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 first CpG dinucleotide at a GC locus selected from the group consisting of cg00300879, cg09552548, and cg14789911 or at a second CpG dinucleotide in linkage disequilibrium with the first CpG dinucleotide at a GC locus selected from the group consisting of cg00300879, cg09552548, and cg14789911, wherein the linkage disequilibrium has a value of $R>0.3$, wherein the at least one first nucleic acid primer detects a methylated or 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 a bisulfite-converted DNA sequence of a first SNP selected from the group consisting of rs11716050, rs6560711, rs3735222, rs6820447, and rs9638144 or a second SNP in linkage disequilibrium with the first SNP selected from the group consisting of rs11716050, rs6560711, rs3735222, rs6820447, and rs9638144, wherein the linkage disequilibrium has a value of $R>0.3$.

2. The kit of claim 1, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide.

3. The kit of claim 1, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide.

4. The kit of any of claims 1-3, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs.

5. The kit of any of claims 1-4, wherein the at least one first nucleic acid primer comprises one or more synthetic or non-natural nucleotides.

6. The kit of any one of claims 1-5, further comprising a solid substrate to which the at least one first nucleic acid primer is bound.

7. The kit of claim 6, wherein the substrate is a polymer, glass, semiconductor, paper, metal, gel or hydrogel.

8. The kit of claim 6, wherein the solid substrate is a microarray or microfluidics card.

9. The kit of any one of claims 1-8, further comprising a detectable label.

10. The kit of any one of claims 1-9, 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.

11. The kit of any one of claims 1-9, further comprising at least a third nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence downstream of the CpG dinucleotide.

12. A method of determining the presence of biomarkers associated with predicting a three-year incidence of CVD using a biological sample from a subject, comprising:

(a) providing a first portion of the biological sample and a second portion of the biological sample, wherein the nucleic acid from at least the first portion is bisulfite converted;

(b) contacting the first portion of the biological sample with a first oligonucleotide primer at least 8 nucleotides in length that is complementary to a sequence that comprises a first CpG dinucleotide at a GC locus selected from the group consisting of cg00300879, cg09552548, and cg14789911, or a second CpG dinucleotide in linkage disequilibrium with the first CpG dinucleotide at a GC locus selected from the group

consisting of cg00300879, cg09552548, and cg14789911, wherein the linkage disequilibrium has a value of R>0.3, wherein the first nucleic acid primer detects a methylated or unmethylated CpG dinucleotide; and

(c) contacting the second portion of the biological sample with a nucleic acid primer at least 8 nucleotides in length that is complementary to a DNA sequence or a bisulfite-converted DNA sequence of a first SNP selected from the group consisting of rs11716050, rs6560711, rs3735222, rs6820447, and rs9638144 or a second SNP in linkage disequilibrium with a first SNP selected from the group consisting of rs11716050, rs6560711, rs3735222, rs6820447, and rs9638144, wherein the linkage disequilibrium has a value of R>0.3,

wherein the percentage of methylation of the CpG dinucleotide at the GC locus selected from the group consisting of cg00300879, cg09552548, and cg14789911, and the identity of the nucleotide at the first SNP selected from the group consisting of rs11716050, rs6560711, rs3735222, rs6820447, and rs9638144 or the second SNP in linkage disequilibrium with the first SNP are biomarkers associated with the three-year incidence of CVD.

13. The method of claim 12, wherein the biological sample is selected from the group consisting of blood and saliva.

14. The method of claim 12, wherein the at least one first nucleic acid primer detects the unmethylated CpG dinucleotide.

15. The method of claim 12, wherein the at least one first nucleic acid primer detects the methylated CpG dinucleotide.

16. The method of claim 12, wherein the at least one first nucleic acid primer comprises one or more nucleotide analogs.

17. The method of claim 12, wherein the at least one first nucleic acid primer comprises one or more synthetic or non-natural nucleotides.

18. The method of claim 12, wherein the window of incidence is three years.