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**COMPOSITIONS AND METHODS FOR DETECTING PREDISPOSITION TO
CARDIOVASCULAR DISEASE**

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ABSTRACT

Methods and compositions are provided for detecting a predisposition for cardiovascular disease in an individual.

COMPOSITIONS AND METHODS FOR DETECTING PREDISPOSITION TO CARDIOVASCULAR DISEASE

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Application No. 62/347,479 filed June 8, 2016, and U.S. Application No. 62/455,468 filed February 6, 2017. Both of these applications are incorporated herein in their entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under R01DA037648 and R44DA041014 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

Cardiovascular Disease (CVD), which consists of Coronary Heart Disease (CHD), Congestive Heart Failure (CHF) and Stroke, is the leading cause of death in the United States. Effective treatments to prevent morbidity and mortality of CVD exist, but their clinical implementation is hindered by inefficient screening techniques. In recent years, others and we have shown that DNA methylation signatures can infer the presence of a variety of disorders related to CVD such as smoking. Unfortunately, when these epigenetic techniques are applied to CVD itself, the power of these methods is diminished, thus limiting their clinical utility. One possible reason for these failures may be the obscuration of epigenetic signature of CVD by *gene x methylation* interaction effects.

A reliable laboratory test would be of practical value in clinical practice, for example, in assisting doctors in prescribing the appropriate treatment for their patients. Accordingly, methods of identifying subjects that have, or are at risk for developing, CVD are needed.

SUMMARY OF THE INVENTION

In certain embodiments, the present disclosure provides a kit for determining methylation status of at least one CpG dinucleotide and a genotype of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide from a gene from **Figure 15** or a first CpG site from **Figure 16**, or a second CpG site that is collinear (e.g., $R > 0.3$) with a first CpG site from **Figure 16**, wherein the at least one first nucleic acid primer detects an unmethylated CpG

dinucleotide; and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or bisulfite converted DNA sequence of a first SNP from **Figure 21** or a second SNP in linkage disequilibrium with a first SNP from **Figure 21**. In some embodiments, the linkage disequilibrium has a value of $R > 0.3$.

In certain embodiments the present disclosure provides a kit for determining methylation status of at least one CpG dinucleotide and a genotype of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a gene from **Figure 17** or a first CpG dinucleotide from **Figure 18** or a second CpG dinucleotide collinear (e.g., $R > 0.3$) with a first CpG site from **Figure 18**, wherein the at least one first nucleic acid primer detects an unmethylated CpG dinucleotide; and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or bisulfite converted DNA sequence of a first SNP **Figure 22** or a second SNP in linkage disequilibrium with a first SNP from **Figure 22**. In some embodiments, the linkage disequilibrium has a value of $R > 0.3$.

In certain embodiments the present disclosure provides a kit for determining methylation status of at least one CpG dinucleotide and a genotype of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide from a gene from **Figure 19** or a first CpG site in **Figure 20** or a second CpG dinucleotide collinear ($R > 0.3$) with a first CpG site from **Figure 20**, wherein the at least one first nucleic acid primer detects an unmethylated CpG dinucleotide; and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or bisulfite converted DNA sequence of a first SNP from **Figure 23** or a second SNP in linkage disequilibrium with a first SNP from **Figure 23**. In some embodiments, the linkage disequilibrium has a value of $R > 0.3$.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs347027.

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5 In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 38364951 in an intergenic region of chromosome 15 wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4937276.

10 In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene, wherein the at least
15 one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary SNP rs17355663.

20 In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid
25 primer at least 8 nucleotides in length that is complementary to SNP rs235807.

30 In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 91171013 of an intergenic region of chromosome 1, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs11579814.

35 In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-

nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs2275187.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 186426136 mapping to chromosome 1 in the Phosducin gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4336803.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18(CDK18) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4951158.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs925613.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide, the kit comprising: at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of

chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs or one or more synthetic or non-natural nucleotides, and wherein the at least one nucleic acid primer detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide, the kit comprising: at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, and wherein the at least one nucleic acid primer detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide; and a detectable label selected from the group consisting of an enzyme label, a fluorescent label, and a colorimetric label.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide, the kit comprising: at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, and wherein the at least one nucleic acid primer detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide; and a solid substrate to which the at least one first nucleic acid primer is bound.

In certain embodiments, the present disclosure provides a method for detecting that a subject is predisposed to or has coronary heart disease comprising: (a) providing a biological sample from the subject; (b) contacting DNA from the biological sample with bisulfite under alkaline conditions; (c) contacting the bisulfite-treated DNA with at least one first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) , wherein the at least one first oligonucleotide probe detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, (d) determining genotype at single nucleotide polymorphism rs347027; and (e) detecting either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, wherein methylation of the CpG dinucleotide at position 92203667 of chromosome 1 is associated with coronary heart disease when genotype of rs347027 is determined.

In certain embodiments, the present disclosure provides a method for measuring the presence of a biomarker in a biological sample from a patient, the improvement comprising

(a) contacting DNA from the biological sample with bisulfite under alkaline conditions; and
(b) contacting the bisulfite-treated DNA with at least one first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3 gene, wherein the at least one first oligonucleotide probe detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, for use in predicting that the patient has coronary heart disease or has an increased likelihood of developing coronary heart disease.

In certain embodiments, the present disclosure provides a method of predicting the presence of biomarkers associated with Cardiovascular Disease (CVD) in a biological sample from a patient, comprising (a) providing a first aliquot from the biological sample and contacting DNA from the first biological sample with bisulfite under alkaline conditions, and (b) providing a second aliquot from the biological sample; (c) contacting (i) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs347027, (ii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 38364951 in an intergenic region of chromosome 15, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4937276, (iii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs17355663, (iv) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs235807, (v) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 91171013 of an intergenic region of chromosome 1, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs11579814, (vi) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a

sequence that comprises a CpG dinucleotide at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs2275187, (vii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 186426136 mapping to chromosome 1 in the Phosducin gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4336803, (viii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18(CDK18) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4951158, and/or (ix) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to rs925613, wherein methylation of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR3 gene, cg20636912, cg16947947, cg05916059, cg04567738, cg16603713, cg05709437, cg12081870, and /or cg18070470, and a G at position 91618766 of chromosome 1, or polymorphisms in rs4937276, rs17355663, rs235807, rs11579814, rs2275187, rs4336803, rs4951158, and/or rs925613 is associated with CVD.

In certain embodiments, the biological sample is a saliva sample.

In certain embodiments, the present disclosure provides a method for detecting one or more copies of a G allele at rs347027 and methylation status at cg13078798 on a nucleic acid sample from a subject at risk for Cardiovascular Disease (CVD), comprising a) performing a genotyping assay on a nucleic acid sample of said human subject to detect the presence of one or more copies of a G allele of the rs347027 polymorphism, and b) performing a methylation assessment at cg13078798 on a nucleic acid sample of said human to detect methylation status to determine if cg13078798 is unmethylated.

In certain embodiments, the present disclosure provides a method of predicting the presence of biomarkers associated with Cardiovascular Disease (CVD) in a biological sample from a patient, comprising detecting one or more pairs of SNPs and CpGs in Table 3 (e.g., SNP rs347027 in conjunction with CpG cg13078798; SNP rs4937276 in conjunction with CpG cg20636912; SNP rs17355663 in conjunction with CpG cg16947947; SNP rs235807 in conjunction with CpG cg05916059; SNP rs11579814 in conjunction with CpG cg04567738;

SNP rs2275187 in conjunction with CpG cg16603713; SNP rs4336803 in conjunction with CpG cg05709437; SNP rs4951158 in conjunction with CpG cg12081870; and/or SNP rs925613 in conjunction with CpG cg18070470).

In certain embodiments, the CVD is Coronary Heart Disease (CHD), Congestive Heart Failure (CHF) and/or Stroke.

In certain embodiments the present disclosure provides a method of determining the presence of a biomarker associated with CHD in a patient sample, the method comprising: (a) isolating nucleic acid sample from the patient sample, (b) performing a genotyping assay on a first aliquot of the nucleic acid sample to detect the presence of at least one SNP, wherein the SNP is selected from a first SNP in **Figure 21** and/or is a second SNP in linkage disequilibrium (e.g., $R > 0.3$) with a first SNP from **Figure 21** to obtain genotype data; and/or (c) bisulfite converting the nucleic acid in a second aliquot of the nucleic acid and performing methylation assessment on a second aliquot of the nucleic acid sample to detect methylation status of at least one gene from **Figure 15** or a first CpG site from **Figure 16** and/or a second CpG site collinear (e.g., $R > 0.3$) with a first CpG from **Figure 16** to obtain methylation data regarding whether a specific CpG residue is unmethylated; and (d) inputting genotype from step (b) and/or methylation data from step (c) into an algorithm that accounts for the contribution of at least one SNP main effect and/or at least one CpG main effect and/or at least one interaction effect (e.g., SNPxSNP, CpGxCpG, SNPxCpG). In some embodiments, the algorithm is Random Forest™ or another algorithm capable of accounting for linear and non-linear effects.

In certain embodiments the present disclosure provides a method of determining the presence of a biomarker associated with stroke in a patient sample, the method comprising: (a) isolating nucleic acid sample from the patient sample, (b) performing a genotyping assay on a first aliquot of the nucleic acid sample to detect the presence of at least one SNP, wherein the SNP is selected from a first SNP in **Figure 22** and/or a second SNP in linkage disequilibrium (e.g., $R > 0.3$) with a first SNP from **Figure 22** to obtain genotype data; and/or (c) bisulfite converting the nucleic acid in a second aliquot of the nucleic acid and performing methylation assessment on a second aliquot of the nucleic acid sample to detect methylation status of at least one gene from **Figure 17** or a first CpG site from **Figure 18** and/or a second CpG site collinear (e.g., $R > 0.3$) with a first CpG from **Figure 18** to obtain methylation data regarding whether a specific CpG residue is unmethylated; and (d) inputting genotype from step (b) and/or methylation data from step (c) into an algorithm that accounts for the contribution of at least one SNP main effect and/or at least one CpG main effect and/or at least one interaction effect (e.g., SNPxSNP, CpGxCpG, SNPxCpG). In some embodiments,

the algorithm is Random Forest™ or another algorithm capable of accounting for linear and non-linear effects.

In certain embodiments the present disclosure provides a method of determining the presence of a biomarker associated with CHF in a patient sample, the method comprising: (a) isolating nucleic acid sample from the patient sample, (b) performing a genotyping assay on a first aliquot of the nucleic acid sample to detect the presence of at least one SNP, wherein the SNP is selected from a first SNP in **Figure 23** and/or a second SNP in linkage disequilibrium (e.g., $R > 0.3$) with a first SNP from **Figure 23** to obtain genotype data; and/or (c) bisulfite converting the nucleic acid in a second aliquot of the nucleic acid and performing methylation assessment on a second aliquot of the nucleic acid sample to detect methylation status of at least one gene from **Figure 19** or a first CpG site from **Figure 20** and/or a second CpG site collinear (e.g., $R > 0.3$) with a first CpG from **Figure 20** to obtain methylation data regarding whether a specific CpG residue is unmethylated; and (d) inputting genotype from step (b) and/or methylation data from step (c) into an algorithm that accounts for the contribution of at least one SNP main effect and/or at least one CpG main effect and/or at least one interaction effect (e.g., SNPxSNP, CpGxCpG, SNPxCpG). In some embodiments, the algorithm is Random Forest™ or another algorithm capable of accounting for linear and non-linear effects.

In certain embodiments, the result comprises a gene-environment interaction effect (SNPxCpG) between the second CpG site collinear (e.g., $R > 0.3$) with the first CpG from **Figure 16** and the first SNP from **Figure 21** or the second SNP in linkage disequilibrium (e.g., $R > 0.3$) with a first SNP from **Figure 21**. In certain embodiments, the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites from **Figure 16** and/or at least two genes from **Figure 15**. In certain embodiments, the result comprises a at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites collinear with the first CpG site from **Figure 16**. In certain embodiments, the result comprises a gene-environment interaction effect (SNPxCpG) between a CpG site collinear (e.g., $R > 0.3$) with the first CpG from **Figure 18** and the first SNP from **Figure 22** or the second SNP in linkage disequilibrium (e.g., $R > 0.3$) with the first SNP from **Figure 22**. In certain embodiments, the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites from **Figure 18** and/or genes from **Figure 17**. In certain embodiments, the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites collinear with the first CpG site from **Figure 18**. In certain embodiments, the result comprises a gene-environment interaction effect (SNPxCpG) between the second CpG site

collinear (e.g., $R > 0.3$) with the first CpG from **Figure 20** and the first SNP from **Figure 23** or the second SNP in linkage disequilibrium (e.g., $R > 0.3$) from the first SNP from **Figure 23**.

In certain embodiments, the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites from **Figure 20** and/or genes from **Figure 19**. In certain embodiments, the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites collinear with the first CpG site from **Figure 20**.

In certain embodiments of the present disclosure, the blood cell is a lymphocyte, such as a monocyte, a basophil, an eosinophil, and/or a neutrophil. In certain embodiments the lymphocyte type is a B-lymphocyte. In certain embodiments, the B-lymphocytes have been immortalized. In certain embodiments, the blood cell type is a mixture of peripheral white blood cells. In certain embodiments, the peripheral blood cell has been transformed into a cell line.

In certain embodiments, the analytical process comprises comparing the obtained profile with a reference profile. In certain embodiments, the reference profile comprises data obtained from one or more healthy control subjects, or comprises data obtained from one or more subjects diagnosed with a substance use disorder. In certain embodiments, the method further comprises obtaining a statistical measure of a similarity of the obtained profile to the reference profile. In certain embodiments, the blood cell or blood cell derivative is a peripheral blood cell. In certain embodiments, the profile is obtained by sequencing of methylated DNA, such as by digital sequencing.

In certain embodiments, the current disclosure can also take the form of a PCR (polymerize chain reaction) assay. In some cases, this will take the form of real time PCR assays (RTPCR) or digital PCR assays. In certain embodiments of these PCR assays, a kit may contain two primers that specifically amplify a region of a target gene and a gene-specific probe that selectively recognizes the amplified region. Together, the primers and the gene specific probes are referred to as a primer-probe set. By measuring the amount of gene specific probe that has hybridized to an amplified segment at a given point of the PCR reaction or throughout the PCR reaction, one who is skilled in the art can infer the amount of nucleic acid originally present at the start of the reaction. In some cases, the amount of probe hybridized is measured through fluorescence spectrophotometry. The number of primer-probe sets can be any integer between 1 and 10,000 probes, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, . . . 9997, 9998, 9999, 10,000. In one kit, all of the probes may be physically located in a single reaction well or in multiple reaction wells. The probes may be in dry or in liquid form. They may be used in a single reaction or in a series of reactions. In certain embodiments, the

probe is an oligonucleotide probe. In certain embodiments, the probe is a nucleic acid derivative probe.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the methods and compositions of matter belong. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the methods and compositions of matter, suitable methods and materials are described below. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

BRIEF DESCRIPTION OF DRAWINGS

Figures 1A-1D. Area under the receiver operating characteristic curve for cg05575921 (A), age+gender+batch+cg05575921 (B), self-reported smoking status (C) and age+gender+batch+ self-reported smoking status (D).

Figure 2. Area under the receiver operating characteristic curve for the CHD prediction model (non-optimized).

Figure 3. Protein Protein Interactome of CHD. Network of top 1000 genes with at least one DNA methylation probe significantly associated with symptomatic CHD.

Figure 4. Venn diagram of DNA methylation probes significantly associated with symptomatic CHD and its conventional modifiable risk factors.

Figure 5. Venn diagram of genes with at least one DNA methylation probe significantly associated with symptomatic CHD and its conventional modifiable risk factors.

Figure 6. ROC curve of the integrated genetic-epigenetic model with the highest average 10-fold cross-validation AUC value.

Figure 7. ROC curve of the conventional risk factor model with the highest average 10-fold cross-validation AUC value.

Figure 8. Partial dependence plots of DNA methylation sites and SNPs.

Figure 9. Two-dimensional histogram of sensitivity and specificity of 10,000 permutations of DNA methylation sites and SNPs.

Figure 10. ROC curve of main effects CHF classification model.

Figure 11. ROC curve of interaction effects CHF classification model.

Figure 12. ROC curve of main effects stroke classification model.

Figure 13. ROC curve of interaction effects stroke classification model.

Figure 14. Flow chart of certain embodiment of method of the invention.

Figure 15. List of genes whose methylation is associated with CHD.

Figure 16. List of CpGs whose methylation is associated with CHD.

Figure 17. List of genes whose methylation is associated with stroke.

Figure 18. List of CpGs whose methylation is associated with stroke.

Figure 19. List of genes whose methylation is associated with CHF.

Figure 20. List of CpGs whose methylation is associated with CHF.

Figure 21. List of SNPs associated with CHD.

Figure 22. List of SNPs associated with stroke.

Figure 23. List of SNPs associated with CHF.

DETAILED DESCRIPTION OF THE INVENTION

The present disclosure provides methods and kits for determining whether a subject has a predisposition to, or likelihood of having or developing cardiovascular disease (CVD).

As shown herein, the methylation status of one or more CpG dinucleotides, alone, or in combination with the genotype and/or the interaction between the genotype and the methylation status (e.g., CH3xSNP), is associated with CVD. As used herein, the term “predisposition” is defined as a tendency or susceptibility for a subject to manifest a condition. For example, a subject is more likely to manifest a condition than is a control subject.

DNA Methylation

DNA does not exist as naked molecules in the cell. For example, DNA is associated with proteins called histones to form a complex substance known as chromatin. Chemical modifications of the DNA or the histones alter the structure of the chromatin without changing the nucleotide sequence of the DNA. Such modifications are described as “epigenetic” modifications of the DNA. Changes to the structure of the chromatin can have a profound influence on gene expression. If the chromatin is condensed, factors involved in gene expression may not have access to the DNA, and the genes will be switched off.

Conversely, if the chromatin is “open,” the genes can be switched on. Some important forms of epigenetic modification are DNA methylation and histone deacetylation. DNA methylation is a chemical modification of the DNA molecule itself and is carried out by an enzyme called DNA methyltransferase. Methylation can directly switch off gene expression by preventing transcription factors binding to promoters. A more general effect is the attraction of methyl-binding domain (MBD) proteins. These are associated with further

enzymes called histone deacetylases (HDACs), which function to chemically modify histones and change chromatin structure. Chromatin-containing acetylated histones are open and accessible to transcription factors, and the genes are potentially active. Histone deacetylation causes the condensation of chromatin, making it inaccessible to transcription factors and causing the silencing of genes.

CpG islands are short stretches of DNA in which the frequency of the CpG sequence is higher than other regions. The "p" in the term CpG indicates that cysteine ("C") and guanine ("G") are connected by a phosphodiester bond. CpG islands are often located around promoters of housekeeping genes and many regulated genes. At these locations, the CG sequence is not methylated. By contrast, the CG sequences in inactive genes are usually methylated to suppress their expression.

As used herein, the term "methylation status" means the determination whether a certain target DNA, such as a CpG dinucleotide, is methylated. As used herein the term "CpG dinucleotide repeat motif" means a series of two or more CpG dinucleotides positioned in a DNA sequence.

About 56% of human genes and 47% of mouse genes are associated with CpG islands. Often, CpG islands overlap the promoter and extend about 1000 base pairs downstream into the transcription unit. Identification of potential CpG islands during sequence analysis helps to define the extreme 5' ends of genes, something that is notoriously difficult with cDNA-based approaches. The methylation of a CpG island can be determined by a skilled artisan using any method suitable to determine such methylation. For example, the skilled artisan can use a bisulfite reaction-based method for determining such methylation.

The present disclosure provides methods to determine the nucleic acid methylation of *TGFBR3* of a patient in order to predict the clinical course and eventual outcome of patients suspected of being predisposed or of having a CHD.

In particular, in certain embodiments of the disclosure, the methods may be practiced as follows. A sample, such as a blood sample, is taken from a patient. In certain embodiments, a single cell type, *e.g.*, lymphocytes, basophils, or monocytes isolated from the blood, may be isolated for further testing. The DNA is harvested from the sample and examined to determine if the *TGFBR3* region is methylated. For example, the DNA of interest can be treated with bisulfite to deaminate unmethylated cytosine residues to uracil. Since uracil base pairs with adenosine, thymidines are incorporated into subsequent DNA strands in the place of unmethylated cytosine residues during subsequent PCR amplifications. Next, the target sequence is amplified by PCR, and probed with a *TGFBR3*-

specific probe. Only DNA from the patient that was methylated will bind to the probe. A specific profile associates with a specific condition.

Methods of determining the patient nucleic acid profile are well known to the art worker and include any of the well-known detection methods. Various PCR methods are described, for example, in *PCR Primer: A Laboratory Manual*, Dieffenbach & Dveksler, Eds., Cold Spring Harbor Laboratory Press, 1995. Other analysis methods include, but are not limited to, nucleic acid quantification, restriction enzyme digestion, DNA sequencing, hybridization technologies, such as Southern Blotting, *etc.*, amplification methods such as Ligase Chain Reaction (LCR), Nucleic Acid Sequence Based Amplification (NASBA), Self-sustained Sequence Replication (SSR or 3SR), Strand Displacement Amplification (SDA), and Transcription Mediated Amplification (TMA), Quantitative PCR (qPCR), or other DNA analyses, as well as RT-PCR, in vitro translation, Northern blotting, and other RNA analyses. In another embodiment, hybridization on a microarray is used.

Single Nucleotide Polymorphism (SNP) Genotyping

Traditional methods for the screening of heritable diseases have depended on either the identification of abnormal gene products (e.g., sickle cell anemia) or an abnormal phenotype (e.g., mental retardation). With the development of simple and inexpensive genetic screening methodology, it is now possible to identify polymorphisms that indicate a propensity to develop disease, even when the disease is of polygenic origin.

Single nucleotide polymorphism (SNP) genotyping measures genetic variations of SNPs between members of a species. A SNP is a single base pair mutation at a specific locus, usually consisting of two alleles (where the rare allele frequency is >1%), and is very common. Because SNPs are conserved during evolution, they have been proposed as markers for use in quantitative trait loci (QTL) analysis and in association studies in place of microsatellites. Many different SNP genotyping methods are known, including hybridization-based methods (such as Dynamic allele-specific hybridization, molecular beacons, and SNP microarrays) enzyme-based methods (including restriction fragment length polymorphism, PCR-based methods, flap endonuclease, primer extension, 5' - nuclease, and oligonucleotide ligation assay), other post-amplification methods based on physical properties of DNA (such as single strand conformation polymorphism, temperature gradient gel electrophoresis, denaturing high performance liquid chromatography, high-resolution melting of the entire amplicon, use of DNA mismatch-binding proteins, SNPLEX and surveyor nuclease assay), and sequencing (such as "next generation" sequencing). See, e.g., US Patent No. 7,972,779.

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A plurality of alleles having distinct organ-functionality (e.g., high and low levels of expression in the heart, or, e.g., high, moderate and low levels of expression in the heart) can arise from one or more polymorphisms in a region of a gene that encodes a polypeptide or can be in a regulatory control sequence that affects expression of the polypeptide, such as a promoter or polyadenylation sequence. Alternatively, relevant alleles can arise from one or more polymorphism at a locus distal to a gene having a direct effect in the identified behavior, wherein the product of that distal locus has an indirect effect on the behavior. A relevant allele can affect a polypeptide at a transcriptional or a translational level and can affect a polypeptide's transcription rate, translation rate, degradation rate, or activity.

Differences between alleles at a brain-functional gene can be characterized in a sample from a subject or from a plurality of subjects by methods for assaying any of the foregoing that are well-known to the skilled artisan. Such methods can include, but are not limited to measuring an amount of an encoded polypeptide and measuring the potential for a polynucleotide sequence to be expressed. Assay methods can detect proteins or nucleic acids directly or indirectly. One can evaluate the suitability of an upstream promoter region for directing transcription of a coding region of the polynucleotide that encodes a polypeptide or can evaluate the suitability of the coding region for encoding a functional polypeptide. The assay methods are specifically contemplated to include screening for the presence of particular sequences or structures of nucleic acids or polypeptides using, e.g., any of various known microarray technologies.

It will be fully appreciated by the skilled artisan that the allele need not have previously been shown to have had any link or association with the disorder phenotype. Instead, an allele and a pathogenic environmental risk factor can interact to predict a predisposition to a disorder phenotype even when neither the allele nor the risk factor bears any direct relation to the disorder phenotype.

Genetic screening (also called genotyping or molecular screening), can be broadly defined as testing to determine if a patient has mutations (or alleles or polymorphisms) that either cause a disease state or are "linked" to the mutation causing a disease state. Linkage refers to the phenomenon that DNA sequences which are close together in the genome have a tendency to be inherited together. Two sequences may be linked because of some selective advantage of co-inheritance. More typically, however, two polymorphic sequences are co-inherited because of the relative infrequency with which meiotic recombination events occur within the region between the two polymorphisms. The co-inherited polymorphic alleles are said to be in "linkage disequilibrium" with one another because, in a given population, they tend to either both occur together or else not occur at all in any particular member of the

population. Indeed, where multiple polymorphisms in a given chromosomal region are found to be in linkage disequilibrium with one another, they define a quasi-stable genetic “haplotype.” In contrast, recombination events occurring between two polymorphic loci cause them to become separated onto distinct homologous chromosomes. If meiotic recombination between two physically linked polymorphisms occurs frequently enough, the two polymorphisms will appear to segregate independently and are said to be in linkage equilibrium.

It would be understood that linkage equilibrium / disequilibrium can be quantitated (using, for example, the Pearson correlation (R) or co-inheritance of alleles (D')). For example, a low level of linkage can be reflected in a correlation (e.g., R value) of about 0.1 or less, a moderate level of linkage is reflected in a R value of about 0.3, while a high level of linkage is reflected in a R value of 0.5 or greater. It also would be understood that, when referring to methylation (i.e. CpGs), collinearity (with an R value) is used as a determination of the linear strength of the association between two CpGs (e.g., a low level of collinearity can be reflected by an R value of about 0.1 or less; a moderate level of collinearity can be reflected by an R value of about 0.3; and a high level of collinearity can be reflected by an R value of about 0.5 or greater).

While the frequency of meiotic recombination between two markers is generally proportional to the physical distance between them on the chromosome, the occurrence of “hot spots” as well as regions of repressed chromosomal recombination can result in discrepancies between the physical and recombinational distance between two markers. Thus, in certain chromosomal regions, multiple polymorphic loci spanning a broad chromosomal domain may be in linkage disequilibrium with one another, and thereby define a broad-spanning genetic haplotype. Furthermore, where a disease-causing mutation is found within or in linkage with this haplotype, one or more polymorphic alleles of the haplotype can be used as a diagnostic or prognostic indicator of the likelihood of developing the disease. This association between otherwise benign polymorphisms and a disease-causing polymorphism occurs if the disease mutation arose in the recent past, so that sufficient time has not elapsed for equilibrium to be achieved through recombination events. Therefore, identification of a haplotype that spans or is linked to a disease-causing mutational change serves as a predictive measure of an individual's likelihood of having inherited that disease-causing mutation. Such prognostic or diagnostic procedures can be utilized without necessitating the identification and isolation of the actual disease-causing lesion. This is significant because the precise determination of the molecular defect involved in a disease process can be difficult and laborious, especially in the case of multifactorial diseases.

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5 The statistical correlation between a disorder and a polymorphism does not necessarily indicate that the polymorphism directly causes the disorder. Rather the correlated polymorphism may be a benign allelic variant which is linked to (*i.e.*, in linkage disequilibrium with) a disorder-causing mutation that has occurred in the recent evolutionary past, so that sufficient time has not elapsed for equilibrium to be achieved through recombination events in the intervening chromosomal segment. Thus, for the purposes of diagnostic and prognostic assays for a particular disease, detection of a polymorphic allele associated with that disease can be utilized without consideration of whether the polymorphism is directly involved in the etiology of the disease. Furthermore, where a given benign polymorphic locus is in linkage disequilibrium with an apparent disease-causing polymorphic locus, still other polymorphic loci which are in linkage disequilibrium with the benign polymorphic locus are also likely to be in linkage disequilibrium with the disease-causing polymorphic locus. Thus these other polymorphic loci will also be prognostic or diagnostic of the likelihood of having inherited the disease-causing polymorphic locus. A broad-spanning haplotype (describing the typical pattern of co-inheritance of alleles of a set of linked polymorphic markers) can be targeted for diagnostic purposes once an association has been drawn between a particular disease or condition and a corresponding haplotype. Thus, the determination of an individual's likelihood for developing a particular disease or condition can be made by characterizing one or more disease-associated polymorphic alleles (or even one or more disease-associated haplotypes) without necessarily determining or characterizing the causative genetic variation.

Many methods are available for detecting specific alleles at polymorphic loci. Certain methods for detecting a specific polymorphic allele will depend, in part, upon the molecular nature of the polymorphism. For example, the various allelic forms of the polymorphic locus may differ by a single base-pair of the DNA. Such single nucleotide polymorphisms (or SNPs) are major contributors to genetic variation, comprising some 80% of all known polymorphisms, and their density in the genome is estimated to be on average 1 per 1,000 base pairs. SNPs are most frequently bi-allelic, or occurring in only two different forms (although up to four different forms of an SNP, corresponding to the four different nucleotide bases occurring in DNA, are theoretically possible). Nevertheless, SNPs are mutationally more stable than other polymorphisms, making them suitable for association studies in which linkage disequilibrium between markers and an unknown variant is used to map disease-causing mutations. In addition, because SNPs typically have only two alleles, they can be genotyped by a simple plus / minus assay rather than a length measurement, making them more amenable to automation.

In one embodiment, allelic profiling can be accomplished using a nucleic acid microarray, which can also be commercialized alone or in combination with one or more kit components. The genetic testing field is rapidly evolving and, as such, the skilled artisan will appreciate that a wide range of profiling tests exist, and will be developed, to determine the allelic profile of individuals in accord with the disclosure.

Nucleic Acids and Polypeptides

The term “nucleic acid” refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, made of monomers (nucleotides) containing a sugar, phosphate and a base that is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues. The terms “nucleic acid,” “nucleic acid molecule,” or “polynucleotide” are used interchangeably and may also be used interchangeably with gene, cDNA, DNA and/or RNA encoded by a gene.

The term “nucleotide sequence” refers to a polymer of DNA or RNA which can be single-stranded or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. A DNA molecule or polynucleotide is a polymer of deoxyribonucleotides (A, G, C, and T), and an RNA molecule or polynucleotide is a polymer of ribonucleotides (A, G, C and U).

A “gene,” for the purposes of the present disclosure, includes a DNA region encoding a gene product, as well as all DNA regions which regulate the production of the gene product, whether or not such regulatory sequences are adjacent to coding and/or transcribed sequences. The term “gene” is used broadly to refer to any segment of nucleic acid associated with a biological function. Genes include coding sequences and/or the regulatory sequences required for their expression. Accordingly, a gene includes, but is not necessarily limited to, promoter sequences, terminators, translational regulatory sequences such as ribosome binding sites and internal ribosome entry sites, enhancers, silencers, insulators, boundary elements, replication origins, matrix attachment sites and locus control regions. For example, “gene” refers to a nucleic acid fragment that expresses mRNA, functional RNA,

or specific protein, including regulatory sequences. "Functional RNA" refers to sense RNA, antisense RNA, ribozyme RNA, siRNA, or other RNA that may not be translated but yet has an effect on at least one cellular process. "Genes" also include non-expressed DNA segments that, for example, form recognition sequences for other proteins. "Genes" can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Gene expression" refers to the conversion of the information, contained in a gene, into a gene product. It refers to the transcription and/or translation of an endogenous gene, heterologous gene or nucleic acid segment, or a transgene in cells. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein. The term "altered level of expression" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

A gene product can be the direct transcriptional product of a gene (*e.g.*, mRNA, tRNA, rRNA, antisense RNA, ribozyme, structural RNA or any other type of RNA) or a protein produced by translation of an mRNA. Gene products also include RNAs which are modified, by processes such as capping, polyadenylation, methylation, and editing, and proteins modified by, for example, methylation, acetylation, phosphorylation, ubiquitination, ADP-ribosylation, myristilation, and glycosylation. The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from post-transcriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA. "Functional RNA" refers to sense RNA, antisense RNA, ribozyme RNA, siRNA, or other RNA that may not be translated but yet has an effect on at least one cellular process.

A "coding sequence," or a sequence that "encodes" a selected polypeptide, is a nucleic acid molecule that is transcribed (in the case of DNA) and translated (in the case of mRNA) into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to, cDNA from viral, prokaryotic or eukaryotic

mRNA, genomic DNA sequences from viral (*e.g.*, DNA viruses and retroviruses) or prokaryotic DNA, and especially synthetic DNA sequences. A transcription termination sequence may be located 3' to the coding sequence.

Certain embodiments of the disclosure encompass isolated or substantially purified nucleic acid compositions. In the context of the present disclosure, an "isolated" or "purified" DNA molecule or RNA molecule is a DNA molecule or RNA molecule that exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or RNA molecule may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived.

By "fragment" is intended a polypeptide consisting of only a part of the intact full-length polypeptide sequence and structure. The fragment can include a C-terminal deletion an N-terminal deletion, and/or an internal deletion of the native polypeptide. A fragment of a protein will generally include at least about 5-10 contiguous amino acid residues of the full-length molecule, preferably at least about 15-25 contiguous amino acid residues of the full-length molecule, and most preferably at least about 20-50 or more contiguous amino acid residues of the full-length molecule, or any integer between 5 amino acids and the full-length sequence.

Certain embodiments of the disclosure encompass isolated or substantially purified nucleic acid compositions. In the context of the present disclosure, an "isolated" or "purified" DNA molecule or RNA molecule is a DNA molecule or RNA molecule that exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or RNA molecule may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule is substantially free of other cellular material or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived.

“Naturally occurring” is used to describe a composition that can be found in nature as distinct from being artificially produced. For example, a nucleotide sequence present in an organism, which can be isolated from a source in nature and which has not been intentionally modified by a person in the laboratory, is naturally occurring.

“Regulatory sequences” and “suitable regulatory sequences” each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences that may be a combination of synthetic and natural sequences.

A “5' non-coding sequence” refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency. A “3' non-coding sequence” refers to nucleotide sequences located 3' (downstream) to a coding sequence and may include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The term “translation leader sequence” refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

A “promoter” refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which directs and/or controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription.

“Promoter” includes a minimal promoter that is a short DNA sequence comprised of a TATA-box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. “Promoter” also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an “enhancer” is a DNA sequence that can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is

capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors that control the effectiveness of transcription initiation in response to physiological or developmental conditions. “Constitutive expression” refers to expression using a constitutive promoter. “Conditional” and “regulated expression” refer to expression controlled by a regulated promoter.

“Operably-linked” refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one of the sequences is affected by another. For example, a regulatory DNA sequence is said to be “operably linked to” or “associated with” a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (*i.e.*, that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

“Expression” refers to the transcription and/or translation of an endogenous gene, heterologous gene or nucleic acid segment, or a transgene in cells. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein. The term “altered level of expression” refers to the level of expression in cells or organisms that differs from that of normal cells or organisms.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) “reference sequence,” (b) “comparison window,” (c) “sequence identity,” (d) “percentage of sequence identity,” and (e) “substantial identity.” As used herein, “reference sequence” is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence;

for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence. As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well-known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller (Myers and Miller, CABIOS, 4, 11 (1988)); the local homology algorithm of Smith *et al.* (Smith *et al.*, Adv. Appl. Math., 2, 482 (1981)); the homology alignment algorithm of Needleman and Wunsch (Needleman and Wunsch, JMB, 48, 443 (1970)); the search-for-similarity-method of Pearson and Lipman (Pearson and Lipman, Proc. Natl. Acad. Sci. USA, 85, 2444 (1988)); the algorithm of Karlin and Altschul (Karlin and Altschul, Proc. Natl. Acad. Sci. USA, 87, 2264 (1990)), modified as in Karlin and Altschul (Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90, 5873 (1993)).

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, Calif.); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wis., USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (Higgins *et al.*, CABIOS, 5, 151 (1989)); Corpet *et al.* (Corpet *et al.*, Nucl. Acids Res., 16, 10881 (1988)); Huang *et al.* (Huang *et al.*, CABIOS, 8, 155 (1992)); and Pearson *et al.* (Pearson *et al.*, Meth. Mol. Biol., 24, 307 (1994)). The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul *et al.* (Altschul *et al.*, JMB, 215, 403 (1990)) are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring

sequence pairs (HSPs) by identifying short words of length “W” in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. “T” is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters “M” (reward score for a pair of matching residues; always >0) and “N” (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity “X” from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, less than about 0.01, or even less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (*e.g.*, BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix. Alignment may also be performed manually by inspection.

For purposes of the present disclosure, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein may be made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By “equivalent program” is intended any sequence comparison program

that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the program.

As used herein, “sequence identity” or “identity” in the context of two nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (*e.g.*, charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have “sequence similarity” or “similarity.” Means for making this adjustment are well known to those of skill in the art. Typically, this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, *e.g.*, as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif.).

As used herein, “percentage of sequence identity” means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

The term “substantial identity” of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, or 94%, or even at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to

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5 a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, 80%, 90%, or even at least 95%.

10 The term “substantial identity” in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, or 94%, or even 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. In certain embodiments, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (Needleman and Wunsch, JMB, 48, 443 (1970)). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the
15 second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. Thus, the disclosure also provides nucleic acid molecules and peptides that are substantially identical to the nucleic acid molecules and peptides presented herein.

20 Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Hybridization of nucleic acids is discussed in more detail below.

Oligonucleotide Probes

As used herein, “primer,” “probe,” and “oligonucleotide” are used interchangeably.
25 The term “nucleic acid probe” or a “probe specific for” a nucleic acid refers to a nucleic acid sequence that has at least about 80%, *e.g.*, at least about 90%, *e.g.*, at least about 95% contiguous sequence identity or homology to the nucleic acid sequence encoding the targeted sequence of interest. A probe (or oligonucleotide or primer) of the disclosure is at least about 8 nucleotides in length (*e.g.*, at least about 8-50 nucleotides in length, *e.g.*, at least about 10-
30 40, *e.g.*, at least about 15-35 nucleotides in length). The oligonucleotide probes or primers of the disclosure may comprise at least about eight nucleotides at the 3' of the oligonucleotide that have at least about 80%, *e.g.*, at least about 85%, *e.g.*, at least about 90% contiguous identity to the targeted sequence of interest.

Primer pairs are useful for determination of the nucleotide sequence of a particular SNP using PCR. The pairs of single-stranded DNA primers can be annealed to sequences within or surrounding the SNP in order to prime amplifying DNA synthesis of the SNP itself.

The first step of the process involves contacting a physiological sample obtained from a patient, which sample contains nucleic acid, with an oligonucleotide probe to form a hybridized DNA. The oligonucleotide probes that are useful in the methods of the present disclosure can be any probe comprised of between about 4 or 6 bases up to about 80 or 100 bases or more. In one embodiment of the present disclosure, the probes are between about 10 and about 20 bases.

The primers themselves can be synthesized using techniques that are well known in the art. Generally, the primers can be made using oligonucleotide synthesizing machines that are commercially available.

The primers or probes of the present disclosure can be labeled using techniques known to those of skill in the art. For example, the labels used in the assays of disclosure can be primary labels (where the label comprises an element that is detected directly) or secondary labels (where the detected label binds to a primary label, *e.g.*, as is common in immunological labeling). An introduction to labels (also called “tags”), tagging or labeling procedures, and detection of labels is found in Polak and Van Noorden (1997) Introduction to Immunocytochemistry, second edition, Springer Verlag, N.Y. and in Haugland (1996) Handbook of Fluorescent Probes and Research Chemicals, a combined handbook and catalogue Published by Molecular Probes, Inc., Eugene, Oreg. Primary and secondary labels can include undetected elements as well as detected elements. Useful primary and secondary labels in the present disclosure can include spectral labels such as fluorescent dyes (*e.g.*, fluorescein and derivatives such as fluorescein isothiocyanate (FITC) and Oregon Green™, rhodamine and derivatives (*e.g.*, Texas red, tetramethylrhodamine isothiocyanate (TRITC), etc.), digoxigenin, biotin, phycoerythrin, AMCA, CyDyes™, and the like), radiolabels (*e.g.*, ³H, ¹²⁵I, ³⁵S, ¹⁴C, ³²P, ³³P), enzymes (*e.g.*, horse-radish peroxidase, alkaline phosphatase) spectral colorimetric labels such as colloidal gold or colored glass or plastic (*e.g.*, polystyrene, polypropylene, latex) beads. The label may be coupled directly or indirectly to a component of the detection assay (*e.g.*, the labeled nucleic acid) according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

In general, a detector that monitors a probe-substrate nucleic acid hybridization is adapted to the particular label that is used. Typical detectors include spectrophotometers,

phototubes and photodiodes, microscopes, scintillation counters, cameras, film and the like, as well as combinations thereof. Examples of suitable detectors are widely available from a variety of commercial sources known to persons of skill. Commonly, an optical image of a substrate comprising bound labeled nucleic acids is digitized for subsequent computer analysis.

Preferred labels include those that use (1) chemiluminescence (using Horseradish Peroxidase and/or Alkaline Phosphatase with substrates that produce photons as breakdown products) with kits being available, *e.g.*, from Molecular Probes, Amersham, Boehringer-Mannheim, and Life Technologies/Gibco BRL; (2) color production (using both Horseradish Peroxidase and/or Alkaline Phosphatase with substrates that produce a colored precipitate) (kits available from Life Technologies/Gibco BRL, and Boehringer-Mannheim); (3) hemifluorescence using, *e.g.*, Alkaline Phosphatase and the substrate AttoPhos (Amersham) or other substrates that produce fluorescent products, (4) fluorescence (*e.g.*, using Cy-5 (Amersham), fluorescein, and other fluorescent labels); (5) radioactivity using kinase enzymes or other end-labeling approaches, nick translation, random priming, or PCR to incorporate radioactive molecules into the labeled nucleic acid. Other methods for labeling and detection will be readily apparent to one skilled in the art.

Fluorescent labels can be used and have the advantage of requiring fewer precautions in handling, and being amendable to high-throughput visualization techniques (optical analysis including digitization of the image for analysis in an integrated system comprising a computer). Preferred labels are typically characterized by one or more of the following: high sensitivity, high stability, low background, low environmental sensitivity and high specificity in labeling. Fluorescent moieties, which are incorporated into the labels of the disclosure, are generally are known, including Texas red, dixogenin, biotin, 1- and 2-aminonaphthalene, p,p'-diaminostilbenes, pyrenes, quaternary phenanthridine salts, 9-aminoacridines, p,p'-diaminobenzophenone imines, anthracenes, oxacarbocyanine, merocyanine, 3-aminoequilenin, perylene, bis-benzoxazole, bis-p-oxazolyl benzene, 1,2-benzophenazin, retinol, bis-3-aminopyridinium salts, hellebrigenin, tetracycline, sterophenol, benzimidazolylphenylamine, 2-oxo-3-chromen, indole, xanthen, 7-hydroxycoumarin, phenoxazine, calicylate, strophanthidin, porphyrins, triarylmethanes, flavin and many others. Many fluorescent labels are commercially available from the SIGMA Chemical Company (Saint Louis, MO), Molecular Probes, R&D systems (Minneapolis, MN), Pharmacia LKB Biotechnology (Piscataway, NJ), CLONTECH Laboratories, Inc. (Palo Alto, CA), Chem Genes Corp., Aldrich Chemical Company (Milwaukee, WI), Glen Research, Inc., GIBCO BRL Life Technologies, Inc. (Gaithersburg, MD), Fluka ChemicaBiochemika Analytika

(Fluka Chemie AG, Buchs, Switzerland), and Applied Biosystems™ (Foster City, CA), as well as many other commercial sources known to one of skill.

Means of detecting and quantifying labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is optically detectable, typical detectors include microscopes, cameras, phototubes and photodiodes and many other detection systems that are widely available.

Oligonucleotide probes may be prepared having any of a wide variety of base sequences according to techniques that are well known in the art. Suitable bases for preparing the oligonucleotide probe may be selected from naturally occurring nucleotide bases such as adenine, cytosine, guanine, uracil, and thymine; and non-naturally occurring or “synthetic” nucleotide bases such as 7-deaza-guanine 8-oxo-guanine, 6-mercaptoguanine, 4-acetylcytidine, 5-(carboxyhydroxyethyl)uridine, 2'-O-methylcytidine, 5-carboxymethylamino-methyl-2-thioridine, 5-carboxymethylaminomethyluridine, dihydrouridine, 2'-O-methylpseudouridine, β ,D-galactosylqueosine, 2'-O-methylguanosine, inosine, N6-isopentenyladenosine, 1-methyladenosine, 1-methylpseudouridine, 1-methylguanosine, 1-methylinosine, 2,2-dimethylguanosine, 2-methyladenosine, 2-methylguanosine, 3-methylcytidine, 5-methylcytidine, N6-methyladenosine, 7-methylguanosine, 5-methylaminomethyluridine, 5-methoxyaminomethyl-2-thiouridine, β ,D-mannosylqueosine, 5-methoxycarbonylmethyluridine, 5-methoxyuridine, 2-methylthio-N6-isopentenyladenosine, N-((9- β -D-ribofuranosyl-2-methylthiopurine-6-yl)carbamoyl)threonine, N-((9- β -D-ribofuranosylpurine-6-yl)N-methyl-carbamoyl)threonine, uridine-5-oxyacetic acid methylester, uridine-5-oxyacetic acid, wybutoxosine, pseudouridine, queosine, 2-thiocytidine, 5-methyl-2-thiouridine, 2-thiouridine, 2-thiouridine, 5-Methyluridine, N-((9-beta-D-ribofuranosylpurine-6-yl)carbamoyl)threonine, 2'-O-methyl-5-methyluridine, 2'-O-methyluridine, wybutosine, and 3-(3-amino-3-carboxypropyl)uridine. Any oligonucleotide backbone may be employed, including DNA, RNA (although RNA is less preferred than DNA), modified sugars such as carbocycles, and sugars containing 2' substitutions such as fluoro and methoxy. The oligonucleotides may be oligonucleotides wherein at least one, or all, of the internucleotide bridging phosphate residues are modified phosphates, such as methyl phosphonates, methyl phosphonotriates, phosphorinorphanolates, phosphoropiperazidates and phosphoramidates (for example, every other one of the internucleotide bridging phosphate residues may be modified as described).

The oligonucleotide may be a “peptide nucleic acid” such as described in Nielsen *et al.*, Science, 254:1497-1500 (1991).

As used herein, a “single base pair extension probe” is a nucleic acid that selectively recognizes a single nucleotide polymorphism (i.e., either the A or the G of an A/G polymorphism). Generally, these probes take the form of a DNA primer (e.g., as in PCR primers) that are modified so that incorporation of the primer releases a fluorophore. One example of this is a Taqman[®] probe that uses the 5' exonuclease activity of the enzyme Taq Polymerase for measuring the amount of target sequences in the samples. TaqMan[®] probes consist of a 18-22 bp oligonucleotide probe, which is labeled with a reporter fluorophore at the 5' end, and a quencher fluorophore at the 3' end. Incorporation of the probe molecule into a PCR chain (which occurs because the probe set is contained in a mixture of PCR primers) liberates the reporter fluorophore from the effects of the quencher. The primer must be able to recognize the target binding site. Some primer extension probes can be “activated” directly by DNA polymerase without a full PCR extension cycle.

The only requirement is that the oligonucleotide probe should possess a sequence at least a portion of which is capable of binding to a known portion of the sequence of the DNA sample. The nucleic acid probes provided by the present disclosure are useful for a number of purposes.

Methods of Detecting Nucleic Acids

A. Amplification

According to the methods of the present disclosure, the amplification of DNA present in a physiological sample may be carried out by any means known to the art. Examples of suitable amplification techniques include, but are not limited to, polymerase chain reaction (including, for RNA amplification, reverse-transcriptase polymerase chain reaction), ligase chain reaction, strand displacement amplification, transcription-based amplification, self-sustained sequence replication (or “3SR”), the Qbeta replicase system, nucleic acid sequence-based amplification (or “NASBA”), the repair chain reaction (or “RCR”), and boomerang DNA amplification (or “BDA”).

The bases incorporated into the amplification product may be natural or modified bases (modified before or after amplification), and the bases may be selected to optimize subsequent electrochemical detection steps.

Polymerase chain reaction (PCR) may be carried out in accordance with known techniques. See, *e.g.*, U.S. Patent Numbers 4,683,195; 4,683,202; 4,800,159; and 4,965,188.

In general, PCR involves, first, treating a nucleic acid sample (*e.g.*, in the presence of a heat

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stable DNA polymerase) with one oligonucleotide primer for each strand of the specific sequence to be detected under hybridizing conditions so that an extension product of each primer is synthesized that is complementary to each nucleic acid strand, with the primers sufficiently complementary to each strand of the specific sequence to hybridize therewith so that the extension product synthesized from each primer, when it is separated from its complement, can serve as a template for synthesis of the extension product of the other primer, and then treating the sample under denaturing conditions to separate the primer extension products from their templates if the sequence or sequences to be detected are present. These steps are cyclically repeated until the desired degree of amplification is obtained. Detection of the amplified sequence may be carried out by adding, to the reaction product, an oligonucleotide probe capable of hybridizing to the reaction product (*e.g.*, an oligonucleotide probe of the present disclosure), the probe carrying a detectable label, and then detecting the label in accordance with known techniques. Various labels that can be incorporated into or operably linked to nucleic acids are well known in the art, such as radioactive, enzymatic, and florescent labels. Where the nucleic acid to be amplified is RNA, amplification may be carried out by initial conversion to DNA by reverse transcriptase in accordance with known techniques.

Strand displacement amplification (SDA) may be carried out in accordance with known techniques. For example, SDA may be carried out with a single amplification primer or a pair of amplification primers, with exponential amplification being achieved with the latter. In general, SDA amplification primers comprise, in the 5' to 3' direction, a flanking sequence (the DNA sequence of which is noncritical), a restriction site for the restriction enzyme employed in the reaction, and an oligonucleotide sequence (*e.g.*, an oligonucleotide probe of the present disclosure) that hybridizes to the target sequence to be amplified and/or detected. The flanking sequence, which serves to facilitate binding of the restriction enzyme to the recognition site and provides a DNA polymerase priming site after the restriction site has been nicked, is about 15 to 20 nucleotides in length in one embodiment. The restriction site is functional in the SDA reaction. The oligonucleotide probe portion is about 13 to 15 nucleotides in length in one embodiment of the disclosure.

Ligase chain reaction (LCR) also can be carried out in accordance with known techniques. In general, the reaction is carried out with two pairs of oligonucleotide probes: one pair binds to one strand of the sequence to be detected; the other pair binds to the other strand of the sequence to be detected. Each pair together completely overlaps the strand to which it corresponds. The reaction is carried out by, first, denaturing (*e.g.*, separating) the strands of the sequence to be detected, then reacting the strands with the two pairs of

oligonucleotide probes in the presence of a heat stable ligase so that each pair of oligonucleotide probes is ligated together, then separating the reaction product, and then cyclically repeating the process until the sequence has been amplified to the desired degree. Detection may then be carried out in like manner as described above with respect to PCR.

According to the methods of the present disclosure, a particular SNP at this locus is detected. Techniques that are useful in the methods of the disclosure include, but are not limited to direct DNA sequencing, PFGE analysis, allele-specific oligonucleotide (ASO), dot blot analysis and denaturing gradient gel electrophoresis, and are well known to a skilled artisan.

There are several methods that can be used to detect DNA sequence variation. Direct DNA sequencing, either manual sequencing or automated fluorescent sequencing can detect sequence variation. Another approach is the single-stranded conformation polymorphism assay (SSCA). This method does not detect all sequence changes, especially if the DNA fragment size is greater than 200 bp, but can be optimized to detect most DNA sequence variation. The reduced detection sensitivity is a disadvantage, but the increased throughput possible with SSCA makes it an attractive, viable alternative to direct sequencing for mutation detection on a research basis. The fragments that have shifted mobility on SSCA gels are then sequenced to determine the exact nature of the DNA sequence variation. Other approaches based on the detection of mismatches between the two complementary DNA strands include clamped denaturing gel electrophoresis (CDGE), heteroduplex analysis (HA) and chemical mismatch cleavage (CMC). Once a mutation is known, an allele specific detection approach such as allele specific oligonucleotide (ASO) hybridization can be utilized to rapidly screen large numbers of other samples for that same mutation. Such a technique can utilize probes which are labeled with gold nanoparticles to yield a visual color result.

Detection of SNPs may be accomplished by sequencing the desired target region using techniques well known in the art. Alternatively, the gene sequences can be amplified directly from a genomic DNA preparation from patient tissue, using known techniques. The DNA sequence of the amplified sequences can then be determined.

There are six well known methods for a more complete, yet still indirect, test for confirming the presence of a mutant allele: 1) single stranded conformation analysis (SSCA); 2) denaturing gradient gel electrophoresis (DGGE); 3) RNase protection assays; 4) allele-specific oligonucleotides (ASOs); 5) the use of proteins which recognize nucleotide mismatches, such as the *E. coli* mutS protein; and 6) allele-specific PCR. For allele-specific PCR, primers are used which hybridize at their 3' ends to a particular *DNMI* mutation. If the particular mutation is not present, an amplification product is not observed. Amplification

Refractory Mutation System (ARMS) can also be used. Insertions and deletions of genes can also be detected by cloning, sequencing and amplification. In addition, restriction fragment length polymorphism (RFLP) probes for the gene or surrounding marker genes can be used to score alteration of an allele or an insertion in a polymorphic fragment. Other techniques for detecting insertions and deletions as known in the art can be used.

In the first three methods (SSCA, DGGE and RNase protection assay), a new electrophoretic band appears. SSCA detects a band that migrates differentially because the sequence change causes a difference in single-strand, intramolecular base pairing. RNase protection involves cleavage of the mutant polynucleotide into two or more smaller fragments. DGGE detects differences in migration rates of mutant sequences compared to wild-type sequences, using a denaturing gradient gel. In an allele-specific oligonucleotide assay, an oligonucleotide is designed which detects a specific sequence, and the assay is performed by detecting the presence or absence of a hybridization signal. In the mutS assay, the protein binds only to sequences that contain a nucleotide mismatch in a heteroduplex between mutant and wild-type sequences.

Mismatches, according to the present disclosure, are hybridized nucleic acid duplexes in which the two strands are not 100% complementary. Lack of total homology may be due to deletions, insertions, inversions or substitutions. Mismatch detection can be used to detect point mutations in the gene or in its mRNA product. While these techniques are less sensitive than sequencing, they are simpler to perform on a large number of samples. An example of a mismatch cleavage technique is the RNase protection method. The riboprobe and either mRNA or DNA isolated from the tumor tissue are annealed (hybridized) together and subsequently digested with the enzyme RNase A that is able to detect some mismatches in a duplex RNA structure. If a mismatch is detected by RNase A, it cleaves at the site of the mismatch. Thus, when the annealed RNA preparation is separated on an electrophoretic gel matrix, if a mismatch has been detected and cleaved by RNase A, an RNA product will be seen which is smaller than the full length duplex RNA for the riboprobe and the mRNA or DNA. The riboprobe need not be the full length of the DNM1 mRNA or gene but can be a segment of either. If the riboprobe comprises only a segment of the DNM1 mRNA or gene, it will be desirable to use a number of these probes to screen the whole mRNA sequence for mismatches.

In similar fashion, DNA probes can be used to detect mismatches, through enzymatic or chemical cleavage. Alternatively, mismatches can be detected by shifts in the electrophoretic mobility of mismatched duplexes relative to matched duplexes. With either

ribo probes or DNA probes, the cellular mRNA or DNA that might contain a mutation can be amplified using PCR before hybridization.

B. Hybridization

The phrase “hybridizing specifically to” refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

“Bind(s) substantially” refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

“Stringent conditions” are those that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate (SSC); 0.1% sodium lauryl sulfate (SDS) at 50 °C, or (2) employ a denaturing agent such as formamide during hybridization, *e.g.*, 50% formamide with 0.1% bovine serum albumin / 0.1% Ficoll / 0.1% polyvinylpyrrolidone / 50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C. Another example is use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS.

Other examples of stringent conditions are well known in the art.

“Stringent hybridization conditions” and “stringent hybridization wash conditions” in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. The thermal melting point (T_m) is the temperature (under defined ionic strength and pH) at which 50% of

the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984); $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, $\%GC$ is the percentage of guanosine and cytosine nucleotides in the DNA, $\% \text{ form}$ is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $>90\%$ identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the T_m for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the T_m ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the T_m ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the T_m . Using the equation, hybridization and wash compositions, and desired temperature, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a temperature of less than 45°C (aqueous solution) or 32°C (formamide solution), the SSC concentration is increased so that a higher temperature can be used. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the T_m for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2 x SSC wash at 65°C for 15 minutes. Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 1 x SSC at 45°C for 15 minutes. For short nucleotide sequences (*e.g.*, about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, less than about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long probes (*e.g.*, >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2 x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode

are substantially identical. This occurs, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids that have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, *e.g.*, hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1 x SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1 x to 2 x SSC (20 x SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5 x to 1 x SSC at 55 to 60°C.

“Northern analysis” or “Northern blotting” is a method used to identify RNA sequences that hybridize to a known probe such as an oligonucleotide, DNA fragment, cDNA or fragment thereof, or RNA fragment. The probe can be labeled with a radioisotope such as ^{32}P , by biotinylation or with an enzyme. The RNA to be analyzed can be usually electrophoretically separated on an agarose or polyacrylamide gel, transferred to nitrocellulose, nylon, or other suitable membrane, and hybridized with the probe, using standard techniques well known in the art.

Nucleic acid sample may be contacted with an oligonucleotide probe in any suitable manner known to those skilled in the art. For example, the DNA sample may be solubilized in solution, and contacted with the oligonucleotide probe by solubilizing the oligonucleotide probe in solution with the DNA sample under conditions that permit hybridization. Suitable conditions are well known to those skilled in the art. Alternatively, the DNA sample may be solubilized in solution with the oligonucleotide probe immobilized on a solid support, whereby the DNA sample may be contacted with the oligonucleotide probe by immersing the solid support having the oligonucleotide probe immobilized thereon in the solution containing the DNA sample.

The term “substrate” refers to any solid support to which the probes may be attached. The substrate material may be modified, covalently or otherwise, with coatings or functional groups to facilitate binding of probes. Suitable substrate materials include polymers, glasses, semiconductors, papers, metals, gels and hydrogels among others. Substrates may have any physical shape or size, *e.g.*, plates, strips, or microparticles. The term “spot” refers to a distinct location on a substrate to which probes of known sequence or sequences are attached. A spot may be an area on a planar substrate, or it may be, for example, a microparticle distinguishable from other microparticles. The term “bound” means affixed to the solid

substrate. A spot is “bound” to the solid substrate when it is affixed in a particular location on the substrate for purposes of the screening assay.

In certain embodiments of the present disclosure, the substrate is a polymer, glass, semiconductor, paper, metal, gel or hydrogel. In certain embodiments of the present disclosure, a kit can further include a solid substrate and at least one control probe, wherein the at least one control probe is bound onto the substrate in a distinct spot.

In certain embodiments of the present disclosure, the solid substrate is a microarray. An “array” or “microarray” is used synonymously herein to refer to a plurality of probes attached to one or more distinguishable spots on a substrate. A microarray may include a single substrate or a plurality of substrates, for example a plurality of beads or microspheres. A “copy” of a microarray contains the same types and arrangements of probes.

Methods for Detecting Coronary Heart Disease

The present disclosure provides a method using bisulfite treated DNA for determining whether a subject has the likelihood of having a CVD by determining methylation status of a CpG dinucleotide repeat or CpG dinucleotide repeat motif region, where the methylation status of the CpG dinucleotide is associated with CVD. In certain embodiments, the method determines the methylation status of a plurality (e.g., any integer between 1 and 10,000, such as at least 100) of CpG dinucleotide repeat motif regions.

Various techniques and reagents find use in the methods of the present disclosure. In one embodiment of the disclosure, blood samples, or samples derived from blood, *e.g.* plasma, circulating, peripheral, lymphocytes, etc. are assayed for the presence of one or more SNPs and/or the methylation status of one or more CpG dinucleotides. A biological sample also can be saliva. Typically, a biological sample that contains nucleic acids is provided and tested.

As used herein, the term “healthy” means that a subject does not manifest a particular condition, and is no more likely than at random to be susceptible to a particular condition.

In certain embodiments, the present disclosure provides a method for detecting that a subject is predisposed to or has coronary heart disease. Such a method typically includes providing a biological sample from the subject; contacting DNA from the biological sample with bisulfite under alkaline conditions; contacting the bisulfite-treated DNA with at least one first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide, wherein the at least one first oligonucleotide probe detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, and detecting either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide,

wherein methylation of the CpG dinucleotide is associated with coronary heart disease. Such a method can further include determining the genotype of a single nucleotide polymorphism (SNP) (e.g., rs347027).

In certain embodiments, the method further comprises contacting the bisulfite-treated DNA with at least one second oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide, where the at least one second oligonucleotide probe detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, whichever is not detected by the at least one first oligonucleotide probe.

In certain embodiments, the method further comprises determining the ratio of methylated CpG dinucleotides to unmethylated CpG dinucleotides. In certain embodiments, the method can include an amplifying step after the contacting step. In certain embodiments, the method can include a sequencing step after the contacting step.

In certain embodiments, a method for measuring the presence of a biomarker in a biological sample from a patient is provided. Such a method can include contacting DNA from the biological sample with bisulfite under alkaline conditions; and contacting the bisulfite-treated DNA with at least one first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide, where the at least one first oligonucleotide probe detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide. Such a method can be used to predict whether or not the patient has coronary heart disease or has an increased likelihood of developing coronary heart disease.

In certain embodiments, a method of predicting the presence of biomarkers associated with Coronary Heart Disease (CHD) in a biological sample from a patient is provided. Such a method typically includes providing a first aliquot from a biological sample and contacting DNA from the first aliquot with bisulfite under alkaline conditions. Such a method also typically includes providing a second aliquot from the biological sample and contacting the bisulfite-treated first aliquot and the second aliquot with the following: (i) a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs347027; (ii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 38364951 in an intergenic region of chromosome 15, and the second aliquot with a nucleic acid primer at

least 8 nucleotides in length that is complementary to SNP rs4937276; (iii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 84206068 of chromosome 4 in the Coenzyme Q2 4-hydroxybenzoate poly-prenyl transferase (COQ2) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs17355663; (iv) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs235807; (v) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 91171013 of an intergenic region of chromosome 1, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs11579814; (vi) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs2275187; (vii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 186426136 mapping to chromosome 1 in the Phosducin gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4336803; (viii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18 (CDK18) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4951158; and/or (ix) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to rs925613.

In certain embodiments, the present disclosure provide a method for detecting one or more copies of a G allele at rs347027 and methylation status at cg13078798 on a nucleic acid sample from a subject at risk for Coronary Heart Disease (CHD), comprising a) performing a genotyping assay on a nucleic acid sample of said human subject to detect the presence of

one or more copies of a G allele of the rs347027 polymorphism, and b) performing a methylation assessment at cg13078798 on a nucleic acid sample of said human to detect methylation status to determine if cg13078798 is unmethylated.

In such a method, methylation of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR3 gene, or at any of positions cg20636912, cg16947947, cg05916059, cg04567738, cg16603713, cg05709437, cg12081870, and /or cg18070470, along with a G at position 1618766 of chromosome 1 or polymorphisms in the SNPs at rs4937276, rs17355663, rs235807, rs11579814, rs2275187, rs4336803, rs4951158, and/or rs925613 are associated with CHD.

Kits for Detecting Coronary Heart Disease

In a further embodiment of the disclosure, there are provided articles of manufacture and kits containing probes, oligonucleotides or antibodies which can be used, for instance, for the applications described above. The article of manufacture comprises a container with a label. Suitable containers include, for example, bottles, vials, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which includes one or more agents that are effective for practicing the methods described herein. The label on the container indicates that the composition can be used for a specific application. The kit of the disclosure will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters and package inserts with instructions for use.

In certain embodiments, the present disclosure provides a kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP). In certain embodiments, a kit as described herein may contain a number of primers that is any integer between 1 and 10,000, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, . . . 9997, 9998, 9999, 10,000. As used herein, the term “nucleic acid primer” or “nucleic acid probes” or “oligonucleotide” encompasses both DNA and RNA primers. In certain embodiments, the primers or probes may be physically located on a single solid substrate or on multiple substrates.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFBR3) gene), and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP

(e.g., SNP rs347027). In some embodiments, the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide. In some embodiments, the at least one second nucleic acid primer has a sequence that detects a G nucleotide at SNP rs347027.

In some embodiments, a kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 92203667 of chromosome 1 within the TGFBR gene), where the at least one third nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 38364951 in an intergenic region of chromosome 15), where the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., rs4937276).

In some embodiments, a kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 38364951 in an intergenic region of chromosome 15), where the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene), where the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs17355663).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene), where the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene), where the at least one first

nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs235807).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene), where the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 91171013 of an intergenic region of chromosome 1), where the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs11579814).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 91171013 of an intergenic region of chromosome 1), wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene), where the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs2275187).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene), wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 186426136 mapping to chromosome 1 in the Phosducin gene), where the at least one first nucleic acid primer detects

the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs4336803).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 186426136 mapping to chromosome 1 in the Phosducin gene), where the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18 (CDK18) gene), where the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs4951158).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18 (CDK18) gene), where the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

A kit as described herein can include at least one first nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene), where the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and at least one second nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a SNP (e.g., SNP rs925613).

In some embodiments, the kit further can include at least one third nucleic acid primer (e.g., at least 8 nucleotides in length) that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide (e.g., at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene), where the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

It would be appreciated that any of the nucleic acid primers, probes or oligonucleotides described herein can include one or more nucleotide analogs and/or one or more synthetic or non-natural nucleotides.

It also would be appreciated that any of the kits described herein can include a solid substrate. In some embodiments, one or more of the nucleic acid primers can be bound to the solid support. Examples of solid supports include, without limitation, polymers, glass, semiconductors, papers, metals, gels or hydrogels. Additional examples of solid supports include, without limitation, microarrays or microfluidics cards.

It also would be appreciated that any of the kits described herein can include one or more detectable labels. In some embodiments, one or more of the nucleic acid primers can be labeled with the one or more detectable labels. Representative detectable labels include, without limitation, an enzyme label, a fluorescent label, and a colorimetric label.

Algorithm for Predicting Post-Surgical Cardiac Events

Any number of algorithms that can capture linear effects (e.g., linear regression) or both linear and non-linear effects (e.g., Random Forest, Gradient Boosting, Neural Networks (e.g., deep neural network, extreme learning machine (ELM)), Support Vector Machine, Hidden Markov model) can be used in the methods described herein. See, for example, McKinney et al., 2011, Appl. Bioinform., 5(2):77-88; Gunther et al., 2012, BMC Genet., 13:37; and Ogutu et al., 2011, BMC Proceedings, 5(Suppl 3):S11. Any type of machine learning algorithm or deep learning neural network algorithm (tuned or non-tuned) capable of capturing linear and/or non-linear contribution of traits for the prediction can be used. See, for example, **Figure 14**. In some instances, a combination of algorithms (e.g., a combination or ensemble of multiple algorithms that capture linear and/or non-linear contributions of traits) is used.

Simply by way of example, Random Forest™ is a popular machine learning algorithm created by Breiman & Cutler for generating “classification trees” (see, for example, “stat.berkeley.edu/~breiman/RandomForests/cc_home.htm” on the World Wide Web). Using standard machine learning and predictive modeling techniques, a diagnostic classifier algorithm was written to be implemented in R and Python programming languages (though it can be implemented in many other programming languages), according to well described guidelines by Breiman & Cutler. A diagnostic classifier algorithm was generated using data from at least two traits (T) and the diagnosis of interest from that population. To determine the output (e.g., diagnosis) for a new individual, one simply determines values for the at least two traits (T) and inputs that information into an algorithm (e.g., the diagnostic classifier algorithm described herein or another algorithm discussed above) that is capable of capturing the linear and non-linear contributions of the traits.

As described herein, the inputs are at least one genotype (e.g., SNP) and the methylation status of at least one CpG dinucleotide, and the outcome can represent a positive or a negative probability (e.g., prediction or diagnosis) for CHD, CHF, stroke or other illnesses. The Traits (T) used to determine the outcome can represent the methylation status of at least one CpG dinucleotide or at least one genotype (e.g., of a SNP), but Traits (T) also can correspond to at least one interaction (e.g., between methylation status and genotype (CpGxSNP), between the methylation status of two different sites (CpGxCpG) or between two different genotypes (SNPxSNP)). It would be appreciated that any such interactions can be visualized using partial dependence plots.

It will be apparent that the present disclosure provides a skilled artisan the ability to construct a matrix in which the methylation status of one or more CpG dinucleotides and one or more genotypes (e.g., SNPs; e.g., at one or more alleles) can be evaluated as described herein, typically using a computer, to identify interactions and allow for prediction of a post-surgical cardiac event. Although such an analysis is complex, no undue experimentation is required as all necessary information is either readily available to the skilled artisan or can be acquired by experimentation as described herein.

The present invention is further detailed in the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below are utilized. All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLE 1

METHYLATION AND GXMETHYLATION EFFECTS IN PREDICTING CARDIOVASCULAR DISEASE

Methylation-based biomarkers are gaining increasing clinical traction for use in guiding diagnosis and therapy. In attempts to identify CpG loci whose methylation status is predictive of cardiovascular disease, a number of investigators have used genome wide approaches combined with clinical diagnostics. In particular, Brenner and colleagues have identified F2RL3 residue cg03636183 as a biomarker for cardiovascular disease (Breitling et al., "Smoking, F2RL3 methylation, and prognosis in stable coronary heart disease," Eur. Heart J., 2012, 33:2841-8). Unfortunately, these analyses have been shown to have been completely confounded by incomplete knowledge of smoking status and did not consider possible confounding genetic variance. In fact, when using biomarker approaches that fully

account for the intensity of smoking, the coronary heart disease signal at cg03636183 disappears. Furthermore, using a genome wide methylation and genetic analyses, combined with biomarker guided smoking assessments, we have recently analyzed data from a large cohort of subjects informative for cardiac disease. We demonstrate that independent of smoking intensity status, that the genetically contextual methylation status, as embodied by methylation-genotype interact (meQTLs) actually contribute better to the prediction of coronary heart disease and that the use of an algorithm that combines local genetic variation and methylation markedly improves prediction of coronary heart disease.

EXAMPLE 2

INCORPORATING GENE X METHYLATION INTERACTIONS INCREASES THE POWER TO PREDICT THE PRESENCE OF CORONARY HEART DISEASE

ABSTRACT

Coronary heart disease (CHD) is the leading cause of death in the United States. Effective treatments to prevent morbidity and mortality of CHD exist, but their clinical implementation is hindered by inefficient screening techniques. In recent years, others and we have shown that DNA methylation signatures can infer the presence of a variety of disorders related to CHD such as smoking. Unfortunately, when these epigenetic techniques are applied to CHD itself, the power of these methods is diminished, thus limiting their clinical utility. One possible reason for these failures may be the obscuration of epigenetic signature of CHD by *gene x methylation* interaction (meQTL) effects. In order to test this possibility, using a stepwise approach, we examined whether incorporation of meQTLs could be used to improve the predictive value of a prior methylation-based assessment by analyzing genetic and epigenetic data from the Framingham Heart Study. In our initial attempt, using Receiver Operator Characteristic (ROC) Area Under the Curve (AUC) analyses focused on F2RL3, we found that the addition of cis- and trans-meQTL at CpG residue cg13751927, which is near a locus previously described by Brenner and colleagues, significantly improved the capacity of a model that included smoking status alone to predict CHD in the training dataset. Subsequent genome-wide meQTL analyses identified a total of 3,265 cis-meQTLs at a FDR of 0.05 and 467,314 significant trans-meQTLs at a FDR of 0.1. Our preliminary analysis suggests that, the inclusion of six additional cis-meQTL further improved the AUC of the existing model with only the F2RL3 meQTL and smoking. This non-optimized model is capable of predicting CHD with 81.9% accuracy. We conclude that incorporating meQTL information in prediction algorithms can markedly improve their power to predict CHD and

that further attempts to improve the ability of the model to predict CHD are possible through additional optimized machine learning models.

INTRODUCTION

Coronary Heart Disease (CHD) is the leading cause of death in the United States whose direct cost to the US economy was estimated to be 108 billion dollars in 2012.¹ Over the past fifty years, a number of medications and devices have been developed to treat CHD. Unfortunately, tens of thousands of Americans continue to die each year because the presence of CHD is not noted until a fatal cardiac event. Conceivably, more effective screening procedures for CHD could lead to the prevention of some of these deaths.¹ But at the current time, the cumbersomeness of certain techniques, such as fasting lipid panels, and/ or the limited predictive ability of others such as electrocardiograms and C-reactive protein levels, limit the effectiveness of the current approaches in identifying CHD.¹⁻³

A number of investigators have proposed that genetic approaches could provide another potential avenue through which to prevent CHD related morbidity and mortality.⁴ Using whole exome and genome sequencing techniques, a number of variants predisposing to CHD have been identified. The relative risk conferred by of many of these variants is often considerable and their presence is sometimes useful for guiding prevention and treatment.⁵ However, the large effect size variants tend to be rare and their presence is not pathognomonic of current disease.⁴ Hence, at the current time, genetic approaches are not generally used for the assessment of the presence or absence of current CHD in general medical practice.

Alternatively, others have proposed that epigenetic techniques might be useful in assessing CHD.⁶⁻⁸ Since replicated peripheral white blood cell DNA methylation signatures for the presence of type 2 diabetes, smoking and drinking have been developed,⁹⁻¹² this suggestion has strong face validity. Notably, using this approach, Brenner and colleagues have proposed that DNA methylation at cg03636183, a CpG residue found in *Coagulation factor II (thrombin) receptor-like 3* (F2RL3), predicts risk for cardiac disease.^{6,13} Although this is an extremely biologically plausible finding, their subsequent studies have demonstrated that the CHD related signal at cg03636183 completely co-segregates with smoking status as indicated by DNA methylation at cg05575921,¹⁴ a CpG residue found in the *aryl hydrocarbon receptor repressor* (AHRR) whose strong predictive power with respect to smoking status has been demonstrated in dozens of studies.¹⁵

However, the failure of the initially intriguing cg03636183 findings to independently identify additional risk outside of that conferred by smoking alone does not mean that methylation approaches for assessing the presence of CHD are destined to fail. Instead, they

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5 suggest that successful approaches need to be more nuanced and that reconsideration of our conceptualization of relationship of methylation status to CHD is in order. For example, the findings by Brenner's group strongly suggest that methylation algorithms for the prediction of current CHD should include an indicator of smoking status. Given the fact that smoking is the largest preventable risk factor for CHD,¹⁶ this is eminently logical. However, in addition, they may need to take into consideration that the long-term effects of exposure to environmental risk factors such as smoking or other cardiac risk factors such as hyperlipidemia may be obscured by gene-environment interactions.

10 The role of gene-environment interactions (GxE) effects in moderating vulnerability to illness is perhaps better appreciated in the behavioral sciences. The basic premise of GxE effects is that the influence of the environment during a developmentally sensitive period of time changes the biological properties of a system in a genetically contextual manner so that in the future-even in the absence of the environmental factor- enhanced vulnerability to illness is present.¹⁷ Critically, because of confounding by the genetic variable, the direct effects of the environmental variable are generally not detectable. Rather, only when considered in the context of genetic variation can these be detected. Though the strength of some GxE findings are controversial, many investigators continue to stress the importance of these GxE effects in the pathogenesis of a variety of behavioral disorders such as depression, post-traumatic stress disorder and antisocial behavior.¹⁸⁻²⁰

20 The physical basis for these GxE effects is thought to vary. For example, at the anatomical level, the GxE effects for behavioral disorders can be manifested by changes in synaptic structure.²¹ However, at the molecular level, the physical manifestation of GxE effects is less certain. But a number of investigators have suggested that changes in DNA methylation may be one potential mechanism through which the physical effects of GxE effects are conveyed.²²

25 Interestingly, the fact that behaviorally relevant changes in the environment can alter DNA methylation and that the degree of those changes is influenced by genetic variation has been known for many years. In our early candidate gene studies, we showed that smoking altered DNA methylation in the promoter region of *monoamine oxidase A (MAOA)*, a key regulator of monoaminergic neurotransmission, and that genotype at the well-characterized promoter associated variable nucleotide repeat (VNTR) altered the percent methylation at the status in both the presence and absence of smoking.^{23,24} Subsequently, methylation changes at those loci were shown to be functional by Volkow and colleagues.²⁵

30 In current terminology, those effects of the VNTR on smoking or basal DNA methylation are now referred to genotype-methylation interaction or methylation quantitative

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trait locus (meQTL) effects. These MAOA meQTL effects had consequence on our ability to detect their relationship to smoking when we conducted our first genome wide studies.

Despite the magnitude of the smoking induced change in DNA methylation in response to smoking, the probes surrounding the *MAOA* VNTR are not among the more highly ranked probes even in studies of DNA from subjects of only one gender. Other observations from those initial studies are equally instructive. First, the local methylation response to smoking was not homogenous. Factor analysis of the methylation status of the 88 CpG residues in the promoter associated islands showed that increases in methylation at one area of the island could be associated with demethylation at others.²⁶ Finally, the effects of smoking on DNA methylation were not static. After time, the signature tended to decay.²³ Hence, from those early studies, it was clear that at MAOA promoter, genetic variation could alter the effects of environmental factor on the local DNA methylation signature in a complex manner.

Subsequent studies suggest that many of these same complexities in response to smoking are evident at the genome wide level. For example, it is clear that at the genome wide level, genetic variation affects the magnitude of the methylation response, and that when attempting to replicate signatures from those of differing ancestries, those meQTL effects may impair the ability to replicate findings at a given locus in a subject pool of a different ancestry.^{27,28} Second, and equally importantly, the reversion of the methylation signatures can be complex.^{28,29} Guida and colleagues specifically examined the epigenomic response to smoking cessation in DNA from a collection of 745 subjects and found two classes of CpG sites, those whose methylation signature reverted with time and those that did not; and concluded that at the genome wide level the “*dynamics of methylation changes following smoking cessation are driven by a differential and site specific magnitude of the smoking induced changes that is irrespective of the intensity and duration of smoking.*”²⁹ In summary, a substantial body of evidence suggests that the genome wide signature to smoking is only partially reversible and that a large chunk of the non-reversible changes may be complexly masked in meQTL effects.

Since smoking is a major risk factor for CHD, this also suggests that a portion of the smoking induced risk present in the epigenome that moderates the risk for CHD may be somewhat non-reversible and masked in meQTL responses. In addition, since smoking is only one of a number of factors can alter risk for CHD and these other factors also may have complex epigenetic signatures, it may well be that interrogation of peripheral WBC DNA methylation may reveal meQTL that moderate risk for CHD and are relatively stable. In this communication, we used regression analytical approaches and the epigenetic and genetic

resources from 324 subjects who participated in the Framingham Heart Study to test whether the addition of meQTL effects can make a contribution to algorithms to predict CHD.

METHODS

Framingham Heart Study. The data used in this study is derived from participants in the Framingham Heart Study (FHS).³⁰ FHS is a longitudinal study aimed at understanding the risks of cardiovascular disease (CVD) and consists of several cohorts including the Original Cohort, Offspring Cohort, Omni Cohort, Third Generation Cohort, New Offspring Spouse Cohort and Second Generation Omni Cohort. Specifically, the Offspring Cohort, initiated in 1971, consisting of the offspring of the Original Cohort and their spouses was used in this study. This cohort consists of 2,483 males and 2,641 females (total of 5,124).³¹ The specific analyses described in this communication were approved by the University of Iowa Institutional Review Board.

Genome-wide DNA Methylation. Of the 5,124 individuals in the Offspring Cohort, only 2,567 individuals (duplicates removed) with DNA methylation data were considered. These individuals were included in the DNA methylation study because they attended the Framingham Offspring 8th exam, provided consent for genetic research, had a buffy coat sample, and had sufficient DNA quantity and quality for methylation profiling. Exam 8 took place between 2005 and 2008. Genomic DNA extracted from their white blood cells was bisulfite converted, then genome-wide DNA methylation was profiled using the Illumina HumanMethylation450 BeadChip (San Diego, CA) at either the University of Minnesota or Johns Hopkins University. The intensity data (IDAT) files of the samples alongside their slide and array information were used to perform the DASEN normalization using the MethyLumi, WateRmelon and IlluminaHumanMethylation450k.db R packages.³² The DASEN normalization performs probe filtering, background correction and adjustment for probe types. Samples were removed if they contained >1% of CpG sites with a detection p-value >0.05. CpG sites were removed if they had a bead count of <3 and/or >1% of samples had a detection p-value >0.05. After DASEN normalization, there were 2,560 samples and 484,241 sites remaining (484,125 CpG sites). CpG sites were grouped by chromosome. Methylation beta values were converted to M values using the beta2m R function in the Lumi package and subsequently converted to z-scores using an R script.³³

Genome-wide Genotype. Of the 2,560 remaining individuals after DNA methylation quality control, 2,406 (1,100 males and 1,306 females) had genome-wide genotype data from the Affymetrix GeneChip HumanMapping 500K Array Set (Santa Clara, CA). This array is capable of profiling 500,568 SNPs in the genome. Quality control was performed at both the sample and SNP probe levels in PLINK. The initial quality control step involved identifying

individuals with discordant sex information. None were identified. Next, individuals with a heterozygosity rate of greater or smaller than the mean $\pm$ 2SD and with a proportion of missing SNPs >0.03 were excluded. Related individuals were also excluded if the identity by descent value was >0.185 (halfway between second and third degree relatives). After performing these sample level quality control steps, 1,599 individuals remained (722 males and 877 females). On the probe level, SNPs with a minor allele frequency $>1\%$, Hardy-Weinberg equilibrium p-value $>10^{-5}$ and SNP missing rate of $<5\%$ were retained. A total of 403,192 SNPs remained after these quality control steps. Using the recode option in PLINK,³⁴ genotypes were coded as 0, 1 or 2.

Phenotypes. In the methylation quantitative trait loci (meQTL) analysis, phenotypes that were considered include age, gender, batch, smoke exposure, and coronary heart disease (CHD) status. Among the 1,599 individuals that passed all quality control steps, 324 were recorded as having CHD at exam 8. These individuals were the training set. CHD was recorded as either prevalent or incident and an individual is diagnosed as having CHD if the Framingham Endpoint Review Committee (panel of three investigators) agrees that one of the following is present: myocardial infarction, coronary insufficiency, angina pectoris, sudden death from CHD, non-sudden death from CHD. For the analysis, CHD was coded as 1 if an individual had either prevalent and/or incident CHD, or 0 otherwise. The age used was the age of an individual at exam 8. Batch was the methylation plate number and smoke exposure was the methylation level at the *aryl hydrocarbon receptor repressor* (AHRR) smoking biomarker, cg05575921. The demographics of the 324 individuals in the training set are summarized in Table 1.

Table 1. Demographic of the 324 individuals in the training set

	CHD present	CHD absent
n		
Male	56	167
Female	23	78
Age		
Male	70.9 $\pm$ 7.0	71.1 $\pm$ 7.8
Female	71.7 $\pm$ 9.2	72.7 $\pm$ 7.9
cg05575921		
Male	-0.389 $\pm$ 1.41	0.277 $\pm$ 1.04
Female	-0.218 $\pm$ 1.16	0.403 $\pm$ 0.90

The remaining 1275 individuals were the testing dataset. The CHD status of these individuals was coded as 0 if CHD was not present, and 1 otherwise. The demographics of these individuals are summarized in Table 2.

Table 2. Demographic of the 1275 individuals in the testing dataset

	CHD present	CHD absent
n		
Male	52	447
Female	49	727
Age		
Male	71.0±8.5	65.0±8.3
Female	72.2±8.9	65.8±8.4
cg05575921 methylation (m-value)		
Male	-0.269±1.02	-0.153±1.02
Female	-0.181±1.00	0.055±0.91

Methylation Quantitative Trait Loci. The meQTL analysis was performed in the training set using the MatrxQTL package in R.³⁵ To determine significant effects of SNP on methylation (meQTL) given CHD status, the following model was interrogated:

$$Meth_i \sim Age + Gender + Batch + cg05575921 + SNP_j + CHD + SNP_j * CHD$$

Cis- and trans-meQTL with a significant $SNP_j * CHD$ term were retained for prediction. The interaction term was of particular interest because the analysis was aimed at uncovering specific SNPs that significantly predicted specific methylation sites given CHD status, after controlling for age, gender, batch, smoke exposure and the main effects of SNP and CHD. In the MatrxQTL package, this was achieved using the modelLINEAR_CROSS model type. The cis distance was chosen to be 500,000 on either side of the site and was performed at the chromosome level. The meQTL analysis was performed on a genome-wide level and for coagulation factor II receptor-like 3 (F2RL3) gene specifically. This was done to determine if there is other meQTL beyond those identified for F2RL3 that better predict CHD.

Receiver Operating Characteristic Curve. An R script was written to perform logistic regression of the models shown below and subsequently calculate the area under the curve (AUC) receiver operating characteristic (ROC)³⁶ using the pROC package in R. This was performed for significant cis-meQTL at a nominal 0.05 level and trans-meQTL at an FDR 0.1 level. In the models listed below, each meQTL is represented by the $SNP_j * meth_i$ term.

$$CHD \sim Age + Gender + Batch + cg05575921 + SNP_j + meth_i + SNP_j * meth_i$$

$$CHD \sim Age + Gender + Batch + cg05575921 + SNP_j + meth_i + SNP_j * meth_i$$

Model Training. A model was trained on the training dataset consisting of 324 individuals. Variables in this model were chosen based on their individual area under the ROC curve (AUC) generated from models described above. A 10-fold cross-validation was

performed to determine the logistic regression threshold for CHD classification. From the average accuracy, a classification threshold of 0.5 was chosen.

Model Testing. Once the training model parameters and the classification thresholds were determined, the trained model was applied on an independent testing dataset. The demographics of the individuals in the testing dataset were described above. Model testing was performed in R.

RESULTS

cg05575921 for smoking status. As discussed earlier, smoking is a major risk factor of CHD. While most studies in the past have used self-reported smoking measures, the reliability and informativeness of these measures is less than optimal. Therefore, in order to minimize the effects of unreliable self-report and to take advantage of the ability of a continuous metric to better capture the amount of smoking consumption, we used a well validated biomarker of smoking, cg05575921.^{14,15,37} While cg05575921 is a strong predictor of self-reported smoking in the 324 individuals ($p\text{-value} = 8.71\text{e-}9$, $R^2 = 0.62$), the strength of cg05575921 as a predictor of CHD outweighs self-reported smoking status ($p\text{-value} = 1.64\text{e-}5$, $R^2 = 0.085$ vs. $p\text{-value} = 0.00218$, $R^2 = 0.042$). This demonstrates that the incorporation of cg05575921 to represent smoke exposure instead of self-reported smoking status would further strengthen the downstream model for CHD prediction.

Methylation quantitative trait loci. The importance of accounting for the confounding effects of interaction between methylation and genotype for CHD prediction was demonstrated by the genome-wide DNA methylation analysis as discussed in the methods section. After controlling for age, gender, batch and cg05575921, CHD was not significantly associated with any methylation CpG sites at an FDR significance level of 0.05. From the meQTL analysis, there were 5,458,462, 3,265, 2,025 and 1,227 significant cis-meQTL at the 0.05 nominal, 0.05 FDR, 0.01 FDR and 0.001 FDR significance levels, respectively. Similarly, there was 467,314 significant trans-meQTL at the 0.1 FDR significance levels. The importance of some of these meQTL is demonstrated using the area under the receiver operating characteristic curve.

Receiver Operator Curve (ROC) of core variables. A ROC curve depicts the tradeoff between the sensitivity and selectivity of a model. Before introducing genetic and epigenetic variables, we established the area under the ROC curve (AUC) for the core variables age, gender, batch, and cg05575921 used in the meQTL model. The AUC of age, gender, batch and cg05575921 were 0.52, 0.51, 0.50, and 0.64, respectively. Collectively, they resulted in an AUC of 0.65, which is almost equal to the AUC of just cg05575921. If self-reported smoking was used instead of cg05575921, its individual and collective AUC is 0.55 and 0.56,

respectively. The ROC curves of these analyses are depicted in Figure 1. Hence, only one core variable, cg05575921, was included in subsequent models.

ROC of CHD prediction in training data. Using cg05575921 and nine SNP-methylation interaction terms for CHD prediction, an AUC of ROC curve of 0.964 was obtained (see Figure 2). The nine interaction terms and their respective AUC with and without the addition of cg05575921 to the model are summarized in Table 3.

Table 3. The list of the 9 meQTLs used to generate the Initial Prediction Model.

SNP	CpG	meQTL AUC	meQTL+cg055 AUC
rs347027	cg13078798	0.728	0.776
rs4937276	cg20636912	0.731	0.770
rs17355663	cg16947947	0.712	0.769
rs235807	cg05916059	0.698	0.765
rs11579814	cg04567738		
rs2275187	cg16603713		
rs4336803	cg05709437		
rs4951158	cg12081870		
rs925613	cg18070470	0.730	0.761

Prediction model. A preliminary logistic prediction model was used to predict CHD in the training data. After 10-fold cross-validation, the classification threshold was set to 0.5. Of the 324 individuals, 299 were included in the prediction due to absence of missing data. Of those 299 individuals, 73 and 226 do and do not have CHD, respectively. This means, if everyone were assigned the majority class (i.e. CHD absent), the prediction accuracy would be 75.6%. The average accuracy of this preliminary model after 10-fold cross-validation was 91%, which is much higher than the baseline.

Model testing. The trained model was used to predict CHD status in the independent testing dataset of 1275 individuals. The model was capable of predicting CHD with an 80% accuracy. This model is yet to be optimized.

DISCUSSION

The results demonstrate that the presence of CHD can be inferred through the use of methylation-genotype interactions derived from meQTL. However, before the results can be discussed, it is important to note several limitations to the current study. First, the Framingham cohort is exclusively White and most subjects are in their mid to late sixties and seventies. Therefore, the current findings may not apply to those of other ethnicities or different age range. Second, outside of cg05575921, the validity of the M (or B-values) for the other probes has not been confirmed by an independent technique such as pyrosequencing. Third, the Illumina array used in the studies is no longer available. Because

of changes in design or availability of probes in the new generation of array, the ability to replicate and extend may be affected.

The current results underscore the value of resources such as the Framingham Heart Study furthering our understanding heart disease. In fact, without this resource, it is fair to say that this type of work would be difficult if not impossible to conduct. Still, even given the current results using this unique data set, a great deal of additional work will be necessary before a screening test such as that described in the current communication can be employed clinically. Most obviously, the current results will have to be replicated and refined in other data sets, then re-tested in research populations representative of their intended future clinical application. The latter point is particularly important because even well-designed cohort studies that were originally epidemiologically sound suffer from retention biases that enrich the remaining pool for less serious illness. This is particularly true with respect to illnesses associated with substance use, because probands with high levels of substance use are more often lost to longitudinal follow-up.³⁸ In addition, because SNP frequencies can vary between ethnicities, the effect size of a given meQTL may also vary. Therefore, extensive testing and development in a variety of ethnically informative cohorts will be necessary.

There may be a hard ceiling for improvement of the AUC. Ironically, this has little to do with the quality or quantity of the epigenetic and genetic data. Rather, the limitation may be the uncertainty in the clinical characterizations. Sadly, even under the best conditions, clinically relevant CHD can remain undetected. This is true even for the FHS cohort. As a result, the “gold standard” itself in the current study is somewhat inaccurate with respect to the actual clinical state. Since this inaccuracy increases the error of even a biomarker that is exactly targeted on the relevant biology, our ability to improve the AUC may be dependent on our ability to derive a more accurate clinical assessment.³⁹

Another limitation to the use this approach is the constantly evolving epidemiology of CHD. Whereas the genetic contribution to CHD is relatively fixed, diets and other environmental exposures continue to vary from generation to generation. Perhaps the best illustration of this limitation can be by considering contribution of smoking to the predictive power of this test in prior generations. Since tobacco was introduced to Europe from the New World in the early 1500s, we can confidently state that the contribution of smoking to CHD in medieval Europe was limited and therefore, the impact of the cg05575921 on predictive power would have be nil. In contrast, because over 40% of US adults smoked in the 1960s,⁴⁰ it is likely that the contribution of smoking behaviors, as captured by cg05575921, to the prediction of CHD would have been significantly greater in subjects from that era. However, smoking is not the only environmental factor that varies from generation to

generation and from cohort to cohort. Over the past 20 years, there have been marked shifts in our understanding and public attitudes towards the amount of saturated and trans-fatty acids in a healthy diet. Since these environment factors also have strong influence on the likelihood of CHD, we would expect that the weighting of meQTLs loading on these dietary factors might vary with respect to age and ethnicity.

The improved predictive power of the smoking methylation biomarker cg05575921 as compared to self-reported smoking is not unexpected. In our initial studies, it has shown to be a potent indicator of current smoking status with an AUC of 0.99 in study that used well screened cases and controls.³⁷ Unreliable self-report for smoking, particularly in high risk cohorts, is a well-established phenomenon.⁴¹⁻⁴⁴ Furthermore, unlike cg05575921, categorical self-report does not capture the intensity of smoking.³⁷ Finally, many subjects who may have participated in the study may have previously smoked, but did not smoke at the Wave 8 interview but still had residual demethylation of AHRR. In each of these instance, the use of the continuous metric may capture additional vulnerability to CHD that is not captured by a dichotomous smoking variable.

Since alcoholism is also a risk for CHD,¹ we were somewhat surprised that our previously established and validated biomarker approach for assessing alcohol intake did not have a greater predictive impact.^{10,45} In our initial models, the addition of methylation status at cg2313759 only improved AUC by 0.015. Although one reason for this failure to show the effect of alcohol use on risk for CHD may be that this marker is not as well validated as our smoking biomarker, there are other reasons as well. First and foremost, as opposed to methylation at cg05575921 which displays a tonic increasing risk for decreased life expectancies at all of levels of exposure, methylation at cg2313759 displays an inverted U-shaped distribution with respect to biological aging. Whether risk for CHD also follows a U shaped distribution with respect to alcohol intake is not known. But it does suggest that any successful algorithm incorporating the main effects of alcohol associated methylation cannot use a simple linear approach.

Our success in finding meQTLs predictive of CHD in the absence of genome wide significant main effects may have significant implications for the searches for marker sets for other common complex disorders of adulthood. Of the top 10 leading causes of death in the United States, using main effects, reliable methylation signatures have been developed only for type 2 diabetes and chronic obstructive pulmonary disease (COPD).^{12,46} Because the ability to find a good biomarker for illness is highly contingent on the reliability of the clinical diagnosis, the success in these two instances may be secondary to the excellent diagnostic reliability of the methods used to diagnose these two disorders, namely the

hemoglobin A1C and spirometry. Additionally, it is important to note that the diagnostic signature for T2DM largely maps to pathways affected by excessive glucose levels while the signature associated with COPD largely overlaps with that of smoking which contributes to 95% of all cases of COPD.^{12,46} Still, because many of the risk factors for other major causes of death, such as stroke, overlap with those for CHD (e.g. smoking), we are optimistic that similar profiles can be generated using this approach.

Unfortunately, the vast majority of adult onset common complex disorders do not have good existing biomarkers or large effect size etiological factors. In these cases, an approach that incorporates meQTLs may be beneficial- the real question is why? Although speculative, based on our experience with local and genome wide data indicates that chronic exposure to cellular stressors leads to a reorganization of the epigenome, which may be only partially reversible. If that disorganization of the genome, regardless of how long it lasts, is causally associated with illness, it can be used as a biomarker for illness. Understanding the reversion time of each of these meQTLs may lead to additional insights. For example, pharmacological interventions may have effects at discrete subsets of these meQTLs. By understanding the relationship between reversion at these loci and therapeutic outcomes, it may be possible to optimize existing medications or more adroitly tailor new combination regimens.

The fact that no main effects of methylation are observed for CHD is not necessarily an indication of lack of epigenetic signature in WBCs. Rather, it speaks to the complexity of the overall genetic architecture. For example, although methylation status at thousands of CpG loci have been associated with smoking status (for review see ^{14,15}) the signal at cg05575921 is one of the few whose signal is not obscured by ethnic specific genetic differences in one population or another.²⁷ This communication shows that the epigenomic response to smoking also includes a plethora of meQTLs. But the necessity of measuring at least two values for each meQTL suggests that translating these findings to improvements in diagnosis, treatment or prevention may be more challenging.

In summary, we report that an algorithm that incorporates information from meQTLs can predict the presence of CHD in the FCS. We suggest that further studies to replicate and expand the generalizability the approach in cohorts of other ethnicities are indicated. We furthermore suggest that similar approaches may lead to the generation of methylation profiles for other common complex disorders such as stroke.

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EXAMPLE 3

SMOKING ASSOCIATED METHYLATION QUANTITATIVE TRAIT LOCI PREFERENTIALLY MAP TO NEURODEVELOPMENTAL PATHWAYS

Smoking is the leading preventable cause of morbidity and mortality in the United States. Smoking exerts its effects indirectly by increasing susceptibility to common complex diseases such as coronary heart disease and coronary obstructive pulmonary disorder. While the association between these disorders and smoking are widely studied, our understanding of the molecular mechanisms through which smoking increasing vulnerability for complex diseases could still be improved. This is especially true for disorders than preferentially involve the central nervous system (CNS). Smoking is a known risk factor for the development of attention deficit hyperactivity disorder and panic disorder. Our study was designed to understand the effects of smoking on DNA methylation in the presence and absence of genetic context in the Framingham Heart Study (FHS). Specifically, data from 1599 individuals from the FHS Offspring cohort were used. These individuals were of European ancestry and were in their early to mid-sixties. The self-reported smoking rate among these individuals was 7.6%. Genome-wide DNA methylation was profiled using the Illumina HumanMethylation 450k BeadChip and the genome-wide SNP data was assessed using the Affymetrix GeneChip HumanMapping 500k Array Set. To understand the effects of smoking on DNA methylation in the absence of genetic variation, we regressed smoking against DNA methylation, controlling for age, gender and batch. After correction for multiple comparisons, methylation status at 525 sites was significant at a 0.05 level. Consistent with prior studies, the top-ranking probe was cg05575921 from the AHRR gene (p-value of 7.65×10^{-155}). Subsequently, to determine the effects of smoking on DNA methylation in the presence of genetic variation, cis and trans-methylation quantitative trait loci (meQTL) analyses were conducted to determine the significant effects of SNP on DNA methylation given smoking status, controlling for age, gender and batch. A total of 126,369,511 cis and 195,068,554,297 trans analyses were performed. Of those, 5294 (0.00419%) and 422,623 (0.00022%) significant cis- and trans-meQTL were generated after correction for multiple comparisons at a 0.05 significance level. To better visualize and compare the connectivity and gene ontology (GO) enrichment between the results of both analyses, we generated protein-protein interaction (PPI) networks. While the DNA methylation analysis mapped to inflammatory pathways, the cis and trans-meQTL analyses mapped to neurodevelopmental

pathways. These neurodevelopmental pathways could provide additional insight into the association of smoking to psychiatric disorders. Furthermore, this study demonstrates that combined genetic and epigenetic analyses may be crucial in better understanding the interplay between environmental variables such as smoking and pathophysiological outcomes.

EXAMPLE 4

INTEGRATED GENETIC AND EPIGENETIC PREDICTION OF CORONARY HEART DISEASE IN THE FRAMINGHAM HEART STUDY

ABSTRACT

Background: Coronary Heart Disease (CHD) is the leading cause of mortality and morbidity in the United States. Unfortunately, the first sign of CHD for some patients is a fatal myocardial infarction. A sensitive method for detecting current CHD or risk for future cardiac events could prevent some of this mortality, but current biomarkers for asymptomatic CHD are both insensitive and non-specific. Recently, others and we have shown that array based DNA methylation assessments accurately predict the degree of cigarette consumption and the smoking associated risk for CHD. However, attempts to extract additional risk for CHD information from these genome wide assessments have not yet been successful.

Methods and Results: Building on the idea that CHD risk factors are a conglomeration of genetic and environmental factors, we use machine learning techniques and integrate genetic, epigenetic and phenotype data (n=2214) from the Framingham Heart Study to build and test a Random Forest classification model for risk for CHD. Our final classifier, was trained on n=1545 individuals and utilized four DNA methylation sites, two SNPs, age and gender, and was capable of predicting CHD status with 78% accuracy in the test set (n=669) and a sensitivity and specificity of 0.75 and 0.80, respectively. In contrast, a model using only CHD risk factors as predictors had an accuracy and sensitivity of only 65% and 0.41, respectively. The specificity was 0.89. Regression analyses of the individual clinical risk factors highlight the strong role of pathways moderated by smoking in CHD pathogenesis.

Conclusions: This study demonstrates the capability of integrated approaches for predicting symptomatic CHD status and suggests that further work could lead to the introduction of a sensitive, readily employable method for detecting asymptomatic CHD.

INTRODUCTION

Coronary Heart Disease (CHD) is the leading cause of death in United States.¹ Effective methods to prevent this mortality and the accompanying morbidity exist, but they

are often employed ineffectively. In fact, sudden cardiac death is the initial presentation in 15% of patients with CHD.^{2, 3}

In efforts to more effectively detect and treat CHD, a number of screening methods for both symptomatic (angina, myocardial infarction) and asymptomatic CHD have been developed. For asymptomatic patients, the intensity of the screening for CHD depends on the level of clinical suspicion. Though clinicians are wary of the potential for cardiac disease at any age, increased attention is paid to individuals with the classic risk factors for CHD defined in the Framingham Heart Study (FHS) including family history of CHD, smoking, elevated systolic blood pressure, diabetes, or anything resembling angina-like chest pain.^{4, 5} Depending on the level of suspicion for CHD, the initial examination typically includes a complete physical exam and a fasting lipid panel that includes low density lipoprotein (LDL), high density lipoprotein (HDL) and triglyceride levels.⁵ The next level of response is normally an electrocardiogram (ECG) followed by more costly and invasive measures including stress testing and cardiac angiography.⁶

Sadly, the most clinically routine tests, the 12 lead ECG and serum lipid screening, are remarkably insensitive for CHD. For example, in a study of 479 patients admitted for acute chest pain with creatine kinase-MB isoenzyme (CK-MB) and troponin T (TnT) confirmed MI, 12 lead ECG were positive only 33% and 28% at admission and post-admission, respectively.⁷ Likewise, serum lipid (cholesterol and triglyceride) screening has been employed for many years. Most relevantly, in the Framingham Heart Study (FHS), using a cutoff of 260 mg/dl, elevated serum cholesterol levels performed at intake failed to identify 2/3 of all the males who developed CHD over the subsequent four years. Hence, for the past decade there has been an increasing call for biomarkers for the prediction and diagnosis of CHD.

Spurred by the lack of sensitivity and specificity of standard procedures such as the ECG and lipid profile, a large number of investigators have attempted to identify biomarkers of asymptomatic CHD and cardiovascular disease (CVD), its closely related disease cluster. Although a variety of approaches, including imaging, mechanical and bio-electrical techniques have been used,⁸⁻¹⁰ the vast majority of investigators have focused on blood based methods because of the 1) proof of principal provided by prior work with triglycerides and cholesterol, 2) clear involvement of blood components such as platelets and white blood cells in CHD and CVD pathogenesis and 3) the ease of integrating blood based approaches into current medical diagnostics.

The majority of these blood-based approaches have focused on circulating lipids and proteins (for review see ^{11, 12}) such as hemoglobin A1C (HbA1c), fibrinogen, vitamin D, C-

reactive protein (CRP), apolipoprotein B (ApoB), apolipoprotein AI (ApoAI), and cholesterol (including high density and low density, HDL and LDL). When the appropriate cutoffs are employed in research settings, each of these markers is modestly informative (Odds or Relative Ratios of 1.5 to 2.5) with respect to the development of future illness.¹¹ In addition, for those with pre-existing disease, cardiac troponin (cTn) levels and high sensitivity (HsCRP) ratios can be informative about future risk.¹¹ However, each of these markers has challenges to their clinical implementation, such as lack of ease of measurement, ethnic variation or limitations in scope of prediction, that have precluded their routine implementation in CHD screening.

Seeking alternative means of creating more effective screening procedures, other investigators have used genetic procedures to identify risk associated variation including more recent genome wide association (GWAS) and exome/genome sequencing studies (Please see O'Donnell and Nabel, 2011 for review).¹³ To date, these studies have isolated approximately 10% of the total genetic risk for CHD.^{14, 15} Notably, many of these SNPs map to lipid and inflammation pathways, both of which are known to be important from prior studies of CHD.¹⁵ Although these studies can predict who is potentially vulnerable to CHD, they do not actually indicate whether an individual has CHD and meta-analyses indicate that at best the contribution of pure genetic approaches to the prediction of CHD will be minimal.¹⁶ As such, genetic approaches have not been incorporated into routine clinical practice.

Epigenetic approaches may provide a new avenue for assessing risk for CHD. It is already well established that epigenetic approaches can quantitatively assess cigarette consumption which may be the largest preventable cause of CHD.^{17, 18} Notably, Hermann Brenner and colleagues have shown that DNA methylation at cg03636183 predicts not only smoking status but risk for MI.^{19, 20} Unfortunately, the risk for CHD and smoking are not independent with their group also showing that the risk for MI connoted by cg03636183 is fully subsumed by smoking status as denoted by methylation at cg05575921, the best established epigenetic biomarker for smoking in all ethnic groups.^{17, 21}

Critical to the current work is the observation that one of the reasons that methylation status markers such as cg03636183 and GPR15 marker cg19859270^{22, 23} do not predict smoking status well in all populations is the presence of genetic confounding of methylation changes by local genetic variation.²² Over the past several years, our understanding of these effects, which were originally described as relatively static interactions (GxMeth),²⁴ has been modified to show that a subset of these interactions can be contextual on the degree of smoking exposure.^{22, 25, 26} In essence, these and other findings demonstrate that at the single

locus level, methylation response to smoking can be better conceptualized as a product of both the degree of smoking exposure and genetic variation. These interaction effects appear to be widespread. Using a genome wide approach, we have recently shown these smoking contextual genetic effects on DNA methylation on a genome wide basis and have shown that nearly $\frac{1}{4}$ of all genes harbor genetically contextual changes in methylation in response to smoking (Dogan et al., in submission).

As opposed to the more easily conceptualized response of a single facet of the methylome to a single environmental factor (smoking), the entirety of the biological response of the peripheral white blood cells (WBC) to the diverse factors that contribute to CHD is likely to be more complex and difficult to reproducibly capture. For example, at the RNA level, significant signatures for micro-RNA^{27, 28} and mRNA²⁹ prepared from blood have been described, but clear utility as clinical tools has not yet come to fruition. Still, their partial success to date indicates that nucleic acids prepared from peripheral WBC possess a larger biological signature that could be harvested through a more systematic approach.

In that hope, we detail the results of an integrated approach that incorporates commonly used machine learning algorithms in combination with both genome wide epigenetic and genetic data from the Framingham Heart Study.

METHODS

Framingham Heart Study. The Framingham Heart Study (FHS) has been described in detail elsewhere.^{30, 31} The clinical, genetic and epigenetic data included in this study is from the Offspring cohort. Specifically, this study included 2,741 of the 5,124 individuals in the Offspring cohort who 1) survived till the eighth examination cycle which was conducted between 2005 and 2008, 2) consented to genetics research, and 3) have peripheral blood genome-wide DNA methylation data. The FHS data was obtained through dbGAP (<https://dbgap.ncbi.nlm.nih.gov>). The University of Iowa Institutional Review Board approved all described analyses.

Genome Wide DNA Methylation. After removing duplicates, DNA methylation data was available for 2,567 individuals. Genome wide DNA methylation of the Offspring cohort was profiled using the Illumina Infinium HumanMethylation450 BeadChip³² (San Diego, CA) array at either University of Minnesota or Johns Hopkins University. The 485,577 probes in this array cover 99% of RefSeq genes with an average of 17 CpG sites per gene within and outside of CpG islands.³²

Probe filtering, background correction and adjustment for probe types were performed on the methylation intensity data (IDAT) files using the MethyLumi, WateRmelon and IlluminaHumanMethylation450k.db R packages.³³ Quality control was performed on the

sample and probe levels. For samples, those with >1% CpG sites with a detection p-value >0.05 were removed while CpG sites with a bead count <3 and/or >1% samples with a detection p-value >0.05 were removed. After quality control, 2,560 unique samples and 484,125 CpG sites remained. Of those CpG sites, 472,822 mapped to autosomes. Due to the bounded nature of methylation beta values ($0 \leq \beta \leq 1$), logistic transformation of beta values to M-values was conducted ($-\infty < M\text{-value} < \infty$) using the beta2m R package, and subsequently converted to z-scores using an R script.³⁴

Genome Wide Genotype. Genome wide SNP data was profiled using the Affymetrix GeneChip HumanMapping 500K (Santa Clara, CA) array. Of the 2,560 individuals remaining after DNA methylation quality control, 2,406 (1,100 males and 1,306 females) had genotype data. Again, quality control was performed at the sample and probe levels. Using PLINK³⁵, samples were examined for discordant sex information, heterozygosity rate greater or smaller than two standard deviations from the mean, and proportion of missing SNPs >0.03. As a result, a total of 111 samples were removed. Population stratification was also performed and no individuals were excluded. Samples were also excluded if their identity by descent value was >0.1875, which is halfway in between second and third degree relatives to ensure that downstream analyses were not influenced by related individuals. As a result of this criterion, a total of 696 individuals were removed, leaving 1599 subjects (722 males and 877 females) for further analyses. Probes were retained if the minor allele frequency was >1%, the Hardy-Weinberg equilibrium p-value was $>10^{-5}$ and the missing rate was <5%. After quality control, 403,192 SNPs remained (472,822 mapped to autosomes). SNPs were coded as 0, 1, 2 per minor allele frequency.

Phenotypes. For each individual, the following data were extracted from the FHS dataset: age, gender, systolic blood pressure (SBP), high-density lipoprotein (HDL) cholesterol level, total cholesterol level, hemoglobin A1C (HbA1c) level, self-reported smoking status, CHD status and date of CHD established.

Data analysis. To identify CHD and conventional modifiable CHD risk factors associated genome wide DNA methylation changes, linear regression analyses were conducted in R as delineated in Equation 1:

$$Meth_i \sim Age + Gender + Batch + X \quad (1)$$

where X represents CHD or conventional modifiable CHD risk factors: SBP, smoking, HDL, total cholesterol and diabetes. Batch represented the DNA methylation laboratory batch.

The association between DNA methylation and CHD or each of the risk factors was determined while controlling for age, gender and batch effects. Bonferroni correction for

multiple comparisons at a genome-wide $\alpha=0.05$ was performed for every regression analysis.³⁶ For each X , a total of 472,822 independent tests were conducted and therefore, only those with a nominal p-value of $1e-07$ ($0.05/472822$) were considered to be significantly associated at the genome wide level.

Network Analysis: A network was generated and Gene Ontology (GO) pathways were identified using STRING Version 10 for symptomatic CHD.³⁷ The STRING database contains information on known and predicted physical (direct) and functional (indirect) associations between proteins. The network included genes with at least one significant main effect DNA methylation locus after genome wide Bonferroni correction for multiple comparisons. Networks were further reduced to include only nodes (proteins) with edges (interactions) with the highest confidence interaction scores of 0.9 or greater. The PPI figure includes nodes with at least one edge. STRING Version 10 was also used to determine the GO enrichment pathways of the network.

Training and Testing Datasets. The goal of this study was to develop an integrated genetic-epigenetic classifier to predict symptomatic CHD. To achieve this, training and testing datasets were prepared. As mentioned previously after DNA methylation and SNP quality control, 1599 subjects remained. However, based on the CHD status and eighth examination cycle dates, the number of individuals reduced from 1599 to 1545 (694 males and 851 females) and these individuals constituted the training set.

To assess the generalizability of the trained model, data from the 696 individuals removed due to relatedness (identity by descent > 0.1875) were used. Similar to the individuals in the training dataset, the CHD status and the eighth examination cycle dates of the individuals in the test dataset were compared to ensure that only those with a CHD status date less than or equal to the eighth examination cycle date are retained. From doing so, the number of individuals in the test set reduced from 696 to 669 (314 males and 355 females).

Variable Reduction. The total number of genetic (SNP) and epigenetic (DNA methylation) probes remaining after quality control measures were 403,192 and 472,822, respectively. Due to the large number of variables (876,014 total, excluding phenotypes), we reduced the search space and minimized redundancy in the predictors as described below.

Linkage disequilibrium based SNP pruning was performed in PLINK³⁵ with a window size of 50 SNPs, window shift of 5 SNPs and a pairwise SNP-SNP LD threshold of 0.5. This reduced the number of SNPs from 403,192 to 161,474. To further reduce the number of SNPs, the chi-squared p-value was calculated between the remaining 161,474 SNPs and CHD status. Those with a chi-squared p-value < 0.1 were retained for model training, resulting in 17,532 SNPs (~4%).

To reduce the number of DNA methylation loci, first, the correlation was calculated between the 472,822 CpG sites and CHD status. CpG sites were retained if the point bi-serial correlation was at least 0.1. A total of 138,815 CpG sites remained. Subsequently, Pearson correlation between those 138,815 sites was calculated. If the Pearson correlation between two loci was at least 0.8, the loci with a smaller point bi-serial correlation was discarded. In the end, 107,799 DNA methylation loci (~23%) remained for model training.

Class Imbalance. Among the 1545 individuals in the training dataset, only 173 were diagnosed with symptomatic CHD. Therefore, the ratio of those with to those without symptomatic CHD is approximately 1:8 (173:1372). This means that if data from all 1545 individuals were to be utilized simultaneously, the baseline prediction accuracy where if all individuals are classified as not having CHD (majority class) will be ~89% (1372/1545). This depicts the major class imbalance in this dataset, which is quite common in medical datasets. It also suggests that accuracy would not be the ideal performance metric. To deal with class imbalance, under-sampling of those without CHD was performed.³⁸ The 1372 individuals without CHD were randomly assigned to eight datasets: 4 with 171 individuals and 4 with 172 individuals, totaling to 1372 individuals. All eight datasets also consisted of the same 173 individuals with CHD, which now balances the classes in each of the eight datasets to a 1:1 ratio (i.e. a 50% baseline accuracy).

Similarly, among the 669 test set individuals, only 71 were diagnosed with CHD, depicting class imbalance. Therefore, 71 individuals without CHD were randomly chosen to ensure the ratio between cases and controls was 1:1.

Model Training and Testing. Using a stratified 10-fold cross-validation approach, Random Forest (RF)³⁹ classification models were built independently using *scikit-learn* in Python⁴⁰ on all eight datasets consisting of genetic, epigenetic and phenotype data. SNPs with smaller chi-squared p-value and methylation sites with a larger correlation with respect to CHD were fed systematically to the model. Feature importance, accuracy and AUC of RF classifiers were used to select important variables for prediction. A grid search was employed to perform 10-fold cross-validation hyper-parameter tuning of the models. The performance metrics of the models were determined. The final model was saved for testing on the test dataset.

To compare the performance of our integrated genetic-epigenetic model to a model with conventional CHD risk factors as predictors, a similar approach was employed to build the model on the training data and subsequently test it on the test dataset.

An alternative approach was implemented in R using the RandomForestTM package. The “*strata*” and “*sampsize*” arguments were used to perform stratified sampling of the

minority class. This is a simpler implementation of the undersampling approach described above. The number of trees (ntree) parameter of this alternative RF classifier was tuned. The same n=1545 training set and n=142 testing set were used to train and test this classifier.

RESULTS

The clinical characteristics of the 1545 subjects used in the primary analyses in this study are given in Table 4. There were more females (n=851) than males (n=694) and they were all of Northern European ancestry. A total of 115 males (~17%) and 58 females (~7%) were diagnosed with symptomatic CHD. Those with symptomatic CHD on average tended to be older, in their early 70s, as opposed to those without symptomatic CHD who tended to be in their mid-60s.

Table 4. Demographic and CHD risk factors of 1545 individuals

	CHD	No CHD
Gender (count)		
Male	115	579
Female	58	793
Age (years)		
Male	71.1±7.4	66.4±8.5
Female	73.0±8.7	66.4±8.6
Total Cholesterol (mg/dL)		
Male	154±33	176±33
Female	172±35	199±36
HDL Cholesterol (mg/dL)		
Male	45±12	50±14
Female	59±17	65±19
HbA1c (%)		
Male	6.0±0.9	5.7±0.8
Female	6.0±0.9	5.7±0.5
SBP (mmHg)		
Male	128±19	130±17
Female	135±18	129±18
cg05575921 (z-score)		
Male	-0.15±1.19	-0.07±1.05
Female	-0.12±1.11	0.08±0.92
Smoker (count)		

Male	12 (10%)	39 (7%)
Female	2 (3%)	64 (8%)

SBP: systolic blood pressure
HbA1c: Hemoglobin A1c

The average HDL and total cholesterol levels were higher among females and those without symptomatic CHD. All total cholesterol averages were <200mg/dL, but only females without symptomatic CHD had an HDL cholesterol level >60mg/dL. More importantly, the ratio between the averages of HDL and total cholesterol were 1:3.4 and 1:3.5 for males with and without symptomatic CHD, respectively, and, 1:2.9 and 1:3.1 for females with and without symptomatic CHD, respectively. The target ratio between total and HDL cholesterol for cardiovascular disease prevention for men is <4.5 and <4.0 for women.⁴¹

Those diagnosed with symptomatic CHD had a higher HbA1c level (6%), on average, than those not diagnosed with symptomatic CHD (5.7%). However, while females with CHD had higher SBP than those without, the opposite was true for males. All SBP averages were larger than 120 mmHg.

Another well-known risk factor for CHD is smoking. Based on self-reported current smoking status, among the men, but not the women, proportionately there were more smokers with symptomatic CHD than without symptomatic CHD. However, methylation status at the smoking biomarker (cg05575921) indicates that both men and women with symptomatic CHD actually smoke more often than those without symptomatic CHD.

Regression Analyses. As a first step of the analyses, the CHD status of the 1545 subjects was regressed against age, gender, cg05575921, SBP, HDL cholesterol, total cholesterol, and percent HbA1c. The summary of the regression outputs with respect to each risk factor is shown in Table 5. The analyses suggest that all conventional risk factors except SBP and HDL cholesterol are significantly associated with CHD status at a 0.05 significance level. More importantly, the trend of slopes suggest that symptomatic CHD is more prevalent in 1) males, 2) older individuals, 3) those with lower total cholesterol, 4) those de-methylated at cg05575921 (i.e. more smoking), and 5) those with higher HbA1c levels.

Table 5. Regression parameters of risk factors of CHD against symptomatic CHD

Risk Factor	Beta	Standard Error	t-statistic	p-value
Gender	-0.0506	0.0173	-2.933	3.41e-03
Age	0.0063	0.0009	6.670	3.57e-11
SBP	-0.0006	0.0005	-1.376	1.69e-01
HDL Cholesterol	-0.0004	0.0005	-0.890	3.73e-01
Total Cholesterol	-0.0014	0.0002	-5.889	4.75e-09
cg05575921	-0.0149	0.0077	-1.932	5.36e-02

HbA1c	0.0465	0.0116	4.003	6.56e-05
SBP: systolic blood pressure				
HbA1c: Hemoglobin A1c				

As the next step, we conducted regression analyses of the relationship of symptomatic CHD to genome wide DNA methylation. After Bonferroni correction, 11,497 methylation sites (2.4%) remained significantly associated with symptomatic CHD. These methylation sites mapped to 6,319 genes. The top 30 sites are shown in Table 6. All significant sites are provided in **Figure 16**.

Table 6. Top 30 significant CpG sites associated with symptomatic CHD

CpG	Beta	Gene	Position	Island Status	Corrected p-value*
cg26910465	6.48E-01	ADAL	TSS200	Island	8.01E-18
cg13567813	6.60E-01	NR1H2	TSS200	Island	2.05E-17
cg09238957	5.98E-01	ORC6L	TSS200	Island	7.97E-17
cg04099813	6.12E-01	TSSC4	TSS1500	S_Shore	1.45E-16
cg07546106	6.29E-01	TAP2	5'UTR	N_Shore	2.40E-16
cg20808462	6.01E-01	HAUS3	5'UTR	Island	5.42E-16
cg16968115	5.92E-01	WDTC1	TSS200	Island	1.25E-15
cg24475210	5.84E-01	MRFAP1	TSS200	Island	1.26E-15
cg03031660	5.84E-01	MRPS7	1stExon	Island	1.45E-15
cg22605179	5.97E-01	EWSR1	5'UTR	Island	3.81E-15
cg02357877	5.71E-01	GBAS	TSS1500	Island	4.04E-15
cg22111723	5.65E-01			Island	4.57E-15
cg06117184	5.67E-01	CKAP2L	1stExon	Island	4.87E-15
cg07478100	5.85E-01	MIS12	TSS1500	Island	5.36E-15
cg15318396	5.83E-01			Island	5.52E-15
cg00544901	5.76E-01	RPS11	TSS1500	Island	5.62E-15
cg24478630	5.88E-01	MOGS	TSS200	S_Shore	5.65E-15
cg04022019	5.90E-01	DCAF13	1stExon	Island	5.86E-15
cg12124516	5.81E-01	MCM6	TSS200	Island	6.41E-15
cg20935862	5.96E-01	C9orf41	TSS1500	Island	6.62E-15
cg07377675	6.00E-01	USP1	TSS200	Island	7.79E-15
cg07734253	5.83E-01	CORO1A	TSS1500	N_Shore	8.16E-15
cg03699307	5.94E-01	GABARAPL2	TSS1500	Island	8.44E-15
cg17360140	5.79E-01	C4orf29	TSS1500	Island	9.10E-15
cg25632648	6.06E-01	KCTD21	TSS200	Island	9.83E-15
cg06339248	5.83E-01	ZDHHC5	5'UTR	Island	1.10E-14
cg24275354	6.24E-01	NDUFA10	Body	N_Shore	1.52E-14
cg25261764	5.93E-01	NARS	1stExon	Island	1.69E-14
cg14172283	5.83E-01	TOMM5	1stExon	Island	2.00E-14
cg01089095	5.69E-01	CHCHD1	TSS200	Island	2.02E-14

* All nominal p-values were adjusted for multiple comparisons by the Bonferroni method.

Due to the large number of genes, network and functional enrichment analyses of the network were performed using data from the top 1000 genes. The network consisted of 952 proteins represented by the nodes and 1,144 interactions represented by the edges. The expected number of edges was 634 with a PPI enrichment p-value of 0, suggesting that interactions between the proteins in the network are likely to have biological relevance. The average node degree and clustering coefficient were 2.4 and 0.85, respectively. This network is depicted in **Figure 3**. The top 10 pathways of this network are shown in Table 7.

Table 7. Top 10 significant PPI network pathways associated with symptomatic CHD

GO Pathway ID	Pathway Description	Observed Gene Count	False Discovery Rate
GO.0044260	cellular macromolecule metabolic process	414	4.53E-18
GO.0043170	macromolecule metabolic process	435	6.54E-17
GO.0044237	cellular metabolic process	476	5.41E-16
GO.0006807	nitrogen compound metabolic process	351	8.54E-16
GO.0034641	cellular nitrogen compound metabolic process	335	8.54E-16
GO.0010467	gene expression	275	5.07E-15
GO.0044238	primary metabolic process	474	1.64E-14
GO.0090304	nucleic acid metabolic process	273	1.64E-14
GO.0008152	metabolic process	516	2.97E-14
GO.0071704	organic substance metabolic process	481	3.55E-14

PPI: protein-protein interaction

From the regression analyses, there were 44,108 (9.3%), 0, 32, 51 and 6 methylation sites significantly associated with cg05575921, SBP, HDL cholesterol, total cholesterol and HbA1c, respectively. The top results for cg05575921, HDL, total cholesterol and HbA1c analyses are given in Table 8 through Table 11.

Table 8. Top 30 significant CpG sites associated with cg05575921 after Bonferroni correction

CpG	Beta	Gene	Position	Island Status	Corrected p-value*
cg21566642	7.10E-01			Island	2.74E-227
cg03636183	7.01E-01	F2RL3	Body	N_Shore	1.01E-223
cg05951221	6.91E-01			Island	1.34E-208
cg01940273	6.68E-01			Island	1.18E-196
cg25648203	5.57E-01	AHRR	Body		2.08E-119
cg21161138	5.37E-01	AHRR	Body		7.19E-113
cg06126421	5.05E-01				6.74E-108

cg09935388	5.02E-01	GFI1	Body	Island	2.91E-94
cg06644428	4.85E-01			Island	7.76E-85
cg15342087	4.73E-01				1.44E-81
cg03329539	4.61E-01			N_Shore	2.30E-76
cg23079012	4.62E-01				2.47E-76
cg11660018	4.42E-01	PRSS23	TSS1500	N_Shore	1.15E-74
cg23916896	4.31E-01	AHRR	Body	N_Shore	3.99E-65
cg12876356	4.34E-01	GFI1	Body	Island	4.30E-65
cg05284742	4.27E-01	ITPK1	Body		2.41E-64
cg19859270	4.29E-01	GPR15	1stExon		7.30E-64
cg14817490	4.24E-01	AHRR	Body		7.27E-62
cg26361535	4.22E-01	ZC3H3	Body		1.18E-61
cg03991871	4.19E-01	AHRR	Body	N_Shore	1.19E-60
cg26703534	4.15E-01	AHRR	Body	S_Shelf	5.17E-60
cg24859433	3.95E-01				1.24E-58
cg12806681	4.08E-01	AHRR	Body	N_Shore	1.53E-56
cg23771366	4.01E-01	PRSS23	TSS1500	N_Shore	2.12E-56
cg18146737	3.99E-01	GFI1	Body	Island	2.59E-53
cg13193840	3.93E-01			Island	1.03E-52
cg27241845	3.73E-01			N_Shore	9.87E-52
cg21322436	3.76E-01	CNTNAP2	TSS1500	N_Shore	2.94E-51
cg25189904	3.89E-01	GNG12	TSS1500	S_Shore	1.23E-50
cg04517079	3.83E-01	FOXP4	Body		5.18E-50

* All nominal p-values were adjusted for multiple comparisons by the Bonferroni method.

Table 9. All 32 significant CpG sites associated with HDL cholesterol after Bonferroni correction

CpG	Beta	Gene	Position	Island Status	Corrected p-value*
cg06500161	-1.38E-02	ABCG1	Body	S_Shore	1.63E-14
cg17901584	1.33E-02	DHCR24	TSS1500	S_Shore	3.39E-13
cg06560379	1.30E-02	NFKBIE	Body	N_Shore	2.36E-12
cg12394289	8.78E-03	EHMT2	Body	N_Shore	1.84E-04
ch.14.1488981R	8.94E-03	RIN3	Body		1.93E-04
cg02076355	9.36E-03	C10orf10	TSS200		2.39E-04
cg03717755	-9.16E-03	MYLIP	Body		4.34E-04
cg10375409	-8.79E-03	CD247	Body	N_Shelf	2.00E-03
cg21669326	8.76E-03				2.06E-03
cg21139312	-7.73E-03	MSI2	Body		2.36E-03
cg11666534	8.60E-03	IGLL1	TSS200		3.10E-03
cg00144180	-7.52E-03	HDAC4	5'UTR		3.87E-03
cg03078551	8.75E-03				4.19E-03
cg15878619	8.45E-03	TUBB	TSS1500	N_Shore	4.48E-03
cg25757877	-8.58E-03	UBE2O	Body		4.96E-03
cg21205288	-8.33E-03				5.04E-03
cg04557677	8.03E-03	JAK3	TSS1500	S_Shore	5.20E-03
cg26313301	-8.68E-03	LDLR	Body	S_Shelf	7.79E-03
cg03290131	8.22E-03	DUSP5	Body		8.43E-03

cg15989436	8.21E-03				8.75E-03
ch.2.207814544R	7.97E-03				1.12E-02
cg08105590	8.28E-03	FAM38A	Body	N_Shore	1.21E-02
cg18407309	7.88E-03	CCL3	TSS200		1.52E-02
ch.2.11889418R	7.80E-03				1.99E-02
cg06007201	7.88E-03	FAM38A	Body	Island	2.06E-02
cg00218409	8.13E-03				2.37E-02
cg13134297	8.08E-03				2.86E-02
cg04605590	7.69E-03				2.97E-02
cg03068497	8.02E-03	GARS	Body	S_Shore	3.24E-02
cg21812670	8.15E-03	SNORD45C	TSS1500		3.53E-02
ch.1.171672612F	7.65E-03				3.55E-02
cg00004667	7.95E-03	ZBTB17	5'UTR		4.11E-02

* All nominal p-values were adjusted for multiple comparisons by the Bonferroni method.

Table 10. Top 30 significant CpG sites associated with total cholesterol after Bonferroni correction

CpG	Beta	Gene	Position	Island Status	Corrected p-value*
cg17901584	6.14E-03	DHCR24	TSS1500	S_Shore	6.96E-12
cg11840035	-4.70E-03				1.01E-05
cg15989436	4.29E-03				3.71E-04
cg15428620	4.16E-03	SFXN3	Body	S_Shore	8.57E-04
cg16460860	4.31E-03			S_Shore	9.63E-04
cg24405567	4.18E-03				1.06E-03
cg27407935	4.22E-03	SREBF1	Body	N_Shelf	1.89E-03
cg25536676	4.14E-03	DHCR24	TSS1500	Island	2.30E-03
cg02560388	4.22E-03				2.38E-03
cg01400685	4.08E-03	FADS2	Body	S_Shore	2.91E-03
cg05932360	4.13E-03	JARID2	Body		2.98E-03
cg04804052	4.14E-03	SMARCA4	TSS200	N_Shelf	3.15E-03
cg01234420	3.80E-03	LOC150381	Body	N_Shelf	4.03E-03
cg22011731	3.95E-03	SQLE	1stExon	S_Shore	4.27E-03
cg21593001	4.05E-03	DTX1	Body	Island	4.49E-03
cg14208102	3.88E-03	TREX1	TSS200		5.22E-03
cg08690876	4.14E-03	CYB5R3	5'UTR		5.33E-03
cg25114611	4.05E-03	FKBP5	TSS1500	S_Shore	6.72E-03
cg03113867	3.91E-03				7.17E-03
cg20519581	4.00E-03			N_Shore	8.11E-03
cg11071448	3.98E-03	SYT2	5'UTR		9.33E-03
cg14254720	3.99E-03	LRRC8C	TSS1500	N_Shore	1.07E-02
cg21645268	3.96E-03	FDFT1	Body	N_Shelf	1.12E-02
cg21443274	-4.10E-03	ZFPM2	Body		1.18E-02
cg03440556	4.04E-03	SCD	Body	S_Shore	1.40E-02
cg09682727	3.67E-03				1.69E-02
cg21108085	3.92E-03	CD82	5'UTR	S_Shelf	1.73E-02
cg22164009	3.89E-03				1.77E-02
cg03611151	3.72E-03	CNR2	5'UTR	S_Shore	1.93E-02
cg19696333	-3.06E-03	IKZF5	5'UTR	Island	2.27E-02

* All nominal p-values were adjusted for multiple comparisons by the Bonferroni method.

Table 11. All 6 significant CpG sites associated with HbA1c after Bonferroni correction

CpG	Beta	Gene	Position	Island Status	Corrected p-value*
cg19693031	-3.63E-01	TXNIP	3'UTR		1.84E-17
cg17901584	-2.67E-01	DHCR24	TSS1500	S_Shore	2.65E-07
cg06500161	2.31E-01	ABCG1	Body	S_Shore	2.21E-04
cg02420024	-2.31E-01	OCA2	Body		3.08E-04
cg04143120	-2.20E-01				2.39E-03
cg04311230	2.05E-01	SOD2	TSS1500	Island	2.08E-02

* All nominal p-values were adjusted for multiple comparisons by the Bonferroni method.

To understand the mapping of significant symptomatic CHD DNA methylation sites to that of its risk factors, **Figures 4 and 5** were generated. The Venn diagram in **Figure 4** shows the overlap in methylation probes between symptomatic CHD and its risk factors, while **Figure 5** depicts overlapping genes mapping to at least one of the probes. As shown in **Figure 5**, the top three intersections in DNA methylation associated genes are between symptomatic CHD and smoking (5229), smoking and total cholesterol (15), and symptomatic CHD, smoking and total cholesterol (13). One gene, DHCR24, was significantly associated with symptomatic CHD and all risk factors.

Integrated Genetic-Epigenetic Random Forest Analyses. Eight RF models were built on the eight datasets consisting of genetic, epigenetic, age and gender data from the 1545 subjects in the training dataset. Standard scikit-learn RF parameters were used to determine the important SNPs and DNA methylation loci. Based on the average accuracy and AUC of the eight classifiers and the Gini index of each variable, four CpG sites (cg26910465, cg11355601, cg16410464 and cg12091641), two SNPs (rs6418712 and rs10275666), age and gender were retained for prediction. Using the tuned parameters (maximum features, minimum samples for each split, information gain criterion, maximum tree depth, number of trees), all eight models were re-fitted to the training dataset. The performance metrics of these stratified 10-fold cross-validated models are shown in Table 12. As depicted in this table, the accuracy ranges from 70-80% between these eight models, which is between a 20-30% increase from the 50% accuracy baseline. More importantly, the sensitivity of the model ranged from 70-82%, while the specificity ranged from 70-79%. The ROC AUC of the eight models ranged from 0.77-0.87. The 10-fold ROC AUC of the best performing model (model 7) is shown in **Figure 6**. All eight models were saved for testing on the test dataset.

Table 12. 10-fold cross-validation performance metrics of the eight integrated genetic-epigenetic models

Model	Accuracy	AUC	Sensitivity	Specificity
1	0.78±0.09	0.82±0.09	0.79±0.12	0.77±0.08
2	0.75±0.05	0.83±0.06	0.78±0.10	0.72±0.08
3	0.79±0.05	0.85±0.07	0.83±0.07	0.76±0.08
4	0.78±0.07	0.84±0.07	0.79±0.12	0.76±0.07
5	0.75±0.06	0.78±0.06	0.70±0.09	0.79±0.09
6	0.70±0.05	0.77±0.05	0.70±0.12	0.70±0.10
7	0.80±0.06	0.87±0.04	0.82±0.08	0.77±0.07
8	0.78±0.06	0.85±0.05	0.82±0.07	0.74±0.08

The demographics and CHD risk factors of the individuals in the testing dataset are summarized in Table 13. Of the 54 females and 88 males, 22 females (~41%) and 49 males (~56%) were diagnosed with symptomatic CHD. Those with symptomatic CHD on average tended to be older, males in their late 60s and females in their early 70s. Males and females without symptomatic CHD were on average in their late 50s and mid-60s, respectively.

Unlike males, the average ages of females with and without symptomatic CHD were comparable between the training and test datasets.

Table 13. Demographics and CHD risk factors of 142 individuals in the test dataset

	CHD	No CHD
Gender (count)		
Male	49	39
Female	22	32
Age (years)		
Male	67.5±8.4	59.6±9.2
Female	72.5±9.0	64.6±10.8
Total Cholesterol (mg/dL)		
Male	141±25	191±32
Female	180±41	187±35
HDL Cholesterol (mg/dL)		
Male	46±11	51±15
Female	62±18	61±18
HbA1c (%)		
Male	5.9±0.9	5.9±1.4
Female	6.3±1.0	6.0±1.0
SBP (mmHg)		
Male	124±19	127±17
Female	136±17	129±15
cg05575921 (z-score)		
Male	-0.46±1.43	-0.26±1.12
Female	0.10±1.12	-0.13±0.93
Smoker (count)		
Male	6	7

Female	1	4
SBP: systolic blood pressure		
HbA1c: Hemoglobin A1c		

All total cholesterol averages were <200mg/dL and only females had average HDL cholesterol levels >60mg/dL. The ratio between the averages of HDL and total cholesterol were 1:3.1 and 1:3.7 for males with and without symptomatic CHD, respectively, and, 1:2.9 and 1:3.1 for females with and without symptomatic CHD, respectively. Again, the ratios were more comparable between both datasets for females than males. However, the ratios were all lower than the target ratio between total and HDL cholesterol for cardiovascular disease prevention, which are <4.5 for men and <4.0 for women.⁴¹

In the test dataset, females tended to have higher HbA1c percentages than males. In addition, females with symptomatic CHD had an average HbA1c >6%. Females also had higher SBP than males. All SBP averages were >120 mmHg. Based on self-reported current smoking status, similar to the training dataset, there were more smokers without symptomatic CHD than with symptomatic CHD. However, when the smoking biomarker, cg05575921, is considered, males tended to be more demethylated than females.

An ensemble of the eight models was used to perform CHD classification in the test dataset. An individual was classified as having CHD if at least four of the eight models voted in favor of CHD. Of the 142 individuals (71 with and 71 without symptomatic CHD) in the test dataset, the CHD status of 110 individuals was predicted correctly, resulting in an accuracy of 77.5%. The confusion matrix of the prediction is shown in Table 14. The test set sensitivity and specificity of the ensemble was 0.75 and 0.80, respectively.

Table 14. Confusion matrix of the integrated genetic-epigenetic ensemble on the test dataset

TRUE	Predicted	
	CHD absent	CHD present
CHD absent	57	14
CHD present	18	53

Conventional CHD Risk Factor Model. To compare the performance of our integrated genetic-epigenetic model to the performance of conventional CHD risk factors in predicting CHD status, another eight RF models were built using age, gender, SBP, HbA1c, total cholesterol, self-reported smoking and HDL cholesterol as predictors. Again, using tuned parameters, the eight RF models were built on the training dataset and tested on the test dataset. The performance metrics of the eight models are summarized in Table 15.

Accuracies of these models on their respective training datasets ranged from 70-76%, while the sensitivity and specificity ranges were 67-74% and 72-79%, respectively. The range of the ROC AUC was 0.72-0.79. While the accuracy and specificity is quite comparable with the integrated genetic-epigenetic models, the conventional risk factors models underperformed with respect to sensitivity and ROC AUC. The 10-fold ROC AUC of the best performing model (model 7) among the eight models is shown in Figure 7. When the ensemble of the eight models was tested on the test dataset, the test accuracy was 64.8%, which is approximately 13% less than that of our integrated genetic-epigenetic ensemble. However, the more important metric is the sensitivity since it shows the degree to which a person with CHD is classified correctly. The sensitivity on the test dataset was only 41%, which is 24% less than that of our integrated genetic-epigenetic ensemble. However, the specificity of the conventional risk factor ensemble was 0.89. The confusion matrix is shown in Table 16.

Table 15. 10-fold cross-validation performance metrics of the eight conventional risk factors models

Model	Accuracy	AUC	Sensitivity	Specificity
1	0.73±0.03	0.77±0.05	0.71±0.07	0.75±0.10
2	0.73±0.07	0.75±0.08	0.74±0.08	0.72±0.09
3	0.75±0.07	0.79±0.06	0.73±0.12	0.77±0.10
4	0.70±0.06	0.75±0.08	0.68±0.10	0.72±0.07
5	0.70±0.06	0.72±0.08	0.67±0.09	0.73±0.10
6	0.71±0.10	0.75±0.10	0.68±0.14	0.75±0.10
7	0.76±0.04	0.79±0.05	0.73±0.11	0.79±0.09
8	0.71±0.10	0.76±0.12	0.68±0.15	0.75±0.11

Table 16. Confusion matrix of the conventional risk factor ensemble on the test dataset

TRUE	Predicted	
	CHD absent	CHD present
CHD absent	63	8
CHD present	42	29

Alternative Random Forest Model. To determine if our ensemble approach consisting of eight models performs better than a single RF model, as described in the methods, one RF model that includes stratified sampling based on the minority class was built in R. The model again included the same four CpGs, two SNPs, age and gender. The classifier was tuned and the classifier with the largest sensitivity was chosen (ntree=500). The training accuracy, AUC, sensitivity and specificity of this model were 82%, 0.83, 0.68 and 0.83, respectively.

While the accuracy, AUC and specificity of this model is comparable to our ensemble model, clearly, the ensemble model provides better sensitivity. When tested on the test set, the single RF model performed with an accuracy, sensitivity and specificity of 76%, 0.66 and 0.86, respectively, demonstrating the increased sensitivity but not specificity provided by the ensemble approach. The comparison between this alternative approach and the ensemble approach is being done on the basis of sensitivity rather than specificity is because, given the application of the classifier in predicting CHD, it is rather important to maximize true positives than true negatives. In other words, the negative impact of having a false negative is much higher than a false positive. However, one of the reasons the sensitivity of the ensemble (ntree=170,000) may not be directly comparable to that of this single RF classifier (ntree=500) is the effective number of trees in the ensemble being much larger than this classifier. Nevertheless, a comparison can be made between one classifier within the ensemble with 20,000 trees and the alternative RF classifier with the same number of trees. The average accuracy, AUC, sensitivity and specificity of the classifier from the ensemble with 20,000 trees were 80%, 0.87, 0.82 and 0.77, respectively. Similarly, the accuracy, AUC, sensitivity and specificity of the alternative RF classifier with 20,000 trees were 82%, 0.83, 0.67 and 0.83. Similar to the prior comparison, the ensemble model performs better with respect to sensitivity than specificity.

While age and gender were included because they are the two non-modifiable risk factors of CHD, we re-fitted the single RF model without age and gender to demonstrate that the performance is not driven solely by these two factors. Without age and gender in the model, the training accuracy, AUC, sensitivity and specificity were 81%, 0.80, 0.65 and 0.83, respectively. On the test dataset, this model performed with an accuracy, sensitivity and specificity of 78%, 0.68 and 0.89, respectively. Therefore, age and gender are not single handedly responsible for the performance of the integrated genetic-epigenetic model. Using conventional risk factors from the training dataset, this alternative RF model performed with an accuracy, AUC, sensitivity and specificity of 77%, 0.77, 0.60 and 0.79, respectively. On the test dataset, it performed with an accuracy, sensitivity and specificity of 69%, 0.61 and 0.77, respectively.

This genetic-epigenetic model was also used to show that the use of a RF model provides an added advantage in capturing possible GxM and MxM interactions, as depicted by the partial dependence plots in Figure 8. Finally, permutation of DNA methylation sites and genotypes was performed to compare the performance of a model consisting of four randomly chosen CpG sites and two randomly chosen SNPs using the training dataset to our integrated model and the conventional risk factor model. A two-dimensional histogram of

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sensitivities and specificities of 10,000 permutations are shown in Figure 9. The largest sensitivity and specificity among these permutations were 0.62 and 0.87, respectively. The training sensitivity and specificity of the single conventional risk factors model of 0.60 and 0.79, respectively, falls well within the sensitivity and specificity of the permutations. The training sensitivity and specificity of the single integrated genetic-epigenetic model of 0.68 and 0.83, respectively, suggests that sensitivity but not the specificity falls outside the permuted values.

DISCUSSION

A better understanding of the relationship of epigenetic changes to the pathogenesis of cardiovascular diseases is essential for the development of improved diagnostics and therapeutics. To the best of our knowledge, we are the first group to examine the relationship between DNA methylation as quantified using the Illumina 450k array and CHD. Therefore, there are limited comparisons that can be made with our results. Nevertheless, our analyses demonstrate that epigenetic signatures with respect to CHD substantially overlap with that of cumulative smoking. This is consistent with the strong well-established relationship between smoking and risk for CHD, where approximately 30% of CHD related deaths in the US each year is attributed to cigarette smoking.^{42, 43} This is not point made lightly. Smoking cessation may be one of the most beneficial, yet underutilized, general interventions in clinical medicine and has also been shown to substantially reduce mortality risk among those with CHD.^{44, 45}

Interesting but not surprisingly, the DNA methylation analysis of all other risk factors described in our study show the wide spread effects of smoking in the remodeling of the epigenome. Prior investigations of the relationship between atherosclerosis and lipid levels, diabetes or hypertension have demonstrated the effect of smoking on these clinical measures.⁴⁶⁻⁴⁸ Our analyses not only identified HDL cholesterol, total cholesterol and HbA1c associated changes in DNA methylation, but also delineated specific loci whose epigenetic signature is modified by smoking and associated with increased risk for CHD. Pending confirmation of the findings by others, the increased precision afforded by extension of the findings in subjects from a diverse set of ethnicities may aid in identifying specific therapeutic interventions for CHD at the individual level.

An additional application for methylation signatures of CHD and its risk factors is as an alternative approach to assess risk for CHD. This idea is particularly attractive given the challenges and limitations in using conventional risk factors to predict the risk for CHD. For instance, most studies use self-reported smoking status, which others and we have shown to be unreliable in more clinical/high risk populations.⁴⁹⁻⁵² These prior findings are especially

relevant given the inconsistency between self-report and cg05575921 methylation in the Offspring cohort used in this study. Another test that is routinely conducted to assess risk for CHD is the fasting serum lipid panel, which assesses total cholesterol, HDL cholesterol, LDL cholesterol and triglyceride levels. While studies have shown that the ratio between total cholesterol and HDL cholesterol are especially predictive of risk for CHD^{53, 54}, others have also shown that information from additional markers such as C-reactive protein is needed to enhance the predictability.⁵⁵ Since these DNA methylation measures are more summative and less influenced by day to day fluctuations in diet, it is possible that they could more exactly constrain the relative contribution each of these metabolic/transcriptional pathways to CHD pathogenesis.

Over the years, the identification of conventional CHD risk factors has led to the development of a number of multivariate risk models. The Framingham Heart Study was a pioneer in this effort developing the Framingham Risk Score for CHD.⁵⁶ This algorithm uses the conventional risk factors (age, gender, total or LDL cholesterol, SBP, diabetes and current smoking) and was developed using the FHS cohort consisting of individuals of European ancestry. Therefore, as expected, this model performed well for white men and women, but hardly generalized to all other ethnic groups. Specifically, in a study that validated this algorithm in an ethnically diverse cohort, the prediction model held for black men and women, but overestimated risk of Japanese Americans, Hispanic men and Native American women.⁵⁷ Hence, there is a need for algorithms that can be used for all members of our society.

One plausible reason for the lack in generalizability is the possible confounding effects of genetic variation. The concept of the potential for genetic confounding of epigenetic signal is widely accepted.⁵⁸ Therefore, the goal of our study was to integrate genetic and epigenetic data to develop a classifier to predict CHD as an alternative to existing algorithms currently available. This approach that mines predictive signal from large and complex genetic and epigenetic datasets is made possible by the advancements in high performance computing systems. Computational techniques such as machine learning have been successfully employed in the fields of genomics and epigenomics.^{59, 60} While logistic regression is the commonly used method for developing binary classification models in medical applications and have been used to analyze microarray data⁶¹, it lacks the ability to capture implicit complex nonlinear relationships. Hence, algorithms capable of detecting complex relationships such as interactions between genetic variation and DNA methylation have an added advantage. In our study, the use of a Random Forest ensemble allowed for a highly accurate, sensitive and specific classification of individuals with CHD. However,

since some genetic risk variants co-sort with ethnic background and may not map to pathways associated with conventional risk factors, it will be necessary to build, test and extend these Random Forest approaches using subjects from all ethnic groups to develop the most generalizable prediction tools.⁶²

While a similar integrated genetic and epigenetic study is not available for comparison, our integrated model clearly outperforms the classifier that uses the Framingham score risk factors. The conventional risk factors model demonstrates the limited predictive value of these risk factors as indicated by a number of studies.⁶³⁻⁶⁵ Moreover, in a study consisting of over 2000 older black and white adults, the Framingham risk score was only capable of distinguishing those who experienced a CHD event versus those who did not after an eight year follow-up at a C-index of 0.577 and 0.583 in women and men, respectively.⁶⁶ The conventional risk factors may not perform as well due to hourly variations of factors such as serum cholesterol level and the use of a single blood pressure measurement instead of an average recorded throughout the day.^{67, 68}

As demonstrated in this manuscript, there are several approaches to building classifiers. In comparing the two methods delineated in this manuscript, the ensemble model performed better than the single RF model with respect to sensitivity and vice versa for specificity. Our reason to favor a model with higher sensitivity is simple. For the classification of diseases such as CHD, a false positive would require further testing but a false negative result could be more detrimental to the patient. However, a test with high sensitivity and specificity is ideal. To achieve that, a larger sample consisting of diverse ethnic groups encompassing both genders is required. Also, while we used the RF algorithm, there are many other algorithms such as Support Vector Machines that can be used as the algorithm underlying a classifier. Nevertheless, our RF model clearly shows non-linearity between methylation sites and SNPs as depicted in the partial dependence plots. Yet, we would like to clarify that the combination of methylation sites and SNPs in our ensemble is only one of many possible combinations that are highly predictive. Based on the permutation results, we demonstrate that the variable reduction step undertaken to enrich for highly predictive methylation and SNP probes provide an edge with respect to sensitivity. However, as the pool of diverse samples increases, a highly predictive yet generalizable classifier will be required.

Our analyses did not take into account the possible effects of medications. This is notable because the current armamentarium of cholesterol lowering agents can have a dramatic effect on the levels of certain risk factors, such as serum cholesterol, that are associated with risk for CHD. Indeed, the presence of these medications may be the reason

why the serum cholesterol level is actually lower in those in the training set who have CHD than in those in the training set without CHD. Unfortunately, it is very difficult to incorporate these types of data into the current analytical approach for a number of reasons. In addition, even if the subjects self-report of prescriptions were accurate, critical information needed to account for their effects, such as medication compliance and the treatment history length are not available. However, in the future, having data such as “pill count” and serum drug level information will be critical if we are to fully understand the effect of medical interventions on epigenetic signatures.

In addition, there are several other limitations in our study. First, our study includes only individuals of European ancestry. However, the incorporation of genetic variation in our model allows for the generalizability between ethnic groups. Nevertheless, additional studies are required to demonstrate this. Second, while our approach predicts symptomatic CHD, the goal is to use this study as a proof of concept towards building a multivariate model capable of forecasting risk for an initial CHD event and subsequently the risk of CHD event recurrence. Further exploration in prospectively biosampled cohorts will be necessary to achieve that goal. Yet, it is important to note that this integrated genetic-epigenetic approach has its advantages. The use of conventional risk factors in calculating risk requires cumbersome testing procedures, the collection of considerable amounts of blood and multiple lab tests. Conceivably, the need for these often cumbersome tests and procedures will be greatly reduced by using a single genetic-epigenetic assay procedure that uses a microgram or less of DNA. More importantly, the pathways associated with specific epigenetic loci with high predictive value could be very useful in guiding therapeutic interventions, management of risk factors and monitoring efficacy of treatments and lifestyle modifications.

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EXAMPLE 5**METHYLATION AND GXMETHYLATION EFFECTS IN PREDICTING CARDIOVASCULAR
DISEASE: STROKE AND CONGESTIVE HEART FAILURE**

Methylation-based biomarkers are gaining increasing clinical traction for use in guiding diagnosis and therapy. Currently, Cologuard, an assay that quantifies DNA methylation in human DNA found in stool samples, is FDA approved for the detection of colon cancer (Lao and Grady 2011). In addition, Smoke Signature™, an DNA methylation assay that detects cigarettes consumption using DNA from blood (Philibert, Hollenbeck et al. 2016), is available for the research market and is being prepared for FDA submission. In attempts to identify CpG loci whose methylation status is predictive of cardiovascular disease, a number of investigators have used genome wide approaches combined with clinical diagnostics. In particular, Brenner and colleagues (Breitling, Salzmann et al. 2012) have identified F2RL3 residue cg03636183 as a biomarker for cardiovascular disease .

Unfortunately, these analyses have been shown to have been completely confounded by incomplete knowledge of smoking status and did not consider possible confounding genetic variance. In fact, when using biomarker approaches that fully account for the intensity of smoking, the coronary heart disease signal at cg03636183 disappears (Zhang, Schöttker et al. 2015). Furthermore, using a genome wide methylation and genetic analyses, combined with biomarker guided smoking assessments, we have recently analyzed data from a large cohort of subjects informative for cardiac disease. We have shown that independent of smoking intensity status, that the genetically contextual methylation status, as embodied by methylation-genotype interact effects actually contribute better to the prediction of coronary heart disease and that the use of an algorithm that combines local genetic variation and methylation markedly improves prediction of coronary heart disease (CVD, Dogan et al., in submission).

However, CVD is only one of three major forms of Cardiovascular Disease (CVD). Stroke and congestive heart failure (CHF) are also prominent forms of CVD. In these examples, we extend our previous work with CVD to show how a combination of genetic variation, as embodied by SNPs, and epigenetic markers, as embodied by the Illumina methylation probes predicts Stroke or CHF.

ABSTRACT

Congestive heart failure (CHF) and stroke are two of the three common types of cardiovascular disease (CVD). Both CHF and stroke affects a large numbers of Americans. While preventative measures such as avoiding smoking can be taken to reduce risk for stroke

and CHF, limited options are available for early detection of risk for these diseases. However, in recent years, the field of epigenetics has provided an alternative approach to understanding complex illnesses. Specifically, DNA methylation signatures may present the opportunity to develop robust clinical tests for CHF and stroke prior to their occurrence. The ability to utilize only DNA methylation and generalize it to a diverse group of individuals could be limited by the presence of confounding genetic effects. Therefore, we integrated genetic and epigenetic data from the Framingham Heart Study to uncover SNPs and DNA methylation sites that collectively increase the predictability of CHF and stroke. Our preliminary analyses suggest that, the incorporation of three DNA methylation sites and three SNPs is capable of classifying CHF status with an area under the curve (AUC) of the receiver operating characteristic (ROC) curve of 0.78 and 0.81 in main effects and interaction effects models, respectively. In assessing the parameters of these models, we show that both DNA methylation and SNP are highly predictive of CHF status when implemented concurrently. Similarly, the AUC of the ROC curve of stroke at 0.85 and 0.86 for the main effects and interaction effects models, respectively, demonstrates the importance of integrating genetic and epigenetic effects. While these models are not optimized and were developed with a relatively small CHF and stroke sample size, we are certain that the more optimized version of this algorithm that accounts for genetic and epigenetic effects developed using a larger cohort could markedly improve our prediction capabilities of the risk for CHF and stroke prior to its occurrence. We are also confident that the presence of genetic information in the algorithm would allow its generalization to different ethnic groups.

INTRODUCTION

Cardiovascular Disease (CVD) includes three distinct diagnostic entities; coronary heart disease (CVD), stroke and congestive heart failure (CHF). By itself, CVD is the leading cause of death in the United States while stroke ranks fourth as a cause of mortality (Centers for Disease Control and Prevention). Over the past fifty years, a number of medications and devices have been developed to treat CVD. Unfortunately, hundreds of thousands of Americans continue to die each year because the presence of CVD is not noted until a fatal thromboembolic or cardiac event. Conceivably, more effective screening procedures for CVD could lead to the prevention of some of these deaths. (Mozaffarian, Benjamin et al. 2016) But at the current time, the cumbersomeness of certain techniques, such as fasting lipid panels, and/ or the limited predictive ability of others such as electrocardiograms and C-reactive protein levels, limit the effectiveness of the current approaches in identifying CVD. (Buckley, Fu et al. 2009, Auer, Bauer et al. 2012, Mozaffarian, Benjamin et al. 2016)

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5 A number of investigators have proposed that genetic approaches could provide another potential avenue through which to prevent CVD related morbidity and mortality.(Paynter, Ridker et al. 2016) Using whole exome and genome sequencing techniques, a number of variants predisposing to CVD have been identified. The relative risk conferred by of many of these variants is often considerable and their presence is sometimes useful for guiding prevention and treatment.(Mega, Stitzel et al.) However, with isolated exceptions, the large effect size variants tend to be rare, often population specific and their presence is not pathognomonic of current disease.(Traylor, Farrall et al. 2012, Paynter, Ridker et al. 2016) Hence, at the current time, genetic approaches are not generally used for the assessment of the presence or absence of current CVD in general medical practice.

10 Alternatively, others have proposed that epigenetic techniques might be useful in assessing CVD.(Sharma, Kumar et al. 2008, Gluckman, Hanson et al. 2009, Breitling, Salzmann et al. 2012) Since replicated peripheral white blood cell DNA methylation signatures for the presence of type 2 diabetes, smoking and drinking have been developed,(Monick, Beach et al. 2012, Toperoff, Aran et al. 2012, Zeilinger, Kühnel et al. 15 2013, Philibert, Penaluna et al. 2014) this suggestion has strong face validity. Notably, using this approach, Brenner and colleagues have proposed that DNA methylation at cg03636183, a CpG residue found in *Coagulation factor II (thrombin) receptor-like 3* (F2RL3), predicts risk for cardiac disease.(Breitling, Salzmann et al. 2012, Zhang, Yang et al. 2014) Although this is 20 an extremely biologically plausible finding, their subsequent studies have demonstrated that the CVD related signal at cg03636183 completely co-segregates with smoking status as indicated by DNA methylation at cg05575921,(Zhang, Schöttker et al. 2015) a CpG residue found in the *aryl hydrocarbon receptor repressor (AHRR)* whose strong predictive power with respect to smoking status has been demonstrated in dozens of studies.(Andersen, Dogan 25 et al. 2015)

However, the failure of the initially intriguing cg03636183 findings to independently identify additional risk outside of that conferred by smoking alone does not mean that methylation approaches for assessing the presence of CVD or other forms of CVD are destined to fail. Instead, they suggest that successful approaches need to be more nuanced and 30 that reconsideration of our conceptualization of relationship of methylation status to CVD is in order. For example, the findings by Brenner's group strongly suggest that methylation algorithms for the prediction of current CVD should include an indicator of smoking status. Given the fact that smoking is the largest preventable risk factor for CVD (Center for Disease Control 2005), this is eminently logical. However, in addition, they may need to take into 35 consideration that the long-term effects of exposure to environmental risk factors such as

smoking or other cardiac risk factors such as hyperlipidemia may be obscured by gene-environment interactions.

The role of gene-environment interactions (GxE) effects in moderating vulnerability to illness is perhaps better appreciated in the behavioral sciences. The basic premise of GxE effects is that the influence of the environment during a developmentally sensitive period of time changes the biological properties of a system in a genetically contextual manner so that in the future-even in the absence of the environmental factor- enhanced vulnerability to illness is present.(Yang and Khoury 1997) Critically, because of confounding by the genetic variable, the direct effects of the environmental variable are generally not detectable. Rather, only when considered in the context of genetic variation can these be detected. Though the strength of some GxE findings are controversial, many investigators continue to stress the importance of these GxE effects in the pathogenesis of a variety of behavioral disorders such as depression, post-traumatic stress disorder and antisocial behavior.(Caspi, McClay et al. 2002, Caspi, Sugden et al. 2003, Kolassa, Ertl et al. 2010)

The physical basis for these GxE effects is thought to vary. For example, at the anatomical level, the GxE effects for behavioral disorders can be manifested by changes in synaptic structure.(McEwen 2007) However, at the molecular level, the physical manifestation of GxE effects is less certain. But a number of investigators have suggested that changes in DNA methylation may be one potential mechanism through which the physical effects of GxE effects are conveyed.(Klengel, Pape et al. 2014)

Interestingly, the fact that behaviorally relevant changes in the environment can alter DNA methylation and that the degree of those changes is influenced by genetic variation has been known for many years. In our early candidate gene studies, we showed that smoking altered DNA methylation in the promoter region of *monoamine oxidase A (MAOA)*, a key regulator of monoaminergic neurotransmission, and that genotype at the well-characterized promoter associated variable nucleotide repeat (VNTR) altered the percent methylation at the status in both the presence and absence of smoking.(Philibert, Gunter et al. 2008, Philibert, Beach et al. 2010) Subsequently, methylation changes at those loci were shown to be functional by Volkow and colleagues.(Shumay, Logan et al. 2012)

In current terminology, those effects of the VNTR on smoking or basal DNA methylation are now referred to genotype-methylation interaction effects. These MAOA interaction effects had consequence on our ability to detect their relationship to smoking when we conducted our first genome wide studies. Despite the magnitude of the smoking induced change in DNA methylation in response to smoking, the probes surrounding the MAOA VNTR are not among the more highly ranked probes even in studies of DNA from

subjects of only one gender. Other observations from those initial studies are equally instructive. First, the local methylation response to smoking was not homogenous. Factor analysis of the methylation status of the 88 CpG residues in the promoter associated islands showed that increases in methylation at one area of the island could be associated with demethylation at others.(Beach, Brody et al. 2010) Finally, the effects of smoking on DNA methylation were not static. After time, the signature tended to decay.(Philibert, Beach et al. 2010) Hence, from those early studies, it was clear that at MAOA promoter, genetic variation could alter the effects of environmental factor on the local DNA methylation signature in a complex manner.

Subsequent studies suggest that many of these same complexities in response to smoking are evident at the genome wide level. For example, it is clear that at the genome wide level, genetic variation affects the magnitude of the methylation response, and that when attempting to replicate signatures from those of differing ancestries, those interaction effects may impair the ability to replicate findings at a given locus in a subject pool of a different ancestry.(Tsaprouni, Yang et al. 2014, Dogan, Xiang et al. 2015) Second, and equally importantly, the reversion of the methylation signatures can be complex.(Tsaprouni, Yang et al. 2014, Guida, Sandanger et al. 2015) Guida and colleagues specifically examined the epigenomic response to smoking cessation in DNA from a collection of 745 subjects and found two classes of CpG sites, those whose methylation signature reverted with time and those that did not; and concluded that at the genome wide level the “*dynamics of methylation changes following smoking cessation are driven by a differential and site specific magnitude of the smoking induced changes that is irrespective of the intensity and duration of smoking.*”(Guida, Sandanger et al. 2015) In summary, a substantial body of evidence suggests that the genome wide signature to smoking is only partially reversible and that a large chunk of the non-reversible changes may be complexly masked in interaction effects.

Since smoking is a major risk factor for CVD in general, and in particular stroke and CVD, this also suggests that a portion of the smoking induced risk present in the epigenome that moderates the risk for CVD may be somewhat non-reversible and masked in interaction effects. In addition, since smoking is only one of a number of factors can alter risk for CVD and these other factors also may have complex epigenetic signatures, it may well be that interrogation of peripheral WBC DNA methylation may reveal interaction effects that moderate risk for CVD and are relatively stable.

So in summary, the use of either genetic or epigenetic information for the prediction of various forms of CVD does not work well. However, it is possible the combinations of

these measurements, in particular those that take into effect interactive effects, could perform superiorly.

In this communication, we used regression analytical approaches and the epigenetic and genetic resources from 324 subjects who participated in the Framingham Heart Study to test whether combinations of environmental (methylation) and genetic information (SNPs) together, or with their interactive effects, can make a better contribution to algorithms to predict CVD.

METHODS

Framingham Heart Study. The data used in this study is derived from participants in the Framingham Heart Study (FHS). (Dawber, Kannel et al. 1963) FHS is a longitudinal study aimed at understanding the risks of cardiovascular disease (CVD) and consists of several cohorts including the Original Cohort, Offspring Cohort, Omni Cohort, Third Generation Cohort, New Offspring Spouse Cohort and Second Generation Omni Cohort. Specifically, the Offspring Cohort, initiated in 1971, consisting of the offspring of the Original Cohort and their spouses was used in this study. This cohort consists of 2,483 males and 2,641 females (total of 5,124). (Mahmood, Levy et al. 2014) The specific analyses described in this communication were approved by the University of Iowa Institutional Review Board.

Genome-wide DNA Methylation. Of the 5,124 individuals in the Offspring Cohort, only 2,567 individuals (duplicates removed) with DNA methylation data were considered.

These individuals were included in the DNA methylation study because they attended the Framingham Offspring 8th exam, provided consent for genetic research, had a buffy coat sample, and had sufficient DNA quantity and quality for methylation profiling. Exam 8 took place between 2005 and 2008. Genomic DNA extracted from their white blood cells was bisulfite converted, then genome-wide DNA methylation was profiled using the Illumina HumanMethylation450 BeadChip (San Diego, CA) at either the University of Minnesota or Johns Hopkins University. The intensity data (IDAT) files of the samples alongside their slide and array information were used to perform the DASEN normalization using the MethyLumi, Watermelon and IlluminaHumanMethylation450k.db R packages. (Pidsley, Y Wong et al. 2013) The DASEN normalization performs probe filtering, background correction and adjustment for probe types. Samples were removed if they contained >1% of CpG sites with a detection p-value >0.05. CpG sites were removed if they had a bead count of <3 and/or >1% of samples had a detection p-value >0.05. After DASEN normalization, there were 2,560 samples and 484,241 sites remaining (484,125 CpG sites). CpG sites were grouped by chromosome. Of those CpG sites, 472,822 mapped to autosomes. Methylation

beta values were converted to M values using the beta2m R function in the Lumi package and subsequently converted to z-scores using an R script.(Du, Kibbe et al. 2008)

Genome-wide Genotype. Of the 2,560 remaining individuals after DNA methylation quality control, 2,406 (1,100 males and 1,306 females) had genome-wide genotype data from the Affymetrix GeneChip HumanMapping 500K Array Set (Santa Clara, CA). This array is capable of profiling 500,568 SNPs in the genome. Quality control was performed at both the sample and SNP probe levels in PLINK. The initial quality control step involved identifying individuals with discordant sex information. None were identified. Next, individuals with a heterozygosity rate of greater or smaller than the mean $\pm$ 2SD and with a proportion of missing SNPs >0.03 were excluded. Related individuals were also excluded if the identity by descent value was >0.185 (halfway between second and third degree relatives). After performing these sample level quality control steps, 1,599 individuals remained (722 males and 877 females). On the probe level, SNPs with a minor allele frequency $>1\%$, Hardy-Weinberg equilibrium p-value $>10^{-5}$ and SNP missing rate of $<5\%$ were retained. A total of 403,192 SNPs remained after these quality control steps. Using the recode option in PLINK,(Purcell, Neale et al. 2007) genotypes were coded as 0, 1 or 2 per minor allele frequency.

Phenotypes. For individuals in this study, their stroke and congestive heart failure (CHF) status were extracted. Since biomaterial for DNA methylation was collected during the eighth examination cycle of the Offspring cohort, only those with a stroke or CHF incidence date prior to this eighth examination were included. Based on this criterion, a total of 1,540 and 1,562 individuals remained for CHF and stroke analyses, respectively.

Among the 1,540 subjects available for CHF analyses, 40 were classified as having CHF. Major criteria of CHF according to the Framingham Study includes paroxysmal nocturnal dyspnea or orthopnea, distended neck veins, rales, increasing heart size by x-ray, acute pulmonary edema on chest x-ray, ventricular S(3) gallop, increased venous pressure >16 cm H₂O, hepatojugular reflux, pulmonary edema, visceral congestion, cardiomegaly shown on autopsy or weight loss on CHF Rx: 10 lbs./5days. Minor criteria include bilateral ankle edema, night cough, dyspnea on ordinary exertion, hepatomegaly, pleural effusion by x-ray, decrease in vital capacity by one-third from maximum record, tachycardia (120 beats per minute or more) or pulmonary vascular engorgement on chest x-ray. To be classified as having CHF, an individual is required to have a minimum of two major or one major and two minor criteria present concurrently. The demographics of these 1,540 individuals are summarized in Table 17.

Table 17. Demographics of the 1,540 individuals in the CHF dataset

	CHF present	CHF absent
n		
Male	22	664
Female	18	836
Age		
Male	72.6±7.2	66.7±8.4
Female	75.5±10.6	66.5±8.4

Among the 1,562 subjects available for stroke analyses, 38 were classified as having had stroke. Stroke encompasses hemorrhagic stroke (subarachnoid hemorrhage or intracerebral hemorrhage), ischemic stroke (cerebral embolism or antherothrombotic brain infarction), transient ischemic stroke or death from stroke. The demographics of these 1,562 subjects are summarized in Table 18.

Table 18. Demographics of the 1,562 individuals in the stroke dataset

	Stroke present	Stroke absent
n		
Male	15	685
Female	23	839
Age		
Male	73.2±9.2	70.0±8.4
Female	73.1±9.2	66.7±8.6

Variable Reduction. The total number of genetic (SNP) and epigenetic (DNA methylation) probes remaining after quality control measures were 403,192 and 472,822, respectively. Due to the large number of variables (876,014 total, excluding possible interaction between SNPs and DNA methylation sites), and to avoid collinearity, variable reduction was performed.

Linkage disequilibrium based SNP pruning was performed in PLINK(Purcell, Neale et al. 2007) with a window size of 50 SNPs, window shift of 5 SNPs and a pairwise SNP-SNP LD threshold of 0.5. This reduced the number of SNPs from 403,192 to 161,474. To further reduce the number of SNPs, the chi-squared p-value was calculated between the remaining 161,474 SNPs and CHF and stroke status. Those with a chi-squared p-value <0.1 were retained for classification analyses, resulting in 15,132 SNPs for CHF and 14,819 SNPs for stroke.

To reduce the number of DNA methylation loci, first, the point bi-serial correlation was calculated between the 472,822 CpG sites and CHF and stroke status. CpG sites were retained if the point bi-serial correlation was at least 0.1. A total of 19,112 and 22,837 CpG

sites remained for CHF and stroke, respectively. Subsequently, Pearson correlations between sites were calculated independently for each illness. If the Pearson correlation between two loci were at least 0.8, the loci with a smaller point bi-serial correlation was discarded. In the end, 10,707 and 9,406 DNA methylation loci remained for the classification analyses of CHF and stroke, respectively.

Receiver Operating Characteristic Curve. A receiver operating characteristic (ROC) curve provides a graphical representation of binary classification performance with varying discrimination thresholds. Therefore, to assess the capability of DNA methylation and SNPs in classifying CHF and stroke, an R script was written to perform logistic regression of the models shown below and subsequently calculate the area under the curve (AUC) of the ROC curve (Beck and Shultz 1986) using the pROC package in R. This was performed systematically using DNA methylation sites that were ordered in descending order of point bi-serial with respect to the illness and SNPs that were order in ascending order of chi-squared p-value with respect to the illness. In the models listed below, SNP*meth term represents the gene-environment interaction.

$$CHF \sim SNP_j + meth_i + SNP_j * meth_i$$

$$Stroke \sim SNP_j + meth_i + SNP_j * meth_i$$

RESULTS

ROC of CHF Classification. Using the top three DNA methylation sites (cg09099697, cg19679281, cg25840850) and SNPs (rs10833199, rs11728055, rs16901105), a model incorporating only main effects were fitted for CHF. The ROC AUC was 0.78 and is shown in **Figure 10**. The model parameters are summarized in Table 19.

Table 19. Parameters of the main effects CHF model

Variable	Estimate	Std. Error	z value	Pr(> z)
cg09099697	0.3856	0.2201	1.752	0.0798
cg19679281	0.3343	0.1942	1.721	0.0852
cg25840850	0.2930	0.2238	1.310	0.1904
rs10833199	0.6222	0.3522	1.767	0.0773
rs11728055	0.3424	0.4367	0.784	0.4331
rs16901105	0.6254	0.4466	1.401	0.1614

To further demonstrate the importance of incorporating both DNA methylation and SNPs in better predicting CHF, interaction terms as depicted in the methods section were included in the CHF model. The ROC AUC for this model increased from the previous model to 0.81 and is shown in **Figure 11**. The model parameters are summarized in Table 20.

Table 20. Parameters of the interaction effects CHF model

Variable	Estimate	Std. Error	z value	Pr(> z)
cg09099697	0.4972	0.2797	1.778	0.0754
cg19679281	0.3602	0.2420	1.489	0.1366
cg25840850	0.3280	0.2915	1.125	0.2605
rs10833199	0.5076	0.5581	0.910	0.3631
rs11728055	0.5905	0.5520	1.070	0.2847
rs16901105	0.3865	0.7489	0.516	0.6058
cg09099697:rs10833199	-1.2780	0.5722	-2.234	0.0255
cg09099697:rs11728055	0.9940	0.7409	1.342	0.1797
cg09099697:rs16901105	0.1493	0.8923	0.167	0.8671
rs10833199:cg19679281	0.7185	0.5258	1.367	0.1718
rs11728055:cg19679281	-0.9245	0.5396	-1.713	0.0867
rs16901105:cg19679281	-0.3603	0.7844	-0.459	0.6460
rs10833199:cg25840850	0.4609	0.4895	0.942	0.3464
rs11728055:cg25840850	-1.2994	0.6516	-1.994	0.0461
rs16901105:cg25840850	0.4543	0.8308	0.547	0.5845

These two models for CHF clearly demonstrate the importance of accounting for both genetic and epigenetic effects. As shown in Table 19, even though only three variables (two CpGs and one SNP) are marginally significant at the 0.05 level with respect to CHF, incorporating gene-environment interactions in the form of SNP-meth interactions strengthens prediction. This is shown in Table 20 where two interaction terms are significant at the 0.05 level in conjunction with one other interaction being marginally significant.

ROC of Stroke Classification. Using the top five DNA methylation sites (cg27209395, cg27551078, cg03130180, cg10319399, cg25861340) and top four SNPs (rs11007270, rs17073262, rs7190657, rs2411130), a main effects model was fitted for stroke. The ROC AUC was 0.85 and is shown in **Figure 12**. The model parameters are summarized in Table 21.

Table 21. Parameters of the main effects stroke model

Variable	Estimate	Std. Error	z value	Pr(> z)
cg27209395	0.2577	0.2225	1.158	0.246728
cg27551078	0.2215	0.1064	2.082	0.037338
cg03130180	-0.0240	0.3378	-0.071	0.943359
cg10319399	-0.4710	0.2880	-1.636	0.101934
cg25861340	-0.4080	0.2716	-1.502	0.133051
rs11007270	1.3498	0.4006	3.369	0.000753
rs17073262	0.8066	0.7543	1.069	0.284923
rs7190657	1.1362	0.3993	2.845	0.004439
rs2411130	1.3714	0.5702	2.405	0.016159

To again demonstrate the importance of DNA methylation sites and SNPs concurrently, an interaction effects model was fitted. The ROC AUC for this model was 0.86 and is shown in **Figure 13**. The model parameters are summarized in Table 22.

Table 22. Parameters of the interaction effects stroke model

Variable	Estimate	Std. Error	z value	Pr(> z)
cg27209395	-2.213e-01	2.866e-01	-0.772	0.4400
cg27551078	2.525e-01	1.131e-01	2.231	0.0257
cg03130180	-7.973e-01	4.729e-01	-1.686	0.0918
cg10319399	-2.266e-01	3.932e-01	-0.576	0.5644
cg25861340	-4.281e-01	3.369e-01	-1.271	0.2037
rs11007270	1.329e+00	6.715e-01	1.980	0.0477
rs17073262	-2.989e+02	1.913e+04	-0.016	0.9875
rs7190657	1.114e-01	9.201e-01	0.121	0.9036
rs2411130	1.235e-02	1.827e+00	0.007	0.9946
cg27209395:rs11007270	1.30E+00	6.68E-01	1.952	0.0509
cg27209395:rs17073262	-2.20E+02	1.40E+04	-0.016	0.9875
cg27209395:rs7190657	2.19E+00	9.00E-01	2.434	0.0149
rs11007270:cg27551078	-2.05E-01	4.76E-01	-0.431	0.6668
rs17073262:cg27551078	1.89E+01	3.32E+03	0.006	0.9955
rs7190657:cg27551078	-6.56E-01	6.82E-01	-0.962	0.3358
rs11007270:cg03130180	8.84E-01	8.43E-01	1.049	0.294
rs17073262:cg03130180	1.18E+01	4.34E+03	0.003	0.9978
rs7190657:cg03130180	2.43E+00	1.18E+00	2.056	0.0398
rs11007270:cg10319399	-3.15E-01	8.41E-01	-0.374	0.7081
rs17073262:cg10319399	-3.18E+01	2.65E+03	-0.012	0.9904
rs7190657:cg10319399	-1.02E+00	8.99E-01	-1.135	0.2565
cg27209395:rs2411130	9.62E-01	1.47E+00	0.654	0.5134
cg27551078:rs2411130	4.32E-01	1.02E+00	0.422	0.673
cg03130180:rs2411130	3.64E+00	2.76E+00	1.319	0.1872
cg10319399:rs2411130	-9.70E-01	1.60E+00	-0.605	0.5453
rs11007270:cg25861340	9.13E-01	7.43E-01	1.229	0.2191
rs17073262:cg25861340	-3.72E+02	2.37E+04	-0.016	0.9875
rs7190657:cg25861340	2.51E-01	5.99E-01	0.418	0.6759
rs2411130:cg25861340	-2.42E+00	2.76E+00	-0.877	0.3804

Once again, these two stroke models demonstrate the importance of genetic and environment in stroke. Both DNA methylation sites and SNPs are highly significant for classifying stroke. Furthermore, the classification performance is likely to increase in additional studies with diverse ethnic backgrounds and larger sample size.

DISCUSSION

The results demonstrate that the presence of stroke or CHF can be inferred through the use of algorithms that take advantage of combination of SNPs, methylation values and or their interaction terms. However, before the results can be discussed, it is important to note

several limitations to the current study. First, the Framingham cohort is exclusively White and most subjects are in their mid to late sixties and seventies. Therefore, the current findings may not apply to those of other ethnicities or different age range. Second, outside of cg05575921, the validity of the M (or B-values) for the other probes has not been confirmed by an independent technique such as pyrosequencing. Third, the Illumina array used in the studies is no longer available. Because of changes in design or availability of probes in the new generation of array, the ability to replicate and extend may be affected.

The current results underscore the value of resources such as the Framingham Heart Study furthering our understanding heart disease. In fact, without this resource, it is fair to say that this type of work would be difficult if not impossible to conduct. Still, even given the current results using this unique data set, a great deal of additional work will be necessary before a screening test such as that described in the current communication can be employed clinically. Most obviously, the current results will have to be replicated and refined in other data sets, then re-tested in research populations representative of their intended future clinical application. The latter point is particularly important because even well-designed cohort studies that were originally epidemiologically sound suffer from retention biases that enrich the remaining pool for less serious illness. This is particularly true with respect to illnesses associated with substance use, because probands with high levels of substance use are more often lost to longitudinal follow-up.(Wolke, Waylen et al. 2009) In addition, because SNP frequencies can vary between ethnicities, the effect size of a given interaction may also vary. Therefore, extensive testing and development in a variety of ethnically informative cohorts will be necessary.

There may be a hard ceiling for improvement of the AUC. Ironically, this has little to do with the quality or quantity of the epigenetic and genetic data. Rather, the limitation may be the uncertainty in the clinical characterizations. Sadly, even under the best conditions, clinically relevant forms of CVD can remain undetected. This is true even for the FHS cohort. As a result, the “gold standard” itself in the current study is somewhat inaccurate with respect to the actual clinical state. Since this inaccuracy increases the error of even a biomarker that is exactly targeted on the relevant biology, our ability to improve the AUC may be dependent on our ability to derive a more accurate clinical assessment.(Philibert, Gunter et al. 2014)

Another limitation to the use this approach is the constantly evolving epidemiology of CVD. Whereas the genetic contribution to CVD is relatively fixed, diets and other environmental exposures continue to vary from generation to generation. Perhaps the best illustration of this limitation can be by considering contribution of smoking to the predictive

power of this test in prior generations. Since tobacco was introduced to Europe from the New World in the early 1500s, we can confidently state that the contribution of smoking to CVD in medieval Europe was limited and therefore, the impact of the cg05575921 on predictive power would have been nil. In contrast, because over 40% of US adults smoked in the 1960s,(Garrett, Dube et al. 2011) it is likely that the contribution of smoking behaviors, as captured by cg05575921, to the prediction of CVD would have been significantly greater in subjects from that era. However, smoking is not the only environmental factor that varies from generation to generation and from cohort to cohort. Over the past 20 years, there have been marked shifts in our understanding and public attitudes towards the amount of saturated and trans-fatty acids in a healthy diet. Since these environment factors also have strong influence on the likelihood of CVD, we would expect that the weighting of interaction effects loading on these dietary factors might vary with respect to age and ethnicity.

The improved predictive power of the smoking methylation biomarker cg05575921 as compared to self-reported smoking is not unexpected. In our initial studies, it has shown to be a potent indicator of current smoking status with an AUC of 0.99 in study that used well screened cases and controls.(Philibert, Hollenbeck et al. 2015) Unreliable self-report for smoking, particularly in high risk cohorts, is a well-established phenomenon. (Caraballo, Giovino et al. 2001, Webb, Boyd et al. 2003, Caraballo, Giovino et al. 2004, Shipton, Tappin et al. 2009) Furthermore, unlike cg05575921, categorical self-report does not capture the intensity of smoking.(Philibert, Hollenbeck et al. 2015) Finally, many subjects who may have participated in the study may have previously smoked, but did not smoke at the Wave 8 interview but still had residual demethylation of AHRR. In each of these instances, the use of the continuous metric may capture additional vulnerability to CVD that is not captured by a dichotomous smoking variable.

Since alcoholism is also a risk for CVD, (Mozaffarian, Benjamin et al. 2016) we were somewhat surprised that our previously established and validated biomarker approach for assessing alcohol intake did not have a greater predictive impact.(Philibert, Penaluna et al. 2014, Brückmann, Di Santo et al. 2016) In our initial models, the addition of methylation status at cg2313759 only improved AUC by 0.015. Although one reason for this failure to show the effect of alcohol use on risk for CVD may be that this marker is not as well validated as our smoking biomarker, there are other reasons as well. First and foremost, as opposed to methylation at cg05575921 which displays a tonic increasing risk for decreased life expectancies at all of levels of exposure, methylation at cg2313759 displays an inverted U-shaped distribution with respect to biological aging. Whether risk for CVD also follows a U shaped distribution with respect to alcohol intake is not known. But it does suggest that

any successful algorithm incorporating the main effects of alcohol associated methylation cannot use a simple linear approach.

Our success in finding algorithms predictive of CVD in the absence of genome wide significant main effects may have significant implications for the searches for marker sets for other common complex disorders of adulthood. Of the top 10 leading causes of death in the United States, using main effects, reliable methylation signatures have been developed only for type 2 diabetes and chronic obstructive pulmonary disease (COPD). (Qiu, Baccarelli et al. 2012, Toperoff, Aran et al. 2012) Because the ability to find a good biomarker for illness is highly contingent on the reliability of the clinical diagnosis, the success in these two instances may be secondary to the excellent diagnostic reliability of the methods used to diagnose these two disorders, namely the hemoglobin A1C and spirometry. Additionally, it is important to note that the diagnostic signature for T2DM largely maps to pathways affected by excessive glucose levels while the signature associated with COPD largely overlaps with that of smoking which contributes to 95% of all cases of COPD. (Qiu, Baccarelli et al. 2012, Toperoff, Aran et al. 2012) Still, because many of the risk factors for other major causes of death, such as stroke, overlap with those for CVD (e.g. smoking), we are optimistic that similar profiles can be generated using this approach.

Unfortunately, the vast majority of adult onset common complex disorders do not have good existing biomarkers or large effect size etiological factors. In these cases, an approach that incorporates interaction effects may be beneficial- the real question is why? Although speculative, based on our experience with local and genome wide data indicates that chronic exposure to cellular stressors leads to a reorganization of the epigenome, which may be only partially reversible. If that disorganization of the genome, regardless of how long it lasts, is causally associated with illness, it can be used as a biomarker for illness. Understanding the reversion time of each of these effects may lead to additional insights. For example, pharmacological interventions may have effects at discrete subsets. By understanding the relationship between reversion at these loci and therapeutic outcomes, it may be possible to optimize existing medications or more adroitly tailor new combination regimens.

In summary, we report that an algorithm that incorporates information from interaction effects can predict the presence of stroke and CHF in the FCS. We suggest that further studies to replicate and expand the generalizability the approach in cohorts of other ethnicities are indicated. We furthermore suggest that similar approaches may lead to the generation of methylation profiles for other common complex disorders such as stroke.

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20 Although the foregoing specification and examples fully disclose and enable the present invention, they are not intended to limit the scope of the invention, which is defined by the claims appended hereto.

All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional
25 embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

The use of the terms "a" and "an" and "the" and similar referents in the context of describing the invention are to be construed to cover both the singular and the plural, unless
30 otherwise indicated herein or clearly contradicted by context. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms (*i.e.*, meaning "including, but not limited to") unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each
35 separate value is incorporated into the specification as if it were individually recited herein.

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5 All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (*e.g.*, “such as”) provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

10 Embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Variations of those embodiments may become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventors expect skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is
15 encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

WHAT IS CLAIMED IS:

1. A kit for determining methylation status of at least one CpG dinucleotide and a genotype of at least one single-nucleotide polymorphism (SNP), the kit comprising
 - at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide from a gene from **Figure 15** or a CpG site from **Figure 16**, or collinear ($R>0.3$) with a CpG site from **Figure 16**, wherein the at least one first nucleic acid primer detects an unmethylated CpG dinucleotide, and
 - at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or bisulfite converted DNA sequence of a first SNP from **Figure 21** or a second SNP in linkage disequilibrium with a first SNP from **Figure 21**, wherein the linkage disequilibrium has a value of $R>0.3$.
2. A kit for determining methylation status of at least one CpG dinucleotide and a genotype of at least one single-nucleotide polymorphism (SNP), the kit comprising
 - at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a gene from **Figure 17** or a CpG dinucleotide from a CpG site in **Figure 18** or a CpG dinucleotide collinear ($R>0.3$) with a CpG site from **Figure 18**, wherein the at least one first nucleic acid primer detects an unmethylated CpG dinucleotide, and
 - at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or bisulfite converted DNA sequence of a first SNP from **Figure 22** or a second SNP in linkage disequilibrium with a first SNP from **Figure 22**, wherein the linkage disequilibrium has a value of $R>0.3$.
3. A kit for determining methylation status of at least one CpG dinucleotide and a genotype of at least one single-nucleotide polymorphism (SNP), the kit comprising
 - at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide from a gene from **Figure 19** or a CpG site in **Figure 20** a CpG dinucleotide collinear ($R>0.3$) with a CpG site from **Figure 20**, wherein the at least one first nucleic acid primer detects an unmethylated CpG dinucleotide, and
 - at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or bisulfite converted DNA sequence of a first

SNP from **Figure 23** or a second SNP in linkage disequilibrium with a first SNP from **Figure 23**, wherein the linkage disequilibrium has a value of $R > 0.3$.

4. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising
at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and
at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs347027.
5. The kit of claim 4, wherein rs347027 comprises a G allele.
6. The kit of claim 4, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the TGFB3 gene, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
7. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising
at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 38364951 in an intergenic region of chromosome 15 wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and
at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4937276.
8. The kit of claim 7, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 38364951 in an intergenic region

of chromosome 15, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

9. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising
at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and
at least one second nucleic acid primer at least 8 nucleotides in length that is complementary SNP rs17355663.
10. The kit of claim 9, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
11. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising
at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and
at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs235807.
12. The kit of claim 11, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.

13. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising
at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 91171013 of an intergenic region of chromosome 1, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and
at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs11579814.
14. The kit of claim 13, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 91171013 of an intergenic region of chromosome 1, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
15. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising
at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and
at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs2275187.
16. The kit of claim 15, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
17. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising

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at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 186426136 mapping to chromosome 1 in the Phosducin gene wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and

at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4336803.

18. The kit of claim 17, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 186426136 mapping to chromosome 1 in the Phosducin gene, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
19. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising

at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18 (CDK18) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and

at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4951158.
20. The kit of claim 19, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18 (CDK18) gene, wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
21. A kit for determining the methylation status of at least one CpG dinucleotide and the presence of at least one single-nucleotide polymorphism (SNP), the kit comprising

at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺

Transporting, Type 2C, Member 1(ATP2C1) gene, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide, and

at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs925613.

22. The kit of claim 21, further comprising at least one third nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
23. The kit of any of claims 1-22, wherein the at least one first primer is at least 10 nucleotides in length and wherein the at least one second primer is at least 10 nucleotides in length.
24. The kit of any of claims 1-22, wherein the at least one first primer is at least 12 nucleotides in length and wherein the at least one second primer is at least 12 nucleotides in length.
25. The kit of any one of claims 1-24, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs.
26. The kit of any one of claims 1-24, wherein the at least one first nucleic acid primer comprises one or more synthetic or non-natural nucleotides.
27. The kit of any one of claims 1-26, further comprising a solid substrate to which the at least one first nucleic acid primer is bound.
28. The kit of claim 27, wherein the substrate is a polymer, glass, semiconductor, paper, metal, gel or hydrogel.
29. The kit of claim 27, wherein the solid substrate is a microarray or microfluidics card.
30. The kit of any one of claims 1-29, further comprising a detectable label.

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31. A kit for determining the methylation status of at least one CpG dinucleotide, the kit comprising: at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs or one or more synthetic or non-natural nucleotides, and wherein the at least one nucleic acid primer detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide.
32. The kit of claim 31, further comprising at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the TGFB3 gene, wherein the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, the opposite that is detected by the at least one first nucleic acid primer.
33. The kit of claim 31 or 32, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide.
34. The kit of claim 31 or 32, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide.
35. The kit of claim 32, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide and wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
36. The kit of claim 32, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide and wherein the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide.
37. The kit of claim 32, further comprising at least a third nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence upstream of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFB3 gene.

38. The kit of claim 37, further comprising at least a fourth nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence downstream of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR gene.
39. The kit of claim 37, wherein the at least third nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.
40. The kit of claim 38, wherein the at least fourth nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.
41. The kit of claim 32, wherein the at least one second nucleic acid primer comprises one or more nucleotide analogs.
42. The kit of claim 33, wherein the at least one second nucleic acid primer comprises one or more synthetic or non-natural nucleotides.
43. The kit of claim 32, further comprising a solid substrate to which the at least one first nucleic acid primer is bound.
44. The kit of claim 43, wherein the substrate is a polymer, glass, semiconductor, paper, metal, gel or hydrogel.
45. The kit of claim 43, wherein the solid substrate is a microarray or microfluidics card.
46. The kit of any of claims 31-45, further comprising a detectable label.
47. A kit for determining the methylation status of at least one CpG dinucleotide, the kit comprising: at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, and wherein the at least one nucleic acid primer detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide; and a detectable label selected from the group consisting of an enzyme label, a fluorescent label, and a colorimetric label.

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48. The kit of claim 47, further comprising at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR gene, wherein the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, the opposite that is detected by the at least one first nucleic acid primer.
49. The kit of claim 47 or 48, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide.
50. The kit of claim 47 or 48, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide.
51. The kit of claim 48, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide and wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
52. The kit of claim 48, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide and wherein the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide.
53. The kit of claim 48, further comprising at least a third nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence upstream of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR gene.
54. The kit of claim 53, further comprising at least a fourth nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence downstream of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR gene.
55. The kit of claim 53, wherein the at least third nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.

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56. The kit of claim 54, wherein the at least fourth nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.
57. The kit of any of claim 47-56, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs.
58. The kit of any of claim 47-56, wherein the at least one first nucleic acid primer comprises one or more synthetic or non-natural nucleotides.
59. The kit of any of claim 47-58, further comprising a solid substrate to which the at least one first nucleic acid primer is bound.
60. The kit of claim 59, wherein the substrate is a polymer, glass, semiconductor, paper, metal, gel or hydrogel.
61. The kit of claim 59, wherein the solid substrate is a microarray or microfluidics card.
62. A kit for determining the methylation status of at least one CpG dinucleotide, the kit comprising: at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB3) gene, and wherein the at least one nucleic acid primer detects either the unmethylated CpG dinucleotide or the methylated CpG dinucleotide; and a solid substrate to which the at least one first nucleic acid primer is bound.
63. The kit of claim 62, further comprising at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence comprising a CpG dinucleotide at position 92203667 of chromosome 1 within the TGFB3 gene, wherein the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide or the methylated CpG dinucleotide, the opposite that is detected by the at least one first nucleic acid primer.
64. The kit of claim 62 or 63, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide.

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65. The kit of claim 62 or 63, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide.
66. The kit of claim 63, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide and wherein the at least one second nucleic acid primer detects the methylated CpG dinucleotide.
67. The kit of claim 63, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide and wherein the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide.
68. The kit of claim 63, further comprising at least a third nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence upstream of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR gene.
69. The kit of claim 68, further comprising at least a fourth nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence downstream of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR gene.
70. The kit of claim 68, wherein the at least third nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.
71. The kit of claim 69, wherein the at least fourth nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.
72. The kit of any of claims 62-71, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs.
73. The kit of any of claims 62-71, wherein the at least one first nucleic acid primer comprises one or more synthetic or non-natural nucleotides.

74. The kit of any of claims 62-73, wherein the substrate is a polymer, glass, semiconductor, paper, metal, gel or hydrogel.
75. The kit of any of claims 62-73, wherein the solid substrate is a microarray or microfluidics card.
76. The kit of any of claims 62-75, further comprising a detectable label.
77. A method of predicting the presence of biomarkers associated with Cardiovascular Disease (CVD) in a biological sample from a patient, comprising
- (a) providing a first aliquot from the biological sample and contacting DNA from the first biological sample with bisulfite under alkaline conditions, and
 - (b) providing a second aliquot from the biological sample;
 - (c) contacting
 - (i) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 92203667 of chromosome 1 within the Transforming Growth Factor, Beta Receptor III (TGFB β 3) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs347027,
 - (ii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 38364951 in an intergenic region of chromosome 15, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4937276,
 - (iii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 84206068 of chromosome 4 in the Coenzyme Q2 4-Hydroxybenzoate Polyprenyltransferase (COQ2) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs17355663,
 - (iv) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 26146070 of chromosome 16 in the Heparan Sulfate 3-O-Sulfotransferase 4 (HS3ST4) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs235807,

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(v) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 91171013 of an intergenic region of chromosome 1, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs11579814,

(vi) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 39491936 of chromosome 1 in the NADH Dehydrogenase (Ubiquinone) Fe-S Protein 5 (NDUFS5) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs2275187,

(vii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 186426136 mapping to chromosome 1 in the Phosducin gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4336803,

(viii) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 205475130 of chromosome 1 in the Cyclin-Dependent Kinase 18 (CDK18) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to SNP rs4951158, and/or

(ix) the first aliquot with a first oligonucleotide probe at least 8 nucleotides in length that is complementary to a sequence that comprises a CpG dinucleotide at position 130614013 of chromosome 3 in the ATPase, Ca⁺⁺ Transporting, Type 2C, Member 1(ATP2C1) gene, and the second aliquot with a nucleic acid primer at least 8 nucleotides in length that is complementary to rs925613,

wherein methylation of the CpG dinucleotide at position 92203667 of chromosome 1 within the TGFBR3 gene, cg20636912, cg16947947, cg05916059, cg04567738, cg16603713, cg05709437, cg12081870, and /or cg18070470, and a G at position 1618766 of chromosome 1 or polymorphisms in rs4937276, rs17355663, rs235807, rs11579814, rs2275187, rs4336803, rs4951158, and/or rs925613 is associated with CVD.

78. The method of claim 77, wherein the biological sample is a saliva sample.

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79. A method of predicting the presence of biomarkers associated with Cardiovascular Disease (CVD) in a biological sample from a patient, comprising detecting one or more pairs of SNPs and CpGs in Table 3.
80. A method for detecting one or more copies of a G allele at rs347027 and methylation status at a CpG at position 92203667 of chromosome 1 on a nucleic acid sample from a subject at risk for Cardiovascular Disease (CVD), comprising
 - a) performing a genotyping assay on a nucleic acid sample of said human subject to detect the presence of one or more copies of a G allele of the rs347027 polymorphism, and
 - b) performing a methylation assessment on a nucleic acid sample of said human to determine if the CpG at position 92203667 of chromosome 1 is unmethylated.
81. The method of any of claims 77-80, wherein the CVD is Coronary Heart Disease (CHD).
82. The method of any of claims 77-80, wherein the CVD is Congestive Heart Failure (CHF).
83. The method of any of claims 77-80, wherein the CVD is stroke.
84. A method of determining the presence of a biomarker associated with CHD in a patient sample, the method comprising:
 - (a) isolating nucleic acid sample from the patient sample,
 - (b) performing a genotyping assay on a first aliquot of the nucleic acid sample to detect the presence of at least one SNP, wherein the at least one SNP is a first SNP from **Figure 21** and/or a second SNP in linkage disequilibrium ($R>0.3$) with a first SNP from **Figure 21** to obtain genotype data; and/or
 - (c) bisulfite converting the nucleic acid in a second aliquot of the nucleic acid and performing methylation assessment on a second aliquot of the nucleic acid sample to detect methylation status of at least one gene from **Figure 15** and/or a first CpG site from **Figure 16** and/or a second CpG site collinear with a first CpG from **Figure 16** to obtain methylation data regarding whether a specific CpG residue is unmethylated; and

- (d) inputting genotype from step (b) and/or methylation data from step (c) into at least one algorithm that accounts for the contribution of at least one SNP main effect and/or at least one CpG main effect and/or at least one interaction effect.
85. A method of determining the presence of a biomarker associated with Stroke in a patient sample, the method comprising:
- (a) isolating nucleic acid sample from the patient sample,
 - (b) performing a genotyping assay on a first aliquot of the nucleic acid sample to detect the presence of at least one SNP, wherein the at least one SNP is a first SNP from **Figure 22** and/or a second SNP in linkage disequilibrium with a first SNP from **Figure 22** to obtain genotype data; and/or
 - (c) bisulfite converting the nucleic acid in a second aliquot of the nucleic acid and performing methylation assessment on a second aliquot of the nucleic acid sample to detect methylation status of at least one gene from **Figure 17** and/or a first CpG site from **Figure 18** and/or a second CpG site collinear with a first CpG from **Figure 18** to obtain methylation data regarding whether a specific CpG residue is unmethylated; and
 - (d) inputting genotype from step (b) and/or methylation data from step (c) into an algorithm that accounts for the contribution of at least one SNP main effect and/or at least one CpG main effect and/or at least one interaction effect.
86. A method of determining the presence of a biomarker associated with CHF in a patient sample, the method comprising:
- (a) isolating nucleic acid sample from the patient sample,
 - (b) performing a genotyping assay on a first aliquot of the nucleic acid sample to detect the presence of at least one SNP, wherein the SNP is a first SNP from **Figure 23** and/or a second SNP in linkage disequilibrium ($R > 0.3$) with a first SNP from **Figure 23** to obtain genotype data; and/or
 - (c) bisulfite converting the nucleic acid in a second aliquot of the nucleic acid and performing methylation assessment on a second aliquot of the nucleic acid sample to detect methylation status of at least one gene from **Figure 19** and/or a first CpG site from **Figure 20** and/or a second CpG site collinear with a first CpG from **Figure 20** to obtain methylation data regarding whether a specific CpG residue is unmethylated; and

(d) inputting genotype from step (b) and/or methylation data from step (c) into an algorithm that accounts for the contribution of at least one SNP main effect and/or at least one CpG main effect and/or at least one interaction effect.

87. The method of any of claim 84-86, wherein the at least one interaction effect is selected from the group consisting of a gene-environment interaction (SNPxCpG) effect, a gene-gene interaction (SNPxSNP) effect, and an environment-environment interaction (CpGxCpG) effect.
88. The method of claim 84, wherein the result comprises a gene-environment interaction effect (SNPxCpG) between the second CpG site collinear with the first CpG from **Figure 16** and the SNP from **Figure 21** or the second SNP in linkage disequilibrium with the first SNP from **Figure 21**.
89. The method of claim 84, wherein the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two genes from **Figure 15** and/or at least two CpG sites from **Figure 16**.
90. The method of claim 84, wherein the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites collinear with the first CpG site from **Figure 16**.
91. The method of claim 85, wherein the result comprises a gene-environment interaction effect (SNPxCpG) between the second CpG site collinear ($R > 0.3$) with the first CpG from **Figure 18** and the SNP from **Figure 22** or the second SNP in linkage disequilibrium with the first SNP from **Figure 22**.
92. The method of claim 85, wherein the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two genes from **Figure 17** and/or at least two CpG sites from **Figure 18**.
93. The method of claim 85, wherein the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites collinear with the first CpG site from **Figure 18**.

94. The method of claim 86, wherein the result comprises a gene-environment interaction effect (SNPxCpG) between the second CpG site collinear with the first CpG from **Figure 20** and the first SNP from **Figure 23** or the second SNP in linkage disequilibrium with the first SNP from **Figure 23**.
95. The method of claim 86, wherein the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two genes from **Figure 19** and/or at least two CpG sites from **Figure 20**.
96. The method of claim 86, wherein the result comprises at least one environment-environment interaction effect (CpGxCpG) between at least two CpG sites collinear with the first CpG site from **Figure 20**.

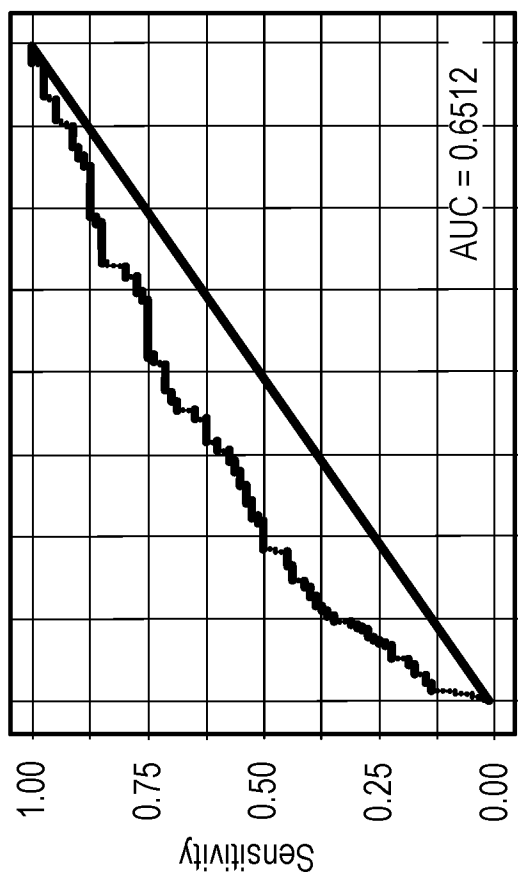


Figure 1A

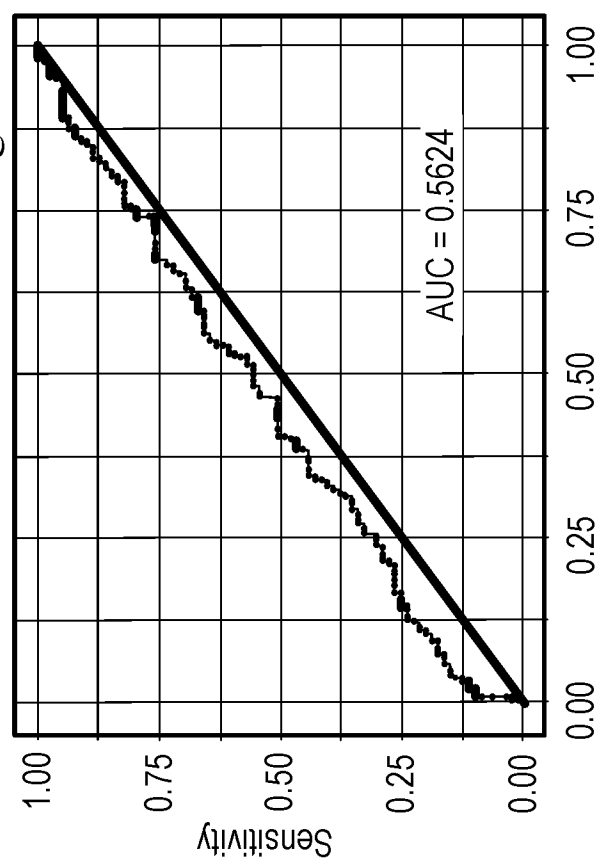


Figure 1B

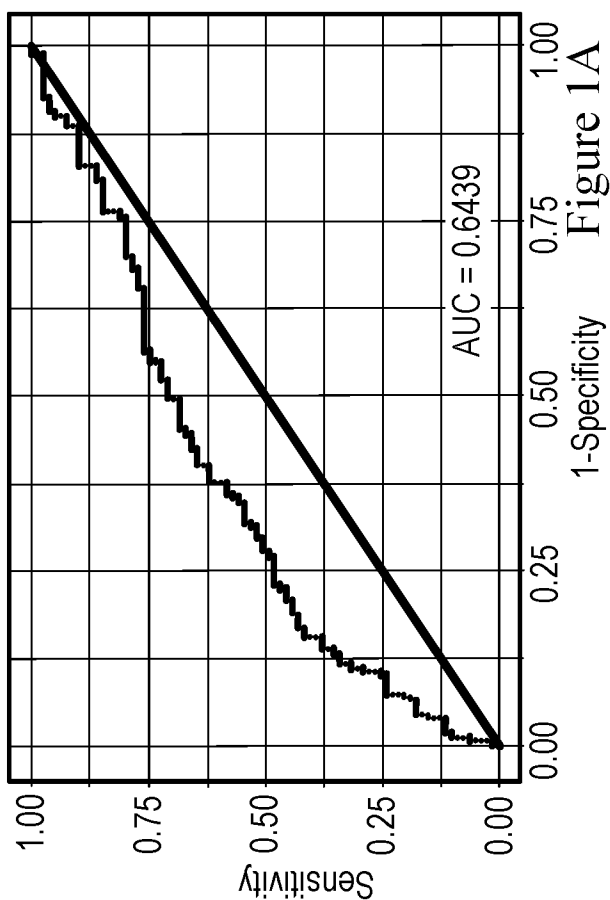


Figure 1C

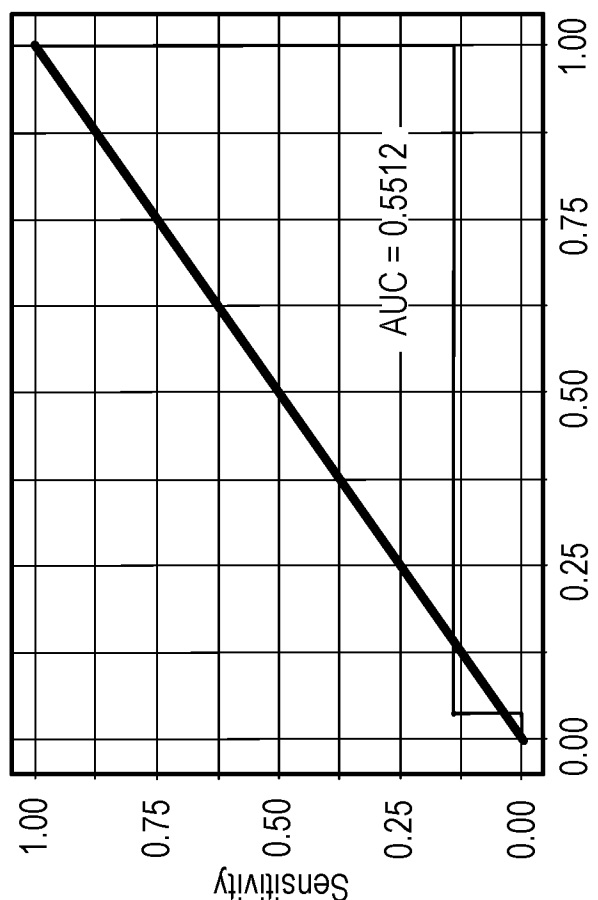


Figure 1D

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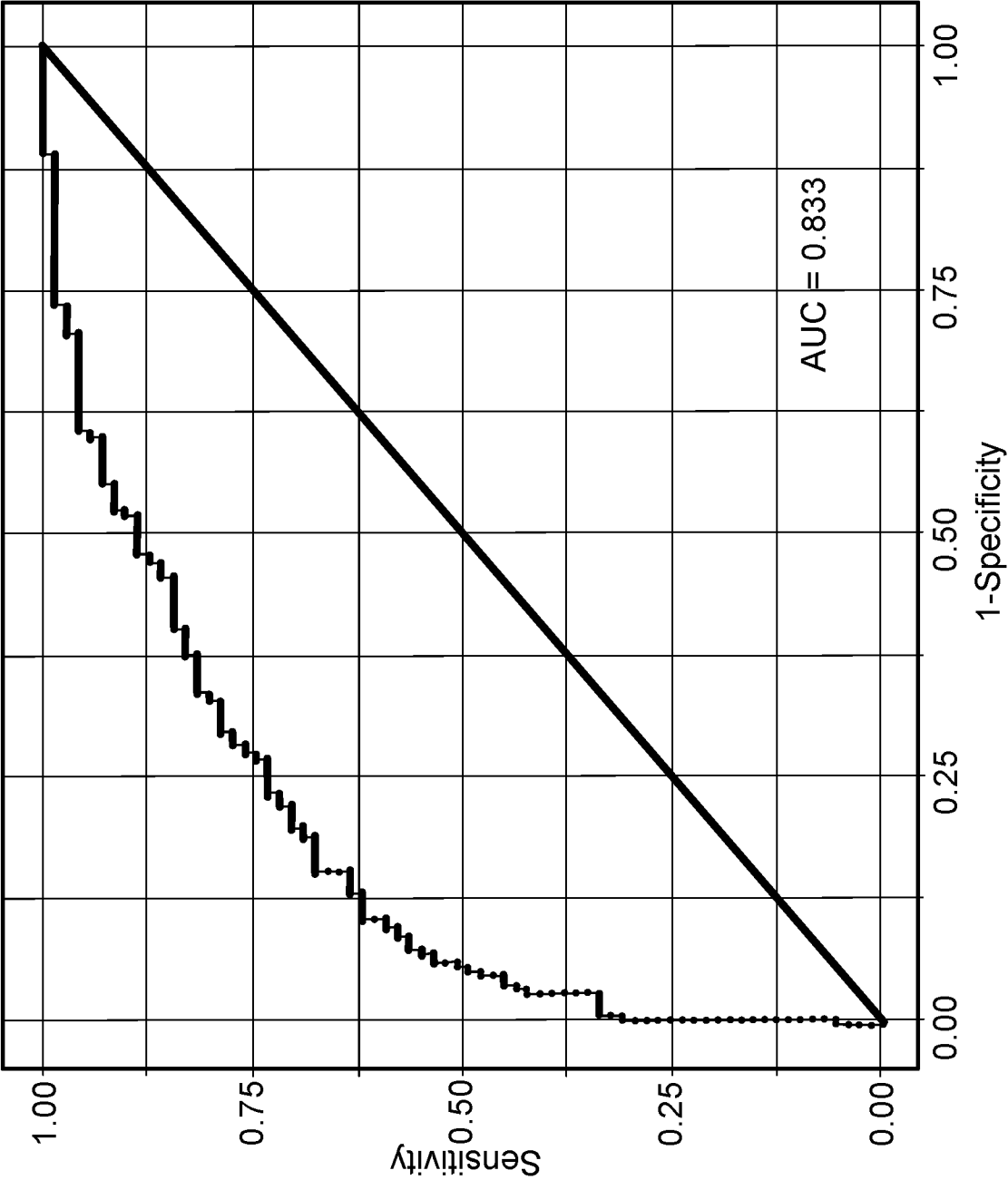


Figure 2

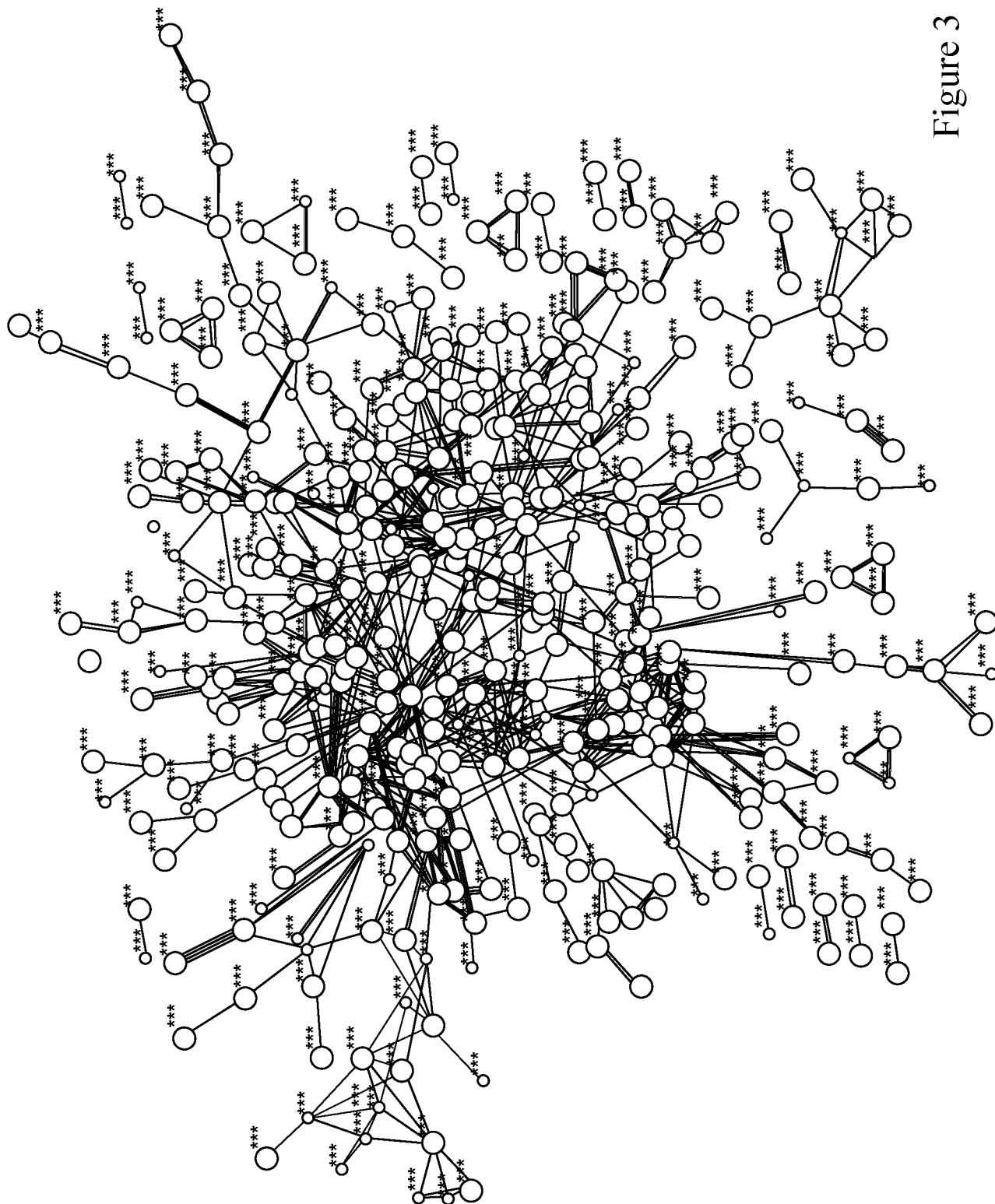


Figure 3

Figure 4

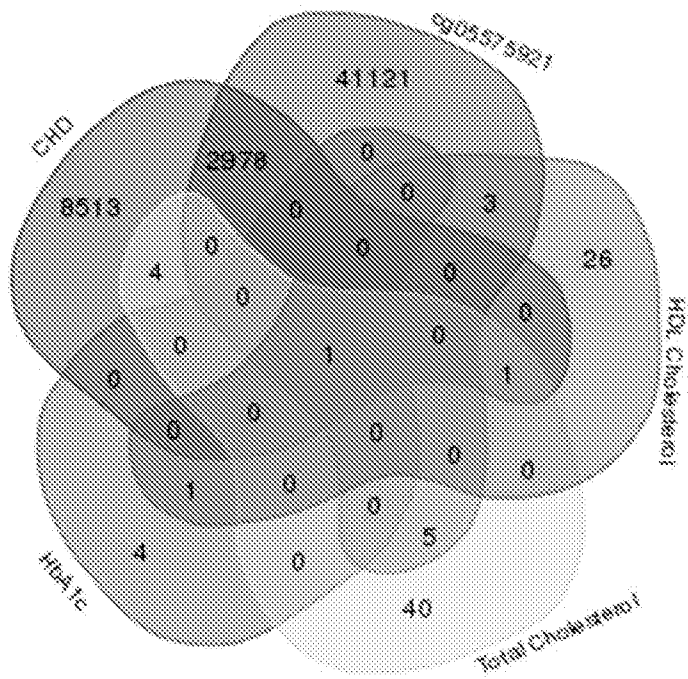


Figure 5

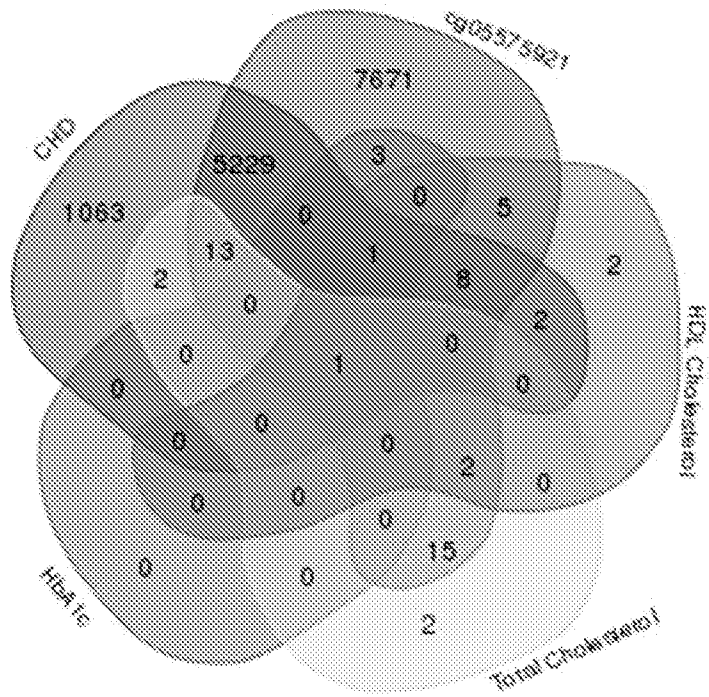


Figure 6.

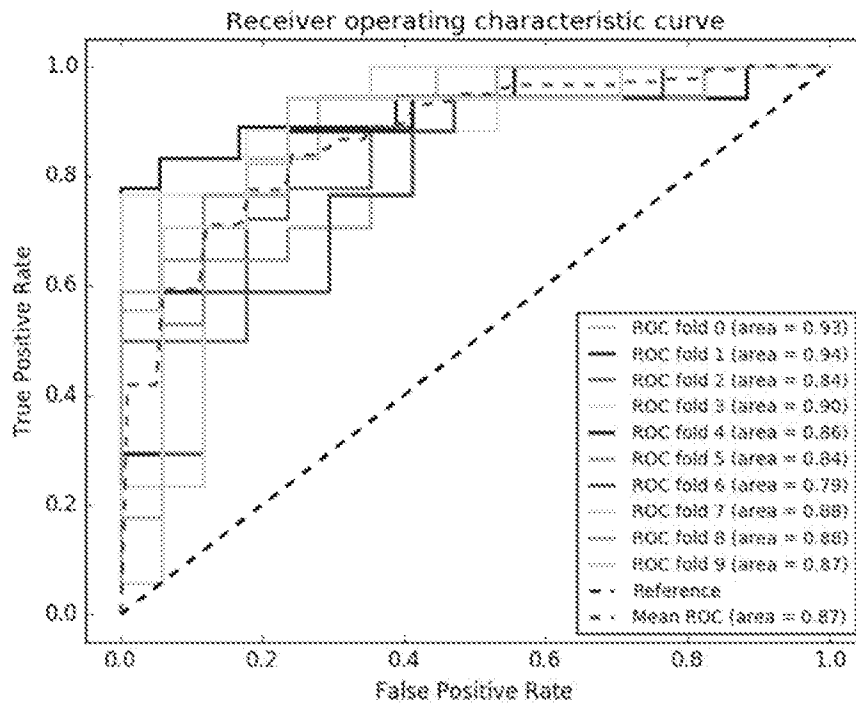
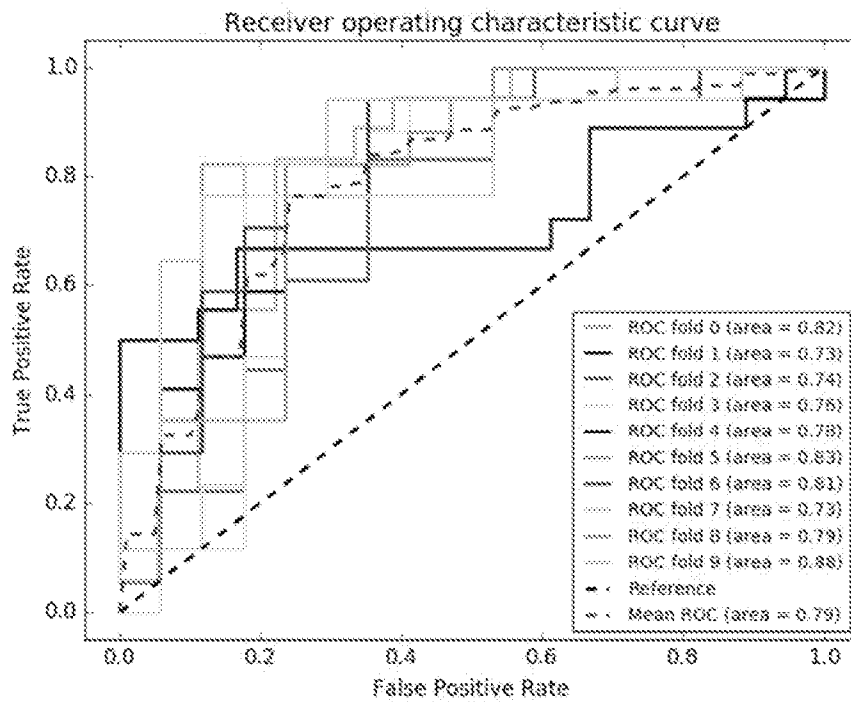


Figure 7.



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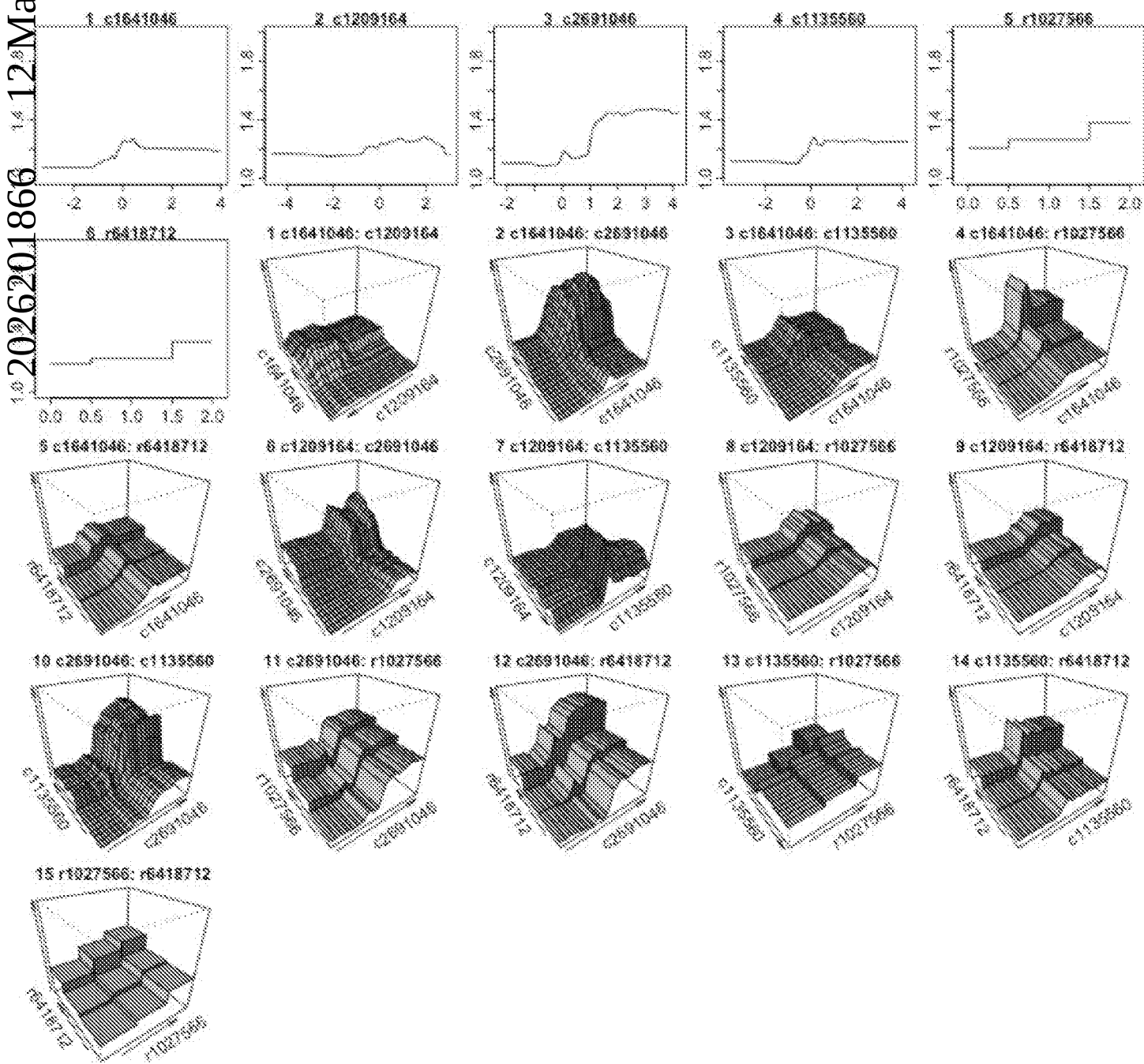


Figure 8

Figure 9.

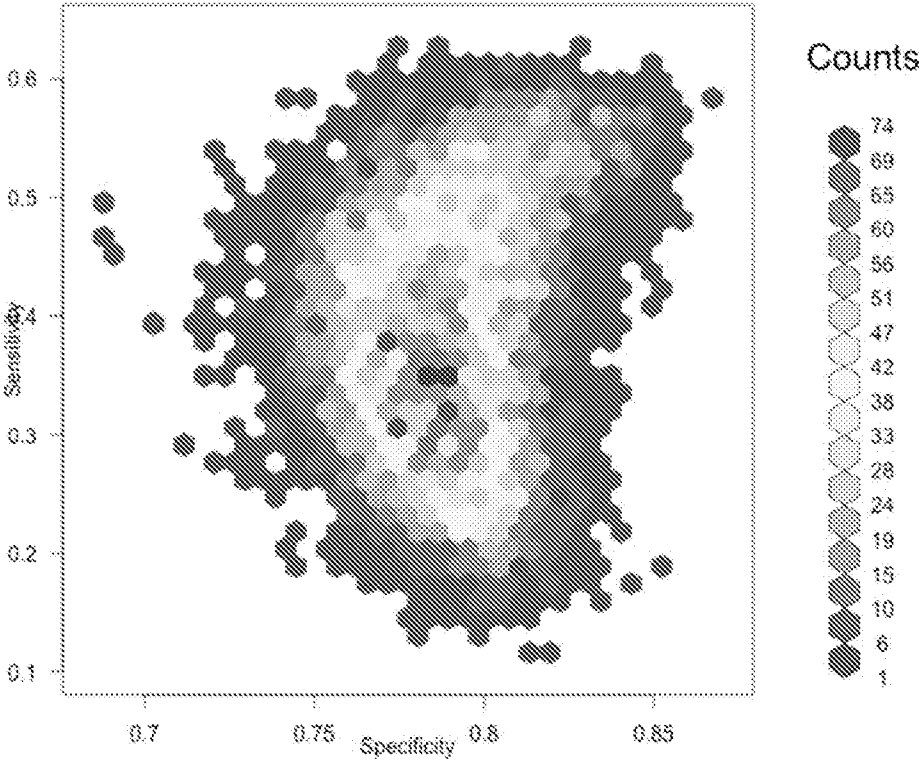


Figure 10

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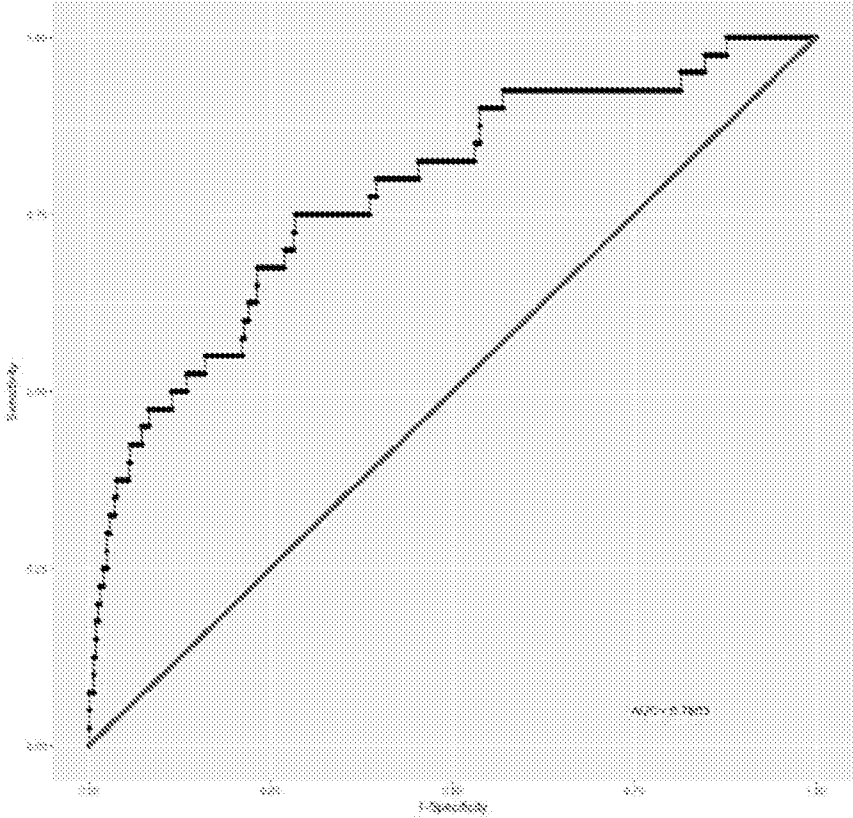


Figure 11

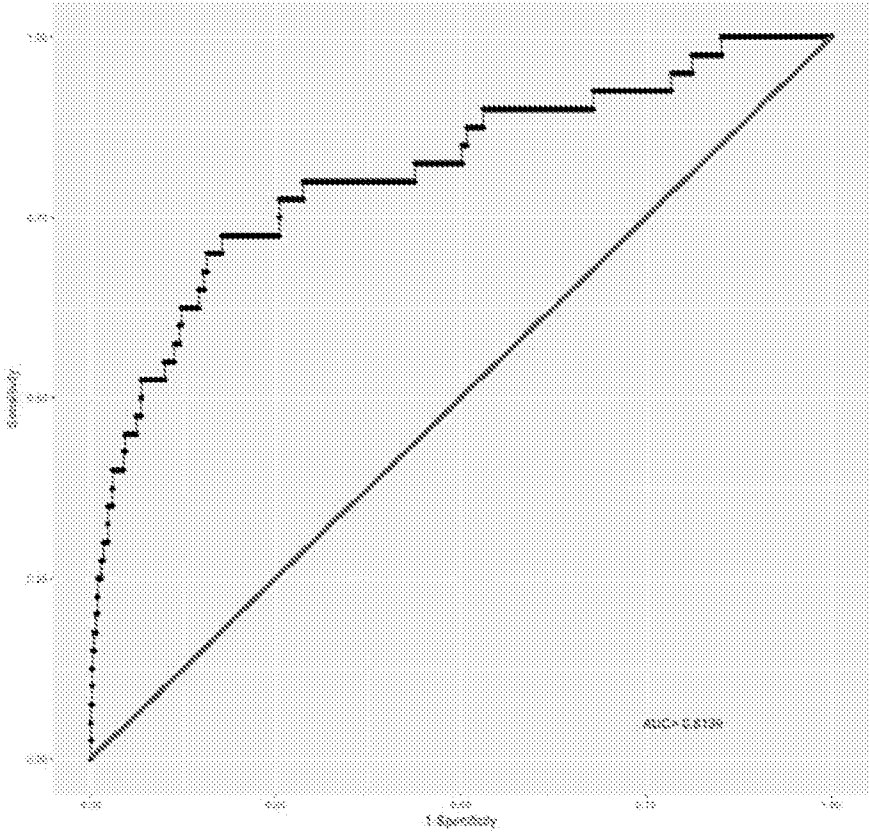


Figure 12

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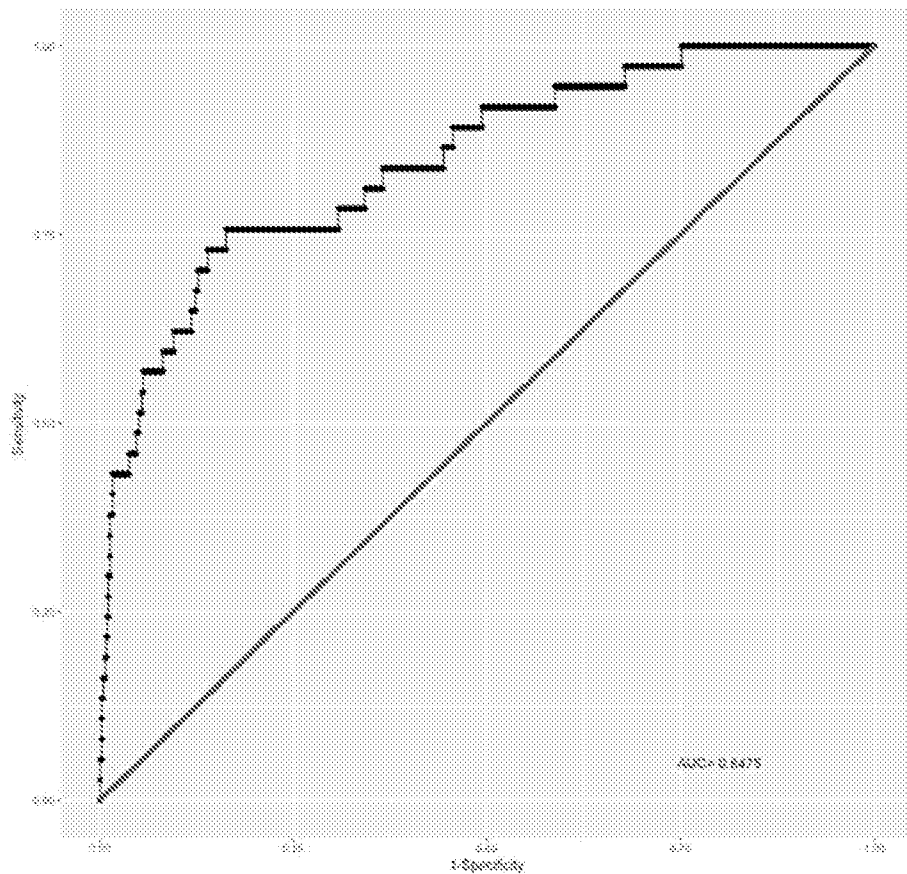


Figure 13

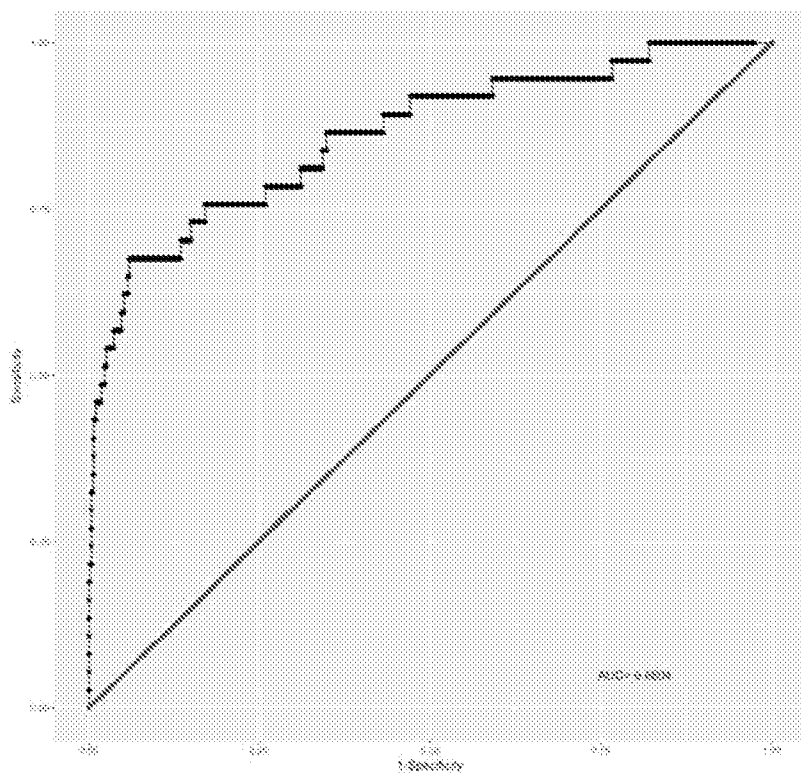
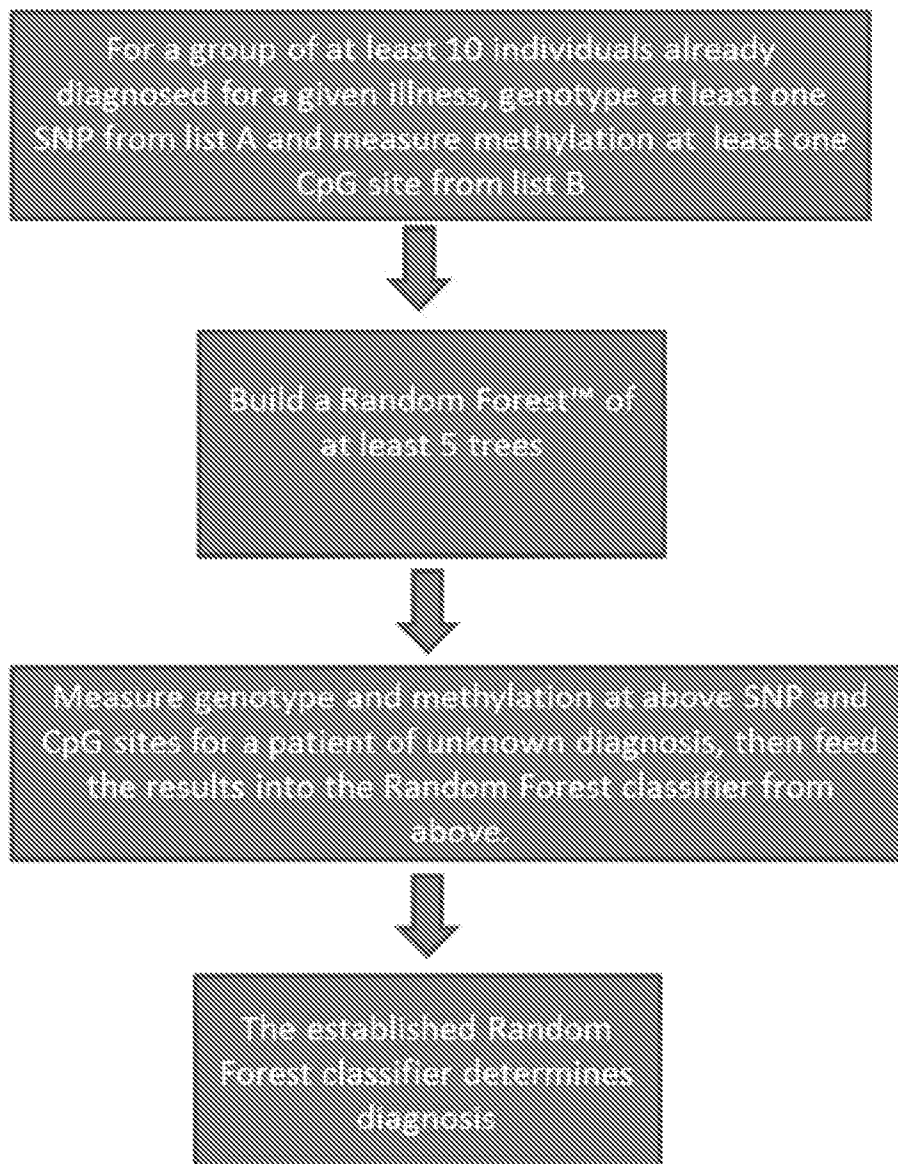


Figure 14



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A2BP1	ACAD9	ACVR2A	ADPRHL2	AK1	ALS2CR8	ANKRD40
A2LD1	ACADM	ADAL	ADRA1B	AK2	ALX3	ANKRD42
A4GALT	ACAP2	ADAM10	ADRA2A	AK3	ALX4	ANKRD44
AACS	ACAP3	ADAM11	ADRA2C	AK3L1	AMDHD2	ANKRD53
AACSL	ACAT2	ADAM12	ADRB2	AK7	AMICA1	ANKRD54
AADAT	ACBD3	ADAM15	ADSL	AKAP1	AMIGO1	ANKRD6
AAK1	ACBD4	ADAM19	AEBP1	AKAP10	AMIGO2	ANKRD9
AANAT	ACBD5	ADAM22	AEBP2	AKAP11	AMIGO3	ANKS1A
AARS2	ACBD6	ADAM23	AEN	AKAP13	AMMECR1L	ANKS1B
AARSD1	ACBD7	ADAM33	AFAP1	AKAP8	AMN1	ANKS3
AASDH	ACCN1	ADAM6	AFARP1	AKAP8L	AMOTL2	ANKS4B
AASDHPPT	ACCN4	ADAM8	AFF1	AKAP9	AMPD2	ANKS6
AATF	ACCN5	ADAM9	AFF3	AKD1	AMPD3	ANLN
AATK	ACCS	ADAMTS12	AFG3L1	AKIRIN1	AMPH	ANO1
ABCA1	ACCSL	ADAMTS14	AFG3L2	AKR1A1	AMZ2	ANO10
ABCA2	ACD	ADAMTS15	AGAP1	AKR1B1	ANAPC1	ANO2
ABCB9	ACE	ADAMTS16	AGAP11	AKR1B15	ANAPC11	ANO5
ABCC1	ACIN1	ADAMTS17	AGAP3	AKR1C2	ANAPC7	ANO6
ABCC5	ACLY	ADAMTS2	AGBL3	AKR1E2	ANG	ANO7
ABCC6P2	ACN9	ADAMTS20	AGBL4	AKR7A3	ANGEL1	ANO8
ABCD3	ACO2	ADAMTS5	AGER	AKT1	ANGEL2	ANO9
ABCD4	ACOT11	ADAMTS7	AGFG1	AKT2	ANGPT4	ANP32A
ABCE1	ACOT13	ADAMTSL2	AGK	AKT3	ANK1	ANP32B
ABCF3	ACOT2	ADAMTSL4	AGMAT	ALAS1	ANKDD1A	ANP32E
ABCG1	ACOT4	ADAP1	AGPAT3	ALCAM	ANKFY1	ANTXR1
ABCG2	ACOT7	ADAR	AGPAT4	ALDH16A1	ANKH	ANTXR2
ABHD10	ACOX1	ADARB1	AGPAT5	ALDH3A2	ANKHD1	ANUBL1
ABHD14A	ACOX3	ADARB2	AGPAT6	ALDH5A1	ANKLE1	ANXA13
ABHD2	ACOXL	ADAT1	AGPAT9	ALDH7A1	ANKLE2	ANXA3
ABHD5	ACP1	ADC	AGRN	ALDH9A1	ANKRD10	ANXA4
ABHD6	ACP6	ADCK2	AGTR1	ALDOA	ANKRD11	ANXA5
ABI2	ACSF3	ADCK5	AHCTF1	ALG10B	ANKRD12	ANXA6
ABI3BP	ACSL1	ADCY10	AHCY	ALG14	ANKRD16	ANXA7
ABL1	ACSL3	ADCY2	AHCYL1	ALG2	ANKRD17	ANXA9
ABL2	ACTB	ADCY3	AHDC1	ALG5	ANKRD18A	AP1AR
ABLIM1	ACTG1	ADCY5	AHI1	ALG9	ANKRD24	AP1B1
ABLIM2	ACTL6A	ADCY9	AHNAK	ALKBH2	ANKRD26	AP1M2
ABO	ACTN1	ADCYAP1	AHNAK2	ALKBH3	ANKRD27	AP2A2
ABR	ACTN2	ADD1	AHR	ALKBH4	ANKRD28	AP2M1
ABT1	ACTN4	ADD2	AHRR	ALKBH5	ANKRD30A	AP2S1
ABTB1	ACTR10	ADD3	AHSG	ALKBH7	ANKRD30B	AP3B1
ABTB2	ACTR1A	ADH1C	AIG1	ALMS1	ANKRD32	AP3B2
ACAA1	ACTR5	ADH5	AIM1	ALOX12B	ANKRD33	AP3D1
ACAA2	ACTR8	ADM	AIMP2	ALOX15	ANKRD33B	AP3M1
ACACA	ACVR1	ADNP	AIP	ALOX5	ANKRD34A	AP3M2
ACACB	ACVR1B	ADPGK	AIRE	ALS2	ANKRD36	AP3S2
ACAD10	ACVR1C	ADPRHL1	AJAP1	ALS2CR4	ANKRD39	AP4E1
AP4S1	ARHGAP12	ARMC6	ATAD3A	ATP6V0C	B4GALT7	BCL2
APAF1	ARHGAP15	ARMC8	ATAD3B	ATP6V0D1	B9D1	BCL2L11
APBB2	ARHGAP17	ARMS2	ATAD3C	ATP6V1B1	BAALC	BCL6
APBB3	ARHGAP19	ARNT2	ATE1	ATP6V1C2	BACE2	BCL7B
APC	ARHGAP20	ARPC1B	ATF1	ATP6V1E1	BACH2	BCLAF1
APCDD1L	ARHGAP21	ARPC2	ATF2	ATP6V1F	BAD	BCO2
APH1A	ARHGAP22	ARPC3	ATF3	ATP6V1G1	BAG2	BCR
APH1B	ARHGAP25	ARPC4	ATF4	ATP6V1H	BAG5	BDH2

Figure 15-1

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API5	ARHGAP29	ARPC5	ATF6B	ATP8A1	BAHCC1	BDP1
APITD1	ARHGAP5	ARPP19	ATF7	ATP8B2	BAI1	BEAN
APLF	ARHGAP9	ARRB1	ATF7IP	ATP8B3	BAI3	BECN1
APLP1	ARHGEF1	ARRB2	ATG12	ATP9A	BAIAP2	BEGAIN
APOA1BP	ARHGEF10	ARRDC2	ATG16L1	ATPBD4	BAIAP2L1	BEND3
APOA4	ARHGEF11	ARSA	ATG16L2	ATPIF1	BAIAP2L2	BEND7
APOB	ARHGEF12	ARSB	ATG2B	ATR	BAK1	BET1
APOBEC3A	ARHGEF15	ARSG	ATG5	ATRN	BAMBI	BET1L
APOBEC3F	ARHGEF16	ARSI	ATG7	ATRNL1	BANP	BFAR
APOBEC3G	ARHGEF17	ARSK	ATHL1	ATXN1	BARHL2	BHLHE23
APOC1	ARHGEF18	ART3	ATIC	ATXN1L	BARX2	BHLHE40
APOL1	ARHGEF19	ARVCF	ATL2	ATXN2	BAT1	BICD1
APOL6	ARHGEF2	ASAH1	ATL3	ATXN2L	BAT2	BICD2
APOLD1	ARHGEF3	ASAH2B	ATM	ATXN3	BAT2L1	BIK
APOM	ARHGEF4	ASAP1	ATOH8	ATXN7	BAT2L2	BIN3
APP	ARHGEF7	ASAP1IT1	ATP11A	ATXN7L1	BAT3	BIRC2
APPL1	ARID1A	ASAP2	ATP11B	ATXN7L3	BAT4	BIRC5
APPL2	ARID1B	ASAP3	ATP13A1	AUH	BAT5	BIRC6
APRT	ARID3A	ASB1	ATP13A2	AURKA	BATF3	BIVM
APTIX	ARID4A	ASB13	ATP1A1	AURKAIP1	BAX	BLCAP
AQP10	ARID5A	ASB18	ATP1A2	AUTS2	BAZ1A	BLM
AQR	ARID5B	ASB6	ATP1B1	AVEN	BAZ2A	BLMH
ARAP1	ARIH2	ASB7	ATP1B2	AVL9	BBC3	BLOC1S2
ARAP2	ARL1	ASF1B	ATP1B3	AVPR1B	BBS10	BLVRA
ARAP3	ARL10	ASGR1	ATP2A2	AXIN1	BBS2	BLZF1
ARC	ARL11	ASH2L	ATP2B2	AXIN2	BBS5	BMF
ARCN1	ARL15	ASL	ATP2B4	AXL	BBS9	BMP2
ARF1	ARL2	ASNS	ATP5B	AZI1	BBX	BMP2K
ARF3	ARL2BP	ASNSD1	ATP5C1	B2M	BCAP29	BMP4
ARF4	ARL3	ASPDH	ATP5D	B3GALNT2	BCAR1	BMP6
ARF5	ARL6	ASPM	ATP5EP2	B3GALT4	BCAR3	BMP7
ARFGAP2	ARL6IP1	ASPSCR1	ATP5G1	B3GALT1	BCAS2	BMP8A
ARFGAP3	ARL6IP4	ASRGL1	ATP5G2	B3GAT2	BCAS3	BMPER
ARFGEF1	ARL6IP5	ASS1	ATP5H	B3GAT3	BCAT1	BMPR1A
ARFIP1	ARL6IP6	ASTN1	ATP5J	B3GNT1	BCAT2	BMPR2
ARGFX	ARL8A	ASXL1	ATP5L	B3GNT7	BCCIP	BMS1
ARGLU1	ARL8B	ASXL2	ATP5SL	B3GNTL1	BCDIN3D	BNC2
ARHGAP1	ARMC10	ATAD1	ATP6V0A2	B4GALNT1	BCL10	BNIP1
ARHGAP10	ARMC5	ATAD2	ATP6V0B	B4GALNT3	BCL11A	BNIP2
BNIP3	BTRC	C11orf83	C14orf28	C17orf80	C1orf151	C20orf199
BOC	BUB1	C11orf9	C14orf38	C17orf82	C1orf152	C20orf20
BOD1L	BUB1B	C11orf91	C14orf39	C17orf85	C1orf156	C20orf26
BOLA1	BUB3	C11orf92	C14orf43	C17orf89	C1orf159	C20orf27
BOLA3	BUD13	C12orf11	C14orf45	C17orf90	C1orf173	C20orf29
BOP1	BUD31	C12orf23	C14orf68	C17orf93	C1orf183	C20orf3
BPHL	BZRAP1	C12orf26	C14orf72	C17orf95	C1orf187	C20orf30
BPNT1	BZW1	C12orf34	C14orf93	C17orf96	C1orf190	C20orf43
BPTF	BZW2	C12orf35	C15orf37	C17orf98	C1orf198	C20orf46
BRCA1	C10orf114	C12orf41	C15orf42	C18orf10	C1orf200	C20orf7
BRCA2	C10orf119	C12orf42	C15orf51	C18orf18	C1orf201	C20orf94
BRD1	C10orf129	C12orf45	C15orf59	C18orf19	C1orf203	C21orf129
BRD2	C10orf131	C12orf49	C15orf60	C18orf20	C1orf212	C21orf15
BRD3	C10orf137	C12orf5	C16orf35	C18orf21	C1orf213	C21orf33
BRD8	C10orf140	C12orf50	C16orf42	C18orf22	C1orf216	C21orf59
BRF1	C10orf18	C12orf53	C16orf46	C18orf34	C1orf220	C21orf63

Figure 15-2

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2026201866	12 Mar 2026	BRI3	C10orf2	C12orf56	C16orf53	C18orf54	C1orf229	C21orf66
		BRI3BP	C10orf32	C12orf57	C16orf55	C18orf55	C1orf25	C21orf70
		BRIX1	C10orf4	C12orf59	C16orf57	C19orf10	C1orf35	C21orf91
		BRMS1	C10orf41	C12orf61	C16orf58	C19orf12	C1orf53	C22orf13
		BRMS1L	C10orf46	C12orf65	C16orf62	C19orf20	C1orf55	C22orf23
		BRP44	C10orf58	C12orf66	C16orf65	C19orf22	C1orf56	C22orf24
		BRP44L	C10orf67	C12orf68	C16orf67	C19orf25	C1orf57	C22orf26
		BRPF1	C10orf75	C12orf73	C16orf68	C19orf28	C1orf58	C22orf28
		BRPF3	C10orf76	C13orf1	C16orf7	C19orf29	C1orf59	C22orf32
		BRSK2	C10orf78	C13orf18	C16orf70	C19orf36	C1orf66	C22orf36
		BRUNOL4	C10orf79	C13orf23	C16orf71	C19orf39	C1orf70	C22orf40
		BRUNOL5	C10orf93	C13orf27	C16orf72	C19orf40	C1orf74	C22orf46
		BRUNOL6	C11orf10	C13orf31	C16orf75	C19orf41	C1orf83	C22orf9
		BRWD1	C11orf17	C13orf35	C16orf80	C19orf48	C1orf85	C2CD4A
		BSCL2	C11orf2	C13orf37	C16orf87	C19orf51	C1orf86	C2CD4D
		BSX	C11orf20	C14orf101	C16orf90	C19orf52	C1orf89	C2orf14
		BTBD1	C11orf21	C14orf102	C16orf92	C19orf55	C1orf9	C2orf15
		BTBD10	C11orf30	C14orf104	C17orf100	C19orf57	C1orf92	C2orf27A
		BTBD12	C11orf34	C14orf106	C17orf101	C19orf6	C1orf93	C2orf27B
		BTBD2	C11orf48	C14orf126	C17orf104	C19orf66	C1orf95	C2orf28
		BTBD7	C11orf49	C14orf133	C17orf106	C19orf69	C1QA	C2orf29
		BTBD9	C11orf51	C14orf135	C17orf42	C1GALT1	C1QL1	C2orf42
		BTC	C11orf54	C14orf138	C17orf48	C1orf101	C1QL2	C2orf43
		BTD	C11orf57	C14orf142	C17orf51	C1orf103	C1QL3	C2orf52
		BTF3	C11orf58	C14orf145	C17orf53	C1orf107	C1QL4	C2orf53
		BTG1	C11orf67	C14orf147	C17orf56	C1orf109	C20orf111	C2orf58
		BTG3	C11orf68	C14orf149	C17orf57	C1orf110	C20orf117	C2orf60
		BTN2A1	C11orf71	C14orf162	C17orf62	C1orf113	C20orf12	C2orf61
		BTN2A2	C11orf75	C14orf174	C17orf66	C1orf115	C20orf151	C2orf62
		BTN3A2	C11orf80	C14orf182	C17orf70	C1orf124	C20orf152	C2orf64
		BTNL2	C11orf82	C14orf21	C17orf77	C1orf125	C20orf196	C2orf68
		C2orf69	C5orf37	C7orf20	C9orf69	CAMK2N1	CBLL1	CCDC46
		C2orf70	C5orf39	C7orf23	C9orf82	CAMK4	CBLN1	CCDC47
		C2orf71	C5orf43	C7orf25	C9orf85	CAMKK2	CBLN3	CCDC49
		C2orf73	C5orf44	C7orf26	C9orf86	CAMSAP1	CBR4	CCDC51
		C2orf74	C5orf45	C7orf27	C9orf89	CAMSAP1L1	CBS	CCDC55
		C2orf77	C5orf51	C7orf36	C9orf93	CAMTA1	CBX1	CCDC57
		C2orf81	C5orf52	C7orf38	C9orf98	CAMTA2	CBX2	CCDC59
		C2orf82	C5orf62	C7orf40	CA12	CAND1	CBX3	CCDC6
		C2orf88	C6orf1	C7orf41	CA13	CAND2	CBX4	CCDC60
		C2orf89	C6orf10	C7orf44	CA4	CANT1	CBX6	CCDC61
		C3orf1	C6orf103	C7orf46	CA5A	CANX	CBX8	CCDC62
		C3orf17	C6orf108	C7orf49	CAB39L	CAP1	CC2D1A	CCDC64
		C3orf18	C6orf118	C7orf50	CABC1	CAPN1	CC2D1B	CCDC64B
		C3orf19	C6orf122	C7orf51	CABIN1	CAPN10	CCAR1	CCDC66
		C3orf24	C6orf125	C7orf52	CABLES1	CAPNS1	CCBE1	CCDC7
		C3orf54	C6orf126	C7orf57	CABLES2	CAPRN1	CCDC105	CCDC72
		C3orf57	C6orf129	C7orf59	CABP7	CAPS2	CCDC106	CCDC77
		C3orf58	C6orf130	C7orf60	CABYR	CAPZA1	CCDC107	CCDC79
		C3orf63	C6orf134	C7orf61	CACHD1	CARD10	CCDC109B	CCDC83
		C3orf71	C6orf136	C7orf64	CACNA1A	CARD11	CCDC111	CCDC84
		C3orf72	C6orf145	C7orf70	CACNA1C	CARD6	CCDC12	CCDC85A
		C3orf75	C6orf147	C7orf71	CACNA1D	CARHSP1	CCDC121	CCDC85B
		C3orf77	C6orf150	C8G	CACNA1G	CARM1	CCDC122	CCDC86
		C4orf10	C6orf163	C8orf12	CACNA2D2	CARS	CCDC123	CCDC88A

Figure 15-3

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C4orf14	C6orf167	C8orf33	CACNB2	CARS2	CCDC126	CCDC88B
C4orf21	C6orf168	C8orf37	CACNG2	CASC1	CCDC129	CCDC88C
C4orf22	C6orf192	C8orf38	CACNG4	CASC5	CCDC13	CCDC90B
C4orf23	C6orf195	C8orf40	CACNG8	CASD1	CCDC134	CCDC92
C4orf29	C6orf203	C8orf42	CACYBP	CASKIN1	CCDC135	CCDC93
C4orf3	C6orf204	C8orf55	CAD	CASKIN2	CCDC136	CCDC96
C4orf32	C6orf217	C8orf59	CADPS2	CASP1	CCDC137	CCHCR1
C4orf33	C6orf218	C8orf76	CAGE1	CASP10	CCDC144B	CCKAR
C4orf34	C6orf221	C9	CALB1	CASP2	CCDC146	CCKBR
C4orf36	C6orf226	C9orf102	CALCA	CASP4	CCDC148	CCL18
C4orf41	C6orf25	C9orf106	CALCB	CASP7	CCDC15	CCL23
C4orf42	C6orf27	C9orf116	CALCOCO2	CASP8AP2	CCDC151	CCL3
C4orf48	C6orf41	C9orf122	CALHM2	CASP9	CCDC157	CCL5
C4orf51	C6orf47	C9orf130	CALM1	CAST	CCDC163P	CCNA2
C4orf52	C6orf48	C9orf140	CALM3	CASZ1	CCDC21	CCND1
C4orf6	C6orf52	C9orf163	CALN1	CATSPER2	CCDC25	CCND2
C5orf13	C6orf64	C9orf171	CALR	CATSPER4	CCDC28A	CCND3
C5orf24	C6orf70	C9orf21	CALU	CATSPERG	CCDC34	CCNDBP1
C5orf27	C6orf72	C9orf25	CAMK1	CAV1	CCDC37	CCNE2
C5orf28	C6orf81	C9orf3	CAMK1D	CBFA2T3	CCDC40	CCNF
C5orf33	C6orf94	C9orf4	CAMK2B	CBFB	CCDC42	CCNJL
C5orf34	C7orf10	C9orf41	CAMK2D	CBLB	CCDC42B	CCNL1
C5orf36	C7orf13	C9orf64	CAMK2G	CBLC	CCDC45	CCNL2
CCNO	CDC25A	CDKN1C	CEP55	CHRNA1	CLK2P	CNTNAP2
CCNT1	CDC25B	CDKN2AIP	CEP57	CHRNA1	CLK3	CNTNAP4
CCNY	CDC25C	CDKN2BAS	CEP63	CHRNA2	CLK4	COASY
CCNYL1	CDC26	CDKN2C	CEP68	CHST1	CLN3	COBL
CCR1	CDC27	CDKN3	CEP72	CHST10	CLN8	COBRA1
CCR6	CDC42BPA	CDNF	CEP76	CHST11	CLOCK	COG1
CCRN4L	CDC42BPB	CDO1	CEP97	CHST12	CLP1	COG2
CCT3	CDC42BPG	CDRT15P	CES3	CHST15	CLPB	COG3
CCT5	CDC42EP2	CDV3	CETN3	CHST2	CLPP	COG4
CCT6A	CDC42EP3	CDX2	CFDP1	CHST6	CLPTM1	COG5
CCT6B	CDC42EP4	CDYL	CFL1	CHSY1	CLPX	COG6
CCT6P1	CDC42EP5	CEACAM16	CFL2	CHTF8	CLSPN	COG7
CCT7	CDC42SE1	CEACAM21	CFLAR	CHUK	CLTA	COIL
CCT8	CDC42SE2	CEACAM5	CGB2	CHURC1	CLTC	COL11A2
CD163L1	CDC7	CEBPB	CGGBP1	CIB1	CLUAP1	COL12A1
CD164	CDC73	CEBPG	CGRRF1	CIDEA	CLUL1	COL18A1
CD226	CDCA2	CEBPZ	CH25H	CIITA	CLVS2	COL1A1
CD248	CDCA4	CECR4	CHAC1	CINP	CLYBL	COL1A2
CD276	CDCA7	CECR6	CHAF1A	CIRBP	CMBL	COL22A1
CD2BP2	CDCA8	CECR7	CHCHD1	CISD1	CMC1	COL25A1
CD300LB	CDCP1	CELA2A	CHCHD2	CISH	CMIP	COL29A1
CD320	CDH11	CELA3A	CHCHD3	CIT	CMPK1	COL2A1
CD34	CDH13	CELA3B	CHCHD5	CITED2	CMPK2	COL5A1
CD38	CDH15	CELSR1	CHCHD6	CKAP2	CMTM7	COL5A3
CD3E	CDH23	CELSR3	CHCHD8	CKAP2L	CN5H6.4	COL6A2
CD3EAP	CDH24	CENPA	CHD3	CKAP5	CNBD1	COL9A3
CD4	CDH26	CENPB	CHD5	CKB	CNBP	COLEC12
CD44	CDH5	CENPBD1	CHD6	CKLF	CNDP2	COMMD1
CD46	CDK11A	CENPC1	CHD7	CKS1B	CNFN	COMMD10
CD48	CDK11B	CENPE	CHEK1	CKS2	CNKSR3	COMMD4
CD55	CDK12	CENPF	CHERP	CLASP1	CNN2	COMMD5
CD58	CDK13	CENPH	CHFR	CLCA4	CNNM2	COPB2

Figure 15-4

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CD59	CDK14	CENPK	CHIC2	CLCN2	CNNM3	COPE
CD81	CDK17	CENPL	CHID1	CLCN6	CNO	COPG
CD83	CDK19	CENPN	CHKA	CLCNKB	CNOT10	COPS6
CD8A	CDK2AP2	CENPO	CHKB	CLDN19	CNOT2	COPS7B
CD9	CDK4	CENPQ	CHKB-CPT1B	CLDN3	CNOT3	COQ10A
CD96	CDK5	CENPT	CHL1	CLDND2	CNOT6	COQ10B
CD97	CDK5R1	CENPV	CHMP2A	CLEC12B	CNOT8	COQ3
CDADC1	CDK5RAP1	CEP120	CHMP2B	CLEC16A	CNP	COQ4
CDAN1	CDK6	CEP135	CHMP7	CLEC17A	CNPY2	COQ6
CDC14A	CDK7	CEP152	CHN2	CLIC1	CNPY3	COQ7
CDC14B	CDK8	CEP164	CHP	CLIC4	CNR2	CORO1A
CDC14C	CDKAL1	CEP170	CHPF2	CLIC6	CNRIP1	CORO1B
CDC20	CDKL2	CEP192	CHPT1	CLIP2	CNST	CORO6
CDC20B	CDKN1A	CEP250	CHRA1	CLIP4	CNTN4	CORO7
CDC23	CDKN1B	CEP350	CHRM5	CLK1	CNTN5	COX10
COX11	CROCC2	CTNNA1	CYBASC3	DAXX	DDX1	DGCR9
COX15	CRTAC1	CTNNA2	CYCS	DAZAP1	DDX10	DGKD
COX16	CRTAP	CTNNA3	CYCSP52	DAZAP2	DDX11	DGKE
COX18	CRTC1	CTNNAL1	CYFIP1	DBF4B	DDX12	DGKH
COX5B	CRTC2	CTNNB1	CYFIP2	DBH	DDX17	DGKI
COX6A1	CRX	CTNNBIP1	CYLD	DBI	DDX19A	DGKZ
COX6B1	CRY2	CTNND2	CYP11A1	DBNDD1	DDX20	DHCR24
COX7A2L	CRYGC	CTNS	CYP17A1	DBNDD2	DDX21	DHODH
COX7B2	CRYGN	CTPS	CYP1A1	DBNL	DDX24	DHPS
COX8A	CRYL1	CTR9	CYP1B1	DBP	DDX27	DHRS12
CPAMD8	CRYM	CTRC	CYP20A1	DBX1	DDX28	DHRS13
CPEB3	CSAD	CTSA	CYP26A1	DCAF10	DDX31	DHRS2
CPEB4	CSDAP1	CTSB	CYP26B1	DCAF12	DDX39	DHRS3
CPLX1	CSDE1	CTSC	CYP27A1	DCAF13	DDX41	DHRS7B
CPN2	CSE1L	CTSO	CYP2A6	DCAF4	DDX42	DHRS7C
CPNE1	CSF1	CTSZ	CYP2A7	DCAF4L1	DDX49	DHRS9
CPNE7	CSF1R	CTTN	CYP2C9	DCAF5	DDX50	DHX16
CPOX	CSF2RB	CTTNBP2NL	CYP2F1	DCAF6	DDX51	DHX29
CPSF1	CSGALNACT2	CTU1	CYP2R1	DCAF7	DDX54	DHX33
CPSF3	CSHL1	CTXN1	CYP3A4	DCAF8	DDX59	DHX34
CPSF3L	CSK	CUBN	CYP3A43	DCAKD	DDX60	DHX35
CPSF6	CSMD1	CUEDC2	CYP3A5	DCBLD1	DECR2	DHX36
CPT1A	CSMD2	CUGBP1	CYP4F12	DCHS1	DEF8	DHX37
CPT2	CSMD3	CUL2	CYP4F2	DCHS2	DEFB125	DHX38
CPZ	CSNK1D	CUL3	CYP4F3	DCK	DEFB132	DHX58
CR1	CSNK1E	CUL4A	CYP4V2	DCLK1	DEK	DHX8
CR1L	CSNK2A1	CUL5	CYP4Z2P	DCLRE1B	DENND1A	DHX9
CRABP2	CSPG4	CUL7	CYP51A1	DCLRE1C	DENND2A	DIABLO
CRAMP1L	CSPG5	CUL9	CYTH1	DCP1A	DENND2C	DICER1
CRB2	CSPP1	CUTA	CYTH2	DCP1B	DENND3	DIDO1
CRBN	CSRNP2	CUX1	CYTH3	DCP2	DENND4B	DIMT1L
CRCP	CSRP1	CUX2	CYTA	DCTD	DENND4C	DIP2B
CREB3L2	CSRP2	CXCL3	CYTSB	DCTN5	DEPDC1B	DIP2C
CREB5	CST2	CXCR1	D2HGDH	DCTN6	DEPDC5	DIRC2
CREBBP	CST3	CXCR2	DAAM1	DCTPP1	DEPDC7	DIS3
CREBL2	CST4	CXCR4	DAB1	DCUN1D1	DERL1	DISC1
CREG1	CST6	CXCR7	DAB2IP	DCUN1D3	DERL2	DKFZP434H168
CRELD1	CSTF1	CXXC1	DACH1	DCUN1D4	DERL3	DKFZp686A1627
CREM	CSTF3	CXXC4	DACT3	DDA1	DET1	DKFZp686O24166
CRHR1	CTAGE5	CXXC5	DAD1	DDAH1	DEXI	DKKL1

Figure 15-5

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CRIP2	CTBP1	CYB561	DAGLB	DDB2	DGAT1	DLAT
CRISPLD2	CTBP2	CYB5B	DAK	DDC	DGAT2	DLC1
CRKL	CTBS	CYB5D2	DALRD3	DDHD2	DGCR14	DLD
CRLS1	CTDSPL	CYB5R1	DAND5	DDN	DGCR2	DLEU1
CRMP1	CTDSPL2	CYB5R3	DAP	DDO	DGCR5	DLG2
CRNKL1	CTF1	CYB5R4	DAP3	DDOST	DGCR6L	DLG4
CROCC	CTH	CYBA	DARS	DDR1	DGCR8	DLGAP1
DLGAP2	DNM1P35	DST	EBF1	EGFL8	ELF3	EPC1
DLGAP3	DNM2	DSTN	EBF3	EGLN2	ELFN2	EPCAM
DLGAP4	DNM3	DTD1	EBPL	EGR1	ELK3	EPDR1
DLGAP5	DNMT1	DTNB	ECD	EHBP1	ELL	EPHA1
DLK1	DNMT3A	DTNBP1	ECE1	EHBP1L1	ELL2	EPHA2
DLK2	DNPEP	DTWD1	ECEL1	EHD1	ELL3	EPHA3
DLL1	DNTTIP2	DTWD2	ECEL1P2	EHD3	ELMO1	EPHA6
DLL3	DOC2A	DTX3	ECHDC3	EHD4	ELMO2	EPHA7
DLL4	DOC2B	DTX4	ECHS1	EHMT1	ELMOD3	EPHA8
DLX3	DOCK1	DTYMK	EDC4	EHMT2	ELOF1	EPHB1
DLX5	DOCK2	DUOX1	EDEM1	EID2	ELOVL1	EPHB3
DLX6AS	DOCK5	DUS2L	EDEM2	EID2B	ELOVL2	EPHB4
DMBT1	DOCK6	DUS3L	EDEM3	EIF1AD	ELOVL5	EPHB6
DMKN	DOCK7	DUSP1	EDF1	EIF1B	ELOVL6	EPHX1
DMP1	DOK5	DUSP11	EDIL3	EIF2AK2	ELOVL7	EPHX3
DMPK	DOLK	DUSP14	EDN1	EIF2AK3	ELP2	EPHX4
DMRTA2	DOLPP1	DUSP18	EDNRB	EIF2AK4	ELP2P	EPM2AIP1
DMTF1	DOM3Z	DUSP28	EEA1	EIF2B1	ELP3	EPN2
DMXL1	DPAGT1	DUSP4	EED	EIF2B4	ELP4	EPO
DMXL2	DPEP2	DUSP5	EEF1A1	EIF2C1	EME1	EPPK1
DNA2	DPEP3	DUSP5P	EEF1A2	EIF2C2	EMID1	EPS8
DNAH1	DPF1	DUSP6	EEF1B2	EIF2C3	EMID2	EPS8L2
DNAH12	DPF3	DUSP7	EEF1D	EIF2S1	EMILIN2	ERAL1
DNAI1	DPH1	DUT	EEF1DP3	EIF2S2	EMILIN3	ERBB2IP
DNAJA2	DPH2	DVL2	EEF1E1	EIF3A	EML3	ERBB3
DNAJB1	DPH3	DVL3	EEF1G	EIF3D	EMX1	ERBB4
DNAJB13	DPH3B	DYDC2	EEF2	EIF3F	EMX2	ERC2
DNAJB14	DPM2	DYM	EEFSEC	EIF3J	ENAH	ERCC3
DNAJB2	DPM3	DYNC1H1	EEPD1	EIF3K	ENC1	ERCC5
DNAJB6	DPP3	DYNC1I1	EFCAB1	EIF3M	ENDOD1	ERCC6
DNAJC1	DPP6	DYNC1I2	EFCAB4A	EIF4A1	ENDOG	ERF
DNAJC10	DPP9	DYNC1LI1	EFCAB5	EIF4A2	ENGASE	ERGIC2
DNAJC13	DPPA2	DYNLL1	EFCAB6	EIF4B	ENO3	ERGIC3
DNAJC21	DPY19L1	DYNLL2	EFCAB7	EIF4E	ENOPH1	ERI1
DNAJC27	DPY19L2P2	DYNLT1	EFCAB9	EIF4E3	ENPP1	ERI3
DNAJC28	DPY19L2P4	DYRK1B	EFEMP2	EIF4EBP2	ENPP7	ERLIN1
DNAJC4	DPY19L4	DYRK2	EFHA1	EIF4ENIF1	ENSA	ERLIN2
DNAJC5	DPYD	DYRK3	EFHA2	EIF4G3	ENTPD4	ERN1
DNAJC7	DPYSL2	DZIP1	EFHD1	EIF4H	ENTPD6	ERO1LB
DNAJC8	DPYSL4	DZIP1L	EFNA1	EIF5	ENY2	ERP29
DNAL4	DPYSL5	E2F1	EFNA2	EIF5A	EP400	ERP44
DNASE2	DR1	E2F3	EFNA3	EIF5B	EP400NL	ESAM
DND1	DRAM1	E2F6	EFNA5	EIF6	EPAS1	ESF1
DNER	DSCR3	E2F8	EFNB2	ELAC2	EPB41	ESPL1
DNLZ	DSE	E4F1	EFR3B	ELANE	EPB41L1	ESPN
DNM1	DSN1	EARS2	EFTUD1	ELAVL1	EPB41L2	ESR1
DNM1L	DSP	EBAG9	EFTUD2	ELF2	EPB49	ESR2
ESRRA	FADS1	FAM157A	FAM46C	FASTK	FDFT1	FLJ22536

Figure 15-6

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ESRRB	FADS6	FAM158A	FAM47E	FASTKD2	FDPS	FLJ25363
ESYT2	FAF1	FAM159A	FAM48A	FASTKD5	FDXR	FLJ31306
ESYT3	FAF2	FAM159B	FAM49B	FAT1	FECH	FLJ33630
ETAA1	FAH	FAM160A2	FAM53A	FAT2	FEM1A	FLJ35220
ETFDH	FAHD1	FAM161B	FAM53B	FAU	FEM1B	FLJ36777
ETHE1	FAHD2A	FAM162A	FAM53C	FBLIM1	FER1L4	FLJ39582
ETNK1	FAHD2B	FAM162B	FAM54B	FBLN1	FERMT2	FLJ41856
ETS1	FAIM	FAM163A	FAM55C	FBLN2	FERMT3	FLJ42709
ETS2	FAM100A	FAM168B	FAM55D	FBLN7	FEZF1	FLJ43390
ETV1	FAM100B	FAM169A	FAM57A	FBRSL1	FGD3	FLJ43663
ETV2	FAM101A	FAM171A2	FAM59A	FBXL12	FGD5	FLJ44606
ETV6	FAM101B	FAM175A	FAM60A	FBXL13	FGD6	FLJ45079
EVC2	FAM103A1	FAM175B	FAM64A	FBXL14	FGF11	FLJ45244
EVPL	FAM104A	FAM176A	FAM65A	FBXL16	FGF12	FLJ45983
EVX1	FAM105A	FAM180A	FAM65B	FBXL17	FGF14	FLJ90757
EVX2	FAM107B	FAM181B	FAM66B	FBXL18	FGF18	FLOT1
EWSR1	FAM108A1	FAM183A	FAM69A	FBXL6	FGF20	FLOT2
EXD3	FAM108B1	FAM183B	FAM72B	FBXL7	FGF22	FLT1
EXO1	FAM108C1	FAM184A	FAM72D	FBXL8	FGF3	FLT3
EXOC2	FAM109A	FAM185A	FAM73B	FBXO11	FGF8	FLYWCH1
EXOC4	FAM10A4	FAM186B	FAM76A	FBXO15	FGF9	FLYWCH2
EXOC6	FAM110A	FAM187B	FAM78A	FBXO18	FGFBP2	FMN1
EXOC7	FAM110B	FAM188A	FAM78B	FBXO22	FGFR1	FMNL1
EXOC8	FAM111A	FAM189A1	FAM7A2	FBXO22OS	FGFR1OP2	FMO5
EXOSC10	FAM111B	FAM189B	FAM82A2	FBXO24	FGFR2	FN3KRP
EXOSC4	FAM113A	FAM18B	FAM82B	FBXO25	FGFR4	FNBP4
EXOSC5	FAM114A2	FAM190A	FAM83H	FBXO28	FGFRL1	FNDC3A
EXOSC6	FAM115A	FAM195B	FAM86A	FBXO30	FGGY	FNDC3B
EXOSC9	FAM115C	FAM198B	FAM86B1	FBXO31	FHIT	FNIP1
EXPH5	FAM116A	FAM19A5	FAM86B2	FBXO32	FIBCD1	FNIP2
EXT1	FAM117B	FAM20B	FAM89A	FBXO33	FILIP1	FNTA
EXTL3	FAM118A	FAM20C	FAM89B	FBXO36	FIS1	FNTB
EYA3	FAM119A	FAM21A	FAM91A1	FBXO38	FIZ1	FOSB
EZH2	FAM119B	FAM21C	FAM96A	FBXO46	FKBP10	FOSL1
EZR	FAM120AOS	FAM32A	FAM96B	FBXO5	FKBP14	FOSL2
F10	FAM120B	FAM36A	FAM98A	FBXO6	FKBP1A	FOXA1
F12	FAM122A	FAM38A	FANCA	FBXO7	FKBP1B	FOXA2
F13A1	FAM125A	FAM38B	FANCC	FBXO8	FKBP2	FOXB1
F13B	FAM125B	FAM3C	FANCE	FBXW4	FKBP3	FOXC1
F2R	FAM128A	FAM3D	FANCF	FBXW9	FKBP4	FOXF1
F2RL3	FAM129A	FAM40A	FANK1	FCAR	FKBPL	FOXJ3
F3	FAM131B	FAM40B	FAR1	FCF1	FLCN	FOXK1
F7	FAM13B	FAM41C	FARP1	FCGRT	FLG	FOXK2
FABP5	FAM13C	FAM43A	FARSA	FCHO2	FLII	FOXN3
FABP6	FAM149A	FAM43B	FAS	FCHSD2	FLJ10038	FOXN4
FADD	FAM150A	FAM46A	FASN	FCRLA	FLJ11235	FOXO1
FOXO3	FYTTD1	GART	GGA3	GLYCTK	GOLGA4	GPSM2
FOXP1	FZD10	GAS2	GGCT	GM2A	GOLGA7	GPSM3
FOXP4	FZD4	GAS5	GGH	GMCL1	GOLGA7B	GPT
FOXR1	FZD5	GAS7	GGPS1	GMCL1L	GOLIM4	GPX1
FOXRED2	FZD7	GAS8	GGT1	GMDS	GOLPH3	GPX6
FPR1	FZR1	GATA2	GGT5	GMEB2	GON4L	GRAMD1C
FPR2	G2E3	GATA3	GGTLC1	GMFB	GOPC	GRASP
FRAS1	G3BP1	GATA5	GH1	GMIP	GORASP1	GRB2
FRAT1	G3BP2	GATA6	GH2	GML	GORASP2	GREB1

Figure 15-7

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FRAT2	G6PC	GATAD2A	GHDC	GMPPA	GOSR2	GREM1
FREQ	GAA	GATAD2B	GHITM	GMPPB	GOT1	GRHL2
FRG1	GAB2	GATS	GHR	GMPR	GOT2	GRHPR
FRG2B	GAB4	GATSL3	GIGYF1	GMPR2	GPATCH1	GRIA1
FRG2C	GABARAP	GBAP1	GIMAP1	GMPS	GPATCH3	GRID1
FRK	GABARAPL1	GBAS	GIMAP4	GNA11	GPBAR1	GRID2
FRMD4A	GABARAPL2	GBP3	GIMAP7	GNA13	GPBP1	GRID2IP
FRMD5	GABARAPL3	GBP4	GIN1	GNA14	GPBP1L1	GRIK4
FRMD6	GABBR1	GBP5	GIN51	GNAI2	GPC1	GRIN1
FRMD8	GABPB1	GBX1	GIN53	GNAI3	GPC6	GRIN2A
FRS3	GABPB2	GCAT	GIPC2	GNAL	GPHN	GRIN2C
FRY	GABRA4	GCDH	GIPR	GNAO1	GPIHBP1	GRIN2D
FRYL	GABRA5	GCH1	GIT2	GNAQ	GPN1	GRINA
FSCN1	GABRB1	GCLM	GJA3	GNAS	GPN2	GRINL1A
FSCN2	GABRD	GCNT4	GJA4	GNASAS	GPN3	GRIP2
FSD1	GABRG3	GCNT7	GJB2	GNB1	GPR108	GRK4
FSD1L	GAD2	GCSH	GJB4	GNB1L	GPR12	GRK5
FSTL3	GADD45B	GDAP1	GLB1	GNB2	GPR123	GRK6
FTHL3	GAK	GDAP2	GLB1L2	GNB2L1	GPR124	GRM4
FTL	GALC	GDE1	GLB1L3	GNB5	GPR125	GRM7
FTO	GALE	GDF1	GLCCI1	GNE	GPR133	GRM8
FTSJD1	GALK1	GDF11	GLI2	GNG10	GPR137	GRN
FUBP1	GALK2	GDF6	GLIS2	GNG12	GPR152	GRPEL1
FUCA1	GALNT10	GDF7	GLIS3	GNG2	GPR153	GRSF1
FUCA2	GALNT2	GDI2	GLO1	GNG4	GPR160	GSK3A
FUK	GALNT3	GNDF	GLOD4	GNG7	GPR177	GSR
FUS	GALNT6	GNPD1	GLP1R	GNGT1	GPR19	GSTA1
FUT10	GALNT7	GNPD5	GLRA3	GNL1	GPR26	GSTCD
FUT11	GALNT8	GEM	GLRX2	GNL2	GPR4	GSTM4
FUT2	GALNTL4	GEMIN6	GLRX5	GNMT	GPR45	GSTO1
FUT4	GALNTL5	GEN1	GLS	GNPAT	GPR63	GSTO2
FUT6	GALNTL6	GFI1	GLT1D1	GNPNAT1	GPR68	GSTP1
FUT8	GAN	GFM1	GLT25D2	GNPTG	GPR89B	GSTZ1
FUZ	GANC	GFM2	GLTPD1	GNRHR2	GPRC5B	GSX2
FXR1	GAPDH	GFOD1	GLTSCR2	GNS	GPRC5C	GTDC1
FXR2	GAPDHS	GFPT2	GLUD1	GOLGA2	GPRC5D	GTF2A1
FXYD3	GAPVD1	GFRA2	GLUL	GOLGA2L1	GPS1	GTF2B
FXYD5	GARS	GGA2	GLYATL1	GOLGA3	GPS2	GTF2E2
GTF2F2	HAND1	HELZ	HIST1H3C	HMGXB4	HPGD	HVCN1
GTF2H2C	HAND2	HEMK1	HIST1H3E	HMHA1	HPS1	HYAL1
GTF2H4	HARS	HERC1	HIST1H3G	HMMR	HPS3	HYAL3
GTF2I	HAS1	HERC2	HIST1H3I	HMSD	HPS5	HYAL4
GTF3C1	HAT1	HERC3	HIST1H3J	HMX3	HPSE	HYI
GTF3C5	HAUS3	HERC5	HIST1H4A	HN1L	HPSE2	HYLS1
GTF3C6	HAUS6	HERPUD2	HIST1H4C	HNF1B	HPX	IAH1
GTPBP1	HAX1	HES1	HIST1H4E	HNRNPA0	HRH4	IBTK
GTPBP3	HBP1	HES4	HIST1H4G	HNRNPA1L2	HRK	ICA1
GTPBP4	HBXIP	HES6	HIST1H4H	HNRNPA2B1	HRNBP3	ICA1L
GTPBP5	HCCA2	HEXA	HIST1H4J	HNRNPA3	HS2ST1	ICAM1
GTPBP8	HCFC1R1	HEXB	HIST1H4K	HNRNPA3P1	HS3ST1	ICAM5
GTSE1	HCFC2	HEXIM2	HIST1H4L	HNRNPAB	HS3ST5	ICK
GUCY1A2	HCG18	HEY2	HIST2H2AB	HNRNPC	HS3ST6	ID1
GUCY2D	HCG22	HFM1	HIST2H2BE	HNRNPCL1	HS6ST3	ID2
GUCY2E	HCG26	HGD	HIST2H2BF	HNRNPD	HSD17B12	ID2B
GUCY2G	HCG27	HGFAC	HIST3H2A	HNRNPF	HSD17B4	IDE

Figure 15-8

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GUF1	HCG4	HGS	HIST3H3	HNRNPH1	HSD3B2	IDH1
GUK1	HCG9	HGSNAT	HIST4H4	HNRNPH3	HSDL1	IDI1
GULP1	HCN1	HHAT	HIVEP1	HNRNPK	HSDL2	IDUA
GUSB	HCN2	HHEX	HIVEP3	HNRNPL	HSF1	IER2
GUSBL2	HCN4	HHIPL1	HK1	HNRNPM	HSF2	IER3
GXYLT2	HCP5	HHLA3	HK2	HNRNPR	HSF2BP	IER3IP1
GYG1	HDAC1	HIAT1	HLA-A	HNRNPU	HSF4	IER5
GYPB	HDAC10	HIBCH	HLA-B	HNRNPUL1	HSP90AB1	IFFO1
GYPC	HDAC11	HIC1	HLA-C	HNRPDL	HSPA12B	IFI27L1
GYS1	HDAC2	HIF1A	HLA-DMB	HOMER3	HSPA13	IFI27L2
GZMM	HDAC4	HIGD2B	HLA-DOA	HOOK1	HSPA14	IFI35
H19	HDAC5	HILS1	HLA-DPB1	HOOK2	HSPA1A	IFIT5
H1F0	HDAC7	HINFP	HLA-DPB2	HOXA1	HSPA1B	IFITM2
H1FX	HDDC2	HIP1R	HLA-DQA1	HOXA10	HSPA1L	IFITM3
H2AFJ	HDDC3	HIPK1	HLA-E	HOXA11AS	HSPA2	IFNAR1
H2AFV	HDGF	HIPK3	HLA-F	HOXB13	HSPA6	IFNAR2
H2AFX	HDGF2	HIPK4	HLA-G	HOXB2	HSPA8	IFNGR2
H2AFY2	HDGFRP3	HIRIP3	HLA-H	HOXB3	HSPB1	IFRD2
H3F3A	HDHD2	HIST1H1D	HLA-J	HOXB4	HSPB6	IFT122
H3F3C	HEATR1	HIST1H1E	HLA-L	HOXB7	HSPBAP1	IFT140
H6PD	HEATR2	HIST1H2AG	HMBS	HOXB8	HSPD1	IFT57
HAAO	HEATR4	HIST1H2AL	HMCN1	HOXB9	HSPE1	IFT80
HABP2	HEATR6	HIST1H2BA	HMG20A	HOXC11	HSPG2	IFT88
HACE1	HEATR7A	HIST1H2BD	HMGA2	HOXD1	HSPH1	IGDCC4
HACL1	HEBP2	HIST1H2BE	HMGB1	HOXD11	HTR6	IGF1R
HADH	HECW1	HIST1H2BF	HMGB1L1	HOXD9	HTR7	IGF2BP1
HADHB	HECW2	HIST1H2BI	HMGB2	HP1BP3	HTRA3	IGF2BP2
HAGH	HELB	HIST1H2BJ	HMGCR	HPCA	HTT	IGF2BP3
HAGHL	HELLS	HIST1H2BN	HMGN1	HPCAL1	HUNK	IGF2R
HAMP	HELQ	HIST1H3A	HMGN3	HPCAL4	HUS1	IGFBP2
IGFBP3	INHA	IRF9	JMJD1C	KCNK1	KIAA0355	KIAA1826
IGFBP4	INHBB	IRGM	JMJD5	KCNK10	KIAA0415	KIAA1841
IGFBP7	INO80	IRS1	JMJD6	KCNK12	KIAA0427	KIAA1875
IGFL2	INO80B	IRS2	JMJD7-PLA2G4B	KCNK15	KIAA0494	KIAA1908
IGFL3	INO80D	IRX2	JMY	KCNK4	KIAA0528	KIAA1949
IGFL4	INPP1	IRX3	JOSD1	KCNK9	KIAA0556	KIAA1967
IGFN1	INPP4B	IRX4	JPH1	KCNMB2	KIAA0649	KIAA1984
IGHMBP2	INPP5A	ISCA1	JPH3	KCNMB4	KIAA0652	KIDINS220
IGSF11	INPP5B	ISCU	JRK	KCNN1	KIAA0664	KIF11
IGSF3	INPP5D	ISL1	JTB	KCNQ1	KIAA0754	KIF13A
IGSF8	INPP5F	ISLR	JUB	KCNQ3	KIAA0892	KIF13B
IGSF9B	INPPL1	ISLR2	JUN	KCNQ4	KIAA0895	KIF15
IK	INSC	ISM1	JUND	KCNQ5	KIAA0895L	KIF16B
IKBIP	INS-IGF2	ISOC1	KANK2	KCNT2	KIAA0907	KIF17
IKBKB	INSM1	ISPD	KANK4	KCNU1	KIAA0913	KIF18A
IKZF1	INSR	ITCH	KARS	KCTD13	KIAA1009	KIF18B
IKZF5	INTS1	ITGA1	KAT2A	KCTD18	KIAA1012	KIF20B
IL12A	INTS12	ITGA11	KAT2B	KCTD2	KIAA1026	KIF21A
IL15	INTS2	ITGA2	KATNAL1	KCTD21	KIAA1033	KIF21B
IL15RA	INTS6	ITGA9	KATNAL2	KCTD6	KIAA1045	KIF22
IL17RA	INTS7	ITGAD	KATNB1	KCTD7	KIAA1143	KIF23
IL17RC	INTS8	ITGAE	KAZALD1	KDELC1	KIAA1191	KIF26B
IL17RD	INTS9	ITGAM	KBTBD11	KDELC2	KIAA1199	KIF3B
IL1RAP	INVS	ITGAV	KBTBD3	KDM2A	KIAA1211	KIF3C
IL21R	IP6K1	ITGB1BP1	KBTBD4	KDM2B	KIAA1244	KIF5C

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IL26	IP6K2	ITGB2	KBTBD6	KDM3A	KIAA1279	KIF6
IL27RA	IPMK	ITGB3BP	KBTBD7	KDM3B	KIAA1310	KIF9
IL28RA	IPO4	ITGB4	KBTBD8	KDM4A	KIAA1324L	KIFC1
IL6ST	IPO7	ITGB5	KCNA3	KDM4B	KIAA1328	KIFC3
IL7	IQCB1	ITGB7	KCNAB2	KDM4C	KIAA1370	KIN
ILDRL	IQCD	ITIH5	KCNE3	KDM5A	KIAA1407	KIR3DL1
ILF3	IQCE	ITM2B	KCNF1	KDM5B	KIAA1409	KIR3DL2
ILK	IQCF1	ITPK1	KCNG3	KDM6B	KIAA1429	KISS1R
IMMT	IQCG	ITPKB	KCNH2	KDR	KIAA1430	KIT
IMP3	IQCK	ITPR1	KCNH3	KHDRBS1	KIAA1462	KLC1
IMP4	IQGAP2	ITPR2	KCNH6	KHNYN	KIAA1522	KLC2
IMPA1	IQGAP3	ITPR3	KCNH8	KIAA0020	KIAA1524	KLC4
IMPA2	IQSEC1	IVD	KCNIP2	KIAA0100	KIAA1530	KLF10
IMPDH1	IRAK1BP1	IVNS1ABP	KCNIP3	KIAA0141	KIAA1543	KLF12
IMPDH2	IRAK3	IWS1	KCNJ10	KIAA0146	KIAA1586	KLF13
INCA1	IRAK4	JAG2	KCNJ11	KIAA0174	KIAA1609	KLF14
INCENP	IREB2	JAGN1	KCNJ12	KIAA0182	KIAA1688	KLF15
INF2	IRF2	JAK2	KCNJ14	KIAA0226	KIAA1712	KLF17
ING1	IRF2BP1	JAM2	KCNJ4	KIAA0232	KIAA1731	KLF2
ING2	IRF2BP2	JARID2	KCNJ5	KIAA0247	KIAA1737	KLF3
ING3	IRF3	JAZF1	KCNJ6	KIAA0284	KIAA1751	KLF5
ING5	IRF4	JDP2	KCNJ9	KIAA0319	KIAA1755	KLF7
KLF9	KRTAP4-11	LDHD	LMAN2	LOC100240735	LOC348926	LOC643719
KLHDC1	KRTAP4-3	LDLRAD1	LMAN2L	LOC100272217	LOC349114	LOC643763
KLHDC3	KRTAP4-8	LDLRAD3	LMBR1	LOC100286844	LOC360030	LOC643923
KLHDC4	KRTAP5-7	LDLRAP1	LMBRD2	LOC100287718	LOC374443	LOC644172
KLHDC8B	KRTAP6-1	LDLOC1L	LMCD1	LOC100287834	LOC387763	LOC644936
KLHL11	KTELC1	LEKR1	LMF1	LOC100302652	LOC388588	LOC645166
KLHL14	KYNU	LEMD2	LMF2	LOC100329108	LOC388692	LOC646498
KLHL17	L1TD1	LEMD3	LMLN	LOC100329109	LOC388789	LOC646762
KLHL18	L2HGDH	LENG1	LMNA	LOC121952	LOC388796	LOC646851
KLHL2	L3MBTL3	LEO1	LMNB1	LOC126536	LOC388946	LOC647121
KLHL21	LACE1	LEPREL1	LMNB2	LOC145783	LOC389033	LOC647288
KLHL22	LACTB2	LEPREL2	LMO1	LOC145814	LOC389332	LOC650368
KLHL23	LAMA3	LEPROTL1	LMO2	LOC145845	LOC389493	LOC651250
KLHL25	LAMA5	LETM1	LMO3	LOC148709	LOC391322	LOC652276
KLHL26	LAMB1	LETM2	LMO4	LOC150776	LOC399744	LOC723972
KLHL28	LAMB2L	LETMD1	LMOD1	LOC151174	LOC399815	LOC728190
KLHL31	LAMB3	LFNG	LMTK3	LOC151534	LOC400027	LOC728392
KLHL33	LAMC3	LGALS12	LMX1B	LOC152217	LOC400043	LOC728407
KLHL7	LAMP1	LGALS14	LNP1	LOC153684	LOC400752	LOC728411
KLK10	LAP3	LGALS3	LNPEP	LOC154761	LOC400794	LOC728643
KLK2	LARP1	LGALS7	LOC100009676	LOC202181	LOC400891	LOC728723
KLRC3	LARP4	LGALS9	LOC100101938	LOC219347	LOC400927	LOC728743
KLRD1	LARS2	LGR4	LOC100128239	LOC220115	LOC401010	LOC728855
KLRG2	LASP1	LGR5	LOC100128292	LOC220429	LOC401052	LOC728875
KNDC1	LASS2	LGR6	LOC100128822	LOC222699	LOC401097	LOC728927
KNTC1	LASS4	LHB	LOC100129716	LOC253724	LOC401431	LOC729080
KPNA1	LASS6	LHFPL2	LOC100129726	LOC254559	LOC404266	LOC729082
KPNA2	LAT	LHFPL3	LOC100129935	LOC255025	LOC440335	LOC729121
KPNA3	LATS2	LHX3	LOC100130015	LOC255167	LOC440356	LOC729156
KPNA4	LBH	LHX4	LOC100130017	LOC282997	LOC440461	LOC729234
KPNA6	LBR	LHX9	LOC100130093	LOC283999	LOC440563	LOC729338
KPNA7	LBXCOR1	LIAS	LOC100130331	LOC284023	LOC440839	LOC729603
KPRP	LCE1A	LIFR	LOC100130581	LOC284379	LOC440905	LOC729668

Figure 15-10

2026201866	12 Mar 2026	KRAS	LCE1E	LIG1	LOC100130691	LOC284551	LOC441046	LOC729678
		KRBA1	LCE1F	LIG4	LOC100130987	LOC284749	LOC441089	LOC730101
		KREMEN2	LCE2B	LILRA6	LOC100133091	LOC285074	LOC441208	LOC731779
		KRIT1	LCE3D	LILRB2	LOC100133315	LOC285548	LOC441455	LOC731789
		KRT1	LCLAT1	LIMK1	LOC100133612	LOC285550	LOC442245	LOC81691
		KRT14	LCMT1	LIN52	LOC100133985	LOC285830	LOC552889	LOC84989
		KRT18	LCN15	LIN54	LOC100133991	LOC286016	LOC595101	LOC91316
		KRT19	LCOR	LINGO3	LOC100134229	LOC338758	LOC619207	LOC92659
		KRT35	LCORL	LINS1	LOC100134713	LOC338799	LOC641367	LOXL1
		KRT72	LDB1	LIPG	LOC100134868	LOC339535	LOC641746	LOXL2
2026201866	12 Mar 2026	KRT76	LDB3	LIPT1	LOC100190938	LOC340357	LOC642006	LOXL3
		KRT86	LDHA	LIX1L	LOC100192426	LOC342346	LOC642587	LPAR1
		KRTAP10-11	LDHAL6A	LLGL1	LOC100216001	LOC344967	LOC643387	LPAR2
		KRTAP19-3	LDHB	LLGL2	LOC100216545	LOC348840	LOC643406	LPAR3
		LPAR6	LRTOMT	MAEA	MAPK8IP1	MCL1	MEIS1	MGC16142
		LPCAT1	LRWD1	MAEL	MAPK8IP2	MCM10	MEIS2	MGC16275
		LPCAT4	LSG1	MAF	MAPK8IP3	MCM2	MELK	MGC23284
		LPHN1	LSM1	MAF1	MAPK9	MCM3	MEN1	MGC26597
		LPHN3	LSM10	MAFB	MAPKAPK2	MCM3APAS	MEP1A	MGC2889
		LPIN1	LSM14B	MAFF	MAPKAPK5	MCM6	MEPCE	MGC34034
2026201866	12 Mar 2026	LPP	LSM2	MAFG	MAPKBP1	MCM7	MERTK	MGC72080
		LRCH3	LSM4	MAFK	MAPKSP1	MCM8	MESDC1	MGLL
		LRCH4	LSM5	MAGI1	MAPRE2	MCOLN1	MESP1	MGMT
		LRFN1	LSM6	MAGI3	MAPRE3	MCOLN2	MET	MGRN1
		LRFN2	LST1	Magmas	MAPT	MCOLN3	METAP2	MIA3
		LRGUK	LTA	MAGOH	MARK2	MCPH1	METRNL	MIAT
		LRIG1	LTB	MAGOH	MARK3	MDC1	METRNL	MICA
		LRIG2	LTBP1	MAL2	MARS	MDFI	METT10D	MICAL3
		LRIT1	LTBP2	MALAT1	MARS2	MDFIC	METT11D1	MICALCL
		LRP1	LTBP3	MAML1	MARVELD1	MDGA1	METTL1	MICALL2
2026201866	12 Mar 2026	LRP10	LTBP4	MAML3	MAS1L	MDH1	METTL10	MICB
		LRP5	LTBR	MAN1A1	MAST1	MDK	METTL13	MIER1
		LRP5L	LTV1	MAN1B1	MAST3	MDM1	METTL2A	MIIP
		LRP6	LUC7L2	MAN2A1	MAST4	MDM2	METTL2B	MIOS
		LRPAP1	LUC7L3	MAN2B2	MAT2A	MDN1	METTL3	MIPOL1
		LRPPRC	LUZP1	MAN2C1	MAT2B	MEA1	METTL4	MIR1180
		LRRC20	LY6D	MANBAL	MATK	MEAF6	METTL5	MIR124-3
		LRRC25	LY6E	MANEAL	MATN1	MECOM	METTL7B	MIR1283-1
		LRRC26	LY6G5C	MANF	MATR3	MECR	METTL9	MIR1297
		LRRC27	LY6H	MAP2K3	MAVS	MED1	MEX3B	MIR1307
2026201866	12 Mar 2026	LRRC28	LY75	MAP2K5	MAX	MED11	MEX3C	MIR132
		LRRC32	LYN	MAP2K6	MAZ	MED12L	MEX3D	MIR1470
		LRRC33	LYNX1	MAP3K1	MBD3	MED13	MFAP1	MIR17HG
		LRRC37B	LYPD3	MAP3K11	MBLAC1	MED16	MFAP2	MIR1908
		LRRC37B2	LYPD6B	MAP3K12	MBLAC2	MED17	MFAP3	MIR1910
		LRRC41	LYRM1	MAP3K14	MBNL1	MED18	MFHAS1	MIR196A1
		LRRC42	LYRM2	MAP3K3	MBOAT2	MED20	MFI2	MIR1973
		LRRC43	LYRM4	MAP3K7IP1	MBOAT7	MED24	MFN2	MIR212
		LRRC47	LYRM5	MAP3K8	MBP	MED25	MFNG	MIR24-2
		LRRC49	LYSMD1	MAP4	MBTD1	MED26	MFSD1	MIR330
2026201866	12 Mar 2026	LRRC4B	LYSMD2	MAP4K5	MBTPS1	MED27	MFSD10	MIR372
		LRRC4C	LYST	MAP6	MC1R	MED30	MFSD2A	MIR375
		LRRC56	LZTFL1	MAP7D1	MCAM	MED4	MFSD2B	MIR492
		LRRC8A	M6PR	MAP9	MCART1	MED7	MFSD5	MIR515-2
		LRRC8D	MACF1	MAPK1	MCART3P	MED8	MFSD8	MIR516A2

Figure 15-11

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LRRFIP1	MACROD1	MAPK11	MCC	MED9	MGA	MIR516B1
LRRFIP2	MAD1L1	MAPK14	MCCD1	MEF2D	MGAT1	MIR517A
LRRK1	MAD2L1	MAPK15	MCF2L	MEGF10	MGAT4A	MIR517B
LRRK2	MAD2L1BP	MAPK1IP1L	MCF2L2	MEGF11	MGAT4C	MIR517C
LRRN1	MAD2L2	MAPK4	MCFD2	MEGF8	MGAT5B	MIR518A1
LRSAM1	MADD	MAPK6	MCHR1	MEGF9	MGC13005	MIR518A2
MIR518F	MMP21	MRPL19	MT1G	MXI1	MZF1	NCBP2
MIR519A1	MMP25	MRPL20	MT1H	MXRA8	N4BP2	NCDN
MIR519A2	MMP28	MRPL21	MT2A	MYADM	N4BP3	NCEH1
MIR519C	MMRN2	MRPL22	MT4	MYADML2	N6AMT2	NCF1C
MIR520A	MNAT1	MRPL23	MTA1	MYB	NAA20	NCK2
MIR520B	MNS1	MRPL24	MTA3	MYBL1	NAA25	NCKAP5
MIR524	MNT	MRPL30	MTBP	MYBPC3	NAA30	NCKIPSD
MIR526A2	MNX1	MRPL32	MTCH1	MYC	NAA35	NCL
MIR526B	MOBKL1A	MRPL37	MTDH	MYCBP	NAALADL2	NCLN
MIR548H3	MOBKL2B	MRPL44	MTERFD1	MYCBP2	NACAP1	NCOA2
MIR548H4	MOBP	MRPL45	MTERFD2	MYCN	NADK	NCOA4
MIR548N	MOCSS3	MRPL46	MTERFD3	MYCNOS	NADSYN1	NCOA5
MIR611	MOG	MRPS14	MTF1	MYEOV2	NAGA	NCOR1
MIR618	MOGS	MRPS15	MTF2	MYF6	NAGK	NCOR2
MIR632	MON1A	MRPS16	MTFMT	MYH10	NANOG	NCRNA00094
MIR636	MON2	MRPS17	MTHFD1	MYH11	NANOS1	NCRNA00095
MIR642	MORG1	MRPS18A	MTHFD1L	MYH3	NANP	NCRNA00115
MIR663	MORN1	MRPS18B	MTHFD2	MYH9	NAP1L4	NCRNA00119
MIR7-2	MORN2	MRPS2	MTHFR	MYL10	NAP1L5	NCRNA00120
MIR760	MORN3	MRPS22	MTHFSD	MYL12A	NAPA	NCRNA00164
MIR9-1	MORN4	MRPS24	MTIF2	MYL12B	NAPG	NCRNA00171
MIS12	MOSPD3	MRPS28	MTIF3	MYL2	NARF	NCRNA00173
MIXL1	MOV10	MRPS31	MTL5	MYL6	NARFL	NCRNA00174
MKI67	MOXD1	MRPS35	MTMR10	MYL6B	NARG2	NCRNA00188
MKI67IP	MPDU1	MRPS36	MTMR14	MYLIP	NARS	NCRNA00189
MKL1	MPHOSPH10	MRPS5	MTMR4	MYLK2	NARS2	NCRNA00219
MKL2	MPHOSPH8	MRPS7	MTMR9	MYLPF	NASP	NDC80
MKLN1	MPL	MRPS9	MTNR1A	MYNN	NAT1	NDE1
MKNK2	MPP7	MRS2	MT01	MYO10	NAT14	NDEL1
MKRN1	MPPE1	MRT04	MTOR	MYO15A	NAT15	NDFIP1
MKX	MPPED1	MS4A10	MTPN	MYO18A	NAT2	NDN
MLC1	MPPED2	MS4A6A	MTR	MYO19	NAV1	NDNL2
MLF1IP	MPRIIP	MSH5	MTRF1L	MYO1C	NAV2	NDRG1
MLKL	MPV17L	MSH6	MTRR	MYO1E	NBEAL1	NDRG3
MLL	MPV17L2	MSI2	MTSS1	MYO1F	NBEAL2	NDRG4
MLL5	MPZL1	MSL1	MTUS2	MYO1G	NBL1	NDUFA10
MLLT1	MRAP2	MSL2	MTX1	MYO3B	NBPF1	NDUFA12
MLLT10	MRAS	MSL3L2	MUC1	MYO5A	NBPF14	NDUFA13
MLLT3	MRC2	MSLN	MUC4	MYO9B	NBPF3	NDUFA2
MLLT6	MRE11A	MSLNL	MUC5B	MYOM2	NBPF9	NDUFA3
MLX	MRFAP1	MSRA	MUC6	MYRIP	NBR1	NDUFA4L2
MLXIPL	MRFAP1L1	MSRB3	MUDENG	MYST1	NCAM1	NDUFA5
MMAB	MRP63	MST1P2	MUS81	MYST2	NCAN	NDUFA6
MMADHC	MRPL1	MSTO1	MUTYH	MYST3	NCAPD2	NDUFA7
MMP15	MRPL12	MSTO2P	MVP	MYST4	NCAPD3	NDUFAB1
MMP17	MRPL16	MSX1	MX1	MYT1	NCAPG	NDUFAF1
MMP19	MRPL18	MT1F	MXD3	MYT1L	NCAPH2	NDUFAF2
NDUFAF3	NFKB1	NLRC3	NR2C2AP	NUDCD1	OCLN	OSBPL9
NDUFB1	NFKBIA	NLRC4	NR2E1	NUDT14	OCM	OSGEP

Figure 15-12

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NDUFB10	NFKBIE	NLRC5	NR2F1	NUDT16	ODF2	OSGIN2
NDUFB5	NFKBIL1	NLRP12	NR2F2	NUDT16L1	ODF2L	OSM
NDUFB6	NFKBIL2	NMB	NR2F6	NUDT18	ODZ2	OSMR
NDUFB7	NFKBIZ	NMD3	NR3C1	NUDT3	ODZ4	OSR2
NDUFC2	NFRKB	NME1	NR3C2	NUDT4	OGDH	OSTCL
NDUFS2	NFYC	NME3	NR4A3	NUDT5	OGDHL	OTOP2
NDUFS5	NGEF	NMT1	NR5A2	NUDT6	OGFOD2	OTP
NDUFV1	NGLY1	NMT2	NR6A1	NUDT8	OGFR	OTUB1
NDUFV2	NGRN	NMU	NRBF2	NUDT9	OGG1	OTUB2
NDUFV3	NHLH1	NOB1	NRBP2	NUF2	OLFM2	OTUD1
NEAT1	NHLH2	NOD1	NRD1	NUFIP1	OLFML2A	OTUD3
NECAB3	NHLRC2	NOL11	NRIP2	NUFIP2	OLFML2B	OTUD6B
NECAP1	NHLRC3	NOL6	NRN1	NUMBL	ONECUT2	OTUD7B
NEDD1	NHLRC4	NOL7	NRP1	NUP133	OPA3	OTX1
NEDD4L	NHP2L1	NOLC1	NRP2	NUP155	OPCML	OTX2
NEDD8	NHSL1	NOM1	NRTN	NUP160	OPN3	OVOL1
NEDD9	NICN1	NOMO3	NRXN2	NUP188	OPRK1	OXNAD1
NEFH	NIF3L1	NOP2	NSD1	NUP210	OPRM1	OXR1
NEFL	NIN	NOP58	NSL1	NUP214	OPTN	OXSRI
NEGR1	NINJ2	NOS1AP	NSMAF	NUP54	OR10G8	OXT
NEIL2	NINL	NOSTRIN	NSMCE1	NUP62	OR10Q1	OXTR
NEIL3	NIP7	NOTCH2NL	NSMCE4A	NUP85	OR12D2	P2RX2
NEK2	NIPA1	NOTCH3	NSUN2	NUP93	OR1A2	P2RX4
NEK3	NIPA2	NOV	NSUN3	NUPL2	OR2L13	P2RY1
NEK4	NIPAL1	NOXA1	NSUN4	NUS1	OR2T33	P4HA1
NEO1	NIPAL3	NPAT	NSUN5	NUSAP1	OR2V2	P4HA3
NEU1	NIPBL	NPB	NT5C	NVL	OR52H1	P4HB
NEURL	NIPSNAP1	NPBWR1	NT5C2	NWD1	OR5D13	P4HTM
NEURL1B	NIPSNAP3A	NPC1	NT5C3	NXF1	OR6V1	PA2G4
NEURL4	NIPSNAP3B	NPC2	NT5DC1	NXN	OR7A10	PABPC1
NEUROG1	NIT2	NPEPPS	NT5DC3	NXPH4	OR7E91P	PABPC4
NEUROG2	NKAIN2	NPFFR1	NT5E	OAF	OR8I2	PABPN1
NF1	NKAIN3	NPHP3	NT5M	OAS1	OR8S1	PABPN1L
NF2	NKD1	NPHP4	NTF4	OAS2	ORAI2	PACRG
NFAT5	NKD2	NPM1	NTM	OAS3	ORC1L	PACS2
NFATC1	NKIRAS1	NPNT	NTN1	OAT	ORC3L	PACSLN1
NFATC2	NKIRAS2	NPR1	NTN3	OAZ2	ORC6L	PAFAH1B2
NFATC2IP	NKTR	NPR3	NTN4	OAZ3	ORMDL1	PAG1
NFATC4	NKX2-1	NQO2	NTNG1	OBFC1	ORMDL2	PAICS
NFE2L1	NKX2-6	NR1D1	NTRK1	OBFC2B	ORMDL3	PAIP1
NFE2L2	NKX2-8	NR1D2	NUB1	OBSCN	OSBPL11	PAIP2
NFIA	NKX6-1	NR1H2	NUBP1	OBSL1	OSBPL1A	PAIP2B
NFIC	NLE1	NR1H3	NUBP2	OCA2	OSBPL2	PAK1
NFIL3	NLGN1	NR2C1	NUCKS1	OCIAD1	OSBPL3	PAK4
NFIX	NLK	NR2C2	NUDC	OCIAD2	OSBPL5	PALM
PALM3	PCCA	PDE5A	PEX7	PHKB	PIP4K2A	PLEKHH3
PAN2	PCCB	PDE6B	PFDN2	PHKG1	PIP4K2C	PLEKHJ1
PANK2	PCDH10	PDE6D	PFDN4	PHKG2	PIP5K1A	PLEKHM1
PANX1	PCDH15	PDE7A	PFKFB3	PHLDA1	PIP5K1B	PLEKHM3
PANX2	PCDH17	PDGFRA	PFKFB4	PHLDA2	PIP5K1C	PLEKHO1
PAOX	PCDH21	PDGFRL	PFKL	PHLDB1	PITPNB	PLEKHO2
PAPL	PCDH9	PDHB	PFKP	PHLDB2	PITPNC1	PLGLA
PAPOLA	PCDHA1	PDIA3	PFN1	PHLDB3	PITPNM3	PLIN1
PAPOLG	PCDHB13	PDIA4	PFN4	PHLPP1	PITRM1	PLK2
PAPPA2	PCDHGA4	PDIK1L	PGAM1	PHOSPHO1	PITX2	PLK3

Figure 15-13

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PAQR3	PCF11	PDK1	PGAM5	PHPT1	PITX3	PLK4
PAQR4	PCGF1	PDLIM1	PGAP1	PHTF2	PIWIL3	PLLP
PARD3	PCGF3	PDLIM3	PGAP2	PHYHIPL	PJA2	PLOD2
PARD3B	PCGF6	PDLIM5	PGAP3	PI4K2B	PKD1	PLXDC2
PARD6A	PCK2	PDLIM7	PGBD4	PIAS1	PKD1L3	PLXNA1
PARD6B	PCLO	PDPK1	PGCP	PIAS2	PKD2	PLXNA2
PARD6G	PCM1	PDPR	PGD	PIAS3	PKM2	PLXNA4
PARL	PCMT1	PDS5A	PGGT1B	PIAS4	PKN1	PLXNB2
PARP1	PCMTD1	PDS5B	PGLS	PIBF1	PKN2	PLXNC1
PARP11	PCNP	PDSS1	PGLYRP2	PICK1	PKN3	PLXND1
PARP15	PCNT	PDSS2	PGM1	PIF1	PKNOX2	PMAIP1
PARP16	PCNX	PDX1	PGM2	PIGB	PKP4	PMEPAP1
PARP2	PCNXL3	PDXDC2	PGM3	PIGG	PLA2G15	PMF1
PARP8	PCOLCE	PDXK	PGP	PIGM	PLA2G6	PML
PARP9	PCOTH	PDZD2	PGPEP1	PIGN	PLAC8	PMM1
PARS2	PCSK2	PDZD7	PGS1	PIGO	PLAG1	PMM2
PARVB	PCSK6	PDZD8	PHACTR1	PIGP	PLAGL1	PMPCB
PASK	PCSK7	PEBP1	PHACTR4	PIGQ	PLAT	PMS1
PATE2	PCTP	PECI	PHAX	PIGT	PLAU	PMS2
PATE4	PCYT1A	PEF1	PHB	PIGU	PLCD1	PMS2L1
PATL1	PDAP1	PEG3	PHC1	PIGV	PLCE1	PMS2L2
PATZ1	PDCD11	PELI1	PHC2	PIGX	PLCH2	PMS2L3
PAWR	PDCD2	PELI2	PHC3	PIGY	PLCL2	PMS2L4
PAX2	PDCD2L	PEMT	PHF1	PIK3AP1	PLD2	PMS2L5
PAX5	PDCD5	PER1	PHF10	PIK3C2G	PLD3	PMVK
PAX6	PDCD6	PER2	PHF11	PIK3CA	PLD5	PNKD
PAX7	PDCD6IP	PER3	PHF12	PIK3CD	PLEC1	PNLIP
PAXIP1	PDCD7	PERP	PHF13	PIK3R2	PLEKHA1	PNMA2
PBLD	PDE10A	PET117	PHF15	PIK3R3	PLEKHA2	PNMT
PBX3	PDE11A	PEX10	PHF17	PIK3R5	PLEKHA6	PNN
PBX4	PDE12	PEX11B	PHF19	PIKFYVE	PLEKHA7	PNO1
PC	PDE3A	PEX12	PHF2	PILRB	PLEKHB1	PNPLA6
PCBD2	PDE3B	PEX13	PHF21A	PIM1	PLEKHF2	PNPLA7
PCBP1	PDE4A	PEX19	PHF21B	PIM3	PLEKHG3	PNPLA8
PCBP2	PDE4B	PEX26	PHF5A	PIN1	PLEKHG4	PNRC2
PCBP3	PDE4D	PEX5	PHGDH	PINK1	PLEKHG5	PODN
PCBP4	PDE4DIP	PEX6	PHIP	PION	PLEKHG6	PODXL
PODXL2	POU6F2	PPP1R3E	PRDX5	PRMT8	PSMA6	PTH1R
POFUT2	PPA1	PPP1R7	PRDX6	PRNP	PSMA7	PTK2
POGK	PPA2	PPP1R8	PRDXDD1P	PROCA1	PSMB1	PTK2B
POLD1	PPAP2B	PPP1R9B	PREB	PROCR	PSMB10	PTMA
POLD2	PPAP2C	PPP2CA	PRELID1	PRODH2	PSMB5	PTMS
POLD3	PPAPDC1A	PPP2R1A	PRELID2	PROKR1	PSMB6	PTP4A1
POLDIP2	PPARG	PPP2R1B	PRELP	PROKR2	PSMB7	PTPMT1
POLE2	PPARGC1A	PPP2R2B	PREP	PROSC	PSMB8	PTPN1
POLG	PPARGC1B	PPP2R3A	PREPL	PRPF19	PSMB9	PTPN12
POLH	PPCDC	PPP2R3C	PREX1	PRPF3	PSMC2	PTPN14
POLI	PPCS	PPP2R5A	PREX2	PRPF31	PSMC3IP	PTPN18
POLK	PPDPF	PPP2R5C	PRHOXNB	PRPF38B	PSMC4	PTPN21
POLN	PPFIA1	PPP2R5D	PRIC285	PRPF40B	PSMC5	PTPN22
POLQ	PPFIA3	PPP3CA	PRICKLE1	PRPF8	PSMC6	PTPN23
POLR1B	PPFIBP2	PPP3CB	PRIM1	PRPSAP2	PSMD1	PTPN4
POLR1C	PPHLN1	PPP3CC	PRIMA1	PRR11	PSMD11	PTPN6
POLR2B	PPIA	PPP3R1	PRKAA1	PRR13	PSMD12	PTPN9
POLR2D	PPIB	PPP4C	PRKAA2	PRR14	PSMD13	PTPRCAP

Figure 15-14

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POLR2E	PPID	PPP4R2	PRKAB2	PRR23C	PSMD2	PTPRE
POLR2G	PPIE	PPP5C	PRKACA	PRR3	PSMD3	PTPRF
POLR2I	PPIH	PPPDE1	PRKACG	PRR5	PSMD4	PTPRG
POLR2J2	PPIL2	PPPDE2	PRKAG2	PRR5L	PSMD6	PTPRJ
POLR2J4	PPIL3	PPRC1	PRKAR1A	PRR7	PSMD7	PTPRK
POLR3B	PPIL4	PPT1	PRKAR1B	PRRC1	PSMD9	PTPRM
POLR3C	PPIL5	PPT2	PRKAR2B	PRRG4	PSME2	PTPRN2
POLR3D	PPM1A	PPY2	PRKCA	PRRT1	PSME3	PTPRO
POLR3K	PPM1E	PQLC1	PRKCB	PRRT2	PSMG1	PTPRS
POLRMT	PPM1F	PQLC3	PRKCD	PRRT4	PSMG2	PTPRU
POLS	PPM1G	PRAGMIN	PRKCDBP	PRSS12	PSMG3	PTPRZ1
POM121	PPM1J	PRAMEF18	PRKCE	PRSS23	PSMG4	PTRF
POM121L10P	PPM1K	PRAMEF20	PRKCG	PRSS38	PSPC1	PTTG1
POM121L2	PPM1L	PRAMEF22	PRKCI	PRSS48	PSPN	PTTG1IP
POMC	PPM1M	PRB2	PRKCSH	PRSS8	PSRC1	PUF60
POMP	PPOX	PRB3	PRKCZ	PRSSL1	PTAFR	PUM1
POMT2	PPP1CA	PRC1	PRKD1	PRTG	PTBP2	PURA
POMZP3	PPP1CB	PRCC	PRKD2	PRUNE2	PTCD3	PURG
PON2	PPP1CC	PRDM11	PRKDC	PSAT1	PTCH1	PUS1
POP1	PPP1R11	PRDM12	PRKG1	PSD2	PTCH2	PUS10
POP7	PPP1R12B	PRDM14	PRKRA	PSD3	PTDSS2	PUSL1
POT1	PPP1R12C	PRDM15	PRKRIP1	PSD4	PTEN	PVR
POTEC	PPP1R14B	PRDM16	PRKRIR	PSG3	PTER	PVRL1
POTED	PPP1R14C	PRDM2	PRMT1	PSIP1	PTGER4	PVRL2
POTEF	PPP1R15A	PRDM5	PRMT10	psiTPTE22	PTGES	PVRL3
POU2F1	PPP1R15B	PRDM6	PRMT2	PSMA1	PTGES2	PVT1
POU3F1	PPP1R2	PRDM8	PRMT3	PSMA2	PTGES3	PWP1
POU3F2	PPP1R2P1	PRDX1	PRMT6	PSMA3	PTGFRN	PWP2
POU6F1	PPP1R3B	PRDX2	PRMT7	PSMA4	PTGIS	PXMP2
PXMP3	RAB8A	RASAL2	RBPJL	RG9MTD1	RNASEH1	RNMTL1
PXMP4	RABAC1	RASD1	RBPMS	RG9MTD2	RNASEH2B	RNPC3
PXN	RABEP2	RASD2	RBX1	RG9MTD3	RNASEH2C	RNPEP
PYCR1	RABGEF1	RASGEF1B	RC3H2	RGL2	RNASEK	RNU5D
PYCR2	RABL4	RASGEF1C	RCAN3	RGMA	RNASEN	RNU5E
PYCRL	RAC2	RASGRP2	RCBTB1	RGMB	RNF103	ROBLD3
PYGB	RACGAP1	RASGRP3	RCBTB2	RGPD2	RNF11	ROBO1
PYGL	RAD1	RASIP1	RCC2	RGPD3	RNF111	ROCK1
PYGM	RAD17	RASL11A	RCCD1	RGPD5	RNF114	ROD1
PYGO1	RAD21	RASSF1	RCE1	RGS16	RNF122	ROGDI
PYGO2	RAD51AP2	RASSF2	RCOR1	RGS17	RNF125	ROMO1
PYY	RAD51L1	RASSF3	RCOR2	RGS19	RNF126	ROPN1L
QARS	RAD52	RASSF4	RCOR3	RGS2	RNF130	RORA
QDPR	RAD9A	RASSF5	RCSD1	RGS20	RNF138	RP11-529I10.4
QKI	RADIL	RASSF6	RDBP	RGS7	RNF139	RP1L1
QPCTL	RAE1	RASSF8	RDH10	RGS8	RNF14	RP5-1022P6.2
QRICH1	RAET1G	RB1	RDH13	RHBDD1	RNF141	RP9P
QRSL1	RAET1K	RB1CC1	REC8	RHBDD2	RNF145	RPA1
QSER1	RAGE	RBAK	RECQL	RHBDF1	RNF152	RPA2
QTRT1	RAI1	RBBP4	RECQL5	RHBDF2	RNF157	RPA3
R3HDM1	RAI14	RBBP6	REEP1	RHEB	RNF160	RPAIN
RAB10	RALB	RBBP8	REEP3	RHEBL1	RNF165	RPAP1
RAB11A	RALGAPA2	RBCK1	REEP4	RHOA	RNF168	RPAP2
RAB11B	RALGAPB	RBKS	REEP5	RHOB	RNF182	RPAP3
RAB11FIP3	RALGDS	RBL1	REEP6	RHOC	RNF187	RPE
RAB11FIP5	RALGPS1	RBM12B	REG3G	RHOD	RNF19A	RPF1

Figure 15-15

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RAB12	RALGPS2	RBM14	REL	RHOF	RNF20	RPF2
RAB14	RALY	RBM15	RELA	RHOG	RNF213	RPGRIP1
RAB15	RALYL	RBM18	RELL1	RHOJ	RNF215	RPGRIP1L
RAB18	RAMP1	RBM19	RERE	RHOT2	RNF216L	RPH3AL
RAB1B	RANBP1	RBM24	RET	RHPN1	RNF220	RPIA
RAB20	RANBP2	RBM27	RETSAT	RHPN2	RNF24	RPL10A
RAB21	RANBP9	RBM33	REV3L	RIC8A	RNF25	RPL10L
RAB22A	RANGRF	RBM34	REXO1	RIC8B	RNF32	RPL13AP20
RAB27A	RAP1A	RBM38	RFC1	RICS	RNF34	RPL13AP5
RAB2A	RAP1B	RBM39	RFC2	RICTOR	RNF39	RPL14
RAB32	RAP1GDS1	RBM42	RFC4	RILPL2	RNF4	RPL18
RAB39	RAP2B	RBM44	RFPL1S	RIMKLA	RNF40	RPL18AP3
RAB3D	RAPGEF6	RBM45	RFPL2	RIMS2	RNF41	RPL19
RAB3GAP1	RAPH1	RBM46	RFT1	RIN3	RNF44	RPL22
RAB40B	RARA	RBM4B	RFTN1	RING1	RNF6	RPL22L1
RAB42	RARB	RBM5	RFWD2	RINL	RNF7	RPL23
RAB43	RARRES1	RBM6	RFX1	RLF	RNF8	RPL23AP53
RAB4B	RASA1	RBM9	RFX2	RLTPR	RNFT1	RPL23AP7
RAB6A	RASA2	RBMXL1	RFX4	RMND1	RNFT2	RPL23AP82
RAB6B	RASA3	RBP1	RFX8	RMND5A	RNGTT	RPL24
RAB7A	RASAL1	RBPJ	RFXANK	RNASE3	RNLS	RPL27
RPL27A	RREB1	S100A7A	SCARNA20	SEC14L2	SERPINE2	SGTA
RPL28	RRM1	S100PBP	SCCPDH	SEC16A	SERPINH1	SGTB
RPL29	RRM2	S1PR1	SCD	SEC22B	SERTAD3	SH2B1
RPL30	RRM2B	S1PR2	SCD5	SEC23A	SERTAD4	SH2B3
RPL31	RRN3	S1PR4	SCFD1	SEC23B	SESN3	SH2D3A
RPL32	RRN3P2	S1PR5	SCFD2	SEC23IP	SETD1A	SH2D5
RPL32P3	RRN3P3	SAA4	SCGB1D4	SEC24B	SETD1B	SH3BGR
RPL36	RRP1	SACM1L	SCGB3A1	SEC24D	SETD2	SH3BP1
RPL37	RRP15	SACS	SCHIP1	SEC31A	SETD3	SH3BP2
RPL37A	RRP7B	SAFB	SCIN	SEC61G	SETD4	SH3BP4
RPL5	RRS1	SALL1	SCLT1	SEC63	SETD7	SH3BP5
RPL6	RSBN1L	SALL3	SCMH1	SECISBP2	SETD8	SH3D20
RPL7	RSF1	SALL4	SCN1B	SECTM1	SETMAR	SH3GL1
RPL8	RSL1D1	SAMD10	SCN4B	SEL1L	SEZ6	SH3PXD2A
RPLP0	RSPH1	SAMD12	SCN8A	SELI	SEZ6L2	SH3PXD2B
RPLP2	RSPH3	SAMD13	SCNM1	SELK	SF3A1	SH3RF3
RPN1	RSPH6A	SAMD4A	SCRIB	SELM	SF3A3	SH3TC1
RPP21	RSPH9	SAMM50	SCRN2	SELPLG	SF3B1	SHANK1
RPP25	RSP04	SAP130	SCRT1	SELS	SF3B4	SHANK2
RPP30	RSPRY1	SAP30	SCRT2	SELT	SFI1	SHANK3
RPP40	RSRC2	SAPS1	SCUBE1	SEMA3A	SFMBT1	SHBG
RPRD1A	RSU1	SAPS2	SCUBE2	SEMA3B	SFMBT2	SHC1
RPRD1B	RTKL1	SAPS3	SCUBE3	SEMA3F	SFRP5	SHC4
RPRD2	RTKN	SARS	SCYL1	SEMA3G	SFRS1	SHD
RPS10P7	RTN1	SARS2	SCYL2	SEMA4B	SFRS11	SHF
RPS11	RTN2	SART1	SCYL3	SEMA4C	SFRS12	SHFM1
RPS12	RTN4	SASH1	SDC1	SEMA5A	SFRS13A	SHH
RPS13	RTN4IP1	SATB1	SDC2	SEMA5B	SFRS14	SHISA3
RPS15	RTN4R	SATB2	SDC4	SEMA6B	SFRS2	SHISA5
RPS15A	RTTN	SAV1	SDCBP	SEMA7A	SFRS2IP	SHMT2
RPS19BP1	RUFY1	SBDS	SDCBP2	SENP1	SFRS3	SHPRH
RPS21	RUFY2	SBDSP	SDCCAG8	SENP2	SFRS4	SHQ1
RPS23	RUNDC2A	SBF1	SDF2L1	SENP3	SFRS6	SHAH2
RPS26	RUNDC2C	SBF2	SDF4	SENP7	SFRS7	SIDT1

Figure 15-16

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RPS27	RUNDC3A	SBK2	SDHA	SEPHS1	SFRS8	SIGIRR
RPS3A	RUNDC3B	SBNO2	SDHAF2	SEPSECS	SFT2D2	SIGLEC10
RPS6KA2	RUNX1	SC5DL	SDHAP3	SERAC1	SFXN5	SIGLEC11
RPS7	RUNX1T1	SCAMP1	SDHB	SERBP1	SGCB	SIK1
RPS9	RUNX2	SCAMP3	SDHC	SERF2	SGCE	SIK3
RPSA	RUNX3	SCAMP4	SDK1	SERINC2	SGEF	SIM2
RPTOR	RUSC1	SCAND1	SDK2	SERINC4	SGK1	SIN3A
RPUSD1	RUVBL2	SCAND3	SDR39U1	SERP1	SGK196	SIP1
RPUSD2	RWDD1	SCARB1	SDR42E1	SERPINB2	SGK269	SIPA1
RPUSD4	RWDD2A	SCARB2	SEC1	SERPINB6	SGMS2	SIPA1L1
RQCD1	RXRA	SCARF2	SEC11A	SERPINB8	SGSH	SIPA1L2
RRAGA	RYR1	SCARNA16	SEC11C	SERPINB9	SGSM1	SIRPA
RRBP1	S100A6	SCARNA2	SEC14L1	SERPIND1	SGSM3	SIRT2
SIRT3	SLC22A17	SLC30A6	SLC4A1AP	SMARCA5	SNORD104	SNUPN
SIRT5	SLC22A18	SLC30A7	SLC4A4	SMARCAD1	SNORD114-15	SNX1
SIRT7	SLC22A18A5	SLC30A9	SLC5A10	SMARCC1	SNORD114-29	SNX11
SIX2	SLC22A23	SLC31A2	SLC5A5	SMARCC2	SNORD114-31	SNX14
SIX4	SLC22A3	SLC33A1	SLC5A7	SMARCD2	SNORD115-1	SNX16
SIX5	SLC22A4	SLC34A2	SLC6A17	SMARCE1	SNORD115-11	SNX17
SKA1	SLC22A5	SLC35A1	SLC6A18	SMC3	SNORD115-13	SNX19
SKA3	SLC23A2	SLC35A3	SLC6A19	SMC4	SNORD115-14	SNX21
SKAP1	SLC24A2	SLC35B1	SLC6A2	SMCR7	SNORD115-15	SNX22
SKAP2	SLC25A11	SLC35D1	SLC6A20	SMCR8	SNORD115-17	SNX29
SKI	SLC25A15	SLC35E1	SLC6A3	SMG6	SNORD115-3	SNX3
SKIL	SLC25A16	SLC35E2	SLC6A5	SMG7	SNORD115-35	SNX32
SKIV2L	SLC25A17	SLC35E3	SLC6A6	SMOC2	SNORD115-38	SNX4
SKP1	SLC25A19	SLC35E4	SLC7A1	SMOX	SNORD115-39	SNX6
SKP2	SLC25A2	SLC35F1	SLC7A10	SMPD1	SNORD115-41	SNX7
SLAIN1	SLC25A21	SLC35F2	SLC7A14	SMPD3	SNORD115-44	SNX8
SLC10A4	SLC25A24	SLC35F5	SLC7A4	SMPD4	SNORD115-6	SNX9
SLC10A7	SLC25A28	SLC36A1	SLC7A6	SMPDL3B	SNORD115-7	SOBP
SLC11A2	SLC25A30	SLC36A4	SLC7A6OS	SMTN	SNORD115-8	SOC51
SLC12A2	SLC25A32	SLC37A1	SLC7A8	SMUG1	SNORD116-8	SOC55
SLC12A4	SLC25A33	SLC37A3	SLC8A1	SMURF1	SNORD1C	SOC56
SLC12A5	SLC25A35	SLC37A4	SLC8A2	SMURF2	SNORD24	SOD1
SLC12A6	SLC25A36	SLC38A1	SLC8A3	SMYD3	SNORD32B	SOLH
SLC12A7	SLC25A38	SLC38A10	SLC9A3	SMYD5	SNORD38A	SON
SLC12A9	SLC25A4	SLC38A2	SLC9A3R2	SNAP23	SNORD42B	SORBS1
SLC13A5	SLC25A40	SLC38A3	SLC9A5	SNAP25	SNORD43	SORBS3
SLC14A2	SLC25A42	SLC38A6	SLC01C1	SNAPC1	SNORD50B	SORCS2
SLC16A1	SLC25A44	SLC38A7	SLC02A1	SNAPC2	SNORD58A	SORD
SLC16A10	SLC25A45	SLC38A9	SLC03A1	SNAPC3	SNORD83A	SORL1
SLC16A12	SLC25A46	SLC39A10	SLC04A1	SNAR-G1	SNORD83B	SOX12
SLC16A13	SLC26A1	SLC39A11	SLC05A1	SNCAIP	SNORD88A	SOX18
SLC16A14	SLC26A10	SLC39A14	SLFN11	SNCG	SNPH	SOX2
SLC16A3	SLC26A11	SLC39A7	SLFN12L	SND1	SNRNP27	SOX5
SLC17A1	SLC26A2	SLC39A8	SLFN5	SNHG10	SNRNP40	SOX7
SLC17A5	SLC26A4	SLC39A9	SLIT1	SNHG12	SNRPA1	SP1
SLC17A7	SLC27A1	SLC41A1	SLIT2	SNHG3-RCC1	SNRPB	SP100
SLC19A1	SLC29A1	SLC41A3	SLIT3	SNHG4	SNRPB2	SP2
SLC19A2	SLC29A2	SLC43A1	SLK	SNHG5	SNRPC	SP3
SLC1A2	SLC29A4	SLC43A2	SLMAP	SNHG6	SNRPD1	SP4
SLC1A3	SLC2A1	SLC44A1	SLTM	SNHG7	SNRPD3	SP7
SLC1A4	SLC2A11	SLC44A2	SLU7	SNHG9	SNRPE	SP8
SLC1A5	SLC2A13	SLC44A3	SMAD3	SNIP1	SNRPF	SPAG1

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SLC1A6	SLC2A3	SLC44A4	SMAD4	SNORA14B	SNRPG	SPAG11A
SLC1A7	SLC2A4	SLC45A4	SMAD7	SNORA20	SNRPN	SPARC
SLC20A1	SLC2A5	SLC46A3	SMAGP	SNORA52	SNTA1	SPATA13
SLC22A15	SLC2A6	SLC48A1	SMAP1	SNORA76	SNTB1	SPATA2
SLC22A16	SLC30A5	SLC4A11	SMARCA4	SNORA8	SNTG2	SPATA20
SPATA5	SRI	STAR	STT3A	SYN3	TAS2R43	TCP11L2
SPATA5L1	SRP14	STARD13	STX11	SYNCRIP	TATDN1	TCTA
SPC25	SRP68	STARD3	STX18	SYNGAP1	TATDN2	TCTE3
SPCS2	SRP72	STARD3NL	STX1A	SYNGR3	TATDN3	TCTEX1D2
SPCS3	SRPK2	STARD4	STX3	SYNPO	TAX1BP1	TCTN1
SPDYA	SRPRB	STARD5	STX4	SYNPO2L	TBC1D1	TDH
SPDYE4	SRRM1	STARD7	STX5	SYNRG	TBC1D12	TDP1
SPDYE7P	SRRM2	STARD9	STX7	SYPL1	TBC1D14	TDRD10
SPEF1	SRRRT	STAT2	STX8	SYT1	TBC1D15	TDRD3
SPEG	SS18	STAT3	STXBP2	SYT17	TBC1D16	TDRKH
SPEN	SSB	STAT5A	STXBP4	SYT3	TBC1D2	TEAD1
SPG11	SSBP1	STAT5B	STXBP5	SYT5	TBC1D22A	TEAD3
SPG21	SSBP2	STAU1	STXBP6	SYT7	TBC1D24	TECPR2
SPG7	SSBP3	STAU2	STYX	SYT9	TBC1D26	TECR
SPHK1	SSBP4	STBD1	STYXL1	SYTL1	TBC1D2B	TEF
SPHK2	SSFA2	STC2	SUCLG1	SYTL2	TBC1D3P2	TEKT4
SPINK2	SSH2	STEAP2	SUCLG2	SYTL3	TBC1D7	TELO2
SPIRE2	SSH3	STEAP4	SUDS3	T	TBCA	TERF2
SPN	SSPN	STIL	SUFU	TAAR6	TBCC	TERF2IP
SPNS3	SSR1	STIM2	SUGT1L1	TACC1	TBCD	TERT
SPOPL	SSTR1	STIP1	SUGT1P1	TACC2	TBCE	TES
SPPL2A	SSX2IP	STK10	SULF1	TACC3	TBCEL	TESK2
SPPL2B	ST13	STK11	SULF2	TACR1	TBL1XR1	TET2
SPR	ST14	STK16	SULT1A2	TAF10	TBL3	TET3
SPRED1	ST20	STK17B	SULT1A3	TAF11	TBRG1	TEX10
SPRED2	ST3GAL1	STK19	SULT1C4	TAF15	TBRG4	TEX2
SPRR2B	ST3GAL2	STK24	SULT2B1	TAF1C	TBX18	TEX264
SPRR2D	ST3GAL3	STK25	SULT4A1	TAF1D	TBX5	TFAM
SPRYD3	ST3GAL4	STK3	SUMO1	TAF4	TBXAS1	TFAMP1
SPSB2	ST3GAL5	STK32B	SUMO2	TAF4B	TCEA1	TFAP2B
SPSB3	ST5	STK32C	SUPT16H	TAF6	TCEA3	TFAP2C
SPTB	ST6GAL1	STK35	SUPT5H	TAF6L	TCEB1	TFAP2E
SPTBN1	ST6GALNAC2	STK36	SUPT6H	TAF7	TCEB3	TFB2M
SPTBN2	ST6GALNAC4	STK38	SUPT7L	TAF8	TCEB3CL	TFCP2
SPTBN4	ST7	STK39	SUSD1	TAGLN	TCERG1	TFDP1
SPTBN5	ST7L	STK40	SUSD4	TAGLN2	TCERG1L	TFEB
SPTY2D1	ST7OT1	STMN1	SUV420H1	TANC1	TCF12	TFG
SQLE	ST8SIA1	STMN3	SUV420H2	TAOK2	TCF20	TFPI
SQRDL	ST8SIA3	STOM	SUZ12	TAOK3	TCF25	TFPT
SQSTM1	ST8SIA4	STOML2	SUZ12P	TAP1	TCF3	TFR2
SR140	ST8SIA6	STOX1	SV2B	TAP2	TCF4	TFRC
SRCIN1	STAC2	STRADA	SV2C	TAPBP	TCF7L1	TGDS
SRD5A3	STAG1	STRAP	SVIL	TAPBPL	TCHH	TGFA
SREBF2	STAG3	STRC	SVIP	TAPT1	TCHP	TGFB2
SRF	STAMPB	STRN	SYCE2	TARSL2	TCL1B	TGFB3
SRFBP1	STAP1	STRN3	SYDE1	TAS1R1	TCP10	TGFBR1
SRGAP1	STAP2	STRN4	SYF2	TAS2R31	TCP11L1	TGFBR2
TGFBR3	TINF2	TMEM11	TMEM233	TNFRSF10B	TP53TG1	TRIM26
TGFBRAP1	TIPIN	TMEM115	TMEM30A	TNFRSF10D	TPBG	TRIM27
TGIF1	TIPRL	TMEM116	TMEM33	TNFRSF11A	TPCN1	TRIM29

Figure 15-18

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TGIF2	TJP2	TMEM120B	TMEM38B	TNFRSF12A	TPCN2	TRIM3
TGM6	TJP3	TMEM121	TMEM41A	TNFRSF13B	TPD52	TRIM31
TGOLN2	TKT	TMEM123	TMEM41B	TNFRSF19	TPD52L1	TRIM33
THADA	TLE2	TMEM126B	TMEM43	TNFRSF1B	TPD52L2	TRIM36
THAP1	TLE3	TMEM128	TMEM44	TNFRSF25	TPI1	TRIM37
THAP11	TLE4	TMEM131	TMEM45A	TNIK	TPK1	TRIM39
THAP2	TLE6	TMEM132A	TMEM5	TNIP2	TPM2	TRIM41
THAP3	TLK1	TMEM132E	TMEM50B	TNK2	TPM4	TRIM43
THAP4	TLR5	TMEM134	TMEM55A	TNKS	TPMT	TRIM44
THAP5	TLX3	TMEM141	TMEM55B	TNKS2	TPR	TRIM45
THAP7	TM2D2	TMEM143	TMEM56	TNPO1	TPRKB	TRIM47
THAP9	TM2D3	TMEM144	TMEM57	TNPO3	TPRX1	TRIM50
THBD	TM4SF4	TMEM145	TMEM59	TNRC18	TPRXL	TRIM54
THBS1	TM7SF2	TMEM146	TMEM61	TNRC6A	TPST1	TRIM58
THBS2	TM7SF3	TMEM14B	TMEM65	TNRC6B	TPST2	TRIM59
THBS3	TM9SF3	TMEM150A	TMEM66	TNS1	TPT1	TRIM60
THEM4	TM9SF4	TMEM151B	TMEM67	TNS3	TPX2	TRIM62
THG1L	TMBIM4	TMEM160	TMEM68	TNXB	TRA2A	TRIM65
THOC1	TMBIM6	TMEM161A	TMEM80	TOB2	TRADD	TRIM7
THOC4	TMC2	TMEM161B	TMEM82	TOLLIP	TRAF3IP1	TRIM71
THOC5	TMC5	TMEM163	TMEM86A	TOM1L1	TRAF4	TRIM73
THOC7	TMC6	TMEM167B	TMEM87B	TOMM22	TRAF5	TRIM8
THOP1	TMC8	TMEM169	TMEM90A	TOMM34	TRAF6	TRIO
THRA	TMCC1	TMEM175	TMEM91	TOMM40	TRAF7	TRIOBP
THRAP3	TMCC2	TMEM179B	TMEM93	TOMM5	TRAFD1	TRIP10
THRB	TMCO1	TMEM18	TMEM99	TOMM6	TRAM1	TRIP11
THSD1P	TMED1	TMEM181	TMEM9B	TOMM7	TRAM2	TRIP4
THSD4	TMED10	TMEM182	TMIE	TOP1MT	TRANK1	TRIT1
THSD7B	TMED2	TMEM184A	TMOD3	TOP1P2	TRAPPC1	TRMT12
THUMPD1	TMED4	TMEM184C	TMPPE	TOP2A	TRAPPC4	TRMT2A
THY1	TMED5	TMEM199	TMPRSS2	TOP2B	TRAPPC6A	TRMT5
TIA1	TMED7	TMEM2	TMPRSS4	TOP3A	TRAPPC6B	TRMT61B
TIAF1	TMED7-TICAM2	TMEM201	TMSB10	TOPBP1	TRAPPC9	TRNAU1AP
TIAM2	TMED9	TMEM209	TMSL3	TOR1A	TRERF1	TRNT1
TIFA	TMEFF1	TMEM212	TMTC2	TOR2A	TRIAP1	TROAP
TIGD3	TMEM100	TMEM214	TMTC3	TOR3A	TRIB1	TROVE2
TIMM10	TMEM101	TMEM216	TMTC4	TOX	TRIB2	TRPC3
TIMM13	TMEM105	TMEM217	TMUB1	TOX2	TRIB3	TRPC4AP
TIMM17A	TMEM106A	TMEM219	TMUB2	TP53	TRIM11	TRPM1
TIMM22	TMEM106B	TMEM22	TMX1	TP53BP1	TRIM14	TRPM2
TIMM44	TMEM106C	TMEM222	TMX3	TP53I13	TRIM15	TRPM4
TIMM50	TMEM107	TMEM223	TNFAIP3	TP53I3	TRIM16L	TRPM7
TIMM8B	TMEM108	TMEM229B	TNFAIP8L1	TP53INP2	TRIM2	TRPS1
TIMP2	TMEM109	TMEM231	TNFRSF10A	TP53RK	TRIM23	TRPV1
TRUB1	TTC4	TXNDC11	UBE4B	UNC84A	UTP3	VPS8
TSC22D1	TTC7B	TXNDC12	UBFD1	UNC93B1	UTRN	VRK2
TSC22D4	TTF2	TXNDC15	UBIAD1	UNCX	UVRAG	VSIG10
TSEN15	TTK	TXNDC16	UBL3	UNG	VAC14	VSNL1
TSEN2	TTLL1	TXNDC17	UBL5	UNK	VAMP4	VSTM2A
TSEN54	TTLL10	TXNDC5	UBL7	UNKL	VANGL2	VSX2
TSG101	TTLL13	TXNIP	UBLCP1	UPF1	VAPA	VTI1A
TSGA10	TTLL2	TXNL1	UBN1	UPF2	VARS	VTI1B
TSGA13	TTLL4	TXNL4A	UBOX5	UPK3B	VASH1	VTRNA1-1
TSGA14	TTLL5	TXNL4B	UBP1	UQCC	VASH2	VTRNA1-2
TSKU	TTLL6	TXNRD1	UBQLN4	UQCR	VASP	VWC2

Figure 15-19

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TSNARE1	TTLL8	TXNRD2	UBR2	UQCRB	VAT1	WAC
TSNAXIP1	TTPA	TYK2	UBTD2	URB2	VAV2	WAPAL
TSPAN1	TTPAL	TYMS	UBTF	USE1	VAV3	WARS2
TSPAN16	TTR	TYRO3	UBXN1	USO1	VCP	WASF1
TSPAN17	TTYH1	TYROBP	UBXN11	USP1	VCPIP1	WASH2P
TSPAN3	TTYH3	TYSND1	UBXN2B	USP15	VDR	WASH3P
TSPAN31	TUB	U2AF1	UBXN6	USP16	VEGFB	WASH5P
TSPAN4	TUBA1A	U2AF2	UBXN7	USP18	VENTX	WASL
TSPAN5	TUBA1B	UBA2	UCHL3	USP19	VENTXP7	WBP1
TSPAN9	TUBA1C	UBA5	UCK1	USP2	VGLL2	WBP11P1
TSPYL3	TUBA3C	UBA52	UCKL1	USP21	VGLL4	WBP2
TSPYL4	TUBA3D	UBA7	UCRC	USP3	VHL	WBP4
TSR1	TUBA8	UBAC1	UFC1	USP32	VIM	WBSCR16
TSSC1	TUBB	UBAC2	UFD1L	USP33	VIPR1	WBSCR17
TSSC4	TUBB1	UBAP2	UFM1	USP36	VIPR2	WBSCR22
TSSK2	TUBB2A	UBASH3B	UFSP1	USP37	VKORC1	WDHD1
TTBK1	TUBB2B	UBB	UFSP2	USP38	VKORC1L1	WDR18
TTBK2	TUBB4	UBC	UGDH	USP39	VOPP1	WDR19
TTC14	TUBB6	UBD	UGGT1	USP4	VPRBP	WDR20
TTC15	TUBB8	UBE2C	UGP2	USP42	VPS11	WDR24
TTC17	TUBBP5	UBE2D1	UGT1A10	USP43	VPS13B	WDR26
TTC18	TUBD1	UBE2D2	UGT8	USP44	VPS13C	WDR27
TTC19	TUBE1	UBE2D3	UHRF1	USP45	VPS18	WDR3
TTC21B	TUBGCP2	UBE2E1	UIMC1	USP46	VPS24	WDR33
TTC22	TUBGCP3	UBE2E2	ULBP1	USP47	VPS26B	WDR34
TTC25	TUBGCP6	UBE2G1	ULBP2	USP48	VPS28	WDR35
TTC26	TULP2	UBE2H	ULBP3	USP49	VPS29	WDR36
TTC27	TULP4	UBE2I	ULK4	USP5	VPS37A	WDR37
TTC28	TUSC2	UBE2J2	UMPS	USP53	VPS37C	WDR4
TTC30A	TUSC3	UBE2K	UNC119B	USP6NL	VPS37D	WDR45L
TTC31	TUT1	UBE2L3	UNC13A	USP7	VPS4A	WDR46
TTC32	TWF1	UBE2N	UNC45A	USPL1	VPS4B	WDR47
TTC35	TWISTNB	UBE2Q1	UNC50	UST	VPS52	WDR48
TTC39A	TWSG1	UBE2W	UNC5A	UTF1	VPS53	WDR5
TTC39B	TXLNA	UBE3A	UNC5B	UTP11L	VPS54	WDR51A
TTC39C	TXN2	UBE3B	UNC80	UTP15	VPS72	WDR51B
WDR52	WRNIP1	YY1	ZCCHC9	ZMYM5	ZNF253	ZNF354A
WDR53	WSB1	YY1AP1	ZDHHC1	ZNF100	ZNF254	ZNF354B
WDR55	WSCD2	ZADH2	ZDHHC11	ZNF101	ZNF256	ZNF354C
WDR59	WTAP	ZAP70	ZDHHC14	ZNF107	ZNF257	ZNF358
WDR60	WTIP	ZAR1	ZDHHC16	ZNF114	ZNF259	ZNF365
WDR62	WWC1	ZAR1L	ZDHHC17	ZNF117	ZNF26	ZNF366
WDR65	WWC2	ZBED5	ZDHHC18	ZNF12	ZNF260	ZNF37A
WDR7	WVOX	ZBP1	ZDHHC20	ZNF121	ZNF263	ZNF37B
WDR70	XAB2	ZBTB1	ZDHHC22	ZNF133	ZNF264	ZNF384
WDR73	XBP1	ZBTB12	ZDHHC23	ZNF134	ZNF266	ZNF385A
WDR74	XCL2	ZBTB16	ZDHHC24	ZNF138	ZNF271	ZNF385B
WDR75	XKR3	ZBTB2	ZDHHC3	ZNF14	ZNF276	ZNF391
WDR76	XKR4	ZBTB20	ZDHHC5	ZNF140	ZNF28	ZNF394
WDR77	XKR5	ZBTB22	ZDHHC7	ZNF141	ZNF280B	ZNF395
WDR8	XKR7	ZBTB24	ZDHHC8	ZNF143	ZNF280D	ZNF396
WDR81	XPC	ZBTB25	ZDHHC8P	ZNF146	ZNF281	ZNF397
WDR82	XPNPEP1	ZBTB26	ZEBl	ZNF148	ZNF282	ZNF398
WDR86	XPNPEP3	ZBTB3	ZFAND1	ZNF155	ZNF284	ZNF410
WDR87	XRCC1	ZBTB34	ZFAND2A	ZNF16	ZNF285A	ZNF414

Figure 15-20

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WDR89	XRCC2	ZBTB4	ZFAND2B	ZNF160	ZNF346	ZNF688
WDR91	XRCC3	ZBTB40	ZFAND3	ZNF167	ZNF419	ZNF689
WDR92	XRCC4	ZBTB42	ZFAND6	ZNF17	ZNF420	ZNF69
WDR93	XRCC6BP1	ZBTB43	ZFC3H1	ZNF174	ZNF426	ZNF691
WDTC1	XRN1	ZBTB45	ZFHX3	ZNF177	ZNF429	ZNF695
WEE1	XRN2	ZBTB46	ZFP1	ZNF181	ZNF43	ZNF697
WFDC3	XYLT1	ZBTB47	ZFP161	ZNF184	ZNF431	ZNF7
WHAMM	XYLT2	ZBTB48	ZFP36L1	ZNF187	ZNF433	ZNF70
WHAMML1	YAF2	ZBTB5	ZFP36L2	ZNF195	ZNF436	ZNF701
WHSC1	YARS	ZBTB7A	ZFP41	ZNF2	ZNF438	ZNF702P
WHSC1L1	YBX1	ZBTB7B	ZFP64	ZNF20	ZNF439	ZNF703
WHSC2	YBX2	ZBTB9	ZFPM1	ZNF207	ZNF440	ZNF705A
WIBG	YEATS2	ZC3H10	ZFPM2	ZNF211	ZNF441	ZNF705D
WIPF2	YIF1A	ZC3H11A	ZFR2	ZNF212	ZNF443	ZNF706
WIPI2	YIF1B	ZC3H12A	ZFYVE1	ZNF213	ZNF444	ZNF784
WISP3	YIPF2	ZC3H12C	ZFYVE16	ZNF214	ZNF446	ZNF786
WNK2	YIPF5	ZC3H13	ZFYVE19	ZNF219	ZNF451	ZNF787
WNK4	YJEFN3	ZC3H15	ZFYVE26	ZNF22	ZNF461	ZNF788
WNT11	YLP1M1	ZC3H3	ZFYVE28	ZNF224	ZNF462	ZNF789
WNT2B	YME1L1	ZC3H6	ZHX2	ZNF225	ZNF467	ZNF79
WNT3	YPEL1	ZC3HAV1	ZIC1	ZNF226	ZNF468	ZNF790
WNT3A	YPEL3	ZCCHC11	ZKSCAN1	ZNF229	ZNF480	ZNF792
WNT5A	YTHDC1	ZCCHC14	ZKSCAN2	ZNF23	ZNF484	ZNF793
WNT5B	YTHDF3	ZCCHC17	ZKSCAN5	ZNF230	ZNF486	ZNF799
WNT9B	YWHA	ZCCHC2	ZMAT3	ZNF236	ZNF487	ZNF8
WRAP53	YWHAH	ZCCHC24	ZMIZ1	ZNF248	ZNF490	ZNF80
WRB	YWHAQ	ZCCHC4	ZMPSTE24	ZNF250	ZNF493	ZNF805
WRN	YWHAZ	ZCCHC8	ZMYM4	ZNF252	ZNF496	ZNF808
ZNF498	ZNF600	ZNF707	ZNF828	ZNF286A	ZNF497	ZNF813
ZNF500	ZNF605	ZNF709	ZNF829	ZNF286B	ZNF560	ZNF814
ZNF506	ZNF607	ZNF71	ZNF83	ZNF292	ZNF561	ZNF815
ZNF507	ZNF608	ZNF710	ZNF830	ZNF295	ZNF562	ZNF816A
ZNF511	ZNF609	ZNF716	ZNF837	ZNF296	ZNF564	ZNF823
ZNF512	ZNF610	ZNF720	ZNF839	ZNF3	ZNF565	ZNF827
ZNF512B	ZNF611	ZNF721	ZNF84	ZNF302	ZNF566	ZSWIM6
ZNF513	ZNF614	ZNF727	ZNF845	ZNF304	ZNF567	ZSWIM7
ZNF514	ZNF619	ZNF735	ZNF860	ZNF311	ZNF57	ZW10
ZNF516	ZNF620	ZNF737	ZNF876P	ZNF317	ZNF570	ZWILCH
ZNF517	ZNF622	ZNF738	ZNF880	ZNF318	ZNF574	ZWINT
ZNF519	ZNF626	ZNF74	ZNF90	ZNF320	ZNF578	ZXDC
ZNF521	ZNF627	ZNF747	ZNF92	ZNF321	ZNF581	ZYG11A
ZNF527	ZNF628	ZNF749	ZNF98	ZNF322B	ZNF582	ZYX
ZNF528	ZNF629	ZNF761	ZNHIT1	ZNF323	ZNF583	ZZZ3
ZNF540	ZNF638	ZNF763	ZNHIT2	ZNF324	ZNF584	
ZNF541	ZNF639	ZNF764	ZNHIT3	ZNF324B	ZNF586	
ZNF543	ZNF641	ZNF766	ZNRD1	ZNF326	ZNF589	
ZNF546	ZNF643	ZNF768	ZNRF1	ZNF330	ZNF593	
ZNF547	ZNF644	ZNF77	ZNRF2	ZNF331	ZNF594	
ZNF549	ZNF649	ZNF770	ZRANB2	ZNF335	ZNF599	
ZNF550	ZNF652	ZNF771	ZSCAN12	ZNF33A	ZNF672	
ZNF551	ZNF655	ZNF773	ZSCAN21	ZNF33B	ZNF680	
ZNF554	ZNF662	ZNF774	ZSCAN29	ZNF34	ZNF681	
ZNF555	ZNF665	ZNF777	ZSCAN5A	ZNF341	ZNF682	
ZNF557	ZNF667	ZNF778	ZSCAN5B	ZNF343	ZNF684	
ZNF559	ZNF668	ZNF780B	ZSWIM5	ZNF345	ZNF687	

Figure 15-21

Gene	Correlation	Mapinfo	Chr	Gene	Correlation	Mapinfo	Chr	Gene	Correlation	Mapinfo	Chr	Gene
TOMM5	-0.355875087	37592468	9	ADAL	-0.369416263	43622671	15	ADAL	-0.369416263	43622671	15	ADAL
USP1	-0.355718933	62901875	1	ORC6L	-0.368456321	46723420	16	ORC6L	-0.368456321	46723420	16	ORC6L
KIAA1191	-0.3556852	175788722	5	TSSC4	-0.365611798	2422520	11	TSSC4	-0.365611798	2422520	11	TSSC4
ABCF3	-0.355620125	183904316	3	NR1H2	-0.365173256	50879636	19	NR1H2	-0.365173256	50879636	19	NR1H2
DUT	-0.355615703	48623432	15	HAUS3	-0.36430563	2243252	4	HAUS3	-0.36430563	2243252	4	HAUS3
RNF4	-0.355580707	2470698	4	MRFAP1	-0.36277689	6642433	4	MRFAP1	-0.36277689	6642433	4	MRFAP1
PHF21B	-0.355575081	45404910	22	WDTC1	-0.362667157	27560829	1	WDTC1	-0.362667157	27560829	1	WDTC1
MAD2L2	-0.355483562	11741009	1	GBAS	-0.362235622	56032049	7	GBAS	-0.362235622	56032049	7	GBAS
PDE12	-0.355372677	57541942	3	TAP2	-0.362071249	32806236	6	TAP2	-0.362071249	32806236	6	TAP2
LOC10021654	-0.355352224	104653126	7	MRPS7	-0.361995457	73257791	17	MRPS7	-0.361995457	73257791	17	MRPS7
NARS	-0.355205982	131909379	10	CKAP2L	-0.361752464	21872664	13	CKAP2L	-0.361752464	21872664	13	CKAP2L
CORO7	-0.355098809	55288998	18	MIS12	-0.36091616	5389857	2	MIS12	-0.36091616	5389857	2	MIS12
PVRL3	-0.355091479	4466888	16	CORO1A	-0.360701477	30194717	17	CORO1A	-0.360701477	30194717	17	CORO1A
ZNF224	-0.355066228	110791400	3	MCM6	-0.35967703	136634144	16	MCM6	-0.35967703	136634144	16	MCM6
SSX2IP	-0.355028754	44598564	19	RPS11	-0.359472362	49999417	2	RPS11	-0.359472362	49999417	2	RPS11
IER3	-0.355007014	85156634	1	DCAF13	-0.359443861	104427717	19	DCAF13	-0.359443861	104427717	19	DCAF13
RILP2	-0.354679968	30712331	6	SPRED2	-0.359215395	38593284	8	SPRED2	-0.359215395	38593284	8	SPRED2
ARPC5	-0.354614315	123921461	12	EWSR1	-0.358719667	65658583	21	EWSR1	-0.358719667	65658583	21	EWSR1
TTC30A	-0.354492711	183605181	1	ZNF829	-0.358025806	29664171	2	ZNF829	-0.358025806	29664171	2	ZNF829
RNF8	-0.354033924	44255255	7	ZDHHC5	-0.357927947	37406949	22	ZDHHC5	-0.357927947	37406949	22	ZDHHC5
C11orf71	-0.353958328	114271629	2	C9orf41	-0.357798005	57435803	19	C9orf41	-0.357798005	57435803	19	C9orf41
ZSWIM7	-0.353487486	15903687	6	ACBD6	-0.357760161	77643594	11	ACBD6	-0.357760161	77643594	11	ACBD6
MRPL18	-0.35348061	160210874	17	MOGS	-0.357714953	180472145	9	MOGS	-0.357714953	180472145	9	MOGS
TRIM45	-0.353473797	117664707	11	TRANK1	-0.357373489	74692696	2	TRANK1	-0.357373489	74692696	2	TRANK1
UBXN6	-0.353410594	4458039	1	CHCHD1	-0.357252974	36986697	3	CHCHD1	-0.357252974	36986697	3	CHCHD1
DNAJB6	-0.35334422	157129685	19	PGAP2	-0.356927065	75541668	10	PGAP2	-0.356927065	75541668	10	PGAP2
C1orf124	-0.353293198	231473791	7	RECQL	-0.356743185	3819031	11	RECQL	-0.356743185	3819031	11	RECQL
GNB1	-0.353260277	1821422	1	ATL2	-0.356545803	21654664	12	ATL2	-0.356545803	21654664	12	ATL2
NIPAZ	-0.353250105	23034700	15	ATAD2	-0.356529845	38604442	2	ATAD2	-0.356529845	38604442	2	ATAD2
CDC25B	-0.353234852	3776921	20	11-Sep	-0.356470204	124408913	8	11-Sep	-0.356470204	124408913	8	11-Sep
BCL2	-0.353193116	60986911	18	C1orf124	-0.356436551	231473786	4	C1orf124	-0.356436551	231473786	4	C1orf124
MIR17HG	-0.353153014	91999862	13	C4orf29	-0.356384274	128886135	1	C4orf29	-0.356384274	128886135	1	C4orf29
MCM7	-0.35281738	99698538	7	PSMB1	-0.356267908	170863399	4	PSMB1	-0.356267908	170863399	4	PSMB1
RTTN	-0.352752991	67873125	18	IWS1	-0.356095802	128284158	6	IWS1	-0.356095802	128284158	6	IWS1
KIAA0020	-0.352751091	2844149	9	C11orf83	-0.356083167	62439314	2	C11orf83	-0.356083167	62439314	2	C11orf83
RAP1B	-0.352746691	69005104	12	PITRM1	-0.356080372	3215066	11	PITRM1	-0.356080372	3215066	11	PITRM1
C1GALT1	-0.352721437	7222050	7	GABARAPL2	-0.356059532	75600014	10	GABARAPL2	-0.356059532	75600014	10	GABARAPL2
GANC	-0.3526641	42565872	15	NPBWR1	-0.355914129	53852274	16	NPBWR1	-0.355914129	53852274	16	NPBWR1

Figure 16-1

cg11338389	11	63742044	-0.35253464	COX8A	cg05533552	11	34074141	-0.349881331	CAPRIN1
cg10185519	16	30621987	-0.352505088	ZNF689	cg11728900	10	13203459	-0.34985572	MCM10
cg11744351	13	30424153	-0.352378107	UBL3	cg22704520	2	200820451	-0.349795351	C2orf60
cg25632648	11	77899776	-0.35231018	KCTD21	cg22223655	18	67872902	-0.349780733	RTTN
cg24692716	6	133119484	-0.352277704	C6orf192	cg04887335	3	196044632	-0.349757753	TCTEX1D2
cg05598205	16	46723426	-0.352256355	ORC6L	cg05907386	19	46195928	-0.349587917	QPCTL
cg26188571	5	179050811	-0.352163814	HNRNPH1	cg07786668	16	73092391	-0.349565761	ZFXH3
cg24275354	2	240964415	-0.352075663	NDUFA10	cg19282742	16	31469983	-0.349456878	ARMIC5
cg19034708	8	17780168	-0.352018329	PCM1	cg16203711	3	169491183	-0.349452418	MYNN
cg26442458	11	65728985	-0.351971658	SART1	cg04912466	11	63742028	-0.349437282	COX8A
cg01532694	8	8243576	-0.351842355	PIGP	cg24591563	3	40498842	-0.349425049	RPL14
cg25696485	21	38445943	-0.351819435	PIGP	cg25807061	7	74306919	-0.349389402	PMS2L5
cg01245787	4	71859630	-0.351805399	DCK	cg05300158	4	140477727	-0.349376124	SETD7
cg04533881	14	50583218	-0.351610642	C14orf138	cg03754076	1	232766254	-0.349370038	
cg02342053	9	37592791	-0.351470964	TOMM5	cg00636124	16	27215281	-0.349364602	JMID5
cg24341498	9	137217390	-0.35144523	RXRA	cg03584288	19	37407041	-0.349320209	ZNF829
cg14229247	9	100745139	-0.351420669	ANP32B	cg19568834	20	34252926	-0.349268405	CPNE1
cg01061025	1	212209225	-0.351336548	INTS7	cg08570275	3	152553089	-0.349215983	P2RY1
cg05982271	4	76555948	-0.351325807	CDKL2	cg11508669	12	6643545	-0.349120673	GAPDH
cg06703062	1	31191648	-0.351283493	MATN1	cg14369264	10	14996383	-0.348977237	DCLRE1C
cg00101895	6	108279135	-0.351042033	SEC63	cg24044479	1	116518910	-0.348959186	SLC22A15
cg11232610	5	140027381	-0.351012033	NDUFA2	cg12426141	15	57210872	-0.348852729	TCF12
cg19594024	19	58919948	-0.351005384	ZNF584	cg07262328	11	35160709	-0.34883205	CD44
cg04049556	2	71357511	-0.350977473	MPHOSPH10	cg23333420	10	105677801	-0.348822412	OBFC1
cg04956913	6	30712436	-0.350940018	IER3	cg02759005	3	53925912	-0.348819472	SELK
cg10284592	11	57434942	-0.350922588	ZDHHC5	cg17221980	6	117996486	-0.348733124	NUS1
cg06939115	16	47007824	-0.350891907	DNAJA2	cg16436509	12	120875898	-0.34868729	COX6A1
cg07743799	20	2821434	-0.350883356	FAM113A	cg10101463	1	202780506	-0.348583286	
cg22702784	2	26100814	-0.350733874	ASXL2	cg18062281	19	19030222	-0.348576964	DDX49
cg11826116	22	39916314	-0.350701027	ATF4	cg12460105	5	68665773	-0.348558635	RAD17
cg15749322	11	82905199	-0.350698438	ANKRD42	cg19233923	11	63753598	-0.348512343	OTUB1
cg07519049	6	154830998	-0.35064233	CNKSR3	cg14664575	19	40476624	-0.348433102	PSMC4
cg04977109	17	46125622	-0.350639743	NFE2L1	cg19859486	3	45730655	-0.348268548	SACM1L
cg21028463	17	74733682	-0.350620143	MIR636	cg13717023	5	53606639	-0.348268378	ARL15
cg00989323	10	49864621	-0.350605578		cg26279152	13	20356101	-0.348260688	PSPC1
cg20819397	9	123964132	-0.350505001	RAB14	cg13390975	5	34915890	-0.348254715	BRX1
cg15072612	6	32862352	-0.350502852		cg03989244	15	72523736	-0.348226451	PKM2
cg03595861	6	26126282	-0.350205476		cg01176150	16	31519952	-0.348099043	C16orf58
cg01438737	20	42086396	-0.350132682	SFRS6	cg12809842	3	196438875	-0.34798469	PIGX
cg15838288	1	228225687	-0.35001719	WNT3A	cg05144147	10	6018955	-0.347911393	IL15RA
cg18493069	6	108582623	-0.349929704	SNX3	cg17696166	17	36981606	-0.347896862	CCDC49

Figure 16-2

cg27110132	16	3661765	-0.34789074	BTBD12	cg05731183	15	68132796	-0.345780026	
cg24356797	19	18682387	-0.347849748	UBA52	cg06642177	6	134496341	-0.345683812	SGK1
cg26858892	12	118573640	-0.3477998	PEBP1	cg13193676	8	80942319	-0.345665718	MRPS28
cg24654547	16	68057165	-0.347750542	DUS2L	cg16041611	6	43139680	-0.345663235	SRF
cg26376168	6	30712439	-0.347656413	IER3	cg16362983	14	50335243	-0.345602286	
cg19954613	22	22020219	-0.347627559	PPIL2	cg21028326	22	50683188	-0.345583858	TUBGCP6
cg26910488	17	66243590	-0.347560803	AMZ2	cg10932242	14	100659592	-0.345556762	
cg01457080	14	77278578	-0.34755422	ANGEL1	cg20940459	1	173793922	-0.345432063	CENPL
cg27275634	20	37590967	-0.3475078	DHX35	cg20349687	2	88927127	-0.34541042	EIF2AK3
cg00080118	6	31126173	-0.347473329	CCHCR1	cg27033716	13	24463018	-0.345404389	PCOTH
cg03951132	20	5931305	-0.347463514	MCM8	cg02184643	11	10879647	-0.345372598	ZBED5
cg08525207	2	3622752	-0.347367499	RPS7	cg21352959	17	62340143	-0.345371598	TEX2
cg20731804	6	42858765	-0.347356586	C6orf226	cg03183872	20	3140552	-0.345353027	FASTKD5
cg04488215	1	174968829	-0.3473125	CACYBP	cg11316940	10	69524027	-0.3453331326	
cg00368987	19	57703364	-0.347300739	ZNF264	cg13799898	9	136858673	-0.345307107	VAV2
cg04553410	7	150864885	-0.347252146	GBX1	cg04726800	3	128598191	-0.345277515	ACAD9
cg14189758	20	36156486	-0.347218357	BLCAP	cg05489143	3	40498640	-0.345275356	RPL14
cg10794915	17	33569985	-0.347155264	SLFN5	cg13872356	11	62341519	-0.345266442	EEF1G
cg15147060	3	88108213	-0.346991106	CGGBP1	cg02594498	15	22893147	-0.34524021	CYFIP1
cg02815282	11	67141135	-0.346921732	LOC100130987	cg02627531	19	52873085	-0.34521987	ZNF880
cg21359254	2	128144817	-0.346861046		cg20994084	17	79269488	-0.345214296	SLC38A10
cg04145065	4	40057559	-0.346845767	N4BP2	cg13360562	15	39872883	-0.34520363	THBS1
cg26439238	13	45563672	-0.346800727	NUFIP1	cg24315188	7	77428849	-0.345162831	PHTF2
cg22493809	1	120838387	-0.346777693	FAM72B	cg05055720	3	49449599	-0.345143613	TCTA
cg06012509	6	43027269	-0.346683899	KLC4	cg21605986	5	175788725	-0.345121854	KIAA1191
cg16993440	5	80597283	-0.346603526	RNU5E	cg22020752	12	22697546	-0.345107002	KIAA0528
cg03837627	17	28443756	-0.346569719	CCDC55	cg00155504	1	11160113	-0.345068005	EXOSC10
cg03133725	12	133563452	-0.346328436	ZNF26	cg08602604	2	198364282	-0.345041863	HSPD1
cg03149313	1	226595334	-0.346305037	PARP1	cg11430659	2	201374471	-0.345027605	KCTD18
cg04278597	1	63154320	-0.346231031	DOCK7	cg06893225	1	24306863	-0.345019478	SFRS13A
cg16370446	4	15683284	-0.346175403	LOC285550	cg04347293	6	32862350	-0.344982957	
cg25180252	10	51828127	-0.346129807	FAM21A	cg05164570	5	140071033	-0.344861201	HARS
cg00730780	10	30316187	-0.346074915	KIAA1462	cg08125972	19	36705377	-0.344833493	ZNF565
cg23077509	3	142166793	-0.346066945	XRN1	cg16120422	12	113590924	-0.344798006	CCDC42B
cg20791839	3	53926047	-0.346041914	SELK	cg15967188	4	2470700	-0.344763143	RNF4
cg02750935	5	145214981	-0.345995489	PRELID2	cg23604584	13	50367114	-0.344602629	KPNA3
cg19180542	10	43047893	-0.345987363	ZNF37B	ch.8.20603847F	8	20559567	-0.344536045	
cg06752163	3	170588210	-0.34598497	RPL22L1	cg03519303	4	139936796	-0.344445444	CCRN4L
cg00603498	17	5322775	-0.345968144	RPAIN	cg18471460	14	54863582	-0.344350015	CDKN3
cg07222113	8	104427719	-0.345951657	DCAF13	cg08809260	2	177054140	-0.344270537	HOXD1
cg25365783	7	108166722	-0.345788162	PNPLA8	cg19545621	2	208491029	-0.344255359	FAM119A

Figure 16-3

cg12646754	1	2574751	-0.34424681		cg05467106	16	30621996	-0.343059665	ZNF689
cg05525867	15	75661090	-0.344245323	MAN2C1	cg21108767	7	99933721	-0.343038938	PILRB
cg08256065	5	77081163	-0.344157358		cg05014952	14	35873130	-0.343036506	NFKBIA
cg10450899	17	685900	-0.344141295	RNMTL1	cg05165580	16	75657337	-0.343003926	ADAT1
cg17868994	9	107526283	-0.344110253	NIPSNAP3B	cg15970156	22	22863219	-0.342934202	ZNF280B
cg23556447	6	90529595	-0.344109611	MDN1	cg05557255	11	2422385	-0.342892148	TSSC4
cg06140118	16	68056778	-0.344096404	DDX28	cg13549897	1	70820344	-0.342862036	HHLA3
cg02083259	16	57220135	-0.344089138	RSPRY1	cg11975206	10	135192160	-0.342797511	PAOX
cg14082963	4	89444434	-0.344044173	PIGY	cg02320003	5	60139293	-0.34271244	ELOVL7
cg02776251	12	62654319	-0.344017998	USP15	cg17168838	19	54663528	-0.342708227	LENG1
cg14400631	11	14666512	-0.344011614	PDE3B	cg10536369	2	170335894	-0.342699288	BBS5
cg03631596	13	73301985	-0.344009358	C13orf37	cg19951638	7	66461658	-0.342659456	SBDS
cg00166327	13	73356072	-0.343955799	PIBF1	cg24269276	17	56084441	-0.342633553	SFRS1
cg16710791	1	193028559	-0.343809007	TROVE2	cg20601096	14	93799719	-0.342627677	KIAA1409
cg14037413	11	9482594	-0.343769054	ZNF143	cg26236440	2	113341947	-0.342625276	CHCHD5
cg18106800	5	94890715	-0.343714226	ARSK	cg26745551	6	97285260	-0.342576277	GPR63
cg26260369	14	68141723	-0.343674296	VT11B	cg10041390	10	89623018	-0.34257548	PTEN
cg17663101	3	49131524	-0.3436661059	QRICH1	cg18283779	2	85107426	-0.342566426	C2orf89
cg25444615	19	24184550	-0.34362926		cg02942644	3	119217190	-0.342547763	C3orf1
cg10037053	6	30181425	-0.343590062	TRIM26	cg09434803	4	26863372	-0.342528142	STIM2
cg17607973	7	100027408	-0.343575086	MEPCE	cg16826947	7	44084618	-0.342488561	DBNL
cg07156296	4	108911347	-0.343545924	HADH	cg20725936	5	175875158	-0.342479582	FAF2
cg21497607	2	74425593	-0.343512873	MTHFD2	cg24647403	3	97483221	-0.342423833	ARL6
cg21840888	18	33709847	-0.343507536	ELP2	cg06069179	17	33288421	-0.342384202	CCT6B
cg08357601	4	71554472	-0.343484954	UTP3	cg03392679	3	71773917	-0.342270192	EIF4E3
cg04845077	9	34126958	-0.343478878	DCAF12	cg13226139	14	45605129	-0.342197272	FKBP3
cg17591343	1	93646016	-0.343439092	TMED5	cg24131747	14	68141730	-0.34214382	VT11B
cg06364629	2	27592939	-0.34337586	EIF2B4	cg27024417	1	32645813	-0.342141324	TXLNA
cg22450146	17	74733660	-0.343370831	MIR636	cg07187585	17	10600923	-0.342113783	C17orf48
cg19695335	20	25604759	-0.343357654	NANP	cg15238008	12	9600875	-0.342103104	DDX12
cg15268622	1	167189846	-0.343305096	POU2F1	cg23627909	14	60337760	-0.342050841	RTN1
cg13129662	17	48227708	-0.343299397	PPP1R9B	cg02146966	17	18967117	-0.341935501	
cg10386445	2	26205648	-0.343295593	KIF3C	cg09172817	18	9915098	-0.341927048	VAPA
cg21076271	14	32546633	-0.343294027	ARHGAP5	cg26260386	4	140477698	-0.341892239	SETD7
cg05165989	2	26101121	-0.343269941	ASXL2	cg14278893	1	145610795	-0.341871099	POLR3C
cg18715511	12	1058965	-0.343259378	RAD52	cg22198449	19	4458029	-0.341806928	UBXN6
cg04210544	13	111806530	-0.343215126	ARHGEF7	cg09507884	11	67084689	-0.341778429	LOC10013098
cg03616195	17	29233260	-0.343207091	C17orf42	cg23285750	10	46223127	-0.341751954	FAM21C
cg14804635	15	75747750	-0.343193716	SIN3A	cg22468803	18	9136381	-0.341654961	ANKRD12
cg25187227	4	40058080	-0.34313652	N4BP2	cg20879576	11	125034747	-0.341634193	PKNOX2
cg17424056	11	46615413	-0.343133568		cg21619228	19	38085153	-0.341616764	ZNF540

Figure 16-4

cg19720917	19	36606221	-0.341572082	POLR2I	cg00582820	3	125314599	-0.340279515	OSBPL11
cg26187219	5	52095812	-0.341547987	ITGA1	cg20064106	2	178257871	-0.340274617	LOC10013069
cg06880557	13	103425546	-0.341516192	C13orf27	cg00533923	6	116892543	-0.340247554	RWDD1
cg23508052	10	102106811	-0.341503998	SCD	cg01547051	7	150777654	-0.340177433	FASTK
cg04310649	10	35416472	-0.341493565	CREM	cg22183232	11	9406733	-0.340165978	IPO7
cg07485181	2	131851172	-0.341466368	FAM168B	cg06027057	14	90849959	-0.340153017	
cg17154187	17	18163844	-0.34141669	SMCR7	cg07532072	22	42016555	-0.340147304	PPDE2
cg12481283	20	19997705	-0.341407558	NAA20	cg08209042	3	196295218	-0.340011253	WDR53
cg12342027	7	44835729	-0.341387876	PPIA	cg21222634	20	57465926	-0.339988699	GNAS
cg24121211	4	128887195	-0.341245085	MFS8	cg04847817	22	28315981	-0.339984914	PITPNB
cg13196826	10	98945664	-0.341208404	SLIT1	cg10977398	3	124606490	-0.339926205	ITGB5
cg18500714	14	100706288	-0.341145751	YY1	cg09947615	4	42659549	-0.339898856	ATP8A1
cg04706880	19	40023151	-0.34113833	EID2B	cg20555477	9	86594889	-0.339896109	HNRNPK
cg04223366	3	66024364	-0.34113271	MAGI1	cg03639675	16	46723204	-0.339853359	ORC6L
cg03956646	8	143750859	-0.341036652	JRK	cg14928532	9	133454630	-0.339830098	LOC10027221
cg18610261	2	37899776	-0.341024743	CDC42EP3	cg15062310	7	100450120	-0.339814389	SLC12A9
cg21824902	1	27560832	-0.341008302	WDTG1	cg25452632	12	56754141	-0.339796555	STAT2
cg14369405	18	32556760	-0.340930302	MAPRE2	cg03762505	1	171750926	-0.339768415	METTL13
cg17865108	17	18086721	-0.340881269	ALKBH5	cg03959891	7	99933717	-0.339753847	PILRB
cg12972275	4	122722461	-0.340847607	EXOSC9	cg08938976	1	247095660	-0.339510494	AHCTF1
cg10952801	17	43568353	-0.340833001	PLEKHM1	cg16696730	21	43916444	-0.339504756	RSPH1
cg05337192	1	108113367	-0.340804487		cg12995410	6	151712734	-0.339426493	ZBTB2
cg09771049	17	66031798	-0.34077698	KPNA2	cg04410587	7	156743073	-0.339404606	NOM1
cg11162385	20	25604740	-0.340764818	NANP	cg15115510	20	33872603	-0.339402915	EIF6
cg11673391	1	10459052	-0.340762424	PGD	cg13654902	19	38853053	-0.339266935	CATSPERG
cg25764824	22	42085083	-0.34073195	NHP2L1	cg00415582	6	43027202	-0.339252662	KLC4
cg22167839	7	35840133	-0.340717966	7-Sep	cg19080138	7	35734733	-0.339233487	HERPUD2
cg13047843	7	101386679	-0.340694773		cg23255280	9	131710198	-0.339211261	DOLK
cg25604067	11	126226068	-0.340686906	ST3GAL4	cg15409468	5	31532111	-0.33920929	RNASEN
cg14871712	9	102861491	-0.340649397	INVS	cg21157115	9	33001303	-0.339133006	APTX
cg02550592	1	762915	-0.340597342	NCRNA00115	cg14735242	2	64371651	-0.339124372	PELI1
cg25597233	5	140027233	-0.340581453	NDUFA2	cg085222087	5	14871910	-0.339113582	ANKH
cg04949346	2	169746998	-0.340572877	SPC25	cg11826708	3	115502895	-0.339095025	
cg14237749	9	136344651	-0.340539992	SLC2A6	cg25794819	19	55629097	-0.339018136	PPP1R12C
cg07093111	17	18585732	-0.340503429	ZNF286B	cg23709121	14	59951523	-0.339011084	C14orf149
cg27619163	17	7982806	-0.340502786	ALOX12B	cg21806917	11	66384012	-0.33900967	RBM14
cg06888550	17	43238612	-0.340497253	HEXIM2	cg13537196	9	15553060	-0.338954497	C9orf93
cg19738812	7	99102438	-0.340461305	ZKSCAN5	cg10845251	19	19314334	-0.338901169	NR2C2AP
cg00102920	6	18156401	-0.340421049	TPMT	cg10545927	1	33117362	-0.338896144	RBBP4
cg09276863	17	60501233	-0.340329001	METTL2A	cg18538332	22	24372958	-0.338876485	LOC391322
cg13423282	19	19174731	-0.340310262	SLC25A42	cg03437731	2	198570720	-0.338864329	MARS2

Figure 16-5

cg04936382	20	36662003	-0.338824445	RPRD1B	cg03228804	16	86589205	-0.337823033	MTHFS
cg13663190	2	73461428	-0.338733202	CCT7	cg18212591	13	103425442	-0.337813706	C13orf27
cg05380793	13	73301995	-0.33869999	C13orf37	cg15806518	9	127177817	-0.337783085	PSMB7
cg05947570	10	89623020	-0.338696742	PTEN	cg10076931	6	27100556	-0.337689661	HIST1H2AG
cg18451983	6	139695471	-0.338677427	CITED2	cg07906495	14	31028426	-0.337584149	G2E3
cg08142263	19	17420206	-0.33866661	DDA1	cg11515196	15	44829065	-0.337575868	EIF3J
cg04226364	17	47865990	-0.338660284	MVST2	cg27084994	5	175875161	-0.337456092	FAF2
cg05376810	17	74511493	-0.338656653		cg11821927	15	45694435	-0.337434226	SPATA5L1
cg02985708	6	32940921	-0.338623166	BRD2	cg09223439	15	65282374	-0.337432597	SPG21
cg24251484	10	119133804	-0.338612263	PDZD8	cg19752449	12	109915316	-0.337347729	UBE3B
cg04844543	3	47324470	-0.338597541	KIF9	cg02286335	10	58121068	-0.337242066	ZWINT
cg08108993	17	38136923	-0.338568569	PSMD3	cg18354764	22	31064165	-0.337224388	DUSP18
cg10392378	6	90348606	-0.338564001	LYRM2	cg07303308	7	128695042	-0.337192042	LOC286016
cg17536750	4	6642118	-0.33855133	MRFAP1	cg04875007	16	2014871	-0.33713364	SNHG9
cg23358710	17	60704660	-0.338546749	MRC2	cg04798796	10	88855483	-0.337109935	GLUD1
cg19929624	18	11851551	-0.338542298	GNAL	cg25937832	3	23958525	-0.33710947	NKIRAS1
cg23924007	4	140099401	-0.338492183		cg11422045	11	43701985	-0.337105913	HSD17B12
cg16340159	2	240322705	-0.338477653	HDAC4	cg08108155	22	29999444	-0.337097091	NF2
cg23472502	6	42420509	-0.338457955	TRERF1	cg22675162	2	70520975	-0.337088686	SNRPG
cg13468174	19	58919984	-0.338454129	ZNF584	cg12174498	8	80942140	-0.337066105	MRPS28
cg08795962	11	93862716	-0.338439787	PANX1	cg26597500	13	73356092	-0.337065249	PIBF1
cg18751306	15	81294292	-0.338412617	MESDC1	cg26149167	19	16187889	-0.336937163	TPM4
cg01154537	10	95462167	-0.338367211	C10orf4	cg14397361	9	140149997	-0.33685328	COBRA1
cg18255595	13	20735871	-0.338346231	GJA3	cg10122932	7	99698990	-0.336815584	MCM7
cg21160472	1	212782112	-0.338299524	ATF3	cg22033189	1	28908551	-0.336801092	SNHG12
cg03780073	15	48624255	-0.3382899	DUT	cg04690289	3	45017999	-0.336741375	ZDHHC3
cg01162436	10	15902292	-0.338252874	FAM188A	cg07987587	22	42486991	-0.336685183	NDUFA6
cg14042131	11	48003169	-0.338229781	PTPRJ	cg14320593	18	47088343	-0.336585646	LIPG
cg05835456	15	43785425	-0.338227429	TP53BP1	cg13023681	2	10444156	-0.336536883	HPCAL1
cg02996684	17	73257924	-0.338182454	GGA3	cg25976786	12	53662079	-0.336502852	ESPL1
cg01040759	2	86116384	-0.338179448	ST3GAL5	cg21869055	19	51522454	-0.336482161	KLK10
cg00965391	11	92930777	-0.33816811	SLC36A4	cg06172942	3	50378529	-0.336440527	RASSF1
cg16026760	19	4791699	-0.338110531	FEM1A	cg01534423	17	18965556	-0.336440304	
cg26693760	6	33267069	-0.338036566	RGL2	cg25423402	1	185286075	-0.336437794	IVNS1ABP
cg03272292	12	48577362	-0.338014964	C12orf68	cg17019204	6	86303781	-0.336395163	SNX14
cg18721605	18	44676421	-0.338008133	HDHD2	cg16587974	5	76383162	-0.336371888	LOC728723
cg27227786	17	54911265	-0.337998411	DGKE	cg09695652	3	139108473	-0.336350018	COPB2
cg10742605	3	18485411	-0.337975785		cg07031532	15	64995684	-0.336327401	OAZ2
cg26674752	10	43634212	-0.337965086	CSGALNACT2	cg15408407	19	1438438	-0.33632339	RPS15
cg18881776	1	28052146	-0.337951707	FAM76A	cg01608030	19	1605680	-0.33630646	UOCR
cg23542858	8	125486752	-0.337873291	RNF139	cg24899068	19	49999470	-0.33629556	RPS11

Figure 16-6

cg15248577	10	7450456	-0.336289824	SFMBT2	cg27417846	2	88927289	-0.334841202	EIF2AK3
cg22974920	21	40686053	-0.336239274	BRWD1	cg26097011	13	103046943	-0.334809987	FGF14
cg19656070	17	3571978	-0.33620493	TMEM93	cg00045190	6	33216612	-0.334802668	
cg02043083	6	150070997	-0.336167693	PCMT1	cg21799605	6	42713881	-0.334798892	TBCC
cg17985418	17	66031785	-0.336153694	KPNA2	cg09000178	16	67063319	-0.334792867	CBFB
cg08533424	17	37009973	-0.336111477	RPL23	cg13883202	3	47422330	-0.334784079	PTPN23
cg23623107	2	128284154	-0.336034419	IWS1	cg02063919	20	50418044	-0.334759579	SALL4
cg03537747	2	27886640	-0.335985854	SLC4A1AP	cg08293367	22	22089752	-0.334757322	YPEL1
cg27376617	7	30518048	-0.335976424	NOD1	cg01888767	5	131832552	-0.334722039	
cg11081185	11	208423	-0.335925672	RIC8A	cg01993413	14	21979151	-0.334646308	METTL3
cg16162927	6	136610857	-0.335914151	BCLAF1	cg06719391	11	2554330	-0.334566917	KCNQ1
cg03719625	19	38806411	-0.335905207	YIF1B	cg19853927	3	153839743	-0.334558308	SGEF
cg02932736	1	67896194	-0.335904392	SERBP1	cg12173535	19	54694174	-0.334525555	MBOAT7
cg12023693	2	102091115	-0.335883486	RFX8	cg06770993	3	49158462	-0.334440256	USP19
cg07281688	12	57082442	-0.33587995	PTGES3	cg09069257	12	94495988	-0.334379901	
cg04966789	14	35591779	-0.335849953	PPP2R3C	cg22813744	11	77899778	-0.334353308	KCTD21
cg00124011	1	14075958	-0.335816174	PRDM2	cg11781847	8	67837483	-0.334340593	SNHG6
cg16632994	5	158690246	-0.335777127	UBLCP1	cg04508286	7	35840410	-0.334324966	7-Sep
cg00166750	8	102138594	-0.335746557		cg10163945	5	115421152	-0.334322447	COMMMD10
cg12700464	11	78128424	-0.335732831	GAB2	cg07623022	16	18801545	-0.334315908	RPS15A
ch.2.223778692R	2	224070448	-0.335658333		cg26900616	4	159593389	-0.334314375	ETFDH
cg01963240	14	54421117	-0.335639893	BMP4	cg03156112	10	22630065	-0.334306438	
cg13189086	15	23034679	-0.33558978	NIP A2	cg23616383	17	7487132	-0.33418011	MPDU1
cg11718235	19	56915184	-0.335579288	ZNF583	cg16458021	21	43430507	-0.334176037	ZNF295
cg03486485	11	14927004	-0.335529526		cg23542284	19	19314328	-0.334093906	NR2C2AP
cg19057882	20	37101373	-0.335494105	RALGAPB	cg05325390	16	23464715	-0.334092741	COG7
cg22916109	15	78730334	-0.335448305	IREB2	cg03373442	13	31736396	-0.334091312	HSPH1
cg05529236	11	62341449	-0.335439973	EEF1G	cg11775492	12	51158663	-0.334088908	ATF1
cg16971831	5	56110935	-0.335391253	MAP3K1	cg02836531	1	78225436	-0.334087771	USP33
cg10035432	14	39644345	-0.335371447	PNN	cg26460378	19	36545594	-0.334084374	WDR62
cg24458288	18	12702185	-0.335350301	CEP76	cg25776555	19	52531777	-0.334015183	ZNF614
cg17488985	6	86159426	-0.335309044	NT5E	cg24429831	19	36120171	-0.334009297	RBM42
cg24218077	11	125495856	-0.335291751	CHEK1	cg18438837	1	42922100	-0.334007624	PPCS
cg25587211	3	43663662	-0.335137657	ANO10	cg21656600	12	111181027	-0.333981092	PPP1CC
cg20009215	6	2765204	-0.335084301	WRNIP1	cg18469778	11	18548623	-0.333980159	TSG101
cg08167214	16	81040017	-0.335066258	CENPN	cg09099697	10	65281856	-0.333966701	REEP3
cg20670292	2	131099506	-0.334908121	IMP4	cg04291082	1	193028561	-0.333948446	TROVE2
cg03092918	10	126107592	-0.334894767	OAT	cg23091255	6	64345855	-0.333910281	
cg14694896	8	104427370	-0.334874376	SLC25A32	cg13519464	19	9938554	-0.333892355	UBL5
cg02410754	1	32410520	-0.334866327		cg02249648	12	1703181	-0.333884751	FBXL14
cg22782929	10	21784432	-0.334849606	C10orf114	cg12109968	20	50383676	-0.333860522	ATP9A

Figure 16-7

cg17417191	1	218458683	-0.333843085	RRP15	cg11980791	9	131084797	-0.333048165	COQ4
cg16465128	16	30389462	-0.333818099	1-Sep	cg24441068	11	32605279	-0.332965766	EIF3M
cg00881254	18	657522	-0.33380022	TYMS	cg05871607	1	28241317	-0.332942938	RPA2
cg04759220	5	78532560	-0.33379053	JMY	cg03054141	12	8234711	-0.332925228	NECAP1
cg17227014	4	6642450	-0.333789496	MRFAP1	cg13912060	14	68141881	-0.332914146	VT11B
cg04273556	9	35096672	-0.333788718	PIGO	cg08703520	19	58978336	-0.332806554	ZNF324
cg16687867	11	111896092	-0.333765466	DLAT	cg16114773	1	20209461	-0.33274614	OTUD3
cg21442773	1	236029828	-0.333760901	LYST	cg08230118	6	30181847	-0.332732541	TRIM26
cg02775028	4	184580387	-0.333708668	C4orf41	cg06746074	3	87276268	-0.332721405	CHMP2B
cg17978996	6	107436496	-0.333702545	BEND3	cg14797322	12	58165899	-0.332706773	FAM119B
cg18264306	3	97483471	-0.333667009	ARL6	cg13676204	14	61447818	-0.332696358	SLC38A6
cg14815005	22	22222162	-0.333664785	MAPK1	cg02455615	11	33183110	-0.332660661	CSTF3
cg13433446	9	128170534	-0.333649537		cg14650559	14	77843620	-0.332652103	C14orf174
cg22512377	22	42475683	-0.333590254	C22orf32	cg18652923	2	109745344	-0.332643816	SH3RF3
cg03883519	4	128886524	-0.3335571	MFSB8	cg09007244	22	51221736	-0.332619131	RPL23AP82
cg26681912	1	169455321	-0.333538715	SLC19A2	cg01840575	2	38977957	-0.332607879	SFRS7
cg03875450	9	98269581	-0.333525673	PTCH1	cg17310611	1	113615709	-0.332607374	LRIG2
cg14532069	18	59993399	-0.333512013	TNFRSF11A	cg21008684	2	157198370	-0.332570497	HDGF2
cg21243939	14	55033137	-0.333490511	SAMD4A	cg06873684	19	4472059	-0.332541702	
cg08402439	4	180980552	-0.333467778		cg13398135	17	80250214	-0.332512383	DLGAP5
cg25264554	3	142166789	-0.33345286	XRN1	cg10130446	14	55658398	-0.332488734	ENPP1
cg14031414	20	13765665	-0.333434352	ESF1	cg21851142	6	132129008	-0.332480761	
cg25296860	13	20702426	-0.333422067		cg27209395	6	26172397	-0.332468423	
cg03456512	7	107531689	-0.333416916	DLD	cg27196102	16	23464713	-0.332459641	COG7
cg13425677	5	56112090	-0.333399843	MAP3K1	cg19049616	17	58042270	-0.332388499	RNFT1
cg09690659	20	33680871	-0.333380273	TRPC4AP	cg18467110	3	140661601	-0.332388305	SLC25A36
cg14838017	1	160232450	-0.333342358	DCAF8	cg25346576	17	28443852	-0.332386846	CCDC55
cg27090007	13	28519388	-0.333333588	ATP5EP2	cg17691309	9	35690459	-0.332372078	TPM2
cg22546696	15	41952645	-0.3333330686	MGA	cg26541587	10	43950885	-0.332361766	ZNF487
cg24663255	8	146228920	-0.3333316172	ZNF252	cg24085655	6	35436189	-0.332342699	RPL10A
cg11652947	17	80605508	-0.3333315291	WDR45L	cg10867947	8	95835263	-0.332322296	INTS8
cg00090767	14	65569376	-0.333308366	MAX	cg14242042	12	24715250	-0.332312405	SOX5
cg26387966	8	144503421	-0.333303594		cg17290332	10	14880008	-0.332273357	CDNF
cg22992588	18	74207551	-0.333283222		cg03803211	2	70313772	-0.332237304	PCBP1
cg08867499	19	33667906	-0.333246525		cg23576473	17	47785586	-0.332213148	SLC35B1
cg24079997	4	52709183	-0.333214481	DCUN1D4	cg24395128	17	57184525	-0.332158046	TRIM37
cg19014302	19	18303893	-0.333200277	MPV17L2	cg06733736	16	3661771	-0.332145324	BTBD12
cg11841349	3	9791615	-0.333154093	OGG1	cg11075994	15	102192790	-0.332097287	TM2D3
cg04175957	15	23207925	-0.333117315	WHAMM1L1	cg13776499	2	12858298	-0.332095052	TRIB2
cg02994863	1	64059297	-0.333092579	PGM1	cg15433422	3	196670053	-0.332087969	LOC152217
cg02246053	17	57184577	-0.333089625	TRIM37	cg18588934	9	132083215	-0.332072066	C9orf106

Figure 16-8

cg04855748	11	64067763	-0.332055228	C11orf20	cg03876184	2	27886755	-0.331155759	SUPT7L
cg11969467	1	174992598	-0.332046422	MRPS14	cg05228735	16	30621825	-0.33113014	ZNF689
cg13112249	22	32870603	-0.331957858	FBXO7	cg04165128	19	52693149	-0.331126428	PPP2R1A
cg03758774	6	32936478	-0.331943135	BRD2	cg21454030	4	17812573	-0.331117392	NCAPG
cg05417615	4	147443478	-0.331926153	SLC10A7	cg18913076	2	99771244	-0.331105406	TSGA10
cg00656411	7	140773422	-0.331922334		cg16788234	11	108093338	-0.331044887	NPAT
cg04364194	1	202114085	-0.33191902	ARL8A	cg13841901	1	45805975	-0.331042314	MUTYH
cg13741289	4	17578858	-0.331910311	LAP3	cg04183933	2	198363868	-0.331036343	HSPD1
cg08655589	3	14444175	-0.33189884	SLC6A6	cg16722292	10	7830180	-0.33100122	KIN
cg16787025	15	51200723	-0.331886894	AP4E1	cg01141237	2	198175400	-0.330992643	
cg06067302	22	40766481	-0.331886115	SGSM3	cg01896926	17	685509	-0.330935504	GLOD4
cg04024692	11	16760046	-0.331876611	C11orf58	cg22825116	2	88991018	-0.330934628	RPIA
cg21914984	2	37899464	-0.331855246	CDC42EP3	cg23528168	5	89770579	-0.330912105	MBLAC2
cg05907686	6	7389956	-0.331796661	CAGE1	cg03857186	2	27255618	-0.330891687	TMEM214
cg24140832	11	236743	-0.331795445	PSMD13	cg06776953	1	149859104	-0.330889713	HIST2H2AB
cg24608684	6	130686865	-0.33179082		cg16697775	6	43543259	-0.330855149	POLH
cg09293699	16	81040972	-0.331787171	CENPN	cg04404789	16	46722505	-0.330808488	ORC6L
cg23792258	6	17988404	-0.331775019	KIF13A	cg02461956	11	134093940	-0.330779359	NCAPD3
cg21777696	11	57283154	-0.331765301	SLC43A1	ch.5.2925238F	5	154966064	-0.330778913	
cg26526596	6	170190117	-0.331751477	C6orf122	cg01456938	4	2470303	-0.330772779	RNF4
cg02656441	13	111367915	-0.331677653	ING1	cg10620501	8	37620046	-0.330734318	PROSC
cg051119514	19	58459218	-0.331599642	ZNF256	cg20692684	10	32735158	-0.330729196	CCDC7
cg10093594	1	206858754	-0.331588177	MAPKAPK2	cg24705286	16	27215306	-0.330717403	JMJD5
cg20288129	3	122745632	-0.331587361	SEMA5B	cg04084597	11	75479652	-0.330714488	DGAT2
cg13601636	19	55385010	-0.331584884	FCAR	cg23060735	22	51066924	-0.330695727	ARSA
cg00911981	3	142297824	-0.331561866	ATR	cg00389713	6	43138877	-0.330690404	SRF
cg04696559	5	36152378	-0.331496606	SKP2	cg26852602	15	83735291	-0.330660947	BTBD1
cg08423350	4	57253668	-0.331474314	AASDH	cg06183820	6	2972097	-0.330587105	SERPINB6
cg16221634	6	73332885	-0.331472593	KCNQ5	cg20214067	12	133065776	-0.330579629	FBRSL1
cg10025462	17	27046956	-0.331415963	SNORD42B	cg27211204	15	99791508	-0.330421962	LRRC28
cg02228635	1	93298093	-0.331368722	RPL5	cg00673674	19	19144826	-0.330408764	SFRS14
cg03509024	3	10184013	-0.331335827	VHL	cg14092529	5	21459600	-0.330396605	LOC728411
cg16706751	7	130792127	-0.331314893	FLJ43663	cg03406394	15	60296138	-0.330384228	FOXB1
cg19956166	2	85980874	-0.331293005	ATOH8	cg10205287	4	100815590	-0.330308839	MAPKSP1
cg09507928	5	140027484	-0.331282327	IK	cg10046127	14	57735694	-0.330305427	MUDENG
cg04219700	1	228594657	-0.331244918	TRIM11	cg08515713	11	64037528	-0.330302972	BAD
cg08794928	6	144537264	-0.331234417		ch.7.3356624R	7	157205374	-0.330248054	DNAJB6
cg24962978	11	118889279	-0.331201305	TRAPPC4	cg11014794	10	93999688	-0.330247179	CPEB3
cg21482837	2	85581528	-0.331193559	ELMOD3	cg17218495	19	11071743	-0.330236689	SMARCA4
cg12564650	5	179050814	-0.331190047	HNRNPH1	cg14645526	11	91959086	-0.330177668	
cg07697850	16	29973177	-0.331174192	TMEM219	cg02888906	11	107798972	-0.330173159	RAB39

Figure 16-9

cg05544840	13	44716513	-0.330172563	cg13022174	18	23671059	-0.329296728	SS18
cg18396041	7	149571256	-0.330142961	cg02750587	1	85156370	-0.329283668	SSX2IP
cg20296188	17	77397067	-0.330124447	cg14209549	10	3215073	-0.329273083	PITRM1
cg09909775	12	45610071	-0.330113482	ch.12.1878964R	12	95773961	-0.329225409	
cg16811230	3	39149235	-0.330102471	cg13992236	6	86352429	-0.329180395	SYNCRIP
cg10289190	9	37422575	-0.330090784	cg24523585	13	49821926	-0.329131905	CDADC1
cg03468945	10	126107610	-0.330046689	cg12482557	8	6693103	-0.329111356	XKR5
cg01606576	14	50065185	-0.330030329	cg24503272	6	160210831	-0.32909182	MRPL18
cg06150468	1	212874085	-0.329986237	cg15605445	10	88470986	-0.329087132	LDB3
cg19759549	3	128211096	-0.329982456	cg03332970	11	124632552	-0.329078936	ESAM
cg14150915	11	66056828	-0.329925721	cg23961842	6	85483800	-0.329056959	
cg18573544	6	38608108	-0.329910686	cg22100476	1	43638037	-0.329045984	WDR65
cg03327386	18	8609878	-0.329888992	cg11594927	6	29720600	-0.329035996	
cg00715047	17	73522054	-0.329888061	cg10533351	20	19997722	-0.329024014	NAA20
cg052223847	10	124913846	-0.329873737	cg25700848	6	7911417	-0.329001846	TXNDC5
cg06015203	14	51297334	-0.329860308	cg25525163	3	38178867	-0.328973986	ACAA1
cg21350283	14	69445743	-0.3298468	cg15617768	10	101492447	-0.328958999	COX15
cg15928538	7	140773578	-0.329823422	cg01747792	20	61806628	-0.328940871	
cg00795915	5	70751728	-0.329814781	ch.21.43742285F	21	44917857	-0.328927234	
cg26570218	2	25195142	-0.329814307	cg12100751	1	109203672	-0.32889872	C1orf59
cg19789848	17	30454741	-0.329802051	cg02127607	17	61920694	-0.328880807	SMARCD2
cg13854983	2	136875315	-0.329784901	cg13383235	7	7680321	-0.328838527	RPA3
cg14810343	5	139028149	-0.329784087	cg08527566	12	95611432	-0.328828162	FGD6
cg05766425	17	48796751	-0.329774497	cg11072887	6	37322624	-0.328795855	RNF8
cg04455180	1	227506639	-0.32972059	cg25136353	10	44185896	-0.328760659	
cg21899921	7	73669227	-0.329717337	cg06942064	1	208417143	-0.328703622	PLXNA2
cg06868961	12	12870959	-0.32970149	cg04453241	17	76374567	-0.328685109	PGS1
cg06366345	14	101459591	-0.329635447	cg21106899	1	11779803	-0.328665514	C1orf187
cg15802848	6	33359461	-0.329613772	cg04496899	1	70820341	-0.328636972	HHLA3
cg21959594	19	1813058	-0.329600725	cg22301261	13	50655392	-0.328630197	DLEU1
cg02036077	22	35653364	-0.329597849	cg07209631	4	89205728	-0.328611241	PPM1K
cg21487637	19	46195684	-0.329549442	cg14225021	2	161126482	-0.328609562	
cg24819738	19	19314415	-0.329524338	cg00345965	1	151226992	-0.328602417	PSMD4
ch.13.1834088F	13	112692382	-0.329479887	cg26761504	19	49140601	-0.328575675	SEC1
cg14119616	11	17099403	-0.329449318	cg14191109	10	70287438	-0.328532882	SLC25A16
cg23000464	19	633785	-0.329422167	cg14229702	15	89164377	-0.328511617	AEN
cg08730330	17	61904790	-0.329415823	cg13710842	5	72251735	-0.328487963	FCHO2
cg18917495	2	74006961	-0.329336715	cg22792272	6	43597128	-0.328464093	MAD2L1BP
cg11712217	17	80455631	-0.329336375	cg12774432	7	141438008	-0.328432793	SSBP1
cg23054379	1	176176226	-0.329317899	cg02690350	17	27620209	-0.328418474	NUFIP2
cg27365208	19	19778986	-0.329312143	cg26220419	11	107880052	-0.328401256	CUL5

Figure 16-10

cg01235203	3	187461998	-0.32838375	BCL6	cg25025968	11	4116056	-0.327515114	RRM1
cg02839220	16	4400790	-0.328375714	Magmas	cg18689253	9	82186806	-0.327509054	TLE4
cg02773889	13	42615649	-0.328371192		cg08723131	20	55043694	-0.327474664	C20orf43
cg02220499	16	19729278	-0.328293789	IQCK	cg26162836	1	160232429	-0.327447023	DCAF8
cg11618704	10	43904553	-0.328267436	HNRNPF	cg25755261	14	35591781	-0.32744401	PPP2R3C
cg24513224	17	10102439	-0.328139158	GAS7	cg058882878	2	37458821	-0.327331685	CEBPZ
cg16604136	1	163291493	-0.328115915	NUF2	cg18766912	15	25683909	-0.327305865	UBE3A
cg15009698	5	77590494	-0.328108638	AP3B1	cg08536977	17	73780663	-0.327288334	UNK
cg12619880	1	44172798	-0.328100592	ST3GAL3	cg01423820	14	77228690	-0.32726969	VASH1
cg07856758	19	37861652	-0.328098838	ZNF527	cg05637795	15	72978746	-0.327263727	HIGD2B
cg03231960	19	49139050	-0.328072515	DBP	cg24465118	20	47895107	-0.327263437	C20orf199
cg06745507	15	44085196	-0.328061446	SERF2	cg042223844	8	42128868	-0.327242973	IKBK
cg14586630	6	74171590	-0.327999254	MTO1	cg08417687	6	108582627	-0.327228651	SNX3
cg15546754	11	68065392	-0.327980846	C4orf14	cg26960647	6	138188928	-0.327209843	TNFAIP3
cg25525207	4	57843836	-0.327976954	NANP	cg05954989	10	135191962	-0.327160735	PAOX
cg06575763	20	25604643	-0.327960038	ATP1B3	cg10663973	4	6642559	-0.327154714	MRFAP1
cg07006042	3	141595655	-0.327941469	ZNF593	cg08739576	7	44144360	-0.32714863	AEBP1
cg23267217	1	26496298	-0.327918017	TUBD1	cg18545992	2	133013028	-0.327148475	NCRNA00164
cg13276752	17	57970287	-0.32790782	SKA3	cg03786924	6	73331680	-0.327139314	KCNQ5
cg11021200	13	21750354	-0.327902494	CCDC42	cg12441052	11	66313700	-0.327094082	ZDHHC24
cg22197033	17	8649004	-0.327888032		cg11739541	12	49582842	-0.327085762	TUBA1A
cg10537699	11	60897371	-0.327887751	KIAA1328	cg00947019	7	44887958	-0.32706042	H2AFV
cg07169535	18	34408654	-0.327864501	RSPH1	cg08863539	19	2841394	-0.327052768	ZNF555
cg07704495	21	43916519	-0.327839196	KLF10	cg07987262	19	19314408	-0.327052731	NR2C2AP
cg18108022	8	103666233	-0.327827313	C21orf66	cg12133425	1	247494926	-0.327046135	ZNF496
cg21740452	21	34143691	-0.327816254	OXSR1	cg02704927	5	65440543	-0.327018464	SFRS12
cg17206034	3	38206839	-0.327753182	MAPKAPK2	cg21308020	4	99182242	-0.327002081	RAP1GDS1
cg23145622	1	206859650	-0.327722951	FIBCD1	cg04350249	20	18488833	-0.326998367	SEC23B
cg26396617	9	133815188	-0.327682279	BMS1	cg27482856	7	99214447	-0.326933242	ZNF498
cg07842594	10	43278214	-0.327675781	ZC3H11A	cg05776084	3	133293427	-0.326924191	CDV3
cg09852199	1	203764897	-0.327674089	RPAIN	cg10767909	19	36980702	-0.326913918	ZNF566
cg15229153	17	5323805	-0.327666371		cg09951650	15	51200814	-0.326852007	AP4E1
cg04575467	8	41997444	-0.327651604	NUFIP2	cg00296291	4	129733887	-0.32679224	PHF17
cg07939768	17	27621433	-0.327641156	MAPKAPK2	cg17662034	8	74207518	-0.326787073	RDH10
cg14153722	1	206858799	-0.327638869	MED11	cg00994924	20	25388641	-0.326735039	GIN51
cg22664368	17	4634740	-0.327607095	ZNF148	cg02226697	8	126010266	-0.326718448	SQLE
cg15094636	3	125094397	-0.327599062	MFNG	cg09742170	7	25021208	-0.32671761	OSBPL3
cg18452324	22	37882397	-0.327582078	USP38	cg00292047	11	33279899	-0.326698839	HIPK3
cg23162983	17	63119174	-0.327577993	UQCR	cg11655486	1	85156638	-0.326677398	SSX2IP
cg05867307	4	144106066	-0.327549394		cg10141938	7	26240087	-0.326676366	HNRNPA2B1
cg11792664	19	1605706	-0.327521905		cg00832928	3	150329458	-0.326674246	SELT

Figure 16-11

cg07458698	2	67624494	-0.326664717	ETAA1	cg07274776	2	203241322	-0.325916478	BMPR2
cg22293500	3	186544871	-0.326626025		cg00061769	1	155658843	-0.325909633	YY1AP1
cg14428767	6	149867359	-0.326613523	PPIL4	cg07163173	2	67624373	-0.325876814	ETAA1
ch.4.3837399F	4	3867601	-0.326602828		cg01109633	17	30263774	-0.325871175	SUZ12
cg02250900	15	51915395	-0.326596709	DMXL2	cg12245040	16	2009320	-0.325848855	NDUFB10
cg03177631	11	18415927	-0.326537506	LDHA	cg08576658	19	56098601	-0.32584852	
cg21122725	4	123843781	-0.326511587	NUDT6	cg13782561	9	94185786	-0.325844458	NFIL3
cg22139878	10	91174299	-0.326508301	IFIT5	cg26549029	12	133286883	-0.32583593	PGAM5
cg25521086	2	113341977	-0.326504199	CHCHD5	cg26100149	5	173315151	-0.325811	CPEB4
cg16898066	6	25726437	-0.326474446	HIST1H2BA	cg21452766	1	70877088	-0.325729334	CTH
cg02625641	15	59041175	-0.326464363	ADAM10	cg12222460	6	14211743	-0.325704805	ABHD5
cg00900054	1	46016580	-0.326437671	AKR1A1	cg18908981	3	43732200	-0.325700868	HSF2
cg01392184	15	41099692	-0.326402001	ZFYVE19	cg16783819	6	122720842	-0.32568702	CCT7
cg08764805	12	95867684	-0.326382203	METAP2	cg19543987	2	73460508	-0.325679713	TGOLN2
cg12637942	11	65190225	-0.32637818	NEAT1	cg01773306	2	85555458	-0.325611789	ODZ4
cg09293387	8	6565827	-0.326374531	AGPAT5	cg15355859	11	79149352	-0.325592413	
cg11995741	6	166797367	-0.326329012	BRP44L	cg09358454	2	157198726	-0.32557561	U2AF2
cg12361356	1	200708503	-0.326300131	CAMSAP1L1	cg08568987	19	56165234	-0.325555557	
cg07383443	12	118573736	-0.32627295	PEBP1	cg16263943	2	144695179	-0.325547228	AKAP11
cg26422134	7	43909318	-0.326268066	MRPS24	cg10391629	13	42846072	-0.325508551	ADD2
cg22370633	10	70092255	-0.326251124	PBLD	cg11220663	2	70994863	-0.325490933	FMNL1
cg23069677	1	36863646	-0.326247862	LSM10	cg24561572	17	43298813	-0.325467769	IFT140
cg22328771	22	50709822	-0.326244795	MAPK11	cg16327326	16	1662895	-0.325411698	
cg07399369	3	142838082	-0.326236812	CHST2	cg27391780	16	30669108	-0.325387182	TMEM222
cg03516836	12	57881693	-0.326214124	MARS	cg13406003	6	127535477	-0.325367572	SRPRB
cg11355601	22	39096475	-0.326122549	JOSD1	cg26528255	1	27652089	-0.325357658	CCDC96
cg17211447	1	10490667	-0.326090256	APITD1	cg24127244	3	133524572	-0.325311963	NPR3
cg24236870	15	42264445	-0.326088433	EHD4	cg04294412	4	7045720	-0.325290186	KBTBD3
cg19510484	12	95868044	-0.326077218	METAP2	cg01822624	5	32710882	-0.325283912	PPPIR12B
cg27467005	19	17622279	-0.326076207	PGLS	cg22024876	11	105948183	-0.325270152	IKZF5
cg22048132	17	60005312	-0.326062196	INTS2	cg05798608	1	202317770	-0.32526046	KARS
cg07001481	17	5389669	-0.32606091	DERL2	cg19696333	10	124768261	-0.325243431	CYP51A1
cg14723664	6	34164073	-0.326046424		cg26812503	16	75681495	-0.32522297	ASGR1
cg13727629	1	2232469	-0.326031111	SKI	cg14283194	7	91763737	-0.325190516	PANX1
cg03888520	22	42978243	-0.326021462	RRP7B	cg19967433	17	7080988	-0.325184747	MIR492
cg20157484	12	46385525	-0.32597696	SFRS2IP	cg19906131	11	93862516	-0.325083036	FUBP1
cg06046434	11	57425242	-0.325958922	CLP1	cg22411415	12	95228201	-0.325056366	BRD2
cg27250139	8	9912632	-0.325949679	MSRA	cg25846022	1	78444909	-0.325033384	RABL4
cg13943141	9	93205862	-0.325941895		cg01872295	6	32937388	-0.325031023	CBR4
cg17859882	6	58287694	-0.325939357	GUSBL2	cg12924408	22	37172025		
cg22272545	2	197036243	-0.325939306	STK17B	cg23834254	4	169931521		

Figure 16-12

cg01153132	6	119400114	-0.325024366	FAM184A	cg07617384	15	74392612	-0.324232748	
cg08674342	5	36152125	-0.324988531	LMBRD2	cg22332388	8	64081173	-0.324192609	YTHDF3
cg22280359	6	83903559	-0.324982256	PGM3	ch.19.11524367R	19	11663367	-0.324190996	
cg254449542	17	1957605	-0.324965792	HIC1	cg08579753	1	39174525	-0.324178189	
cg14538868	2	37458838	-0.32495014	CEBPZ	cg16558358	17	80416024	-0.324149559	NARF
cg19921130	15	81294134	-0.32493694	MESDC1	ch.1.3903344F	1	201984137	-0.324148319	ELF3
cg14555127	7	35841578	-0.324857256	7-Sep	cg20952324	3	9773343	-0.324123713	BRPF1
cg27132050	15	45021149	-0.324809094		cg03100196	7	143077761	-0.324118202	ZYX
cg02972188	12	58165945	-0.324789555	METTL1	cg07740989	6	74230681	-0.324100074	EEF1A1
cg02508567	2	85361184	-0.324776309	TCF7L1	cg02773756	6	27799308	-0.324098135	HIST1H4K
cg22164238	1	110162488	-0.324766824	AMPD2	cg27573591	7	127672152	-0.324089021	SND1
cg09131135	2	27886635	-0.324748043	SLC4A1AP	cg23109134	10	7830051	-0.324027008	ATP5C1
cg07745102	7	111204826	-0.324743251		cg24198128	19	18682398	-0.323992027	UBA52
cg06564818	18	33162094	-0.324742507		cg121110529	3	141030588	-0.323968331	
cg26477793	10	104262085	-0.324725205	ACTR1A	cg16987848	8	356385	-0.323873848	FBXO25
cg26446827	20	18268978	-0.324719315	ZNF133	cg13790879	2	239336104	-0.323860169	ASB1
cg10698964	15	50647173	-0.324710544	FLJ10038	cg23521964	10	127408065	-0.323816189	C10orf137
cg27438040	6	136611664	-0.324708659	BCLAF1	cg10922622	9	108210153	-0.323814357	FSD1L
cg08261858	1	246887303	-0.324686816	SCCPDH	cg23664192	6	34725288	-0.323781194	SNRPC
cg08908148	7	39606013	-0.324672541	C7orf36	cg20617957	13	100085203	-0.323779967	
cg12018042	14	57735703	-0.324662831	MUDENG	cg07500976	19	13261292	-0.323774553	IER2
cg04055703	5	39074730	-0.324655194	RICTOR	cg21522303	17	74581331	-0.323701579	ST6GALNAC2
cg14140830	3	47020973	-0.324586715	NBEAL2	cg22682162	6	97731065	-0.323646018	MIR548H3
cg00143700	13	49107116	-0.32457104	RCBTB2	cg04892170	10	128076910	-0.323599224	ADAM12
cg15093003	10	123687697	-0.324553876	ATE1	cg17718302	6	27858637	-0.323594574	HIST1H3J
cg01170099	14	82000431	-0.324505423	SEL1L	cg09084877	6	30181302	-0.323571762	TRIM26
cg12429444	1	20988133	-0.324491178	DDOST	cg27574168	18	54318782	-0.323523157	WDR7
cg14940636	12	56498092	-0.324480936	PA2G4	cg08524221	17	74732291	-0.323493781	SFRS2
cg23374376	19	39390198	-0.324467272	SIRT2	cg23843362	10	104677600	-0.323487052	CNNM2
cg04064611	7	72298987	-0.3244459461	SBDSP	cg27326518	1	226187335	-0.323484557	C1orf55
cg15203817	19	36980483	-0.3244456458	ZNF566	cg05105845	14	55369781	-0.323476095	GCH1
cg26337884	10	52751119	-0.324381202	PRKG1	cg15738138	17	40976420	-0.323443222	BECN1
cg16302650	6	149867607	-0.324375372	PPIL4	cg01446164	11	2421746	-0.323419794	
cg04798523	4	103749125	-0.324368642	UBE2D3	cg25335190	6	27791899	-0.323389975	HIST1H4J
cg10916494	6	86388066	-0.324357434	SNHG5	cg07720856	2	232572668	-0.323317117	PTMA
cg14907986	6	24645932	-0.324349458	KIAA0319	cg04853151	1	54519244	-0.323310252	C1orf83
cg10341991	3	48229869	-0.324338049	CDC25A	cg14795047	12	38710433	-0.323262895	ALG10B
cg18110359	2	45179970	-0.324285248		cg21797405	5	139944339	-0.323255048	APBB3
cg26633120	2	105654408	-0.324261682	MRP59	cg03299121	2	68384913	-0.323209398	PNO1
cg12219045	22	44894262	-0.32424612	LDOC1L	cg18282264	7	6048883	-0.323198034	AIMP2
cg02249930	10	70166207	-0.32423633	RUFY2	cg05243144	19	46273434	-0.323179055	DMPK

Figure 16-13

cg04473235	5	77080995	-0.32317354	cg19469297	7	45151440	-0.322263518	TBRG4
cg22594055	5	131832675	-0.323147221	cg04476741	1	11724884	-0.322205816	FBXO6
cg01351869	15	80215929	-0.323110631	C15orf37	6	31783364	-0.322150938	HSPA1A
cg25486143	3	50378527	-0.323081941		1	207669576	-0.322149922	CR1
cg01058931	16	25269641	-0.323061952	ZKSCAN2	1	64055717	-0.322125161	
cg10130401	17	46970032	-0.323052963	ATP5G1	17	61699522	-0.322116732	MAP3K3
cg08699435	20	19997606	-0.323042722	NAA20	1	109234813	-0.322065257	PRPF38B
cg13303229	5	154136254	-0.323033169	LARP1	20	3451306	-0.322063417	ATRN
cg22311942	17	73201390	-0.323032374	NUP85	7	94286834	-0.322037174	SGCE
cg01528792	9	73027862	-0.323014216	KLF9	1	93646535	-0.322020513	TMED5
cg11661269	1	39339371	-0.322981793	MYCBP	16	85482380	-0.322018847	
cg03162359	12	45610751	-0.322961344	ANO6	19	50180725	-0.322018282	PRMT1
cg07387199	17	62502055	-0.322944049	CDC45	16	81478990	-0.322004356	CMIP
cg02759489	4	55098483	-0.322864602	PDGFRA	2	15731793	-0.321997128	DDX1
cg09881819	3	129034470	-0.322863335	H1FX	10	103816089	-0.321994977	C10orf76
cg26689765	5	52083512	-0.322837183	ITGA1	12	8551501	-0.321942755	
cg17998013	3	15643079	-0.32282921	HACL1	7	138125259	-0.321928381	
cg13902357	6	31324280	-0.322825841	HLA-B	3	183736084	-0.32189395	ABCC5
cg19672384	6	168132359	-0.322815494		19	47164782	-0.321877832	DACT3
cg25136709	7	143599409	-0.322814727	FAM115A	14	23058032	-0.321863068	DAD1
cg10170443	5	72794209	-0.322812808	BTF3	14	23341280	-0.321857359	LRP10
cg08613513	1	52870060	-0.322743742	ORC1L	12	120884702	-0.321852337	TRIAP1
cg09514055	1	43919573	-0.322726322	HYI	4	25162214	-0.321845294	SEPSECS
cg20427059	2	131851445	-0.322721337	FAM168B	4	15683224	-0.321833927	LOC285550
cg18238734	12	26986119	-0.32269329	ITPR2	11	58939272	-0.321822163	DTX4
cg15660466	17	49230788	-0.32267049	NME1	2	87035620	-0.321816277	CD8A
cg26805238	1	144931980	-0.322666073	PDE4DIP	10	75541665	-0.32175145	CHCHD1
cg11543665	19	8373294	-0.322633174	CD320	1	145209930	-0.32174593	NOTCH2NL
cg03761979	4	57843892	-0.322632778	C4orf14	3	73159953	-0.321722166	
cg14919823	3	14166510	-0.32263013	TMEM43	18	51796328	-0.321686299	POLI
cg26938153	7	137686926	-0.32258273	CREB3L2	7	99102391	-0.321676935	ZKSCAN5
cg06391926	16	1832733	-0.322551841	NUBP2	12	132195732	-0.321650788	SFRS8
cg12938135	13	20356591	-0.322536412	PSPC1	13	50510822	-0.32163652	C13orf1
cg27239157	3	183145817	-0.322484551	MCF2L2	3	48956015	-0.3216358	ARIH2
cg18912981	7	7222021	-0.322438059	C1GALT1	1	67519814	-0.32163229	SLC35D1
cg00597713	6	42947103	-0.322377818	PEX6	11	94964516	-0.321537357	SESN3
cg04771550	17	8079827	-0.322358831	TMEM107	16	70380558	-0.321504451	DDX19A
cg18534872	10	58121066	-0.322328227	ZWINT	14	103799810	-0.32150326	EIF5
cg05964952	12	51633050	-0.322288042	DAZAP2	12	133532978	-0.321453317	ZNF605
cg05091519	11	31839552	-0.322284208	PAX6	9	107526202	-0.321430955	NIPSNAP3B
cg02167732	14	81687645	-0.322281649	GTF2A1	18	34408166	-0.32141394	C18orf10

Figure 16-14

cg13467399	9	133588111	-0.32136029	ABL1	cg07909497	12	9600950	-0.32062983	DDX12
cg27201871	17	79212816	-0.32133625	C17orf56	cg05907029	1	197872227	-0.320610732	C1orf53
cg18199720	1	115054041	-0.321335395	TRIM33	cg03671660	21	40554907	-0.320603863	PSMG1
cg23264557	5	89770687	-0.321314646	MBLAC2	cg10029411	13	50746245	-0.32059706	FAM10A4
cg14226747	4	657927	-0.321302376	PDE6B	cg03727342	9	6758683	-0.320587997	KDM4C
cg24966682	6	24666810	-0.321297592	ACOT13	cg16989148	17	46125619	-0.320578206	NFE2L1
cg05899183	16	66968638	-0.321293986	FAM96B	cg06591456	7	4814952	-0.320569011	KIAA0415
ch.14.1499103R	14	93412334	-0.321275943	ITPK1	cg08278266	5	141071625	-0.320560037	
cg14210872	1	155294935	-0.321249623	RUSC1	cg11225935	12	498478	-0.320538087	KDM5A
cg17323045	14	58764804	-0.321247072	FLJ1306	cg20127188	22	21996426	-0.320533792	SDF2L1
cg01547622	5	49962954	-0.321241363	PARP8	cg19125715	8	67525489	-0.320523485	MYBL1
cg11150308	17	74068434	-0.321196292	SRP68	cg11337525	19	45418417	-0.320450231	APOC1
cg00318899	3	50284137	-0.321186065	GNAI2	cg26526379	7	26416184	-0.320445104	
cg09913796	17	27181988	-0.321184802	ERAL1	cg15889838	5	131832312	-0.320428934	NPC2
cg15006843	1	205720633	-0.321171607	NUCKS1	cg03323770	14	74960890	-0.320393237	C19orf40
cg19761211	16	70415365	-0.321166532	ST3GAL2	cg07727872	19	33463030	-0.320379934	NUFIP2
cg23304339	19	37862045	-0.321147788	ZNF527	cg17006779	17	27621172	-0.320378565	HSPH1
cg01911237	8	134582305	-0.321000636	ST3GAL1	cg02318347	13	31735110	-0.320378274	C1orf183
cg10101074	13	46961818	-0.32096891	C13orf18	cg26623550	1	112281629	-0.320374349	SULF2
cg10234952	20	55926623	-0.320929929	RAE1	cg18124201	20	46414952	-0.32036769	RNF145
cg24909975	6	160147912	-0.320926955	WTAP	cg01657408	5	158634989	-0.32036192	FANCA
cg02466926	10	127408000	-0.320888054	C10orf137	cg20573831	16	89882393	-0.320293448	LOC400027
cg15427567	14	21458055	-0.320848398	METT11D1	cg17576719	12	46121221	-0.320279495	PHLDB2
cg02611874	10	46194725	-0.320811407	NFKBIL2	cg02908709	3	111578238	-0.320272316	CD2BP2
cg13390998	8	145670370	-0.320810211	CCDC72	cg00270311	16	30366760	-0.320264176	C3orf54
cg25858682	3	48481793	-0.320806895	ECD	cg05550371	3	49841167	-0.320240443	GATSL3
cg15213114	10	74927623	-0.320799709	SOD1	cg10998744	22	30685926	-0.320178203	MIR632
cg18841894	21	33031735	-0.320796465	ARFIP1	cg08209724	17	30677138	-0.320151273	FANCF
cg21618713	4	153701330	-0.320791499	NUP62	cg23302316	11	22647430	-0.320114875	SEC61G
cg07934604	4	139010141	-0.320790128	CALR	cg14648311	17	17359737	-0.320088258	IRF2BP2
cg17177829	19	50432927	-0.320765551	CCT6P1	cg08310974	7	54827110	-0.320069399	LEPROTL1
cg25392269	19	13049289	-0.320743229	ZNF398	cg06527865	1	234746497	-0.320046632	ARL6
cg16410464	7	65215907	-0.3206974	MIIP	cg06927280	8	29953601	-0.320044476	ATP5H
cg05046597	7	148823741	-0.320685163	CAV1	cg13968953	3	97483466	-0.320011219	CTSC
cg24953506	1	12079889	-0.320673355	DDX49	cg26207995	17	58045920	-0.320010155	FBXO36
cg22126032	7	116166529	-0.32064921	C16orf65	cg04547425	17	73043127	-0.319974067	DNAIC13
cg09964705	19	19030333	-0.32064293	ZNF441	cg01742905	11	88071023	-0.319971303	B2M
cg01386121	16	22012560	-0.320640591	HRK	cg01014179	2	230787137	-0.319962207	
cg01421963	19	11877743	-0.320634917	CHD6	cg15050398	6	28829182	-0.319952016	
cg05642446	12	117316716	-0.32063475		cg18352988	3	132136600	-0.319945447	
cg04139300	20	40247070	-0.320630349		cg24134304	15	45003680	-0.319937355	

Figure 16-15

cg24942186	3	55521373	-0.319934646	WNT5A	cg19909712	11	17374669	-0.319280435	DKFZp686O24
cg03396809	3	48282488	-0.319916354	ZNF589	cg27100316	1	151735804	-0.319255246	OAZ3
cg11877577	6	133135687	-0.319874698	RPS12	cg24041036	14	58711637	-0.319250288	PSMA3
cg13452400	2	7006280	-0.319819407	CMPK2	cg26929161	20	50701266	-0.319246729	ZFP64
cg15916192	12	63025948	-0.31981197		cg18039855	11	57434952	-0.319226027	ZDHHC5
cg25072436	2	30454560	-0.319811559	LBH	cg07323055	20	3140559	-0.319221291	FASTKD5
cg02580528	1	183441376	-0.319795522	SMG7	cg04620101	15	101835123	-0.319219805	SNRPA1
cg05639842	21	43639440	-0.319782302	ABCG1	cg08452546	5	118323860	-0.319216659	DTWD2
cg17903246	3	100053926	-0.31977701	NIT2	cg07080177	17	75243417	-0.319149171	
ch.8.39446R	8	1206157	-0.319765689		cg03354957	1	246729501	-0.319129299	CNST
cg27394038	6	36562217	-0.319752212	SFRS3	cg18251360	22	20067313	-0.319127844	DGCR8
cg21753290	20	37376903	-0.319721195	ACTR5	cg26998900	18	5238137	-0.319115253	C18orf18
cg14535006	20	18448030	-0.319712801	C20orf12	cg02342362	19	12792713	-0.319074367	DHPS
cg12144374	8	123793325	-0.319694376	ZHX2	cg20173334	8	42698483	-0.319056129	THAP1
cg14078059	12	65174660	-0.319690859		cg01449415	16	3184811	-0.319045677	ZNF213
cg26118675	2	96256841	-0.319684739	TRIM43	cg09885409	21	34697563	-0.319009414	IFNAR1
cg16970804	5	43042108	-0.319666523	LOC153684	cg15305172	6	116892775	-0.3189988	RWDD1
cg22149837	17	41150293	-0.319651372	RPL27	cg10396609	4	89378025	-0.318986561	HERC5
cg14714046	6	41341654	-0.319643486		cg15884202	7	158649092	-0.318963767	WDR60
cg00531307	14	50998683	-0.319628429	MAP4K5	cg00046560	15	101835624	-0.318953983	SNRPA1
cg15814736	11	63439115	-0.319612295	ATL3	cg07315521	16	71929403	-0.318926095	KIAA0174
cg12995162	2	129079641	-0.319605245		cg08605641	8	96146723	-0.31891987	PLEKHF2
cg15123824	2	85581917	-0.319585923	ELMOD3	cg00125159	1	228290140	-0.318919165	C1orf35
cg05468351	5	21459598	-0.319580627	LOC728411	cg18976974	8	103990325	-0.31886373	
cg16273215	1	155100190	-0.319572454	EFNA1	cg19478983	7	120590592	-0.318846808	ING3
cg03214297	22	38453296	-0.319539001	PICK1	cg03555836	8	41422764	-0.318836096	
cg08391020	5	74344779	-0.319535462		cg09048062	11	129892327	-0.318799468	
cg11761572	19	39390455	-0.319511445	SIRT2	cg25559069	6	33134799	-0.31878808	COL11A2
cg16895948	1	145610875	-0.319500108	POLR3C	cg02252000	7	130792943	-0.318754447	FLJ43663
cg09914581	2	11606494	-0.31942943	E2F6	cg26020585	1	235491765	-0.318725294	GGPS1
cg18745406	8	134309938	-0.319428293	NDRG1	cg11656992	17	79818741	-0.318708371	P4HB
cg14123153	12	6602654	-0.319396147	NCAPD2	cg17572663	8	27950635	-0.318703702	ELP3
cg06872176	1	68697386	-0.319374869	GPR177	cg17424134	2	27616206	-0.318700799	FTHL3
cg23006223	4	57843834	-0.319363247	C4orf14	cg01476820	2	86333266	-0.318690077	PTCD3
cg04305134	10	75173374	-0.319346905	ANXA7	cg03651680	2	46926842	-0.318677691	SOC5
cg21654379	3	32864307	-0.319339391	TRIM71	cg03432151	15	89745000	-0.318657951	ABHD2
cg04628413	16	28962222	-0.319335418	NFATC2IP	cg18296227	10	99205774	-0.318632007	ZDHHC16
cg02447185	17	71228623	-0.31931176	C17orf80	cg25784395	22	40742943	-0.318619229	ADSL
cg26450188	19	46850188	-0.319299618	PPP5C	cg11996632	16	70284893	-0.318613349	EXOSC6
cg03436558	16	75657345	-0.319293675	ADAT1	cg19402413	1	247453950	-0.31859291	
cg25495613	7	134895782	-0.319290408	WDR91	cg06029050	11	74660429	-0.318592152	SPCS2

cg062333552	17	5322836	-0.318583811	RPA1N	cg17323493	7	151573944	-0.31782972	PRKAG2
cg00666849	2	85839032	-0.318581343	C2orf68	cg20546928	8	27167985	-0.317788159	PTK2B
cg027772905	2	203484258	-0.318571577		cg23483707	13	44453835	-0.317758439	C13orf31
cg10203523	4	6711606	-0.318556894	MRFAP1L1	cg10502884	10	125852315	-0.317724567	
cg26151531	22	19842652	-0.318547473	GNB1L	cg26856330	19	19314312	-0.317722426	NR2C2AP
cg11072373	4	100485070	-0.318511974	RG9MTD2	cg23587005	12	9600941	-0.31769931	DDX12
cg19294125	20	25604737	-0.318503772	NANP	cg06820286	22	29664179	-0.317667424	EWSR1
cg14834466	11	67981677	-0.318490985	SUV420H1	cg20423427	18	67873036	-0.317644484	RTTN
cg03410722	16	85588815	-0.318393771		cg03773681	2	63815918	-0.317634832	MDH1
cg10451977	15	45507901	-0.318385842		cg07917842	17	29672644	-0.317620083	NF1
cg16427488	8	86132835	-0.318362584	C8orf59	cg05025913	11	7539248	-0.317603976	PPFIBP2
cg01458420	20	48532416	-0.31833503	SPATA2	cg07500433	5	63986130	-0.317557954	FAM159B
cg08643953	3	132379052	-0.318333507	UBA5	cg00343022	3	38178135	-0.317549845	ACAA1
cg07509872	17	26574551	-0.318321054	PPY2	cg18633432	3	135915556	-0.317535357	MSL2
cg26624026	19	18416001	-0.318312224		cg11332388	1	42922083	-0.317508674	PPCS
cg21056475	5	110428269	-0.318302024	WDR36	cg11792281	17	26443366	-0.317503456	NLK
cg05396178	6	27833129	-0.318283962	HIST1H2AL	cg00023288	2	44223284	-0.317498439	LRPPRC
cg21071625	19	39217605	-0.318281465	ACTN4	cg19423311	16	27413904	-0.317490447	IL21R
cg07979357	19	14142353	-0.318257333	IL27RA	cg23665065	14	102781012	-0.317487681	
cg02600494	17	73257794	-0.318232739	MRPS7	cg04402021	19	1094921	-0.317487072	POLR2E
cg15254860	3	167813494	-0.318226119	GOLIM4	cg04722620	19	54982598	-0.317485236	CDC42EP5
cg04671334	19	35224921	-0.318225653	ZNF181	cg24603490	12	47473995	-0.317483244	AMIGO2
cg15139906	19	48018631	-0.318220403	NAPA	cg12188830	3	57741926	-0.31747084	SLMAP
cg05526438	5	174350112	-0.318206885		cg10035607	16	30366449	-0.317464299	CD2BP2
cg22822383	19	58987261	-0.31819855	ZNF446	cg16861047	1	116518978	-0.317460593	SLC22A15
cg08686311	20	825052	-0.318162649	FAM110A	cg03831869	16	3508546	-0.317446036	NAT15
cg02653800	10	60095305	-0.318124029	UBE2D1	cg26759552	7	139877471	-0.317432117	LOC10013422
cg05171480	13	32420488	-0.318108464	EEF1DP3	cg08582555	22	21356051	-0.317405036	FLJ39582
cg22396798	15	43478022	-0.318098867	CCNDBP1	cg17055717	20	32700280	-0.317358429	EIF2S2
cg04295991	13	21348012	-0.318095056	N6AMT2	cg10541361	1	235667946	-0.317336445	B3GALNT2
cg21120664	21	44299807	-0.318080906	WDR4	cg20303592	10	116697907	-0.317311403	TRUB1
cg03774520	1	32238105	-0.318032599		cg23572376	6	1610120	-0.317305549	FOXC1
cg23515325	19	1194462	-0.318024235	TMEM231	cg18238491	18	47901440	-0.317274509	SKA1
cg08713543	16	75575906	-0.317988903	SLC6A2	cg01718711	8	8860266	-0.317265628	ERI1
cg03860054	16	55691102	-0.317985928	SFRS12	cg09823679	13	53425813	-0.317185343	
cg09001528	5	65440474	-0.31795392	MKL1	cg15993873	15	44719935	-0.317175926	CTDSPL2
cg06207852	22	41033162	-0.317880418	E2F6	cg16015499	1	159888603	-0.317167085	TAGLN2
cg12858075	2	11606497	-0.317863207	CRKL	cg11041264	20	33872554	-0.317160612	EIF6
cg15575339	22	21272441	-0.317842899	ADNP	cg18611281	2	27805844	-0.317100457	ZNF512
cg05279707	20	49547986	-0.317842816	PGAP2	cg26455541	4	26321238	-0.317087024	RBPJ
cg08098619	11	3818841	-0.317839785		cg11432034	3	13520913	-0.3170766	HDAC11

Figure 16-17

cg00477061	18	77794585	-0.317073557	C18orf22	cg17976065	17	15902694	-0.316587368	ZSWIM7
cg14162457	13	113444243	-0.317066079	ATP11A	cg27308130	3	126422683	-0.316577097	CHCHD6
cg02303317	10	135122580	-0.317048209	TUBGCP2	cg13402292	21	37667921	-0.316576392	
cg08875433	6	29604148	-0.317044591		cg11229390	6	32122082	-0.316571087	PPT2
cg02063458	16	48190773	-0.317041547		cg25825740	17	80036910	-0.316562865	FASN
cg09746604	3	15919583	-0.317015865		cg00028636	12	6876321	-0.316561751	PTMS
cg03801946	16	4303664	-0.317012306		cg04931453	9	101983720	-0.316538558	ALG2
cg23048068	8	82192604	-0.317002317	FABP5	cg05797656	17	61851352	-0.316534057	DDX42
cg06790069	1	40203513	-0.31698387	PPIE	cg06329143	18	48556512	-0.316532328	SMAD4
cg04122974	22	39916495	-0.316977852	ATF4	cg26473728	6	33359147	-0.316511087	KIFC1
cg02164516	15	41576100	-0.316975036	LOC729082	cg00367659	17	33288544	-0.31651086	CCT6B
cg15345154	10	16563586	-0.316973964	C1QL3	cg11726572	18	658602	-0.316501562	TVMS
cg07557355	1	155904306	-0.316970418	KIAA0907	cg13643774	9	132176807	-0.316451603	
cg17415239	16	29937734	-0.316963136	KCTD13	cg17996757	7	131013207	-0.316443626	MKLN1
cg04757284	17	18585734	-0.316959024	ZNF286B	cg06148997	2	107084783	-0.316432183	RGPD3
cg05964529	12	110906245	-0.316956112	GNP3	cg00461978	15	75661184	-0.316418729	MAN2C1
cg20872579	4	6643098	-0.316929638	MRFAP1	cg06083525	1	27216957	-0.316411254	GNP2
cg18803079	1	64014643	-0.316900309	EFCAB7	cg06005571	3	52188725	-0.316350406	WDR51A
cg22167498	19	8451051	-0.31689544		cg02775353	7	101814109	-0.316345726	CUX1
cg19484299	2	234775274	-0.316893115	MSL3L2	cg06578951	19	19030513	-0.316344214	DDX49
cg03324837	17	61044407	-0.316888657		cg06020459	5	64858893	-0.316340679	CENPK
cg27072387	2	33171699	-0.316854653	LTBP1	cg07951488	4	41992560	-0.316324269	SLC30A9
cg03017824	1	227915338	-0.316851439	LOC100130093	cg06548512	1	146522492	-0.316319221	
cg19461392	12	26349002	-0.316848597	SSPN	cg24001556	20	5591874	-0.316312757	RP5-1022P6.2
cg11976407	1	33814857	-0.316848549	PHC2	cg24079591	14	103851511	-0.316308634	MARK3
cg04347624	3	101498377	-0.316817908	FAM55C	cg03314080	2	178129903	-0.316303911	NFE2L2
cg22512322	3	64009096	-0.316777866	PSMD6	cg10826045	19	36631318	-0.316302248	CAPNS1
cg22211971	17	73257917	-0.316770696	GGA3	ch.19.1004238R	19	30753371	-0.316289741	
cg20632873	1	155948126	-0.316760195	ARHGEF2	cg23371542	6	31334738	-0.316285184	
cg27049318	5	68514098	-0.316758021	MRPS36	cg12745769	19	21579993	-0.31625756	ZNF493
cg11575912	19	5828299	-0.316747049	NRTN	cg14385337	7	113726252	-0.316204654	TMED7
cg09227150	10	102475578	-0.316746332		cg00645922	5	114962179	-0.316195809	EVC2
cg10470489	8	41686324	-0.316694877	ANK1	cg17255450	4	5710372	-0.316190761	BMPR2
cg17212073	17	7818956	-0.316694101	LOC284023	cg04940109	2	203240432	-0.316185543	TNFRSF13B
cg25142954	15	41245554	-0.316692394	CHAC1	cg13195185	17	16875596	-0.316183199	
cg04729371	11	111637213	-0.316645245	PPP2R1B	cg06024111	6	43597558	-0.316151626	MAD2L1BP
cg27287791	15	49103304	-0.316644621	CEP152	cg26428889	7	116311825	-0.316147795	MET
cg12722217	15	44487545	-0.316627014	FRMD5	cg10055227	16	58768320	-0.316145339	GOT2
cg24691578	11	45869488	-0.316624188	CRY2	cg02725437	6	90348314	-0.316145138	LYRM2
cg08316775	2	73964643	-0.316617024	TPRKB	cg03768106	11	111957237	-0.316134758	TIMM8B
cg18515171	17	58156344	-0.316609868	HEATR6	ch.19.683370F	19	16239180	-0.31608497	RAB8A

Figure 16-18

cg04233747	5	145214971	-0.316038752	PRELID2	cg16859906	16	68298978	-0.315462252	SLC7A6
cg18078305	2	65215753	-0.316028995	SLC1A4	cg17513693	6	32122084	-0.315449268	PPT2
cg26548134	22	41185283	-0.316006968	SLC25A17	cg06329197	16	27214832	-0.315441256	JMJD5
cg11227637	4	103749288	-0.316003535	UBE2D3	cg24000232	1	166808428	-0.315423291	POGK
cg26330063	5	14614735	-0.315981747	FAM105A	cg01117273	3	112738650	-0.315411432	C3orf17
cg13111374	4	17812581	-0.315974869	NCAPG	cg07885039	3	143690495	-0.315404499	C3orf58
cg10063260	14	104181875	-0.315972665	XRCC3	cg16750914	2	55646622	-0.315317218	CCDC88A
cg16579347	3	155572233	-0.315961605	SLC33A1	cg22124117	15	43028932	-0.315260277	CDAN1
cg02881434	3	101394920	-0.315949831	LOC100009676	cg04907171	5	139135794	-0.315247374	EVA3
cg20332930	11	82997207	-0.315941074	CCDC90B	cg13129888	1	28415099	-0.315219116	TCEB1
cg04372675	8	107283146	-0.315934161	OXR1	cg04252558	8	74884436	-0.315191576	COG2
cg16222848	13	42846088	-0.315914052	AKAP11	cg12052812	1	230778592	-0.31517789	CUTA
cg13546538	9	111754815	-0.315884772	CTNNAL1	cg03511311	6	33385541	-0.315147746	C18orf54
cg23639257	17	73663270	-0.315880044	RECQL5	cg12538597	11	85906334	-0.315146266	SNX7
cg14460708	3	172428874	-0.315879175	NCEH1	cg08390021	18	51884793	-0.315136993	FNTB
cg20433014	15	75018583	-0.31585114	CYP1A1	cg16232504	1	99127707	-0.315131026	PCGF1
cg02005549	4	106629965	-0.315840601	GSTCD	cg10740670	14	65453617	-0.315107181	HNRNPH3
cg03841667	22	41986013	-0.315835653	PMM1	cg02006147	2	74734710	-0.315100834	PAK1
cg26258330	8	82633130	-0.315829806	ZFAND1	cg20053981	10	70091610	-0.315090558	RTTN
cg13657659	2	208632393	-0.315778484	FZD5	cg26996201	11	77122864	-0.315084387	NEDD4L
cg06536503	6	42750688	-0.31575931	MRPL12	cg06118578	18	67872897	-0.31505969	NT5C2
cg00672574	17	79669841	-0.315752305	CUTA	cg12876333	18	55710995	-0.315031304	DAXX
cg02854226	6	33385965	-0.315725102	VDR	cg09865173	10	104952209	-0.315016935	NUP133
cg05909891	12	19565983	-0.315712495	TOR1A	cg21286626	6	33290780	-0.315015701	CCT6A
cg02522757	12	48298992	-0.315702476	GPATCH3	cg18877635	1	229643817	-0.314966372	TSNARE1
cg21374864	9	132586569	-0.315701176	PRKAR1A	cg02753865	7	56119046	-0.314949027	YIF1A
cg04971263	1	27227008	-0.315675891	NKIRAS1	cg14563732	8	143474839	-0.314932065	GRIN2A
cg14235783	11	65420518	-0.315670955	USPL1	cg16145821	11	66056771	-0.314910696	CDKN2BAS
cg02501334	17	66508232	-0.315653515	TNFRSF10D	cg09622330	16	10205262	-0.314900072	GLS
cg17782025	3	23958698	-0.315632621	HNRNPU	cg00718440	9	21995312	-0.314896239	MCM8
cg12531328	13	31192104	-0.315619562	FUCA2	cg02640306	2	191745287	-0.314877216	TOMM40
cg01456571	8	23021325	-0.315615915	MXN1	cg27367554	20	5930982	-0.314866565	LOC644936
cg22320000	1	245027629	-0.315589973	FANCC	cg21549639	19	45394156	-0.314854594	NIPAZ
cg13380562	6	143832576	-0.315571447	DDAH1	cg15639469	5	79596224	-0.314848503	EIF4A1
cg05060949	7	156798581	-0.315567652	PRDX6	cg07483245	15	23034598	-0.314795593	ZNF566
cg14115740	9	98054883	-0.315557555	ADAR	cg04303571	17	25680876	-0.314787095	MCM3
cg24448326	1	85930306	-0.31553667	TEX264	cg21240492	17	7476105	-0.314777556	GFMD1
cg17859081	1	173446963	-0.315523547	METTL10	cg22852149	19	36980565	-0.314760904	TRAFD1
cg20705565	1	154580699	-0.315522085		cg07837434	6	52149679		
cg18685883	3	51705045	-0.315493148		cg24667363	3	158362181		
cg20025072	10	126480608	-0.315482712		cg18350792	12	112563442		

Figure 16-19

cg20122548	15	45694411	-0.3147572	SPATA5L1	cg27479693	17	17495173	-0.314115064	PEMT
cg05236391	19	6361348	-0.314740074	CLPP	cg02847589	1	22778394	-0.314093777	ZBTB40
cg10427040	17	74261306	-0.314713728	FAM100B	cg11699826	1	26438425	-0.314091519	PDIK1L
cg20116574	20	44718168	-0.314695262	NCOA5	cg24382801	6	37665291	-0.314080732	MDGA1
cg03101422	2	136876737	-0.314683549	CXCR4	cg23818142	2	170550784	-0.314080047	C2orf77
cg25053079	6	31778519	-0.31468268	HSPA1L	cg03162131	11	82905106	-0.31406978	ANKRD42
cg15642758	15	83876612	-0.314675343	HDGFRP3	cg00347862	15	71184758	-0.314065904	LRRC49
cg24354901	1	202777590	-0.314667965	KDM5B	cg02015280	7	134671225	-0.314061078	AGBL3
cg02234820	1	85358327	-0.314630703	LPAR3	cg06911282	8	11660733	-0.314024935	FDFT1
cg10009297	17	34890195	-0.314630019	MYO19	cg11213348	3	38206830	-0.313946753	OXSR1
cg13301155	15	82338574	-0.314620159	MEX3B	cg04464219	8	98657199	-0.313939983	MTDH
cg03099492	10	94833214	-0.314584322	CYP26A1	cg17171485	6	138725799	-0.313937011	HEBP2
cg05447186	20	3869454	-0.314580771	PANK2	cg12856612	22	42228819	-0.313929974	SREBF2
cg04417028	11	110583882	-0.31457063	ARHGAP20	ch.20.54687769F	20	55254362	-0.313916315	GRK6
cg19556901	15	25414769	-0.314559251	SNORD115-1	cg05614346	5	176858608	-0.313897293	C13orf1
cg18418962	18	2571633	-0.31454915	METTL4	cg25486979	13	50510739	-0.31384795	
cg13694772	3	9773336	-0.31453798	BRPF1	cg07751641	5	134826244	-0.313809214	
cg26068292	18	57360307	-0.314530589	CCBE1	cg00590869	8	37962609	-0.313805501	ASH2L
cg07586906	1	160250600	-0.314518743	PEX19	cg00087098	4	76598919	-0.313789221	G3BP2
cg19236745	11	33182890	-0.314496307	CSTF3	cg00935782	12	56498920	-0.313782479	PA2G4
cg01209943	14	54863601	-0.314481719	CDKN3	cg24565496	16	1021302	-0.313744641	LMF1
cg07206840	1	110949893	-0.314480105	HBXIP	cg06627361	12	498468	-0.313740268	KDM5A
cg26490839	19	49999468	-0.314471008	RPS11	cg04965811	10	101492459	-0.313724711	COX15
ch.11.2738269F	11	130342732	-0.314470238	ADAMTS15	cg17738494	3	9773251	-0.313702376	BRPF1
cg10266188	1	32645867	-0.3144461336	TXLNA	cg04882175	6	131122610	-0.313695633	
cg25287247	2	86946958	-0.314444225	RMND5A	cg10313675	1	209957739	-0.313693084	C1orf74
cg09977865	6	33385582	-0.314428286	CUTA	cg22094042	11	450123	-0.313671343	PTDSS2
cg01049274	8	146228340	-0.31441972	ZNF252	cg09225973	6	150232183	-0.3136569	
cg17490921	11	116658887	-0.314408635	ZNF259	cg12091642	14	61104566	-0.313648862	MYT1L
cg06784830	17	7486996	-0.314406881	MPDU1	cg04680209	2	1941133	-0.313647679	HPSE
cg12039286	8	143533193	-0.314406393	GNA13	cg04599631	4	84256200	-0.313631727	
cg03182819	17	63053327	-0.314403563	DTYMK	cg09214920	1	108743318	-0.313623682	SLC25A24
cg10460130	2	242625978	-0.314376936	ARAP2	cg12581035	12	9067477	-0.31358959	PHC1
cg06588087	4	36245610	-0.314371059	CANX	cg23677570	7	74489617	-0.313564664	WBSCR16
cg07831432	5	179125659	-0.31434941	TRIM39	cg21372200	3	50375735	-0.313555931	RASSF1
cg08127941	6	30293955	-0.314304646	CDK17	cg07911523	22	32871416	-0.313424356	FBXO7
cg11545360	12	96793417	-0.314278106	FAM36A	cg16193765	21	45527559	-0.313408896	PWP2
cg02228207	1	244998759	-0.314267612	CDC48	cg06177002	6	31370956	-0.313382674	MICA
cg12751733	1	38157745	-0.314249719	CACNA1G	cg04865575	10	27443031	-0.31336713	YME1L1
cg16766889	17	48637951	-0.314168303	JDP2	cg14968603	10	102046143	-0.313357898	BLOC1S2
cg02921269	14	75894323	-0.314157785		cg24861394	8	11141871	-0.313341739	MTMR9

Figure 16-20

cg03538717	3	79068441	-0.3133318939	ROBO1	cg19011063	5	170171465	-0.312604099	
cg07185974	3	18485529	-0.313291446		cg19406117	4	77228196	-0.31260208	STBD1
cg11674773	1	54518492	-0.313273236	TMEM59	cg02768471	1	155231827	-0.312597618	SCAMP3
cg14157947	18	20513080	-0.313271394	RBBP8	cg26890010	1	70876953	-0.312584027	CTH
cg16854524	4	83931902	-0.313267561	LIN54	cg25230151	11	35441107	-0.312575367	SLC1A2
cg12399453	1	27648454	-0.313253477	TMEM222	cg09295542	6	88986071	-0.312573243	
cg04791162	14	62331287	-0.313204112		cg02283836	14	52118711	-0.312573076	FRMD6
cg13249876	10	32217968	-0.313203077	ARHGAP12	cg20549080	10	103892662	-0.312572442	PPRC1
cg08602689	13	103452535	-0.313201285	BIVM	cg26567249	8	97247842	-0.312567105	UQCRB
cg06039171	20	57599526	-0.313182948	TUBB1	cg00459078	17	43024659	-0.31254579	KIF18B
cg17092583	11	735575	-0.31316707		cg07066932	1	24285945	-0.312525345	PNRC2
cg01936270	2	38303680	-0.313163724	CYP1B1	cg09134840	1	235530680	-0.31252441	TBCE
cg12391087	1	244012456	-0.313092666		cg23908998	10	22292698	-0.312508657	DNAJC1
cg08451517	8	125383826	-0.313067357	TMEM65	cg13612958	19	18303626	-0.312432183	MPV17L2
cg10029427	6	31778258	-0.313063644	HSPA1L	cg12955252	20	32891324	-0.312402774	AHCY
cg23955684	3	16555288	-0.313041653	RFTN1	cg15142485	2	240323713	-0.3123785	HDAC4
cg08184792	12	48592270	-0.313031799		cg04530460	6	42858550	-0.312373143	C6orf226
cg15309223	1	54519091	-0.313030393	TMEM59	cg02657830	1	27152905	-0.312331236	ZDHHC18
cg07509420	16	740472	-0.312997001	WDR24	cg10639412	2	33824684	-0.312321857	FAM98A
cg01997230	3	13937190	-0.312992094		cg22846149	20	56064151	-0.312319239	HMGB1L1
cg10210086	16	84837307	-0.312990249		cg01430870	2	99954399	-0.312310125	EIF5B
cg24334002	22	42087946	-0.3129473	C22orf46	ch.12.78471492F	12	79947361	-0.31228268	
cg04583149	19	1207124	-0.312938042	STK11	cg07639697	19	11850005	-0.312259286	ZNF823
cg12380209	10	120515094	-0.312919137	C10orf46	cg12835684	12	53645647	-0.312259282	MFSD5
cg07335234	3	185304496	-0.312901017	SEN2	cg01320614	2	86115591	-0.312256233	ST3GAL5
cg21144673	22	42017783	-0.312828234	PPDE2	cg10122474	14	88459471	-0.312253961	GALC
cg10553894	11	68550534	-0.312815938	CPT1A	cg00483446	3	67048774	-0.312227391	KBTBD8
cg21542094	10	6243955	-0.312812907	PFKFB3	cg21610999	17	8661909	-0.312214307	SPDYE4
cg08591058	17	25681106	-0.31277814		cg02470625	7	39453784	-0.312195627	POU6F2
cg23317683	7	99698554	-0.312748966	MCM7	cg10261819	16	22448417	-0.312186035	RRN3P3
cg25252777	19	56709056	-0.31274811		cg12569089	20	35724525	-0.312175162	RBL1
cg16317734	11	94822598	-0.312726255	ENDOD1	cg22256960	15	77711686	-0.312152953	PDS5B
cg01488306	1	197037504	-0.312717361	F13B	cg09774198	13	33160713	-0.312129442	MEX3C
cg06995565	16	75590339	-0.312709713	TMEM231	cg15901997	18	48723744	-0.312126192	C4orf48
cg19438583	5	1585122	-0.31266495	SDHAP3	cg04731813	4	2043086	-0.312109391	
cg12712846	1	181058068	-0.312653477	IER5	cg11748640	19	5691196	-0.312087368	RPL36
cg08346494	11	70049962	-0.312649574	FADD	cg16080746	4	87928530	-0.312082237	AFF1
cg18882576	2	191184621	-0.312640816	HIBCH	cg03931027	5	138609848	-0.312077003	SNHG4
cg17476752	19	24184762	-0.312629479		cg08439970	6	74230786	-0.312049726	EEF1A1
cg04529582	20	30697510	-0.312615295	TM9SF4	cg18436128	14	65439236	-0.31204719	RAB15
cg09463047	17	36104218	-0.312604493	HNF1B	cg15032638	10	51565035	-0.312010206	NCOA4

Figure 16-21

cg23063986	4	128886308	-0.312010108	MFSD8	cg23361901	6	4019100	-0.311457675	
cg01741121	14	24701991	-0.311995322	GMPR2	cg04122790	1	229762148	-0.31145005	URB2
cg10006762	11	65342202	-0.311993608	EHP11	cg20232119	6	31778558	-0.311434108	HSP11
cg16257334	6	30881842	-0.311990634	GTF2H4	cg03700218	16	1832709	-0.311425685	SPSB3
cg17145587	2	230579435	-0.311956796	DNER	cg26196213	6	29617956	-0.311419256	
cg26258108	2	232329189	-0.311904844	NCL	cg03503975	22	46518455	-0.311408219	GIN1
cg18423859	18	60986742	-0.311896537	BCL2	cg04564312	5	102456179	-0.311406209	IPO4
cg20099147	19	56652066	-0.311876004	ZNF444	cg01913958	14	24658184	-0.311394684	PKN2
cg24622726	9	91926624	-0.311872136	CKS2	cg16228804	1	89150099	-0.311383786	TMTC3
cg03512355	12	121837704	-0.311856927	RNF34	cg21641552	12	88535903	-0.311363177	CHURC1
cg11368578	7	150754936	-0.311833839	CDK5	cg11177179	14	65381159	-0.311359427	STK32B
cg14868663	14	77923968	-0.311807926	C14orf133	cg19764048	4	5053152	-0.311354382	TTC7B
cg12654140	17	46842970	-0.311804284	TTL6	cg12720152	14	91087476	-0.311342047	IKZF5
cg22063259	15	74428820	-0.311800399	ISLR2	cg17834180	10	124768240	-0.311338609	MFNG
cg10553515	7	5013490	-0.311790555	RNF216L	cg01765930	22	37881422	-0.311336552	SCN8A
cg23480499	12	95867566	-0.311774415	METAP2	cg27575217	12	51984358	-0.311336453	MRAP2
cg06330324	22	31031670	-0.311744645	SLC35E4	cg15411280	6	84747508	-0.311334544	ZNF343
cg17983571	10	65186953	-0.311742516	JMJD1C	cg20546810	20	2489835	-0.311326468	NDNL2
cg11723896	17	34136427	-0.311708393	TAF15	cg01665633	15	29562142	-0.311315041	KIF23
cg23639922	10	103892660	-0.311690979	PPRC1	cg20762182	15	69727293	-0.311298714	DAP3
cg11371394	2	105946583	-0.311684665	TGFBAP1	cg13088939	1	155659111	-0.311282538	DDX10
cg22786826	16	2564780	-0.311664077	ATP6V0C	cg24631920	11	108535736	-0.311244961	
cg07033880	15	85923739	-0.311661358	AKAP13	cg07937578	4	25487481	-0.311230164	
cg04270788	1	89356964	-0.311646715	GTF2B	ch.3.21287957F	3	21312953	-0.31122769	
cg25902627	11	88071152	-0.311636913	CTSC	cg03573109	16	85849619	-0.311221409	ZNF302
cg02568557	11	129288930	-0.311633811	BARX2	cg22685123	19	35168238	-0.311173235	ABHD14A
cg25966751	14	74098320	-0.311632275		cg26791985	3	52008971	-0.311170877	METTL2A
cg09150633	5	148206173	-0.311612062	ADRB2	cg20275462	17	60501228	-0.311163602	PRKAB2
cg23243994	7	139045033	-0.311590734	LUC7L2	cg24403497	1	146644500	-0.311156458	LRRCD
cg08027110	12	57082200	-0.311589665	PTGES3	cg10463708	1	90309205	-0.311154244	MAGI3
cg26278858	15	40401256	-0.311565525	BMF	cg18539474	1	113933413	-0.311144325	GNAL
cg08817965	17	38574364	-0.311557758	TOP2A	cg24643211	18	11851603	-0.311139178	PSMD1
cg21930443	17	28443747	-0.31155749	CCDC55	cg12968077	2	231921504	-0.311137139	EIF3D
cg25781121	3	48282641	-0.31153991	ZNF589	cg14240963	22	36925312	-0.31113281	PARVB
cg12353549	17	30771552	-0.31150551	PSMD11	cg00367327	22	44419885	-0.3111081963	ZNF876P
cg10282920	2	95831790	-0.311493502	ZNF2	cg17030981	4	205522	-0.311053017	CBX6
cg16497340	5	180601183	-0.311491519		cg06060673	22	39268830	-0.311051901	SMC3
cg24451858	11	75379620	-0.311487056	MAP6	cg19882663	3	180308459	-0.311006881	SLC22A16
cg11739675	12	104852151	-0.311467348	CHST11	cg15124560	10	112327767	-0.310993498	DAAM1
cg08965527	16	84178213	-0.311458198	HSDL1	cg24926253	6	110799072	-0.310993018	
cg16720880	9	33265144	-0.311457945	SUGT1P1	cg04381122	14	59655332		

Figure 16-22

cg04010712	3	42003234	-0.310971927	ULK4	cg15485323	6	26234460	-0.31040183	HIST1H1D
cg12760261	5	122758659	-0.310954843	CEP120	cg26974158	5	118788130	-0.310394783	HSD17B4
cg01902998	14	65346633	-0.310954012		cg25882709	1	224517832	-0.310381947	NVL
cg00098718	15	81072600	-0.310943813	KIAA1199	cg20295040	1	192778396	-0.310376629	RGS2
cg211119375	2	44393385	-0.310941186		cg08118646	4	99850258	-0.310362001	EIF4E
cg27158084	6	149813350	-0.310880851		cg04696149	2	37552545	-0.310354955	
cg06867829	12	24715508	-0.310855578	SOX5	cg20259594	3	15920154	-0.310314802	RAI1
cg07195197	16	1662150	-0.310851937	IFT140	cg15906409	17	17685582	-0.310307309	TRA2A
cg10700459	6	30231675	-0.31084726	HLA-L	cg05501276	7	23571514	-0.310304828	PRDX1
cg16050957	16	24550743	-0.310839405	RBBP6	cg14219630	1	45987336	-0.310282221	CD164
cg162223510	6	136610388	-0.31083644	BCLAF1	cg00615550	6	109703901	-0.310266408	BUB3
cg13260314	6	3900192	-0.310809318		cg03423968	10	124914448	-0.310265171	MTFMT
cg23465426	6	32847377	-0.310804367	PPP1R2P1	cg06929872	15	65322164	-0.310263064	SFRS8
cg19138325	12	129429698	-0.310787979	GLT1D1	cg05759182	12	132195987	-0.310256508	GMCL1
cg09928842	8	135845050	-0.310785667		cg18133008	2	70056632	-0.310253914	TMEM9B
cg21950493	12	110907285	-0.310767027	GNP3	cg11310299	12	14923421	-0.310237641	KIF18A
cg26014017	1	38019849	-0.310757279	SNIP1	cg10371306	11	8985977	-0.310234835	NOL6
cg04210100	2	9614471	-0.310757023	IAH1	cg08967200	11	28129733	-0.310224134	KIF22
cg05732749	22	42467120	-0.310710639	NAGA	cg02738677	3	133265129	-0.310220997	RBM12B
cg01199952	13	25591486	-0.310694165		cg03863549	9	33474004	-0.310183401	TAF7
cg13615109	9	27610826	-0.310682333		cg04078251	16	29802448	-0.310169295	INPP1
cg01245284	12	76426035	-0.310653084	PHLDA1	cg07538747	8	94753418	-0.310151829	NUBP2
cg07660645	19	17392438	-0.310651422	ANKLE1	cg20560182	5	140700478	-0.310149367	
cg09986574	9	135544256	-0.310637644	DDX31	cg25110245	2	191209022	-0.310146761	
cg04982748	12	66696283	-0.310592246	HELB	cg09118169	16	1833616	-0.310123881	
cg18105335	19	37019307	-0.310590173	ZNF260	cg19102035	6	28864611	-0.310122362	
cg14128369	6	34231203	-0.310584514		cg02717437	18	14132207	-0.3101214	ZNF519
cg12124647	19	20749738	-0.310578389	ZNF737	cg00049253	1	231473541	-0.310118095	EXOC8
cg02200456	11	2923436	-0.310577221	SLC22A18AS	cg12091641	8	145180933	-0.310103328	
cg26406994	4	99182798	-0.310540847	RAP1GDS1	cg27429194	17	3099847	-0.310092412	OR1A2
cg00164500	2	132416160	-0.310538722		cg11726911	1	6241120	-0.310084667	CHD5
cg26473844	5	37834909	-0.310508489	GDNF	cg03820909	10	127407979	-0.310062111	C10orf137
cg00314018	20	3776260	-0.310498132	CDC25B	cg12790134	8	67578787	-0.310052978	VCPIP1
cg06058395	18	13726784	-0.310496038	C18orf19	cg25134231	2	122288051	-0.310038735	CLASP1
ch.4.8394628F	4	8343728	-0.310490626		cg14377370	4	17812264	-0.310022859	NCAPG
cg25826526	20	61426675	-0.310461276	C20orf20	cg13603859	5	145827007	-0.310022832	TCERG1
cg13929053	6	3068474	-0.310439582		cg07730007	12	107377277	-0.310017507	MTERFD3
cg07353572	1	91966518	-0.310426926	CDC7	cg06576783	6	53572893	-0.30998009	
cg01092811	3	131100455	-0.31041985	NUDT16	cg25498327	5	68389852	-0.3099672	SLC30A5
cg16063617	5	128430663	-0.310416734	ISOC1	cg09063111	22	31503870	-0.309973367	SELM
cg17308959	3	15643111	-0.31040967	HACL1	cg03082763	19	12662438	-0.309973248	ZNF564

Figure 16-23

cg02718464	13	41384019	-0.309964545	SUGT111	cg11356029	5	72112729	-0.309328399	TNPO1
cg24669932	1	8877431	-0.309957815	RERE	cg04576025	5	1386550	-0.309317824	
cg10239816	10	101190596	-0.309953822	GOT1	cg24427993	6	30418847	-0.309316734	
cg22048948	2	99225318	-0.309889634	C2orf64	cg16576664	19	51611660	-0.309309	CTU1
cg00208412	10	99609481	-0.30982282	GOLGA7B	cg09978545	11	66035829	-0.309288893	RAB1B
cg11488569	9	130186546	-0.309874293	ZNF79	cg14064229	2	42588497	-0.309275025	COX7A2L
cg26112390	12	100550390	-0.309863508	GOLGA2L1	cg21410080	21	43639862	-0.309263997	ABCG1
cg09843086	7	131013189	-0.309842788	MKLN1	cg11819799	10	105452339	-0.30926266	SH3PXD2A
cg20850195	17	62223337	-0.309805432	SNORA76	cg02971882	4	71554083	-0.309258765	UTP3
cg26796563	16	68344861	-0.309784497	PRMT7	cg17574857	5	147763476	-0.309251558	FBXO38
cg20054027	11	66610720	-0.309783946	RCE1	cg20951334	2	86669446	-0.309238473	KDM3A
cg16501572	11	71934660	-0.309781631	INPPL1	cg07391436	5	145214979	-0.309233064	PRELID2
cg16147336	1	51435387	-0.30975064	CDKN2C	cg14553224	17	56084507	-0.309205101	SFRS1
cg04974899	20	25177027	-0.309749165	ENTPD6	cg19675288	6	166582206	-0.30919056	T
cg09281539	20	20693126	-0.309738063	RALGAPA2	cg00267325	6	29691936	-0.309184837	HLA-F
cg08037327	7	150211061	-0.309728585	GIMAP7	cg12610061	1	40916055	-0.309183854	ZNF643
cg12349683	15	68133070	-0.309720432	HHLA3	cg17896229	20	5294595	-0.30917879	PROKR2
cg01557883	1	70820063	-0.309719717	PTPN12	cg05092885	4	106629795	-0.309169309	INTS12
cg00403457	7	77166947	-0.309712411	CH25H	ch.15.99448522F	15	101630999	-0.309168091	
cg00933696	16	11327141	-0.309672325		cg22350160	1	46016574	-0.309166433	AKR1A1
cg24568842	10	90967160	-0.309661868		cg04970352	11	44327399	-0.309165028	ALX4
cg07699084	3	123307740	-0.30964294		cg25478109	3	179322476	-0.30915821	NDUFB5
cg08358671	1	185286807	-0.309610866	IVNS1ABP	cg24947163	15	23086952	-0.309135818	NIPA1
cg20768342	1	85483948	-0.309605089	MCOLN3	cg00215350	17	6555120	-0.309093776	C17orf100
cg00966077	16	1401335	-0.309556153	C16orf42	cg21411757	12	93771484	-0.309089927	NUDT4
cg11733478	11	88071037	-0.309540219	CTSC	cg06449906	5	77072222	-0.309075428	TBCA
cg26507704	15	25314647	-0.30953877	SNORD116-8	cg25993851	11	46722334	-0.309066398	ARHGAP1
cg07515367	17	45401150	-0.309530681	C17orf57	cg10001590	17	21729117	-0.309047162	
cg11676109	11	118992413	-0.309529962	HINFP	cg19510792	5	16935695	-0.309042736	MYO10
cg14870242	14	55034646	-0.309508258	SAMD4A	cg09356401	2	64068331	-0.309038662	UGP2
cg22984041	3	161090118	-0.309445163	C3orf57	cg24152845	15	25414763	-0.309009332	SNORD115-1
cg15799959	10	38146444	-0.309426878	ZNF248	cg27518692	17	61627470	-0.30897399	DCAF7
cg07968927	13	115080364	-0.309416353	ZNF828	cg14256840	7	64197047	-0.308966434	
cg16513467	10	28822500	-0.309390525	WAC	cg19501543	1	35875651	-0.308951201	ZMYM4
cg16341592	3	112931182	-0.30938636	BOC	cg17159242	2	3623060	-0.30891525	RP57
cg06160898	3	45187312	-0.309383291	CDCP1	cg07793810	10	101989373	-0.308892578	CHUK
cg14621103	7	1178041	-0.30938325	C7orf50	cg00734724	15	41408630	-0.308881017	INO80
cg17131070	1	243418713	-0.30935382	SDCCAG8	cg16989797	9	139378060	-0.30887793	C9orf163
cg16056849	7	35225695	-0.30934228		cg27026509	1	36348944	-0.30886745	EIF2C1
cg10585870	19	14530314	-0.309333683	DDX39	cg26053083	11	14995770	-0.308860659	
cg00533084	1	156698170	-0.309330586	C1orf66	cg08400563	2	201729555	-0.308853596	CLK1

Figure 16-24

cg12271800	19	59028764	-0.308817426	ZBTB45
cg20908993	14	67826378	-0.308811976	EIF2S1
cg14094460	4	43900946	-0.308803308	
cg27659478	17	73891062	-0.308782907	TRIM65
cg14407698	9	34458886	-0.308776983	C9orf25
cg03218988	11	62341521	-0.308770933	EEF1G
cg24726668	14	39736238	-0.308756003	CTAGE5
cg02566518	10	75531971	-0.30872194	FUT11
cg17001531	1	16825540	0.309175372	
cg08524474	10	49813208	0.309188516	ARHGAP22
cg11566832	10	88659593	0.309358545	BMPR1A
cg26164151	11	44749353	0.309778003	
cg12586707	4	74738902	0.309811367	
cg01266707	17	37824461	0.310151696	PNMT
cg10274208	13	41351044	0.31049244	
ch.8.2353618R	8	119282796	0.310724538	SAMD12
cg11964099	17	3905835	0.31085308	
cg01194336	12	66627997	0.310951911	IRAK3
cg03183745	19	17577087	0.311037602	
cg08541880	3	137833983	0.311204357	DZIP1L
cg23869307	17	42297441	0.311749709	UBTF
cg02850329	1	24829455	0.3119366	RCAN3
cg26547359	10	16859530	0.312483668	RSU1
cg17105206	16	67211972	0.312769436	KIAA0895L
cg17079026	2	95858880	0.312782194	
cg17847344	5	158478734	0.313906358	EBF1
cg16704344	5	141616127	0.315140712	
cg08529748	19	52407630	0.315600775	ZNF649
cg01806195	14	102701850	0.316556217	RAGE
cg07930620	12	96431556	0.316776736	
cg18362448	19	18544419	0.316786853	SSBP4
cg07212416	16	28385626	0.320695478	
cg08293303	5	176731731	0.321332977	PRELID1
cg00742472	14	31889912	0.322585238	

Figure 16-25

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A2LD1	ADAP1	ALDH3B2	AP3B2	ARPC3	ATXN7L1	BMI1
AACS	ADAR	ALG10B	AP3D1	ARPC5	ATXN7L3	BMP4
AAK1	ADARB1	ALG5	AP4E1	ARPP19	AUTS2	BMP8A
AASDH	ADARB2	ALKBH2	AP4S1	ARRB1	AVEN	BMP8B
ABCA17P	ADAT1	ALKBH5	APAF1	ARSA	AVL9	BMPR1A
ABCB9	ADCK2	ALOX12B	APBB2	ARSG	AXIN2	BMPR2
ABCC1	ADCK5	ALOX5	APC	ART3	AXL	BMS1
ABCC5	ADCYAP1	ALS2CR11	APH1B	ASAH1	B3GALNT2	BNIP2
ABCF2	ADD1	ALS2CR4	APITD1	ASAP1	B3GALT4	BPHL
ABCF3	ADD2	ALX4	APOA1BP	ASAP3	B3GALT1	BPTF
ABCG1	ADD3	AMDHD2	APOL1	ASB7	B3GAT3	BRAF
ABCG2	ADNP	AMFR	APOL2	ASGR1	B3GNT2	BRCA1
ABHD2	ADPGK	AMIGO2	APOLD1	ASNS	B3GNTL1	BRD1
ABI2	ADPRHL1	AMMECR1L	APOM	ASPDH	B4GALNT4	BRD2
ABL1	ADRA2C	AMN1	APRT	ASPG	B4GALT7	BRI3
ABLM1	ADRB2	AMOTL2	APTIX	ASPSR1	B9D1	BRIX1
ABR	ADRBK1	AMPD2	AQP10	ASTN1	BACE1	BRPF1
ABTB1	ADRBK2	AMZ2	ARAP1	ASXL2	BAD	BRPF3
ABTB2	AEBP1	ANG	ARAP2	ATAD1	BAHCC1	BRSK2
ACAA1	AEBP2	ANGEL1	ARAP3	ATAD2	BAIAP2	BRUNOL4
ACACB	AFARP1	ANK1	ARF1	ATAD3A	BAIAP2L1	BRUNOL5
ACAD10	AFF4	ANKDD1A	ARFGAP1	ATAD3B	BANP	BRWD1
ACAD9	AFG3L2	ANKH	ARFGEF1	ATAD3C	BARD1	BTBD10
ACADM	AGAP1	ANKLE1	ARHGAP1	ATE1	BARX2	BTBD12
ACADSB	AGAP11	ANKLE2	ARHGAP10	ATF3	BAT1	BTBD2
ACAT2	AGAP3	ANKRD11	ARHGAP12	ATF4	BAT2	BTBD9
ACBD5	AGFG1	ANKRD12	ARHGAP19	ATG12	BAT2L2	BTC
ACBD6	AGL	ANKRD18A	ARHGAP21	ATG5	BAT3	BTG2
ACCN4	AGPAT4	ANKRD26	ARHGAP22	ATG7	BATF3	BTN2A2
ACE	AGPAT5	ANKRD27	ARHGAP5	ATIC	BAX	BTN3A2
ACO2	AGRN	ANKRD30A	ARHGAP9	ATL2	BBC3	C10orf105
ACOT4	AHCYL2	ANKRD30B	ARHGEF1	ATL3	BBS5	C10orf114
ACOT7	AHDC1	ANKRD31	ARHGEF10	ATOH8	BCAR1	C10orf129
ACOX3	AHI1	ANKRD33B	ARHGEF11	ATP11A	BCAS3	C10orf137
ACP6	AHNAK2	ANKRD36	ARHGEF15	ATP11B	BCAT1	C10orf18
ACSF3	AHR	ANKRD42	ARHGEF16	ATP12A	BCKDHB	C10orf32
ACSL1	AHRR	ANKRD44	ARHGEF2	ATP13A1	BCL11A	C10orf4
ACSL3	AIG1	ANKRD53	ARID1A	ATP1A2	BCL2	C10orf46
ACTG1	AIM1	ANKRD6	ARID1B	ATP5G2	BCL9	C10orf58
ACTL6A	AIMP2	ANKS1B	ARID4A	ATP5J	BCLAF1	C10orf93
ACTN1	AIRE	ANKS3	ARID5B	ATP5SL	BCO2	C11orf10
ACTR5	AK2	ANO10	ARIH2	ATP6V0A1	BCR	C11orf20
ACVR1B	AK3	ANO5	ARL1	ATP6V0A2	BDH2	C11orf34
ADAM10	AK7	ANO6	ARL10	ATP6VOC	BDP1	C11orf45
ADAM11	AKAP10	ANO7	ARL15	ATP6VOD1	BEAN	C11orf54
ADAM12	AKAP11	ANO8	ARL3	ATP6V0E2	BEND3	C11orf58
ADAM19	AKAP13	ANP32A	ARL6	ATP6V1E1	BEND7	C11orf61
ADAM22	AKD1	ANP32B	ARL8A	ATP6V1F	BEST4	C11orf67
ADAM3A	AKIRIN1	ANP32E	ARL8B	ATP6V1H	BHLHE23	C11orf68
ADAM6	AKR1A1	ANTXR2	ARMC10	ATP8B2	BIK	C11orf71
ADAM9	AKR1B15	ANTXRL	ARMC5	ATP8B3	BIN3	C11orf83
ADAMTS12	AKR1C2	ANUBL1	ARMC6	ATP9A	BIRC5	C11orf9
ADAMTS5	AKT1	ANXA3	ARPC1A	ATR	BLCAP	C12orf26
ADAMTS7	AKT1S1	ANXA4	ARPC1B	ATXN2	BLOC1S3	C12orf57
ADAMTS8	ALDH3A2	AP2M1	ARPC2	ATXN7	BLVRA	C12orf68

Figure 17-1

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C13orf27	C1orf201	C5orf36	CALR	CCDC55	CDH23	CHST12
C13orf37	C1orf203	C5orf42	CAMK1	CCDC57	CDH24	CHST2
C14orf101	C1orf216	C5orf45	CAMK2B	CCDC6	CDH5	CHST6
C14orf102	C1orf229	C5orf52	CAMKK2	CCDC64B	CDK11A	CHTF8
C14orf104	C1orf230	C6orf10	CAMSAP1	CCDC77	CDK17	CHUK
C14orf138	C1orf25	C6orf103	CAMSAP1L1	CCDC79	CDK19	CHURC1
C14orf145	C1orf35	C6orf122	CAND1	CCDC83	CDK5R1	CIAPIN1
C14orf182	C1orf59	C6orf129	CAND2	CCDC86	CDK6	CIB4
C14orf4	C1orf63	C6orf153	CANT1	CCDC88B	CDKL2	CINP
C15orf37	C1orf83	C6orf163	CANX	CCDC88C	CDKN1B	CIR1
C15orf51	C1orf85	C6orf192	CAPN10	CCDC9	CDKN3	CIRBP
C15orf59	C1orf93	C6orf195	CAPRIN1	CCDC90B	CDR2	CISD1
C16orf13	C1QA	C6orf201	CAPRIN2	CCDC96	CDV3	CISH
C16orf35	C1QL1	C6orf203	CARD10	CCDC99	CDYL	CKAP2L
C16orf42	C1QL3	C6orf211	CARD11	CCHCR1	CEBPG	CKAP4
C16orf52	C1QL4	C6orf226	CARD6	CCKAR	CEBPZ	CKAP5
C16orf58	C20orf111	C6orf48	CARM1	CCKBR	CECR6	CKB
C16orf7	C20orf196	C6orf72	CASD1	CCL4	CELSR1	CLCA4
C16orf70	C20orf199	C6orf94	CASKIN1	CCL5	CELSR3	CLCNKB
C16orf75	C20orf20	C7orf10	CASP10	CCND2	CENPBD1	CLEC12B
C16orf87	C20orf30	C7orf13	CASP4	CCNY	CENPL	CLEC16A
C16orf88	C20orf43	C7orf23	CASP8AP2	CCNYL1	CENPN	CLIC1
C16orf90	C20orf46	C7orf27	CASP9	CCR1	CENPT	CLIC4
C17orf101	C20orf94	C7orf40	CASZ1	CCRN4L	CENPV	CLIC6
C17orf42	C21orf129	C7orf41	CATSPER2	CCT5	CEP110	CLIP2
C17orf48	C21orf15	C7orf46	CATSPERG	CCT6A	CEP120	CLIP4
C17orf51	C21orf91	C7orf49	CAV1	CCT6B	CEP135	CLK1
C17orf56	C22orf23	C7orf57	CAV3	CCT7	CEP152	CLN6
C17orf62	C22orf32	C7orf64	CBFA2T3	CD276	CEP164	CLP1
C17orf66	C22orf34	C7orf70	CBFB	CD300LB	CEP55	CLPB
C17orf85	C22orf40	C8orf38	CBLN1	CD34	CEP68	CLSTN3
C17orf98	C22orf9	C8orf40	CBLN3	CD3E	CEP72	CLUAP1
C18orf22	C2CD4D	C8orf55	CBR4	CD44	CERK	CLUL1
C18orf8	C2orf27A	C9orf102	CBX1	CD46	CFL1	CMC1
C19orf10	C2orf27B	C9orf103	CBX8	CD58	CFL2	CMIP
C19orf20	C2orf28	C9orf106	CC2D1A	CD59	CFLAR	CMPK2
C19orf21	C2orf53	C9orf116	CCBE1	CD81	CHAC1	CNBD1
C19orf22	C2orf60	C9orf170	CCDC102B	CD8A	CHAF1B	CNIH
C19orf25	C2orf69	C9orf171	CCDC107	CDADC1	CHAT	CNKSR3
C19orf28	C2orf71	C9orf3	CCDC111	CDC14C	CHCHD1	CNNM2
C19orf29	C2orf76	C9orf40	CCDC122	CDC20B	CHCHD2	CNNM4
C19orf40	C2orf88	C9orf41	CCDC129	CDC25A	CHCHD5	CNO
C19orf47	C3orf37	C9orf69	CCDC13	CDC25B	CHD5	CNOT10
C19orf61	C3orf58	C9orf86	CCDC134	CDC25C	CHD9	CNOT2
C19orf66	C3orf71	C9orf89	CCDC137	CDC26	CHEK1	CNOT6
C19orf73	C4orf14	C9orf93	CCDC148	CDC27	CHFR	CNOT8
C1GALT1	C4orf21	C9orf98	CCDC150	CDC42BPG	CHID1	CNST
C1orf113	C4orf22	CA13	CCDC157	CDC42EP3	CHKA	CNTN4
C1orf122	C4orf29	CACNA1C	CCDC25	CDC42SE2	CHMP2B	CNTNAP2
C1orf124	C4orf34	CACNA1D	CCDC42	CDC7	CHN1	CNTNAP4
C1orf151	C4orf41	CACNA1G	CCDC42B	CDC73	CHN2	COBL
C1orf152	C4orf42	CACNG4	CCDC45	CDCA4	CHPF2	COBRA1
C1orf159	C4orf43	CAD	CCDC46	CDCP1	CHPT1	COG3
C1orf190	C4orf6	CAGE1	CCDC49	CDH13	CHRD	COG7
C1orf198	C5orf28	CALCB	CCDC51	CDH15	CHRM3	COL11A2

Figure 17-2

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COL18A1	CTAGE1	DCAF11	DHRS7B	DPH2	EFNB2	EPOR
COL1A1	CTBP1	DCAF12	DHX35	DPM3	EFR3B	EPS8L1
COL22A1	CTBP2	DCAF13	DHX36	DPP9	EFTUD1	EPS8L2
COL6A2	CTDSPL	DCAF4	DHX37	DPYSL4	EFTUD2	ERAL1
COLEC12	CTF1	DCAF8	DIABLO	DRAM1	EGR1	ERBB2
COMMD1	CTNNA1	DCAKD	DIAPH1	DRG1	EHBP1L1	ERBB2IP
COMMD4	CTNNAL1	DCHS2	DICER1	DSCR3	EHD4	ERBB3
COPB2	CTNNB1	DCK	DIDO1	DST	EHMT2	ERCC3
COQ4	CTRC	DCLRE1B	DIP2C	DSTN	EID2	ERCC5
CORO1A	CTSA	DCLRE1C	DIRAS2	DSTYK	EID2B	ERF
CORO1B	CTXN1	DCTN5	DISC1	DTWD1	EIF1B	ERI1
CORO1C	CUEDC2	DCUN1D4	DKFZp434J0226	DTWD2	EIF2AK2	ERMAP
CORO7	CUGBP1	DDA1	DKFZP686I15217	DTX3	EIF2AK3	ESAM
COX11	CUL3	DDAH1	DKFZp686O2416	DTX4	EIF2AK4	ESCO2
COX15	CUL5	DDI2	DKKL1	DTYMK	EIF2B4	ESF1
COX5B	CUL7	DDOST	DLAT	DULLARD	EIF2C2	ESPL1
COX6A1	CUX1	DDX10	DLD	DUS2L	EIF3D	ESPN
COX6B1	CXCR1	DDX11	DLG4	DUSP11	EIF3F	ESR1
COX8A	CXCR2	DDX12	DLGAP1	DUSP14	EIF3J	ESR2
CPA5	CXCR4	DDX20	DLGAP2	DUSP18	EIF3M	ETAA1
CPAMD8	CXXC4	DDX28	DLGAP5	DUSP4	EIF4E3	ETFB
CPEB3	CXXC5	DDX31	DLK2	DUSP5	EIF4EBP2	ETFDH
CPEB4	CYB561	DDX39	DLL1	DUSP7	EIF4ENIF1	ETNK1
CPNE1	CYB5D2	DDX41	DLX3	DUT	EIF4G3	ETS1
CPSF3L	CYB5R1	DDX42	DMP1	DYDC2	EIF5	EVC2
CPSF7	CYB5R2	DDX49	DMTF1	DYNC1H1	EIF6	EWSR1
CPT1A	CYBA	DDX50	DMXL1	DYNC1I1	ELFN2	EXD3
CRABP2	CYCSP52	DDX51	DMXL2	DYNLL1	ELMO1	EXOC6
CRAMP1L	CYFIP1	DDX60	DNAH17	DYNLL2	ELMO2	EXOSC10
CRBN	CYLD	DECR2	DNAH3	DYNLT1	ELMOD3	EXOSC9
CRCP	CYP27A1	DEF8	DNAJA2	DYRK2	ELOVL7	EZH2
CREB3L2	CYP2F1	DEFB125	DNAJB1	DZIP1L	ELP2	EZR
CREM	CYP2U1	DEK	DNAJB13	E2F1	ELP2P	F12
CRHR1	CYP3A5	DENND2A	DNAJB2	E2F8	ELP3	F2R
CRIP2	CYP4F2	DENND2C	DNAJB6	EARS2	ELP4	F7
CRISPLD2	CYP4F22	DENND3	DNAJC1	EBF1	EMID1	FABP5
CRKL	CYP4V2	DEPDC5	DNAJC14	EBF4	EMILIN2	FAF2
CROCC	CYP51A1	DERL2	DNAJC19	EBPL	EML3	FAH
CRTAC1	CYTH1	DERL3	DNAJC27	ECD	EML4	FAHD1
CRTAP	CYTH3	DET1	DNAJC4	ECEL1	EMX2	FAHD2A
CRTC2	CY TSA	DGAT2	DNASE2	EDC3	ENGASE	FAIM2
CRYM	CYTSB	DGCR2	DNER	EDEM1	ENPP1	FAIM3
CSAD	DAAM1	DGCR5	DNM1	EDF1	ENTPD5	FAM105A
CSF1	DAB1	DGCR6	DNM2	EEF1D	ENTPD6	FAM107B
CSGALNACT2	DACH1	DGCR6L	DNM3	EEF1G	ENY2	FAM109A
CSK	DAP	DGKD	DNMT1	EEFSEC	EP400NL	FAM10A4
CSNK2B	DAP3	DGKE	DNPEP	EEPD1	EPCAM	FAM113A
CSPG4	DAXX	DGKG	DOCK2	EFCAB5	EPHA1	FAM115A
CSPG5	DAZAP1	DGKZ	DOCK3	EFCAB7	EPHA8	FAM115C
CSRNP2	DAZAP2	DHCR24	DOCK7	EFCAB9	EPHB1	FAM117B
CSRP1	DBI	DHODH	DOK7	EFEMP2	EPHB3	FAM119A
CSRP2	DBNDD1	DHPS	DOLPP1	EFHA1	EPHB4	FAM119B
CST2	DBNDD2	DHRS12	DONSON	EFHD1	EPHX4	FAM122A
CST3	DBNL	DHRS2	DPEP3	EFNA1	EPM2AIP1	FAM129A
CSTF3	DBP	DHRS3	DPF1	EFNA3	EPN2	FAM129B

Figure 17-3

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FAM131B	FBRSL1	FOXC1	GAPDHS	GMPPA	GSTM2	HIATL1
FAM149B1	FBXL12	FOXK1	GAR1	GMPR	GSTO1	HIC1
FAM150A	FBXL14	FOXN3	GAS7	GNA13	GTDC1	HIF1A
FAM157A	FBXL18	FOXN4	GAS8	GNAI2	GTF3C1	HIP1
FAM159A	FBXL7	FOXP1	GATA2	GNAL	GTF3C5	HIPK1
FAM163A	FBXO22	FOXP4	GATA6	GNAS	GTPBP1	HIPK3
FAM168B	FBXO27	FOXRED2	GATAD2A	GNB1	GTPBP5	HIST1H1T
FAM175A	FBXO31	FPR1	GATAD2B	GNB1L	GTPBP8	HIST1H2AG
FAM180A	FBXO46	FRAT1	GBAS	GNB5	GUCY1A2	HIST1H2AL
FAM185A	FBXO7	FRG1	GBP3	GNG7	GUCY2G	HIST1H2BA
FAM186B	FBXW4	FRG2B	GBP4	GNL2	GUK1	HIST1H2BD
FAM188A	FBXW9	FRG2C	GBX1	GNMT	GULP1	HIST1H3A
FAM189A1	FCAR	FRMD4A	GCAT	GNPAT	GUSB	HIST1H3C
FAM18B2	FCF1	FRMD8	GCDH	GNRHR2	GUSBL2	HIST1H3G
FAM198B	FCHO2	FRS3	GCH1	GOLGA2	GYG1	HIST1H3I
FAM38A	FCHSD2	FRYL	GCNT4	GOLGA2L1	GYPB	HIST1H4J
FAM3D	FDFT1	FSCN1	GCNT7	GOLGA3	H1FX	HIST1H4K
FAM40A	FECH	FSCN2	GCSH	GOLGA7B	H6PD	HIST2H2BA
FAM40B	FER1L4	FSD1L	GDE1	GORAB	HABP2	HIST2H2BE
FAM41C	FERMT2	FSIP1	GDF1	GORASP1	HACL1	HIST3H3
FAM43A	FGF14	FST	GDF11	GORASP2	HADH	HIVEP1
FAM46A	FGFBP2	FTHL3	GDF7	GOT1	HAGH	HLA-B
FAM46C	FGFR1	FTL	GDNF	GOT2	HAGHL	HLA-DPB2
FAM49B	FGFR1OP	FTSJD1	GDPD5	GPATCH1	HAMP	HLA-F
FAM54A	FGFR4	FUBP1	GEN1	GPATCH3	HAND2	HLA-H
FAM54B	FGFRL1	FUK	GFI1	GPHN	HAUS3	HLA-J
FAM55C	FIBCD1	FUT8	GFPT2	GPR107	HAUS6	HLA-L
FAM55D	FIS1	FXR1	GFRA2	GPR108	HAUS8	HMBS
FAM59A	FKBP10	FXR2	GGA3	GPR133	HCCA2	HMG20A
FAM64A	FKBP2	FXYD5	GGT1	GPR137	HCG18	HMGB1L1
FAM65A	FKBP3	FYTTD1	GGTLC1	GPR137B	HCG22	HMGN1
FAM65B	FLG	FZD3	GHITM	GPR137C	HCG26	HMGN3
FAM72B	FLII	FZD5	GHR	GPR153	HCG27	HMGXB3
FAM73B	FLJ25363	FZD7	GIMAP7	GPR155	HCG9	HMGXB4
FAM76A	FLJ31306	FZR1	GIN1	GPR157	HCN1	HNF1B
FAM7A2	FLJ39582	G3BP1	GIN51	GPR161	HCN2	HNRNPA0
FAM82A2	FLJ41350	GAA	GIPR	GPR177	HCN3	HNRNPA1
FAM82B	FLJ41603	GABARAP	GJA3	GPR63	HDAC1	HNRNPCL1
FAM83H	FLJ43390	GABARAPL2	GJB2	GPRC5B	HDAC10	HNRNPF
FAM86A	FLJ44606	GABARAPL3	GLB1	GPRC5D	HDAC4	HNRNPH1
FAM91A1	FLJ45244	GABBR1	GLB1L2	GPS2	HDGFRP3	HNRNPK
FAM96B	FLJ90757	GABPB1	GLB1L3	GPSM3	HEATR2	HNRNPL
FANCC	FLOT1	GABPB2	GLI3	GPX1	HEATR6	HNRNPM
FANK1	FLYWCH1	GABRA5	GLIS2	GPX3	HEATR7A	HNRNPU
FAR1	FLYWCH2	GABRD	GLOD4	GPX6	HEBP2	HOOK2
FARP1	FMN1	GAD2	GLP1R	GRASP	HELLS	HOXA1
FASN	FMN2	GADD45B	GLRX3	GRHPR	HELQ	HOXB13
FASTK	FN3KRP	GAK	GLRX5	GRID1	HERC2	HOXB2
FASTKD2	FNBP4	GALC	GLT1D1	GRID2IP	HERC3	HOXB4
FASTKD5	FNDC3B	GALNT10	GLT8D1	GRIN2A	HERPUD2	HOXB7
FAT1	FNDC4	GALNT14	GLTPD1	GRIN2D	HES3	HOXC11
FAT2	FNIP2	GALNT8	GLYCTK	GRM8	HES6	HOXD1
FAT4	FNTA	GALNTL6	GMCL1	GRN	HEXIM2	HP1BP3
FBLIM1	FNTB	GANC	GMEB2	GRSF1	HGSNAT	HPCAL1
FBN1	FOXBI	GAPDH	GML	GSR	HHLA3	HPCAL4

Figure 17-4

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HPS1	IL15RA	JAZF1	KIAA1191	KPNA3	LNPEP	LOC644936
HPS5	IL17RA	JMJD1C	KIAA1274	KRAS	LOC100129935	LOC646762
HPX	IL27RA	JMJD5	KIAA1324L	KRIT1	LOC100130093	LOC647979
HRK	ILDR1	JMJD6	KIAA1328	KRT14	LOC100130581	LOC650368
HRNBP3	ILF3	JMY	KIAA1409	KRT72	LOC100130987	LOC728392
HS3ST1	IMP4	JOSD1	KIAA1429	KRT8	LOC100133091	LOC728411
HS3ST4	IMPA2	JRK	KIAA1462	KRTAP4-7	LOC100133315	LOC728723
HS3ST5	INADL	JUN	KIAA1522	KRTAP4-8	LOC100133991	LOC728927
HS6ST1	ING1	KANK2	KIAA1530	KRTAP5-7	LOC100134229	LOC729121
HSD17B12	ING2	KARS	KIAA1543	KRTAP6-1	LOC100216001	LOC729156
HSDL1	INHA	KATNAL2	KIAA1609	KSR2	LOC100216545	LOC729234
HSF2	INO80	KBTBD3	KIAA1712	KY	LOC100268168	LOC729603
HSP90AB1	INPP1	KBTBD6	KIAA1751	KYNU	LOC100329108	LOC729991-MEF2
HSPA14	INPP4B	KBTBD7	KIAA1804	L1TD1	LOC100329109	LOC731789
HSPA1A	INS-IGF2	KCNAB2	KIAA1841	LAP3	LOC126536	LOC91316
HSPA1L	INSM2	KCNAB3	KIAA1949	LARP1	LOC143666	LOC92973
HSPA6	INTS1	KCNG3	KIAA1967	LARS	LOC150776	LONP1
HSPBAP1	INTS2	KCNIP2	KIDINS220	LASS2	LOC151174	LOXL2
HSPC157	INTS6	KCNJ10	KIF11	LASS4	LOC151534	LPAR2
HSPD1	INTS7	KCNJ11	KIF13A	LASS6	LOC154761	LPAR6
HSPE1	INVS	KCNJ12	KIF13B	LATS2	LOC202181	LPCAT1
HSPG2	IP6K2	KCNJ4	KIF16B	LBH	LOC220429	LPCAT4
HTR7	IPO4	KCNJ9	KIF17	LCE1A	LOC285550	LRIG2
HTR7P	IPO5	KCNK13	KIF18B	LCE1E	LOC285830	LRIT1
HTT	IPO7	KCNK15	KIF21A	LCE2B	LOC286016	LRP10
HUNK	IPPK	KCNK9	KIF22	LCLAT1	LOC338758	LRP5
HVCN1	IQCE	KCNMB4	KIF23	LCOR	LOC339535	LRRC26
HYI	IQCF1	KCNN1	KIF26B	LCORL	LOC340357	LRRC28
ICA1	IQCG	KCNQ1	KIF3C	LDHAL6A	LOC342346	LRRC33
ICA1L	IQCK	KCNQ3	KIF9	LDHD	LOC344967	LRRC8B
ICAM3	IQSEC1	KCNQ4	KIFC1	LDLRAP1	LOC348926	LRRFIP1
ICAM5	IRAK3	KCNQ5	KIFC3	LDOC1L	LOC349114	LRRFIP2
ICK	IRAK4	KCNT2	KLC1	LENG1	LOC388428	LRRN1
ID2B	IRF2	KCTD12	KLC2	LEPROTL1	LOC388588	LRTOMT
IDE	IRF2BP1	KCTD18	KLC4	LGALS14	LOC388789	LSG1
IER3	IRF4	KCTD2	KLF10	LGALS7	LOC388796	LSM10
IFI27L1	IRGM	KCTD21	KLF17	LGALS7B	LOC399744	LSM14B
IFIT5	IRX3	KCTD6	KLF3	LGR4	LOC400657	LSM2
IFNAR1	ISOC1	KDELC2	KLF5	LHX4	LOC400927	LTBP1
IFRD2	ISOC2	KDM2B	KLF7	LIAS	LOC401052	LTC4S
IFT122	ITCH	KDM5B	KLF9	LIFR	LOC401097	LUC7L2
IFT140	ITFG3	KDM6B	KLHDC2	LIMD2	LOC401127	LUC7L3
IFT57	ITGA1	KIAA0020	KLHDC3	LIN52	LOC401431	LUZP1
IFT80	ITGA11	KIAA0141	KLHDC4	LIPT1	LOC404266	LY6H
IFT88	ITGAM	KIAA0182	KLHL11	LITAF	LOC440905	LY75
IGF1R	ITGB5	KIAA0232	KLHL17	LIX1L	LOC440910	LYN
IGF2BP1	ITM2B	KIAA0319	KLHL20	LLGL1	LOC440926	LYPD3
IGFBP7	ITM2C	KIAA0355	KLHL25	LLGL2	LOC441089	LYRM1
IGFL2	ITPR2	KIAA0513	KLHL26	LMAN2	LOC441208	LYRM2
IGFL3	ITSN1	KIAA0664	KLK10	LMBRD2	LOC441455	LYST
IGSF3	IWS1	KIAA0754	KLRC2	LMF1	LOC441601	LZTR1
IGSF8	JAGN1	KIAA0892	KLRG2	LMF2	LOC641367	MACF1
IKBIP	JAK2	KIAA0895L	KNDC1	LMO4	LOC641746	MACROD1
IKBKB	JAK3	KIAA1012	KNTC1	LMOD1	LOC643406	MAD1L1
IKZF5	JAM2	KIAA1026	KPNA2	LMX1B	LOC644669	MAD2L1

Figure 17-5

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MAD2L1BP	MCOLN1	MIR142	MRPL37	MYRIP	NDUFB6	NPBWR1
MAD2L2	MCOLN3	MIR1470	MRPL38	MYST3	NEAT1	NPC1
MAFG	MDGA2	MIR17HG	MRPL44	MYST4	NEDD4L	NPC2
MAFK	MDK	MIR1908	MRPS17	MYT1L	NEDD8	NPFFR1
MAGI1	MDM2	MIR210	MRPS24	MZF1	NEFH	NPHP4
MAGI3	MDN1	MIR24-2	MRPS28	N4BP2	NEU1	NPM1
Magmas	ME2	MIR375	MRPS31	N6AMT2	NEURL	NPR1
MAN2B2	MEA1	MIR492	MRPS7	NAA20	NEUROG1	NPR3
MAN2C1	MECOM	MIR517A	MRPS9	NAA30	NF1	NQO2
MANEAL	MED1	MIR517B	MRS2P2	NAAA	NF2	NR1D1
MAP1S	MED13	MIR517C	MS4A10	NAALADL1	NFATC1	NR2C1
MAP2K4	MED24	MIR518A1	MSH3	NACAP1	NFATC2	NR2C2AP
MAP3K1	MED8	MIR518A2	MSH5	NANOS1	NFATC2IP	NR2F1
MAP3K11	MED9	MIR518F	MSH6	NANP	NFATC4	NRBF2
MAP3K12	MEGF10	MIR519A1	MSI2	NAP1L4	NFE2L1	NRIP2
MAP3K14	MEGF11	MIR519C	MSL1	NAP1L5	NFIC	NRN1
MAP3K6	MEGF6	MIR520A	MSL2	NAPA	NFIL3	NRTN
MAP4	MEIS2	MIR596	MSRB3	NARF	NFKB2	NSD1
MAP4K1	MEP1A	MIR618	MST1P2	NARG2	NFKBIA	NSMAF
MAPK1	MEPCE	MIR632	MSTO2P	NARS	NFKBIE	NSMCE4A
MAPK11	MESDC1	MIR636	MT4	NAT2	NFKBIL1	NSUN2
MAPK8IP1	MESP1	MIR639	MTA1	NBL1	NFKBIL2	NT5DC3
MAPK8IP2	METRNL	MIS12	MTA2	NBN	NFYC	NT5M
MAPKAPK2	METT10D	MITF	MTCH1	NBPF1	NGF	NTF4
MAPKAPK5	METTL13	MKI67IP	MTDH	NBPF14	NGLY1	NTM
MAPRE2	METTL2A	MKL2	MTERFD3	NBPF16	NHEDC2	NTN4
MAPRE3	METTL2B	MKNK2	MTF2	NBPF3	NHLH1	NUBP2
MAPT	MEX3B	MKRN1	MTFMT	NBPF9	NHLRC3	NUCKS1
MARK3	MEX3C	MLKL	MTHFD2	NBR1	NHP2L1	NUDT22
MAST3	MEX3D	MLLT1	MTHFD2L	NCAM1	NIF3L1	NUDT3
MAT2B	MFAP2	MLLT10	MTHFSD	NCAPD2	NINJ2	NUDT6
MATK	MF12	MLLT6	MTL5	NCAPD3	NIPA1	NUDT8
MATN1	MFSD10	MLX	MTO1	NCAPG	NIPA2	NUDT9
MAVS	MFSD2A	MMP19	MTR	NCAPH2	NIPSNAP3B	NUFIP1
MBLAC1	MFSD5	MMP21	MTRF1L	NCBP2	NIT2	NUFIP2
MBLAC2	MFSD8	MNX1	MTUS2	NCEH1	NKAIN2	NUP133
MBNL1	MGA	MOBK13	MUC1	NCF1C	NKAIN3	NUP153
MBOAT2	MGAT4A	MOC52	MUDENG	NCK1	NKD2	NUP188
MBOAT7	MGAT4C	MOGS	MUTYH	NCKIPSD	NKIRAS1	NUP210
MBP	MGC23284	MORG1	MVP	NCL	NKX2-8	NUP93
MBTD1	MGLL	MORN3	MXD3	NCOA5	NLK	NUS1
MCAM	MGMT	MORN4	MYADM	NCRNA00115	NLRP7	NVL
MCART1	MIA	MOV10	MYADML2	NCRNA00164	NMB	NXF1
MCART3P	MICA	MOXD1	MYBL1	NCRNA00171	NME1	NXN
MCC	MICAL1	MPDU1	MYC	NCRNA00173	NMNAT1	OAS1
MCCD1	MICAL3	MPL	MYCNOS	NCRNA00189	NMNAT2	OAS3
MCF2L	MICALCL	MPPE1	MYH10	NDE1	NMT1	OAT
MCHR1	MICALL2	MPV17L2	MYH9	NDEL1	NMT2	OAZ2
MCL1	MICB	MRAP2	MYL12A	NDN	NMU	OAZ3
MCM10	MIIP	MRC2	MYNN	NDRG1	NOL11	OBFC1
MCM3AP	MIOS	MRE11A	MYO10	NDUFA2	NOL7	OBSL1
MCM3APAS	MIR1253	MRFAP1	MYO19	NDUFA3	NOM1	OCEL1
MCM6	MIR1275	MRPL12	MYO1G	NDUFA6	NOS3	OCIAD1
MCM7	MIR1297	MRPL16	MYO5A	NDUFAB1	NOSTRIN	OCIAD2
MCM8	MIR1307	MRPL18	MYO9B	NDUFB5	NOTCH3	ODC1

Figure 17-6

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ODF2	PAPPA2	PFDN1	PLCD1	PON2	PRDX3	PSMG1
ODZ4	PARD6G	PFKFB3	PLCH2	POP1	PRDX5	PSMG2
OGDH	PARP1	PFKP	PLD2	POU2F1	PRDX6	PSPC1
OGFOD1	PARP11	PFN2	PLD3	POU3F2	PRDXDD1P	PTBP2
OGG1	PARP15	PGAM1	PLEC1	PP14571	PRELID1	PTCH1
OLFM2	PARVB	PGAP2	PLEKHA1	PPA1	PRELID2	PTCH2
OLFML2B	PATE2	PGBD2	PLEKHA5	PPAPDC1A	PREX1	PTEN
OMP	PATE4	PGD	PLEKHA6	PPARGC1B	PRHOXNB	PTGES
ONECUT2	PAX2	PGLS	PLEKHA7	PPCDC	PRIC285	PTGES2
OPTN	PAX5	PGM1	PLEKHB1	PPCS	PRICKLE1	PTGES3
OR10G8	PAX6	PGM3	PLEKHG4	PPFIA1	PRIM1	PTGFRN
OR12D2	PAX7	PGS1	PLEKHG6	PPFIBP2	PRKACA	PTH1R
OR1A2	PCBP2	PHAX	PLEKHH1	PPHLN1	PRKAG2	PTK2
OR2L8	PCDH15	PHC1	PLEKHH3	PPIB	PRKCA	PTMA
OR2M2	PCDH21	PHC2	PLEKHM1	PPIE	PRKCB	PTMS
OR2V2	PCDP1	PHF10	PLEKHO2	PPIL2	PRKCD	PTPMT1
OR52H1	PCGF3	PHF13	PLGLA	PPIL4	PRKCG	PTPN1
OR5H1	PCGF6	PHF14	PLIN3	PPM1F	PRKCCQ	PTPN12
OR6P1	PCM1	PHF15	PLK4	PPM1J	PRKCZ	PTPN22
OR8S1	PCMT1	PHF17	PLXNA1	PPM1K	PRKD1	PTPN6
ORC6L	PCMTD1	PHF19	PLXNA2	PPM1L	PRKRA	PTPN7
ORMDL3	PCNP	PHF21A	PLXNA4	PPM1M	PRKRIR	PTPRG
OSBPL11	PCNT	PHF21B	PLXNC1	PPP1CC	PRMT1	PTPRJ
OSBPL2	PCOTH	PHLDB1	PLXND1	PPP1R12B	PRND	PTPRN2
OSBPL9	PCTP	PHLPP2	PMAIP1	PPP1R12C	PROCA1	PUM1
OSCAR	PCYT1A	PHPT1	PMS2	PPP1R14B	PROKR2	PURA
OSGIN1	PDCD2L	PHTF2	PMS2L3	PPP1R15B	PROSC	PURB
OSTCL	PDCD6	PI4K2B	PMS2L5	PPP1R16B	PRPF3	PURG
OTOP2	PDCD6IP	PI4KAP2	PNKD	PPP1R2P1	PRPF31	PUS1
OTUB1	PDCD7	PIBF1	PNKP	PPP1R3B	PRPF38B	PUS10
OTUD1	PDE2A	PICK1	PNLIP	PPP1R3E	PRPF40B	PUS7
OTUD3	PDE3B	PIGG	PNMT	PPP1R9B	PRPF6	PVRL1
OVOL1	PDE4DIP	PIGO	PNN	PPP2CA	PRR11	PVRL2
OXSRI	PDE6D	PIGP	PNPLA2	PPP2R3C	PRR14	PVRL3
P2RX2	PDE7A	PIGT	PNPLA7	PPP2R5A	PRR3	PVT1
P2RX4	PDGFA	PIGV	PNPLA8	PPP2R5C	PRR5	PWWP2B
P2RY1	PDGFRL	PIGX	PODXL	PPP3CB	PRRC1	PXMP3
P4HA3	PK2	PIGY	POGK	PPP3CC	PRRT2	PYCR1
P4HB	PDLIM1	PIK3AP1	POLD1	PPP3R1	PRRT4	PYGB
PA2G4	PDLIM5	PIK3R5	POLD3	PPP4C	PRSS1	PYY
PABPC4	PDPK1	PILRB	POLDIP2	PPP4R4	PRSS48	QKI
PABPN1	PDX1	PIN1	POLDIP3	PPP5C	PSAT1	QPCTL
PACS2	PDXDC1	PINK1	POLR2C	PPPDE1	PSD3	QRICH1
PACSIN1	PDXDC2	PION	POLR2E	PPPDE2	PSD4	QRS11
PACSIN3	PDXK	PIP5K1A	POLR2G	PPT2	PSG3	QSOX1
PAG1	PDZD8	PITPNB	POLR2I	PPTC7	PSG6	QTRT1
PAIP2B	PEBP1	PITRM1	POLR3C	PPY2	PSIP1	RAB11FIP1
PAK1	PEL12	PKD2	POLR3D	PQLC1	PSMA3	RAB11FIP5
PALM	PEPD	PKDCC	POLR3K	PQLC3	PSMB1	RAB12
PAN2	PER2	PKM2	POLRMT	PRAGMIN	PSMC4	RAB14
PANK2	PET117	PKN1	POM121C	PRAMEF22	PSMC5	RAB18
PANX1	PEX10	PKNOX2	POM121L10P	PRC1	PSMD1	RAB1A
PANX2	PEX19	PLAGL1	POMC	PRDM16	PSMD11	RAB1B
PAOX	PEX26	PLAU	POMT2	PRDM2	PSMD4	RAB27A
PAPOLA	PEX7	PLCB1	POMZP3	PRDX1	PSME3	RAB2A

Figure 17-7

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RAB37	RBPM52	RNF152	RQCD1	SCARNA20	SFRP5	SLC25A17
RAB39	RCAN3	RNF157	RRAGC	SCCPDH	SFRS1	SLC25A19
RAB3D	RCBTB1	RNF165	RRBP1	SCD	SFRS12	SLC25A2
RAB3GAP1	RCC2	RNF185	RREB1	SCGB1D1	SFRS13A	SLC25A28
RAB40B	RCOR1	RNF187	RRM1	SCHIP1	SFRS14	SLC25A32
RAB40C	RCOR2	RNF215	RRM2B	SCIN	SFRS6	SLC25A33
RAB42	RDBP	RNF216L	RRN3	SCMH1	SFRS7	SLC25A40
RAB43	RDH10	RNF220	RRN3P3	SCN8A	SFRS8	SLC25A42
RAB4B	RDH14	RNF24	RRP1	SCRIB	SFTPB	SLC25A44
RAB7A	RECQL	RNF25	RRP7B	SCRN2	SCEF	SLC26A11
RABL4	REEP1	RNF34	RSPH1	SCRT1	SGK1	SLC26A4
RAD17	REEP3	RNF39	RSPO4	SCYL1	SGSM3	SLC26A6
RAD23B	REG3G	RNF4	RSPRY1	SCYL2	SGTB	SLC27A3
RAD52	REL	RNF44	RSU1	SDC4	SH2B3	SLC29A1
RADIL	RELA	RNF8	RTKN2	SDCBP	SH3BP4	SLC29A2
RAGE	RELL1	RNFT1	RTN1	SDCCAG3	SH3BP5	SLC29A4
RALBP1	REM2	RNFT2	RTN2	SDCCAG8	SH3GL1	SLC2A4
RALGAPB	RER1	RNGTT	RTN4RL2	SDF2L1	SH3GLB2	SLC2A5
RALGPS1	RET	RNMTL1	RTTN	SDHA	SH3PXD2A	SLC2A6
RALY	RFPL3	RNU5E	RUFY1	SDHAP3	SH3PXD2B	SLC2A9
RANBP2	RFWD2	ROPN1L	RUFY2	SDK1	SH3TC1	SLC30A9
RANBP9	RFWD3	RORA	RUNDC2A	SDR42E1	SHANK2	SLC35D1
RANGAP1	RFX8	RP5-1022P6.2	RUNX2	SEC11A	SHANK3	SLC35E4
RAP1A	RG9MTD1	RPA2	RUSC1	SEC14L1	SHBG	SLC35F5
RAP1B	RGL2	RPA3	RUVBL2	SEC16A	SHFM1	SLC37A3
RAP1GDS1	RGL3	RPAIN	RWDD1	SEC23A	SHISA3	SLC38A10
RAP2A	RGMA	RPF1	RWDD2A	SEC23B	SHIAH2	SLC38A3
RAPGEF6	RGNEF	RPF2	RXRA	SEC63	SIGLEC11	SLC38A6
RARA	RGPD2	RPGRIP1	RYR1	SEL1L	SIGLEC8	SLC38A7
RARB	RGPD3	RPH3AL	S1PR1	SELK	SIK1	SLC39A11
RARRES1	RGS17	RPL10A	S1PR2	SELT	SIN3A	SLC39A6
RASA2	RGS7	RPL10L	S1PR5	SEMA3A	SIRT2	SLC39A7
RASGEF1A	RGS9	RPL13AP20	SACM1L	SEMA3F	SIRT4	SLC41A3
RASGEF1B	RHAG	RPL13AP5	SACS	SEMA4C	SIX2	SLC43A1
RASGEF1C	RHBDF2	RPL14	SAFB2	SEMA5B	SKA1	SLC43A2
RASGRP3	RHBDL3	RPL18	SALL3	SENP2	SKI	SLC44A1
RASSF1	RHEB	RPL22L1	SALL4	SEPHS1	SKP1	SLC44A2
RASSF4	RHOC	RPL23	SAMD10	SEPSECS	SLC10A4	SLC45A4
RASSF6	RHOD	RPL23AP53	SAMD12	SEPX1	SLC10A7	SLC4A1AP
RBBP4	RHOG	RPL23AP82	SAMD4A	SERAC1	SLC12A5	SLC6A1
RBCK1	RHOT2	RPL31	SAP30	SERINC4	SLC12A9	SLC6A19
RBM12B	RHPN1	RPL32	SAPS2	SERPINB2	SLC13A5	SLC6A2
RBM14	RIC8A	RPL36	SAPS3	SERPINB6	SLC16A10	SLC6A6
RBM15	RICS	RPP21	SART1	SESN3	SLC19A1	SLC7A14
RBM24	RICTOR	RPRD1B	SASH1	SETD1A	SLC19A2	SLC8A1
RBM27	RILPL2	RPS11	SATB1	SETD1B	SLC1A2	SLC9A3
RBM34	RIMBP2	RPS12	SATB2	SETD5	SLC1A4	SLC03A1
RBM38	RING1	RPS13	SAV1	SETD7	SLC1A5	SLC05A1
RBM42	RMND1	RPS15	SBF1	SETMAR	SLC22A15	SLFN12L
RBM44	RMND5A	RPS15A	SBK2	SEZ6L2	SLC22A18AS	SLFN5
RBM5	RNASEH2B	RPS21	SBNO2	SF1	SLC22A3	SLIT1
RBM6	RNASEN	RPS6KA2	SCAF1	SF3B1	SLC22A4	SLK
RBM9	RNF139	RPS7	SCAMP1	SFI1	SLC22A5	SLTM
RBPJ	RNF14	RPS9	SCARB1	SFMBT1	SLC23A2	SMAD3
RBPJL	RNF141	RPTOR	SCARF2	SFMBT2	SLC25A16	SMAD7

Figure 17-8

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SMAGP	SNX6	STAG3	TAF4	TFG	TMEM214	TPMT
SMARCA4	SNX8	STAP2	TAGLN2	TFPI	TMEM217	TPRKB
SMARCC2	SOCS1	STARD3	TANC1	TGFA	TMEM219	TPRX1
SMARCD2	SOCS4	STARD9	TAP2	TGFBR1	TMEM222	TPST2
SMARCE1	SOLH	STAT2	TAPT1	TGFBR2	TMEM229B	TRA2A
SMC3	SORBS3	STAT5B	TARM1	TGOLN2	TMEM231	TRADD
SMCR7	SOX18	STAU1	TAS1R3	THADA	TMEM43	TRAFD1
SMCR8	SOX2	STAU2	TAS2R43	THAP9	TMEM50B	TRAM2
SMG6	SOX5	STBD1	TATDN3	THBS1	TMEM57	TRANK1
SMOC2	SP1	STEAP2	TAX1BP1	THBS2	TMEM59	TRAPPC1
SMPD3	SP100	STK10	TBC1D1	THOC7	TMEM61	TRAPPC2L
SMPD4	SP140L	STK11	TBC1D10C	THRA	TMEM65	TRAPPC6A
SMURF2	SP4	STK17B	TBC1D13	THSD4	TMEM68	TRAPPC6B
SMYD3	SP8	STK24	TBC1D14	THSD7B	TMEM80	TRAPPC9
SNAPIN	SPATA5L1	STK25	TBC1D15	THUMPD1	TMEM82	TREM1
SND1	SPDYE4	STK32C	TBC1D16	THUMPD2	TMEM86A	TRERF1
SNHG12	SPEG	STK35	TBC1D17	THYN1	TMEM87B	TRIB2
SNHG3	SPG11	STK40	TBC1D2	TIMM22	TMEM93	TRIM11
SNHG4	SPHK1	STOX2	TBC1D26	TIMP2	TMIE	TRIM26
SNHG5	SPIRE2	STRBP	TBC1D3P2	TINF2	TMPRSS2	TRIM27
SNHG6	SPN	STRN3	TBCA	TIPIN	TMPRSS4	TRIM28
SNHG9	SPPL2A	STRN4	TBCB	TIRAP	TMSL3	TRIM35
SNIP1	SPPL2B	STX19	TBCC	TJP3	TMUB1	TRIM36
SNORA14B	SPR	STX1A	TBCD	TLCD1	TMX1	TRIM37
SNORA26	SPRED1	STX1B	TBCEL	TLE2	TNFAIP8L1	TRIM39
SNORA76	SPRED2	STXBP4	TBKBP1	TLE3	TNFRSF10C	TRIM43
SNORD114-29	SPRR2D	STYX	TBL1XR1	TLE4	TNFRSF10D	TRIM44
SNORD114-31	SPRY2	SUCLG2	TBL3	TLN1	TNFRSF12A	TRIM45
SNORD115-1	SPSB1	SUDS3	TBXAS1	TM7SF2	TNFRSF13B	TRIM47
SNORD115-11	SPSB2	SUFU	TCEA3	TMBIM1	TNIP2	TRIM54
SNORD115-14	SPTB	SUGT1L1	TCEB1	TMBIM4	TNKS2	TRIM65
SNORD115-15	SPTBN4	SUGT1P1	TCEB3CL	TMC5	TNPO1	TRIM7
SNORD115-17	SQRDL	SULF1	TCF12	TMC6	TNPO3	TRIM71
SNORD115-19	SQSTM1	SULT1A2	TCF25	TMED1	TNRC18	TRIOBP
SNORD115-3	SRD5A3	SULT1A3	TCF3	TMED10	TNRC6A	TRIP10
SNORD115-38	SRF	SULT2B1	TCF7	TMED5	TNRC6B	TRMT12
SNORD115-39	SRI	SUPT16H	TCTA	TMED9	TNS3	TRNT1
SNORD115-44	SRP68	SUPT7L	TCTE1	TMEFF1	TNXB	TROAP
SNORD115-6	SRPK2	SUV39H2	TCTEX1D2	TMEM107	TOMM40	TROVE2
SNORD115-7	SS18	SUV420H1	TDH	TMEM108	TOMM5	TRPM1
SNORD115-8	SSB	SUZ12	TDP1	TMEM111	TOMM70A	TRPM4
SNORD116-2	SSBP4	SYCE2	TDRD10	TMEM116	TOP1P2	TSC2
SNORD116-8	SSH2	SYCP3	TEAD1	TMEM134	TOP2B	TSC22D1
SNORD32B	SSH3	SYDE1	TEAD3	TMEM136	TOPBP1	TSEN15
SNORD38A	SSR1	SYF2	TECPR2	TMEM143	TOR1A	TSG101
SNORD42B	SSX2IP	SYNGAP1	TECTA	TMEM144	TOR2A	TSGA13
SNORD74	ST13	SYNGR3	TERF2	TMEM145	TOX2	TSNARE1
SNRPA1	ST20	SYNPO	TERF2IP	TMEM151B	TP53BP1	TSNAXIP1
SNRPC	ST3GAL1	SYT9	TERT	TMEM163	TP53I13	TSPAN16
SNRPD1	ST3GAL2	SYTL2	TEX2	TMEM179B	TP53RK	TSPAN17
SNUPN	ST3GAL4	T	TEX264	TMEM18	TPBG	TSPAN18
SNX14	ST5	TACC2	TFAP4	TMEM181	TPCN1	TSPAN3
SNX19	ST8SIA4	TAF11	TFB1M	TMEM189	TPCN2	TSPAN31
SNX22	ST8SIA6	TAF15	TFDP1	TMEM201	TPD52	TSPAN4
SNX3	STAG1	TAF1C	TFEB	TMEM205	TPK1	TSPAN5

Figure 17-9

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TSR1	UBLCP1	VPS37D	YAP1	ZMPSTE24	ZNF429	ZNF643
TSSC1	UBP1	VPS52	YARS	ZMYM4	ZNF431	ZNF649
TSSC4	UBR3	VPS54	YBX2	ZMYM5	ZNF433	ZNF653
TSSK2	UBTD2	VRK1	YIPF5	ZNF10	ZNF436	ZNF662
TTC14	UBTF	VSNL1	YLPM1	ZNF100	ZNF439	ZNF664
TTC22	UBXN1	VTA1	YPEL1	ZNF101	ZNF440	ZNF665
TTC28	UBXN11	VTI1B	YPEL3	ZNF107	ZNF441	ZNF669
TTC30A	UBXN6	WASF1	YTHDF3	ZNF12	ZNF444	ZNF689
TTC31	UCK1	WASH3P	YWHAH	ZNF133	ZNF462	ZNF7
TTC39A	UCRC	WASH5P	YWHAQ	ZNF14	ZNF467	ZNF70
TTC7B	UFC1	WASL	YWHAZ	ZNF141	ZNF480	ZNF701
TTK	UFSP2	WBSCR22	YY1	ZNF143	ZNF484	ZNF702P
TTLL1	UGGT1	WDR20	YY1AP1	ZNF146	ZNF485	ZNF703
TTLL6	UGT1A10	WDR26	ZAR1L	ZNF148	ZNF487	ZNF705D
TTPAL	UHRF1BP1	WDR27	ZBBX	ZNF184	ZNF490	ZNF706
TTR	ULBP2	WDR34	ZBED5	ZNF195	ZNF491	ZNF709
TTYH3	ULBP3	WDR4	ZBTB1	ZNF20	ZNF493	ZNF716
TUB	ULK1	WDR47	ZBTB12	ZNF207	ZNF496	ZNF717
TUBA1A	UMPS	WDR51A	ZBTB17	ZNF213	ZNF498	ZNF718
TUBA1B	UNC80	WDR52	ZBTB2	ZNF219	ZNF511	ZNF735
TUBA3C	UNC84A	WDR53	ZBTB4	ZNF22	ZNF514	ZNF737
TUBA3D	UNKL	WDR55	ZBTB40	ZNF224	ZNF521	ZNF738
TUBA4B	UPK3B	WDR59	ZBTB41	ZNF229	ZNF527	ZNF747
TUBB	UQCR	WDR60	ZBTB42	ZNF235	ZNF528	ZNF749
TUBB1	URB2	WDR62	ZBTB45	ZNF236	ZNF530	ZNF761
TUBB4	USF2	WDR65	ZBTB46	ZNF252	ZNF534	ZNF764
TUBB6	USP1	WDR7	ZBTB7A	ZNF254	ZNF540	ZNF766
TUBD1	USP15	WDR70	ZBTB9	ZNF257	ZNF541	ZNF768
TUBGCP2	USP18	WDR73	ZC3H11A	ZNF259	ZNF543	ZNF777
TUBGCP6	USP19	WDR74	ZC3H12C	ZNF26	ZNF547	ZNF784
TXLNA	USP2	WDR8	ZC3HAV1L	ZNF264	ZNF549	ZNF787
TXNIP	USP32	WDR82	ZCCHC14	ZNF267	ZNF550	ZNF788
TXNL4A	USP33	WDTC1	ZCCHC2	ZNF276	ZNF555	ZNF8
TXNRD1	USP34	WDYHV1	ZCCHC24	ZNF28	ZNF557	ZNF80
TYK2	USP36	WEE1	ZDHH1C1	ZNF280B	ZNF559	ZNF808
TYMS	USP4	WHAMM	ZDHH1C16	ZNF286B	ZNF562	ZNF813
TYRO3	USP42	WHSC1	ZDHH1C19	ZNF295	ZNF564	ZNF814
TYROBP	USP43	WHSC2	ZDHH1C23	ZNF3	ZNF565	ZNF816A
U2AF2	USP49	WIZ	ZDHH1C3	ZNF311	ZNF566	ZNF821
UAP1	USP53	WNK4	ZDHH1C4	ZNF317	ZNF57	ZNF826
UBA5	USP7	WNT11	ZDHH1C5	ZNF321	ZNF570	ZNF827
UBA52	UTP15	WNT3A	ZDHH1C7	ZNF322B	ZNF578	ZNF829
UBASH3B	UTP3	WNT5A	ZEB1	ZNF323	ZNF583	ZNF83
UBB	UTRN	WRB	ZFAND2B	ZNF324	ZNF584	ZNF837
UBC	VAC14	WRN	ZFAND3	ZNF335	ZNF589	ZNF839
UBD	VAPA	WRNIP1	ZFHX3	ZNF33A	ZNF593	ZNF845
UBE2H	VARS	WSCD2	ZFP1	ZNF33B	ZNF594	ZNF860
UBE2I	VASH1	WTAP	ZFP36L2	ZNF354A	ZNF605	ZNF876P
UBE2K	VCPIP1	WWC1	ZFP64	ZNF358	ZNF609	ZNF880
UBE2Q1	VDAC3	XAB2	ZFYVE19	ZNF366	ZNF610	ZNF90
UBE3A	VGLL4	XBP1	ZFYVE9	ZNF384	ZNF611	ZNF98
UBIAD1	VIPR2	XKR5	ZHX2	ZNF385A	ZNF618	ZNHIT1
UBL3	VKORC1L1	XRCC3	ZKSCAN1	ZNF385B	ZNF619	ZNHIT3
UBL5	VPS18	XRN1	ZKSCAN5	ZNF395	ZNF627	ZSCAN2
UBL7	VPS37C	YAF2	ZMIZ1	ZNF397	ZNF638	ZSCAN29

Figure 17-10

12 Mar 2026
ZSCAN5B
ZSWIM1
ZSWIM7
ZWILCH
ZWINT
ZXDC
ZYG

2026201866

Gene	Correlation	Mapinfo	Chromosome	Gene	Correlation	Mapinfo	Chromosome
MCM10	-0.158183678	13203459	10	Gene			
GLTPD1	-0.158077141	1260496	1	BMS1	-0.185834649	26172397	6
SAMD4A	-0.15796925	55033137	14		-0.172882298	43278214	10
MATN1	0.157968394	43361618	10	RPP21	-0.172168945	34191979	6
HCG27	-0.157826226	31191648	1	PLEC1	0.17081525	30312857	6
RUNDC2A	-0.157753658	67745999	11	FAH	0.170417571	145018285	8
	-0.157753366	31165843	6	SLC9A3	0.166645603	80445147	15
	0.157619259	12070685	16	NR2F1	0.165587106	524683	5
	0.15730284	195380764	3	SLC4A1AP	0.165290855	92920498	5
FLYWCH1	-0.15715639	2972941	16	ZNF593	0.165117862	27906671	2
CSTF3	-0.156891668	33183110	11	DUSP18	-0.16388116	26496298	1
RANBP9	0.156886635	13712174	6	LRP10	-0.163879852	31064165	22
ZFYVE19	-0.156885196	41099692	15	PRRC1	-0.162761622	23341280	14
ARPP19	-0.15688342	52861112	15	C21orf91	0.162356683	126853253	5
CCDC6	-0.156802852	61666667	10	CEBPZ	0.162213611	19192027	21
PON2	0.156799443	95064397	7	DGCR6L	-0.161405725	37458728	2
TLCD1	0.156755573	27053269	17	SAPS3	-0.161241262	20307980	22
UFC1	-0.156626247	161122156	1	ZNF496	-0.161035122	68228228	11
GLB1	0.156541726	113690888	4	ANO6	-0.1610061	247494983	1
CASZ1	-0.156537909	33138513	3	NBPF1	-0.16087252	45610071	12
EID2	0.156406513	10856739	1	NEU1	-0.160580305	16941426	1
VKORC1L1	-0.156119654	40030840	19	SUV39H2	0.160442832	31831876	6
CORO1B	0.156111043	65338716	7	GABBR1	-0.16042562	14921550	10
MIR518F	0.156106431	67211017	11	EXOSC9	0.160263001	29600642	6
LOC10013005	-0.156054823	54202347	19	FAM113A	-0.160131027	122722461	4
TAS2R43	-0.155978128	227915338	1	KIAA1191	-0.159960915	33217368	6
C17orf85	0.155859829	142092835	5	MEGF6	-0.159883389	2821434	20
JMJD6	-0.15573673	11244939	12	NFKBIL2	-0.159808113	175788722	5
SOX18	0.155647707	3749224	17	FAM41C	-0.159767459	3447740	1
WDR4	0.155558463	74722752	17	CUL5	0.15965711	145669602	8
GMPPA	0.155458296	62681243	20	GATA2	0.159570325	805102	1
	-0.155442677	44300012	21	CXXC5	-0.159465263	107880052	11
	-0.155385813	220363586	2	ZNF20	0.159406457	139028606	5
	-0.155247556	40950037	3	ADRBK1	-0.159405023	128211096	3
	-0.155225225	158649092	7	MAD2L2	0.159339878	12251201	19
	-0.155050672	68132796	15	LIFR	0.159131526	67034540	11
TERT	0.154937677	96889416	15	PHF10	-0.158916423	11741009	1
GNB1L	0.154921571	1295267	5		0.158619383	38556796	5
NANP	-0.154916257	19842652	22		-0.15846813	63392087	7
	-0.154890478	25604737	20		-0.158465591	170125165	6
					0.158350786	48463113	1

Figure 18-1

cg25270498	17	81037414	0.154850868	METRNL	cg11675492	20	60640074	0.153055593	TAF4
cg16246252	11	119535621	0.154835931	PVRL1	cg05874913	2	160569340	0.153047444	7-Mar
cg07483273	19	2901388	0.15482523	ZNF57	cg22037798	1	231473786	-0.153018104	C1orf124
cg14116162	11	64052260	0.154813114	BAD	cg09319020	17	7304467	-0.152929383	
cg16326998	7	5553266	0.154742278	FBXL18	cg14276772	2	10588646	0.15290302	ODC1
cg02445395	7	157659455	-0.154741029	PTPRN2	cg22704520	2	200820451	-0.152868301	C2orf60
cg19731367	10	95256484	0.15469021	CEP55	cg12459358	17	719896	0.152866944	
cg02994863	1	64059297	-0.154659001	PGM1	cg23572228	7	4923575	0.152850265	RADIL
cg11855759	17	9548802	0.154602589	USP43	cg15994267	1	805352	0.152794359	FAM41C
cg12822074	11	57243865	0.154588285	RTN4RL2	cg25653296	15	35413975	-0.152764061	
cg14694896	8	104427370	-0.154578413	SLC25A32	cg04479472	7	1231443	-0.152726596	
cg26105280	1	11159908	-0.15440444	EXOSC10	cg10945667	13	91999862	-0.152718728	MIR17HG
cg25753024	11	67070913	0.154332796	SSH3	cg26520012	10	42672589	0.152701062	
cg02881082	14	101694374	-0.154218759	FABP5	cg14804635	15	75747750	-0.152687177	SIN3A
cg23048068	8	82192604	-0.154203444	NCRNA00164	cg01043397	6	30689219	0.152650354	TUBB
cg18545992	2	133013028	-0.154183608	RORA	cg23966123	14	105886028	0.152642204	MTA1
cg08700690	15	60884630	-0.154106201	ERBB2IP	cg16063617	5	128430663	-0.152641525	ISOC1
cg22100652	6	28834404	0.154011378	AP4E1	cg13854983	2	136875315	-0.152597109	CXCR4
cg07172256	5	65220910	-0.153896215	CEBPZ	cg08224208	19	15218165	0.152595494	SYDE1
cg09951650	15	51200814	-0.153867717	MICALL2	cg10041390	10	89623018	-0.152572899	PTEN
cg05882878	2	37458821	-0.153736187	SERAC1	cg01026613	2	27255450	0.152543587	TMEM214
cg21535156	7	1499152	0.153696744	FASN	cg15062310	7	100450120	-0.152532561	SLC12A9
cg04246357	6	158589294	0.153694605	EHP1L1	cg18190323	4	113486291	0.152467613	C4orf21
cg25825740	17	80036910	-0.153670657	PDX1	cg25964984	22	30783371	0.152440628	RNF215
cg18765439	11	65343343	-0.153582145	CNBD1	cg13468174	19	58919984	-0.152435099	ZNF584
cg12815918	13	28498544	0.153549663	POLD1	cg17428043	1	180200104	-0.152423454	LHX4
cg20630812	8	87877422	-0.153539903	TUBB1	cg12576688	1	2344112	0.152423351	PEX10
cg06945456	19	50887879	0.153532538	SNORD115-7	cg25632648	11	77899776	-0.152399685	KCTD21
cg06039171	20	57599526	-0.153500523	MUTYH	cg04407579	13	99228509	0.152394376	STK24
cg10462593	15	79042505	-0.153481813	DENND3	cg26633120	2	105654408	-0.152372242	MRPS9
cg00977301	15	25427487	-0.15347267	FAM122A	cg23473419	17	74732838	0.152313596	MIR636
cg15105252	17	17295483	0.153472309	CUX1	cg02951344	11	85522279	0.152262611	SYTL2
cg10990665	14	102522832	-0.153463291	LOC401431	cg27572074	19	42419406	0.152251113	
cg13841901	1	45805975	-0.153408611	MEPCE	cg11508669	12	6643545	-0.152244554	GAPDH
cg12895810	8	142138638	0.153379282	PGS1	cg16310717	12	4383619	-0.152207064	CCND2
cg02765496	9	71393662	-0.153268715	UBXN1	cg18069309	15	42867567	-0.152075913	STARD9
cg09951433	7	101843287	0.153226233		cg04286540	6	29944636	0.152072306	HCG9
cg18396041	7	149571256	-0.153173819		cg04194728	6	150232017	-0.152035648	
cg17607973	7	100027408	-0.153115784		cg13662093	20	33865505	0.152016464	
cg04453241	17	76374567	-0.153081865		cg12375025	18	67873125	-0.152003547	RTTN
cg09491948	11	62446595	-0.153066122		cg26097011	13	103046943	-0.152001466	FGF14

Figure 18-2

cg26192815	2	240722597	-0.151988227		cg09833174	7	143059591	0.150834506	FAM131B
cg06327849	3	129035119	0.151974022	H1FX	cg10241701	1	117113180	-0.150829598	CD58
cg13972460	20	1165703	0.151963336	C20orf46	cg26528255	1	27652089	-0.150820246	TMEM222
cg06361278	17	25783929	0.151933678		cg10955633	7	957950	-0.150813737	ADAP1
cg08391321	5	112630695	0.151846152	MCC	cg14563732	8	143474839	-0.150801927	TSNARE1
cg16600432	14	64970085	0.151762215	ZBTB1	cg22995176	7	76139470	0.150745944	UPK3B
cg13129662	17	48227708	-0.151661424	PPP1R9B	cg17154187	17	18163844	-0.150744467	SMCR7
cg13550107	18	32558066	-0.151648823	MAPRE2	cg16609139	11	23962902	-0.150726414	
cg08916879	7	2946518	0.151629537	CARD11	cg05947570	10	89623020	-0.150713259	PTEN
cg19169976	17	48071254	0.151611041	DLX3	cg24654547	16	68057165	-0.150704372	DUS2L
cg23737366	1	9149026	-0.15160714	SLC2A5	cg01485266	19	2476132	-0.150699276	GADD45B
cg27367469	5	100239529	0.151604881	ST8SIA4	cg12314527	22	19110193	0.150555397	DGCR2
cg09695652	3	139108473	-0.151596807	COPB2	cg06352483	1	28052575	0.150468906	FAM76A
cg16527939	1	1253970	-0.151510937	CPSF3L	cg16968115	1	27560829	-0.150466659	WDTC1
cg05337192	1	108113367	-0.15150932	RPS15	cg21035471	17	77005669	0.150428762	CANT1
cg21956150	19	1438388	0.151462566		cg06117184	2	113522207	-0.150396687	CKAP2L
cg05585551	6	167314745	-0.151421935	MFSD5	cg06099276	16	49315812	0.1503915	CBLN1
cg12586596	12	53645731	-0.151387904	POLR3D	ch.8.2353618R	8	119282796	0.150370073	SAMD12
cg20806085	8	22108223	-0.151379731		cg24363298	3	50242671	0.150302309	SLC38A3
cg16328462	8	36636824	-0.151367967		cg18735798	3	194392871	0.150186096	LSG1
cg02036077	22	35653364	-0.151317152	HMGXB4	cg04607442	13	21872219	0.150166347	
cg18877635	1	229643817	-0.151285503	NUP133	cg20368463	18	77673604	0.150153225	PQLC1
cg18157915	17	61852003	-0.151278011	DDX42	cg08526140	19	53693063	-0.150119594	ZNF665
cg00900124	2	69969033	0.151173458	ANXA4	cg16221634	6	7332885	-0.150092848	KCNQ5
cg22933020	5	77072365	0.151118739	TBCA	cg26805238	1	144931980	-0.150090824	PDE4DIP
cg12152193	5	175954583	-0.151112219	RNF44	cg17001531	1	16825540	0.150086507	NEUROG1
cg18116217	10	3215066	-0.151105762	PITRM1	cg04063589	5	134871973	0.150084505	S1PR1
cg27218469	2	7005960	0.151096478	CMIPK2	cg02628801	1	101701963	-0.150081278	PGAM1
cg13195185	17	16875596	-0.151084988	TNFRSF13B	cg18268492	10	99185986	0.1500765	TUBB
cg05717050	12	20935811	-0.151072047		cg05217468	6	30689475	-0.150076046	AKD1
cg06995549	1	43282720	0.151050549	ERMAP	cg20917554	6	110012378	0.150042794	
cg12930714	14	24835006	0.151015028	NFATC4	cg09852107	11	57226342	0.150036158	GMPR
cg27664881	5	179234149	0.151014383	SQSTM1	cg15365536	6	16266181	-0.150015549	RUNX2
cg16226300	6	133136135	0.151001866	RPS12	cg17115147	6	45345601	0.15001509	CDC20B
cg08602604	2	198364282	-0.150957472	HSPD1	cg05005023	5	54469138	0.150011061	MAP1S
cg16504641	6	137143711	0.150918302	PEX7	cg04022891	19	17836889	-0.149999536	CTBP2
cg10069734	2	120124354	0.150897259	DBI	cg05882699	10	126840591	0.149983516	CPA5
cg26681912	1	169455321	-0.150884714	SLC19A2	cg15649111	7	129988860	-0.149884514	
cg06439489	5	176044620	-0.15085924		cg23091255	6	64345855	-0.149860681	CFLAR
cg04099813	11	2422520	-0.150844198	TSSC4	cg03974286	2	201980638	0.149842516	
cg03860054	16	55691102	-0.150839379	SLC6A2	cg05762326	10	92591168	-0.149770187	HTR7

Figure 18-3

cg21028463	17	74733682	-0.149757537	MIR636	cg04215179	7	23719682	0.148995326	C7orf46
cg11175310	10	16859107	-0.1497555971	RSU1	cg20382057	2	69969052	0.14898319	ANXA4
cg08264848	12	120740020	0.149741428	SIRT4	cg22813744	11	77899778	-0.14890876	KCTD21
cg13364389	13	112876974	-0.14971626		cg08984586	5	175963618	-0.148907793	RNF44
cg09044296	5	176739296	0.14966717	MXD3	cg16174274	7	148679906	0.148894155	
cg15389153	3	42819341	-0.149656056		cg05719877	11	114271629	-0.14884886	C11orf71
cg13390975	5	34915890	-0.149649837	BRX1	cg13676204	14	61447818	-0.148843602	SLC38A6
cg10282371	8	38854376	-0.149644383	ADAM9	cg09634134	5	321681	0.148839064	AHRR
cg07951488	4	41992560	-0.149640297	SLC30A9	cg16105080	1	239806917	-0.148817779	CHRM3
cg22017132	6	42927199	-0.149632595	GNMT	cg11336323	19	41946040	0.148807561	ATP5SL
cg06207460	9	4741011	0.149573639	AK3	cg14119392	14	95623926	-0.148806362	FLJ45244
cg14376275	1	171810570	0.149515353	DNM3	cg21347733	2	220306674	0.148797663	SPEG
cg22852149	19	36980565	-0.149501651	ZNF566	cg02772905	2	203484258	-0.148796864	
cg10157951	12	122108328	-0.149488889	MORN3	cg06756227	15	77712488	0.148794181	HMG20A
cg02656441	13	111367915	-0.149484667	ING1	cg11059266	4	48782139	0.14877356	FRYL
cg23540765	19	1173635	0.149467405	SBNO2	cg16458507	12	113376293	0.148763956	OAS3
cg27564108	1	150585651	0.149431297		cg24951396	12	125473687	-0.148763294	DHX37
cg22860534	11	68813585	-0.149420958		cg26507704	15	25314647	-0.148729954	SNORD116-8
cg16249355	17	76310516	0.14939609		cg02357877	7	56032049	-0.148728823	GBAS
cg06646346	11	6280988	0.149368024	CCKBR	cg15825725	11	82905263	0.148715548	ANKRD42
cg24475210	4	6642433	-0.149348708	MRFAP1	cg09127400	6	30712331	-0.148685932	IER3
cg09220050	20	48770642	0.149347117	TMEM189	cg13834567	19	42817981	0.148665613	TMEM145
cg11177179	14	65381159	-0.149283356	CHURC1	cg05300158	4	140477727	-0.148640487	SETD7
cg11949866	1	10754891	0.149280852	CASZ1	cg04407100	10	133729658	0.14863168	
cg20919306	17	11924526	0.149272336	MAP2K4	cg03392679	3	71773917	-0.148602006	EIF4E3
cg26300597	3	128840676	0.149264485	RAB43	cg06928982	1	36851566	0.148587241	STK40
cg07370464	17	43394456	0.149260284	MAP3K14	cg07179693	11	32605281	-0.14858278	EIF3M
cg05112967	7	63353492	-0.149240706		cg06330324	22	31031670	-0.148580156	SLC35E4
cg17391518	19	59028285	-0.1492221852	ZBTB45	cg06366345	14	101459591	-0.148574915	SNORD114-3:
cg14229247	9	100745139	-0.149199219	ANP32B	cg17753475	2	180477963	-0.148564496	ZNF385B
cg09664684	4	38665613	0.149115513	KLF3	cg16704344	5	141616127	0.14855801	
cg07928105	7	75368414	0.149108155	HIP1	cg23387220	4	53578496	0.148481521	SNORA26
cg22591103	3	159944037	-0.149088107	LOC401097	cg15408407	19	1438438	-0.148464886	RPS15
cg26164151	11	44749353	0.14908218		cg13455597	9	2844149	-0.148462079	KIAA0020
cg00045190	6	33216612	-0.149081913		cg14397361	9	140149997	-0.148402564	COBRA1
cg25629442	17	77070844	0.149072973	ENGASE	cg09200668	13	31773954	0.148378923	B3GALT1
cg01532694	8	8243576	-0.149068077		cg01196996	4	39481740	-0.148338225	LOC401127
cg26976888	7	12628091	-0.149064685	SCIN	cg05544840	13	44716513	-0.148331982	
cg14036868	2	38604442	-0.14906092	ATL2	cg17324887	11	18720217	0.148297822	TMEM86A
cg23193446	10	15210836	0.149017758	NMT2	cg09706833	21	46824938	0.148289888	COL18A1
cg09011732	2	74730507	0.14900727	LOC151534	cg16591054	19	50145354	-0.148289371	SCAF1

cg27642943	19	11457439	0.148286047	TMEM205	cg26487629	16	19418116	-0.147739286	
cg02350644	2	133111454	-0.148266521		cg08187779	8	102217898	0.147702744	ZNF706
cg22690046	1	36863663	-0.148265602	LSM10	cg18818993	14	91087882	-0.14769999	TTC7B
cg27275634	20	37590967	-0.148263529	DHX35	cg16020249	1	27930640	0.147684057	AHDC1
cg00934735	5	180582587	-0.148252309	OR2V2	cg15889649	15	79055693	-0.147668507	ADAMTS7
cg14443077	11	68606701	0.148202821	CPT1A	cg04936382	20	36662003	-0.147661501	RPRD1B
cg20363309	17	57184465	-0.148191888	TRIM37	cg27619163	17	7982806	-0.1476506	ALOX12B
cg00226085	6	58172067	-0.148186913		cg08977130	3	176915099	0.147646178	TBL1XR1
cg12013492	11	46143011	0.148176619	PHF21A	cg14902146	15	90294607	-0.147634919	MESP1
cg08117032	8	38325144	0.148141221	FGFR1	cg11975206	10	135192160	-0.14760049	PAOX
cg27109030	19	2702898	0.148111743	GNG7	cg08557876	16	81130217	0.147593758	GCSH
cg26258108	2	232329189	-0.148113939	NCL	cg06100147	7	143059260	0.147576716	FAM131B
cg18915437	12	62654245	-0.148107202	USP15	cg11224423	12	56136943	0.147552317	GDF11
cg03371986	5	138089103	0.148102031	CTNNA1	cg04323979	2	220306667	0.147546626	SPEG
cg07661849	4	146686236	-0.148082645	ZNF827	cg16370446	4	15683284	-0.147533266	LOC285550
cg26115276	5	178977181	0.148058168	RUFY1	cg13979277	9	129388281	0.14753005	LMX1B
cg10734432	8	145180544	-0.148048134		cg11070069	6	105389370	0.147527638	
cg01176150	16	31519952	-0.148044789	C1orf58	cg23060872	2	71205685	0.147509904	ANKRD53
cg15233329	22	32340329	-0.148043181	YWHAH	cg09141413	16	19896246	0.147501869	GPRC5B
cg25211006	1	43971496	-0.148026322		cg24517252	1	249200781	0.147484551	PGBD2
cg14494313	8	18248453	-0.14801893	NAT2	cg17598704	4	148885518	-0.14746688	ARHGAP10
cg23955334	1	1543828	-0.148008444		cg17734983	15	25456897	-0.147459422	SNORD115-1
cg03989244	15	72523736	-0.147993159	PKM2	cg16203711	3	169491183	-0.14744457	MYNN
cg27649653	19	58789751	0.147977673	ZNF8	cg16263627	15	100339283	-0.147430448	C15orf51
cg18604876	3	5164258	0.147973745	ARL8B	cg05938683	1	85156187	0.147394476	SSX2IP
cg16250722	6	31478166	-0.147964231	MICB	cg08342588	6	34494976	0.14739182	PACSIN1
cg26929161	20	50701266	-0.147950104	ZFP64	cg24692716	6	133119484	-0.147371456	C6orf192
cg25658641	17	19557814	-0.147938892	ALDH3A2	cg04977109	17	46125622	-0.147360657	NFE2L1
cg00014203	17	7757969	0.147909582	KDM6B	cg11983363	2	32578646	-0.147349467	
cg02918483	4	84406202	0.147891149	FAM175A	cg26548134	22	41185283	-0.147312649	SLC25A17
cg03631596	13	73301985	-0.147889449	C13orf37	cg11654179	12	57998762	0.147310319	DTX3
cg15692992	13	112710428	0.147881968		cg05102651	8	28351601	0.147237007	FZD3
cg20965255	17	37607625	-0.147871346	MED1	cg09990596	14	102227939	0.147212069	PPP2R5C
cg20423427	18	67873036	-0.147868534	RTTN	cg24152238	15	26327408	0.147206306	
cg27102918	6	20024152	0.147853428		cg18436758	1	21113190	0.147196044	HP1BP3
cg17064520	10	98591758	0.147817311	LCOR	cg20568408	14	90425050	-0.147186139	TDP1
cg12266953	2	20866261	-0.14780131	GDF7	cg02416013	16	11891051	0.147177449	
cg08502759	11	10562853	0.147777139	RNF141	cg11228874	1	1813727	-0.147129492	GNB1
cg03982544	11	17036042	0.147771177	PLEKHA7	cg24085655	6	35436189	-0.147075727	RPL10A
cg11523350	11	117171073	0.147762515	BACE1	cg16989332	4	175216323	0.147059924	KIAA1712
cg04364194	1	202114085	-0.147739331	ARL8A	cg14170181	9	5114002	-0.147057911	JAK2

Figure 18-5

cg01249134	18	577110	-0.147007892		cg02866761	22	17565664	0.146504678	IL17RA
cg193385725	18	21166173	0.147003965	NPC1	cg23459174	14	82295989	-0.146501189	
cg17414733	19	21688647	0.146998767	ZNF429	cg25704749	2	241526252	0.146490289	CAPN10
cg07987587	22	42486991	-0.146993117	NDUFA6	cg25559069	6	33134799	-0.146488868	COL11A2
cg23271318	20	44509620	0.146976731	ZSWIM1	cg12078510	19	53030774	0.146463725	ZNF808
cg16834212	3	67706500	0.146967171	SUCLG2	cg03083562	8	126007153	-0.146451536	
cg23059868	1	1649451	0.146903206	CDK11A	cg01266707	17	37824461	0.146424743	PNMT
cg16458021	21	43430507	-0.146878634	ZNF295	cg26450188	19	46850188	-0.146423466	PPP5C
cg24839520	3	129749648	-0.14687072		cg05170366	10	34063213	-0.146398386	
cg14128369	6	34231203	-0.146865351	SRF	cg19447629	12	82766859	-0.146394834	C12orf26
cg16041611	6	43139680	-0.146858375		cg16868190	18	12377377	0.146394378	AFG3L2
cg21161069	7	32768311	0.146847352	LOC441208	cg16170495	6	30042626	0.146376432	RNF39
cg06183820	6	2972097	-0.146833498	SERPINB6	cg25818882	19	12886379	0.146371446	HOOK2
cg22199361	20	5081567	0.146831171	C20orf30	cg11818149	2	132795839	0.146362461	
cg22885777	19	15947555	0.146807253		cg242023851	6	111136481	0.146359632	CDK19
cg05256172	2	26139506	0.146805524	SFRS6	cg22345896	2	173399001	-0.146339284	C22orf40
cg01438737	20	42086396	-0.14680045	KLC1	cg14382318	22	46646383	-0.146331275	EFHA1
cg08142571	14	104096390	0.146793709	GOLGA3	cg25299201	13	22178312	0.146325742	
cg19837214	12	133402551	-0.146741638	CDKL2	cg17575113	10	43188688	-0.146294783	HLA-B
cg05982271	4	76555948	-0.146715608	CCDC148	cg02718200	6	31324269	0.146286938	SMARCC2
cg13896783	2	159313876	0.146714173	CCR1	cg26841507	12	56583252	0.146274253	POMZP3
cg13144783	3	46249795	0.146710472	ANO10	cg15290081	7	76254647	-0.146270174	DNASE2
cg25587211	3	43663662	-0.146704921	ZNF324	cg25490276	19	12992844	0.146248054	AMIGO2
cg07100957	19	58982330	-0.146683061	DGKG	cg09933058	12	47473799	0.14623361	
cg10730421	3	186078847	-0.146680082	PIIL2	cg22506343	3	127173672	-0.146233006	CHTF8
cg19954613	22	22020219	-0.146668083		cg08555160	16	69166339	0.146214468	IGSF8
cg06832605	20	26319303	-0.14666373	KIAA1967	cg12390003	1	160068671	0.14619861	
cg17687970	8	22462467	0.146651288	SOLH	cg03056129	1	89593910	-0.146183951	
cg02360300	16	577976	0.146646328	NARS	cg21961512	4	8692854	-0.146144174	
cg25261764	18	55288998	-0.146644714	ARL15	cg02095553	9	134428624	-0.146111046	IKZF5
cg13717023	5	53606639	-0.146634461	ZNF90	cg19696333	10	124768261	-0.146096847	SLCOSA1
cg14766646	19	20187337	-0.146607817	DDX51	cg07212416	16	28385626	0.146072461	ZNF514
cg22672078	12	132628386	0.146593884	CCT7	cg10824802	8	70747252	-0.146035521	PI4K2B
cg22160784	2	73460416	-0.146590936	ABL1	cg05588757	2	95825608	0.146019956	BRSK2
cg13467399	9	133588111	-0.146587138	FAM64A	cg25020699	4	25247397	-0.146009634	COL11A2
cg27248073	17	6347727	0.146579927	LMOD1	cg18509719	11	1469746	0.146001258	PRR3
cg16903217	1	201915950	0.146572934	RBM9	cg01243297	6	33160292	0.145999539	SLC38A7
cg08532569	22	36424620	0.146562289	C16orf13	cg00260647	6	30524003	0.145993935	CDC25B
cg16757281	16	685785	0.146532775	ZNF276	cg08855361	16	58718334	0.145979776	
cg04751069	16	89787483	-0.146530595	KIAA1191	cg07003055	20	3776921	-0.145976739	
cg21605986	5	175788725	-0.146527533		cg06642177	6	134496341	-0.145968281	SGK1

Figure 18-6

cg08293303	5	176731731	0.145960531	PRELID1	cg092338957	16	46723420	-0.145535827	ORC6L
cg111737710	19	37959864	-0.145958036	ZNF570	cg04584087	3	129159014	-0.145534147	IFT122
cg17092583	11	735575	-0.145931918		cg19545258	7	73703601	0.145521537	CLIP2
cg00161367	6	153323552	0.145925226	MTRF1L	cg14780883	15	25466402	-0.145511238	SNORD115-1
cg20390253	18	77793812	0.14592137	C18orf22	cg09887955	1	202129854	0.145506281	PTPN7
cg08779779	2	200322566	0.14589524	SATB2	cg03657031	19	54385215	0.145500388	PRKCG
cg11232610	5	140027381	-0.145872418	NDUFA2	cg20681747	7	66949602	0.145499417	
cg15617768	10	101492447	-0.145866683	COX15	cg11532971	6	106676381	-0.145493496	ATG5
cg04200362	2	73341598	-0.14585801	RAB11FIP5	cg23983067	10	43277941	-0.1454877	BMS1
cg12646754	1	2574751	-0.145836637		cg15057823	6	42981704	0.145448952	MEA1
cg01245787	4	71859630	-0.145833742	DKK	cg05047465	10	27793441	-0.145445233	RAB18
cg17508063	12	53298678	-0.14582112	KRT8	cg10370564	19	39522418	0.1454394	FBXO27
cg13452400	2	7006280	-0.145813123	CMIPK2	cg02113521	15	22892956	0.145426434	CYFIP1
cg12673840	5	133193418	-0.14580572		cg16943083	18	500817	0.145421286	COLEC12
cg05776084	3	133293427	-0.145799061	CDV3	cg09293387	8	6565827	-0.145417185	AGPAT5
cg03031660	17	73257791	-0.145794474	MRPS7	cg06260874	8	6010288	-0.145412078	
cg10964421	8	23021093	0.145788903	TNFRSF10D	cg20012885	18	12377404	0.145409524	AFG3L2
cg24500304	1	235291357	0.145779595	SNORA14B	cg20284698	3	48956327	0.145396196	C3orf71
cg16008009	3	47620532	0.145774457	CSPG5	cg14102005	14	56645376	-0.145391458	PELI2
cg04901121	13	25321731	-0.145769462		cg02466749	9	98054877	-0.145380955	FANCC
cg13137533	17	43973292	-0.145765755	MAPT	cg05956803	5	137666464	-0.145374184	CDC25C
cg23627909	14	60337760	-0.14576489	RTN1	cg07804735	3	113157476	-0.145352523	WDR52
cg21914984	2	37899464	-0.145750906	CDC42EP3	cg09744376	3	53080176	0.145351412	SFMBT1
cg26260369	14	68141723	-0.145750822	VTI1B	cg17043191	11	79968672	-0.145346972	
cg24589549	3	49391282	-0.145739237		cg15050398	6	28829182	-0.14532152	
cg05865161	7	97557134	0.145735851		cg07455051	2	128051853	-0.145316194	ERCC3
cg16168311	1	156561947	0.145732033	APOA1BP	cg16884295	22	21018314	-0.145308823	
cg00090619	6	33160286	0.145723342	COL11A2	cg17430214	6	41246904	0.145250217	TREM1
cg11572675	2	86155952	0.14571672		cg00311921	22	19119464	-0.145208327	TSSK2
cg09075525	13	25940208	-0.145716233		cg04223844	8	42128868	-0.14519515	IKKB
cg24294159	1	150947566	-0.145699521	LASS2	cg23213688	1	231473791	-0.14518404	C1orf124
cg27018005	7	134249247	-0.145685962	AKR1B15	cg06046629	3	53698952	-0.145171704	CACNA1D
cg17847344	5	158478734	0.145651466	EBF1	cg07786668	16	73092391	-0.145161769	ZFXH3
cg02611874	10	46194725	-0.145649318		cg12198254	3	11521788	-0.145160379	ATG7
cg08573907	13	101628998	-0.145646169		cg12575136	18	32820987	0.145142575	ZNF397
cg09564990	10	113748602	-0.145626619		cg23281018	1	944789	0.145140116	
cg20275462	17	60501228	-0.145620732	METTL2A	cg07135388	1	160040411	-0.14511769	KCNJ10
cg19722371	12	102271755	0.145616081	DRAM1	cg25495217	7	6048875	-0.145117516	PMS2
cg01409734	12	112563185	0.145600525	TRAFD1	cg06551493	7	77166702	0.145111403	PTPN12
cg16613143	17	2415359	-0.145596296	METT10D	cg10700459	6	30231675	-0.145109586	HLA-L
cg23377236	6	3809610	-0.145590335		cg07195197	16	1662150	-0.145100701	IFT140

Figure 18-7

cg13947043	9	88141545	-0.145099533		cg06221470	7	2353869	0.144667213	SNX8
cg16340159	2	240322705	-0.145078412	HDAC4	cg11974096	2	233470647	-0.144663044	EFHD1
cg12442236	22	37823644	0.145070768	ELFN2	cg17452570	5	179886642	-0.144645355	
cg17371350	17	655677	0.145023974	ELP2P	cg13754687	2	40573036	-0.14463748	SLC8A1
cg25932599	4	1005201	0.145023631	FGFR11	cg03926050	12	111020225	0.144636428	PPTC7
cg14537800	4	15964950	0.145009257	FGFBP2	cg19197523	8	124428674	0.144635607	WDYHV1
cg22468803	18	9136381	-0.145006366	ANKRD12	cg05168344	22	21340160	0.144634469	LZTR1
cg11027325	2	239148674	0.145003153	HES6	cg15605011	1	110162477	0.144633593	AMPD2
cg13741289	4	17578858	-0.14499938	LAP3	cg04510639	17	74722764	0.14463114	JMJD6
cg09599399	6	32121843	-0.144988081	PPT2	cg15272186	6	29709610	-0.144621593	LOC285830
cg14284925	22	42315998	0.144986058		cg199445078	4	16944288	-0.144603269	
cg06536503	6	42750688	-0.144978543		cg09392386	17	63557887	0.144596393	AXIN2
cg10101463	1	202780506	-0.144936548		cg11038081	19	44810637	-0.144588905	ZNF235
cg02568557	11	129288930	-0.144914637	BARX2	cg01606770	1	97279796	0.144586107	PTBP2
cg24274354	1	13034580	-0.14490222	PRAMEF22	cg01950479	22	23528162	0.144584154	BCR
cg25798026	22	32149910	0.144886889	DEPDC5	cg05844625	6	29976071	-0.144572468	HLA-J
cg26937912	16	89945578	-0.144875539	TCF25	cg20676350	1	22961885	-0.144570767	C1QA
cg01240047	14	91224692	0.144849038	TTC7B	cg14172283	9	37592468	-0.144566093	TOMM5
cg01289140	6	41862737	0.144840768	USP49	cg13956095	17	81037419	0.144559264	METRNL
cg23868848	8	128806661	0.144835314	PVT1	cg10274208	13	41351044	0.144549353	
cg19226007	17	43045068	0.14481882	C1QL1	cg13806031	10	103454441	0.14453662	FBXW4
cg24448326	1	85930306	-0.144814465	DDAH1	cg23727520	3	121741145	0.14453208	ILDR1
cg25352856	1	180472145	-0.144808397	ACBD6	cg18622281	20	43977112	0.144489422	SDC4
cg25696485	21	38445943	-0.144804471	PIGP	cg27479418	10	126107594	0.144486055	OAT
cg19367232	2	68478649	0.14478426	PPP3R1	cg00556514	3	38066524	0.144483144	PLCD1
cg01400712	2	25352206	0.144779628	EFR3B	cg11228480	12	133066511	0.144474531	FBRSL1
cg17895522	10	44788915	0.144766133		cg10685336	3	149688848	0.144470583	PFN2
cg02153829	12	119034267	-0.14476336		cg05516746	10	5884061	-0.144460997	
cg17841838	19	3626645	0.144749137	C19orf29	cg06691810	8	27168883	-0.144459918	TRIM35
cg20769334	22	50913335	0.144745105	SBF1	cg23924753	14	81979997	-0.144447173	SEL1L
cg09197288	14	94550812	-0.144737186	IFI27L1	cg26036626	1	16085597	0.14444652	FBLIM1
cg25966751	14	74098320	-0.144732878		cg13433446	9	128170534	-0.144430504	
cg13668025	3	67706320	0.144721538	SUCLG2	cg06384413	17	46671215	0.144418991	LOC404266
cg13637402	9	139009863	0.144718052	C9orf69	cg03610000	11	128392383	0.144414893	ETS1
cg10446401	2	101619230	0.14471167	RPL31	cg20611850	19	41284006	0.144411711	RAB4B
cg10753423	7	143318009	0.144709219	FAM115C	cg22031336	4	89079809	-0.144411092	ABCG2
cg00494761	2	86564659	0.14470112	REEP1	cg07959380	16	89894648	0.144408344	SPIRE2
cg12502155	15	85201891	0.1447	NMB	cg07022554	16	1993481	0.144399564	SEPX1
cg22167498	19	8451051	-0.144680036		cg05445051	6	107349292	-0.144394343	C6orf203
cg06456464	1	9352752	0.144677234	SPSB1	cg22201516	19	32715740	0.144392486	
cg04533881	14	50583218	-0.144667878	C14orf138	cg19146902	11	47516584	-0.144349217	CUGBP1

Figure 18-8

cg06936779	1	151171405	0.144346412	PIP5K1A	cg19707448	17	25779279	-0.143980789	
cg10252138	17	58120427	-0.144343746		cg07084801	15	66648876	0.143975257	TIPIN
cg06708122	5	64969231	-0.144326784	SGTB	cg02100343	1	31538517	-0.143974948	PUM1
cg11877270	2	65658583	-0.144326086	SPRED2	cg11673391	1	10459052	-0.143972279	PGD
cg14551186	9	131012492	0.144306766	DNM1	cg08580796	6	79943404	-0.143966736	HMGN3
cg15481483	19	23299728	0.144302895		cg26789283	22	41682348	-0.143911495	RANGAP1
cg20521389	8	21645509	0.144299686	GFRA2	cg07591229	2	241922908	0.143907587	
cg21871583	3	15374148	0.144294533	SH3BP5	cg09913796	17	27181988	-0.143903324	ERAL1
cg00631837	22	45404212	0.144293286	PHF21B	cg01444712	7	150210785	-0.143896834	GIMAP7
cg12525736	1	228269915	0.144287586	ARF1	cg14910854	2	132254702	-0.143880243	LOC150776
cg09172423	11	62446602	-0.144280739	UBXN1	cg13614812	17	21254058	-0.14387046	
cg08213444	5	784871	0.144268688		cg18416950	17	46620413	0.143847756	HOXB2
cg23069677	1	36863646	-0.14424909	LSM10	cg03183872	20	3140552	-0.14384028	FASTKD5
cg16710791	1	193028559	-0.144244488	TROVE2	cg15312192	3	125412355	-0.143836547	
cg26387966	8	144503421	-0.144239401		cg03907612	6	41703314	0.143794968	TFEB
cg26561207	5	171615258	0.144224081	STK10	cg17436327	6	170863443	-0.143765511	PSMB1
cg09046255	16	30662126	0.144212928	PRR14	cg19034708	8	17780168	-0.143750386	PCM1
cg02874321	11	94166952	-0.144199147	MRE11A	cg16538289	6	41703332	0.143744694	TFEB
cg21501096	14	24454443	-0.144181828		cg12449510	7	97910870	0.143737786	BR13
cg10341991	3	48229869	-0.144178374	CDC25A	cg23645831	1	15944060	0.143735139	DDI2
cg01069104	3	18467441	0.144163346	SATB1	cg07899263	13	99293508	-0.143725785	SERAC1
cg19340909	1	1821422	-0.144161502	GNB1	cg11582617	6	158589302	0.14370099	
cg00636124	16	27215281	-0.144151508	JMJD5	cg12644885	1	154297985	0.143692522	ATP8B2
cg18517677	9	131799243	0.144149085	FAM73B	cg24875440	1	27986375	0.143692289	
cg13657659	2	208632393	-0.144135344	FZD5	cg27035087	6	28834254	0.143678491	
cg07646714	11	34378884	0.144119567	ABTB2	cg24684520	10	120543329	-0.143673806	
cg08411512	20	25846519	0.144113136		cg26674132	19	9434637	0.14367065	ZNF559
cg03215858	10	15025727	-0.144112377		cg11527367	1	144612646	-0.143653884	C1orf152
cg15617548	2	171785815	0.144108409	GORASP2	cg24631920	11	108535736	-0.143653819	DDX10
cg02918146	7	99725667	0.144100791	MBLAC1	cg03020271	19	4867550	0.143636953	PLIN3
cg02330114	3	43663594	0.144080811	ANO10	cg12991976	12	83053192	-0.143636883	
cg09905732	16	928154	-0.144074294	LMF1	cg13601636	19	55385010	-0.143633914	FCAR
cg11199036	3	129325693	0.144055593	PLXND1	cg26511840	5	137827785	0.143632918	
cg27310761	14	90798393	0.144054452	C14orf102	cg08975295	12	37936063	-0.143628507	
cg01559663	8	53852274	-0.144040489	NPBWR1	cg04903936	11	19262692	-0.143612358	E2F8
cg01698167	4	11430908	-0.144033258	HS3ST1	cg09691861	4	77870047	-0.143597049	11-Sep
cg15318396	21	38593284	-0.144026267		cg06462174	17	30813688	0.143583845	CDK5R1
cg12361356	1	200708503	-0.144024427	CAMSAP11	cg03793778	19	39264720	-0.1435794	LGALS7
cg11396746	16	1877632	0.143998564	FAHD1	cg10827434	1	84944976	0.1435725	RPF1
cg05954989	10	135191962	-0.14399806	PAOX	cg07033880	15	85923739	-0.143563052	AKAP13
cg16120422	12	113590924	-0.143985496	CCDC42B	cg23924007	4	140099401	-0.143549456	

Figure 18-9

cg00544901	19	49999417	-0.143546047	RPS11	cg21922468	19	42417238	0.143163113	
cg00997262	16	19421265	-0.143545731	TMC5	cg04473235	5	77080995	-0.143153178	
cg13241807	11	33757992	0.143532971	CD59	cg05941299	14	23095661	-0.143153023	
cg06910299	4	2758074	0.143528707	TNIP2	cg05157470	6	28937310	-0.143136263	
cg18574403	17	77070839	0.143517544	ENGASE	cg187332869	19	6739680	0.143133536	TRIP10
cg18471460	14	54863582	-0.143503877	CDKN3	cg23084309	19	6280164	0.143129689	MLLT1
cg21799605	6	42713881	-0.143495991	TBCC	cg26932860	7	75938875	-0.14311066	
cg08328124	16	28251274	-0.143486281		cg04836154	11	62439314	-0.143108776	C11orf83
cg09020181	22	46467123	0.143466327		cg18045461	22	29601862	0.143102873	EMID1
cg16840889	6	107077549	0.143443188	QRS1	cg19038917	10	106014565	0.143094361	GSTO1
cg24104633	14	67999913	0.143425776	PLEKHH1	cg11575912	19	5828299	-0.143078231	NRTN
cg21216828	19	15560076	0.143413768	MIR1470	cg27621528	2	241392617	0.143077502	PP14571
cg06510563	19	11308259	0.143411473	KANK2	cg17700415	8	145901039	0.14307031	
cg15786664	6	28917329	-0.14340202		cg07575812	5	138883510	-0.143066702	
cg19149264	3	187571176	0.143398382		cg11724493	6	33168040	0.143061784	SLC39A7
cg07559730	19	53497048	0.143397989	ZNF702P	cg25486143	3	50378527	-0.143055206	RASSF1
cg20856750	15	41444887	-0.143397234		cg25923207	11	62192276	0.14305433	
cg21422400	1	1747243	-0.143393336	GNB1	cg24106894	15	48623432	-0.143046805	DUT
cg01218180	6	168079427	0.143367827		cg17053098	6	33137183	-0.143031785	COL11A2
cg14162034	15	78112026	0.143365993		cg25221281	11	106698622	-0.14301587	GUCY1A2
cg18075720	19	45349207	0.143360144	PVRL2	cg13249096	3	48670922	0.14300549	SLC26A6
cg23717752	17	21360435	0.143353962		cg27121095	18	77155145	0.142999981	NFATC1
cg21285133	1	150209464	-0.143344346	ANP32E	cg07416975	4	699435	0.142996122	PCGF3
cg02775353	7	101814109	-0.14330473	CUX1	cg14303778	8	1616111	-0.142988403	DLGAP2
cg08249899	16	20975258	0.143298089	DNAH3	cg16040094	14	52240877	-0.14298482	
cg06305175	2	228337254	-0.143271754	AGFG1	cg15209934	19	52800385	0.142978259	ZNF480
cg01353139	8	124170018	0.143267543		cg10122932	7	99698990	-0.142963883	MCM7
cg22229470	6	168107104	0.143264081		cg19255053	1	184944109	-0.142957611	FAM129A
cg05598205	16	46723426	-0.143255291	ORC6L	cg11786428	2	132560627	-0.142954203	C2orf27B
cg14860917	8	18871440	0.143254218	PSD3	cg14162457	13	113444243	-0.142953758	ATP11A
cg05990936	9	95858257	0.14324035	C9orf89	cg00303723	19	18304398	0.142945962	MPV17L2
cg14654948	6	36164803	0.143237102	BRPF3	cg03238901	19	10047197	0.14293808	OLFM2
cg24015081	14	105144033	-0.143235808		cg18751306	15	81294292	-0.142925444	MESDC1
cg24297454	6	30689211	0.143228083	TUBB	cg12429444	1	20988133	-0.142916935	DDOST
cg18782651	7	65969785	-0.143222905		cg09275602	7	66370330	-0.142909278	
cg10616859	7	2586532	-0.143215146	C7orf27	cg13738615	9	109624741	0.142894432	ZNF462
cg13985271	9	97140681	-0.143195614	HIATL1	cg13140465	15	23085026	-0.142879507	NIPA1
cg02861733	1	153930593	0.143169875	CRTC2	cg00710870	7	102793411	-0.142865435	
cg08348387	2	242158123	0.143168425	ANO7	cg01779076	2	201980642	0.142863153	CFLAR
cg08163906	14	102227932	0.143165814	PPP2R5C	cg03951132	20	5931305	-0.142846926	MCM8
cg21352959	17	62340143	-0.14316438	TEX2	cg24131747	14	68141730	-0.142827403	VT11B

Figure 18-10

cg23783768	10	45454944	-0.14281714	RASSF4	cg01712432	6	28480974	-0.142512411	GPX6
cg16436509	12	120875898	-0.142804624	COX6A1	cg06895436	8	82434543	-0.142507543	
cg02083412	8	1649758	0.142804564	DLGAP2	cg25876975	15	77363192	0.142506067	TSPAN3
cg19071627	7	98923091	0.142802756	ARPC1A	cg08377569	16	30538014	0.142502767	ZNF768
cg06793377	22	51112536	0.142800765	SHANK3	cg11399053	11	130781648	-0.142501298	SNX19
cg25290175	2	71248774	-0.142795628		cg08283318	19	51859473	-0.1424988	ETFB
cg18715525	5	179223116	0.142782785	LTC4S	cg23762487	6	31165673	0.142497893	HCG27
cg22223655	18	67872902	-0.142779322	RTTN	cg15813550	20	62221886	-0.14249465	GMEB2
cg06012509	6	43027269	-0.142776386	KLC4	cg04792380	12	105162318	-0.142481018	
cg10757027	7	150783788	0.142767561	AGAP3	cg04383836	17	9559049	-0.142479059	USP43
cg04956913	6	30712436	-0.142759546	IER3	cg20632863	12	99038768	-0.142476177	APAF1
cg27226043	11	1770394	0.142757482	HCCA2	cg10515630	1	248342467	-0.142472392	OR2M2
cg23488616	6	159065864	0.142744978	DYNLT1	cg14368881	9	21396078	-0.142471663	
cg10534439	2	69969029	0.142716442	ANXA4	cg19366591	1	92951355	-0.142470941	GFI1
cg04887335	3	196044632	-0.142713408	TCTEX1D2	cg10772238	7	11013365	0.142467978	PHF14
cg23806411	16	49890167	0.14270233		cg10392378	6	90348606	-0.142467808	LYRM2
cg09013204	13	79183513	0.142701032		cg25245266	22	38349536	-0.142465333	C22orf23
cg18451256	2	128284158	-0.142672764	IWS1	cg05621343	11	134146253	0.142441131	GLB1L3
cg08661899	6	132722664	0.142671747	MOXD1	cg21926875	2	47596410	0.142412816	EPCAM
cg24385902	6	144617301	-0.14265619	UTRN	cg08782481	6	27839916	0.142406517	HIST1H3I
cg08163160	12	7052390	-0.142654223	C12orf57	cg25406872	5	172385821	0.142402108	LOC1002681e
cg04553410	7	150864885	-0.142645841	GBX1	cg05832051	19	54369469	0.142386925	MYADM
cg01283712	14	106919294	-0.142644348		cg20627546	1	1451383	-0.142376434	ATAD3A
cg15967188	4	2470700	-0.142630041	RNF4	cg15172514	6	31478236	-0.14237425	MICB
cg02283811	11	576060	0.142628062	LOC143666	cg08485259	3	196590644	-0.14235179	
cg08007338	1	180123948	0.142626313	QSOX1	cg23917680	4	323517	-0.142345395	
cg14870242	14	55034646	-0.142620511	SAMID4A	cg22852134	11	71618618	-0.142344736	LOC10013331
cg02436290	12	130877573	-0.142616715		cg23945273	4	120987944	0.142343661	MAD2L1
cg14732699	8	128750039	0.142608737	MYC	cg21981298	11	1824157	-0.142337353	
cg18511212	10	38715824	-0.14259973	LOC399744	cg04474988	10	131770171	0.142315488	
cg14385738	1	114414340	0.142588711	PTPN22	cg01013595	16	3130324	-0.142310554	
cg27502066	17	74380231	0.142573972	SPHK1	cg26094752	14	35099088	-0.142310546	SNX6
cg21121496	19	55592930	0.142573836	EPS8L1	cg04041474	2	219187843	0.142308846	PNKD
cg24122991	12	6985221	-0.142557538		cg13171979	16	57497010	-0.142303606	POLR2C
cg06791151	3	37034956	-0.14255306	EPM2AIP1	cg06717289	15	75978121	-0.14229569	CSPG4
cg12856433	11	44084185	-0.14255263		cg19415767	6	7108058	0.142276348	RREB1
cg04599297	10	26505442	0.142551284	GAD2	cg26014952	3	196366994	-0.142237153	LRRC33
cg03326059	11	13690160	-0.142538135	FAR1	cg05712126	22	29601860	0.14222413	EMID1
cg09607178	6	29978432	-0.142522516	NCRNA00171	cg01289656	12	51984945	0.142213782	SCN8A
cg14858951	17	38257028	-0.142518626	NR1D1	cg18500714	14	100706288	-0.142201896	YY1
cg22611419	17	77070824	0.142517668	ENGASE	cg06412409	21	43426532	-0.14219949	ZNF295

Figure 18-11

cg25004737	2	204209718	-0.142197125	ABI2	cg04738301	12	96184580	-0.141935596	NTN4
cg12814147	7	142375072	-0.142192922		cg01204669	15	101176097	-0.141935058	ASB7
cg27159032	19	9272145	-0.142191574	ZNF317	cg04293891	19	53239200	-0.141920287	ZNF611
cg21938149	5	107746626	-0.142176772		cg27505348	4	8441964	0.141913942	ACOX3
cg01547051	7	150777654	-0.142172982	FASTK	cg11450546	19	43965012	-0.141888269	LYPD3
cg19695335	20	25604759	-0.142171678	NANP	cg13406003	6	127535477	-0.14188261	
cg03027379	6	31462183	0.142170333		cg16807577	16	22019998	0.141871988	C16orf52
cg11427898	15	38544983	0.142170114	SPRED1	cg10260072	6	42421084	0.141871489	TRERF1
cg19678315	6	168760112	-0.142165811		cg07244326	1	161360101	0.141865317	
cg03797305	16	30209202	-0.14215647	SULT1A3	cg16406226	20	42086458	0.141856851	SFRS6
cg24066601	6	26271455	0.14215023	HIST1H3G	cg15072612	6	32862352	-0.14185641	
cg00531400	12	125348358	0.142133097	SCARB1	cg03324464	1	116022091	-0.1418497	
cg23322277	8	145215781	-0.142130657	HEATR7A	cg02759005	3	53925912	-0.141844314	SELK
cg01383268	17	71088868	0.142127037	SLC39A11	cg27272293	12	76531007	-0.141842382	
cg07478100	17	5389857	-0.14211707	MIS12	cg26460378	19	36545594	-0.141835413	WDR62
cg06695833	19	18220682	0.142114498	MAST3	cg12774559	11	68519071	0.141833839	MTL5
cg21840888	18	33709847	-0.142085542	ELP2	cg25916505	18	32820654	0.141824258	ZNF397
cg24147024	3	40526345	-0.142082431	ZNF619	cg00715047	17	73522054	-0.141821991	LLGL2
cg10003974	7	47552912	-0.142079527	TNS3	cg02125554	16	90238222	-0.141816151	
cg18590611	1	40745926	-0.142075841	ZMPSTE24	cg16792258	2	239631449	-0.141797001	PTPMT1
cg14664575	19	40476624	-0.142074211	PSMC4	cg26054336	11	47586799	-0.141779422	
cg07636117	2	237072957	0.142058112		cg10912077	1	87794075	-0.14177516	LMO4
cg07290865	4	187053574	-0.142039486		cg20395128	19	4243436	-0.141773642	
cg13795627	1	157015873	0.142034642	ARHGEF11	cg24647506	10	130366835	-0.141772232	
cg24909975	6	160147912	-0.14203111	WTAP	cg08290850	6	44238228	0.141767615	CDH24
cg14645856	6	18368844	-0.142030473		cg23946709	14	23527317	0.141757281	RAB43
cg10583683	15	23034700	-0.142022398	NIP2	cg23409587	3	128840680	0.141754097	RDBP
cg01708236	6	44233446	0.142022054	NFKBIE	cg18335034	6	31922445	-0.141748701	
cg02785793	19	16125592	-0.142018398	LOC126536	cg04337618	16	777215	0.141742206	HAGHL
cg21898708	6	31802157	0.142015279	C6orf48	cg00080118	6	31126173	-0.141736423	CCHCR1
cg27267227	16	29888023	0.142015148	SEZ6L2	cg10977398	3	124606490	-0.14173491	ITGB5
cg04611493	2	100863359	-0.142013888		cg26973045	18	77711805	0.141731284	PQLC1
cg00591353	16	83670892	0.142012139	CDH13	cg15413566	7	8301971	0.14172299	ICA1
cg17436946	4	39699568	0.141994616	UBE2K	cg26668872	16	3546216	-0.141722347	C16orf90
cg08867249	12	9067433	0.141991897	PHC1	cg16144447	1	36184773	0.141718692	C1orf216
cg10831504	12	69005104	-0.141978329	RAP1B	cg00223042	2	65126816	-0.141718172	
cg04912466	11	63742028	-0.1419616	COX8A	cg14712964	3	9773672	0.141713337	BRPF1
cg23971381	11	58736000	-0.141957257		cg21290290	1	2518275	0.141711404	C1orf93
cg00848394	3	52188768	-0.141943752	WDR51A	cg11162385	20	25604740	-0.141705047	NANP
cg13353472	19	39343117	0.141940595	HNRNPL	cg10318313	11	3014937	-0.141700008	NAP1L4
cg04515258	17	78825412	-0.141938228	RPTOR	cg12242204	11	62607811	0.141681385	WDR74

Figure 18-12

cg10637425	17	79008593	0.141677728	BAIAP2
cg07377675	1	62901875	-0.141672587	USP1
cg10709925	3	149768629	-0.141669894	
cg26910867	11	68228179	0.141669732	SAPS3
cg13260314	6	3900192	-0.141668974	
cg15646967	7	43795266	-0.141661539	
cg21811549	7	63667594	-0.141657689	ZNF735
cg17251379	20	55966551	0.141657407	RBM38
cg08120389	17	19881268	0.141644612	AKAP10
cg22183232	11	9406733	-0.141639999	IPO7
cg04310649	10	35416472	-0.141639965	CREM
cg20977357	19	24184933	-0.141634699	
cg27110132	16	3661765	-0.141628529	BTBD12
cg27084994	5	175875161	-0.141626706	FAF2
cg07867325	3	73159953	-0.141616613	
cg01436664	3	128997925	0.141614884	C3orf37
cg04140754	12	124196328	0.141609326	ATP6V0A2
cg23411981	14	105940377	-0.141607704	CRIP2

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A2BP1	AKAP13	ATOH8	C10orf137	C2orf60	CCRN4L	CKAP2L
AASDHPPT	AKAP8	ATP13A1	C10orf78	C2orf68	CCT6P1	CKS2
AATF	AKNA	ATP1B1	C10orf95	C3orf18	CCT7	CLK1
ABCA7	ALDH3B1	ATP1B3	C11orf21	C3orf21	CD34	CLN8
ABCB9	ALDH5A1	ATP5C1	C11orf34	C3orf54	CD44	CLU
ABCD3	ALDOA	ATP6V0E2	C11orf41	C3orf57	CD58	CMIP
ABCF3	ALG12	ATPGD1	C11orf83	C3orf63	CD59	CN5H6.4
ABCG1	ALG6	ATR	C11orf93	C3orf71	CD9	CNKSR3
ABCG2	ALKBH4	ATRN	C12orf26	C4orf10	CDAN1	CNNM2
ABL1	ALKBH5	AVIL	C12orf61	C4orf34	CDC20	CNOT6
ABLM1	ALOX12B	AZI1	C13orf31	C4orf41	CDC25A	COBRA1
ABLM2	AMIGO1	AZU1	C13orf37	C4orf48	CDC25B	COG2
ABR	AMOTL1	B3GALNT2	C14orf133	C5orf24	CDC42EP4	COG8
ABTB2	AMT	B9D1	C14orf138	C5orf43	CDC42SE2	COL18A1
ACAA1	AMZ2	BAHCC1	C14orf174	C6orf27	CDC73	COL23A1
ACBD6	ANK1	BAIAP2L1	C15orf37	C6orf81	CDCA4	COL7A1
ACCN3	ANKH	BAIAP3	C16orf13	C7orf50	CDH23	COMMD3
ACOT2	ANKRD12	BAMBI	C16orf42	C7orf51	CDK13	COMMD6
ACOT4	ANKRD16	BANP	C16orf57	C7orf70	CDK2AP1	COPS8
ACOT7	ANKRD26	BBS5	C16orf59	C8orf73	CDK6	COQ6
ACP1	ANKRD27	BCAM	C16orf87	C9orf106	CDKN1B	CORO7
ACSL1	ANKRD39	BCAP29	C16orf89	C9orf139	CDKN1C	COX18
ACSL3	ANP32B	BCAS3	C17orf42	C9orf140	CDNF	COX19
ACTN4	ANXA5	BCCIP	C17orf48	C9orf69	CEACAM8	COX5B
ACTR5	AP2A2	BCL2	C17orf57	C9orf98	CEBPE	COX8A
ACVR2A	AP3B1	BCL2L11	C17orf59	CA5A	CEBPG	CPEB1
ADAD1	AP3D1	BCR	C17orf70	CABC1	CECR2	CPEB3
ADAL	AP3M2	BDP1	C17orf89	CACNA1C	CECR4	CPNE1
ADAM10	AP4S1	BECN1	C17orf91	CACNA2D4	CELSR1	CPT2
ADAM22	APP	BEND3	C17orf95	CACYBP	CELSR3	CR2
ADAM30	AREG	BICC1	C17orf96	CALHM1	CENPA	CRADD
ADCY3	ARFGAP3	BICD1	C18orf18	CALHM2	CENPN	CREB3L2
ADCY4	ARHGAP26	BICD2	C18orf19	CALM2	CEP170	CRNKL1
ADD2	ARHGAP27	BID	C18orf22	CALN1	CEP63	CROT
ADHFE1	ARHGAP5	BLM	C18orf55	CALR	CEP72	CRTC2
ADNP	ARHGEF3	BMF	C19orf10	CAMK1D	CEP78	CRYM
ADORA2B	ARID1B	BMP1	C19orf25	CAMTA1	CGGBP1	CSF1
ADRB2	ARL15	BMP8A	C19orf29	CANX	CGRRF1	CSGALNACT2
AFF1	ARL2	BMPR2	C1orf106	CARD14	CH25H	CSNK1E
AGA	ARL8A	BMS1	C1orf124	CATSPERG	CHCHD1	CSNK1G3
AGAP1	ARMC8	BOC	C1orf216	CBFA2T3	CHD6	CTBP1
AGPAT2	ARNTL	BRD1	C1orf53	CBFB	CHEK1	CTDP1
AGPAT5	ARPP-21	BRD4	C1orf59	CCDC12	CHERP	CTDSPL
AGRN	ASB1	BRIX1	C1orf95	CCDC148	CHKB	CTF1
AGTRAP	ASB13	BRP44	C1orf97	CCDC33	CHKB-CPT1B	CTNS
AHCY	ASB6	BRP44L	C1QL1	CCDC40	CHMP6	CTPS
AHCYL1	ASGR1	BRPF1	C1R	CCDC41	CHN1	CUTA
AHDC1	ASXL2	BRWD1	C1S	CCDC6	CHN2	CUX1
AHNAK	ATAD2	BSN	C20orf117	CCDC72	CHPF2	CUX2
AIFM2	ATF3	BSPRY	C20orf27	CCDC85A	CHRA1	CXCR1
AIM1	ATG12	BTBD10	C20orf43	CCDC90A	CHSY1	CXCR2
AK2	ATG16L2	BTBD12	C21orf59	CCDC96	CHSY3	CXXC5
AKAP1	ATHL1	BTNL9	C21orf66	CCHCR1	CIB1	CYB5R3
AKAP10	ATL2	BTRC	C22orf32	CCND3	CITED2	CYFIP1
AKAP11	ATL3	BZW2	C2orf15	CCNL2	CKAP2	CYP1B1

Figure 19-1

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CYP20A1	DUT	FAF1	FNIP1	GPX4	IFFO1	KIAA0415
CYP26A1	DYNC1LI2	FAHD2B	FNTA	GREM1	IFI27	KIAA0892
CYP2R1	E2F3	FAIM	FOXC1	GRHPR	IFNAR1	KIAA1191
CYP2U1	EARS2	FAM100B	FOXO2	GRK4	IFT122	KIAA1586
CYP4F3	ECSIT	FAM103A1	FOXJ1	GSK3A	IFT140	KIAA1731
CYP51A1	EEA1	FAM113A	FOXO1	GSTP1	IGF2BP2	KIF20B
CYTH3	EEFSEC	FAM125A	FRY	GTDC1	IGSF8	KIF9
CYTSB	EEPD1	FAM125B	FRYL	GTF2A1	IGSF9B	KIFC1
DALRD3	EFNA3	FAM129A	FUCA2	GTF2E2	IKBKB	KIFC3
DAZAP1	EFR3B	FAM149B1	FUT10	GTF2H4	IKZF5	KIN
DBP	EHD3	FAM158A	FUT11	GTPBP1	IL15RA	KLC2
DCAF7	EHD4	FAM163A	FUT4	GTSE1	IL17RC	KLF10
DCI	EID2B	FAM168B	FZD1	GUSBL2	IL31RA	KLF2
DCP1A	EIF2B4	FAM184A	G2E3	H1FX	ILF3	KLF5
DCUN1D2	EIF2S2	FAM188A	GAB2	H2AFY2	IMP3	KLF6
DCUN1D4	EIF3A	FAM21A	GADD45A	HAGH	IMP4	KLHL2
DDIT4	EIF3J	FAM46B	GALC	HDAC1	IMPDH1	KLHL21
DDX12	EIF4E3	FAM63A	GALK1	HDAC4	INCENP	KLHL25
DDX19B	EIF4H	FAM7A2	GALNT6	HDAC7	INPP5A	KLHL8
DEF8	EIF5B	FAM91A1	GATSL3	HDLBP	INPP5K	KPNA2
DENND4B	ELAC2	FANCF	GBAS	HERC4	INPPL1	KPNA3
DEPDC6	ELANE	FANCL	GCH1	HERC5	INTS7	KRAS
DERL3	ELL2	FASTK	GCKR	HERPUD2	IPO9	KRT17
DGAT2	ELMO3	FASTKD5	GDAP2	HES6	IQCE	KY
DGKH	ELOVL3	FAT3	GDF7	HEXB	IREB2	LAG3
DGKZ	ELP2	FBLIM1	GFI1	HGD	IRF1	LARP1
DHRS3	EME2	FBRSL1	GFOD1	HGS	IRF2BP2	LASS4
DHRS7B	ENOPH1	FBXL14	GFRA3	HGSNAT	IRF4	LBH
DHRS9	ENPP1	FBXO2	GGA3	HHLA3	ISOC1	LBR
DHX16	ENSA	FBXO32	GGH	HIAT1	ITGA5	LCLAT1
DIRC2	EPAS1	FBXO33	GGT6	HIF1A	ITIH4	LCN6
DLAT	EPDR1	FBXO7	GIN51	HINFP	ITPKB	LCORL
DLD	EPHB1	FEM1A	GLB1L3	HIPK3	ITPR3	LDB3
DLL1	EPM2A	FEM1B	GLCCI1	HIRIP3	IWS1	LDHA
DMPK	EPN3	FGD6	GLDC	HIVEP3	JAK3	LEPRE1
DMTF1	EPPK1	FGF14	GLOD4	HJURP	JMJD5	LETM1
DMXL1	ERBB2IP	FGFR1OP	GLTSCR1	HK1	JMY	LGALS12
DMXL2	ERC1	FHIT	GLUD1	HLA-DPA1	JOSD1	LHB
DNAH10	ERCC1	FIBCD1	GMPPA	HLX	JPH2	LHPP
DNAJA2	ERCC3	FITM2	GNA12	HNRNPA2B1	JPH4	LITAF
DNAJB6	ERN1	FKBP1A	GNA13	HNRNPA3	KARS	LLGL2
DNAJC1	ESF1	FKBP4	GNAI2	HNRNPAB	KCNAB2	LMBRD2
DNAJC13	ESPL1	FKBP5	GNG10	HNRNPH1	KCNMA1	LMF1
DNLZ	ESR2	FLI1	GNL3	HNRNPM	KCNQ1	LMNB1
DOCK9	ETFDH	FLII	GOLGA4	HNRNPR	KCNQ4	LMO2
DOLPP1	ETV3L	FLJ13197	GOLGA7B	HNRNPU	KCNQ5	LMO4
DPYSL2	EVPL	FLJ33630	GOLGA8B	HS6ST1	KCNS1	LMO7
DTWD2	EXOC8	FLJ35220	GORASP1	HSD3B7	KCTD5	LOC100128239
DTX1	EXOSC4	FLJ39582	GPR107	HSF2BP	KDM4A	LOC100128822
DTX4	EXTL3	FLJ43663	GPR176	HTT	KDM5B	LOC100130581
DTYMK	EZR	FLJ45244	GPR44	HYI	KHK	LOC100130987
DUS2L	F12	FLOT1	GPR56	HYLS1	KIAA0146	LOC100132354
DUSP11	F2R	FNDC1	GPR63	IBTK	KIAA0174	LOC100134229
DUSP14	FA2H	FNDC3A	GPR97	ID1	KIAA0284	LOC100144603
DUSP5	FADD	FNDC3B	GPS2	IDI1	KIAA0368	LOC100189589

Figure 19-2

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LOC100270710	MAPK1IP1L	MRPL20	NFKBIA	PARD3B	PLEKHA6	PTAFR
LOC151534	MAPKAPK2	MRPS24	NGLY1	PARP12	PLEKHG3	PTCH2
LOC153684	MAPKBP1	MRS2	NHLRC4	PARP8	PLEKHG6	PTDSS2
LOC202181	MARCO	MSH3	NHP2L1	PARVB	PLEKHO1	PTEN
LOC253724	MARK2	MSL2	NHSL1	PAXIP1	PLK4	PTGER2
LOC25845	MARK3	MTERFD1	NID2	PBX3	PLXNA2	PTGER4
LOC283404	MAT2A	MTHFD1L	NIPA2	PCGF1	PMS2L2	PTGS1
LOC284023	MBLAC2	MTHFD2	NIPSNAP3B	PCID2	PNN	PTK2B
LOC284837	MCAM	MTIF3	NKIRAS1	PCK2	PNPLA8	PTPN23
LOC285830	MCC	MTMR10	NLGN2	PCM1	POGK	PTPN5
LOC389033	MCCC2	MTO1	NOB1	PCMT1	POLR1B	PTPRE
LOC401431	MCF2L	MTRF1L	NOL7	PCNT	POM121L2	PTRH1
LOC647121	MCF2L2	MTX1	NOM1	PCSK7	POU2F1	PTTG1
LOC728264	MCM2	MUM1	NOSTRIN	PDCD11	PPARA	PUF60
LOC728411	MCM5	MUTYH	NPAT	PDCD5	PPARGC1B	PUM1
LOC730755	MCM6	MX1	NPC2	PDE3B	PPBPL1	PUSL1
LOC93622	MCM7	MXD3	NPHP4	PDIA4	PPHLN1	PVRL3
LOXHD1	MCM8	MYBL1	NPLOC4	PDIK1L	PPIF	PVRL4
LPAR1	MDGA1	MYL12B	NR1H2	PDP2	PPIL2	PWWP2A
LPAR5	MDH2	MYO15A	NR1H3	PDPK1	PPIL4	PXMP2
LRBA	MDK	MYST2	NRSN2	PDS5B	PPP1CC	PXMP3
LRP5	MDN1	N4BP2	NRXN2	PDXDC1	PPP1R12C	PXN
LRRC26	MED12L	N6AMT2	NSMAF	PDXK	PPP1R14B	PYCR2
LRRC28	MEN1	NAA35	NT5DC1	PEBP1	PPP1R7	QKI
LRRC3	MESDC1	NAAA	NTN1	PEBP4	PPP1R9B	QPCTL
LRRC56	METAP1	NADK	NTN3	PECI	PPP2R2A	QPR2
LRRC8A	METTL9	NANP	NTN4	PER2	PPP2R2B	QRICH1
LRRC8D	MEX3C	NAP1L4	NUBP2	PFKL	PPP2R3C	RAB10
LRRFIP2	MFSD1	NARF	NUDT16L1	PGAP2	PPP3CA	RAB11FIP3
LSP1	MFSD3	NBPF1	NUDT3	PGD	PPP4C	RAB11FIP4
LUC7L3	MFSD4	NCAPG	NUDT4	PGLYRP4	PPPDE1	RAB12
LYPLA1	MGA	NCBP2	NUDT6	PGM1	PRDM14	RAB32
LYRM4	MGAT5B	NCK1	NUP153	PGP	PRDM15	RAB5C
LYST	MGRN1	NCKAP5L	NUP210	PGS1	PRDM2	RAD23A
LZTS2	MIB2	NCL	NXT1	PHACTR3	PRDX1	RAET1K
MACF1	MICAL2	NCOA5	OAS2	PHC2	PRDX6	RAGE
MACROD1	MIR146B	NCOR1	OAT	PHF15	PREP	RAI1
MAD2L1BP	MIR17HG	NCOR2	OAZ1	PHKG1	PRICKLE1	RALB
MAEA	MIR191	NCRNA00115	OCIAD1	PHLDA1	PRKAG2	RALGAPB
MAFF	MIR24-2	NDFIP1	OGFRL1	PHLPP1	PRKCA	RALY
MAFG	MIRLET7I	NDUFA10	ORAOV1	PIGY	PRKD2	RANBP2
MAG	MIS12	NDUFA6	ORC6L	PILRB	PROSC	RAP1B
Magmas	MKRN2	NDUFAF2	OSBPL1A	PIM3	PRPF8	RAP1GDS1
MAN2A1	MLLT1	NDUFS2	OSBPL5	PITPNB	PRR3	RAP2B
MAN2C1	MMAB	NDUFS6	OSCAR	PITPNC1	PRRX2	RAPH1
MANF	MMRN2	NDUFV1	OTUD4	PKD1	PRSS8	RASA1
MAP3K1	MOGS	NEIL3	OTUD7B	PKIG	PRTN3	RASA3
MAP3K11	MORN1	NEK11	P2RX4	PKM2	PSD4	RASGEF1B
MAP3K12	MORN2	NEK3	P2RY2	PKNOX1	PSMB9	RASSF1
MAP3K3	MPG	NEK9	P4HB	PKNOX2	PSMD1	RASSF10
MAP3K6	MPHOSPH6	NEO1	PABPC1	PLAUR	PSMD11	RASSF4
MAP3K8	MPO	NEURL	PANK4	PLBD2	PSMD6	RB1CC1
MAP6	MPRIP	NF2	PANX1	PLCL1	PSMG1	RBBP6
MAPK1	MPV17L2	NFIC	PAOX	PLD1	PSMG2	RBM14
MAPK11	MRP63	NFKB1	PAQR7	PLEC1	PSPC1	RBX1

Figure 19-3

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RCAN3	RXRA	SIK3	SNORA30	TCTA	TRIM33	VDR
RCOR1	S100A11	SIKE1	SNRPA1	TEAD3	TRIM37	VKORC1
RDH10	S1PR4	SILV	SNRPF	TECPR1	TRIM52	VPS13C
RDH13	SACM1L	SIM2	SNX10	TENC1	TRIM59	VPS16
REEP3	SAMD13	SIN3A	SNX14	TERF2	TRIM7	VPS29
RELT	SAMD4A	SIRT2	SNX17	TES	TRIM71	VPS52
REPS1	SAP130	SIT1	SNX20	TGFB3	TROVE2	VRK1
RET	SARS	SIVA1	SNX24	TGFB1	TRPV4	VTI1B
REV3L	SAV1	SKA1	SP4	TGFB1R1	TSEN2	VTRNA1-3
RFC4	SBNO2	SKI	SPAG4	THAP11	TSKU	VWA1
RFTN1	SC65	SLC11A2	SPATA13	THBS1	TSPAN18	VWCE
RFWD2	SCAMP1	SLC12A9	SPATA20	THRA	TSTD2	WDFY2
RGS17	SCAMP4	SLC16A1	SPCS3	TIGD3	TTC15	WDR27
RGS6	SCAND1	SLC16A3	SPEN	TIMM13	TTC30A	WDR4
RHOB	SCARF1	SLC1A5	SPOPL	TIMM22	TTC36	WDR51B
RHOF	SCD	SLC22A18AS	SPTBN5	TIMP2	TTC7B	WDR60
RICTOR	SCLY	SLC22A4	SREBF1	TJP2	TTLL1	WDR76
RILPL1	SCN2B	SLC25A13	SREBF2	TLE3	TTLL4	WDR81
RNASE12	SCN8A	SLC25A16	SRF	TM2D3	TUBA1B	WHAMM
RNASE2	SCT	SLC25A18	SRGAP3	TMCC3	TUBA3E	WHAMML1
RNASEH2B	SDCBP	SLC25A29	SRRT	TMEM105	TUBG2	WNT3
RNF11	SDCBP2	SLC25A4	SS18	TMEM127	TUBGCP2	WNT5A
RNF126	SEC1	SLC25A42	SS18L1	TMEM146	TUBGCP3	WRNIP1
RNF14	SEC23B	SLC26A2	SSB	TMEM14B	TUBGCP6	WSCD2
RNF149	SEC31A	SLC27A1	SSH3	TMEM150A	TUFM	WTAP
RNF168	SEC31B	SLC27A3	ST3GAL2	TMEM175	TUSC2	XRN2
RNF187	SEMA4C	SLC2A1	ST6GALNAC4	TMEM18	TXLNA	YAF2
RNF4	SEMA5B	SLC2A11	STARD5	TMEM2	TXNDC12	YARS
RNF8	SEN2	SLC2A6	STARD7	TMEM201	TXNDC15	YIF1A
RNH1	SEN3	SLC33A1	STARD9	TMEM22	TXNDC16	YIPF2
RNU5E	SEPHS1	SLC35E1	STAT5A	TMEM231	TYK2	YPEL3
ROGDI	SERBP1	SLC35F1	STIM2	TMEM43	TYMS	YTHDF3
RORA	SERPINB13	SLC36A4	STK17B	TMEM64	U2AF1	YWHAH
RP5-1022P6.2	SESN3	SLC37A3	STK36	TMEM65	U2AF2	YWHAQ
RPAIN	SETD2	SLC39A4	STRADB	TMEM79	UBE2E2	YY1
RPL10A	SETD3	SLC43A2	STX1B	TMEM93	UBE2J2	ZADH2
RPLP0	SETD7	SLC45A4	STYXL1	TMEM9B	UBE2L3	ZBP1
RPP40	SETD8	SLC46A2	SUGT1L1	TMTC4	UBE3A	ZBTB1
RPS11	SF3A1	SLC46A3	SUSD1	TNFAIP3	UBLCP1	ZBTB16
RPS15	SFMBT1	SLC6A6	SYF2	TNPO1	UHRF1BP1	ZBTB2
RPS21	SFMBT2	SLC7A5	SYNGR2	TOB2	UIMC1	ZBTB25
RPS3A	SFRS2IP	SLC7A6	SYNJ2	TOLLIP	UNC45A	ZBTB4
RPTOR	SFRS4	SLC7A7	SYNPO	TOMM40	UQCR	ZBTB42
RPUSD1	SFRS8	SLFN12L	TAF15	TOMM5	URB2	ZBTB48
RRAGC	SFXN5	SMAD4	TAF4	TOP3A	USP1	ZBTB7B
RRBP1	SGCE	SMARCA4	TAP2	TRA2A	USP14	ZC3H12C
RREB1	SGK1	SMCR5	TBC1D10B	TRAM1	USP21	ZC3H18
RRN3P3	SGK196	SMCR7	TBC1D14	TRAM2	USP3	ZC3H6
RRS1	SGMS2	SMPD4	TBCD	TRANK1	USP36	ZCCHC10
RTKN	SGSM3	SNAPC2	TCEA2	TRAPPC3	USP38	ZCCHC2
RTTN	SH3D20	SNCG	TCEA3	TRIM17	USP39	ZDHHC3
RUFY2	SH3GL1	SND1	TCF12	TRIM25	USP46	ZDHHC5
RUNX3	SHC1	SNHG12	TCF25	TRIM26	UVVAG	ZEB2
RUSC1	SIDT1	SNHG7	TCF7L1	TRIM27	VAPA	ZFHX3
RWDD1	SIGLEC9	SNHG9	TCN2	TRIM28	VAV2	ZFP161

Figure 19-4

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ZFYVE28
ZMYND12
ZMYND8
ZNF174
ZNF252
ZNF26
ZNF264
ZNF295
ZNF324
ZNF324B
ZNF365
ZNF385A
ZNF451
ZNF487
ZNF496
ZNF507
ZNF551
ZNF574
ZNF584
ZNF586
ZNF593
ZNF622
ZNF644
ZNF672
ZNF689
ZNF706
ZNF710
ZNF76
ZNF767
ZNF777
ZNF787
ZNF805
ZNF853
ZNHIT2
ZNR2
ZSCAN29
ZSWIM6
ZWINT

Illumina Probe	Chr	Mapinfo	Correlation	Gene	Illumina Probe	Chr	Mapinfo	Correlation	Gene
cg09099697	10	65281856	-0.193379401	REEP3	cg05639842	21	43639440	-0.163110259	ABCG1
cg19679281	2	58468512	-0.185685097	FANCL	cg00911981	3	142297824	-0.16303639	ATR
cg25840850	2	237994627	-0.185054516	COPS8	cg04875007	16	2014871	-0.162049943	SNHG9
cg08503002	3	183903768	-0.184334999	ABCF3	cg10122932	7	99698990	-0.161865279	MCM7
cg15147060	3	88108213	-0.181815672	CGGBP1	cg09089230	17	1588195	-0.161658514	PRPF8
cg07249227	21	43430503	-0.178346706	ZNF295	cg17491846	19	19431584	-0.161623054	KIAA0892
cg14157244	2	170655474	-0.1753330946	SSB	cg09693228	4	2965311	-0.161609044	GRK4
cg25072436	2	30454560	-0.174710628	LBH	cg13875899	6	5004148	-0.161551284	RPP40
cg10122474	14	88459471	-0.173252955	GALC	cg10035432	14	39644345	-0.161504145	PNN
cg01493617	17	79650915	-0.172916428	HGS	cg00329447	8	145028170	0.16145763	PLEC1
cg14167673	15	63796729	-0.172333193	USP3	cg07326074	16	2510388	-0.161334732	C16orf59
cg18845832	1	184943573	-0.171089644	FAM129A	cg22929219	22	35796023	-0.161015227	MCM5
cg14092529	5	21459600	-0.171049555	LOC728411	cg19594691	2	20646743	-0.160915427	RHOB
cg18022279	1	231473268	-0.170919895	C1orf124	cg23635560	2	27473369	0.160806621	
cg20366603	17	7218821	-0.17014871	GPS2	cg09682913	2	30455589	-0.160789982	LBH
cg07852756	4	152021104	-0.169669026	RPS3A	cg16643542	19	827843	0.160786219	AZU1
cg00477061	18	77794585	-0.169560714	C18orf22	cg03754076	1	232766254	-0.160692897	
cg01910197	22	35796030	-0.169135137	MCM5	cg21122725	4	123843781	-0.16062274	NUDT6
cg20116574	20	44718168	-0.169087579	NCOA5	cg21120249	9	139921971	0.160105625	C9orf139
cg09531225	4	82393079	-0.169005298	RASGEF1B	cg24919790	10	90967918	-0.160034928	CH25H
cg04396495	5	60626910	-0.168951894	ZSWIM6	cg20966828	9	74384075	-0.160020427	TMEM2
cg17813364	7	149321879	-0.168877571	ZNF767	cg22094042	11	450123	-0.159993886	PTDSS2
cg01446164	11	2421746	-0.168532183		cg18565702	13	113241891	-0.15987487	TUBGCP3
cg14374980	8	29397161	0.167331051		cg23474794	1	182584178	-0.159554489	B9D1
cg09730697	2	96931861	-0.16727242	TMEM127	cg09537354	17	19266363	-0.159538084	NDUFA10
cg067533281	1	6086652	-0.167253216	KCNAB2	cg24275354	2	240964415	-0.159497264	DPYSL2
cg02276695	19	19774628	-0.166913495	ATP13A1	cg02787772	8	26435434	-0.159492158	DCP1A
cg26223989	18	60189751	-0.166720544	ZCCHC2	cg111198734	3	53381585	-0.159099556	ARID1B
cg05907029	1	197872227	-0.165768203	C1orf53	cg08308556	6	157342734	-0.158975294	
cg25937832	3	23958525	-0.165467301	NKIRAS1	cg10849092	15	40574697	-0.158964065	PKNOX1
cg17019204	6	86303781	-0.165254339	SNX14	cg19764539	21	44394723	-0.158881867	NOL7
cg25371036	11	94500749	0.165007581	AMOTL1	cg05884522	6	13615538	-0.158869514	BICD2
cg10391629	13	42846072	-0.164969318	AKAP11	cg08439468	9	95526812	-0.158781541	MTHFD1L
cg11075316	3	160167725	-0.1648335814	TRIM59	cg21610516	6	151186758	-0.1587097	PIM3
cg04613791	20	1373260	-0.164725767	FKBP1A	cg23962478	22	50354086	-0.158709561	CYTSB
cg21545849	20	40247209	-0.164421404	CHD6	cg14931122	17	20059106	-0.15870089	ATP1B3
cg09185754	10	1095081	-0.164167608	ID1	cg07006042	3	141595655	-0.158690134	WNT3
cg08925142	4	18023851	-0.163893057	LCORL	cg00126034	17	44896162	-0.158665168	PVRL4
cg17329534	1	154980743	0.163804997	ZBTB7B	cg04891053	1	161053558	0.158627481	
cg07730301	11	67777952	0.163310193	ALDH3B1	cg24909975	6	160147912	-0.158614432	WTAP

Figure 20-1

cg08277003	1	26827064	-0.158480859		cg23640903	6	13487662	-0.155506941	GFOD1
cg21411757	12	93771484	-0.158479848	NUDT4	cg05534807	11	75379613	-0.155504427	MAP6
cg01320040	21	43430494	-0.158438631	ZNF295	cg09417530	8	91658296	-0.155421184	TMEM64
cg04749129	2	27008876	-0.158436626	CENPA	cg09818930	16	31106315	-0.155320895	VKORC1
cg14406138	2	139259159	-0.158392558	SPOPL	cg05639310	4	2420719	-0.155140387	ZFYVE28
cg23097985	8	22552961	-0.15837277		cg05641961	15	90776927	-0.155071173	CIB1
cg26910465	15	43622671	-0.158296018	ADAL	cg00661010	6	153323879	-0.155035423	MTRF1L
cg03713996	12	132195583	-0.158236103	SFRS8	cg04441780	15	83479272	-0.154991006	WHAMM
cg11656992	17	79818741	-0.158233802	P4HB	cg12133425	1	24749426	-0.154977542	ZNF496
cg24282486	6	139308723	-0.158157764	REPS1	cg23983067	10	43277941	-0.154910806	BMS1
cg07906495	14	31028426	-0.157971888	G2E3	cg10227077	19	2495139	-0.154890048	
cg20518446	11	62315034	0.157823248	AHNAK	cg03727756	1	51425478	-0.154806964	FAF1
cg12516875	22	46463543	0.157779508		cg22124117	15	43028932	-0.154776905	CDAN1
cg08582555	22	21356051	-0.15777625	FLJ39582	cg02835038	21	47743854	-0.154625803	PCNT
cg05087909	2	9771142	-0.157747549	YWHAQ	cg09189896	2	85766104	-0.154596961	MAT2A
cg03989244	15	72523736	-0.157650562	PKM2	cg26826852	20	37377424	-0.154579717	ACTR5
cg07567376	10	60271505	0.157585237	BICC1	cg20291674	6	159240077	-0.154493667	EZR
cg09150006	6	158652830	-0.157566627		cg11050116	8	17780536	-0.154483705	PCM1
cg05462360	17	18218585	-0.157490209	TOP3A	cg09885409	21	34697563	-0.154407914	IFNAR1
cg15814736	11	63439115	-0.157488041	ATL3	cg07195197	16	1662150	-0.15440381	IFT140
cg22594055	5	131832675	-0.157449138		cg06202737	2	128166279	0.154390569	
cg06987053	16	87947779	0.157444381	CA5A	cg02824291	7	154795251	-0.154361789	PAXIP1
cg04294412	4	7045720	-0.157299983	CCDC96	cg11188633	11	105948590	-0.15430898	AASDHPP
cg04790357	5	40680416	-0.157007678	PTGER4	cg22014600	13	21750851	-0.154308871	MRP63
cg07323055	20	3140559	-0.156926112	FASTKD5	cg08846566	8	80803954	-0.154188217	
cg00635481	6	35226917	-0.156906537	ZNF76	cg20010135	16	30996822	0.154174877	HSD3B7
cg04759220	5	78532560	-0.156859586	JMY	cg05072774	3	49840536	-0.15414679	C3orf54
cg24497877	1	1244060	-0.15682909	PUSL1	cg27575217	12	51984358	-0.154137378	SCN8A
cg005333923	6	116892543	-0.156767322	RWDD1	cg25869317	15	101792241	-0.154031117	CHSY1
cg14621103	7	1178041	-0.156765598	C7orf50	cg16246698	12	133263907	-0.153891022	PXMP2
cg16026760	19	4791699	-0.156709071	FEM1A	cg26408609	7	87563569	-0.153686832	ADAM22
cg04741133	5	43042726	-0.156706477	LOC153684	cg17295834	13	29132547	0.153683996	
cg07743799	20	2821434	-0.156605326	FAM113A	cg15825175	8	103668090	-0.153678281	KLF10
cg21338479	7	101459330	-0.15650623	CUX1	cg08703520	19	58978336	-0.153643968	ZNF324
cg06534892	6	13615533	-0.15637744	NOL7	cg11614451	3	160167729	-0.153641965	TRIM59
cg12878260	5	139028156	-0.156302588	CXXC5	cg17218495	19	11071743	-0.153611813	SMARCA4
cg24742444	12	49524560	-0.156142645	TUBA1B	cg17910478	1	228581288	0.153555604	
cg09881819	3	129034470	-0.155802742	H1FX	cg23727007	6	29716796	-0.153508764	LOC28583
cg12020639	1	110527249	-0.155635439	AHCYL1	cg08424876	3	196669195	-0.153383167	NCBP2
cg13382714	14	31495002	-0.155627697	AP4S1	cg09837385	3	39149225	-0.153375787	GORASP1
cg20752878	17	7080538	0.155570925	ASGR1	cg14974722	17	35306061	-0.153371377	AATF

Figure 20-2

cg14397361	9	140149997	-0.153309057	COBRA1	cg04123995	17	71308339	-0.150918461	CDC42EP2
cg06123753	2	60593185	0.153281414		cg16859906	16	68298978	-0.150914093	SLC7A6
cg16710791	1	193028559	-0.153267263	TROVE2	cg11204983	6	82957301	-0.150911872	IBTK
cg18221226	12	124997487	0.153261211	NCOR2	cg07642705	16	2014817	-0.150831191	SNHG9
cg17727929	21	38069338	-0.153254996		cg23092788	4	949558	0.150827511	TMEM175
cg00232265	5	1814816	-0.153252737	NDUFS6	cg23706268	13	51484060	-0.150779916	RNASEH2I
cg00248174	10	43600239	-0.153169685	RET	cg01025283	3	138327728	-0.15077408	FAIM
cg02249648	12	1703181	-0.153117313	FBXL14	cg17978996	6	107436496	-0.150653997	BEND3
cg05501276	7	23571514	-0.152912497	TRA2A	cg15901997	18	48723744	-0.150636021	MEX3C
cg05468351	5	21459598	-0.152911507	LOC728411	cg12570942	2	242626270	-0.150572219	DTYMK
cg12922931	21	33984727	-0.152902343	C21orf59	cg14945578	20	3776324	-0.150567537	CDC25B
cg24395307	7	39990042	-0.152765999	CDK13	cg24640588	4	1283718	-0.150530252	MAEA
cg06912282	1	1563001	0.152708218	MIB2	cg19804488	17	73760363	0.150502464	GALK1
cg01943813	6	24495061	-0.152647113	ALDH5A1	cg01102854	11	63605717	0.150488304	MARK2
cg16007497	4	74713356	0.152454835	PPBPL1	cg22043361	14	64970199	-0.15047175	ZBTB1
cg10786622	6	17706560	-0.152409545	NUP153	cg16971831	5	56110935	-0.150460325	MAP3K1
cg11075994	15	102192790	-0.152309844	TM2D3	cg22332388	8	64081173	-0.150359955	YTHDF3
cg12133664	12	94217493	0.152046022	CRADD	cg26541587	10	43950885	-0.150328936	ZNF487
cg05669853	6	107435226	0.152011974	BEND3	cg24085655	6	35436189	-0.150295392	RPL10A
cg17626178	2	205410273	-0.151976152	PARD3B	cg15818008	11	112126170	0.15028977	C11orf34
cg08884209	5	73981306	-0.151931335	HEXB	cg15684661	5	1795014	0.150277861	
cg26337430	1	43232221	-0.151895538	LEPRE1	cg16395133	6	150326394	-0.150241954	RAET1K
cg06478398	19	1479426	-0.151864871	C19orf25	cg20890156	8	53627208	-0.150238928	RB1CC1
cg18455653	20	17662865	-0.151859378	RRBP1	cg10414829	10	88719259	0.15017174	SNCG
cg10338848	16	7701595	0.151809987	A2BP1	cg21753290	20	37376903	-0.150140034	ACTR5
cg25609649	2	19547730	-0.151784709		cg02043083	6	150070997	-0.150111476	PCMT1
cg19847945	17	60783784	0.151708191	10-Mar	cg02006147	2	74734710	-0.150089989	PCGF1
cg06764670	1	110052490	-0.151705335	AMIGO1	cg01049274	8	146228340	-0.150047572	ZNF252
cg11967952	1	52498983	-0.151696194	TXNDC12	cg16811230	3	39149235	-0.149965796	GORASP1
cg08096946	3	122514224	-0.151585448	DIRC2	cg18613834	7	65215902	-0.149929372	CCT6P1
cg02357725	15	75932598	-0.151580256	IMP3	cg24781737	11	66034681	0.149919889	KLC2
cg05180153	19	11039414	-0.15157422	YIPF2	cg18199720	1	115054041	-0.149877242	TRIM33
cg24298255	19	58280994	-0.151430693	ZNF586	cg04081402	22	31003587	0.149871454	TCN2
cg03647327	6	28891109	-0.151357238	TRIM27	cg02631957	5	122847966	-0.149774738	CSNK1G3
cg04410161	6	116892488	-0.151305719	RWDD1	cg27193080	3	129160612	0.14976515	IFT122
cg04794887	4	1858231	-0.151286531	LETM1	cg26745551	6	97285260	-0.149685651	GPR63
cg03519303	4	139936796	-0.15122989	CCRN4L	cg07793203	2	9771347	-0.149655797	YWHAQ
cg03966045	2	202316319	-0.151183333	STRADB	cg12359279	21	42797953	-0.149655305	MX1
cg20137586	12	95043552	-0.151125738	TMCC3	cg23955684	3	16555288	-0.149647391	RFTN1
cg09840736	3	47205788	-0.150944043	SETD2	cg05988158	22	51021418	-0.14964072	CHKB-CPT
cg19080138	7	35734733	-0.150935037	HERPUD2	cg04258457	17	62207789	-0.149635563	ERN1

Figure 20-3

cg16103421	15	102068632	0.149520412		cg05738924	2	144995448	0.14829255	GTDC1
cg10972821	17	55163212	-0.149514625	AKAP1	cg17154187	17	18163844	-0.148283886	SMCR7
cg11909217	16	23569246	-0.149498547	EARS2	cg06058395	18	13726784	-0.148280468	C18orf19
cg08629647	22	46692562	-0.14949374	GTSE1	cg02357877	7	56032049	-0.148259756	GBAS
cg22084410	3	51987688	0.149484748		cg23320649	3	50604613	0.148240924	C3orf18
cg09841203	13	52733292	-0.14947635	NEK3	cg12100751	1	109203672	-0.148232565	C1orf59
cg02110858	8	145028222	0.149448761	PLEC1	cg27414860	16	4852427	-0.148207496	ROGD1
cg25296860	13	20702426	-0.149415589		cg15967188	4	2470700	-0.148189045	RNF4
cg13267195	11	67777215	0.149414279	ALDH3B1	cg12243976	12	133563125	-0.148089896	ZNF26
cg05001598	9	114246158	-0.149291453	KIAA0368	cg24097153	12	122231765	-0.147940216	RHOF
cg05500574	19	58962884	-0.149286244	ZNF324B	cg24848615	19	3368396	0.147907846	NFIC
cg10480239	22	23522307	0.149217989	BCR	cg17024199	17	74881747	0.147840184	MGAT5B
cg19656070	17	3571978	-0.149217902	TMEM93	cg18770186	8	141521259	-0.14783855	CHRA1
cg19761211	16	70415365	-0.149210318	ST3GAL2	cg02932736	1	67896194	-0.147837458	SERBP1
cg02818189	1	25173236	0.149159776		cg25562925	2	25110049	0.147817341	ADCY3
cg24904084	5	14653382	-0.149150582	FASTK	cg23018091	1	32758168	0.147772105	HDAC1
cg26975609	7	150777587	-0.149148473	DUT	cg21442773	1	236029828	-0.147753262	LYST
cg24106894	15	48623432	-0.149130669	IFT122	cg12962778	12	54778312	0.147736731	ZNF385A
cg04584087	3	129159014	-0.14912679	EFNA3	cg01385795	11	14913124	-0.147717124	CYP2R1
cg11688696	1	155052192	0.149031833	DBP	cg15541611	10	104211319	0.147692866	C10orf95
cg03231960	19	49139050	-0.149009914	ZNF805	cg22512633	4	39640549	-0.147683986	C4orf34
cg26758863	19	57752111	-0.148965348	DEF8	cg00049253	1	231473541	-0.147665885	EXOC8
cg01134297	16	90014983	-0.148947814	C3orf57	cg22796393	3	50375250	-0.1476625	RASSF1
cg22984041	3	161090118	-0.148900293	RAP1GDS1	cg25753024	11	67070913	0.147655116	SSH3
cg21308020	4	99182242	-0.148888958	KRT17	cg16664617	19	17607007	0.147639896	SLC27A1
cg27236973	17	39781997	0.148859457		cg06186940	12	93322861	-0.147610253	EEA1
cg16263943	2	144695179	-0.148838578	C13orf37	cg19906131	11	93862516	-0.14760571	PANX1
cg03631596	13	73301985	-0.14879802	PFKL	cg01318248	1	226736816	-0.147569449	C1orf95
cg05129930	21	45719797	-0.148776087	CCDC6	cg14319655	19	15490716	-0.147489505	AKAP8
cg11017226	10	61666667	-0.148766615	EID2B	cg14235783	11	65420518	-0.147480169	MAP3K12
cg04706880	19	40023151	-0.148758074	ZNF672	cg18070593	12	53891718	0.147478964	
cg02016753	1	249132838	-0.148746861	GTF2H4	cg10620680	1	178025100	0.14747724	C13orf37
cg25467336	7	2757616	0.148681857	ZNF787	cg05380793	13	73301995	-0.147471604	PLK4
cg16257334	6	30881842	-0.148652748	ZNF174	cg10393416	4	128802077	-0.147435391	SCAMP1
cg18473162	19	56631888	-0.148616405	TRIM27	cg06994657	5	77656066	-0.147364293	CRNKL1
cg05663418	16	3451086	-0.148552528	C16orf87	cg04275707	20	20033092	-0.147318515	C6orf81
cg25589651	6	28891121	-0.148551078	LBR	cg18357736	6	35705549	0.147287498	BRPF1
cg06793581	16	46865077	-0.148541202	DDX19B	cg20952324	3	9773343	-0.147279052	GNL3
cg18764107	1	225615669	-0.148444024	SLC6A6	cg05573699	3	52720067	-0.147278181	FAM158A
cg14244577	16	70332878	0.148366225		cg25953341	14	24610919	-0.147276991	
cg08655589	3	14444175	-0.148293474		cg16512867	3	136581189	-0.147259919	NCK1

Figure 20-4

cg15602950	3	45731220	-0.147239041	SACM1L	cg09000830	1	94883752	-0.146442665	ABCD3
cg16243665	19	5720655	-0.147212861	TMEM146	cg09853387	7	139877374	-0.146426779	LOC10013
cg04265971	4	2470698	-0.147199336	RNF4	cg08346494	11	70049962	-0.146402613	FADD
cg20383686	1	6052612	-0.147193576	NPHP4	cg15746187	1	11713123	0.146352023	FBXO2
cg08223393	1	955701	-0.147192362	AGRN	cg08863777	11	94278457	0.146344438	FUT4
cg04911669	6	73697178	0.147184786	KCNQ5	cg21599869	2	239335445	-0.146300923	ASB1
cg04128145	16	69373507	-0.147170843	COG8	cg11997536	19	16176297	0.146257897	
cg13637733	15	70390233	-0.147146093	TLE3	cg10403048	19	15490832	-0.14624772	AKAP8
cg13173552	1	16091599	0.147133852	FBLIM1	cg18406718	4	102269374	-0.146239528	PPP3CA
cg16672637	17	74138356	0.147127412	FOXJ1	cg03077062	2	73299091	-0.146230884	SFXN5
cg06391926	16	1832733	-0.147095962	NUBP2	cg04910183	1	193090988	-0.146203037	CDC73
cg03200502	6	24403107	-0.147083317	MRS2	cg14078059	12	65174660	-0.14617734	
cg22974920	21	40686053	-0.147061565	BRWD1	cg25463963	19	47214580	0.146147025	PRKD2
cg02547025	2	30454275	-0.14703693	LBH	cg16080746	4	87928530	-0.146130849	AFF1
cg10912077	1	87794075	-0.146988366	LMO4	cg11159591	1	208417937	-0.146129471	PLXNA2
cg05146683	18	23670721	-0.146883897	SS18	cg03959891	7	99933717	-0.146083138	PILRB
cg05544840	13	44716513	-0.146878083		cg06180363	19	59056346	-0.14607458	TRIM28
cg11338666	17	3539646	-0.146825216	CTNS	cg27366007	15	91479184	0.146067898	UNC45A
cg08408668	19	1173241	0.146823834	SBNO2	cg16887862	1	1243669	-0.146055799	PUSL1
cg02303317	10	135122580	-0.146813202	TUBGCP2	cg00473462	5	472545	-0.146048822	LOC25845
cg10028071	10	22604918	-0.146799716	COMMD3	cg01249735	7	156742241	-0.146046155	NOM1
cg17492326	8	124780746	-0.146792534	FAM91A1	cg16374343	17	1014352	0.146009788	ABR
cg06150454	3	185364870	0.146760841	IGF2BP2	cg09339301	6	163836245	-0.146007077	QKI
cg02832646	16	81040020	-0.146760802	CENPN	cg00736299	16	4730465	0.145977834	MGRN1
cg21806917	11	66384012	-0.146757252	RBM14	cg09858777	16	4743966	-0.145949666	NUDT16L
cg13676763	9	129262204	0.146725124	FAM125B	cg14686845	8	6565560	-0.145949231	AGPAT5
cg16229180	19	1103746	-0.146693326	GPX4	cg08810813	16	686527	-0.145942912	C16orf13
cg18100007	17	29815661	-0.146691364	RAB11FIP4	cg18917495	2	74006961	-0.145880939	DUSP11
cg13443911	9	101866107	0.146690776	TGFBF1	cg16687867	11	111896092	-0.145871726	DLAT
cg18162528	11	133826660	-0.146661922	IGSF9B	cg19468028	22	17639712	-0.145870811	CECR4
cg19189965	12	123459820	-0.146654704	ABC9	cg14644065	9	130476625	0.145856379	PTRH1
cg03623771	17	79650928	-0.14665005	HGS	cg21818333	3	130745442	-0.145853626	NEK11
cg14831946	7	90893731	-0.146601178	FZD1	cg00811377	6	30636608	0.14584128	DHX16
cg01866597	16	837896	-0.146586783	RPUSD1	cg26933453	19	17530662	-0.145817678	FAM125A
cg05455036	1	202828149	0.14655374		cg11801411	17	1628727	0.14580947	WDR81
cg24258716	8	143820480	-0.146541264		cg21667796	11	63804119	-0.145807112	MACROD1
cg04488215	1	174968829	-0.146540086	CACVBP	cg09055943	21	43431271	-0.145764734	ZNF295
cg11694433	15	63796712	-0.146522576	USP3	cg16026299	1	84764375	-0.145737234	SAMD13
cg16843718	22	50322571	0.146511153		cg26998900	18	5238137	-0.145714389	C18orf18
cg09346030	10	13390377	-0.146485284	SEPHS1	cg07168181	7	2884124	-0.145683843	GNA12
cg15884202	7	158649092	-0.146450039	WDR60	cg19514721	5	141813298	0.145677927	

Figure 20-5

cg01313966	18	47901443	-0.145649922	SKA1	cg16788234	11	108093338	-0.144584744	NPAT
cg24001556	20	5591874	-0.145636981	RP5-1022P6.2	cg02016838	11	109963531	-0.144564254	ZC3H12C
cg07617384	15	74392612	-0.145606454		cg01259782	16	21313973	0.144545051	CRYM
cg13430225	1	53662423	-0.145427102	CPT2	cg08133912	19	47747483	-0.144533911	
cg21243939	14	55033137	-0.145400717	SAMD4A	cg11436767	11	46401422	0.144518118	MDK
cg00421624	1	153746588	0.145345528	SLC27A3	cg23659250	22	50174065	0.144496308	BRD1
cg01574390	16	21623651	0.145328826	METTL9	cg25372103	6	170599661	-0.144484397	DLL1
cg19591588	3	45730799	-0.145316484	SACM1L	cg16928487	17	17741425	0.144471087	SREBF1
cg24000232	1	166808428	-0.145293301	POGK	cg10463708	1	90309205	-0.144457118	LRRC8D
cg03512248	1	28517610	0.145288929	PTAFR	cg20227213	3	37284559	-0.144454047	GOLGA4
cg03236816	19	36618904	-0.145262962		cg05867307	4	144106066	-0.144441974	USP38
cg23408670	17	36831499	-0.145247503	C17orf96	cg07535605	18	158294	-0.144410067	USP14
cg18794664	1	42922694	-0.145191673	ZMYND12	cg21740452	21	34143691	-0.144386437	C21orf66
cg18925864	17	48624421	-0.145180463	SPATA20	cg07097722	20	43247325	-0.144373596	PKIG
cg01693598	1	47998637	0.145157565		cg01406317	16	4397291	0.144364867	Magmas
cg08285587	7	152161197	-0.145141416	LOC100128822	cg04569651	5	177956199	0.144299333	COL23A1
cg12124516	2	136634144	-0.145097583	MCM6	cg07471962	14	55368706	-0.144297295	GCH1
cg25414605	11	67182672	0.145069327	ATPGD1	cg21160472	1	212782112	-0.144296979	ATF3
cg11464438	2	113957041	0.145052514	PSD4	cg15441731	14	74036128	-0.144240375	ACOT2
cg24331354	3	14444067	-0.145018838	SLC6A6	cg10101470	1	90286633	-0.144223979	LRRC8D
cg13190306	11	18415923	-0.144959234	LDHA	cg17338544	11	44559989	0.144210963	
cg19916323	19	16653199	-0.144953856	CHERP	cg04690289	3	45017999	-0.144200383	ZDHH3
cg23200000	1	245027629	-0.144947456	HNRNPU	cg10298855	14	35874025	-0.14418808	NFKBIA
cg19696103	5	132354130	0.144938565	ZCCHC10	cg03183872	20	3140552	-0.144150199	FASTKD5
cg26449680	22	38714272	0.144934305	CSNK1E	cg09527615	11	94883350	0.144140151	
cg20080702	10	74046947	0.144867036		cg00367327	22	44419885	-0.144127129	PARVB
cg26761504	19	49140601	-0.144863958	SEC1	cg24099956	11	113907379	0.14411921	
cg08723131	20	55043694	-0.144850307	C20orf43	cg19240052	22	42475693	-0.144112873	C22orf32
cg17290332	10	14880008	-0.144849792	CDNF	cg07315521	16	71929403	-0.144070658	KIAA0174
cg02569115	17	76922138	0.144810669	TIMP2	cg27637895	1	118472247	-0.143998043	GDAP2
cg13189086	15	23034679	-0.144801106	NIPAZ	cg23959009	4	83352458	-0.143981513	ENOPH1
cg05978546	5	131132739	-0.144799677	FNIP1	cg08136416	21	44060833	0.143980372	
cg08802167	14	74959978	-0.144795178	NPC2	cg19529645	17	79196743	-0.143977208	AZI1
cg14871856	8	30515337	-0.144786495	GTF2E2	cg21403330	7	1178030	-0.143965672	C7orf50
cg26215227	14	55518143	-0.144776671	MAPK1IP1L	cg21012061	1	205568557	0.143952643	MFSD4
cg27564108	1	150585651	0.144764715		cg25123308	2	113300087	-0.143919987	POLR1B
cg11826961	17	38221639	0.144763914	THRA	cg06233552	17	5322836	-0.143905247	RPAIN
cg16048537	5	39074780	-0.144750624	RICTOR	cg03725309	1	109757585	0.143897155	SARS
cg09932345	1	1710561	-0.144653677	NADK	cg19426773	6	139309558	-0.143892848	REPS1
cg00957688	1	36183672	0.14464267	C1orf216	cg12586707	4	74738902	0.143822018	
cg02244204	5	625213	0.144640223	CEP72	cg01733795	17	7465439	-0.14381146	SENP3

Figure 20-6

cg10080401	22	22210635	0.143800265	MAPK1	cg10107890	2	44314289	0.143254484	
cg16573386	1	1334508	-0.14378666	CCNL2	cg10393931	7	95951432	-0.143252546	SLC25A13
cg20102034	2	74653166	0.143758904	RTKN	cg06177860	15	60884785	-0.143249002	RORA
cg05048680	1	1342566	-0.143758879	MRPL20	cg00715047	17	73522054	-0.143246665	LLGL2
cg04593445	16	2265125	-0.143750317	PGP	cg04928693	1	155178248	0.14323694	MTX1
cg10427040	17	74261306	-0.143731837	FAM100B	cg13639083	9	100957746	0.143236274	
cg09456216	2	175870288	-0.143721701	CHN1	cg07851008	2	109335747	-0.14322934	RANBP2
cg13380562	6	143832576	-0.143704172	FUCA2	cg22766770	17	18218566	-0.143180143	TOP3A
cg06003169	4	103422460	-0.143675707	NFKB1	cg00608540	5	180627973	0.143164608	TRIM7
cg10093594	1	206858754	-0.143666241	MAPKAPK2	cg24014462	17	12921391	-0.143160808	ELAC2
cg06329143	18	48556512	-0.143662321	SMAD4	cg04309350	8	67341294	-0.14314686	RRS1
cg13807549	9	116444721	0.143653248		cg01332181	19	47290716	-0.143143759	SLCIA5
cg24694913	19	58978210	-0.14362171	ZNF324	cg13801946	17	61699522	-0.14313367	MAP3K3
cg23908998	10	22292698	-0.143614577	DNAJC1	cg08700690	15	60884630	-0.143048803	RORA
cg11723896	17	34136427	-0.143574196	TAF15	cg14592933	7	26416122	-0.14302871	
cg20835353	7	99698988	-0.143554889	MCM7	cg10051414	22	38598733	-0.143026203	MAFF
cg09039698	16	30007384	-0.143550055	HIRIP3	cg27579771	5	142431272	0.143019345	ARHGAP2
cg00533407	7	150745278	0.14354925	ACCN3	cg19594024	19	58919948	-0.14295505	ZNF584
cg08161931	8	145028402	0.143530309	PLEC1	cg07536998	4	178363522	-0.142939512	AGA
cg16588137	4	186064512	-0.143516018	SLC25A4	cg17923377	22	50174057	0.1429254	BRD1
cg15686615	4	6781565	0.14351396		cg18167179	14	74058881	-0.142923356	ACOT4
cg12445422	11	113920436	0.143508166		cg15783696	16	68564277	-0.142916685	
cg26952697	6	148881461	0.143506126		cg02505296	8	63951123	-0.142910631	GGH
cg13883202	3	47422330	-0.14350314	PTPN23	cg10604550	5	43001210	0.142904319	NXT1
cg10124993	14	105478712	0.143441685	CDC4	cg26752655	20	23331282	-0.14289375	
cg08451517	8	125383826	-0.143430215	TMEM65	cg06704539	7	102105256	-0.142870548	ALKBH4
cg20468415	8	41592973	0.143423115	ANK1	cg11673391	1	10459052	-0.142813926	PGD
cg26775866	5	159849193	0.143406385	PTTG1	cg11210652	12	32260091	-0.142812635	BICD1
cg01305745	16	31106788	0.143398108	VKORC1	cg08915922	1	42127381	-0.142801393	HIVEP3
cg21279955	1	153747551	0.143392101	SLC27A3	cg00929964	6	30879921	0.142783337	GTF2H4
cg01437482	14	100772378	-0.14338621	SLC25A29	cg23054379	1	176176226	-0.142772794	RFWD2
cg27605748	5	42951711	-0.143378774		cg12143717	8	145133263	-0.142764142	EXOSC4
cg01905773	17	79297618	0.143374854	TMEM105	cg13371705	12	2452955	0.142736454	CACNA1C
cg03029755	17	76265444	0.143353737		cg18045172	6	32801648	-0.142733855	TAP2
cg22666115	6	30182186	-0.143347521	TRIM26	cg02839220	16	4400790	-0.142727983	Magmas
cg01307174	3	35722556	0.143306493	ARPP-21	cg10648908	22	43253189	-0.142655385	ARFGAP3
cg06708720	12	1099075	0.143301954	ERC1	cg14461650	2	101925089	-0.142625869	RNF149
cg15420687	5	159546321	-0.143293962	PWWP2A	cg27661869	17	61627703	-0.142616659	DCAF7
cg03361810	8	42010162	-0.143289592	AP3M2	cg23044186	5	141228416	0.142608028	
cg21550006	2	97760606	-0.143273409	FAHD2B	cg15444566	15	63796413	-0.142599782	USP3
cg14815005	22	22222162	-0.143256624	MAPK1	cg03240232	12	113448327	0.142569771	OAS2

Figure 20-7

cg05289892	11	67070816	0.142568423	SSH3	cg10277631	14	53019580	-0.142036723	TXNDC16
cg20669049	19	55573572	0.142560169	RDH13	cg03536846	8	120886254	-0.142033842	DEPDC6
cg162335860	1	62902122	-0.142547332	USP1	cg04792715	3	49058577	-0.142024737	MIR191
cg26478485	10	112257641	-0.142529671	DUSP5	cg27413118	2	238969595	-0.142023689	SCLY
cg24899068	19	49999470	-0.142527579	RPS11	cg12616531	4	8160892	-0.142000222	ABLM2
cg02141084	12	8834151	0.142487773		cg13309513	17	40811520	-0.141993264	TUBG2
cg00798281	6	33041697	0.142451642	HLA-DPA1	cg07188523	6	44528793	0.141982609	IMPDH1
cg16501572	11	71934660	-0.142432178	INPPL1	cg06372654	7	128044655	0.141964604	RAB10
cg23651356	6	153452954	0.142417229	RGS17	cg17959183	2	26297671	0.141872897	GPR44
cg11355601	22	39096475	-0.142413325	JOSD1	cg19254163	11	60623782	0.141865552	
cg12700464	11	78128424	-0.142339	GAB2	cg16679302	16	85622276	0.141858724	ZSCAN29
cg14183540	11	3175007	0.142321201	OSBPL5	cg26789400	15	43663318	-0.141845397	
cg02271677	2	130939252	-0.142314268	SMPD4	cg26902127	16	88513285	0.141838083	
cg23572376	6	1610120	-0.142308491	FOXC1	cg17029062	3	32859445	-0.141837757	TRIM71
cg23233742	5	139077894	0.142308414	CDC25A	cg06654628	5	150018914	0.141829279	SYNPO
cg10341991	3	48229869	-0.142298724	DYNC11I2	cg01896926	17	685509	-0.141827087	GLOD4
cg09504873	16	66774626	0.142286216	SLFN12L	cg03327386	18	8609878	-0.141798651	RAB12
cg03182688	17	33825300	0.142276211	SIC16A1	cg07485181	2	131851172	-0.141787096	FAM168B
cg24347098	1	113456650	0.142266323		cg00881254	18	657522	-0.141784809	TYMS
cg12707346	12	64960957	0.142266268	SIKE1	cg24231804	15	67316861	0.141781051	
cg08339208	1	115323327	-0.142265519	PPPIR12C	cg02956542	1	153321421	0.141771061	PGLYRP4
cg25794819	19	55629097	-0.142249393	ZNF26	cg03666053	4	2765951	-0.141764691	BSPRY
cg08382497	2	232469534	-0.142239341	WHAMM1L1	cg02003202	9	116111459	0.141745034	
cg16250856	12	133563128	-0.142224566		cg01701959	1	51443542	-0.141710805	ARL15
cg04175957	15	23207925	-0.142211301	LSP1	cg01196404	5	53606491	-0.141701685	EPDR1
cg04366628	4	26290463	0.142208378	H1FX	cg24953179	7	37960251	-0.141698998	WRNIP1
cg09060789	11	1884988	0.142206128	QRICH1	cg01067849	6	2765587	-0.141662958	LARP1
cg12276904	3	129035177	-0.142193542	NDFIP1	cg22512536	5	154134507	-0.141608708	IKZF5
cg17663101	3	49131524	-0.142177838	KPNA2	cg19696333	10	124768261	-0.141598301	ACOT7
cg17323243	5	141488153	-0.142177803	CDC20	cg27316808	1	6453995	-0.141587484	DCUN1D2
cg09771049	17	66031798	-0.142169758	MAP3K6	cg27560367	13	114144049	0.141549134	NRXN2
cg06699484	5	132166328	-0.142138577	KPNA2	cg09129050	11	64478374	0.141521271	KARS
cg08263040	1	43824491	-0.142123673	LOC283404	cg26812503	16	75681495	-0.141501297	DHRS3
cg26161024	1	27693840	0.142122906	CYBR3	cg26937389	1	12677975	-0.141468946	F12
cg17985418	17	66031785	-0.142106255	GNA13	cg25962774	5	176831364	-0.141442173	FNDC1
cg09802818	12	52604609	0.142096244	HNRNPA3	cg14971597	6	159590578	-0.141422488	PPHLN1
cg10250355	22	43045158	-0.142086732	EIF4H	cg24452366	12	42719850	-0.141402578	
cg09580608	17	63052483	-0.142086287	FAM188A	cg06635946	22	46470016	0.141376824	SGK196
cg05434655	2	178078121	-0.142084203		cg25861458	8	42948482	-0.141313584	P2RY2
cg13353389	7	73609617	0.142056986		cg01550445	11	72929983	0.141308444	
cg01162436	10	15902292	-0.142039844		cg09317239	10	21818060	0.141301174	

Figure 20-8

cg00355829	3	128326679	0.141284711		cg13850871	9	139583773	0.140769543	
cg14389547	19	3398778	0.141281524	NFIC	cg14533881	17	79361650	0.14076785	
cg02463426	19	16683387	-0.14127762	SLC35E1	cg22033189	1	28908551	-0.140764715	SNHG12
cg02775028	4	184580387	-0.141272302	C4orf41	cg17457912	17	1617102	0.140762759	C17orf91
cg08116711	7	101596218	0.141271838	CUX1	cg00164196	2	162095477	-0.140757784	
cg12665973	15	42867875	-0.141268104	STARD9	cg25347941	22	43486472	0.140741734	TTL1
cg04888030	2	113033033	-0.141257674	ZC3H6	cg03954150	18	71815372	-0.140736768	C18orf55
cg14428767	6	149867359	-0.141255695	PPIL4	cg25213720	5	176734343	0.140693163	MXD3
cg24798115	7	149157735	-0.141232962	ZNF777	cg25021247	3	49460162	0.140685924	AMT
cg26490839	19	49999468	-0.14121366	RPS11	cg01035038	14	88459686	-0.140684248	GALC
cg22162404	19	8273842	-0.141213142	LASS4	cg02197392	19	13049544	-0.140650309	CALR
cg01411894	6	86303454	-0.141204473	SNX14	cg14031414	20	13765665	-0.140607259	ESF1
cg00666849	2	85839032	-0.14118894	C2orf68	cg14229247	9	100745139	-0.140572797	ANP32B
cg08669096	11	121229765	0.141179606		cg03646967	3	61196428	-0.140569709	FHIT
cg26904702	1	153746899	0.14117201	SLC27A3	cg18001714	5	14871894	-0.140563924	ANKH
cg23267217	1	26496298	-0.141171116	ZNF593	cg25944720	6	106958640	-0.140512105	AIM1
cg27203184	7	100081966	0.141163475	C7orf51	cg18751306	15	81294292	-0.140504767	MESDC1
cg11690666	17	80415469	0.141067206	NARF	cg13475822	3	9210116	-0.140498751	SRGAP3
cg03399927	11	64036876	-0.141064683		cg05729480	17	75276428	0.140490295	9-Sep
cg02793948	11	68095662	0.141047963	LRP5	cg13752043	9	131644109	-0.140487766	LRRC8A
cg07383443	12	118573736	-0.141036051	PEBP1	cg18467978	19	47134906	0.140469522	
cg01153872	2	240323819	-0.14101712	HDAC4	cg23281075	1	31538727	-0.14045366	PUM1
cg13567813	19	50879636	-0.141011242	NR1H2	cg24668150	10	27389076	-0.14043479	ANKRD26
cg09864245	11	33746426	0.141011047	CD59	cg17665608	10	43633793	-0.140424471	CSGALNA1
cg26987179	17	40307119	-0.140992169	RAB5C	cg15440973	14	24610792	-0.140422901	FAM158A
cg20107653	22	42228989	-0.140975054	SREBF2	cg13053396	12	7168545	0.1404228	C1S
cg22111723	13	21872664	-0.140965278		cg12419348	17	54991398	-0.140408612	TRIM25
cg13717023	5	53606639	-0.14095761	ARL15	cg15238008	12	9600875	-0.14038581	DDX12
cg13672514	12	123869502	0.140948561	SETD8	cg04468671	12	132337407	0.14032159	
cg08527566	12	95611432	-0.140939378	FGD6	cg05006942	16	69776039	0.140302667	NOB1
cg05465755	9	91926196	-0.140914728	CKS2	cg26227101	1	14075870	-0.140293274	PRDM2
cg16001977	22	32340332	-0.140909322	YWHAH	cg11162385	20	25604740	-0.140288363	NANP
cg20288129	3	122745632	-0.140901438	SEMA5B	cg04426007	4	166129241	-0.140279294	KLHL2
cg00779206	12	2914519	0.140898497	FKBP4	cg03295933	19	1479358	-0.140261436	C19orf25
cg20577878	16	66914781	-0.140887469	PDP2	cg08092393	14	64970675	-0.140255646	ZBTB25
cg14426371	9	113714986	-0.140880317	LPAR1	cg17341174	7	97923834	0.140240012	BAIAP2L1
cg14156905	1	17193979	0.140877411		cg02385710	11	64884962	-0.14022812	ZNHIT2
cg03071793	16	11682634	0.140835067	LITAF	cg02130266	22	17078353	-0.140180673	
cg00286773	11	12207449	0.140831425	MICAL2	cg07945480	4	2964972	-0.140170738	GRK4
cg07326768	15	86337453	-0.140827552	KLHL25	cg00431050	10	103985730	0.140165615	ELOVL3
cg26896160	1	6454004	-0.140799114	ACOT7	cg20310071	8	77912528	-0.140140087	PXMP3

Figure 20-9

cg07172256	5	65220910	-0.140124048	ERBB2IP	cg15102777	10	127511674	-0.139766363	BCCIP
cg05914712	19	33864373	-0.140108759	CEBPG	cg02083189	1	100503813	-0.139761249	HIAT1
cg23684603	4	185747386	-0.140107225	ACSL1	cg04159215	10	126182324	0.139755036	LHP
cg25039902	14	103063148	-0.140103012	RCOR1	cg26580576	4	6675790	-0.139743417	LOC93622
cg18176482	1	161128720	0.140094983	USP21	cg17193921	22	50683583	-0.139738644	TUBGCP6
cg15500658	1	16174610	-0.14007385	SPEN	cg07810106	5	131630122	-0.139734148	SLC22A4
cg02070289	5	43066798	-0.14005195		cg01377696	20	32581542	-0.139731316	RALY
cg00509610	3	12528629	0.140050677	TSEN2	cg04705952	1	160066587	0.139712804	IGSF8
cg01398415	1	226309536	-0.140048		cg00594118	9	140150000	-0.139707838	COBRA1
cg25136353	10	44185896	-0.140047889		cg02999224	14	23284559	0.139700564	SLC7A7
cg27234239	2	121010047	-0.140014512	RALB	cg24608684	6	130686865	-0.139682436	
cg01441777	22	38714416	0.140013072	CSNK1E	cg02994588	1	24828970	-0.139670677	RCAN3
cg22499237	16	2587546	-0.140001227	PDPK1	cg17442852	17	1478889	0.139662547	SLC43A2
cg17526741	5	126366741	-0.139982332	3-Mar	cg10610348	19	2427956	-0.139661366	TIMM13
cg26260386	4	140477698	-0.139979578	SETD7	cg23872935	5	130599536	-0.139649183	CDC42SE2
cg03576863	16	69415422	0.139973796	TERF2	cg07274776	2	203241322	-0.139639797	BMPR2
cg20521685	17	10600763	-0.139971177	C17orf48	cg10287970	6	7115345	0.139628123	RREB1
cg27467996	5	179921670	-0.139956085	CNOT6	cg20670292	2	131099506	-0.139620627	IMP4
cg22248011	6	52442381	-0.139946299	TRAM2	cg24534743	1	27884345	0.139607926	AHDC1
cg09048062	11	129892327	-0.13994208		cg11429664	15	91260578	-0.139605859	BLM
cg17418708	2	204400358	-0.139939352	RAPH1	cg24732796	11	133907497	-0.139594535	LOC10012
cg07824483	17	79882042	0.139934863	MAFG	cg16185365	3	196230308	-0.139589869	RNF168
cg15638207	6	5261560	-0.139934528	LYRM4	cg00536939	11	47279352	0.139589455	NR1H3
cg04738301	12	96184580	-0.139933106	NTN4	cg08502703	21	45138838	-0.139570156	PDXK
cg00484122	2	20579065	0.139926336		cg08794928	6	144537264	-0.139564831	
cg02093647	2	148602395	-0.139916596	ACVR2A	cg04296257	2	219536679	-0.139554224	STK36
cg08867893	10	64134160	-0.139904822	ZNF365	cg02178957	16	85964200	0.139546843	FAM46B
cg05105845	14	55369781	-0.139904698	GCH1	cg24312792	1	27337638	0.139519683	SETD3
cg19695335	20	25604759	-0.139843104	NANP	cg00763768	14	99947408	-0.1395129	PLEKHA6
cg03479527	8	145637966	0.139835399	SLC39A4	cg24537993	1	204275926	0.139488917	NUDT6
cg03951132	20	5931305	-0.13983285	MCM8	cg00019301	4	123843794	-0.139481422	HAGH
cg00546897	21	45232232	0.139824625	LOC284837	cg03638642	16	1877211	-0.139461012	C17orf95
cg16340159	2	240322705	-0.139814047	HDAC4	cg25699034	17	74721824	0.139455215	CLU
cg11357670	13	114143948	0.139813506	DCUN1D2	cg19442470	8	27470225	0.139449051	LEPRE1
cg25365783	7	108166722	-0.139803966	PNPLA8	cg19044674	1	43232628	-0.139412398	KLHL21
cg08452546	5	118323860	-0.139797182	DTWD2	cg01881062	1	6660403	0.139406873	EIF3J
cg23535768	15	68570349	-0.139787616	FEM1B	cg11515196	15	44829065	-0.139404162	MOGS
cg15543443	6	33386036	-0.139783399	CUTA	cg07321171	2	74692645	-0.139397731	
cg01854842	20	49547693	-0.1397828	ADNP	cg03598938	2	191502738	0.139395724	MIR17HG
cg00083188	10	79314844	0.13977793	KCNMA1	cg10945667	13	91999862	-0.139385185	
cg03926751	4	88140261	0.139772908	KLHL8	cg12995410	6	151712734	-0.139358518	ZBTB2

Figure 20-10

cg00443276	17	15848206	-0.139346001	ADORA2B	cg01811416	1	227127838	-0.138869417	CABC1
cg27286107	3	88108209	-0.139307682	CGGBP1	cg14694952	4	3076907	-0.138855297	HTT
cg26188571	5	179050811	-0.139300554	HNRNPH1	cg01422009	16	125896	0.138854555	MPG
cg10646145	2	9235600	0.139272066		cg01089095	10	75541668	-0.138838044	CHCHD1
cg26712763	17	21030248	-0.13924529	DHRS7B	cg01794932	1	1209696	-0.138827943	UBE2J2
cg03499675	6	31744339	0.13923966	C6orf27	cg05954120	1	156254757	0.138823075	TMEM79
cg06014792	17	7382760	-0.139213431	ZBTB4	cg26336164	19	4791680	-0.138807544	FEM1A
cg10045354	11	111169427	0.139206535	C11orf93	cg17892917	3	107823424	0.138806082	
cg19698084	10	91461284	-0.13920132	KIF20B	cg14804635	15	75747750	-0.138802427	SIN3A
cg09384035	8	104131768	0.139195976		cg19256675	7	74988891	-0.138763337	PMS2L2
cg04624363	5	176433907	-0.13917953	UIMC1	cg11826708	3	115502895	-0.138755663	
cg06656994	1	179713176	-0.139155881	FAM163A	cg14631910	8	10590511	-0.138752046	
cg01015663	1	23729692	0.139153583	TCEA3	cg23251057	14	69480702	0.138750491	
cg00816008	16	82203996	-0.139136639	MPHOSPH6	cg12582330	1	2473224	0.138744956	
cg06875162	1	28184973	0.13913165		cg02201963	18	12702795	-0.138741927	PSMG2
cg01313320	2	46526265	-0.13912913	EPAS1	cg16722292	10	7830180	-0.138735291	KIN
cg15494556	20	56196212	0.139107576	ZBP1	cg25998745	8	142028625	0.138730232	
cg15787552	7	21467063	-0.139085932	SP4	cg14315992	4	48833004	-0.138712052	OClAD1
cg26900616	4	159593389	-0.139073229	ETFDH	cg00583733	16	30075102	0.138694408	ALDOA
cg16772514	17	43046872	0.139070601	C1QL1	cg10603824	17	48943588	-0.138687412	
cg06395692	6	28891945	-0.139070023	TRIM27	cg00965795	2	27957843	0.138679328	SS18L1
cg15408407	19	1438438	-0.139035451	RPS15	cg05713474	20	60718893	-0.138678366	LOC10018
cg01165297	16	475440	-0.139033611	RAB11FIP3	cg20874785	2	74612674	0.138674288	PCK2
cg18730422	6	4135609	-0.139019655	PECI	cg09378756	14	24569543	0.138666023	CYP51A1
cg14567424	11	67349598	0.138979769	GSTP1	cg14283194	7	91763737	-0.138635504	TTC15
cg05209463	4	2935884	-0.13897162	C4orf10	cg15971879	2	3467236	0.138623752	
cg07187585	17	10600923	-0.138968833	C17orf48	cg00967073	1	244443687	0.138622679	IRF4
cg11699826	1	26438425	-0.138966568	PDIK1L	cg26433102	6	391441	-0.138609316	PCK2
cg26349332	9	37592199	-0.138957679	TOMM5	cg10264529	14	24562064	0.138607106	SLC37A3
cg13423282	19	19174731	-0.138952777	SLC25A42	cg01012242	7	140043078	0.138602232	SND1
cg24431349	17	18218572	-0.138947622	TOP3A	cg22951727	7	127292125	-0.138594467	SLC16A1
cg05251190	10	104196206	0.138946207	MIR146B	cg08491025	1	113498799	-0.138593326	SLC12A9
cg22512322	3	64009096	-0.138937161	PSMD6	cg05049628	11	72525270	-0.138588931	SEC31A
cg17735043	5	21459472	-0.13892543	LOC728411	cg15062310	7	100450120	-0.13858048	FASTK
cg12410310	11	63275838	0.138913747	LGALS12	cg12923613	4	83812206	-0.138580184	MTHFD2
cg05051152	8	124408913	-0.138912109	ATAD2	cg01547051	7	15077654	-0.138555847	C3orf21
cg04497885	19	42747008	-0.138906723	GSK3A	cg21497607	2	74425593	-0.13854892	
cg03621988	3	113251716	-0.138892334	SIDT1	cg08996788	3	194992260	-0.138528886	
cg00993543	2	159313345	-0.138885239	CCDC148	cg07414961	17	70587753	-0.138526223	ANKH
cg01620248	14	105265453	0.138877746	ZBTB42	cg09238598	5	14871908	-0.138525044	
cg18482175	6	10747728	-0.13887497	TMEM14B	cg14702655	14	72398920	-0.138498344	RGS6

Figure 20-11

cg14284211	6	35570224	0.138495526	FKBP5	cg22992588	18	74207551	-0.138023751	
cg01098651	18	77439095	-0.138486195	CTDP1	cg23067438	22	42228994	-0.138001194	SREBF2
cg04355250	12	113796401	-0.138484317	PLBD2	cg06218044	6	105851256	-0.137979885	PREP
cg19925518	10	90851787	0.138475989		cg17661220	20	3693179	0.137957723	
cg21937128	1	150971889	0.138454318	FAM63A	cg19117777	5	109024969	-0.137954855	MAN2A1
cg22512377	22	42475683	-0.13842818	C22orf32	cg03633458	19	852284	0.137914434	ELANE
cg13390332	17	78971641	0.138420336	CHMP6	cg18307957	1	9649516	-0.137905494	TMEM201
cg03949755	7	26437999	-0.138410898		cg10502957	12	123757070	0.137897352	CDK2AP1
cg27241907	3	23244637	-0.138410397	UBE2E2	cg16041611	6	43139680	-0.137893849	SRF
cg07388806	6	7108895	-0.138389639	RREB1	cg04005943	10	73350048	0.137890391	CDH23
cg191114543	3	46996484	0.138383862	CCDC12	cg09572053	6	34360501	-0.137846377	NUDT3
cg01719220	16	58035188	-0.13838198	C16orf57	cg25140066	2	30670679	-0.137844293	LCLAT1
cg27108047	17	73257286	-0.138375664	GGA3	cg22916109	15	78730334	-0.137843807	IREB2
cg21289924	10	120839943	-0.138345419	EIF3A	cg10460130	2	242625978	-0.137838585	DTYMK
cg22396980	8	146228348	-0.138336171	ZNF252	cg23459643	5	149109544	-0.137834001	PPARGC1I
cg19971804	2	39102883	-0.138334169	MORN2	cg20153322	12	120703977	0.137819343	PXN
cg22546696	15	41952645	-0.138325776	MGA	cg23483707	13	44453835	-0.1378172	C13orf31
cg22407744	2	136634157	-0.138294936	MCM6	cg05824432	16	2301222	-0.137811767	DCI
cg19673549	5	54916621	0.138272725		cg21120664	21	44299807	-0.137809884	WDR4
cg12455363	7	27200671	-0.138269405		cg17501485	22	24191984	-0.137809769	
cg25678231	1	157069611	0.138259653	ETV3L	cg06818484	8	145051287	-0.137800965	PLEC1
cg15223102	19	33166151	-0.138236403	ANKRD27	cg22032626	12	50203811	0.137791607	NCKAP5L
cg00858400	16	87904580	0.138224791	SLC7A5	cg02508567	2	85361184	-0.137764112	TCF7L1
cg13810234	9	139622243	-0.138161929	SNHG7	cg14766148	2	128786246	-0.13776139	SAP130
cg23921523	21	45876245	0.138157575	LRRC3	cg00395632	22	50709221	-0.137753647	MAPK11
cg21826784	1	11795937	0.138148466	AGTRAP	cg21656600	12	111181027	-0.137744367	PPP1CC
cg20687038	3	127317259	-0.138143028	MCM2	cg25976786	12	53662079	-0.137736289	ESPL1
cg14195992	8	48265917	0.138140171	KIAA0146	cg032222009	2	129077232	0.137734333	HS6ST1
cg19198358	8	1725179	0.138122524	CLN8	cg07517005	1	6051606	-0.137725508	NPHP4
cg11975206	10	135192160	-0.138102579	PAOX	cg085222087	5	14871910	-0.137724723	ANKH
cg03209127	1	235668099	-0.138097688	B3GALNT2	cg11070000	14	64805073	-0.137719025	ESR2
cg10971750	14	97264166	-0.138089169	VRK1	cg23890469	10	88715317	0.137709708	MMRN2
cg00982830	12	82752388	-0.138082947	C12orf26	cg27024417	1	32645813	-0.137703766	TXLNA
cg09030452	3	64008884	-0.138077091	PSMD6	cg16405432	14	95973710	0.137657788	
cg14569415	2	220363584	-0.138074785	GMPPA	cg26337070	2	85999873	0.137657072	ATOH8
cg02676144	1	25174677	-0.138073265		cg04482628	1	36581751	0.137652192	
cg03156112	10	22630065	-0.138061452		cg01231779	14	52535887	-0.137644363	NID2
cg02367949	11	94964516	-0.138053063	SESN3	cg08767710	7	149570989	-0.137623136	ATP6V0E2
cg19306970	1	221055097	0.138052194	HLX	cg13304638	17	80834089	0.137583066	TBCD
cg02294302	1	47906276	0.138051433	FOXO2	cg18130076	11	66384026	-0.137581855	RBM14
cg03691549	12	53443911	0.138049721	TENC1	cg10069121	1	152009711	0.137577548	S100A11

Figure 20-12

cg21369679	16	47007757	-0.137565628	DNAJA2
cg07556261	20	35484900	0.137558735	C20orf117
cg14306819	2	128052889	0.137543739	ERCC3
cg20752795	2	20866407	-0.137542736	GDF7
cg16252717	19	39390344	-0.137536146	SIRT2
cg10588135	17	59329903	0.137518966	BCAS3
cg14143241	3	14166563	-0.137514663	TMEM43
cg24714742	1	91487571	-0.137513992	ZNF644
cg06642177	6	134496341	-0.137496047	SGK1
cg10129391	4	54582825	0.137489435	AKAP13
cg08211967	15	85923708	-0.137488614	
cg12363903	5	134526269	0.13746002	DLD
cg03456512	7	107531689	-0.137455535	BTBD10
cg13393276	11	13484763	-0.137447544	PSPC1
cg12938135	13	20356591	-0.137438874	
cg13573745	9	97405553	0.137433787	QPRT
cg02640604	16	29690271	0.137421976	SCD
cg23508052	10	102106811	-0.13740472	

Figure 20-13

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SNP	ChiSquare p value	SNP	ChiSquare p value	SNP	ChiSquare p value	SNP	ChiSquare p value
rs6418712	2.18E-08	rs756827	9.32E-06	rs4240151	2.72E-05	rs5925800	4.98E-05
rs11924095	1.42E-07	rs7049377	9.44E-06	rs5972323	2.74E-05	rs11066587	5.01E-05
rs3889602	1.63E-07	rs5949715	9.49E-06	rs4625170	2.79E-05	rs601300	5.08E-05
rs4358964	5.01E-07	rs5980073	9.57E-06	rs7061674	2.83E-05	rs1416244	5.13E-05
rs7888371	5.16E-07	rs12390162	9.59E-06	rs5907076	2.86E-05	rs2864894	5.15E-05
rs3131441	6.21E-07	rs5957709	9.83E-06	rs5943627	2.90E-05	rs4748099	5.18E-05
rs5932058	7.58E-07	rs2056491	1.00E-05	rs12689291	2.93E-05	rs1285582	5.24E-05
rs5933886	9.11E-07	rs12393815	1.02E-05	rs5910006	2.94E-05	rs4830819	5.28E-05
rs6640916	1.12E-06	rs10881990	1.03E-05	rs572249	2.94E-05	rs6525672	5.46E-05
rs6457816	1.23E-06	rs582132	1.07E-05	rs5925762	2.96E-05	rs1906321	5.49E-05
rs12690204	1.51E-06	rs7884737	1.08E-05	rs6616265	2.97E-05	rs7882491	5.51E-05
rs1875619	1.82E-06	rs806643	1.12E-05	rs1582412	3.01E-05	rs205828	5.53E-05
rs5972470	1.82E-06	rs1040474	1.12E-05	rs222108	3.07E-05	rs6528055	5.60E-05
rs17365948	1.84E-06	rs2027822	1.18E-05	rs321034	3.11E-05	rs12688712	5.72E-05
rs5929410	1.86E-06	rs4830923	1.19E-05	rs644429	3.11E-05	rs8031759	5.81E-05
rs1540705	1.95E-06	rs4497115	1.21E-05	rs2100684	3.41E-05	rs5934763	5.87E-05
rs2239431	2.15E-06	rs17337541	1.22E-05	rs5921682	3.42E-05	rs4358925	5.91E-05
rs6608067	2.40E-06	rs1986011	1.24E-05	rs5936019	3.44E-05	rs5918514	5.99E-05
rs1073274	2.61E-06	rs203995	1.28E-05	rs5970907	3.49E-05	rs6623334	6.00E-05
rs6638536	2.63E-06	rs4475664	1.32E-05	rs2407769	3.52E-05	rs2830582	6.06E-05
rs5932609	2.66E-06	rs5969461	1.33E-05	rs6523640	3.52E-05	rs2048637	6.07E-05
rs4240003	2.76E-06	rs5942191	1.33E-05	rs5916610	3.53E-05	rs5928121	6.15E-05
rs5908325	3.03E-06	rs5929657	1.39E-05	rs5910831	3.58E-05	rs2233048	6.16E-05
rs6866970	3.13E-06	rs5920401	1.43E-05	rs11094849	3.61E-05	rs6641786	6.20E-05
rs1268602	3.23E-06	rs5937156	1.44E-05	rs2190567	3.65E-05	rs12706350	6.24E-05
rs41359256	3.43E-06	rs1425843	1.46E-05	rs17341595	3.65E-05	rs5949779	6.31E-05
rs3747276	3.48E-06	rs914936	1.50E-05	rs760580	3.66E-05	rs10514576	6.40E-05
rs5961804	3.61E-06	rs2858278	1.51E-05	rs1894571	3.71E-05	rs9927211	6.54E-05
rs5972354	3.73E-06	rs6640037	1.52E-05	rs2066364	3.74E-05	rs1937567	6.56E-05
rs5968401	3.85E-06	rs9325663	1.53E-05	rs484369	3.77E-05	rs1980775	6.69E-05
rs6834019	3.90E-06	rs16995825	1.53E-05	rs16998872	3.84E-05	rs12127143	6.74E-05
rs3827468	3.95E-06	rs17377726	1.55E-05	rs4825213	3.84E-05	rs5966508	6.75E-05
rs1016824	4.00E-06	rs5985781	1.56E-05	rs5933350	3.85E-05	rs5978240	6.79E-05
rs7830923	5.42E-06	rs1474804	1.61E-05	rs1230820	3.99E-05	rs7884069	6.83E-05
rs1004991	5.59E-06	rs10521847	1.70E-05	rs3935725	4.02E-05	rs1012454	6.83E-05
rs10496147	5.89E-06	rs981780	1.71E-05	rs6629434	4.03E-05	rs4844071	6.95E-05
rs16994895	6.16E-06	rs5972463	1.71E-05	rs7052935	4.11E-05	rs762875	7.03E-05
rs4421510	6.33E-06	rs5927921	1.74E-05	rs807185	4.24E-05	rs16985984	7.18E-05
rs10783884	6.65E-06	rs5971598	1.74E-05	rs4131420	4.31E-05	rs17390	7.27E-05
rs5974336	6.82E-06	rs5950604	1.84E-05	rs5974239	4.36E-05	rs2961375	7.29E-05
rs9813811	6.84E-06	rs5945723	1.96E-05	rs4829909	4.37E-05	rs2224048	7.31E-05
rs6640079	7.13E-06	rs7050981	2.03E-05	rs1448514	4.49E-05	rs5939895	7.33E-05
rs6631703	7.15E-06	rs2316179	2.10E-05	rs6530108	4.51E-05	rs6631847	7.43E-05
rs2223315	7.53E-06	rs5976289	2.10E-05	rs2842687	4.54E-05	rs10856497	7.51E-05
rs7882576	7.53E-06	rs2131927	2.27E-05	rs10863224	4.59E-05	rs2742587	7.82E-05
rs17312192	8.18E-06	rs5929842	2.30E-05	rs176034	4.63E-05	rs5972314	7.95E-05
rs6619299	8.44E-06	rs1837943	2.32E-05	rs10081857	4.71E-05	rs5941725	7.97E-05
rs6609614	8.73E-06	rs5921205	2.39E-05	rs5991450	4.74E-05	rs1019089	8.04E-05
rs1866934	8.77E-06	rs5990899	2.42E-05	rs1203564	4.78E-05	rs1478550	8.04E-05
rs10275666	8.99E-06	rs5980078	2.49E-05	rs5926901	4.83E-05	rs5970748	8.13E-05
rs16856394	9.07E-06	rs1031914	2.51E-05	rs5987947	4.84E-05	rs1378389	8.15E-05
rs9018	9.11E-06	rs6540394	2.55E-05	rs5941511	4.88E-05	rs2611019	8.16E-05
rs2369786	9.27E-06	rs6634590	2.59E-05	rs5908093	4.97E-05	rs11796000	8.18E-05

Figure 21-1

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rs5970768	8.20E-05	rs5961787	0.0001163	rs9996437	0.0001552	rs5908994	0.00019894
rs2214180	8.23E-05	rs952836	0.0001178	rs6525581	0.0001559	rs7881785	0.00019919
rs633203	8.23E-05	rs5922641	0.0001178	rs7392062	0.0001561	rs17261572	0.00019993
rs5915507	8.30E-05	rs4826673	0.0001179	rs6744831	0.0001567	rs16966903	0.00020151
rs12008641	8.32E-05	rs12950579	0.0001195	rs11865044	0.0001575	rs287771	0.00020449
rs797252	8.32E-05	rs5953410	0.0001205	rs225048	0.0001593	rs12868476	0.00020535
rs677066	8.45E-05	rs4074209	0.0001219	rs10521585	0.0001604	rs5934025	0.00020568
rs3747687	8.45E-05	rs196356	0.000122	rs1602407	0.0001608	rs10999786	0.00020737
rs2014867	8.48E-05	rs3126111	0.0001225	rs5906156	0.0001622	rs12065003	0.00021065
rs6528845	8.54E-05	rs10511632	0.0001231	rs1005911	0.0001645	rs10506534	0.00021266
rs12842964	8.56E-05	rs766118	0.0001232	rs5935270	0.0001645	rs5942608	0.00021305
rs5965947	8.56E-05	rs2800662	0.0001234	rs5910616	0.0001648	rs1029454	0.00021385
rs28201	8.59E-05	rs17250761	0.0001241	rs16910276	0.0001651	rs6521151	0.00021455
rs234491	8.65E-05	rs5979707	0.0001249	rs9906017	0.0001654	rs1949951	0.00021598
rs11864276	8.65E-05	rs1795577	0.0001253	rs715171	0.0001659	rs8169	0.00021632
rs11079344	8.66E-05	rs2889001	0.0001255	rs4655316	0.0001704	rs17317628	0.00021656
rs10507930	8.80E-05	rs6637507	0.0001259	rs12007404	0.0001704	rs6643887	0.00021728
rs7061270	8.89E-05	rs5956542	0.0001264	rs16828505	0.0001711	rs1463435	0.00021845
rs2719873	8.89E-05	rs12559140	0.0001276	rs1324823	0.0001714	rs11572381	0.00021978
rs3781383	9.14E-05	rs9324789	0.0001277	rs6609302	0.0001725	rs2025580	0.00022028
rs4828210	9.23E-05	rs5917513	0.0001285	rs5908542	0.0001732	rs620787	0.00022055
rs1115361	9.26E-05	rs5934731	0.0001291	rs10500548	0.0001739	rs5915785	0.00022097
rs1656651	9.28E-05	rs17145430	0.0001292	rs41451152	0.0001749	rs4460557	0.00022105
rs6527243	9.32E-05	rs2787566	0.0001295	rs5935573	0.0001749	rs17505622	0.00022175
rs178715	9.37E-05	rs5974714	0.0001298	rs1015825	0.0001753	rs6645778	0.000222
rs5961648	9.42E-05	rs2312984	0.00013	rs10509870	0.0001759	rs5934137	0.0002221
rs3126289	9.47E-05	rs16989935	0.0001311	rs2238917	0.0001771	rs5927057	0.00022234
rs4844224	9.55E-05	rs10220201	0.0001317	rs5971556	0.0001774	rs5974808	0.00022543
rs831167	9.66E-05	rs722847	0.0001332	rs12836051	0.0001794	rs7296677	0.00022642
rs6621132	9.69E-05	rs7879492	0.000134	rs1072149	0.0001802	rs5974406	0.00022652
rs6616008	9.81E-05	rs979848	0.0001344	rs5944269	0.0001825	rs7056902	0.00022687
rs3095633	9.87E-05	rs5910248	0.0001353	rs17108506	0.0001831	rs4129094	0.0002275
rs5937126	9.90E-05	rs2254392	0.0001356	rs11942278	0.000184	rs225041	0.00022965
rs5935292	9.94E-05	rs41356547	0.0001357	rs6653828	0.0001849	rs6522693	0.00023004
rs2316351	1.00E-04	rs1546885	0.0001368	rs1977059	0.0001858	rs9948310	0.00023122
rs6654427	0.0001012	rs1609538	0.0001375	rs12852982	0.0001868	rs5984750	0.00023273
rs11795905	0.0001028	rs5984526	0.0001399	rs1869562	0.0001882	rs5989582	0.00023303
rs5927267	0.0001037	rs1033388	0.0001409	rs2266910	0.0001882	rs6603421	0.00023331
rs3125579	0.0001039	rs10173586	0.0001424	rs11096119	0.0001885	rs1361651	0.00023409
rs6530045	0.0001047	rs7062414	0.0001427	rs3828983	0.0001886	rs5957470	0.00023523
rs17541189	0.0001065	rs12391688	0.0001427	rs7527017	0.0001889	rs2748475	0.00023607
rs4830233	0.0001065	rs17020606	0.000143	rs11094826	0.0001899	rs1529405	0.0002374
rs4830335	0.0001073	rs2903676	0.0001434	rs11095248	0.0001902	rs5955303	0.00023785
rs5943240	0.0001092	rs5949319	0.0001445	rs7631725	0.0001915	rs5956460	0.00023913
rs17013157	0.0001097	rs7061076	0.0001449	rs3772601	0.0001916	rs5905768	0.00023913
rs6520412	0.0001098	rs5918075	0.0001453	rs17341330	0.000192	rs477233	0.00024383
rs11549009	0.0001102	rs6847617	0.0001457	rs6523584	0.0001921	rs5972363	0.00024529
rs12014135	0.0001123	rs7879771	0.0001482	rs4826634	0.0001921	rs6528142	0.0002455
rs5907551	0.0001125	rs1322199	0.0001498	rs845122	0.0001923	rs473838	0.00024605
rs4759438	0.0001128	rs331345	0.0001512	rs17758599	0.0001925	rs9894417	0.00024623
rs991256	0.0001131	rs6636113	0.0001523	rs978390	0.000196	rs6418754	0.00024754
rs5986271	0.0001133	rs1263913	0.0001527	rs13403523	0.000197	rs942459	0.00024803
rs5919700	0.0001138	rs6654492	0.000153	rs6627910	0.000198	rs6641022	0.00024868
rs1906299	0.0001159	rs41495649	0.0001533	rs17120381	0.0001985	rs6530511	0.00024868
rs17034357	0.000116	rs13158981	0.0001552	rs6611276	0.0001989	rs12307589	0.00025279

Figure 21-2

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rs7738055	0.0002545	rs10470321	0.0003026	rs10880022	0.0003503	rs6624074	0.00040852
rs5972240	0.000255	rs500879	0.0003028	rs7663471	0.0003504	rs5950893	0.00040955
rs17004107	0.000257	rs7776126	0.000303	rs1293919	0.0003531	rs17321050	0.00040995
rs17597375	0.0002606	rs5926307	0.0003041	rs2025278	0.0003532	rs4240155	0.00041035
rs8126456	0.0002615	rs17650556	0.0003048	rs5932574	0.0003535	rs2902210	0.00041373
rs850635	0.0002615	rs1726206	0.0003049	rs4787348	0.0003541	rs707289	0.00041472
rs4447684	0.0002623	rs16970170	0.0003056	rs12325649	0.0003545	rs4829035	0.00041524
rs5910867	0.0002634	rs1882354	0.000306	rs4526506	0.0003556	rs10765861	0.00042006
rs2192276	0.0002646	rs2199809	0.0003087	rs11252547	0.0003564	rs5911622	0.00042111
rs9552517	0.0002657	rs900450	0.0003092	rs5981268	0.0003579	rs736818	0.00042362
rs821038	0.0002669	rs1353456	0.0003092	rs1158755	0.0003594	rs4826609	0.00042385
rs12687579	0.0002671	rs7707177	0.0003101	rs12513356	0.0003598	rs5936684	0.00042754
rs2127064	0.000268	rs2979322	0.0003104	rs4425925	0.0003599	rs975166	0.00042873
rs10483818	0.0002683	rs12489946	0.0003105	rs7909677	0.0003624	rs5990013	0.00042922
rs2588288	0.0002696	rs682176	0.0003119	rs11899367	0.0003626	rs11218131	0.00042925
rs6984890	0.0002696	rs16861267	0.0003121	rs9698796	0.0003626	rs7952006	0.00042961
rs7891415	0.0002699	rs5916520	0.0003124	rs2926458	0.000365	rs1204399	0.00043114
rs5951458	0.0002704	rs5940942	0.0003145	rs17159801	0.000366	rs5916245	0.00043141
rs4307646	0.0002706	rs7577881	0.0003149	rs400439	0.0003666	rs11092739	0.00043174
rs16923297	0.0002707	rs178685	0.0003151	rs35906400	0.0003668	rs4969661	0.00043509
rs964528	0.0002716	rs41376146	0.0003152	rs6943487	0.000367	rs10459940	0.00043593
rs233655	0.0002722	rs17076490	0.000317	rs12159204	0.0003684	rs1858934	0.00043806
rs5972177	0.0002727	rs4844164	0.0003173	rs12007523	0.0003694	rs17542763	0.00043984
rs5927923	0.0002728	rs6825299	0.0003177	rs41477549	0.0003702	rs13385578	0.00044122
rs4623700	0.0002731	rs11092309	0.0003186	rs4825158	0.0003711	rs979127	0.00044359
rs815869	0.0002755	rs5990540	0.0003186	rs4474149	0.0003725	rs2521385	0.00044378
rs11169170	0.0002758	rs5916657	0.00032	rs4288315	0.0003741	rs17300926	0.00044465
rs1703946	0.0002765	rs17019491	0.0003209	rs9806181	0.0003746	rs2051727	0.00044614
rs5915287	0.0002766	rs5906161	0.0003213	rs845188	0.0003796	rs376165	0.00044636
rs5923929	0.0002785	rs6964079	0.0003219	rs1018794	0.0003811	rs41333050	0.00044645
rs5935153	0.0002791	rs12320268	0.000323	rs9988299	0.0003831	rs1125142	0.00044666
rs17035686	0.0002794	rs10498926	0.0003234	rs5936963	0.000384	rs3128282	0.00044785
rs6590392	0.0002796	rs5934746	0.0003248	rs5926173	0.0003851	rs5915856	0.00044819
rs10961079	0.0002801	rs2428447	0.0003255	rs4262422	0.0003856	rs228392	0.00044905
rs7190458	0.0002815	rs4733372	0.0003258	rs6551290	0.0003857	rs5979977	0.00045173
rs454992	0.0002818	rs5942185	0.0003269	rs7853273	0.0003864	rs1380722	0.00045353
rs4330825	0.0002819	rs5910842	0.0003269	rs6624381	0.0003874	rs4072191	0.00045626
rs7718116	0.0002845	rs1007942	0.000329	rs5919772	0.0003877	rs1342321	0.00045872
rs5923736	0.0002854	rs4679029	0.0003291	rs11797927	0.0003881	rs11209241	0.00046002
rs5917288	0.0002874	rs161630	0.0003316	rs12558359	0.0003889	rs17148289	0.00046048
rs17259400	0.0002877	rs7225465	0.000332	rs11051643	0.0003898	rs763696	0.00046106
rs1268027	0.0002883	rs2238973	0.0003321	rs6527192	0.0003907	rs119301	0.00046154
rs5908591	0.0002906	rs1980789	0.0003322	rs653618	0.0003912	rs4892897	0.00046276
rs1116372	0.000292	rs4969659	0.000334	rs11091070	0.0003928	rs5974275	0.00046481
rs5973375	0.0002929	rs10944520	0.0003345	rs331347	0.000393	rs7138534	0.00046643
rs4828959	0.0002933	rs6894882	0.0003347	rs194293	0.0003947	rs5981088	0.00046668
rs2805962	0.0002946	rs1368769	0.0003387	rs12398801	0.000397	rs16981858	0.00046792
rs2266790	0.0002954	rs5911136	0.0003396	rs6630002	0.0004003	rs4080381	0.00046951
rs17134173	0.0002965	rs5906947	0.0003405	rs10161783	0.0004012	rs5966774	0.00046957
rs4829169	0.0002979	rs11265318	0.0003409	rs5918081	0.0004023	rs5010471	0.00047054
rs5924002	0.0002984	rs400586	0.0003423	rs1540301	0.000403	rs6829976	0.00047179
rs5916870	0.0002984	rs16901105	0.0003441	rs5968948	0.0004052	rs9803580	0.00047386
rs17575611	0.0002986	rs12037400	0.0003464	rs11943130	0.0004057	rs623695	0.00047778
rs7325627	0.0002995	rs5930036	0.0003484	rs4829934	0.0004057	rs17411883	0.00047844
rs2632086	0.0003	rs765304	0.0003497	rs2451678	0.0004074	rs568707	0.00048002

Figure 21-3

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rs6639416	0.0004815	rs17254207	0.0005789	rs4291390	0.0007037	rs12526341	0.00081451
rs5922023	0.0004871	rs5971110	0.0005803	rs5934442	0.0007097	rs13027348	0.00081934
rs4573436	0.0004873	rs4827600	0.0005816	rs5929803	0.00071	rs11122275	0.00082208
rs7553222	0.0004896	rs107621	0.0005817	rs5906073	0.0007102	rs10126138	0.00082342
rs5935138	0.0004924	rs5982635	0.0005822	rs6619657	0.0007102	rs12560013	0.00082359
rs16905445	0.000494	rs10467741	0.0005836	rs6641050	0.0007117	rs11071467	0.0008263
rs12661742	0.0004942	rs206050	0.0005856	rs17219483	0.0007146	rs4824228	0.00082668
rs4844477	0.0004953	rs9887051	0.0005859	rs12844438	0.0007152	rs1650590	0.00082727
rs5956652	0.0004953	rs11125548	0.0005869	rs16975213	0.000717	rs17481221	0.00082949
rs17278485	0.0004981	rs1620574	0.0005872	rs719499	0.0007192	rs6617632	0.00083014
rs5918494	0.0004989	rs4893429	0.0005916	rs206599	0.0007203	rs1926114	0.00083271
rs4827622	0.0005006	rs1454500	0.0005939	rs7166105	0.0007227	rs7534148	0.00083301
rs5973843	0.000501	rs11152555	0.0006033	rs7585736	0.0007258	rs10521956	0.00083588
rs41536847	0.0005023	rs1999923	0.0006051	rs5935385	0.0007272	rs16985419	0.00083752
rs17097997	0.0005037	rs4827618	0.0006064	rs292199	0.0007285	rs7475474	0.00084211
rs41525448	0.0005061	rs5959364	0.0006094	rs10521981	0.000729	rs10522007	0.00084988
rs6628810	0.0005151	rs2436065	0.0006113	rs4503229	0.0007333	rs8077332	0.00085439
rs661342	0.0005164	rs6632790	0.0006121	rs2858222	0.0007341	rs10505725	0.00085591
rs10091938	0.0005199	rs5951580	0.0006157	rs6633000	0.0007345	rs1948558	0.00085744
rs4830677	0.0005234	rs6526513	0.0006165	rs5908778	0.000737	rs588427	0.00085768
rs11083957	0.0005258	rs659521	0.0006173	rs17190904	0.0007407	rs11120869	0.00086064
rs16994558	0.0005259	rs1935404	0.0006215	rs2040416	0.0007449	rs1453329	0.00086212
rs10855477	0.0005266	rs9493709	0.0006253	rs6636518	0.000749	rs2540769	0.00086341
rs7827160	0.0005307	rs987017	0.0006288	rs16870514	0.0007502	rs5972873	0.00086447
rs6420139	0.0005313	rs7719299	0.0006294	rs5930699	0.0007511	rs6694388	0.00086642
rs1159223	0.0005332	rs5978122	0.0006311	rs4830633	0.0007512	rs12710568	0.00086771
rs12012009	0.0005348	rs4571411	0.0006315	rs5904763	0.0007571	rs17835106	0.00086787
rs871156	0.0005352	rs10820175	0.0006335	rs9450829	0.0007574	rs2179049	0.00086814
rs1029308	0.0005371	rs7826323	0.0006341	rs601552	0.0007607	rs6641173	0.00086901
rs2224095	0.000538	rs4300782	0.0006386	rs17325827	0.000763	rs12854960	0.00087142
rs6528940	0.0005402	rs12848856	0.000639	rs2561435	0.0007671	rs1581706	0.00087214
rs533054	0.0005411	rs5974183	0.0006394	rs3920502	0.0007711	rs10983233	0.00087462
rs719199	0.0005414	rs10498670	0.00065	rs10867945	0.000772	rs2570306	0.00087673
rs11092138	0.0005426	rs12557389	0.0006557	rs7066452	0.0007721	rs1482821	0.00087723
rs367985	0.0005428	rs5955132	0.0006559	rs3752627	0.0007733	rs3819662	0.00087727
rs5927035	0.0005436	rs1937561	0.0006571	rs5921731	0.0007735	rs2521651	0.00087842
rs2150010	0.0005491	rs17315366	0.0006586	rs4829829	0.0007749	rs177680	0.00087873
rs2806022	0.0005492	rs4816165	0.0006598	rs2499416	0.0007751	rs4306056	0.00088598
rs5922797	0.0005526	rs4545218	0.0006607	rs5942091	0.0007773	rs9892139	0.00088887
rs9501885	0.0005543	rs10948714	0.0006631	rs1879610	0.0007783	rs5971421	0.00090017
rs5916284	0.0005549	rs9539143	0.0006638	rs5921690	0.0007815	rs12594048	0.000905
rs1937178	0.0005553	rs6756191	0.0006687	rs10521556	0.0007822	rs4957169	0.00090574
rs6633864	0.0005566	rs2534697	0.000669	rs5979463	0.0007844	rs972655	0.00090696
rs4457887	0.0005566	rs6641482	0.0006705	rs603315	0.0007877	rs5918053	0.00090798
rs12855563	0.000557	rs4826184	0.0006735	rs11167418	0.0007897	rs2731014	0.00090985
rs17333127	0.0005586	rs6634857	0.0006768	rs5945977	0.0007901	rs9556491	0.00091076
rs2106913	0.0005588	rs17133347	0.0006835	rs6610918	0.0007913	rs6527730	0.00091126
rs5972512	0.0005591	rs5936657	0.0006842	rs5958482	0.0007936	rs4805410	0.00091207
rs845445	0.0005609	rs6629310	0.0006887	rs4826217	0.0007957	rs2269466	0.00091562
rs1929363	0.0005655	rs954911	0.0006927	rs12689414	0.0008024	rs6520724	0.0009168
rs1493061	0.0005677	rs7026753	0.0006931	rs6629756	0.0008031	rs7064695	0.00091999
rs41516347	0.0005749	rs629846	0.000696	rs919037	0.0008037	rs12556842	0.00092038
rs4811738	0.0005754	rs11055460	0.0006964	rs6685296	0.0008042	rs7880724	0.00092092
rs2519196	0.0005787	rs5978787	0.0007027	rs17017422	0.000806	rs5980419	0.00092491
rs4240068	0.0005788	rs5928378	0.0007027	rs9321951	0.0008092	rs2858769	0.00093018

Figure 21-4

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rs6608501	0.0009307	rs2595146	0.0010466	rs6624219	0.0011488	rs17270765	0.00129065
rs4826225	0.0009321	rs17721991	0.0010499	rs4824580	0.0011488	rs5922289	0.00129082
rs6634178	0.0009336	rs1336832	0.0010509	rs1409134	0.0011522	rs5967919	0.0012912
rs2050979	0.0009391	rs1195395	0.0010554	rs2227142	0.001155	rs5931583	0.0012916
rs4830507	0.0009416	rs1115799	0.001057	rs5950978	0.0011578	rs16936151	0.00129237
rs11925620	0.0009444	rs17057631	0.0010576	rs4365962	0.001158	rs5951426	0.00129292
rs17069764	0.0009485	rs6675190	0.0010581	rs2238149	0.0011589	rs17127885	0.00129522
rs1126140	0.000952	rs13328515	0.001059	rs2225969	0.0011607	rs1540281	0.00129564
rs6034572	0.0009538	rs12454155	0.0010668	rs1318833	0.0011673	rs17627141	0.00129723
rs16945163	0.0009598	rs5909509	0.0010698	rs5934013	0.0011696	rs3926503	0.00130058
rs532856	0.0009605	rs2855259	0.0010721	rs7526407	0.0011725	rs556111	0.00130131
rs5926763	0.0009627	rs5979403	0.0010745	rs2109563	0.0011798	rs2050775	0.00130267
rs1414073	0.000964	rs217932	0.0010747	rs10494345	0.0011812	rs3918084	0.00130515
rs2188133	0.0009669	rs6527577	0.0010799	rs6568219	0.0011828	rs6637465	0.0013055
rs1556618	0.0009677	rs555063	0.0010838	rs1731475	0.0011854	rs4643744	0.00131142
rs5972174	0.0009691	rs2807171	0.0010871	rs1921938	0.0011871	rs12198920	0.00131572
rs12556700	0.000974	rs5980285	0.0010881	rs5918486	0.0011888	rs2242903	0.00132036
rs3865999	0.0009746	rs1876415	0.0010892	rs6539020	0.0011913	rs5934628	0.00132716
rs1795594	0.0009772	rs5937005	0.0010927	rs5934039	0.001192	rs1898271	0.00132906
rs5927141	0.0009772	rs6710956	0.0010931	rs2804591	0.0011987	rs17333065	0.00133026
rs4923429	0.0009788	rs2838246	0.0010953	rs5927105	0.0011996	rs17388907	0.00133253
rs5931086	0.0009797	rs11027538	0.0010957	rs9550218	0.0012001	rs11245246	0.00133309
rs12623857	0.0009827	rs5935784	0.0010957	rs10491777	0.0012044	rs17329378	0.00133565
rs5977273	0.0009846	rs6953339	0.0010984	rs7772349	0.0012062	rs6568048	0.00133669
rs17222293	0.0009871	rs12861218	0.0010989	rs7888015	0.0012082	rs2748855	0.00133812
rs1788244	0.0009883	rs5926757	0.0010991	rs1207469	0.0012085	rs1921944	0.00134784
rs12489983	0.000991	rs6528766	0.0010996	rs823066	0.0012129	rs5972815	0.00134984
rs5935925	0.0009926	rs858079	0.0011001	rs3127080	0.0012149	rs848622	0.00135153
rs4304064	0.0009931	rs17031214	0.0011027	rs5927572	0.0012169	rs5920040	0.00135298
rs5979606	0.0009936	rs11094371	0.001103	rs5940848	0.0012173	rs7885172	0.0013536
rs5963786	0.0009941	rs2660006	0.001103	rs10491766	0.0012186	rs1482832	0.00135902
rs3095571	0.0009943	rs209990	0.0011066	rs6636303	0.001222	rs7884783	0.00135948
rs12689742	0.0009958	rs5910840	0.0011078	rs1859168	0.0012221	rs7055913	0.00136155
rs11204227	0.0009971	rs2182285	0.0011081	rs11773573	0.0012258	rs16990063	0.00136575
rs5910186	0.0010018	rs7864957	0.001109	rs5920671	0.0012272	rs7296488	0.00136746
rs4824801	0.0010032	rs7876945	0.0011093	rs11215380	0.0012315	rs7541884	0.00137536
rs5942617	0.0010088	rs4586824	0.0011095	rs868117	0.0012316	rs10033375	0.00137654
rs11265310	0.0010127	rs12427587	0.001111	rs12488162	0.0012335	rs12689966	0.00137944
rs6609568	0.0010133	rs11091237	0.001113	rs5935787	0.0012355	rs17807973	0.00138259
rs2117234	0.0010147	rs1736649	0.0011138	rs5933842	0.0012355	rs283446	0.00138287
rs2027803	0.0010149	rs539181	0.0011167	rs6942273	0.0012407	rs5907830	0.00138383
rs5972224	0.0010172	rs4912577	0.0011168	rs175737	0.001243	rs209234	0.0013862
rs7683566	0.0010222	rs41483250	0.0011192	rs6461569	0.0012451	rs1397169	0.00138675
rs6081140	0.0010227	rs3176595	0.0011224	rs2627530	0.0012473	rs9644996	0.00139061
rs41342947	0.0010265	rs1436971	0.0011225	rs2107528	0.0012481	rs2071780	0.0013915
rs5989532	0.0010268	rs17576350	0.0011233	rs3013028	0.001249	rs5977928	0.00139204
rs2904124	0.0010271	rs11095630	0.0011237	rs10906798	0.0012527	rs6520655	0.0013922
rs12568255	0.0010288	rs17801315	0.0011241	rs488163	0.0012555	rs4484871	0.00139362
rs1997481	0.0010294	rs2057521	0.0011296	rs4920416	0.0012609	rs6608087	0.00139487
rs13073001	0.0010296	rs2050909	0.0011357	rs10993042	0.0012658	rs16999222	0.00139818
rs943498	0.0010309	rs6530556	0.0011377	rs6418053	0.0012695	rs11806541	0.00140033
rs6520279	0.001034	rs16962802	0.0011417	rs6617714	0.0012709	rs5920370	0.00140055
rs11165120	0.0010392	rs4903444	0.001146	rs4824895	0.0012764	rs923820	0.00140444
rs1537720	0.0010433	rs2746112	0.0011465	rs1727451	0.0012792	rs5957567	0.00140597
rs12078096	0.0010453	rs2264844	0.001147	rs2474853	0.0012867	rs9408314	0.00140658

Figure 21-5

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rs5922256	0.0014107	rs17114702	0.0015632	rs5943053	0.0017117	rs7250197	0.00186604
rs11652587	0.0014151	rs7053403	0.0015636	rs4870397	0.0017119	rs16912030	0.00186738
rs7063248	0.0014167	rs6546227	0.0015637	rs7338471	0.0017123	rs10511264	0.00187045
rs1927272	0.0014169	rs845118	0.0015662	rs17285811	0.0017147	rs2001510	0.00187687
rs7053410	0.0014268	rs6639974	0.0015672	rs6471286	0.0017158	rs6110699	0.00188002
rs9287640	0.0014272	rs5934683	0.0015705	rs154756	0.0017212	rs17304062	0.00188456
rs12876111	0.0014272	rs5931630	0.0015745	rs12468338	0.0017262	rs11084878	0.001886
rs7974374	0.0014275	rs5920606	0.0015758	rs9865038	0.0017279	rs1470909	0.00188901
rs6608592	0.0014275	rs5950249	0.0015801	rs10492879	0.0017306	rs996058	0.00189152
rs35091279	0.0014328	rs12687753	0.0015821	rs10521972	0.0017341	rs12559003	0.00189466
rs6639695	0.0014366	rs16825798	0.0015822	rs9813304	0.0017341	rs16984818	0.00189607
rs5908724	0.001437	rs3911610	0.0015847	rs12832235	0.0017387	rs17108228	0.00189804
rs2428720	0.0014416	rs7018599	0.0015862	rs6600090	0.0017404	rs10121216	0.00189981
rs4827044	0.0014425	rs10519262	0.0015915	rs202777	0.001743	rs4376434	0.00190068
rs2278945	0.0014439	rs4828437	0.0015932	rs5911660	0.0017449	rs5906928	0.00190483
rs2285633	0.0014448	rs4830050	0.0015935	rs16868212	0.0017461	rs11062532	0.00190736
rs7058159	0.0014463	rs5981065	0.0015945	rs536097	0.0017465	rs743896	0.00191456
rs17170955	0.0014534	rs5917963	0.0016033	rs4134051	0.0017497	rs960066	0.00191551
rs9678479	0.001459	rs2292804	0.0016069	rs10512989	0.0017533	rs2594854	0.00191843
rs16911103	0.0014627	rs196580	0.0016091	rs4478749	0.0017537	rs2010606	0.00192018
rs17160154	0.0014637	rs2448853	0.001611	rs7806810	0.0017562	rs1944390	0.00192316
rs5944690	0.0014675	rs3895063	0.001613	rs5909187	0.0017585	rs5977298	0.00192621
rs5909721	0.0014686	rs378414	0.001615	rs6548098	0.0017697	rs6629277	0.00193512
rs479036	0.0014713	rs17131080	0.0016195	rs5970645	0.0017727	rs1003169	0.00193579
rs6636107	0.0014741	rs7684025	0.0016207	rs4826690	0.0017746	rs1342219	0.00193875
rs17246141	0.0014745	rs3117460	0.0016233	rs5930020	0.0017758	rs11048606	0.00193905
rs2320009	0.0014802	rs13102624	0.0016254	rs2727184	0.0017819	rs17276881	0.00194542
rs5933743	0.0014819	rs7069744	0.0016296	rs482796	0.0017832	rs7539893	0.00194681
rs12387720	0.0014827	rs815419	0.0016532	rs11256530	0.0017877	rs2748302	0.00194729
rs11564026	0.0014856	rs3008972	0.0016556	rs16989995	0.001793	rs7192139	0.00194778
rs11052552	0.0014918	rs10881582	0.0016567	rs5908051	0.0017936	rs17532490	0.00194952
rs5950402	0.0014937	rs12185961	0.0016569	rs7644001	0.0017987	rs10081808	0.00195023
rs5916697	0.0014972	rs41476844	0.0016573	rs7699969	0.0018013	rs134767	0.00195514
rs33123	0.0015029	rs12836085	0.0016577	rs17517294	0.0018017	rs4893622	0.00195681
rs2010818	0.001516	rs9988960	0.0016585	rs1634347	0.0018019	rs1493594	0.00195769
rs2092909	0.0015183	rs5920650	0.0016594	rs2384424	0.0018025	rs2612326	0.00195822
rs10521922	0.0015189	rs3746250	0.0016605	rs5905013	0.0018053	rs5974210	0.00195929
rs959694	0.001522	rs10168890	0.0016628	rs1898810	0.0018267	rs1216714	0.00196133
rs7762850	0.0015233	rs7669737	0.0016635	rs1370865	0.0018291	rs6645884	0.00196248
rs7422689	0.0015278	rs2335519	0.0016669	rs916658	0.0018319	rs7193282	0.00196351
rs8024593	0.0015279	rs5936438	0.0016672	rs11163235	0.0018342	rs11002824	0.00196678
rs2281808	0.0015303	rs5921608	0.0016688	rs4759285	0.0018349	rs6641732	0.00196842
rs16950388	0.0015358	rs2144732	0.0016707	rs1016553	0.0018367	rs617156	0.00197332
rs1041236	0.0015406	rs10521748	0.001672	rs17726411	0.001837	rs11150186	0.00197476
rs5944691	0.0015407	rs7403021	0.0016816	rs11682110	0.0018404	rs1592293	0.00198202
rs7562854	0.0015416	rs1978147	0.0016858	rs10521352	0.0018423	rs11597065	0.00198347
rs2521413	0.0015448	rs12010464	0.0016867	rs4408025	0.0018454	rs1986391	0.00198544
rs2982104	0.0015459	rs816971	0.0016878	rs3803214	0.0018455	rs5931020	0.00198622
rs6087099	0.0015482	rs1558089	0.0016902	rs17584901	0.0018506	rs12273505	0.0019876
rs6637454	0.0015498	rs5928685	0.0016944	rs7879462	0.0018512	rs407746	0.00198929
rs13148770	0.0015528	rs898249	0.0016961	rs10521683	0.0018528	rs2498044	0.00199083
rs2129557	0.0015529	rs2239477	0.0017006	rs5937001	0.0018591	rs7879064	0.00199267
rs25699	0.001557	rs2742899	0.0017085	rs4889442	0.0018601	rs5923840	0.00199562
rs12338324	0.0015587	rs7844594	0.0017097	rs17300660	0.0018626	rs10785219	0.00199979
rs8044444	0.0015599	rs1916827	0.00171	rs6567560	0.0018643	rs1033952	0.00200103

Figure 21-6

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rs5931055	0.0020028	rs1237597	0.0021771	rs5925658	0.0023131	rs2984344	0.00246824
rs12191972	0.002008	rs5940217	0.002181	rs2522942	0.0023136	rs2074321	0.00247031
rs5933686	0.0020202	rs4830882	0.0021828	rs3002415	0.0023155	rs17594762	0.00247953
rs1600705	0.0020212	rs2205637	0.0021837	rs6960667	0.0023205	rs3763496	0.00248049
rs1277992	0.0020237	rs41393746	0.002184	rs2428212	0.0023236	rs821931	0.00248293
rs1293888	0.002026	rs17745898	0.0021873	rs2312033	0.0023243	rs7602129	0.00248309
rs6676084	0.0020293	rs13111857	0.0021882	rs2271688	0.0023296	rs875494	0.00248916
rs17280555	0.002033	rs35731709	0.0021926	rs7034379	0.0023315	rs2373571	0.00248984
rs12672637	0.0020338	rs814953	0.0021952	rs12396885	0.0023329	rs7062292	0.00249602
rs17338737	0.0020338	rs5974063	0.0021968	rs1563295	0.0023346	rs5953564	0.00250443
rs11698063	0.002034	rs4844144	0.0022003	rs17421554	0.0023381	rs1839148	0.00250556
rs17191803	0.0020384	rs5970756	0.0022013	rs1194565	0.0023395	rs2971381	0.00251669
rs5961501	0.002039	rs5920654	0.0022092	rs4784307	0.00234	rs2294456	0.0025179
rs461011	0.0020393	rs11077573	0.0022125	rs4431713	0.0023405	rs217994	0.00251793
rs10975141	0.0020444	rs5923649	0.0022151	rs5952630	0.0023424	rs12285681	0.00252214
rs7563563	0.0020447	rs17589482	0.0022165	rs5926145	0.0023439	rs3812243	0.00252829
rs2702239	0.0020457	rs850638	0.0022191	rs10282982	0.0023469	rs17520378	0.00252979
rs2237785	0.0020475	rs10736703	0.0022224	rs1011624	0.002357	rs41456245	0.00253124
rs5927077	0.0020518	rs12012062	0.0022238	rs1366934	0.0023595	rs7988462	0.00253455
rs1354504	0.0020574	rs12625924	0.0022256	rs2782669	0.002361	rs905362	0.00253683
rs7334189	0.0020581	rs1924680	0.0022269	rs10521427	0.002361	rs10848161	0.00253872
rs12013728	0.0020647	rs5910937	0.0022306	rs2071191	0.0023637	rs10745676	0.0025398
rs2694710	0.0020746	rs2833537	0.0022321	rs2231496	0.0023638	rs16831204	0.00254301
rs10495660	0.0020749	rs17316731	0.0022339	rs7844288	0.0023654	rs11147630	0.0025433
rs1942598	0.0020759	rs10502407	0.0022349	rs16956948	0.0023699	rs1933405	0.00255057
rs35209885	0.0020815	rs12450386	0.0022371	rs5972687	0.0023713	rs5925593	0.00255282
rs7431265	0.0020884	rs985703	0.0022383	rs13110602	0.0023725	rs4811792	0.00255362
rs9444074	0.0020914	rs5907001	0.0022385	rs4825511	0.0023805	rs4825476	0.00255601
rs5931595	0.0020952	rs3130076	0.0022438	rs4467269	0.002381	rs2642589	0.0025603
rs9851426	0.0020977	rs4240057	0.0022439	rs3118077	0.0023811	rs17552796	0.00256075
rs17246029	0.0020978	rs4839775	0.0022529	rs318168	0.0023861	rs199638	0.0025622
rs12852223	0.0021021	rs17694541	0.0022531	rs17800362	0.0023866	rs41329849	0.00256368
rs1607653	0.0021044	rs16989447	0.0022536	rs2091648	0.0023886	rs4300141	0.00257031
rs980494	0.0021102	rs5971790	0.0022545	rs1382410	0.0023923	rs5972809	0.00257265
rs256003	0.0021111	rs9546325	0.0022554	rs7653913	0.0023932	rs5962299	0.00257416
rs5910841	0.0021176	rs10033826	0.0022562	rs11766540	0.0023952	rs203644	0.0025798
rs32274	0.0021198	rs1841135	0.0022586	rs10021331	0.0023986	rs333910	0.00258065
rs5951582	0.0021202	rs4782854	0.0022705	rs6917645	0.0023996	rs4499720	0.00258417
rs1742852	0.002123	rs5750467	0.0022741	rs7894582	0.0024021	rs7061865	0.00258863
rs12525343	0.0021258	rs2316997	0.0022782	rs2960660	0.0024043	rs4636358	0.0025911
rs1926282	0.0021268	rs1345320	0.0022796	rs2614578	0.0024048	rs41464946	0.00259324
rs527174	0.0021283	rs1284440	0.0022822	rs12327672	0.0024061	rs7500985	0.00259625
rs17794389	0.0021286	rs641284	0.0022834	rs10991736	0.0024147	rs17155887	0.00259717
rs960230	0.0021297	rs1921946	0.0022847	rs6017996	0.0024217	rs10031347	0.00259808
rs2984915	0.0021299	rs2804356	0.0022851	rs202273	0.0024224	rs17210369	0.00259939
rs41494755	0.0021301	rs1962051	0.0022871	rs13264791	0.0024225	rs17404243	0.00259966
rs6610466	0.0021361	rs5925749	0.0022889	rs10333	0.0024249	rs4755454	0.00260627
rs11105027	0.0021466	rs3121454	0.0022892	rs16999801	0.002425	rs4595494	0.00260748
rs7746596	0.0021479	rs819558	0.0022917	rs213535	0.0024416	rs7302566	0.00260924
rs12687206	0.0021508	rs741928	0.0022934	rs41464344	0.0024428	rs10811434	0.00261524
rs7878715	0.0021513	rs17353229	0.0022942	rs1997480	0.0024462	rs7056866	0.00261615
rs3860829	0.0021528	rs13265492	0.0023063	rs2201665	0.0024515	rs959931	0.00261706
rs5957111	0.0021589	rs5935593	0.002309	rs17731407	0.0024533	rs1025952	0.00261784
rs5922247	0.0021674	rs1553690	0.0023098	rs4281059	0.0024544	rs17280621	0.00261818
rs12851930	0.0021722	rs5970981	0.0023109	rs5905163	0.0024547	rs808517	0.00262687

Figure 21-7

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rs12333603	0.0026322	rs5964314	0.0027994	rs17537048	0.0029885	rs240188	0.00320274
rs5973570	0.0026351	rs16864788	0.0028088	rs239757	0.0029912	rs9365789	0.00320424
rs7882753	0.002646	rs1551343	0.0028097	rs237150	0.002998	rs2460488	0.0032044
rs1918560	0.0026505	rs6638777	0.002815	rs5747353	0.0030026	rs13389178	0.00321331
rs7885928	0.0026556	rs17794578	0.0028154	rs4697350	0.0030033	rs1020256	0.00321663
rs10028553	0.0026571	rs10118551	0.002822	rs1999270	0.0030053	rs4696645	0.00321765
rs679327	0.0026622	rs12690384	0.0028235	rs10435425	0.0030055	rs7882055	0.00322128
rs10961168	0.0026708	rs7867360	0.0028295	rs1277767	0.0030107	rs5927962	0.00322171
rs1839436	0.0026752	rs9559772	0.0028322	rs4503268	0.0030114	rs4787053	0.00322545
rs9348837	0.0026794	rs2064652	0.0028358	rs6625472	0.0030162	rs12851954	0.00322738
rs11948744	0.0026817	rs5945705	0.0028361	rs5928187	0.0030182	rs7312853	0.00323082
rs5944563	0.0026828	rs1565471	0.0028392	rs3744760	0.0030249	rs9501975	0.0032327
rs5910718	0.0026838	rs6636538	0.0028403	rs869738	0.0030287	rs10522017	0.00323398
rs1857853	0.0026868	rs4826780	0.0028414	rs7611544	0.00303	rs12688897	0.00323836
rs2869076	0.0026872	rs10860397	0.0028427	rs4526502	0.003033	rs4633929	0.00324201
rs3775121	0.0026903	rs2158536	0.0028451	rs9503670	0.003041	rs10999085	0.00324237
rs878073	0.0026919	rs779984	0.0028482	rs6535220	0.0030427	rs2146951	0.00324626
rs4396581	0.0026921	rs2925175	0.0028662	rs6715785	0.0030452	rs7312700	0.00324792
rs16911991	0.002695	rs17219901	0.0028746	rs2825603	0.0030486	rs36047913	0.00324935
rs4119090	0.0026975	rs17399240	0.0028751	rs721431	0.0030507	rs747145	0.00324975
rs2172693	0.0026975	rs16876827	0.0028758	rs7963886	0.0030538	rs2060978	0.00326257
rs1898799	0.002701	rs17002433	0.0028809	rs9350228	0.0030559	rs6658076	0.00327437
rs9520124	0.0027101	rs5979643	0.0028809	rs5953847	0.0030565	rs2016751	0.0032874
rs5905042	0.0027104	rs5949507	0.0028931	rs2248314	0.003059	rs3772505	0.00328972
rs4107962	0.0027118	rs3744758	0.0028934	rs2290674	0.0030597	rs7822711	0.00329723
rs12849629	0.0027188	rs761685	0.0029	rs2595479	0.003063	rs5945546	0.00329999
rs17337757	0.0027215	rs6520623	0.0029025	rs909379	0.0030663	rs12559632	0.00330103
rs17245537	0.0027239	rs7179956	0.0029038	rs12516361	0.0030664	rs1965009	0.00330437
rs728340	0.0027251	rs3771685	0.0029054	rs11151771	0.003069	rs5927408	0.00331134
rs4917653	0.0027278	rs916352	0.0029217	rs316720	0.0030696	rs1874274	0.00331507
rs1558690	0.0027309	rs1547396	0.0029277	rs115571	0.0030791	rs2748312	0.00331579
rs5909876	0.0027353	rs12618771	0.0029313	rs2049661	0.0030804	rs3027369	0.00331871
rs2238971	0.0027371	rs16960253	0.0029335	rs5924031	0.0030854	rs1169081	0.00332104
rs696975	0.0027412	rs7325885	0.0029382	rs1354269	0.0030862	rs938661	0.0033234
rs11800756	0.0027475	rs1032075	0.0029391	rs1037104	0.0030947	rs2290376	0.00332458
rs5928271	0.0027514	rs6573309	0.0029434	rs10470297	0.0030975	rs7622802	0.00332616
rs7095944	0.002752	rs4844364	0.0029462	rs17324835	0.0030986	rs34985771	0.00332852
rs16894192	0.0027534	rs3764763	0.0029476	rs7989613	0.0030997	rs6638361	0.00332862
rs11796631	0.0027545	rs1921152	0.0029485	rs5918463	0.0031039	rs2471105	0.00332998
rs9526447	0.0027545	rs5981241	0.0029486	rs12134393	0.0031045	rs3135154	0.00333373
rs2206684	0.0027591	rs2842772	0.00295	rs1055919	0.0031067	rs196987	0.00333595
rs7641386	0.0027595	rs1218124	0.0029549	rs6609303	0.0031183	rs17104169	0.00334024
rs6527779	0.0027613	rs17338057	0.0029584	rs11103505	0.0031232	rs942602	0.00334173
rs12431261	0.0027632	rs2030253	0.0029594	rs317089	0.0031419	rs418544	0.00334287
rs6908911	0.0027649	rs7779937	0.0029604	rs1457608	0.0031596	rs6748518	0.00334315
rs6619699	0.0027657	rs4631605	0.0029626	rs9315031	0.0031601	rs5911634	0.00334528
rs2840811	0.0027668	rs7868409	0.0029658	rs34745199	0.0031648	rs2144497	0.00335158
rs2162919	0.002776	rs6100719	0.0029684	rs1915601	0.0031654	rs7201592	0.00335163
rs1351260	0.0027817	rs2820694	0.0029693	rs9922955	0.0031654	rs9399704	0.00335386
rs1581286	0.0027844	rs10483477	0.0029695	rs6112546	0.003171	rs2236153	0.00336477
rs10826588	0.0027849	rs768198	0.0029717	rs2156975	0.0031727	rs17091245	0.00336891
rs5966755	0.0027926	rs418886	0.0029749	rs6128676	0.0031732	rs4826897	0.0033848
rs4825731	0.0027933	rs16953757	0.0029769	rs17319056	0.0031795	rs4749305	0.00338501
rs2836503	0.0027944	rs5973160	0.0029799	rs7584187	0.0031913	rs798159	0.00339438
rs4318894	0.0027961	rs6609257	0.0029843	rs2611605	0.0031928	rs5934551	0.0033963

Figure 21-8

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rs4452953	0.0034007	rs11796660	0.0035869	rs1034461	0.0038374	rs10511568	0.00401354
rs7222649	0.0034017	rs5933309	0.0035929	rs384225	0.0038424	rs12007973	0.00401441
rs17081893	0.0034026	rs2211221	0.0035955	rs4830299	0.0038435	rs8050204	0.0040171
rs4363313	0.0034081	rs6575728	0.0036085	rs16833171	0.0038452	rs4655643	0.00402414
rs8060992	0.0034106	rs7919211	0.0036099	rs17805883	0.0038454	rs4484340	0.00402587
rs9937119	0.0034108	rs4939921	0.0036148	rs12613322	0.0038462	rs11915789	0.00403255
rs1198723	0.0034179	rs3128809	0.003615	rs865525	0.0038514	rs4345730	0.0040398
rs5927062	0.0034254	rs2875248	0.0036185	rs4240039	0.0038606	rs6633866	0.00404001
rs16997510	0.0034354	rs41391344	0.0036234	rs2992177	0.0038645	rs2267592	0.00405032
rs1544867	0.0034376	rs7202180	0.0036311	rs5919988	0.0038663	rs10498850	0.0040597
rs1554310	0.0034386	rs7826857	0.0036348	rs11676482	0.0038678	rs110133	0.00406725
rs2238993	0.003439	rs5954822	0.0036367	rs10521726	0.0038751	rs5918362	0.00407197
rs12852291	0.0034442	rs5925924	0.003638	rs17743398	0.0038885	rs10893379	0.00407291
rs1462811	0.0034484	rs2291985	0.0036389	rs11176397	0.0038945	rs5954267	0.00407985
rs2870758	0.0034486	rs12976023	0.0036399	rs633691	0.0039039	rs17260618	0.00408233
rs1537415	0.0034522	rs7885942	0.0036463	rs5927914	0.0039071	rs4827023	0.00408343
rs5962954	0.0034563	rs4278071	0.003651	rs7719176	0.0039074	rs5921851	0.00408877
rs4740583	0.0034579	rs11619328	0.0036594	rs7586131	0.0039101	rs11580624	0.004096
rs2429799	0.0034611	rs403558	0.0036804	rs17641840	0.0039134	rs6033377	0.0040983
rs6628825	0.003464	rs17051672	0.0036873	rs4828941	0.003918	rs7278294	0.00409833
rs2058655	0.0034653	rs3008922	0.0036874	rs11038227	0.0039192	rs1017190	0.0041036
rs34191540	0.003467	rs5927678	0.0036882	rs4593704	0.003922	rs1882407	0.00410628
rs5975291	0.0034672	rs10521432	0.0036935	rs2107425	0.0039248	rs684573	0.00410707
rs1021734	0.0034701	rs13256218	0.0037045	rs5982925	0.0039284	rs9842287	0.00411098
rs4277226	0.0034749	rs5911548	0.0037078	rs10085385	0.003929	rs11129517	0.00411194
rs1884694	0.0034765	rs9522357	0.0037085	rs9376702	0.0039316	rs12621754	0.00411712
rs4830775	0.0034838	rs893465	0.0037086	rs2961401	0.0039317	rs6481864	0.00412961
rs1864277	0.0034847	rs5923658	0.0037116	rs6676380	0.0039338	rs4258586	0.00413439
rs652582	0.0034849	rs10808361	0.0037121	rs7787946	0.003939	rs9895315	0.00413935
rs738085	0.0034905	rs1277964	0.0037132	rs17790821	0.0039407	rs10454141	0.00414685
rs5920949	0.0034914	rs4827289	0.0037153	rs5765532	0.0039423	rs2092255	0.00415235
rs1937076	0.0034916	rs2765379	0.0037168	rs5942880	0.0039443	rs16899194	0.00415637
rs17608192	0.0034931	rs7708097	0.0037231	rs2508420	0.0039498	rs411751	0.00416171
rs11156966	0.0034966	rs2376973	0.003725	rs1427087	0.003954	rs2573668	0.00416774
rs2103520	0.003498	rs1152202	0.0037286	rs5949581	0.003954	rs10924848	0.00416907
rs783404	0.0034986	rs2908784	0.0037308	rs6463443	0.0039581	rs12949329	0.00417518
rs376886	0.0034987	rs851235	0.003742	rs5938377	0.0039589	rs8101738	0.00417741
rs5905820	0.0035065	rs36038231	0.003748	rs10253752	0.0039603	rs4524307	0.0041816
rs5940034	0.0035147	rs2164787	0.0037502	rs823031	0.0039614	rs5927693	0.00418473
rs17122882	0.0035164	rs10196963	0.0037513	rs11013860	0.0039632	rs5748307	0.0041927
rs16855137	0.0035166	rs12598492	0.0037552	rs17273882	0.0039694	rs903471	0.00421122
rs952489	0.0035187	rs5990571	0.0037712	rs2157272	0.0039731	rs6639205	0.00421309
rs2568447	0.0035232	rs17095458	0.0037738	rs17239044	0.0039735	rs11234201	0.00421742
rs939348	0.0035232	rs16974638	0.0037754	rs579005	0.0039742	rs5933374	0.00421821
rs1181065	0.003524	rs9394524	0.0037792	rs917640	0.0039746	rs1458961	0.00421919
rs7975082	0.0035325	rs1318761	0.0037818	rs6637203	0.00398	rs6726739	0.00422111
rs5904980	0.003541	rs10126799	0.0037993	rs10504398	0.0039825	rs754133	0.00422691
rs7120805	0.0035481	rs12557491	0.0038043	rs6991826	0.0039872	rs808802	0.00423544
rs10184858	0.0035549	rs2292893	0.0038051	rs5963545	0.0039963	rs17138834	0.00423809
rs2225609	0.0035563	rs5765558	0.0038059	rs1840485	0.003999	rs9730979	0.00423983
rs8037065	0.0035572	rs31465	0.0038093	rs1124814	0.0040021	rs17398001	0.00424094
rs6812536	0.003568	rs733099	0.0038105	rs749516	0.0040037	rs4734058	0.00424127
rs1206920	0.0035713	rs41491649	0.0038106	rs2737424	0.0040079	rs2562784	0.00424606
rs6132672	0.0035746	rs2952131	0.0038211	rs5905498	0.0040083	rs4957159	0.00424724
rs2523990	0.003585	rs981066	0.0038251	rs6594805	0.0040101	rs3113053	0.00424805

Figure 21-9

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rs8033429	0.004255
rs2040577	0.0042552
rs6718080	0.0042557
rs17148800	0.0042603
rs9950126	0.0042613
rs232569	0.0042633
rs17093688	0.0042635
rs4940732	0.0042677
rs5915280	0.0042691
rs10151548	0.0042727
rs12011691	0.0042742
rs41408045	0.0042805
rs2327951	0.0042865
rs10193163	0.0042878
rs5920962	0.0042885
rs7052650	0.004293
rs4076999	0.0042957
rs13406485	0.0042981
rs11217364	0.0043033
rs5928184	0.0043047
rs5928022	0.0043048
rs7912575	0.004307
rs1338097	0.0043073
rs4300862	0.0043077
rs5963436	0.0043151
rs17103027	0.0043259
rs236064	0.004332
rs12394920	0.0043394

Figure 21-10

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SNP	ChiSquare P value	SNP	ChiSquare P value	SNP	ChiSquare P value
rs11007270	5.14E-19	rs658339	1.18E-09	rs7620921	1.91E-09
rs17073262	2.61E-18	rs11894357	1.19E-09	rs17150942	1.92E-09
rs7190657	1.58E-12	rs7813492	1.19E-09	rs7696347	1.93E-09
rs2411130	1.74E-12	rs10991286	1.25E-09	rs17101921	1.93E-09
rs1346861	6.09E-12	rs17045475	1.28E-09	rs17070374	1.93E-09
rs2503730	1.28E-11	rs10509275	1.30E-09	rs17665636	1.93E-09
rs773969	1.45E-11	rs1026842	1.33E-09	rs11016169	1.94E-09
rs4448502	2.51E-11	rs17135958	1.34E-09	rs1800130	1.95E-09
rs11935979	5.47E-11	rs10521073	1.34E-09	rs16945738	1.95E-09
rs8066895	5.51E-11	rs16829525	1.36E-09	rs2116732	1.95E-09
rs4837165	1.45E-10	rs12809590	1.37E-09	rs4544694	1.96E-09
rs2122189	1.51E-10	rs7236104	1.37E-09	rs4832055	1.98E-09
rs4743886	1.55E-10	rs6016319	1.38E-09	rs135080	2.01E-09
rs9813883	2.18E-10	rs13294648	1.38E-09	rs341971	2.02E-09
rs11902772	2.36E-10	rs8048037	1.40E-09	rs1391048	2.03E-09
rs17041032	2.57E-10	rs9893250	1.41E-09	rs10033823	2.03E-09
rs7949670	2.78E-10	rs10000609	1.42E-09	rs11063757	2.03E-09
rs12716680	3.69E-10	rs2707671	1.43E-09	rs11882629	2.06E-09
rs2139622	4.13E-10	rs12058586	1.47E-09	rs856127	2.07E-09
rs17644677	4.38E-10	rs16940712	1.47E-09	rs12141445	2.08E-09
rs10924674	4.44E-10	rs1017329	1.52E-09	rs9855339	2.12E-09
rs1443903	4.90E-10	rs17245098	1.52E-09	rs441394	2.12E-09
rs16907736	5.20E-10	rs16954194	1.54E-09	rs8069306	2.13E-09
rs2458707	5.73E-10	rs12679740	1.57E-09	rs3135679	2.14E-09
rs1488831	5.98E-10	rs3731194	1.59E-09	rs16839691	2.18E-09
rs17058945	6.22E-10	rs10989383	1.60E-09	rs10746431	2.25E-09
rs41524446	6.36E-10	rs12481485	1.62E-09	rs11158527	2.25E-09
rs1862725	6.38E-10	rs4140637	1.65E-09	rs1545653	2.28E-09
rs12405213	6.49E-10	rs459289	1.67E-09	rs2898097	2.29E-09
rs16873285	6.91E-10	rs17223923	1.69E-09	rs7612956	2.32E-09
rs16969423	7.46E-10	rs10469061	1.70E-09	rs9428247	2.42E-09
rs17084123	7.60E-10	rs1974880	1.72E-09	rs17071555	2.50E-09
rs41358349	7.69E-10	rs16986733	1.73E-09	rs6972733	2.72E-09
rs2365177	7.78E-10	rs7664613	1.76E-09	rs6849870	2.87E-09
rs10081321	7.84E-10	rs17459522	1.77E-09	rs2664089	3.07E-09
rs13226886	7.98E-10	rs953216	1.77E-09	rs17127235	3.15E-09
rs10116858	8.37E-10	rs11028121	1.78E-09	rs2064873	3.29E-09
rs16996744	8.45E-10	rs17130723	1.78E-09	rs1397706	3.79E-09
rs9968025	8.53E-10	rs10847143	1.78E-09	rs9511646	4.49E-09
rs2114656	8.98E-10	rs17129180	1.79E-09	rs10507779	4.91E-09
rs12427758	9.10E-10	rs11973158	1.80E-09	rs16977815	5.00E-09
rs1893912	9.10E-10	rs7325039	1.81E-09	rs12645640	5.04E-09
rs7616638	9.38E-10	rs7746075	1.83E-09	rs3828983	5.06E-09
rs17701478	9.66E-10	rs16877066	1.84E-09	rs10272660	5.09E-09
rs4736240	9.80E-10	rs2833537	1.84E-09	rs9673539	5.66E-09
rs6071448	1.09E-09	rs17305183	1.84E-09	rs16828720	5.74E-09
rs10272511	1.09E-09	rs1003106	1.85E-09	rs17198456	1.44E-08
rs17134173	1.10E-09	rs2595146	1.87E-09	rs12424995	2.75E-08
rs10514526	1.14E-09	rs7231918	1.88E-09	rs8175963	2.94E-08
rs222809	1.15E-09	rs6801556	1.88E-09	rs7329263	3.06E-08
rs12166759	1.16E-09	rs11892351	1.89E-09	rs17154065	3.36E-08
rs4140425	1.16E-09	rs16899203	1.89E-09	rs17125102	5.31E-08
rs11109787	1.17E-09	rs1215834	1.89E-09	rs10161762	8.14E-08

Figure 22-1

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rs874511	9.81E-08	rs7792701	5.42E-06	rs159619	2.06E-05
rs4906417	1.13E-07	rs4751881	5.44E-06	rs6867140	2.08E-05
rs16894463	1.48E-07	rs7601609	5.45E-06	rs4899628	2.08E-05
rs2220197	1.69E-07	rs7561649	5.46E-06	rs7081304	2.09E-05
rs11082879	1.86E-07	rs17447468	5.62E-06	rs4145262	2.09E-05
rs2702894	1.94E-07	rs6907667	5.67E-06	rs3010711	2.11E-05
rs3101089	2.26E-07	rs41385047	5.81E-06	rs9896209	2.12E-05
rs17322650	2.77E-07	rs16868514	5.95E-06	rs12100022	2.16E-05
rs7995725	2.78E-07	rs1461698	5.96E-06	rs7148698	2.18E-05
rs11245373	2.95E-07	rs17213769	6.05E-06	rs10483600	2.20E-05
rs16850673	3.27E-07	rs7048449	6.07E-06	rs9362046	2.23E-05
rs777805	3.33E-07	rs10159565	6.11E-06	rs7746931	2.26E-05
rs2137873	3.55E-07	rs4476905	6.45E-06	rs16861032	2.31E-05
rs7083512	3.63E-07	rs10252992	6.67E-06	rs606670	2.33E-05
rs1374778	3.78E-07	rs2493215	6.74E-06	rs1978147	2.34E-05
rs2845573	4.19E-07	rs1353645	7.32E-06	rs4748946	2.37E-05
rs2374506	4.67E-07	rs17135053	8.44E-06	rs2879725	2.44E-05
rs11249163	4.86E-07	rs7814691	8.82E-06	rs2136781	2.54E-05
rs17488361	4.97E-07	rs13235564	8.83E-06	rs4425537	2.56E-05
rs11230550	5.37E-07	rs6708183	9.80E-06	rs3124736	2.57E-05
rs4257980	5.80E-07	rs10838120	1.01E-05	rs7775112	2.60E-05
rs17247907	6.88E-07	rs2642556	1.04E-05	rs17827168	2.64E-05
rs16975213	9.37E-07	rs9864435	1.04E-05	rs993250	2.65E-05
rs4687113	1.08E-06	rs4239555	1.08E-05	rs7527246	2.67E-05
rs12997980	1.11E-06	rs7221984	1.08E-05	rs13178377	2.67E-05
rs17027550	1.12E-06	rs17294110	1.11E-05	rs1936763	2.71E-05
rs11824839	1.16E-06	rs17109825	1.12E-05	rs41415147	2.71E-05
rs1076725	1.17E-06	rs10929654	1.17E-05	rs4455878	2.72E-05
rs12395234	1.18E-06	rs3852823	1.21E-05	rs12788831	2.73E-05
rs7030479	1.20E-06	rs2657475	1.22E-05	rs17059620	2.76E-05
rs2305885	1.27E-06	rs4689349	1.27E-05	rs9829645	2.81E-05
rs6924108	1.39E-06	rs7673636	1.34E-05	rs11961118	2.81E-05
rs9646957	1.52E-06	rs6437301	1.38E-05	rs31887	2.82E-05
rs17055923	1.56E-06	rs6005515	1.38E-05	rs16975860	2.88E-05
rs9302221	1.84E-06	rs7828571	1.39E-05	rs1359140	2.89E-05
rs9568130	2.01E-06	rs1413254	1.39E-05	rs1341140	2.89E-05
rs3934577	2.33E-06	rs16980981	1.48E-05	rs17347454	2.91E-05
rs17172689	2.39E-06	rs7249111	1.49E-05	rs9820153	2.92E-05
rs4852262	2.44E-06	rs7814667	1.51E-05	rs9287767	2.93E-05
rs13142375	3.25E-06	rs4300229	1.59E-05	rs6925493	2.93E-05
rs995385	3.78E-06	rs1446216	1.63E-05	rs10489643	2.96E-05
rs6716674	3.83E-06	rs6547193	1.64E-05	rs17169595	3.01E-05
rs1152934	4.14E-06	rs2785173	1.72E-05	rs6760222	3.04E-05
rs8098902	4.43E-06	rs11778669	1.76E-05	rs2496331	3.04E-05
rs12064275	4.48E-06	rs29426	1.82E-05	rs12447986	3.07E-05
rs1005427	4.54E-06	rs9609441	1.83E-05	rs1978949	3.12E-05
rs11066699	4.57E-06	rs41497849	1.84E-05	rs3135806	3.13E-05
rs13338089	4.58E-06	rs735311	1.85E-05	rs2778913	3.17E-05
rs17777478	4.71E-06	rs41478351	1.92E-05	rs41353849	3.20E-05
rs16952725	4.94E-06	rs12232279	1.92E-05	rs9577246	3.20E-05
rs1571362	4.94E-06	rs135439	1.96E-05	rs2998734	3.24E-05
rs9954459	5.23E-06	rs17652855	2.00E-05	rs17003277	3.24E-05
rs1962511	5.24E-06	rs7660043	2.00E-05	rs7905885	3.25E-05
rs886206	5.36E-06	rs16952975	2.03E-05	rs16872626	3.26E-05
rs9573196	5.41E-06	rs9592510	2.05E-05	rs17071212	3.27E-05

Figure 22-2

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		111/122	
rs7290510	3.31E-05	rs2089051	4.57E-05
rs2489386	3.33E-05	rs10851713	4.58E-05
rs17136184	3.39E-05	rs6072574	4.62E-05
rs6112602	3.41E-05	rs1338007	4.62E-05
rs7258075	3.42E-05	rs774507	4.66E-05
rs4894094	3.44E-05	rs2115055	4.78E-05
rs16867583	3.46E-05	rs726085	4.96E-05
rs735665	3.47E-05	rs4378299	5.00E-05
rs17078168	3.49E-05	rs2363768	5.01E-05
rs9635390	3.52E-05	rs16955607	5.03E-05
rs16964764	3.57E-05	rs17190037	5.07E-05
rs17434013	3.58E-05	rs10957260	5.08E-05
rs16980975	3.61E-05	rs13231718	5.08E-05
rs11014853	3.63E-05	rs2848872	5.13E-05
rs1517440	3.64E-05	rs1441492	5.17E-05
rs12323400	3.65E-05	rs10019120	5.17E-05
rs17600829	3.67E-05	rs17130391	5.18E-05
rs11971669	3.74E-05	rs16853335	5.18E-05
rs328389	3.74E-05	rs1402982	5.24E-05
rs7511818	3.75E-05	rs8021182	5.24E-05
rs17063661	3.76E-05	rs17104310	5.25E-05
rs17009821	3.76E-05	rs41431549	5.27E-05
rs735183	3.83E-05	rs777831	5.31E-05
rs17161652	3.84E-05	rs4448295	5.35E-05
rs11780949	3.86E-05	rs4693997	5.44E-05
rs2035882	3.88E-05	rs8037800	5.47E-05
rs2127388	3.88E-05	rs6456652	5.49E-05
rs9397087	3.92E-05	rs12102352	5.53E-05
rs16991630	3.93E-05	rs16860778	5.55E-05
rs2203428	3.94E-05	rs12419474	5.57E-05
rs618393	3.96E-05	rs16943976	5.64E-05
rs138465	3.98E-05	rs16934126	5.65E-05
rs16855587	3.99E-05	rs822519	5.67E-05
rs17684354	4.01E-05	rs12603217	5.70E-05
rs7197514	4.03E-05	rs17028456	5.70E-05
rs6739610	4.03E-05	rs1325350	5.71E-05
rs2672458	4.06E-05	rs2824903	5.74E-05
rs10514852	4.10E-05	rs12489946	5.81E-05
rs17738653	4.13E-05	rs9928871	5.83E-05
rs10956341	4.18E-05	rs1980789	5.89E-05
rs17828913	4.19E-05	rs9882757	5.90E-05
rs3744951	4.20E-05	rs2112626	5.91E-05
rs6956087	4.25E-05	rs17144649	6.00E-05
rs7556491	4.25E-05	rs10242657	6.03E-05
rs7176139	4.27E-05	rs16837404	6.16E-05
rs6711283	4.29E-05	rs10927530	6.16E-05
rs9327170	4.32E-05	rs2010905	6.17E-05
rs900501	4.32E-05	rs7284708	6.19E-05
rs10166067	4.36E-05	rs16902902	6.19E-05
rs11239131	4.37E-05	rs12248406	6.21E-05
rs10985431	4.40E-05	rs7952006	6.22E-05
rs10521469	4.42E-05	rs6461068	6.25E-05
rs9296758	4.43E-05	rs17011669	6.27E-05
rs1861269	4.49E-05	rs821585	6.27E-05
rs10498889	4.53E-05	rs12592927	6.31E-05
		rs17081073	6.33E-05
		rs16946234	6.33E-05
		rs1966049	6.33E-05
		rs41390551	6.33E-05
		rs6813350	6.34E-05
		rs2470592	6.39E-05
		rs17248007	6.41E-05
		rs11113904	6.57E-05
		rs909966	6.57E-05
		rs10492479	6.58E-05
		rs11200820	6.61E-05
		rs2588153	6.64E-05
		rs6061414	6.64E-05
		rs17037858	6.65E-05
		rs17088891	6.67E-05
		rs2075005	6.69E-05
		rs11256896	6.70E-05
		rs3751609	6.71E-05
		rs17110716	6.72E-05
		rs17738584	6.72E-05
		rs16945302	6.75E-05
		rs742058	6.76E-05
		rs6947391	6.77E-05
		rs11066417	6.79E-05
		rs7540790	6.86E-05
		rs361386	6.87E-05
		rs2506363	6.91E-05
		rs6930572	6.95E-05
		rs17143029	6.97E-05
		rs17359763	7.00E-05
		rs7753282	7.00E-05
		rs11934409	7.01E-05
		rs2127994	7.03E-05
		rs16926940	7.04E-05
		rs11802583	7.05E-05
		rs6564988	7.05E-05
		rs17019886	7.07E-05
		rs6725530	7.07E-05
		rs17644551	7.08E-05
		rs4553462	7.09E-05
		rs11049300	7.10E-05
		rs17162892	7.10E-05
		rs379387	7.11E-05
		rs11978507	7.12E-05
		rs41421146	7.12E-05
		rs9643874	7.13E-05
		rs1392481	7.15E-05
		rs17076068	7.15E-05
		rs13335336	7.15E-05
		rs34442697	7.16E-05
		rs11988203	7.16E-05
		rs2834567	7.16E-05
		rs11077913	7.18E-05
		rs167901	7.20E-05
		rs1333345	7.20E-05

Figure 22-3

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rs16863892	7.23E-05	rs11698155	0.0001198	rs4278478	0.0001867
rs6967655	7.24E-05	rs4690374	0.0001207	rs7465564	0.0001868
rs3118205	7.25E-05	rs6127676	0.0001266	rs4499448	0.0001873
rs17135109	7.25E-05	rs4669573	0.0001271	rs11601059	0.0001893
rs16871387	7.27E-05	rs524811	0.0001279	rs2610808	0.0001928
rs6534884	7.29E-05	rs7034055	0.0001302	rs11117209	0.0001941
rs925219	7.29E-05	rs4524459	0.0001307	rs708436	0.0001942
rs13439821	7.32E-05	rs2410200	0.0001359	rs10503636	0.000197
rs10944520	7.32E-05	rs17807611	0.0001363	rs7847263	0.0001996
rs16842165	7.36E-05	rs8050204	0.0001381	rs7084614	0.0002045
rs17103118	7.38E-05	rs7157772	0.0001407	rs4435942	0.0002056
rs17021261	7.38E-05	rs6534890	0.0001408	rs183805	0.000207
rs7560153	7.39E-05	rs7224403	0.0001413	rs2729547	0.0002085
rs1774929	7.39E-05	rs4856008	0.0001428	rs6698441	0.0002088
rs12381471	7.44E-05	rs587952	0.000143	rs4670949	0.0002096
rs9590070	7.49E-05	rs1629888	0.0001438	rs16882008	0.0002123
rs17195435	7.51E-05	rs10516697	0.0001442	rs4307284	0.0002203
rs6855048	7.55E-05	rs1174305	0.0001444	rs10514492	0.0002206
rs6887404	7.56E-05	rs17675810	0.0001447	rs12402548	0.0002215
rs1526959	7.62E-05	rs10492314	0.0001456	rs2032821	0.0002294
rs7776218	7.73E-05	rs17212829	0.0001458	rs4045515	0.0002337
rs17157380	7.83E-05	rs8057123	0.0001472	rs1659284	0.0002349
rs11143178	7.87E-05	rs869901	0.0001474	rs10964337	0.0002365
rs9910447	8.21E-05	rs9477397	0.000148	rs9873736	0.0002378
rs16824224	8.35E-05	rs3744171	0.0001515	rs1451890	0.0002379
rs10845920	8.44E-05	rs10487884	0.0001548	rs608665	0.000239
rs6868941	8.53E-05	rs6974087	0.0001574	rs1078324	0.0002399
rs9357123	8.54E-05	rs9365114	0.0001577	rs1020723	0.0002419
rs17181606	8.61E-05	rs7611795	0.0001593	rs4784805	0.0002426
rs639595	8.79E-05	rs501213	0.0001603	rs10505446	0.0002446
rs9427477	8.88E-05	rs10490000	0.0001605	rs1370138	0.0002482
rs10175061	9.04E-05	rs16904805	0.0001665	rs13279286	0.0002494
rs11581227	9.08E-05	rs911225	0.0001671	rs9352838	0.0002507
rs17666079	9.23E-05	rs17666735	0.0001672	rs4872206	0.0002528
rs9313810	9.52E-05	rs17378053	0.0001682	rs10804866	0.0002548
rs1489170	9.62E-05	rs7907913	0.0001691	rs4325261	0.000259
rs943327	9.63E-05	rs9946486	0.0001695	rs10737025	0.0002599
rs7776583	9.71E-05	rs6824902	0.0001696	rs41347750	0.0002648
rs16938000	9.83E-05	rs6066395	0.0001699	rs17619264	0.0002691
rs9570793	9.99E-05	rs10515813	0.000171	rs12757377	0.0002699
rs17432461	0.0001015	rs6747341	0.000171	rs1448809	0.0002703
rs6046762	0.0001078	rs4557033	0.0001715	rs11188759	0.0002709
rs7978045	0.0001093	rs34379411	0.0001729	rs17642885	0.0002714
rs437518	0.0001093	rs1156942	0.000174	rs4499238	0.0002733
rs1407877	0.0001105	rs12147724	0.0001743	rs10492055	0.0002779
rs6112481	0.0001116	rs7739957	0.0001743	rs12418818	0.0002783
rs16929898	0.0001117	rs9689350	0.0001748	rs6936494	0.0002808
rs3929907	0.0001139	rs253910	0.0001749	rs9544230	0.0002824
rs16929280	0.0001142	rs16823725	0.0001762	rs930655	0.0002839
rs2476163	0.0001142	rs10490665	0.0001779	rs35653399	0.000289
rs17172341	0.0001159	rs2219652	0.0001781	rs11234429	0.0002891
rs16937734	0.0001163	rs17508331	0.0001814	rs17167995	0.0002915
rs7248144	0.0001174	rs4774941	0.0001837	rs16918784	0.0002918
rs6584984	0.0001179	rs2895	0.0001864	rs6794287	0.0002943
rs10458204	0.0001197	rs16995302	0.0001866	rs10839595	0.0002982

Figure 22-4

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rs10510819	0.0002997	rs6086496	0.0004182	rs341497	0.0005481
rs4668298	0.0003002	rs883010	0.00042	rs6714881	0.0005487
rs4833840	0.000304	rs1432693	0.0004234	rs572609	0.0005498
rs16892009	0.0003071	rs17011927	0.0004273	rs10811539	0.0005498
rs11192252	0.0003075	rs12755278	0.0004316	rs12676658	0.0005499
rs11215482	0.0003078	rs3113053	0.0004351	rs17044304	0.0005512
rs6508341	0.0003125	rs7574709	0.0004373	rs1407214	0.0005585
rs841779	0.000315	rs4839801	0.0004382	rs17146892	0.0005586
rs2457715	0.0003166	rs13030985	0.000439	rs196580	0.0005607
rs9398226	0.0003177	rs11080775	0.0004419	rs17425397	0.0005622
rs7646819	0.0003186	rs40590	0.0004455	rs16866574	0.0005627
rs6063367	0.000324	rs666051	0.0004468	rs17031621	0.0005635
rs6862877	0.000328	rs7149693	0.0004497	rs277094	0.0005648
rs1523074	0.0003322	rs10755055	0.0004586	rs10503493	0.0005655
rs2175465	0.0003338	rs12156924	0.0004593	rs10856827	0.0005656
rs10860877	0.000336	rs750571	0.0004594	rs851023	0.0005688
rs6990760	0.0003398	rs6994723	0.0004604	rs41496150	0.0005693
rs1996671	0.0003421	rs7925366	0.0004616	rs13388047	0.0005708
rs2198207	0.0003433	rs1076884	0.0004623	rs665036	0.0005732
rs12127407	0.0003433	rs4418560	0.0004657	rs12467020	0.0005735
rs17561681	0.000346	rs9893321	0.000466	rs17651026	0.000574
rs1891987	0.0003481	rs17811677	0.0004686	rs16870976	0.0005745
rs3821285	0.0003514	rs11675929	0.0004705	rs6133374	0.0005762
rs17458000	0.0003541	rs1583646	0.0004717	rs1607807	0.0005794
rs7091524	0.0003556	rs11751618	0.0004718	rs1684674	0.0005814
rs2828789	0.0003569	rs6107483	0.000473	rs5995594	0.0005863
rs12423492	0.0003573	rs628606	0.0004731	rs11265310	0.0005888
rs388	0.0003589	rs670271	0.0004745	rs2105158	0.0005916
rs13265557	0.0003619	rs816546	0.0004764	rs17745803	0.0005919
rs17123864	0.0003631	rs6854741	0.0004783	rs17642119	0.0005948
rs1978300	0.0003643	rs4440674	0.0004846	rs10885348	0.0005974
rs9942632	0.0003647	rs10514444	0.0004861	rs9371388	0.0005983
rs16936184	0.0003647	rs834130	0.0004911	rs1564048	0.0006011
rs973009	0.000369	rs12174997	0.000494	rs9492415	0.0006066
rs11218313	0.0003748	rs41339754	0.0004951	rs16893890	0.0006078
rs6066693	0.0003757	rs10503795	0.0005005	rs10910443	0.0006089
rs17824132	0.0003766	rs6934260	0.0005008	rs12061312	0.000613
rs1239904	0.0003776	rs6458330	0.0005077	rs16966632	0.0006247
rs11820515	0.0003832	rs6490506	0.0005078	rs3024676	0.0006305
rs6736779	0.0003847	rs16856202	0.0005188	rs4595229	0.000641
rs4240446	0.000385	rs10974007	0.0005192	rs868928	0.0006452
rs6963233	0.000385	rs11653617	0.0005212	rs41445146	0.0006465
rs947919	0.0003857	rs41386450	0.0005225	rs2819820	0.0006552
rs6874596	0.0003894	rs10839585	0.0005264	rs9621532	0.0006578
rs1005948	0.0003944	rs4754276	0.0005297	rs1856107	0.00066
rs7725377	0.0003958	rs17816553	0.0005306	rs283027	0.0006608
rs7772387	0.0003996	rs6446391	0.0005307	rs753725	0.0006672
rs10850171	0.0004014	rs9941114	0.0005334	rs7223092	0.0006677
rs326141	0.0004072	rs3748006	0.0005335	rs4076124	0.00067
rs17119912	0.0004112	rs4942165	0.0005352	rs7172232	0.0006747
rs10047208	0.000413	rs12351443	0.0005375	rs16892504	0.0006747
rs2527853	0.0004133	rs11859738	0.0005394	rs6995938	0.0006757
rs705970	0.000414	rs2272094	0.0005437	rs7926940	0.0006759
rs1399358	0.0004153	rs12447958	0.0005439	rs6977788	0.0006857
rs7010545	0.0004174	rs7744512	0.0005441	rs9813811	0.0006857

Figure 22-5

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rs12454921	0.0006911	rs12701006	0.0008747	rs16897892	0.0010566
rs6435822	0.0006916	rs7967638	0.0008837	rs11216466	0.0010593
rs34918490	0.0006962	rs1943387	0.0008857	rs17653411	0.0010645
rs10431282	0.0007071	rs2350415	0.0009072	rs17190412	0.0010676
rs4370778	0.0007108	rs7123782	0.0009079	rs2065968	0.0010685
rs12135026	0.0007119	rs6727051	0.0009098	rs10491598	0.0010703
rs16932063	0.0007151	rs4717229	0.0009108	rs7001472	0.0010726
rs1574399	0.0007183	rs4695345	0.000918	rs7713655	0.0010729
rs12925964	0.0007184	rs2297154	0.0009184	rs6923835	0.0010763
rs1764416	0.0007226	rs2268389	0.0009197	rs751625	0.0010872
rs1439025	0.0007248	rs400214	0.0009244	rs11158850	0.0010917
rs6512152	0.0007266	rs16981495	0.0009295	rs10519971	0.0010921
rs6936315	0.0007285	rs8026993	0.0009325	rs2067589	0.0010937
rs10458732	0.0007287	rs2044538	0.0009331	rs7221278	0.0010952
rs4936823	0.0007297	rs7320986	0.0009354	rs1672989	0.0010955
rs247355	0.0007312	rs6805279	0.0009396	rs10880010	0.0010979
rs17072878	0.0007328	rs1605864	0.0009411	rs11807765	0.0010987
rs6602515	0.0007376	rs11074481	0.0009431	rs17089826	0.001102
rs1888140	0.0007377	rs12404945	0.0009483	rs10492719	0.0011062
rs17011839	0.000739	rs442208	0.0009528	rs3024994	0.0011064
rs4774725	0.0007543	rs17101811	0.0009555	rs1317928	0.0011076
rs4291550	0.0007576	rs1647646	0.0009579	rs11101085	0.0011197
rs2785245	0.0007588	rs12024134	0.0009588	rs355127	0.0011241
rs6482455	0.0007589	rs11135418	0.0009669	rs17363431	0.0011276
rs1998927	0.0007607	rs10767929	0.0009692	rs1417676	0.0011281
rs5917746	0.0007615	rs2170057	0.0009794	rs16837190	0.0011287
rs6732885	0.0007662	rs11892488	0.0009795	rs12718224	0.001129
rs16927476	0.0007694	rs10517845	0.0009808	rs16834810	0.0011294
rs10510233	0.0007768	rs2099305	0.0009821	rs10140983	0.0011323
rs17227203	0.0007793	rs10762774	0.0009884	rs1613776	0.0011362
rs6421008	0.0007923	rs7155312	0.0009919	rs6556757	0.0011415
rs17830967	0.0007929	rs2034598	0.0009937	rs7800059	0.0011432
rs11929326	0.0007939	rs7753049	0.000995	rs17084040	0.001147
rs11215936	0.000798	rs9868264	0.0010095	rs7633800	0.0011488
rs6766260	0.0008037	rs4671694	0.0010108	rs7324489	0.0011521
rs305423	0.0008071	rs4797092	0.0010121	rs384134	0.0011541
rs10951911	0.0008096	rs9890514	0.0010122	rs16940610	0.0011616
rs11606886	0.0008134	rs3848110	0.001014	rs17610832	0.0011618
rs16966835	0.0008154	rs10509052	0.0010218	rs12632003	0.0011628
rs2179307	0.0008163	rs10437704	0.0010223	rs7986406	0.001168
rs3852545	0.0008236	rs2337251	0.0010246	rs4481316	0.0011694
rs17232873	0.0008254	rs41508049	0.001025	rs11574637	0.001174
rs17284999	0.000827	rs16948360	0.0010304	rs11199375	0.0011742
rs6998419	0.0008284	rs16983057	0.0010324	rs11005278	0.0011743
rs700228	0.0008378	rs16823172	0.0010367	rs2830993	0.00118
rs1337645	0.0008446	rs3806402	0.0010371	rs1628891	0.0011818
rs4979807	0.000848	rs17669038	0.001039	rs7787896	0.0011831
rs9360049	0.0008518	rs12611846	0.0010391	rs2084903	0.0011837
rs6979341	0.0008523	rs703602	0.001047	rs8078588	0.0011842
rs1742852	0.0008621	rs9904198	0.0010488	rs12048640	0.0011878
rs7794464	0.0008634	rs41514051	0.0010493	rs7296488	0.0011924
rs735173	0.0008641	rs1163760	0.0010496	rs4140577	0.0011967
rs4468514	0.0008711	rs6779915	0.0010534	rs10850536	0.0012037
rs964745	0.0008731	rs1405217	0.0010548	rs638191	0.0012061
rs7182710	0.0008735	rs17747953	0.0010553	rs11212290	0.001208

Figure 22-6

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rs16965693	0.0012129
rs1354308	0.0012129
rs3923096	0.0012137
rs12142665	0.0012186
rs6718149	0.0012323
rs2277176	0.0012361
rs8089224	0.001239
rs765336	0.0012403
rs16872733	0.0012421
rs17393206	0.001245
rs17710558	0.001246
rs1212595	0.001247
rs11037407	0.0012477
rs353206	0.0012559
rs11122414	0.0012644
rs994769	0.0012645

Figure 22-7

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SNP	ChiSquare p value	SNP	ChiSquare p value	SNP	ChiSquare p value
rs10833199	8.83E-19	rs7696347	3.56E-09	rs4132421	6.38E-09
rs11728055	2.87E-17	rs4899015	3.85E-09	rs7129236	6.41E-09
rs16901105	4.52E-17	rs11219832	3.99E-09	rs3096660	6.44E-09
rs12325649	4.92E-17	rs222809	4.01E-09	rs2303723	6.55E-09
rs2632086	1.68E-16	rs4306358	4.11E-09	rs7547381	6.57E-09
rs997860	7.91E-12	rs35005996	4.14E-09	rs7868409	6.57E-09
rs10277013	1.16E-11	rs11160571	4.21E-09	rs16883001	6.57E-09
rs17154797	1.18E-11	rs16949908	4.27E-09	rs10510498	6.57E-09
rs17055141	1.52E-11	rs2896061	4.33E-09	rs7006266	6.58E-09
rs17586131	1.54E-11	rs17654944	4.40E-09	rs1904928	6.58E-09
rs11729371	1.85E-11	rs2862116	4.43E-09	rs6100719	6.59E-09
rs4300782	1.91E-11	rs2296066	4.45E-09	rs17116121	6.64E-09
rs8139654	2.25E-11	rs9321466	4.46E-09	rs10868851	6.69E-09
rs9552517	2.53E-11	rs17191803	4.51E-09	rs16996490	6.78E-09
rs2815732	2.70E-11	rs7188054	4.57E-09	rs17174407	6.79E-09
rs11626422	2.83E-11	rs17701478	4.69E-09	rs17148966	6.79E-09
rs7069744	4.87E-11	rs12111154	4.71E-09	rs41472047	6.91E-09
rs10773005	1.85E-10	rs297779	4.86E-09	rs6100783	6.99E-09
rs13429130	3.55E-10	rs1413512	4.87E-09	rs11935748	7.02E-09
rs9312755	3.99E-10	rs10044755	4.95E-09	rs16983712	7.02E-09
rs1039119	4.30E-10	rs4568238	4.97E-09	rs17015855	7.03E-09
rs17155293	5.16E-10	rs1497169	4.99E-09	rs16827988	7.04E-09
rs2449539	6.97E-10	rs41388249	5.00E-09	rs7934354	7.05E-09
rs268299	1.07E-09	rs1439332	5.01E-09	rs3962573	7.06E-09
rs9979508	1.15E-09	rs1198006	5.05E-09	rs17043686	7.08E-09
rs2048495	1.24E-09	rs41386447	5.15E-09	rs17836464	7.08E-09
rs10991581	1.30E-09	rs6589527	5.26E-09	rs16893391	7.10E-09
rs13176869	1.47E-09	rs1821542	5.28E-09	rs16847237	7.10E-09
rs11787939	1.60E-09	rs415208	5.29E-09	rs17524193	7.10E-09
rs17128560	1.61E-09	rs2725663	5.33E-09	rs17065451	7.11E-09
rs8022177	1.64E-09	rs1915462	5.35E-09	rs7137705	7.13E-09
rs960078	2.18E-09	rs17121606	5.35E-09	rs7648240	7.15E-09
rs4320103	2.20E-09	rs16910061	5.36E-09	rs17017662	7.27E-09
rs2711493	2.36E-09	rs12694400	5.42E-09	rs10957818	7.27E-09
rs5026429	2.50E-09	rs6517876	5.54E-09	rs17834140	7.33E-09
rs7119574	2.53E-09	rs17080859	5.57E-09	rs2154399	7.40E-09
rs17713163	2.54E-09	rs7210897	5.58E-09	rs1782786	7.40E-09
rs41524446	2.57E-09	rs17023472	5.62E-09	rs6441299	7.51E-09
rs10280397	2.63E-09	rs2279023	5.63E-09	rs9828738	7.54E-09
rs10053788	2.84E-09	rs42772	5.67E-09	rs7982110	7.56E-09
rs8015614	2.84E-09	rs4740238	5.68E-09	rs4837165	7.56E-09
rs6858024	2.84E-09	rs12059815	5.70E-09	rs6481454	7.59E-09
rs16986733	2.85E-09	rs1017931	5.70E-09	rs17128992	7.66E-09
rs8021182	2.89E-09	rs355954	5.72E-09	rs16931982	7.85E-09
rs11562945	2.96E-09	rs16956948	5.81E-09	rs16839691	8.05E-09
rs10748449	2.99E-09	rs9385824	5.81E-09	rs9513390	8.18E-09
rs3187141	3.00E-09	rs7923915	6.01E-09	rs9428247	8.26E-09
rs1341994	3.09E-09	rs17660851	6.11E-09	rs12509766	8.44E-09
rs9992080	3.17E-09	rs17326067	6.21E-09	rs7735510	8.82E-09
rs11106069	3.19E-09	rs1932637	6.28E-09	rs10509275	8.99E-09
rs955943	3.22E-09	rs3866687	6.30E-09	rs16904515	9.01E-09
rs2830017	3.31E-09	rs4503463	6.32E-09	rs7204905	9.84E-09
rs7718362	3.43E-09	rs2022105	6.35E-09	rs17033273	9.85E-09

Figure 23-1

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rs996793	1.01E-08	rs6989128	2.21E-06	rs10880288	2.24E-05
rs4839854	1.06E-08	rs12608629	2.30E-06	rs9609775	2.25E-05
rs17770834	1.07E-08	rs957434	2.66E-06	rs10768703	2.34E-05
rs4743886	1.11E-08	rs3929907	2.81E-06	rs1539400	2.43E-05
rs245675	1.12E-08	rs6663174	2.86E-06	rs10515762	2.45E-05
rs17000486	1.15E-08	rs6560752	3.40E-06	rs7840975	2.51E-05
rs16856394	1.30E-08	rs4401694	3.88E-06	rs4745006	2.57E-05
rs41465145	1.34E-08	rs2427995	4.11E-06	rs11259475	2.69E-05
rs10850269	1.45E-08	rs7822802	4.16E-06	rs138465	2.71E-05
rs9591488	1.55E-08	rs10434137	4.40E-06	rs1786734	2.85E-05
rs41456546	1.57E-08	rs7711505	4.41E-06	rs735311	2.86E-05
rs9511646	1.57E-08	rs10431210	4.64E-06	rs727190	2.95E-05
rs6957661	1.74E-08	rs10490904	5.65E-06	rs1423616	2.97E-05
rs502518	1.76E-08	rs4691370	5.74E-06	rs10267502	3.05E-05
rs7978453	1.77E-08	rs2722552	5.92E-06	rs16988320	3.12E-05
rs7634813	1.82E-08	rs17769092	5.94E-06	rs10935018	3.20E-05
rs13479	2.01E-08	rs17045404	6.09E-06	rs9577481	3.28E-05
rs9384060	2.41E-08	rs2043265	6.56E-06	rs3852528	3.38E-05
rs1009295	2.50E-08	rs17063761	6.76E-06	rs4752432	3.41E-05
rs850942	2.67E-08	rs10509376	6.91E-06	rs17528635	3.44E-05
rs1077747	2.93E-08	rs12158070	7.34E-06	rs12644895	3.45E-05
rs6722636	3.17E-08	rs17114703	8.07E-06	rs12901876	3.46E-05
rs17212829	3.65E-08	rs6135697	8.20E-06	rs6765656	3.47E-05
rs41348748	4.25E-08	rs13220654	9.17E-06	rs9436667	3.56E-05
rs1021379	4.41E-08	rs12260362	9.29E-06	rs17676550	3.57E-05
rs10975141	5.00E-08	rs6034984	9.39E-06	rs6665865	3.70E-05
rs10733352	5.47E-08	rs17801458	9.86E-06	rs16912196	3.78E-05
rs1248551	7.65E-08	rs12110175	1.02E-05	rs2301857	4.02E-05
rs16922192	7.86E-08	rs1493506	1.12E-05	rs879428	4.10E-05
rs10777800	2.49E-07	rs1254703	1.24E-05	rs6994642	4.29E-05
rs10494170	2.69E-07	rs16931326	1.29E-05	rs2689132	4.30E-05
rs16919123	2.97E-07	rs17124464	1.29E-05	rs6494165	4.39E-05
rs11860355	2.98E-07	rs9552533	1.31E-05	rs7737968	4.43E-05
rs10495153	4.27E-07	rs4592605	1.33E-05	rs1423304	4.46E-05
rs1254672	6.04E-07	rs1492689	1.34E-05	rs9497352	4.75E-05
rs17652341	6.09E-07	rs503554	1.36E-05	rs9302577	4.75E-05
rs11187403	6.29E-07	rs4772416	1.38E-05	rs17514618	4.86E-05
rs9959126	6.98E-07	rs11193528	1.38E-05	rs1927272	4.91E-05
rs17324835	7.02E-07	rs9532930	1.40E-05	rs10490898	4.94E-05
rs17541562	7.61E-07	rs17330898	1.42E-05	rs17141840	5.01E-05
rs7595832	7.72E-07	rs2154704	1.44E-05	rs6850330	5.09E-05
rs35805164	7.81E-07	rs17156145	1.49E-05	rs1950851	5.14E-05
rs16884886	8.18E-07	rs1594424	1.52E-05	rs5969903	5.19E-05
rs10511116	8.94E-07	rs661149	1.59E-05	rs1446216	5.24E-05
rs10882332	9.16E-07	rs11043229	1.60E-05	rs9328948	5.31E-05
rs13158321	9.55E-07	rs10004741	1.65E-05	rs1872043	5.41E-05
rs11122825	9.57E-07	rs4355718	1.67E-05	rs7504430	5.43E-05
rs1522779	9.85E-07	rs711826	1.67E-05	rs11052464	5.46E-05
rs1123595	1.06E-06	rs11146539	1.72E-05	rs1523648	5.56E-05
rs9298792	1.16E-06	rs11252747	1.86E-05	rs9296344	5.61E-05
rs9287482	1.21E-06	rs16871320	1.91E-05	rs13374152	5.68E-05
rs897656	1.57E-06	rs10902933	2.01E-05	rs383855	5.79E-05
rs2389883	1.71E-06	rs2977537	2.19E-05	rs16920386	5.80E-05
rs7628803	1.82E-06	rs570880	2.22E-05	rs17009291	5.84E-05
rs16918253	1.84E-06	rs17564083	2.22E-05	rs16929074	6.08E-05

Figure 23-2

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rs13399239	6.10E-05	rs17004068	8.42E-05	rs4476905	0.000106
rs7540790	6.11E-05	rs13334391	8.45E-05	rs17655252	0.0001063
rs7302965	6.11E-05	rs12430149	8.46E-05	rs10107255	0.000107
rs6503858	6.14E-05	rs2131247	8.57E-05	rs2838484	0.0001081
rs3826149	6.16E-05	rs9302218	8.58E-05	rs1286220	0.0001081
rs4575739	6.31E-05	rs4509408	8.60E-05	rs9950823	0.0001087
rs2887208	6.33E-05	rs17757989	8.60E-05	rs4296747	0.0001088
rs7895335	6.38E-05	rs6436168	8.63E-05	rs16912743	0.0001091
rs17010429	6.50E-05	rs6757928	8.70E-05	rs17066406	0.0001094
rs11139727	6.51E-05	rs16952642	8.73E-05	rs12381471	0.0001111
rs3940202	6.52E-05	rs17300991	8.78E-05	rs17168413	0.0001115
rs11007270	6.55E-05	rs4751276	8.79E-05	rs6925493	0.000112
rs16903084	6.60E-05	rs11065386	8.81E-05	rs17125701	0.0001125
rs590732	6.66E-05	rs4241471	8.82E-05	rs7786553	0.000113
rs824211	6.68E-05	rs2429010	8.83E-05	rs11925269	0.0001135
rs7018599	6.69E-05	rs10927510	8.88E-05	rs871387	0.0001139
rs16962248	6.72E-05	rs7986574	8.90E-05	rs12820818	0.0001142
rs6590743	6.79E-05	rs11607727	8.99E-05	rs470029	0.0001145
rs41425044	6.79E-05	rs7914927	9.09E-05	rs17084772	0.0001146
rs435945	6.94E-05	rs17232035	9.23E-05	rs7076586	0.0001149
rs17143392	6.95E-05	rs17777477	9.23E-05	rs17145374	0.0001152
rs16894744	6.97E-05	rs17744902	9.24E-05	rs6597472	0.0001157
rs17631686	6.98E-05	rs10976785	9.24E-05	rs3889602	0.000116
rs1971603	7.01E-05	rs189509	9.28E-05	rs17044733	0.0001162
rs12416804	7.11E-05	rs1116864	9.32E-05	rs17083131	0.0001168
rs16966786	7.18E-05	rs17073748	9.32E-05	rs10174991	0.0001169
rs11673919	7.22E-05	rs10159565	9.33E-05	rs2101210	0.000117
rs17758987	7.27E-05	rs3739216	9.33E-05	rs4461205	0.0001171
rs1514589	7.34E-05	rs6836600	9.41E-05	rs131390	0.0001171
rs1229670	7.39E-05	rs1445871	9.43E-05	rs7095435	0.0001174
rs7116979	7.49E-05	rs17144393	9.48E-05	rs1355554	0.0001177
rs6538486	7.52E-05	rs7525079	9.56E-05	rs475842	0.0001178
rs10447132	7.56E-05	rs17016123	9.66E-05	rs4335774	0.0001179
rs2526565	7.58E-05	rs2888686	9.71E-05	rs16954432	0.0001181
rs7115217	7.63E-05	rs4284619	9.74E-05	rs12430547	0.0001182
rs4979530	7.73E-05	rs16886698	9.79E-05	rs17804486	0.000119
rs17069212	7.96E-05	rs12159204	9.84E-05	rs6684802	0.000119
rs1333345	7.98E-05	rs6964079	9.85E-05	rs833986	0.0001193
rs2423672	7.99E-05	rs16875172	9.98E-05	rs2658072	0.0001195
rs7342882	8.00E-05	rs1426284	9.99E-05	rs17101993	0.0001197
rs10930700	8.04E-05	rs17155568	0.0001012	rs2266910	0.0001199
rs562907	8.05E-05	rs17046231	0.0001014	rs10505414	0.0001203
rs34277810	8.05E-05	rs10250922	0.0001015	rs7832507	0.000121
rs17732220	8.09E-05	rs9495484	0.0001033	rs4469890	0.0001214
rs11239303	8.18E-05	rs6456652	0.0001037	rs412841	0.0001218
rs1389750	8.23E-05	rs9930732	0.000104	rs4402410	0.000122
rs7921998	8.24E-05	rs7236945	0.000104	rs7115657	0.0001222
rs17427680	8.26E-05	rs1469488	0.0001042	rs9565932	0.0001225
rs8007742	8.28E-05	rs546528	0.0001042	rs4405320	0.0001226
rs10521469	8.29E-05	rs10073428	0.0001043	rs10966485	0.0001236
rs16842165	8.29E-05	rs3791320	0.0001043	rs16954906	0.0001239
rs17450699	8.32E-05	rs879362	0.0001043	rs12406698	0.0001239
rs10895889	8.33E-05	rs17215946	0.0001045	rs6571823	0.0001248
rs6413523	8.36E-05	rs9957971	0.0001058	rs1512432	0.0001252
rs9289448	8.41E-05	rs4742424	0.000106	rs11074925	0.0001258

Figure 23-3

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rs1937934	0.0001261	rs2422677	0.000137	rs11831258	0.0001739
rs11068096	0.0001268	rs17014869	0.000137	rs17505435	0.0001744
rs10087433	0.0001269	rs1393355	0.0001371	rs959454	0.0001754
rs11935340	0.0001269	rs157673	0.0001372	rs442332	0.0001767
rs3934900	0.000127	rs1737502	0.0001373	rs4845016	0.0001774
rs17446338	0.0001273	rs41477845	0.0001381	rs11022250	0.0001778
rs9402750	0.0001275	rs6862763	0.0001381	rs16848847	0.0001782
rs16920467	0.0001276	rs17088255	0.0001382	rs4720801	0.0001846
rs6881226	0.0001277	rs9924092	0.000139	rs1485591	0.0001854
rs1448127	0.0001286	rs17143671	0.0001392	rs7792597	0.0001886
rs4932976	0.000129	rs17122763	0.0001396	rs11870481	0.0001892
rs16944056	0.0001292	rs904317	0.0001398	rs2068929	0.0001916
rs11862196	0.0001292	rs3096378	0.0001398	rs9568232	0.0001927
rs11184329	0.0001293	rs10256108	0.0001399	rs7321954	0.0001948
rs16892989	0.0001296	rs1346861	0.0001401	rs13101295	0.0001967
rs28607918	0.0001297	rs2939967	0.0001401	rs10919966	0.0002021
rs11864276	0.0001308	rs4932445	0.0001408	rs17069141	0.0002026
rs3206354	0.0001309	rs17348537	0.0001409	rs837727	0.0002044
rs1893836	0.0001312	rs6481313	0.0001413	rs7604415	0.0002056
rs7611514	0.0001312	rs2824903	0.0001416	rs1927551	0.0002094
rs8110995	0.0001312	rs7776126	0.0001417	rs2165565	0.0002099
rs10437704	0.0001315	rs2681314	0.0001418	rs17058450	0.000214
rs41461646	0.0001317	rs2963794	0.0001421	rs1546914	0.0002156
rs17109410	0.0001318	rs7540706	0.0001424	rs3915055	0.000216
rs11219735	0.0001327	rs9358928	0.0001432	rs11081336	0.000216
rs8109860	0.0001328	rs920967	0.000144	rs16978425	0.0002169
rs9615766	0.0001334	rs10518794	0.0001451	rs17322057	0.000221
rs2962249	0.0001336	rs565742	0.0001462	rs10828685	0.0002227
rs740553	0.0001337	rs994638	0.0001463	rs17728260	0.0002245
rs6453220	0.0001337	rs643099	0.0001472	rs7858066	0.0002247
rs4600958	0.0001338	rs2996368	0.0001472	rs4993355	0.0002284
rs10920462	0.0001339	rs7938742	0.0001477	rs6124562	0.0002344
rs972178	0.0001339	rs6035213	0.0001485	rs896186	0.0002403
rs6467723	0.0001341	rs12555797	0.0001502	rs10736996	0.000243
rs11645072	0.0001343	rs10491116	0.0001502	rs173389	0.0002444
rs4072879	0.0001348	rs11644455	0.000153	rs673471	0.0002482
rs2879725	0.0001352	rs17162823	0.0001539	rs16846246	0.0002538
rs9928871	0.0001354	rs9838009	0.000154	rs17653822	0.0002549
rs3027209	0.0001355	rs6951874	0.0001544	rs7182308	0.0002611
rs376535	0.0001358	rs9943843	0.0001556	rs746385	0.0002618
rs2025278	0.000136	rs2218066	0.0001557	rs11245257	0.0002623
rs2140756	0.0001361	rs4778099	0.0001577	rs7613256	0.0002656
rs6912037	0.0001361	rs4676312	0.0001598	rs1421346	0.0002666
rs16872626	0.0001361	rs4917745	0.0001614	rs4880511	0.00027
rs16914121	0.0001363	rs11247377	0.0001628	rs33157	0.0002727
rs2445174	0.0001363	rs10225776	0.0001633	rs1617936	0.0002737
rs1482619	0.0001364	rs6132977	0.0001637	rs10936578	0.000274
rs1906969	0.0001364	rs16994140	0.0001647	rs6563177	0.0002806
rs10509148	0.0001366	rs2344752	0.0001655	rs313161	0.0002865
rs544789	0.0001367	rs11677881	0.0001672	rs8463	0.0002865
rs750339	0.0001367	rs6598912	0.0001673	rs16926787	0.0002915
rs16981660	0.0001367	rs7811465	0.0001674	rs7959960	0.0002921
rs17674478	0.0001367	rs699181	0.0001694	rs1536945	0.0002997
rs245957	0.0001368	rs948173	0.0001698	rs35241893	0.000301
rs12257536	0.000137	rs10884039	0.000172	rs1372540	0.0003014

Figure 23-4

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rs17165412	0.0003014	rs9263597	0.0004274	rs5976816	0.0005863
rs496190	0.000302	rs1976192	0.0004299	rs4603275	0.0005939
rs2243544	0.000305	rs4689915	0.0004302	rs274035	0.0005981
rs10183197	0.0003062	rs4978438	0.0004313	rs17415059	0.0006031
rs4072661	0.0003069	rs41509648	0.0004315	rs4757064	0.0006039
rs10816972	0.0003081	rs7969825	0.0004402	rs2043778	0.0006071
rs1603199	0.0003087	rs2281649	0.0004419	rs12312105	0.0006094
rs719926	0.0003103	rs16921893	0.0004459	rs4750048	0.0006109
rs16915382	0.0003104	rs12083416	0.0004498	rs17033398	0.0006125
rs7324589	0.0003108	rs11982286	0.0004505	rs4505340	0.0006159
rs9865234	0.000312	rs7772922	0.0004526	rs2024788	0.0006173
rs4264593	0.0003184	rs17184428	0.0004541	rs11220051	0.0006216
rs17092188	0.0003187	rs10873349	0.0004553	rs10772075	0.0006226
rs315782	0.0003194	rs7973206	0.0004597	rs11165315	0.0006341
rs9830956	0.0003245	rs1836655	0.0004617	rs2287045	0.0006353
rs7141908	0.000326	rs10032829	0.0004706	rs4242340	0.0006359
rs16931010	0.0003286	rs8060064	0.0004715	rs1735469	0.0006364
rs6690583	0.0003311	rs4869890	0.0004759	rs2070334	0.0006367
rs12359591	0.0003337	rs534150	0.0004793	rs11615777	0.0006371
rs911782	0.000337	rs6008573	0.0004818	rs2445333	0.0006415
rs12026625	0.0003379	rs10256786	0.0004823	rs1893791	0.0006426
rs2211011	0.0003382	rs9586181	0.0004839	rs6981251	0.0006439
rs4243965	0.0003397	rs7955585	0.0004923	rs10860097	0.0006564
rs7357322	0.0003426	rs1340048	0.0004928	rs349973	0.0006567
rs1934020	0.0003429	rs6705877	0.0004943	rs2199154	0.0006583
rs4132554	0.0003435	rs1598745	0.0004965	rs8078261	0.0006608
rs17168361	0.0003492	rs10247439	0.000497	rs16958089	0.0006622
rs10518891	0.0003498	rs9856242	0.0004983	rs7324699	0.0006777
rs12610253	0.0003506	rs6501834	0.0004994	rs2237961	0.0006782
rs4637494	0.0003535	rs28606996	0.0005122	rs248848	0.0006785
rs2279018	0.0003544	rs1631596	0.000513	rs2685468	0.0006841
rs12262851	0.0003613	rs10767075	0.0005132	rs17684734	0.0006854
rs16898687	0.0003621	rs11913750	0.0005147	rs10170236	0.0006928
rs772443	0.0003665	rs12927476	0.0005158	rs283735	0.0006937
rs41521048	0.0003685	rs6465381	0.0005167	rs9405232	0.0006972
rs7599985	0.0003689	rs1861710	0.0005173	rs6047797	0.0006977
rs4935838	0.0003747	rs7524430	0.0005207	rs17282840	0.0006988
rs104664	0.0003766	rs10860397	0.0005231	rs7882576	0.0007015
rs6724110	0.0003779	rs4782712	0.0005253	rs488156	0.000706
rs2461202	0.0003815	rs8126456	0.0005342	rs4242245	0.000707
rs1869176	0.0003819	rs4776292	0.0005368	rs17007695	0.000707
rs7594094	0.0003849	rs879872	0.0005368	rs17169771	0.0007073
rs7022605	0.0003888	rs10283737	0.0005375	rs2674885	0.0007106
rs17566231	0.000395	rs41468946	0.0005382	rs6892850	0.0007118
rs1939631	0.0003952	rs41376144	0.0005547	rs7327101	0.0007174
rs2600960	0.000399	rs4930027	0.0005572	rs11928296	0.000723
rs2811608	0.0004022	rs5952804	0.0005598	rs7480288	0.0007352
rs323451	0.0004025	rs447136	0.0005663	rs7772387	0.0007353
rs333165	0.0004027	rs12805072	0.0005709	rs17001349	0.0007355
rs7199063	0.0004042	rs185435	0.0005719	rs10512441	0.0007379
rs7563563	0.0004058	rs10977348	0.0005724	rs1818806	0.0007399
rs464466	0.0004069	rs3843718	0.0005733	rs11002432	0.0007409
rs6996216	0.0004086	rs16862435	0.0005739	rs41440247	0.0007441
rs7921993	0.0004112	rs11611673	0.0005797	rs12508229	0.0007458
rs17296412	0.0004139	rs1436879	0.0005849	rs16929280	0.0007491

Figure 23-5

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rs7913128	0.000751	rs4695881	0.0009128	rs9576072	0.0010531
rs16912372	0.0007512	rs11189359	0.0009171	rs12757377	0.0010626
rs2387595	0.0007568	rs2286720	0.0009182	rs3791624	0.0010643
rs7089591	0.0007576	rs2973488	0.0009184	rs11071385	0.0010647
rs12990870	0.0007577	rs4628973	0.0009205	rs206910	0.0010665
rs9922955	0.0007662	rs329235	0.0009205	rs7303167	0.0010678
rs4921698	0.0007719	rs2241520	0.0009276	rs10509810	0.0010686
rs7951875	0.0007774	rs11071467	0.0009349	rs1980775	0.0010769
rs319301	0.0007778	rs12540569	0.0009355	rs4430519	0.001082
rs16964802	0.0007843	rs1011624	0.0009419	rs4463179	0.0010827
rs671873	0.0007878	rs16989701	0.0009455	rs1740720	0.0010887
rs17029241	0.0007884	rs7875389	0.0009459	rs12637343	0.0010895
rs11130377	0.0007908	rs17822462	0.0009467	rs2439631	0.0010896
rs12601491	0.0007919	rs6595788	0.0009474	rs4761615	0.0010938
rs834487	0.0007941	rs1165207	0.0009474	rs218815	0.0010944
rs8113032	0.0007956	rs1888924	0.0009476	rs1449546	0.0010947
rs10261536	0.0007962	rs1882426	0.0009495	rs17627078	0.0010981
rs6887277	0.0007969	rs17630766	0.0009523	rs1153744	0.0011002
rs4677259	0.0007972	rs7316431	0.0009604	rs7070722	0.0011011
rs9843448	0.0007995	rs237238	0.0009607	rs244990	0.0011066
rs16933168	0.0008038	rs7324229	0.0009627	rs12144146	0.0011132
rs616749	0.0008058	rs1322199	0.000963	rs17306064	0.0011133
rs9694859	0.0008099	rs739104	0.0009636	rs1607237	0.0011156
rs7577271	0.0008165	rs2833457	0.0009644	rs16982350	0.0011172
rs7311216	0.0008249	rs11956184	0.0009715	rs12490417	0.0011177
rs7046184	0.0008262	rs3851333	0.0009761	rs6027005	0.0011216
rs6741676	0.0008274	rs2934118	0.000977	rs2156646	0.0011284
rs294711	0.0008291	rs954882	0.0009792	rs7591341	0.0011337
rs6870006	0.0008321	rs17728526	0.0009845	rs12675500	0.0011392
rs1023853	0.0008406	rs12666205	0.0009875	rs10507004	0.001147
rs4789753	0.0008436	rs670232	0.0009877	rs2283029	0.0011492
rs4131667	0.0008462	rs41484050	0.0009882	rs12201626	0.0011563
rs764502	0.0008476	rs314583	0.0009926	rs6069285	0.0011628
rs2306936	0.0008513	rs1944469	0.0009945	rs2472680	0.0011833
rs654694	0.0008522	rs6812348	0.0009949	rs12705150	0.0011848
rs782702	0.0008541	rs7873050	0.0009979	rs9650197	0.0011877
rs2633019	0.0008565	rs17016013	0.0010024	rs16838718	0.001189
rs4813377	0.0008587	rs994813	0.0010033	rs12247030	0.0011986
rs11106868	0.0008596	rs4622487	0.0010054	rs16907322	0.0012026
rs11602880	0.0008598	rs7954351	0.0010078	rs2046357	0.0012093
rs754233	0.0008617	rs1180657	0.0010107	rs10038062	0.0012105
rs4391826	0.0008645	rs10079961	0.0010139	rs6517304	0.0012118
rs1982265	0.0008655	rs17425397	0.0010142	rs797252	0.0012201
rs10812021	0.0008667	rs2391214	0.0010222	rs9864057	0.0012207
rs3812704	0.000871	rs9829295	0.0010249	rs12463085	0.0012258
rs13088856	0.0008736	rs10515149	0.0010287	rs2900476	0.001226
rs12584035	0.0008756	rs675893	0.0010342	rs4890173	0.0012274
rs17156347	0.0008757	rs17356585	0.0010364	rs4843632	0.0012278
rs7087658	0.0008847	rs17638906	0.0010394	rs257962	0.0012362
rs2518827	0.0008898	rs11595510	0.0010401	rs4750655	0.0012365
rs9285163	0.0008931	rs7869264	0.001042	rs7220621	0.0012419
rs17517294	0.0008973	rs893460	0.0010453	rs7495602	0.0012422
rs33995980	0.000902	rs150568	0.0010475	rs192680	0.0012483
rs2061840	0.0009095	rs12212981	0.0010522	rs4235441	0.0012524
rs2285663	0.0009105	rs3087684	0.0010522	rs7527274	0.0012566

Figure 23-6

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rs13432866	0.0012592
rs7047314	0.0012592
rs943165	0.0012621
rs6892944	0.0012664
rs6963728	0.0012686
rs4684269	0.0012721
rs4775229	0.0012777
rs11660443	0.0012777
rs10106438	0.0012795
rs4983243	0.0012818
rs41460547	0.0012832
rs10257375	0.0012834
rs10884470	0.0012835
rs11020149	0.0012901
rs11698292	0.001294
rs2451678	0.001295

Figure 23-7