%
5-hydroxytryptamine (serotonin) receptor 3B	HTR3B	rs1176744	0.25	0.18	0.31	0.43	1.84	ATAGTGTGGACATTGAAAGAT[A/C]CCCTGACCTTCCCTATGTTT (SEQ ID NO. 60)	35.7%
protein kinase, AMP-activated, gamma 1 non-catalytic subunit	PRKAG1	rs2293445	0.35	0.31	0.46	0.27	2.83	AAAAGTGTTTCCCAGAAACCC[A/G]CCATCCCTTTATCCTTTTAT (SEQ ID NO. 61)	34.9%
apolipoprotein A-II	APOA2	rs5085	0.18	0.26	0.28	0.04	2.75	CAGACTCTAGAGACTGAAATT[C/G]AAGGCCCAGTTCTTGCTGTT (SEQ ID NO. 62)	16.7%
apolipoprotein H (beta-2-glycoprotein I)	APOH	rs8178847	0.08	0.06	0.06	0.08	2.05	TACCTACGTTTGCAACACTTC[A/G]TGTTTATAAGCCATCAGCTG (SEQ ID NO. 63)	8.9%
carnitine palmitoyltransferase 1A (liver)	CPT1A	rs2228502	0.97	0.92	0.9	0.86	3.09	TTCAGTTTCATCTAACGTCAC[A/G]AAGAACGCTGCTTTCTCCAC (SEQ ID NO. 64)	6.0%
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	rs1438732	0.18	0.09	0.09	0.17	2.82	TTAGGGACTTTCAAAAACTCA[C/G]ACTCTTGGGTTCTGACCCTG (SEQ ID NO. 65)	14.8%
adrenergic, alpha-2A-, receptor	ADRA2A	rs1800544					3.06	TGGGAGTTGGCCATGCAGCTC[C/G]GGGCCGACGGAGCAGAACGC (SEQ ID NO. 66)	34.6%
adrenergic, beta-2-, receptor, surface	ADRB2	rs1042713	0.33	0.53	0.39	0.48	0.00	GCCTTCTTGCTGGCACCCAAT[A/G]GAAGCCATGCGCCGGACCAC (SEQ ID NO. 67)	22.4%
D-amino-acid oxidase	DAO	rs2070586	0.15	0.31	0.38	0.44	2.32	TTGCCAGGAGCTGAGGTCTGC[A/G]GGAGGAGAGTTGTGAGTGAA (SEQ ID NO. 68)	18.2%
choline acetyltransferase	CHAT	rs8178990	0.08	0	0	0	1.87	CCAGCAGGGCCTTGTAGCTGA[A/G]TACACCAGAGATGAGGCTGG (SEQ ID NO. 69)	5.5%
monoamine oxidase B	MAOB	rs1181252					2.83	AGTGGGAAGCAGCAACATAGA[A/G]TGGCTTTTCAAGAAATAAAC (SEQ ID NO. 70)	3.9%
phosphoinositide-3-kinase, class 3	PIK3C3	rs4121817	0.14	0.3	0.35	0.18	2.67	CAGCACTCCGAATGAAGGCTG[A/G]CAGTGAAACTGAATTACTTA (SEQ ID NO. 71)	11.7%
retinoic acid receptor, beta	RARB	rs2033447	0.11	0.2	0.22	0.58	2.85	ATGCCGGGTGCTAGAGATACA[A/G]CAGTGAACATGACAAAGTTC (SEQ ID NO. 72)	14.1%
apolipoprotein E	APOE	rs439401	0.62	0.46	0.35	0.88	2.91	GAGAACTGAGGGGGTGGGAGG[A/G]GAAGAGAGTGCCGGCGGCTC (SEQ ID NO. 73)	35.7%

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dystrobrevin binding protein 1	DTNBP1	rs2743867	0.08	0.06	0.09	0.31	2.83	GATTAAATGCATTCTGCCACA[A/G]TTCTCATTATTTTCATAGTC (SEQ ID NO. 74)	10.4%
glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	GAD2	rs8190586					2.45	CACCCGCCATCAATCCTGCCG[A/G]CTCTGGCCGCTCTGCCTCAT (SEQ ID NO. 75)	3.1%
acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	ACAT1	rs10890819	0.22	0.29	0.35	0	2.74	ACCAGAAGCTAGCATAATGGA[A/G]TATCGCCCCTCACTTTGTTC (SEQ ID NO. 76)	31.5%
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	rs3761740	0.14	0.03	0.05	0.03	3.01	CGTCAGAAATGTGTGGTGGGG[A/C]CATATTAGTGGTGACAGGTT (SEQ ID NO. 77)	9.6%
dopa decarboxylase (aromatic L-amino acid decarboxylase)	DDC	rs1466163	0.83	0.99	0.99	0.93	3.20	GGCTGGTTGGAGCCTCTCCCC[A/G]GGCAGCAGCCCTGGTGGAGA (SEQ ID NO. 78)	10.9%
5-hydroxytryptamine (serotonin) receptor 3B	HTR3B	rs2276307	0.17	0.18	0.3	0.08	2.64	CCTTCTCTCTTGGGCCAAGGA[A/G]TTTCTGCTCTATTGCATGTT (SEQ ID NO. 79)	19.5%
platelet/endothelial cell adhesion molecule (CD31 antigen)	PECAM1	rs1131010					1.33	AACCTCACTTAACATTTTGGC[A/G]TGGGAATGGCAATTATCTGC (SEQ ID NO. 80)	4.7%
scavenger receptor class B, member 1	SCARB1	rs4765623	0.42	0.31	0.44	0.43	2.91	GATTTTGCCCAGTGGCTCTCC[A/G]AGGTGGCTGTACTGATGGAC (SEQ ID NO. 81)	36.5%
protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1	rs3792822					2.84	GATGTGGATACTGAGCCTCGC[A/G]GCTTATATGATTGCTCACAG (SEQ ID NO. 82)	17.2%
apolipoprotein E	APOE	rs429358		0	0.01	0.02	1.38	GGTACTGCACCAGGCGGCCGC[A/G]CACGTCCTCCATGTCCGCGC (SEQ ID NO. 83)	26.8%
nitric oxide synthase 3 (endothelial cell)	NOS3	rs1549758					2.05	TGGGTCCCCCCGCACAGAGCC[A/G]TCCTGCTGCCGGTAGCCCGC (SEQ ID NO. 84)	29.4%
5,10-methylenetetrahydrofolate reductase (NADPH)	MTHFR	rs2066470		0.01	0.01	0.01	3.02	CCGGAGTCTCTCATGCCGCTC[A/G]GGGTCCAGGCCCGGGGTGGA (SEQ ID NO. 85)	9.6%
angiopoietin 1	ANGPT1	rs1283694	0.86	0.88	0.9	0.88	3.13	CAAACCCTTTCCACTCCATTA[A/T]AAGAACATGAATCCTGATAA (SEQ ID NO. 86)	17.4%
peroxisome proliferative activated receptor, gamma	PPARG	rs1801282	0.08	0.02	0.06	0	3.48	CTGGGAGATTCTCCTATTGAC[C/G]CAGAAAGCGATTCCTTCACT (SEQ ID NO. 87)	12.0%
solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	SLC6A4	rs2020933	0.05	0.07	0.01	0.39	3.12	TTTTGTCCAGAAAAGTGAACC[A/T]GGTCAATGGATTATTTATGA (SEQ ID NO. 88)	11.2%
phosphofructokinase, platelet	PFKP	rs6901	0.66	0.74	0.86	0.69	2.49	AGGACCCATCCTGGATCATCC[A/G]ATGAGCAGCCGTGGCGCTCG (SEQ ID NO. 89)	28.9%
apolipoprotein C-IV	APOC4	rs2288911	0.45	0.68	0.72	0.7	3.29	CTCCGGACGGGCACAGAGAGG[A/C]TTTATAGTGGTTGAGACCCA (SEQ ID NO. 90)	49.2%
adiponectin receptor 2	ADIPOR2	rs2058112	0.13	0	0.01	0.13	2.71	TCTTCTTGCCCTACATACTTC[A/G]AAAGCCCTTGGAGAAATCCT (SEQ ID NO. 91)	13.0%

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catechol-O-methyltransferase	COMT	rs4680	0.52	0.26	0.24	0.29	2.64	CGGATGGTGGATTTCGCTGGC[A/G]TGAAGGACAAGGTGTGCATG (SEQ ID NO. 92)	47.9%
selectin P (granule membrane protein 140kDa, antigen CD62)	SELP	rs6131	0.2	0.19	0.19	0.32	2.71	GTCAGCACCTGGAAGCCCCCA[A/G]TGAAGGAACCATGGACTGTG (SEQ ID NO. 93)	19.8%
apolipoprotein L, 3	APOL3	rs132653	0.86	0.98	0.98	0.37	2.80	GTTCCAGGGTATATCTCAGAG[A/C]CTGGAGAACGTGTCTGGTTA (SEQ ID NO. 94)	17.4%
fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	FLT1	rs2296189	0.11	0.21	0.09	0.27	3.34	GATTTTGTCAAAGATAGATTC[A/G]GGAGCCATCCATTTCAGAGG (SEQ ID NO. 95)	22.4%
dopamine beta-hydroxylase (dopamine beta-monooxygenase)	DBH	rs4531					3.16	AGGACCCTGGACCCCCGAAGG[A/C]AAGGCCGGCTTCCTCTGGGT (SEQ ID NO. 96)	7.6%
interleukin 1, beta	IL1B	rs1143634	0.22	0	0.07	0.1	2.57	AGCCTCGTTATCCCATGTGTC[A/G]AAGAAGATAGGTTCTGAAAT (SEQ ID NO. 97)	20.3%
phosphoenolpyruvate carboxykinase 1 (soluble)	PCK1	rs8192708	0.1	0	0	0.03	3.03	AAAGAATCTTGTCCCCAACAG[A/G]TTCTGGGTATAACCAACCCT (SEQ ID NO. 98)	7.6%
cytochrome P450, family 3, subfamily A, polypeptide 4	CYP3A4	rs2740574	0.98	1	1	0.25	2.43	ACAGCCATAGAGACAAGGGCA[A/G]GAGAGAGGCGATTTAATAGA (SEQ ID NO. 99)	9.1%
cytochrome P450, family 2, subfamily D, polypeptide 6	CYP2D6	rs7286458					1.35	ACGCTGGGCTGCACGCTACCC[A/G]CCAGGTCCCCTGCCACTGCC (SEQ ID NO. 100)	7.3%
angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)	AGT	rs5049					2.82	TGTGTAACTCGACCCTGCACC[A/G]GCTCACTCTGTTCAGCAGTG (SEQ ID NO. 101)	11.2%
acetyl-Coenzyme A carboxylase alpha	ACACA	rs2229416					2.96	GTTAGAGACTGAAAGCTTTCA[A/G]ATGAACAGAATTGATACTGG (SEQ ID NO. 102)	13.3%
dopamine receptor D3	DRD3	rs9288993	0.03	0	0	0.23	2.77	GGCAGGTAATGATATTGTGAC[A/G]TGGAGAATGTGCACTTAGAA (SEQ ID NO. 103)	5.2%
TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	TEK	rs600728	0.08	0.32	0.31	0.26	2.76	GGCTCCACGACAATGAGTACA[A/G]CTGTGGTCCGTGGCTTCTTG (SEQ ID NO. 104)	9.1%
phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	rs10494851	0.01	0	0	0.17	2.84	AAGGGGACTGTGAGAAAAAAA[A/G]TGTTCATGAGGCTCGAGTCC (SEQ ID NO. 105)	1.0%
v-akt murine thymoma viral oncogene homolog 2	AKT2	rs4802071	0.73	0.68	0.63	0.76	1.57	CAGTTCAGTTGGTTTTAGTAT[A/G]TTCAGAGTTGTGCATCCATC (SEQ ID NO. 106)	34.9%
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	PRKAG2	rs1029947	0.12	0.41	0.52	0.33	3.22	GTTGGCTCTACTCATTTCCTC[A/G]TCGTCATTCTCTTGTAGTCA (SEQ ID NO. 107)	14.8%

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cytochrome P450, family 1, subfamily A, polypeptide 2	CYP1A2	rs2470890	0.64	0.12	0.18	0	3.41	AGAATGGTGGTGTCTTCTTCA[A/G]TTGATGGAGAAGCGCAGCCG (SEQ ID NO. 108)	43.2%
cytochrome P450, family 3, subfamily A, polypeptide 4	CYP3A4	rs12333983	0.12	0.34	0.3	0.84	2.37	AATTAGATTGGAATGGATGTA[A/T]CCGTGTATATTCATACCCTT (SEQ ID NO. 109)	23.2%
paraoxonase 1	PON1	rs662	0.36	0.57	0.68	0.78	3.43	ATTTTCTTGACCCCTACTTAC[A/G]ATCCTGGGAGATGTATTTGG (SEQ ID NO. 110)	34.4%
apolipoprotein C-III	APOC3	rs4520					2.52	CTTGGTGGCGTGCTTCATGTA[A/G]CCCTGCATGAAGCTGAGAAG (SEQ ID NO. 111)	29.4%
microsomal triglyceride transfer protein (large polypeptide, 88kDa)	MTP	rs3816873	0.24	0.12	0.21	0.26	3.66	CGCCCCTTTACCTTTCCATGG[A/G]TTAGATGAAGGAGCGTAGGT (SEQ ID NO. 112)	25.0%
phosphoinositide-3-kinase, catalytic, gamma polypeptide	PIK3CG	rs4727666	0.84	0.87	0.96	0.52	3.07	GCTCTTAGAACTAGCTACAAA[A/G]ATATTTCATATGTTTATGTC (SEQ ID NO. 113)	26.0%
apoptosis, caspase activation inhibitor	AVEN	rs504714	0.95	0.91	0.88	0.4	3.30	ACTTGTAATTATGCGTGGAGT[A/T]GTTAACTGTATTTTTTACAC (SEQ ID NO. 114)	6.5%
peptide YY	PYY	rs231460					2.42	TGCTCACCCTAGGATGGAGGG[A/G]GCAGTGGGGGCTGGTTAGGA (SEQ ID NO. 115)	22.1%
selectin E (endothelial adhesion molecule 1)	SELE	rs5361	0.09	0.01	0.02	0.02	1.73	GCCTGTACCAATACATCCTGC[A/C]GTGGCCACGGTGAATGTGTA (SEQ ID NO. 116)	30.5%
cytochrome P450, family 2, subfamily C, polypeptide 19	CYP2C19	rs11188092	0.2	0.02	0	0.26	2.87	GCAAGCCCTATTAGACATATA[A/C]TTTTCCCAACTTTTCCCTTT (SEQ ID NO. 117)	21.9%
phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	rs10513055	0.2	0.01	0	0.1	3.36	GGGTAGGAAATTAAGTGAATA[A/C]TTTTTGTGATCCAAGAAAGA (SEQ ID NO. 118)	18.5%
apolipoprotein A-I	APOA1	rs4225					2.83	CTTTTAAGCAACCTACAGGGG[A/C]AGCCCTGGAGATTGCAGGAC (SEQ ID NO. 119)	45.1%
interleukin 10	IL10	rs3024492					2.86	GAAATGAGCAAGAGATCTGAC[A/T]CCAGGAGTCTTTCCTCATTT (SEQ ID NO. 120)	24.2%
glycogen synthase kinase 3 beta	GSK3B	rs10934502	0.06	0.49	0.5	0.36	2.98	GCTTCCTTATGTAAAATGTAG[A/G]TATTTCTAAAGTAACGCAAT (SEQ ID NO. 121)	22.4%
Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	HIF1A	rs2301108	0.94	0.78	0.76	0.19	3.12	CTACTGGAAGATTAGCCACGT[A/G]TTGAGTTTTGTCTTTGCATT (SEQ ID NO. 122)	12.8%
ATP-binding cassette, sub-family B (MDR/TAP), member 1	ABCB1	rs1128503	0.61	0.31	0.42	0.88	3.03	ACTCTGCACCTTCAGGTTCAG[A/G]CCCTTCAAGATCTAXCAGGA (SEQ ID NO. 123)	39.6%
apolipoprotein B (including Ag(x) antigen)	APOB	rs3791981	0.1	0.07	0.04	0.49	3.51	TTTTCCAAAGATGATCTCTCC[A/G]GAGCTATTGTTTCTTCATTC (SEQ ID NO. 124)	12.8%
phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	rs10515070	0.25	0.8	0.76	0.44	3.12	AGATTCCTCCCTGTACGATAG[A/T]GTCTTACTTTTCCACTTTGC (SEQ ID NO. 125)	29.2%

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insulin receptor substrate 1	IRS1	rs1801123	0.05	0.26	0.33	0.42	3.24	CCTTCTCTATGCTGCAACAGC[A/G]GATGATTCTTCCTCTTCCAC (SEQ ID NO. 126)	14.3%
melanocortin 3 receptor	MC3R	rs6024725	0.33	0.21	0.27	0.62	3.14	CCTAGAGACATATCTCAGTTA[A/G]GTTTTAGCCTCACCAGTATT (SEQ ID NO. 127)	33.3%
cholinergic receptor, muscarinic 3	CHRM3	rs7520974	0.53	0.46	0.51	0.75	3.50	CAGCTGAAAGAAAGACAAATA[A/G]TAGATACCCACTGCATGGCT (SEQ ID NO. 128)	43.5%
apolipoprotein L, 2	APOL2	rs1001293	0.12	0.01	0.15	0.49	3.08	TTCTTGAGTCCGTCTGTCTGG[A/G]TGGGAACCCAGTCTTTACCA (SEQ ID NO. 129)	12.8%
lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	LIPA	rs6586179	0.11	0.04	0.09	0.18	3.28	ACCCTGCATTCTGAGGGGTCT[A/G]GAGGGAAACTGACAGCTGTG (SEQ ID NO. 130)	10.4%
leptin receptor	LEPR	rs8179183	0.1	0.02	0.13	0.13	3.48	TAATGGAGATACTATGAAAAA[C/G]GAGAAAAATGTCACTTTACT (SEQ ID NO. 131)	21.1%
ATP-binding cassette, sub-family B (MDR/TAP), member 1	ABCB1	rs2032582	0.61	0.5	0.48	1	2.76	TAGTTTGACTCACCTTCCCAG[A/C]ACCTTCTAGTTCTTTCTTAT (SEQ ID NO. 132)	38.5%
lipase, hepatic	LIPC	rs936960	0.88	1	1	0.77	2.87	CAGAGCACGAGGCTGATTTTC[A/C]ATCCCAGTGTGGGCCACACC (SEQ ID NO. 133)	11.5%
peroxisome proliferative activated receptor, gamma	PPARG	rs4135268	0.04	0.06	0.09	0.03	3.33	ATTAACCCATGGTCCAGAAAT[C/G]ATGGGTTGTTAAATGACCAA (SEQ ID NO. 134)	6.0%
hypothetical protein MGC4093	MGC4093	rs1982072	0.69	0.53	0.47	0.82	2.78	TACGATTCTCACCCCATATTT[A/T]CAAGCCTAGTCCAAGGATTA (SEQ ID NO. 135)	33.1%
retinoic acid receptor, alpha	RARA	rs4890109	0.05	0	0	0	3.41	GGCTGCTCAGGGCCTCGTCCA[A/C]CCCCAGCCTGACAGAGAGCT (SEQ ID NO. 136)	2.9%
angiotensin II receptor, type 1	AGTR1	rs931490	0.81	0.84	0.86	0.98	2.01	GGCGCCCCCTGGACTTCTGCT[A/G]GAATTTAGATTTAAATAGAT (SEQ ID NO. 137)	25.0%
platelet/endothelial cell adhesion molecule (CD31 antigen)	PECAM1	rs4072032	0.63	0.51	0.51	0.89	2.80	AGTGCCCGATATACATTAAGT[A/G]CTTAATAAATGACTGCTACC (SEQ ID NO. 138)	46.6%
angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	ACE	rs4333	0.51	0.77	0.56	0.45	3.38	CTGACCCCAAGAGCGAGGGGA[A/G]CCCAACTCTGTGCTCTCACC (SEQ ID NO. 139)	47.4%
neuropeptide Y	NPY	rs1468271		1	1	1	2.66	GACCCTGTAATTTTCAGAAAC[A/G]CACATAGGAGTGGGTGTCTG (SEQ ID NO. 140)	4.9%
titin-cap (telethonin)	TCAP	rs931992	0.7	0.52	0.58	0.1	2.50	TACCTGGACGCTGGCTGCCCC[A/C]CGGTCAGAGGTCTGGGGTCC (SEQ ID NO. 141)	39.3%
pyruvate kinase, muscle	PKM2	rs2856929	0.21	0.42	0.28	0.15	2.46	CAGGCTCAGGGTCTAAATTCC[A/G]TATCCTTTCTTCCATACCCT (SEQ ID NO. 142)	19.3%
dopamine receptor D3	DRD3	rs167771	0.83	0.78	0.82	0.13	3.22	TGCTCCAAAGTCTATCACAAT[A/G]ATCCTCTTTTCCATAAAGCC (SEQ ID NO. 143)	24.5%
phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	rs1356413	0.02	0.05	0.03	0.08	2.96	TTTAGACATATGCCTCTATAT[C/G]CTTCTATAATTATTAATAGT (SEQ ID NO. 144)	4.4%
apolipoprotein L, 5	APOL5	rs2076672	0.2	0.06	0.06	0.04	0.87	CTCAGTTCCTCTGCTGTCTCC[A/G]TCCTTGCCCCATCCTCCAGG (SEQ ID NO. 145)	39.3%
lipase, hepatic	LIPC	rs417344	0.09	0.09	0.06	0.07	3.08	TTTCCTAATTTTGCAGTTGAG[A/G]TTTAAGAGGTTGGGAACTGG (SEQ ID NO. 146)	14.8%

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tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A	rs4149578	0.11	0.31	0.15	0.33	1.23	ATGGGGCCCTGGGGAGAGAGC[A/G]TGGCAAGTTCTCAGCATTCG (SEQ ID NO. 147)	12.5%
glycogen synthase 1 (muscle)	GYS1	rs2287754	0.07	0.1	0.03	0.02	2.87	CGGGAAGCTTGCAAGACGCTC[A/G]GCTTCCTATTGCAAGACCGC (SEQ ID NO. 148)	8.9%
disrupted in schizophrenia 1	DISC1	rs821616	0.31	0.14	0.07	0.39	3.69	GCTTGTCGATTGCTTATCCAG[A/T]GCCTACAGCTCCAGGAAGCC (SEQ ID NO. 149)	25.3%
phosphofructokinase, platelet	PFKP	rs10508244	0.06	0.08	0.11	0.21	2.67	CACACACTAACATGCAGAAAC[A/G]TACTACCTCACACTCAAATG (SEQ ID NO. 150)	10.2%
lipoprotein lipase	LPL	rs268	0.01	0	0	0	3.13	ACAATCTGGGCTATGAGATCA[A/G]TAAAGTCAGAGCCAAAAGAA (SEQ ID NO. 151)	1.0%
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	rs1801714					0.24	TTCAGCAGGAGCTGGGCCCTC[A/G]GGCCCAGTGGCTGGGCTGGA (SEQ ID NO. 152)	2.6%
cholesteryl ester transfer protein, plasma	CETP	rs5880	0.05	0	0	0	2.85	GATATCGTGACTACCGTCCAG[C/G]CCTCCTATTCTAAGAAAAGC (SEQ ID NO. 153)	5.7%
scavenger receptor class B, member 1	SCARB1	rs10846744	0.14	0.63	0.6	0.81	3.11	TAGCTTATCAGGTTTATTGCT[C/G]TCCATCTGTATCACCTGCCT (SEQ ID NO. 154)	19.0%
apolipoprotein M	APOM	rs707922					3.19	CCTGTTTTATGAGATTTTAAC[A/C]CCTTACCTTGATTCCTAGGA (SEQ ID NO. 155)	10.4%
growth hormone releasing hormone	GHRH	rs6032470	0.16	0.24	0.24	0.61	3.15	AGCCCCAGTCCTTACCGGAAC[A/G]GTAGAGGCTTAACAAACATT (SEQ ID NO. 156)	16.1%
solute carrier family 12 (potassium/chloride transporters), member 4	SLC12A4	rs7200210	0.06	0	0.01	0.48	3.14	CAAGAGCTCCCTACCCAGGAA[A/G]CCCAAGCCTCACCCAGAATG (SEQ ID NO. 157)	7.0%
cytochrome P450, family 2, subfamily D, polypeptide 6	CYP2D6	rs1135821					0.00	CCCTTGGGAACGCGGCCCGAA[A/G]CCCAGGATCTGGGTGATGGG (SEQ ID NO. 158)	1.0%
interleukin 1 receptor, type I	IL1R1	rs2192752					3.66	CCTTTTAATGGCCATCAATAA[A/C]ACAGCCTGACTAGTTCAACA (SEQ ID NO. 159)	22.4%
cholecystokinin A receptor	CCKAR	rs3822222	0.13	0.17	0.34	0.13	3.04	AAACTGACCTCCAACATGGAT[A/G]ATGGGGACCGACTTGTGGGG (SEQ ID NO. 160)	13.3%
gamma-aminobutyric acid (GABA) A receptor, alpha 4	GABRA4	rs1398176	0.06	0.04	0.11	0.2	3.39	AAATAAAAAGAATGCAGCCCA[A/G]TGTGGGGTAAGTAAAAGGAT (SEQ ID NO. 161)	16.9%
acetyl-Coenzyme A carboxylase alpha	ACACA	rs8081866	0.79	0.69	0.64	0.38	2.97	GAGAAGCTCCCATCTAGCTGT[A/G]TATGATAGGGGGTTTATCTG (SEQ ID NO. 162)	24.0%
ornithine aminotransferase (gyrate atrophy)	OAT	rs2807071	0.82	0.97	0.92	0.93	3.22	GGTTAGGGAGACTAGCAATTA[A/G]TTGAGAAGATGTAGTTTGAC (SEQ ID NO. 163)	16.1%
apolipoprotein L, 4	APOL4	rs2005590	0.23	0.09	0.07	0.49	2.07	TGCCTGATTTTGTCACTGAAC[A/G]ATGAGCATGATTTTTCCAGG (SEQ ID NO. 164)	26.8%
phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	rs7641983	0.18			0.4	2.48	CTCATAAAGAGCCAGACAAAA[A/G]GAAAAAAAACCCAGAAATTA (SEQ ID NO. 165)	26.0%
Williams Beuren syndrome chromosome region 14	WBSCR14	rs6967107	0.1	0	0	0.07	1.60	GGAATCTCACAGGCCTTCACC[A/C]CTCTCCCCTGCCCTTTCTCA (SEQ ID NO. 166)	6.5%

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hypothetical protein FLJ32252	FLJ32252	rs619698	0.65	0.24	0.26	0.73	2.35	TGGGACAGGTGCGCTCCCAGA[A/C]GGGATCCTGTCGCCAGTTCT (SEQ ID NO. 167)	38.5%
gamma-aminobutyric acid (GABA) A receptor, alpha 2	GABRA2	rs1442061	0.25	0.07	0.06	0.28	3.16	GGGTGTGCCCTCTAGATTTAG[C/G]CAGAGATCTATCCAGTGTAT (SEQ ID NO. 168)	25.3%
glycogen synthase kinase 3 beta	GSK3B	rs4688046	0.06	0.48	0.5	0.36	3.01	TAGTAAACTATTTCTTCCCAT[A/G]GGAGAAGATGGATTCTTTTC (SEQ ID NO. 169)	21.6%
tyrosine hydroxylase	TH	rs3842726					2.17	GCCCCACATCTGTGCCACAGA[C/G]ACAGACCCTGGGATCCTCAG (SEQ ID NO. 170)	3.9%
5-hydroxytryptamine (serotonin) receptor 5A	HTR5A	rs1440451	0.99	1	1	0.46	2.63	CTTGTTCATGATGAGATTATA[C/G]CTGATCTGACGTGAGAATGC (SEQ ID NO. 171)	3.6%
paraoxonase 1	PON1	rs854572	0.56	0.48	0.41	0.05	2.67	GGTGCCTCTGTACAACCATGT[C/G]TCTCTTCTCTGCTGTCTGCT (SEQ ID NO. 172)	47.7%
paraoxonase 1	PON1	rs3917550	0.18	0.04	0.08	0.1	2.91	AGCAACGTCTTGCTGTTTTTC[A/G]GAGGTAGAGGGCTGCTTTCT (SEQ ID NO. 173)	13.5%
uncoupling protein 3 (mitochondrial, proton carrier)	UCP3	rs826082	0.01	0	0	0.54	2.76	GCCCCACCCACTCTCCTGACT[A/T]TCGGGAGCAAACCAGTAGAG (SEQ ID NO. 174)	4.2%
5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	HTR7	rs1891311	0.1	0.18	0.17	0.3	3.49	AATGACCGGTTATACTCTTCT[A/G]TAAAGGAATCCTGGAGGTGT (SEQ ID NO. 175)	6.8%
cholinergic receptor, nicotinic, alpha polypeptide 7	CHRNA7	rs3087454					3.28	TAGCCATACTCCAGAAAAAAT[A/C]AATAAATTCCCTTGGCCCCA (SEQ ID NO. 176)	34.4%
ATP-binding cassette, sub-family G (WHITE), member 5 (sterolin 1)	ABCG5	rs4148189	0.09	0.08	0.07	0.64	3.29	TTCAACAAGCCTGCTTACTGC[A/G]GTTAGTTGTGACCATTGTCT (SEQ ID NO. 177)	16.7%
cholesteryl ester transfer protein, plasma	CETP	rs1800776					0.01	ATGATCTCAGAGGCTGTATAC[A/C]CACCCAGAGTTATTTTATGC (SEQ ID NO. 178)	6.8%
glutamate decarboxylase 1 (brain, 67kDa)	GAD1	rs3791850	0.18	0.03	0.07	0.14	2.94	CACAACAAGGGTTTAGCTCTA[A/G]GGAGAGCAGAGGCAGGATGA (SEQ ID NO. 179)	22.1%
angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	ACE	rs4305	0.6	0.71	0.52	0.08	2.52	ATTGAGTGGCTGGGGCCTGGC[A/G]CAGCCAGAAATGACAGTGGC (SEQ ID NO. 180)	46.9%
apoptosis, caspase activation inhibitor	AVEN	rs563895	0.89	0.78	0.74	0.31	3.29	GCCAATGCAGATTTATCCTCC[A/G]CCCTTCTCCAACCTGTTCTA (SEQ ID NO. 181)	16.1%
glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	GAD2	rs7072137	0.18	0.06	0.02	0.32	3.14	TGCTCACTATATGCCAATAGC[A/G]TCCCACAACCACTGATTGTG (SEQ ID NO. 182)	9.9%
neuropeptide Y receptor Y5	NPY5R	rs11100494	0.08	0.13	0.14	0.1	3.42	CAGAAAGATGTCATCATCCAG[A/C]ATTGCGTCCACACAGTCAAC (SEQ ID NO. 183)	7.0%
cytochrome P450, family 3, subfamily A, polypeptide 5	CYP3A5	rs4646450	0.18	0.34	0.27	1	3.44	GAGCGAGAGGACGCTATTGCA[A/G]TGCCACGTGAAGTGAATTGT (SEQ ID NO. 184)	20.8%

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intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	rs5491	0	0.08	0.06	0.25	3.21	GCACCTCCTGTGACCAGCCCA[A/T]GTTGTTGGGCATAGAGACCC (SEQ ID NO. 185)	2.6%
glycogen synthase 1 (muscle)	GYS1	rs5447					2.19	CTGGTTGGGAGCCTTCCCGAC[A/G]TGAACAAGATGCTGGATAAG (SEQ ID NO. 186)	0.0%
malate dehydrogenase 1, NAD (soluble)	MDH1	rs1255	0.81	0.99	0.97	0.99	3.36	CGAACAAGGACGCTTTGAAGA[A/G]GTGGAATTACTGTGCAAGGA (SEQ ID NO. 187)	28.1%
dopamine receptor D2	DRD2	rs2471857	0.17	0.5	0.42	0.17	2.71	CTTCCCAGTTGCACTAACAGA[A/G]CCTTTGATTCAGTTCAGCAA (SEQ ID NO. 188)	18.8%
gamma-aminobutyric acid (GABA) A receptor, alpha 4	GABRA4	rs3762611	0.07	0.14	0.19	0.07	2.60	CTCTCTCGTTTGGGAAAAATA[A/G]CGGAAGAACTAGTGTATCCT (SEQ ID NO. 189)	9.6%
glutamate decarboxylase 1 (brain, 67kDa)	GAD1	rs701492	0.27	0.3	0.3	0.23	1.64	GGAGGGAAATTAAAATGAAGA[A/G]TCAATGAGATTGCACATGAA (SEQ ID NO. 190)	16.9%
acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	ACAT1	rs11212515	0.22	0.31	0.35	0.01	2.84	GGATTGCAATAAAGGGAAGGA[A/T]GAAGGATGATTTTGGCTTGA (SEQ ID NO. 191)	31.0%
cholinergic receptor, muscarinic 1	CHRM1	rs2067477	0.1	0.14	0.06	0	2.64	TACCACGTACCTGCTCATGGG[A/C]CACTGGGCTCTGGGCACGCT (SEQ ID NO. 192)	11.2%
selectin P (granule membrane protein 140kDa, antigen CD62)	SELP	rs1800808	0.13	0.18	0.21	0.01	3.60	ATGTGAATAATAAGGATAATA[A/G]TCACCAAATACATAGACATG (SEQ ID NO. 193)	11.7%
cholesteryl ester transfer protein, plasma	CETP	rs1532624	0.51	0.29	0.36	0.1	3.16	TCTGCCCCTTTGGGCTGCAGC[A/C]TCACAAGCTGTGTGGCGTTG (SEQ ID NO. 194)	40.1%
adrenergic, beta-2-, receptor, surface	ADRB2	rs1042718	0.19	0.34	0.52	0.35	2.91	CCCATTCAGATGCACTGGTAC[A/C]GGGCCACCCACCAGGAAGCC (SEQ ID NO. 195)	19.5%
retinoid X receptor, alpha	RXRA	rs3118536	0.84				2.14	CTGCAGGTGCACGGTTTCCTG[A/C]TTGCCCAGGTGTCTCTGAGC (SEQ ID NO. 196)	19.0%
apolipoprotein E	APOE	rs405509	0.5	0.34	0.25	0.76	2.70	GAGGACACCTCGCCCAGTAAT[A/C]CAGACACCCTCCTCCATTCT (SEQ ID NO. 197)	46.6%
phosphoinositide-3-kinase, catalytic, gamma polypeptide	PIK3CG	rs849404	0.09	0.06	0.02	0.23	3.31	TCTGGTTGAATAAAGGTTCTT[A/G]AAAACCTCCTGAGTCAGGAC (SEQ ID NO. 198)	13.5%
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	PRKAG2	rs6960931	0.08	0.2	0.14	0.23	3.44	TCTGGGAAATGCAAGGCACAC[A/G]GCCAAGTGTGGTGGGGGTAG (SEQ ID NO. 199)	11.5%
adenosine A1 receptor	ADORA1	rs903361	0.68	0.51	0.64	0.68	3.44	AGTGGTCAGGCTTCACCCAGT[A/G]CTACAGAGCAGATCTGGGAC (SEQ ID NO. 200)	37.8%
phosphofructokinase, muscle	PFKM	rs2269935	0.15	0.28	0.21	0.05	3.47	CGGCAATTAGACTGGCTAGAG[A/C]CACCTCAGTCAGGCTCTCCC (SEQ ID NO. 201)	22.7%
retinoid X receptor, alpha	RXRA	rs3750546					1.43	CCTGAGGATGAAGGGGCGTCC[A/G]TGGCCAGGCAGCAGTGAGAA (SEQ ID NO. 202)	12.0%
lipase, hormone-sensitive	LIPE	rs10422283	0.03	0.07	0.03	0.33	0.89	GGAAGGAACCTCGTACATCCT[A/G]CGGGGCAGTGGGGACAGCGT (SEQ ID NO. 203)	26.0%
phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	rs2292459	0.8	0.48	0.51	0.41	1.67	ATTCTCTTTCTCCCTTTCTTC[A/G]AAACAGGCCCTGAAGTATGA (SEQ ID NO. 204)	6.3%

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cytochrome P450, family 3, subfamily A, polypeptide 5	CYP3A5	rs15524	0.07	0.33	0.27	0.76	3.05	TTCTTGAAGACCAAAGTAGAA[A/G]TCCTTAGAATAACTCATTCT (SEQ ID NO. 205)	12.2%
paraoxonase 1	PON1	rs705381	0.02	0.86	0.84	0	2.48	GGTGGGGGCTGACCGCAAGCC[A/G]CGCCTTCTGTGCACCTGGTC (SEQ ID NO. 206)	26.0%
acetyl-Coenzyme A carboxylase beta	ACACB	rs2430683	0.94	0.91	0.84	0.72	2.96	CCAGCAAACACCAGGCTACCA[A/C]GGATCCCAAAGATGCCAAAA (SEQ ID NO. 207)	12.0%
dopamine receptor D3	DRD3	rs167770	0.71	0.67	0.76	0.28	2.80	TGGCTTCAGCTTGTAAAGCTT[A/G]GAAACATTCTGAAACAACAT (SEQ ID NO. 208)	34.1%
dopamine receptor D5	DRD5	rs2867383	0.33	0.52	0.43	0.5	0.77	GCCTGTGGTCACAGAGCTCCT[A/G]AGTGGCAGAACTCAACTTGA (SEQ ID NO. 209)	33.3%
similar to SALL4B	LOC391530	rs10460960	0.92	0.73	0.71	0.59	2.55	CCATACTGAAAATGCTAGTCC[A/G]CCAAGCACACTTTGAGATCA (SEQ ID NO. 210)	12.8%
TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	TEK	rs617333	0.89	1	1	0.96	3.16	TGAAATCCTTTTCCCTGCTTT[A/C]CTCCAGCACTTGGGGGATGT (SEQ ID NO. 211)	15.6%
glycogen synthase kinase 3 beta	GSK3B	rs334555	0.8	1	1	1	3.34	AATTATATCTTATTATTAAAA[C/G]TCTACCAACTCAAAGCTTCC (SEQ ID NO. 212)	15.4%
cytochrome P450, family 1, subfamily A, polypeptide 2	CYP1A2	rs762551	0.69	0.67	0.61	0.57	3.28	CAAAGGGTGAGCTCTGTGGGC[A/C]CAGGACGCATGGTAGATGGA (SEQ ID NO. 213)	32.8%
histamine receptor H1	HRH1	rs901865	0.83	0.93	0.93	0.68	3.23	CTCATTGGCGCAAGAGCAGCC[A/G]CCAGTTATGGCTCACTCCCT (SEQ ID NO. 214)	19.8%
cholesteryl ester transfer protein, plasma	CETP	rs5883	0.06	0	0	0.13	2.94	AGCTACCTTGGCCAGCGAGTG[A/G]AAGACTCGCTCAGAGAACCA (SEQ ID NO. 215)	6.8%
somatostatin	SST	rs2162189					3.13	TCTAGAAGGCATCCAGGCCTC[A/G]CCTCTTTCATGTGCAGCTTT (SEQ ID NO. 216)	11.5%
dopamine receptor D1	DRD1	rs1799914	0	0.07	0.13	0	2.26	CAACTTCTTTGTCATCTCCTT[A/G]GCTGTGTCAGATCTCTTGGT (SEQ ID NO. 217)	0.3%
oxidised low density lipoprotein (lectin-like) receptor 1	OLR1	rs2742115	0.27	0.54	0.56	0.18	2.89	ACATGTGTACACGTGGTGTAT[A/G]TTAAAAACTTCAGGCTCTCT (SEQ ID NO. 218)	24.5%
lipase, hepatic	LIPC	rs1800588	0.26	0.39	0.59	0.53	2.84	TGCAGAAAACCCTTCACCCCC[A/G]TGTCAAAAGGAGCTGACGAA (SEQ ID NO. 219)	25.0%
peroxisome proliferative activated receptor, gamma	PPARG	rs6809631	0.21	0.41	0.44		3.37	GGAGAGGGAAAAATAAAGTTA[A/T]TGCATGTCCCAGTTTCCTCA (SEQ ID NO. 220)	27.3%
phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	rs706713	0.25	0.74	0.74	0.43	3.10	TTTCCTTCCAATATATTCTAC[A/G]TAAGTTCCCGGAAAGTCCCC (SEQ ID NO. 221)	27.9%
adrenergic, alpha-2A-, receptor	ADRA2A	rs521674	0.73	0.31	0.32	0.19	1.49	TTCTACTCCCTCTTCCCCTTA[A/T]TGAAGGATGCTGTGTGTACA (SEQ ID NO. 222)	33.3%
solute carrier family 39 (zinc transporter), member 7	SLC39A7	rs1547387	0.13	0.04	0.05	0.02	2.96	GCAACCCGGACATGGACACTC[C/G]CACAGTGGTGAGGAAGAGAC (SEQ ID NO. 223)	9.9%
apolipoprotein C-III	APOC3	rs2071521					3.53	ACAGCTCCTGTTGCCATAGGA[A/G]GGAGCTGGGTGAGATACTAG (SEQ ID NO. 224)	43.2%

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phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3Cb	rs1663554	0.59	0.98	0.98	0.19	2.80	AAAAACTTTTTCTGATCCCTT[A/C]CTTTTGAAAAGCCCATTAAT (SEQ ID NO. 225)	45.6%
adrenergic, beta-1-, receptor	ADRB1	rs1801253	0.68	0.75	0.85	0.59	0.93	TGCGCGCGCAGCAGAGCAGTC[C/G]CTGGAAGGCCTTGCGGAAGT (SEQ ID NO. 226)	19.0%
adiponectin receptor 2	ADIPOR2	rs7975375	0.13	0.07	0.09	0.23	2.61	CTTTTCACAGGAAAATTTCTT[A/G]GGAGTCTATTGTCACTGTCT (SEQ ID NO. 227)	14.6%
uncoupling protein 3 (mitochondrial, proton carrier)	UCP3	rs2734830					2.93	CGCATCGGCCTCTATGACTCC[A/G]TCAAGCAGGTGTACACCCCC (SEQ ID NO. 228)	1.6%
uncoupling protein 2 (mitochondrial, proton carrier)	UCP2	rs660339	0.38	0.43	0.46	0.5	3.52	ACACCGCGGTACTGGGCGCTG[A/G]CTGTAGCGCGCACTGGCCCC (SEQ ID NO. 229)	40.9%
lipase, hepatic	LIPC	rs11632618	0.01	0	0	0	2.59	TGCAATGAAATGCTCTGTCGG[A/G]TTGGGGTTGTCTAATTGCCT (SEQ ID NO. 230)	6.3%
cholinergic receptor, muscarinic 2	CHRM2	rs324651	0.11	0.03	0	0.25	3.07	TCATCAATCCATGAAACTTAG[A/C]ATAATACTGATAAATTGAAT (SEQ ID NO. 231)	13.5%
autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	AIRE	rs1003854	0.35	0.19	0.27	0.08	2.76	CATTGCGTATTATCAGGAAAA[A/G]AATACTGTCTATTAAAGAAA (SEQ ID NO. 232)	23.7%
dopamine receptor D5	DRD5	rs2227852	0.99			0	1.31	CTCATCARCTTCTACATCCCC[A/G]TTGCCATCATGATCGTGACC (SEQ ID NO. 233)	2.9%
acetylcholinesterase (YT blood group)	ACHE	rs3757868	0.14	0	0.01	0.03	1.81	ATGCGGGTGGGGAGGTGAGAG[A/G]TTGGCGACATTGACGGGAGG (SEQ ID NO. 234)	13.8%
phosphoinositide-3-kinase, class 2, gamma polypeptide	PIK3C2G	rs12582982	0.11	0.46	0.52	0.14	2.89	TAAAGTTTGACTTTTCCTATT[C/G]GTAGCTCACTTGAAGACAAA (SEQ ID NO. 235)	16.9%
corticotropin releasing hormone receptor 1	CRHR1	rs1396862	0.2	0	0	0	2.93	GACCAGGGCTTCTGAACTGCA[A/G]AGGTGCTTTTTCCTAAAACC (SEQ ID NO. 236)	18.8%
insulin receptor	INSR	rs7254060	0.92	0.86	0.89	0.32	3.48	AAGGGCATTTGCATTCAAAGG[A/G]TTCTAAACGGAAAATGACAA (SEQ ID NO. 237)	10.4%
guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	GNAO1	rs1190762	0.12	0.1	0.15	0.27	3.18	AGACTTCCCCAGGAAAGTCCT[A/C]TGTGTCTTGTATTTGGTTAC (SEQ ID NO. 238)	8.9%
cytochrome P450, family 3, subfamily A, polypeptide 4	CYP3A4	rs4986910	0.01	0	0	0	1.74	ATGTTCATGAGAGCAAACCTC[A/G]TGCCAATGCAGTTTCTGGGT (SEQ ID NO. 239)	0.3%
adrenergic, alpha-1A-, receptor	ADRA1A	rs573542	0.97	0.97	0.78	0.79	1.19	AGTGAGGCTTGGAAAGGCGTC[A/G]TGGACAGACCTGGGTCGCTT (SEQ ID NO. 240)	26.3%
angiopoietin 1	ANGPT1	rs1283718	0.11	0.07	0.09	0.08	3.25	CTTCAAAAAGTGAAACTAACT[A/C]CTCGTTTCTGGTAAAGAGCC (SEQ ID NO. 241)	7.0%
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	rs3846662	0.47	0.57	0.53	0.93	2.59	CCAGTTTAAAAATACATCATA[A/G]GTAAGGCAATGAGAAGAGTT (SEQ ID NO. 242)	47.1%
neuropeptide Y receptor Y5	NPY5R	rs6837793	0.9	0.99	0.99		2.81	ATGAATTGTCACTCAGAAGAA[A/G]CTTAATAGGCATTAATACTA (SEQ ID NO. 243)	12.0%

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ATP-binding cassette, sub-family C (CFTR/MRP), member 8	ABCC8	rs3758947	0.19	0.31	0.24	0	2.70	TGCTTTGAGCAAGGGTACCCC[A/G]CTCTGAGAATTCCCAGCCAT (SEQ ID NO. 244)	15.1%
interleukin 1 receptor, type I	IL1R1	rs2228139	0.08	0	0	0.08	3.09	TTCTGCTTAAATATGGCTTGT[C/G]CATTATAACATAAGTTAGGC (SEQ ID NO. 245)	7.0%
phosphoinositide-3-kinase, catalytic, delta polypeptide	PIK3CD	rs6541017	0.14	0.2	0.34	0.14	3.17	TTTCCCTCTACTCAGTTATCC[A/G]ATTATTCATGACTAGATGAG (SEQ ID NO. 246)	14.8%
gamma-aminobutyric acid (GABA) A receptor, alpha 2	GABRA2	rs11503016					2.86	CCATAGATCCAAACATCTTTA[A/T]CTATCCATGTATTTGAGTAG (SEQ ID NO. 247)	14.6%
adenosine A2a receptor	ADORA2A	rs3761422	0.63	0.66	0.68	0.66	2.10	TCAAGGGCCTTGCTGGGGGCA[A/G]ACAAGGTGGAACATAACACG (SEQ ID NO. 248)	36.7%
insulin-like growth factor 1 (somatomedin C)	IGF1	rs5742612	0.03	0.27	0.27	0.04	3.00	TTGTCCCAGTTGCCAAGTGAG[A/G]GGTGTGATCTCATTTCCTAG (SEQ ID NO. 249)	3.9%
guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	GNAO1	rs4784642	0.44	0.6	0.55	0.43	3.14	ATTTTCTTCTGGGTGGCCCTA[A/G]ACTGCTTTCTTTTTCCCCAT (SEQ ID NO. 250)	46.1%
scavenger receptor class B, member 2	SCARB2	rs894251	0.09	0.46	0.4	0.19	3.31	CTCAGGAGGCCTTACTGTGCC[A/G]TGGTTCTTGCCCTTTGATTT (SEQ ID NO. 251)	13.8%
phosphoinositide-3-kinase, class 2, gamma polypeptide	PIK3C2G	rs10841044	0.12	0	0	0.02	3.44	AACCAATTCTGGCCTTTAAAG[A/C]AGTCTCTTTATCTCATTCCC (SEQ ID NO. 252)	15.4%
retinoic acid receptor, alpha	RARA	rs9904270	0.14	0.31	0.42	0.08	3.35	GCCTTCCCCTTAGAGAAGAGC[A/G]CCTGCCAGACAAGGGAGAAG (SEQ ID NO. 253)	14.1%
ATP-binding cassette, sub-family C (CFTR/MRP), member 8	ABCC8	rs722341	0.07	0.04	0.03	0	2.78	TTCTGCAGAGCTTCTTCTCCT[A/G]TCTCCCACATGACTAATGTT (SEQ ID NO. 254)	13.0%
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	rs281432	0.48	0.26	0.36	0.64	3.03	ATAGGGAGTCATGGAGGGTTT[C/G]TGAGCAGGCCAGGGATTAGA (SEQ ID NO. 255)	46.4%
nitric oxide synthase 3 (endothelial cell)	NOS3	rs1799983	0.66	0.89	0.93	0.93	2.58	CAGAAGGAAGAGTTCTGGGGG[A/C]TCATCTGGGGCCTGCAGCAG (SEQ ID NO. 256)	29.7%
cytochrome P450, family 2, subfamily C, polypeptide 19	CYP2C19	rs4986893	0	0.03	0.05	0	2.39	CAGGATTGTAAGCACCCCCTG[A/G]ATCCAGGTAAGGCCAAGTTT (SEQ ID NO. 257)	0.0%
vascular cell adhesion molecule 1	VCAM1	rs1041163	0.08	0.09	0.18	0.18	3.07	ACCAAATATCTAGGGATCAGA[A/G]AAATTGATTCAGGAAATACT (SEQ ID NO. 258)	18.0%
apolipoprotein F	APOF	rs4301822	0	0	0	0.59	2.92	TCTAAGTCATAGCTCTTGATT[A/G]TGGCCCACCCCCAGTAGGGA (SEQ ID NO. 259)	6.3%
5-hydroxytryptamine (serotonin) receptor 3A	HTR3A	rs1150226	0.93	1	1	0.63	2.82	TTATGTCACCCTGGGGAGTAA[A/G]AGAATGGTCTTCCTGCTCCT (SEQ ID NO. 260)	11.2%
dystrobrevin binding protein 1	DTNBP1	rs1018381	0.08	0.06	0.09	0.31	2.89	ATCTGCCGGTGATTCAACAGC[A/G]TGCGGAACCTGCATGACGTT (SEQ ID NO. 261)	9.9%

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coagulation factor II (thrombin)	F2	rs5896	0.05	1	1	0	3.32	GTAGTGTAGCACCAGGGTCCC[A/G]TGGTGCTGCTGTCGGGGTTG (SEQ ID NO. 262)	12.5%
protein kinase, AMP-activated, beta 1 non-catalytic subunit	PRKAB1	rs1062688	0	0	0	0	0.57	CCTCCGGGGCGTCTTATGGCC[A/C]CCATGCCGCTCCAGCGCGGC (SEQ ID NO. 263)	9.9%
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	rs5927	0.73	0.93	0.96	0.65	2.87	GACACAGCACACAACCACCCG[A/G]CCTGTTCCCGACACCTCCCG (SEQ ID NO. 264)	24.0%
adenosine A3 receptor	ADORA3	rs2298191	0.28	0.26	0.31	0.12	2.31	TAGGAATGGGCAAATGAAGTG[A/G]CCTTCTGCCCCAGCCTCTCT (SEQ ID NO. 265)	30.5%
amiloride binding protein 1 (amine oxidase (copper-containing))	ABP1	rs1049793	0.31	0.54	0.61	0.67	3.01	GCTCAAAGACCACGGGCGGGT[C/G]CCAGGGGTCGTTCTGGTGGT (SEQ ID NO. 266)	33.3%
superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	SOD1	rs2070424	0.09	0.53	0.39	0.19	3.03	CATAGCTTTGTTAGCTATGCC[A/G]GTAATTAACAGGCATAACTC (SEQ ID NO. 267)	8.9%
glycogen synthase 2 (liver)	GYS2	rs1871143	0.87	0.7	0.85	0.55	2.40	AGCCAGGAGCTTTCCTGGGCG[A/C]TTTTTGTACAGGATCTCATT (SEQ ID NO. 268)	22.4%
microsomal triglyceride transfer protein (large polypeptide, 88kDa)	MTP	rs745075	0.09	0	0	0.05	3.17	TGATTTCTTGCATACTTTATT[A/G]AGCAAAATCCATGAGAAGTG (SEQ ID NO. 269)	11.7%
histamine receptor H2	HRH2	rs686874	0.04	0.24	0.1	0.39	3.04	TGAGATCTAGTAGAAGGACAC[A/G]TCTTGAATTGGGTCATGCTT (SEQ ID NO. 270)	6.5%
LOC441301	LOC441301	rs4726107	0.05	0	0	0.02	2.52	TGGGGACAGAGGCTAAATACT[A/G]CCCCCTCCCCTTTTCTACTT (SEQ ID NO. 271)	8.6%
dopamine receptor D4	DRD4	rs4987059					2.79	TTTGCAAGCACTTTCTCTTCT[A/G]CACGTTTGGAACCTACCCCG (SEQ ID NO. 272)	6.8%
proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-melanocyte stimulating hormone/ beta-melanocyte stimulating hormone/ beta-endorphin)	POMC	rs3769671	0.05	0.06	0.02	0.03	2.45	TTATAAACTGACACACACACA[A/C]AAAAAATCCACACACACTTT (SEQ ID NO. 273)	3.4%
adrenergic, alpha-2A-, receptor	ADRA2A	rs1800545					0.66	AGGAGCTCGGAGCAAGAAGGC[A/G]CCCACCGAGAGCGTCTGAAG (SEQ ID NO. 274)	25.0%
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	rs1433099	0.69	0.78	0.73	0.38	3.03	TAATAAATATTAAGGGTGACC[A/G]GTGACTCAGGCTCTGCCTCT (SEQ ID NO. 275)	28.9%
corticotropin releasing hormone	CRH	rs3176921	0.07	0	0	0.63	2.92	CTGCAGAAGCAAGGCCAATAA[A/G]TCTCTCAAAATGCAGTTCAA (SEQ ID NO. 276)	15.1%
cytochrome P450, family 7, subfamily A, polypeptide 1	CYP7A1	rs3808607	0.63	0.59	0.43	0.42	3.52	AGTCAACATATATTTGAGAGA[A/C]CTTCAACTTATCAAGTATTG (SEQ ID NO. 277)	39.8%
Oxytocin (Neurophysin 1)	OXT	rs877172	0.33	0.46	0.49	0.49	2.94	GGTGAAGAGGCTGATGGGGCC[A/C]AGCAGGTCACAGAGCTCATC (SEQ ID NO. 278)	34.1%
retinoic acid receptor, beta	RARB	rs1290443	0.11	0.16	0.17	0.36	2.43	AGAAGCTCTTTCATGTTGTCA[A/G]TTTTAGAAATCCAAATCATT (SEQ ID NO. 279)	16.4%
somatostatin receptor 3	SSTR3	rs2071710	0.19	0.7	0.57	0.2	2.51	CACGTTGACGATGTTGAGCAC[A/G]TAGAAGGGCATCCAGCAGAG (SEQ ID NO. 280)	25.0%

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peroxisome proliferative activated receptor, alpha	PPARA	rs1800206	0.04	0	0	0	2.59	TGTGTGACATCCCGACAGAAA[C/G]GCACTTGTGAAATCGACAAT (SEQ ID NO. 281)	7.3%
apolipoprotein E	APOE	rs446037					2.02	AGACACAGGTGACCCAACTCC[A/C]ATGGCTGGCCTAGGCCCCTC (SEQ ID NO. 282)	1.0%
malate dehydrogenase 1, NAD (soluble)	MDH1	rs2278718	0.25	0.17	0.21	0.01	3.12	CTCCCTAGAGTTACACACGCT[A/C]TCTCTCCCGCCAATTGCCGG (SEQ ID NO. 283)	24.2%
thioredoxin reductase 2	TXNRD2	rs737865					3.17	TTTGGATTTTTCCAGCCAGGG[A/G]TTTTTGTGTCCTGTTGCTTT (SEQ ID NO. 284)	28.9%
insulin receptor substrate-1	IRS1	rs4675096	0.08	0.2	0.13	0.63	3.03	AGTGTTTTCCAAGGTGTGATT[A/G]AAAATGGAGATTTCTTACCT (SEQ ID NO. 285)	11.7%
apolipoprotein L, 3	APOL3	rs132661	0.33	0.86	0.81	0.32	3.36	TTCCGCTCTCCCTCTGAGAGT[A/G]TATTACTGTGCTTCAATACA (SEQ ID NO. 286)	36.5%
protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1	rs461404	0.67	0.67	0.86	0.67	2.34	CATTAGGCACTGTTTTGTTCC[A/G]AGGAAGATATTGCAGGAGAA (SEQ ID NO. 287)	31.8%
microcephaly, primary autosomal recessive 1	MCPH1	rs2515449	0.07	0	0		2.64	AATTTCAACTTATAAACATAC[A/G]TTGCTATAAATATGTTCAAT (SEQ ID NO. 288)	6.5%
Corticotropin-releasing hormone receptor 2	CRHR2	rs107540	0.77	0.47	0.65	0.58	1.82	AGGGACTGGAGCCTGCTGCCC[A/G]GCACGGTGGTCACACCCTGG (SEQ ID NO. 289)	35.2%
v-akt murine thymoma viral oncogene homolog 1	AKT1	rs2494746	0.92	0.26	0.34	0.56	2.68	GGGGATGGAGAAGGCAGGATG[C/G]GGCAGGAGGCCTTGGGGGGA (SEQ ID NO. 290)	13.5%
retinoic acid receptor, beta	RARB	rs322695	0.23	0.08	0.07	0.02	2.69	CCTGTAGGATTGTGTTCCTCT[A/G]AAACTGTCCCCTAAATTATG (SEQ ID NO. 291)	16.7%
phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	rs870995					2.71	TCAGGTATTAGCACTTGAAAT[A/C]TAACTTCTTTATGAAGCTCC (SEQ ID NO. 292)	44.8%
5-hydroxytryptamine (serotonin) receptor 3B	HTR3B	rs3758987	0.23	0.15	0.33	0.48	3.25	ACAGCCTTTACCTAAGGCAGT[A/G]CTCTTGCTGACATTCAGGAC (SEQ ID NO. 293)	29.2%
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	rs5030390	0.11	0	0	0	3.33	CCCAAAGCTGAGAAGTGGGAC[A/G]CCCCAGCACACCCTCCCCCA (SEQ ID NO. 294)	8.1%
phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	rs10494852	0.72	0.71	0.72	0.11	3.16	AACTGAAAGCAGTTTAATCTC[A/G]CCAGAGCCACTGAAGGAGTT (SEQ ID NO. 295)	30.7%
angiotensin II receptor, type 1	AGTR1	rs12695902	0.08	0	0	0.09	3.32	CATCAGGATTATCAGCATTTA[A/G]GCCAGAGTTGCAAATTAAGT (SEQ ID NO. 296)	9.1%
apolipoprotein E	APOE	rs7412					1.21	CGGCCTGGTACACTGCCAGGC[A/G]CTTCTGCAGGTCATCGGCAT (SEQ ID NO. 297)	29.4%
insulin receptor substrate 1	IRS1	rs1801278	0.06	0.02	0.08	0.1	2.79	AGACTGGGCCCTGCACCTCCC[A/G]GGGCTGCTAGCATTTGCAGG (SEQ ID NO. 298)	7.8%
phosphofructokinase, liver	PFKL	rs2838549	0.07	0	0	0.11	0.70	GGACACTGGTTCCACCTCCGC[A/G]TGGCTGTACAGTGCTGCCGA (SEQ ID NO. 299)	15.1%

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kinase insert domain receptor (a type III receptor tyrosine kinase)	KDR	rs2305948	0.07	0.16	0.08	0.29	3.41	AGCACCTTAACTATAGATGGT[A/G]TAACCCGGAGTGACCAAGGA (SEQ ID NO. 300)	13.0%
tumor necrosis factor, alpha-induced protein 6	TNFAIP6	rs3771892					2.00	CAGCACCTAGCAAAATACCCC[A/G]TGGTATGATGTTCAAAGTAA (SEQ ID NO. 301)	17.7%
apolipoprotein B (including Ag(x) antigen)	APOB	rs1801701	0.05	0	0	0	3.09	TCAGATGGAAAAATGAAGTCC[A/G]GATTCATTCTGGGTCTTTCC (SEQ ID NO. 302)	7.0%
5-hydroxytryptamine (serotonin) receptor 6	HTR6	rs9659997	0.69	0.19	0.1	0.43	3.66	ACAAATGCTCTGAGTCACCAC[A/G]CTGCGGCTCAGATGCTATGA (SEQ ID NO. 303)	39.1%
cytochrome P450, family 3, subfamily A, polypeptide 4	CYP3A4	rs1851426	0.98	1	1		3.41	CACACAGCATCAAGGACTCCA[A/G]TAAGATGGTCCCAGCCTCTT (SEQ ID NO. 304)	9.4%
cytochrome P450, family 2, subfamily C, polypeptide 19	CYP2C19	rs4244285	0.15	0.26	0.28	0.17	2.83	CACTATCATTGATTATTTCCC[A/G]GGAACCCATAACAAATTACT (SEQ ID NO. 305)	15.1%
endothelin 1	EDN1	rs5369	0.91	1	1		2.87	CACAAAGGCAACAGACCGTGA[A/G]AATAGATGCCAATGTGCTAG (SEQ ID NO. 306)	13.0%
ankyrin repeat domain 1 (cardiac muscle)	ANKRD1	rs4933200	0.13	0.21	0.3	0.44	3.30	CAGTTAGAATTGTCAATCTAG[A/G]TGGGGACAACTCATTATTTT (SEQ ID NO. 307)	15.1%
adrenergic, alpha-2B-, receptor	ADRA2B	rs2229169	0.72	0.52	0.69	0.77	2.59	CTTCTTCAGCTACAGCCTGGG[A/C]GCCATCTGCCCGAAGCACTG (SEQ ID NO. 308)	28.1%
brain-derived neurotrophic factor	BDNF	rs6265	0.18	0.63	0.34	0	3.30	TTGGCTGACACTTTCGAACAC[A/G]TGATAGAAGAGCTGTTGGAT (SEQ ID NO. 309)	18.0%
lipase, gastric	LIPF	rs814628	0.14	0.23	0.38	0	3.56	ATCGACTTCATTGTAAAGAAA[A/G]CTGGACAGAAGCAGCTACAC (SEQ ID NO. 310)	18.5%
angiopoietin 1	ANGPT1	rs2514869	0.87	0.71	0.68	0.82	3.40	GGCAAAGTTTCATCTATTAGC[A/G]ATAAAATGTGAATTTTCTGC (SEQ ID NO. 311)	13.0%
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	rs1951795	0.85	0.73	0.75	0.07	3.38	ACTTATTTCAGTGGTTCAAAA[A/C]ATTTCTTCAACGCTTAACCA (SEQ ID NO. 312)	25.8%
cytochrome P450, family 2, subfamily D, polypeptide 6	CYP2D6	rs11568728					0.90	ACCCGCATCTCCCACCCCCAG[A/G]ACGCCCCTTTCGCCCCAACG (SEQ ID NO. 313)	12.8%
acetyl-Coenzyme A carboxylase beta	ACACB	rs2241220	0.88	0.73	0.73	0.76	3.17	ATCGAAGTTACGCATCCGGTT[A/G]AGTTCCAGCTGGAAGGCCAG (SEQ ID NO. 314)	19.3%
adenosine A2b receptor	ADORA2B	rs2015353	0.46	0.11	0.16		2.81	AAAGTAGAACATACCAGGCCG[A/G]GAGAACAACATGTGCTGCTT (SEQ ID NO. 315)	47.1%
brain-derived neurotrophic factor	BDNF	rs2049045	0.18	0	0	0	3.47	AAATCTCTCTTCTTCGATAAA[C/G]TTCCCAGGAGGTAACCCAAT (SEQ ID NO. 316)	17.4%
5-hydroxytryptamine (serotonin) receptor 2A	HTR2A	rs6312	0.93	0.99	1	0.77	3.43	AACAAATGTATCTCATGTGTG[A/G]ACCCTGAAGACAAATGTAAG (SEQ ID NO. 317)	6.8%
histamine N-methyltransferase	HNMT	rs12691940	0.36	0.28	0.31	0.48	3.23	AATCAACCAAGTGGAAGAAAG[A/G]ATATCAGAGTCTGAAGACAA (SEQ ID NO. 318)	38.3%
disrupted in schizophrenia 1	DISC1	rs1322783	0.88	0.88	0.85	0.81	3.43	ATCACTCCTCTTCTAGCATCT[A/G]TTACATTTTCTGGCATTTCT (SEQ ID NO. 319)	15.9%

Gene	Symbol	SNP	CEU	HCB	JPT	YRI	Gen-Score	Sequence Context	MAF
cytochrome P450, family 2, subfamily D, polypeptide 6	CYP2D6	rs1058171					2.04	AACCTGCGCATAGTGGTGGCT[A/G]ACCTGTTCTCTGCCGGGATG (SEQ ID NO. 320)	0.0%
hypothetical protein MGC4093	MGC4093	rs1800469	0.69	0.55	0.48	0.78	2.32	AGGGGGCAACAGGACACCTGA[A/G]GGATGGAAGGGTCAGGAGGC (SEQ ID NO. 321)	33.6%
retinoid X receptor, alpha	RXRA	rs4917348	0.11				3.02	GGTGGGGTTAGAGGGGATGGT[A/G]CCTGGCAGTGTGCAGCAGAC (SEQ ID NO. 322)	19.0%
tumor necrosis factor, alpha-induced protein 6	TNFAIP6	rs1046668	0.14	0.23	0.13	0.23	3.07	GCGTCTTTACAGATCCAAAGC[A/G]AATTTTTAAATCTCCAGGCT (SEQ ID NO. 323)	17.2%
lipase, hepatic	LIPC	rs6083	0.42	0.72	0.94	0.64	3.57	GTCTTTCTCCAGATGATGCCA[A/G]TTTTGTGGATGCCATTCATA (SEQ ID NO. 324)	39.6%
fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	FLT1	rs748253	0.7	0.76	0.76		3.27	GCCCTGGTTTCCTCCAGTATG[A/C]CTGCAAAATTTCCTCTCCAT (SEQ ID NO. 325)	37.8%
haptoglobin	HP	rs2070937	0.48	0.44	0.4	0.71	3.37	CCAATGTACTTTCCTGAATGC[A/G]GCCAGAAACTGAGCCCACCC (SEQ ID NO. 326)	43.8%
ghrelin precursor	GHRL	rs26312					3.20	GCTGTTGCTGCTCTGGCCTCT[A/G]TGAGCCCCGGGAGTCCGCAG (SEQ ID NO. 327)	14.3%
angiotensin I converting enzyme (peptidyl-dipeptidase A)	ACE	rs1800764	0.6	0.69	0.52	0.08	2.49	ATTTGCAAAGTATGTACAGCA[A/G]CCCCCCCTTATCCTCAGTGG (SEQ ID NO. 328)	47.9%
acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	ACAT2	rs15982	0.67	0.56	0.58	0.48	3.54	CCCTCCTTCAATATTGACCTA[A/G]CGGGGGAGAAAAGATTTAGA (SEQ ID NO. 329)	30.5%
histamine N-methyltransferase	HNMT	rs1801105	0.13	0.04	0.02	0	3.38	TTTACGTTCTCGAGGTTCGAT[A/G]TCTTGGCTACAAGCTCTAAA (SEQ ID NO. 330)	8.6%
lipoprotein lipase	LPL	rs295	0.23				2.80	GATGCACCTACTAGACACCTA[A/C]TCTGCGCTAGATGGTGGGGG (SEQ ID NO. 331)	26.6%
apolipoprotein L, 3	APOL3	rs132642	0.88	0.99	0.98	1	3.10	GTCAGTGACTGGAGAGCTCCA[A/T]GGAAAGTCTCTCAGTGACCT (SEQ ID NO. 332)	11.7%
adrenergic, beta-3-, receptor	ADRB3	rs4994					1.60	TGGTCTGGAGTCTCGGAGTCC[A/G]GGCGATGGCCACGATGACCA (SEQ ID NO. 333)	8.6%
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	PRKAG2	rs1860743	0.85				2.57	AAAAGGCCTCTGGGGCAGGGA[A/G]GAATGTCCTTTAATGGGGAC (SEQ ID NO. 334)	9.6%
nitric oxide synthase 3 (endothelial cell)	NOS3	rs1800783	0.6	0.88	0.94	0.57	3.17	CATGCTGGAGGAGACAACAGA[A/T]CCCAAGTCTGGCTTCCATAT (SEQ ID NO. 335)	37.5%
carnitine palmitoyltransferase II	CPT2	rs1799821	0.56	0.74	0.77	0.2	3.11	GCCAAGGATGGCTCTACTGCC[A/G]TCCACTTTGAGCACTCTTGG (SEQ ID NO. 336)	46.1%
Choline Kinase Beta	CHKB	rs1064344					3.11	TGTGGTATCTTTACTGGAACC[A/G]ATAAATGCACCTCTGGCTCT (SEQ ID NO. 337)	7.8%
phosphoinositide-3-kinase, class 3	PIK3C3	rs3813065	0.15	0.3	0.35	0.4	3.06	CAAAAATTGGAATTTTGCCAG[A/G]TTTAAATTCCAGTGGCCTTC (SEQ ID NO. 338)	12.8%
gamma-aminobutyric acid (GABA) A receptor, alpha 2	GABRA2	rs3756007	0.08	0.26	0.11	0	2.93	CAGTTTAAAGTCCAGGGTGTT[A/G]TTATTACGTGTGCGCAAAAC (SEQ ID NO. 339)	6.3%

Gene	Symbol	SNP	CEU	HCB	JPT	YRI	Gen-Score	Sequence Context	MAF
tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	rs1061622	0.25	0.2	0.16	0.16	3.53	GTGGACGTGCAGACTGCATCC[A/C]TGCTTGCATTCCCAGGGATG (SEQ ID NO. 340)	22.1%
fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	FLT1	rs10507383	0.07	0.01	0	0.11	2.96	CCCTTTCAGCAACAACACCAT[C/G]GGTAGAAATATGATGCAGCG (SEQ ID NO. 341)	8.1%
dopamine receptor D2	DRD2	rs1799978	0.03	0.14	0.11	0.13	2.49	CCCAGCCTGCAATCACAGCTT[A/G]TTACTCTGGGTGTGGGTGGG (SEQ ID NO. 342)	9.9%
cytochrome P450, family 3, subfamily A, polypeptide 5	CYP3A5	rs4646458	0.02	0.31	0.25	0.53	2.01	ATTTTCCTTTTTTATTCTTTC[A/C]TTTTCCCTCCTTTTCTGAAT (SEQ ID NO. 343)	8.3%
5-hydroxytryptamine (serotonin) receptor 2A	HTR2A	rs659734	0.93	1	1	0.83	3.07	CTGGTAGGAAATTGAACTGAA[A/G]TCATAAACGGAAAGCAGCTA (SEQ ID NO. 344)	7.6%
galanin	GAL	rs694066	0.06	0.01	0	0.32	2.02	TTCTAAGTCCTCTGCCATGCC[A/G]GGAAAGCCTGGGTGCACCCA (SEQ ID NO. 345)	13.0%
resistin	RETN	rs3219177					2.62	CCAGGGATCAGTGAGGTCTCT[A/G]AGACCCTTGGGGAGCTTGCC (SEQ ID NO. 346)	19.5%
choline acetyltransferase	CHAT	rs885834	0.59	0.22	0.32	0.16	2.46	ACGACGCCGTGCCGGGAATAG[A/G]GAAGCAGTGTGAGGACCACA (SEQ ID NO. 347)	40.1%
selectin E (endothelial adhesion molecule 1)	SELE	rs5368	0.08	0.32	0.14	0.04	3.09	ACTCAAGTTGAGTTGATCCAT[A/G]TAATTCAAATCCCTCCTCAC (SEQ ID NO. 348)	12.0%
protein kinase, AMP-activated, alpha 2 catalytic subunit	PRKAA2	rs2796516	0.17	0.34	0.4	0.27	3.03	GAACTTTTATAGGTTGCTGGA[A/G]GGAATGTAAATTAGTGCAAA (SEQ ID NO. 349)	15.6%
cholinergic receptor, nicotinic, alpha polypeptide 7	CHRNA7	rs1355920	0.9	0.77	0.83	0.45	3.00	ATCAACTGAGGAAGATAATAA[A/G]CTATAAAAAGATGAAAAGGA (SEQ ID NO. 350)	12.8%
apolipoprotein A-I	APOA1	rs5070					2.93	GCCACGGGGATTTAGGGAGAA[A/G]GCCCCCCGATGGTTGGCTCC (SEQ ID NO. 351)	35.2%
acetyl-Coenzyme A carboxylase beta	ACACB	rs34274	0.9	0.82	0.69	0.35	3.42	CTCTATGATTTCACAGTGATG[A/G]GCTCAAGTATGTGTCTGCTT (SEQ ID NO. 352)	20.3%
angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)	AGT	rs4762	0.08	0.08	0.1	0.04	2.96	GCTGTGAACACGCCCACCACC[A/G]TGGACAGCAGCAGCTGGGCC (SEQ ID NO. 353)	12.5%
5-hydroxytryptamine (serotonin) receptor 1D	HTR1D	rs676643	0.16	0.31	0.19	0.22	3.25	AGGTTCATCTTGACGCATCCT[A/G]AGCTACTTAACTTCGGTTCC (SEQ ID NO. 354)	17.7%
glycogen synthase 2 (liver)	GYS2	rs1478290					3.01	AATGTGGCTGAAGCCAAAAGC[A/C]TAATGAATGAGGGGAAGCCT (SEQ ID NO. 355)	31.3%
acetylcholinesterase (YT blood group)	ACHE	rs3847063	0.46	0.83	0.91	0.1	3.00	TCTTCCCTGGTATGACCTGAC[A/G]TCCATCTGACATGGTCCCTG (SEQ ID NO. 356)	44.8%
phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	rs40318	0.8	0.78	0.78	1	2.90	AATAGATGACTGTGAACAGTG[A/G]TGGCCAGGGAACTATCTTCA (SEQ ID NO. 357)	17.2%

Gene	Symbol	SNP	CEU	HCB	JPT	YRI	Gen-Score	Sequence Context	MAF
vascular endothelial growth factor	VEGF	rs833060	0.3	0.46	0.4	0.15	2.93	GGGCGTCAGAGCAGACTGTCT[A/C]CCCAAAGAATCCTCCGAAGG (SEQ ID NO. 358)	29.7%
cytochrome P450, family 2, subfamily C, polypeptide 9	CYP2C9	rs1057910	0.06			0	1.30	GTGCACGAGGTCCAGAGATAC[A/C]TTGACCTTCTCCCCACCAGC (SEQ ID NO. 359)	15.4%
glycogen synthase 2 (liver)	GYS2	rs2306179	0.8	0.71	0.85	0.57	3.39	TTTCAGTAGGTTTGCAGGGAA[A/G]CCAACTCAAAGCTATATCTG (SEQ ID NO. 360)	25.5%
acetyl-Coenzyme A carboxylase alpha	ACACA	rs4795180	0.12	0.5	0.31	0.03	2.97	TTCCTGGCCACACTGAGAAAC[A/C]CCTCCTTTCCTTCGACACAT (SEQ ID NO. 361)	12.5%
leptin receptor	LEPR	rs7602					3.15	CTTGGAGAGGCAGATAACGCT[A/G]AAGCAGGCCTCTCATGACCC (SEQ ID NO. 362)	22.1%
cytochrome P450, family 3, subfamily A, polypeptide 5	CYP3A5	rs6976017	0.04	0.02	0.02	0.13	3.11	CTGGGACTGTGGATGGATGTA[A/G]TTTCGTTTTTTCTAGTCTGT (SEQ ID NO. 363)	4.4%
interleukin 1, alpha	IL1A	rs1800794	0.31	0.07	0.14	0	2.95	AAGCATGGATCTGGGAGGAAA[A/G]CAGCTTGTGTGAGTTGGATA (SEQ ID NO. 364)	24.0%
adrenergic, beta-1-, receptor	ADRB1	rs2429511	0.4	0.58	0.67	0.27	3.24	TCCTGGCTTCCTTCTGGACCC[A/G]CAAGGGGCAGTCTCAAAATA (SEQ ID NO. 365)	46.6%
adenosine A3 receptor	ADORA3	rs1415793	0.81	0.77	0.81	0.76	2.85	ACACACATGTTCAGCCCAACT[A/G]GAGCCTTTTGTCAGTAAGTC (SEQ ID NO. 366)	22.4%
5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	HTR7	rs1935349	0.12	0.21	0.31	0.5	2.76	TTATAGATTGTCCAGACATGA[A/G]CAGATCTATCACCTGACCAC (SEQ ID NO. 367)	15.6%
lipoprotein lipase	LPL	rs328	0.13	0.09	0.15	0.03	2.85	ACAAGTCTCTGAATAAGAAGT[C/G]AGGCTGGTGAGCATTCTGGG (SEQ ID NO. 368)	10.2%
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	rs10515521	0.16	0	0	0.11	3.03	CCTAATCTAAAATTTTCTATT[A/G]CTACATCAAGGGAACAATTT (SEQ ID NO. 369)	16.7%
retinoic acid receptor, gamma	RARG	rs10082776	0.07	0.21	0.27	0.64	3.22	TCCCAAGGTGAATGATGGTCT[A/G]AGGACTTCTGGTGGAGAGAA (SEQ ID NO. 370)	13.3%
apolipoprotein B (including Ag(x) antigen)	APOB	rs676210	0.19	0.69	0.67	0.17	2.62	ATGTGGGGAAGCTGGAATTCT[A/G]GTATGTGAAGGTCAGGAACT (SEQ ID NO. 371)	22.4%
carnitine palmitoyltransferase 1A	CPT1A	rs597316	0.31	0.11	0.23	0.09	2.70	CGGGGAGGAGGCCCTAATTGT[C/G]CAATGGGGGCCGCGTAAATG (SEQ ID NO. 372)	31.3%
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	rs6196	0.17	0.06	0.07	0.14	2.76	CAGAAGTTTTTTGATATTTCC[A/G]TTTGAATATTTTGGTATCTG (SEQ ID NO. 373)	16.4%
adrenergic, alpha-1A-, receptor	ADRA1A	rs2229126	0.03	0.07	0.02	0	1.92	CCTCAGTGAGAACGGGGAGGA[A/T]GTCTAGGACAGGAAAGATGC (SEQ ID NO. 374)	1.6%
serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	SERPINE1	rs6092					3.42	ACCTGCCTAGTCCTGGGCCTG[A/G]CCCTTGTCTTTGGTGAAGGG (SEQ ID NO. 375)	12.8%
cytochrome P450, family 3, subfamily A, polypeptide 4	CYP3A4	CYP3A4_5					2.28	ATACTTATTGAGAGAAAGAAT[C/G]GATCCAAAAAATCAAATCTT (SEQ ID NO. 376)	0.0%
interleukin 6 (interferon, beta 2)	IL6	rs2069827	0.1	0	0	0	2.97	AAGAAGAGATCTCTTCAAGAT[A/C]GATAAAACAGTGACCTCTGT (SEQ ID NO. 377)	8.3%

Gene	Symbol	SNP	CEU	HCB	JPT	YRI	Gen-Score	Sequence Context	MAF
tumor necrosis factor (ligand) superfamily, member 6	TNFSF6	rs6700734	0.33	0.08	0.16	0.34	3.38	AAATAAACCAGAAATTGGTAA[A/G]TCATCACATGGAAATCAAAT (SEQ ID NO. 378)	24.2%
cholinergic receptor, nicotinic, alpha polypeptide 7	CHRNA7	rs2221223	0.16	0.03	0.01	0.08	2.93	GAATTGGTCCACCAGCAAAAC[A/C]CATTTGCTTCTCCGTGGACT (SEQ ID NO. 379)	16.4%
peptide YY	PYY	rs1058046	0.72	0.27	0.33	0.44	2.34	GGAAAAGAGACGGCCCGGACA[C/G]GCTTCTTTCCAAAACGTTCT (SEQ ID NO. 380)	26.6%
brain-derived neurotrophic factor	BDNF	rs908867	0.12	0.01	0.08	0.09	1.05	GCACCTACACCAACAATTCAG[A/G]GTATCCCACTGTAAGATATA (SEQ ID NO. 381)	6.8%
ATP-binding cassette, sub-family B (MDR/TAP), member 1	ABCB1	rs1045642					2.92	GGCCTCCTTTGCTGCCCTCAC[A/G]ATCTCTTCCTGTGACACCAC (SEQ ID NO. 382)	33.9%
retinoid X receptor, gamma	RXRG	rs157864	0.17	0.12	0.32	0.24	2.89	ATGATATTGAATTAAAGGAAA[A/G]TGAATGGTCTCAGTCAGAGA (SEQ ID NO. 383)	10.7%
cholecystokinin B receptor	CCKBR	rs1805002	0.04	0.01	0.07	0.09	2.78	GGCACATTCATCTTTGGCACC[A/G]TCATCTGCAAGGCGGTTTCC (SEQ ID NO. 384)	3.9%

Table 11: Summary of SNP assay results.

Good runs	Count	Fraction
0	68	18%
1	31	8%
2	55	14%
3	140	36%
4	67	17%
5	23	6%
Grand Total	384	

What is claimed is

1. A physiogenomics method for predicting an individual's response to the environment comprising:
    (a) selecting a plurality of genetic markers based on an analysis of the entire human genome or a fraction thereof;
    (b) identifying significant covariates among demographic data and the other phenotypes by principal component analysis;
    (c) performing for each selected genetic marker an unadjusted association test using genetic data
    (d) using permutation testing to obtain a non-parametric and marker complexity probability value for identifying significant genetic markers; and
    (e) constructing a physiogenomic model by linear regression analyses and model parameterization for the dependence of said patient's response to treatment with respect to said genetic markers; and
    (f) identifying one or more genes not associated with a particular outcome in said patient to serve as a physiogenomic control.

2. The method according to claim 1, wherein the step of selecting a plurality of genetic markers comprises DNA screening using a fixed array.

3. The method according to claim 1, wherein the step of selecting a plurality of genetic markers comprises DNA screening using a liquid array.

4. The method according to claim 1, wherein the step of selecting a plurality of genetic markers comprises DNA screening using a random array.

5. The method according to claim 4, wherein the random array is a microbead array comprising microbeads with an average diameter less than or equal to 2 microns.

6. The method according to claim 1, wherein said phenotypes are endophenotypes.

7. The method according to claims 1-5, wherein said covariates are determined by generating a covariance matrix for all markers and selecting each significantly correlated marker for use as a covariate in the association test for each marker, and wherein serological and baseline outcomes are tested by linear regression.

8. The method according to claims 1-5, wherein said permutation testing comprises

selecting an original data set;

creating a plurality of permuted data sets that differ from the original data set by having a response variable permuted at random with respect to a marker;

performing the same tests on the original data set and the plurality of permuted data sets to obtain a non-parametric estimate of the null distribution of the test statistics, and

determining the false positive rate of a marker by determining where in the distribution of test results corresponding to the permuted data sets lies the test result corresponding to the original data set.

9. The method of claim 8, wherein the number of data sets in the plurality of data sets is at least 1000, and wherein a marker is selected for model building when test results corresponding to the original data set are in the top 50.

10. The method of claims 1-5, wherein said linear regression model in the construction of said physiogenomic model has the form

$$R = R_o + \sum_i \alpha_i M_i + \sum_i \beta_i D_i + \varepsilon$$

wherein R is the respective phenotype variable, M_i represents the genetic marker variables, D_i are the demographic covariates, and ε is the residual unexplained variation.

11. A method for treating an individual suffering from a disease or disorder, said method comprising the steps of

preparing a physiogenomics database, said physiogenomics database comprising a plurality of ensembles of genetic markers obtained from a plurality of people, wherein each ensemble of a genetic markers is associated with a physiological response to a treatment;

obtaining genotype and phenotype data of the individual; and

comparing the genotype data of the individual with said plurality of ensembles of genetic markers in said physiogenomics database;

calculating a predicted physiological response of the individual to each treatment associated with each ensemble of genetic markers, and

recommending a treatment regimen based on said calculation.

12. The method of claim 11, further comprising ranking the predicted physiological response of the individual as percentile against the physiological responses of the people whose ensembles of genetic markers constitute the database.

13. The method of claim 11, wherein the step of preparing a physiogenomics database further comprises

selecting a plurality of ensembles of genetic markers based on an analysis of the entire human genome or a fraction thereof;

identifying significant covariates among demographic data and the other phenotypes by principal component analysis;

performing for each selected genetic marker an unadjusted association test using genetic data

using permutation testing to obtain a non-parametric and marker complexity probability ("p") value for identifying significant markers, wherein the significance is shown by $p<0.05$; and

constructing a physiogenomic model by linear regression analyses and model parameterization for the dependence of said patient's response to treatment with respect to said markers, wherein said physiogenomic model has $p<0.05$; and

identifying one or more genes not associated with a particular outcome in said patient to serve as a physiogenomic control.

14. An assay for constructing a physiogenomic database, wherein said assay comprises

a plurality of subpopulations of oligonucleotide probes, wherein all of the oligonucleotide probes in each subpopulation are capable of hybridizing with an oligonucleotide selected from the group consisting of SEQ ID NOs 1-384,

a plurality of binding sites, wherein each binding site binds one of the subpopulations of oligonucleotides.

15. The assay according to claim 14, wherein each binding site of the plurality of binding sites is on a separate bead.

16. The assay according to claim 15, wherein the bead has an average diameter less than or equal to 2 microns.

17. The assay according to claim 16, wherein said beads are fixed on a surface of a solid support.

18. The assay according to claim 14, wherein each of said subpopulations is attached on a discrete area on the surface of a solid support.

19. The assay according to claim 14, wherein said plurality of subpopulations of oligonucleotide probes comprises oligonucleotide probes capable of hybridizing with at least about 10 oligonucleotides selected from the group of oligonucleotides consisting of SEQ ID NOs 1-384.

20. The assay according to claim 14, wherein said plurality of subpopulations of oligonucleotide probes comprises oligonucleotide probes capable of hybridizing with at least about 20 oligonucleotides selected from the group of oligonucleotides consisting of SEQ ID NOs 1-384.

21. The assay according to claim 14, wherein said plurality of subpopulations of oligonucleotide probes comprises oligonucleotide probes capable of hybridizing with at least about 50 oligonucleotides selected from the group of oligonucleotides consisting of SEQ ID NOs 1-384.

22. The assay according to claim 14, wherein said plurality of subpopulations of oligonucleotide probes comprises oligonucleotide probes capable of hybridizing with at least about 100 oligonucleotides selected from the group of oligonucleotides

consisting of SEQ ID NOs 1-384.

23. The assay according to claim 14, wherein said plurality of subpopulations of oligonucleotide probes comprises oligonucleotide probes capable of hybridizing with at least about 200 oligonucleotides selected from the group of oligonucleotides consisting of SEQ ID NOs 1-384.

24. The assay according to claim 14, wherein said plurality of subpopulations of oligonucleotide probes comprises oligonucleotide probes capable of hybridizing with at least about 300 oligonucleotides selected from the group of oligonucleotides consisting of SEQ ID NOs 1-384.

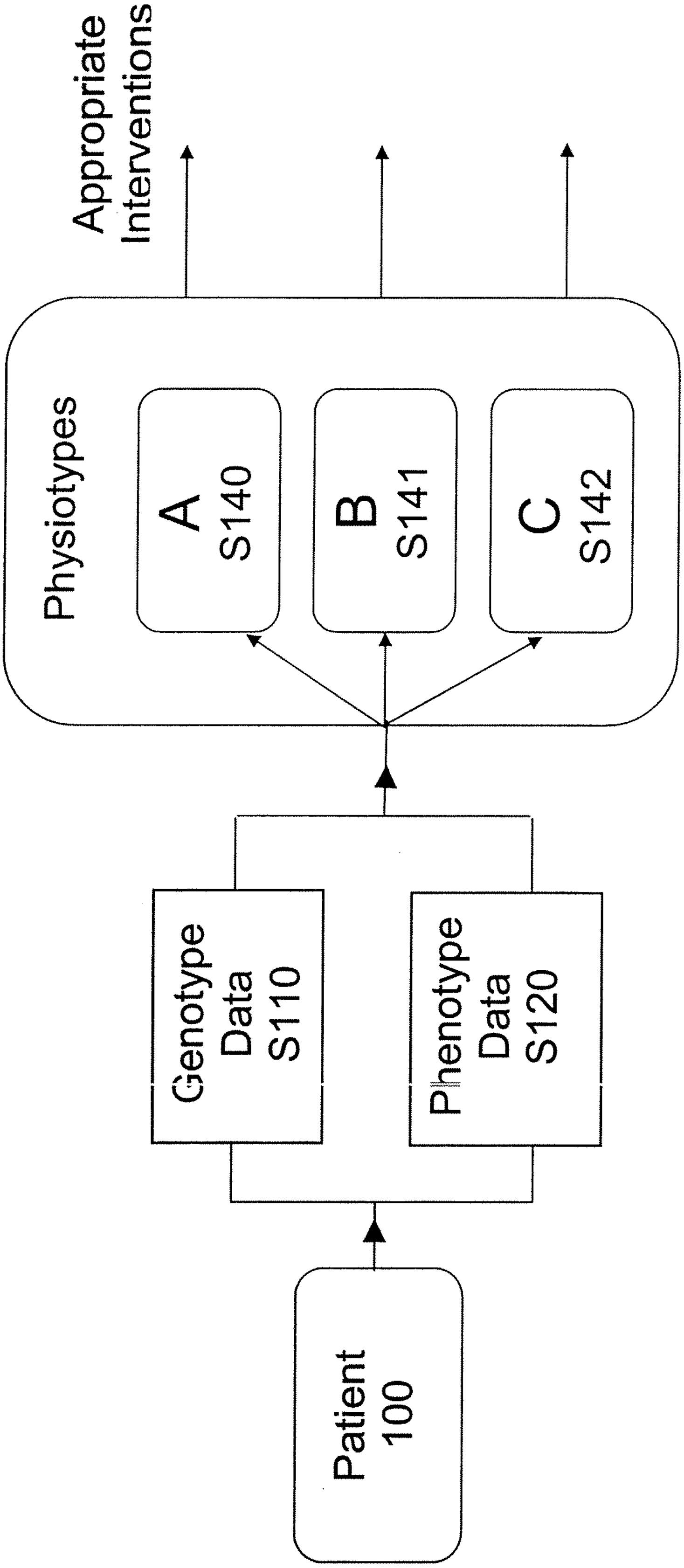
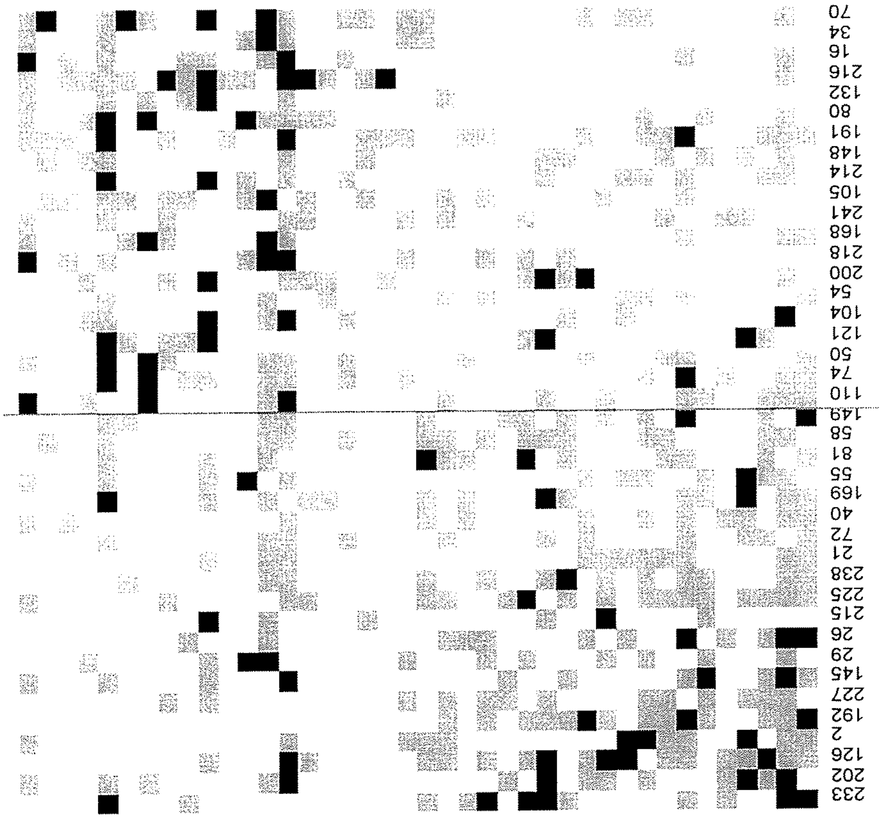

Patient
100
Genotype
Data
S110
Phenotype
Data
S120
Physiotypes
A
S140
B
S141
C
S142
Appropriate
Interventions

FIGURE 1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218
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149
58
81
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29
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227
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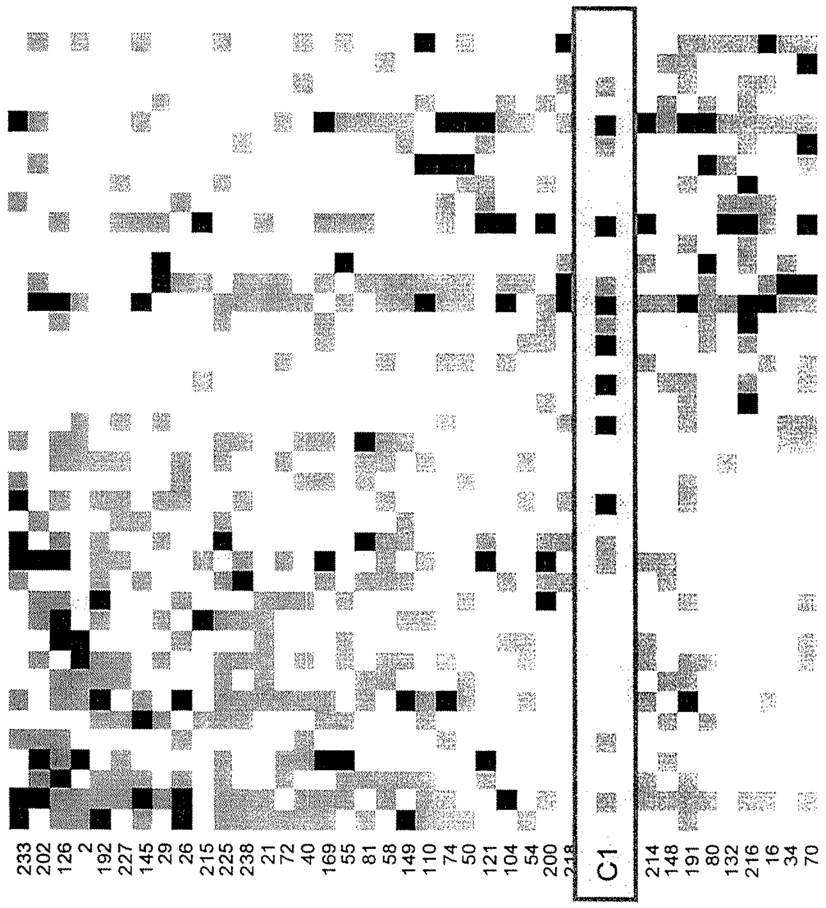
2
126
202
233

FIGURE 2a



Multi-Gene SNP Ensemble places test Individual C1 at 86th percentile risk ranking

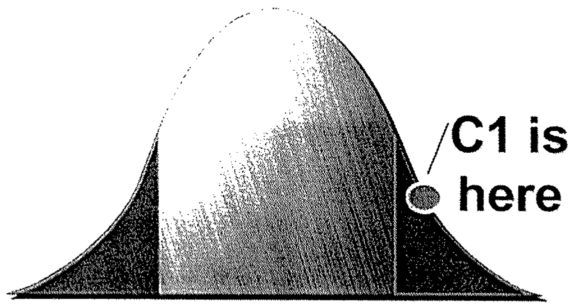


FIGURE 2b

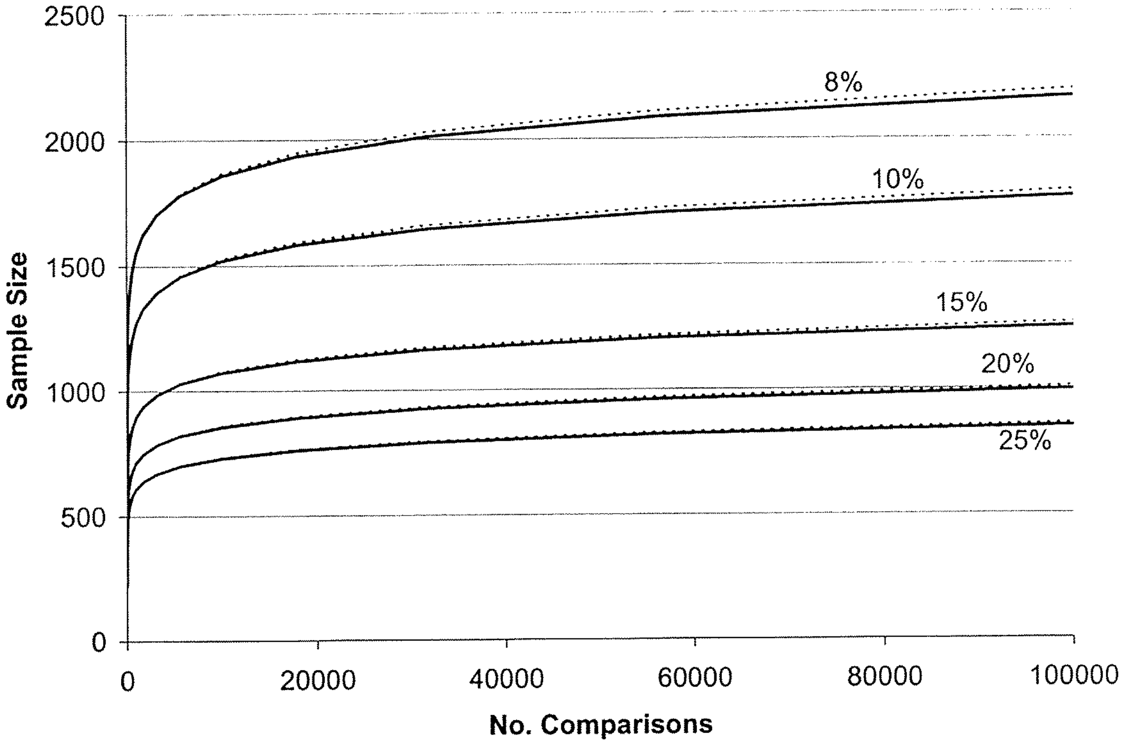
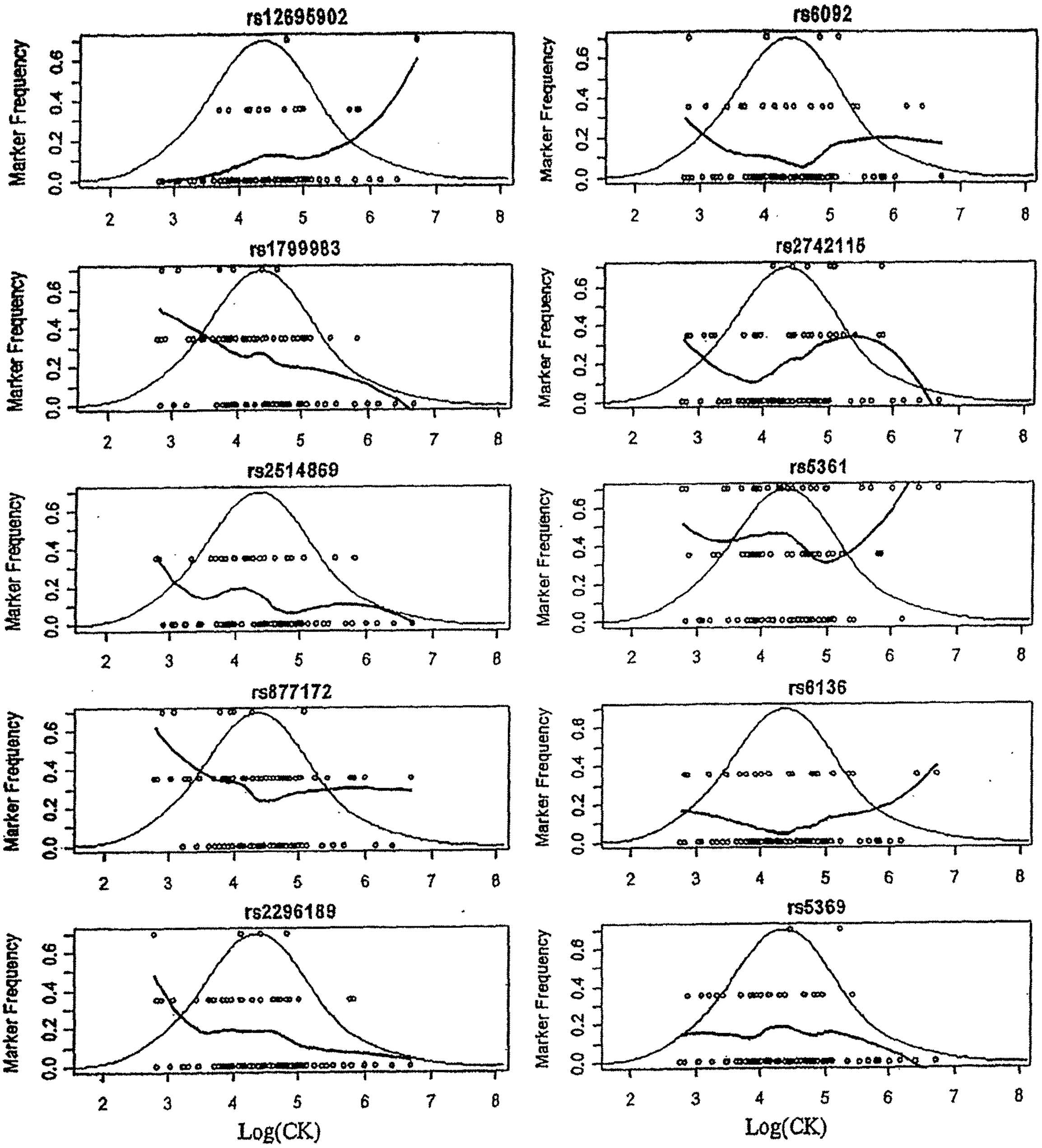

2500
2000
1500
1000
500
0
Sample Size
0
20000
40000
60000
80000
100000
No. Comparisons
8%
10%
15%
20%
25%

FIGURE 3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rs6092
rs1799983
rs2742115
rs2514869
rs5361
rs877172
rs6136
rs2296189
rs5369
Marker Frequency
0.0
0.2
0.4
0.6
2
3
4
5
6
7
8
Log(CK)

FIGURE 4