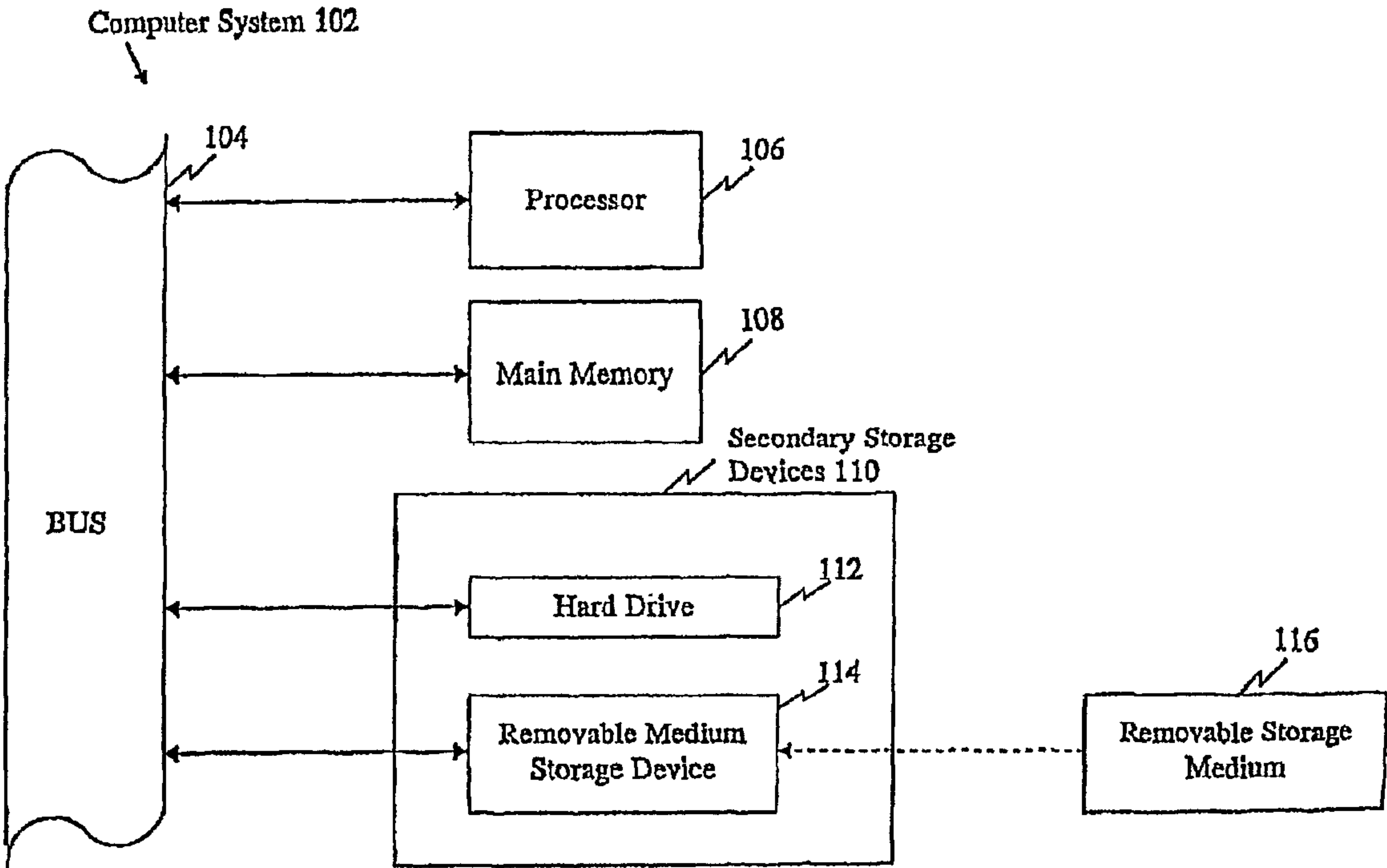




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(54) **Titre :** POLYMORPHISMES NUCLEOTIDES SIMPLES ASSOCIES A DES TROUBLES CARDIOVASCULAIRES ET A UNE
REPONSE AU MEDICAMENT, LEURS PROCEDES DE DETECTION ET D'UTILISATION

(54) **Title:** SINGLE NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND STATIN
RESPONSE, METHODS OF DETECTION AND USES THEREOF



(57) **Abrégé/Abstract:**
A method is provided for indicating whether a human has an increased risk for a myocardial infarction (MI), or whether a human's risk for MI is reduced by treatment with an HMG-CoA reductase inhibitor, e.g. a statin such as pravastatin, atorvastatin, simvastatin, cerivastatin, or lovastatin. The method comprises testing nucleic acid from the human for presence or absence of a single nucleotide polymorphism at position 101 of SEQ ID NO:191 or its complement. Presence of G at position 101 of SEQ ID NO:191 or C at position 101 of the complement indicates that the human has increased risk for MI and that the risk is reduced by such treatment. Also provided are polynucleotides useful for such testing.

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ABSTRACT

A method is provided for indicating whether a human has an increased risk for a myocardial infarction (MI), or whether a human's risk for MI is reduced by treatment with an HMG-CoA reductase inhibitor, e.g. a statin such as pravastatin, atorvastatin, simvastatin, cerivastatin, or lovastatin. The method comprises testing nucleic acid from the human for presence or absence of a single nucleotide polymorphism at position 101 of SEQ ID NO:191 or its complement. Presence of G at position 101 of SEQ ID NO:191 or C at position 101 of the complement indicates that the human has increased risk for MI and that the risk is reduced by such treatment. Also provided are polynucleotides useful for such testing.

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**SINGLE NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND STATIN RESPONSE, METHODS OF
DETECTION AND USES THEREOF**

5 FIELD OF THE INVENTION

The present invention is in the field of cardiovascular disorders and drug response, particularly acute coronary events and statin treatment of acute coronary events. In particular, the present invention relates to specific single nucleotide polymorphisms (SNPs) in the human genome, and their association with acute coronary events and/or variability in the
10 responsiveness to statin treatment (including preventive treatment) between different individuals. The naturally-occurring SNPs disclosed herein can be used as targets for the design of diagnostic reagents and the development of therapeutic agents, as well as for disease association and linkage analysis. In particular, the SNPs of the present invention are useful for, for example, identifying whether an individual is likely to experience an acute coronary event
15 (either a first or recurrent acute coronary event), for predicting the seriousness or consequences of an acute coronary event in an individual, for prognosing an individual's recovery from an acute coronary event, for evaluating the likely response of an individual to statins for the treatment/prevention of acute coronary events, for providing clinically important information for the prevention and/or treatment of acute coronary events, and for screening and selecting
20 therapeutic agents. The SNPs disclosed herein are also useful for human identification applications. Methods, assays, kits, and reagents for detecting the presence of these polymorphisms and their encoded products are provided.

BACKGROUND OF THE INVENTION

25 CARDIOVASCULAR DISORDERS AND RESPONSE TO STATIN TREATMENT

Cardiovascular disorders include, for example, acute coronary events such as myocardial infarction and stroke.

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Myocardial Infarction

Myocardial infarction (MI) is the most common cause of mortality in developed countries. It is a multifactorial disease that involves atherogenesis, thrombus formation and propagation. Thrombosis can result in complete or partial occlusion of coronary arteries. The luminal narrowing or blockage of coronary arteries reduces oxygen and nutrient supply to the cardiac muscle (cardiac ischemia), leading to myocardial necrosis and/or stunning. MI, unstable angina, or sudden ischemic death are clinical manifestations of cardiac muscle damage. All three endpoints are part of the Acute Coronary Syndrome since the underlying mechanisms of acute complications of atherosclerosis are considered to be the same.

Atherogenesis, the first step of pathogenesis of MI, is a complex interaction between blood elements, mechanical forces, disturbed blood flow, and vessel wall abnormality. On the cellular level, these include endothelial dysfunction, monocytes/macrophages activation by modified lipoproteins, monocytes/macrophages migration into the neointima and subsequent migration and proliferation of vascular smooth muscle cells (VSMC) from the media that results in plaque accumulation.

In recent years, an unstable (vulnerable) plaque was recognized as an underlying cause of arterial thrombotic events and MI. A vulnerable plaque is a plaque, often not stenotic, that has a high likelihood of becoming disrupted or eroded, thus forming a thrombogenic focus. Two vulnerable plaque morphologies have been described. A first type of vulnerable plaque morphology is a rupture of the protective fibrous cap. It can occur in plaques that have distinct morphological features such as large and soft lipid pool with distinct necrotic core and thinning of the fibrous cap in the region of the plaque shoulders. Fibrous caps have considerable metabolic activity. The imbalance between matrix synthesis and matrix degradation thought to be regulated by inflammatory mediators combined with VSMC apoptosis are the key underlying mechanisms of plaque rupture. A second type of vulnerable plaque morphology, known as "plaque erosion", can also lead to a fatal coronary thrombotic event. Plaque erosion is morphologically different from plaque rupture. Eroded plaques do not have fractures in the plaque fibrous cap, only superficial erosion of the intima. The loss of endothelial cells can expose the thrombogenic subendothelial matrix that precipitates thrombus formation. This process

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could be regulated by inflammatory mediators. The propagation of the acute thrombi for both plaque rupture and plaque erosion events depends on the balance between coagulation and thrombolysis. MI due to a vulnerable plaque is a complex phenomenon that includes: plaque vulnerability, blood vulnerability (hypercoagulation, 5 hypothrombolysis), and heart vulnerability (sensitivity of the heart to ischemia or propensity for arrhythmia).

Recurrent myocardial infarction (RMI) can generally be viewed as a severe form of MI progression caused by multiple vulnerable plaques that are able to undergo pre-rupture or a pre-erosive state, coupled with extreme blood coagulability.

10 The incidence of MI is still high despite currently available preventive measures and therapeutic intervention. More than 1,500,000 people in the US suffer acute MI each year (many without seeking help due to unrecognized MI), and one third of these people die. The lifetime risk of coronary artery disease events at age 40 years is 42.4% for men (one in two) and 24.9% for women (one in four) (Lloyd-Jones DM; *Lancet*, 1999 353: 15 89-92).

The current diagnosis of MI is based on the levels of troponin I or T that indicate the cardiac muscle progressive necrosis, impaired electrocardiogram (ECG), and detection of abnormal ventricular wall motion or angiographic data (the presence of acute thrombi). However, due to the asymptomatic nature of 25% of acute MIs (absence of 20 atypical chest pain, low ECG sensitivity), a significant portion of MIs are not diagnosed and therefore not treated appropriately (e.g., prevention of recurrent MIs).

Despite a very high prevalence and lifetime risk of MI, there are no good prognostic markers that can identify an individual with a high risk of vulnerable plaques and justify preventive treatments. MI risk assessment and prognosis is currently done 25 using classic risk factors or the recently introduced Framingham Risk Index. Both of these assessments put a significant weight on LDL levels to justify preventive treatment. However, it is well established that half of all MIs occur in individuals without overt hyperlipidemia. Hence, there is a need for additional risk factors for predicting predisposition to MI.

30 Other emerging risk factors are inflammatory biomarkers such as C-reactive protein (CRP), ICAM-1, SAA, TNF α , homocysteine, impaired fasting glucose, new lipid

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markers (ox LDL, Lp-a, MAD-LDL, etc.) and pro-thrombotic factors (fibrinogen, PAI-1). Despite showing some promise, these markers have significant limitations such as low specificity and low positive predictive value, and the need for multiple reference intervals to be used for different groups of people (e.g., males-females, smokers-non smokers, hormone replacement therapy users, different age groups). These limitations diminish the utility of such markers as independent prognostic markers for MI screening.

Genetics plays an important role in MI risk. Families with a positive family history of MI account for 14% of the general population, 72% of premature MIs, and 48% of all MIs (Williams R R, *Am J Cardiology*, 2001; 87:129). In addition, replicated linkage studies have revealed evidence of multiple regions of the genome that are associated with MI and relevant to MI genetic traits, including regions on chromosomes 14, 2, 3 and 7 (Broeckel U, *Nature Genetics*, 2002; 30: 210; Harrap S, *Arterioscler Thromb Vasc Biol*, 2002; 22: 874-878, Shearman A, *Human Molecular Genetics*, 2000, 9; 9,1315-1320), implying that genetic risk factors influence the onset, manifestation, and progression of MI. Recent association studies have identified allelic variants that are associated with acute complications of coronary heart disease, including allelic variants of the ApoE, ApoA5, Lpa, APOCIII, and Klotho genes.

Genetic markers such as single nucleotide polymorphisms are preferable to other types of biomarkers. Genetic markers that are prognostic for MI can be genotyped early in life and could predict individual response to various risk factors. The combination of serum protein levels and genetic predisposition revealed by genetic analysis of susceptibility genes can provide an integrated assessment of the interaction between genotypes and environmental factors, resulting in synergistically increased prognostic value of diagnostic tests.

Thus, there is an urgent need for novel genetic markers that are predictive of predisposition to MI, particularly for individuals who are unrecognized as having a predisposition to MI. Such genetic markers may enable prognosis of MI in much larger populations compared with the populations that can currently be evaluated by using existing risk factors and biomarkers. The availability of a genetic test may allow, for example, appropriate preventive treatments for acute coronary events to be provided for susceptible individuals (such preventive treatments may include, for example, statin

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treatments and statin dose escalation, as well as changes to modifiable risk factors), lowering of the thresholds for ECG and angiography testing, and allow adequate monitoring of informative biomarkers.

Moreover, the discovery of genetic markers associated with MI will provide novel
5 targets for therapeutic intervention or preventive treatments of MI, and enable the development of new therapeutic agents for treating MI and other cardiovascular disorders.

Stroke

10 Stroke is a prevalent and serious disease. Stroke is the most common cause of disability, the second leading cause of dementia, and the third leading cause of mortality in the United States. It affects 4.7 million individuals in the United States, with 500,000 first attacks and 200,000 recurrent cases yearly. Approximately one in four men and one
15 in five women aged 45 years will have a stroke if they live to their 85th year. About 25% of those who have a stroke die within a year. For that, stroke is the third leading cause of mortality in the United States and is responsible for 170,000 deaths a year. Among those who survive the stroke attack, 30 to 50% do not regain functional independence.

Stroke occurs when an artery bringing oxygen or nutrients to the brain either ruptures, causing the hemorrhagic type of strokes, or gets occluded, causing the
20 thrombotic/embolic strokes that are collectively referred to as ischemic strokes. In each case, a cascade of cellular changes due to ischemia or increased cranial pressure leads to injuries or death of the brain cells. In the United States, the majority (about 80-90%) of strokes are ischemic, including 31% large-vessel thrombotic (also referred to as large-vessel occlusive disease), 20% small-vessel thrombotic (also referred to as small-vessel
25 occlusive disease), and 32% embolic or cardiogenic (caused by a clot originating from elsewhere in the body, e.g., from blood pooling due to atrial fibrillation, or from carotid artery stenosis). The ischemic form of stroke shares common pathological etiology with atherosclerosis and thrombosis. 10-20% of strokes are of the hemorrhagic type, involving bleeding within or around the brain. Bleeding within the brain is known as cerebral
30 hemorrhage, which is often linked to high blood pressure. Bleeding into the meninges surrounding the brain is known as a subarachnoid hemorrhage, which could be caused by

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a ruptured cerebral aneurysm, an arteriovenous malformation, or a head injury. The hemorrhagic strokes, although less prevalent, pose a greater danger. Whereas about 8% of ischemic strokes result in death within 30 days, about 38% of hemorrhagic strokes result in death within the same time period.

5 Known risk factors for stroke can be divided into modifiable and non-modifiable risk factors. Older age, male sex, black or Hispanic ethnicity, and family history of stroke are non-modifiable risk factors. Modifiable risk factors include hypertension, smoking, increased insulin levels, asymptomatic carotid disease, cardiac vessel disease, and hyperlipidemia. Information derived from the Dutch Twin Registry estimates the
10 heritability of stroke as 0.32 for stroke death and 0.17 for stroke hospitalization.

The acute nature of stroke leaves physicians with little time to prevent or lessen the devastation of brain damage. Strategies to diminish the impact of stroke include prevention and treatment with thrombolytic and, possibly, neuroprotective agents. The success of preventive measures will depend on the identification of risk factors and
15 means to modulate their impact.

Although some risk factors for stroke are not modifiable, such as age and family history, other underlying pathology or risk factors of stroke such as atherosclerosis, hypertension, smoking, diabetes, aneurysm, and atrial fibrillation, are chronic and amenable to effective life-style, medical, and surgical treatments. Early recognition of
20 patients with these risk factors, and especially those with a family history, with a non-invasive test of genetic markers will enable physicians to target the highest risk individuals for aggressive risk reduction.

Statin Treatment

25 Coronary heart disease (CHD) accounts for approximately two-thirds of cardiovascular mortality in the United States, with CHD accounting for 1 in every 5 deaths in 1998, which makes it the largest single cause of mortality (*American Heart Association. 2001 Heart and Stroke Statistical Update. Dallas, TX: American Heart Association. 2000*). Stroke is the third leading cause of death, accounting for 1 of every
30 15 deaths. Reduction of coronary and cerebrovascular events and total mortality by treatment with HMG-CoA reductase inhibitors (statins) has been demonstrated in a

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number of randomized, double blinded, placebo controlled prospective trials (Waters, D.D., *What do the statin trials tell us?* Clin Cardiol, 2001. 24(8 Suppl): p. III3-7, Singh, B.K. and J.L. Mehta, *Management of dyslipidemia in the primary prevention of coronary heart disease.* Curr Opin Cardiol, 2002. 17(5): p. 503-11). These drugs have their
 5 primary effect through the inhibition of hepatic cholesterol synthesis, thereby upregulating LDL receptor in the liver. The resultant increase in LDL catabolism results in decreased circulating LDL, a major risk factor for cardiovascular disease. In addition, statins cause relatively small reductions in triglyceride levels (5 to 10%) and elevations in HDL cholesterol (5 to 10%). In a 5 year primary intervention trial (WOSCOPS),
 10 pravastatin decreased clinical events 29% compared to placebo in hypercholesterolemic subjects, achieving a 26% reduction in LDL-cholesterol (LDL-C) (Shepherd, J., et al., *Prevention of coronary heart disease with pravastatin in men with hypercholesterolemia.* West of Scotland Coronary Prevention Study Group; N Engl J Med, 1995. 333(20): p. 1301-7). In a similar primary prevention trial (AFCAPS/TexCAPS) (Downs, J.R., et al.,
 15 *Primary prevention of acute coronary events with lovastatin in men and women with average cholesterol levels: results of AFCAPS/TexCAPS. Air Force/Texas Coronary Atherosclerosis Prevention Study.* Jama, 1998. 279(20): p. 1615-22) in which subjects with average cholesterol levels were treated with lovastatin, LDL-C was reduced an average of 25% and events decreased by 37%.

20 Secondary prevention statin trials include the CARE (Sacks, F.M., et al., *The effect of pravastatin on coronary events after myocardial infarction in patients with average cholesterol levels. Cholesterol and Recurrent Events Trial investigators.* N Engl J Med, 1996. 335(14): p. 1001-9) and LIPID (treatment with pravastatin) (*Prevention of cardiovascular events and death with pravastatin in patients with coronary heart disease and a broad range of initial cholesterol levels. The Long-Term Intervention with Pravastatin in Ischaemic Disease (LIPID) Study Group.* N Engl J Med, 1998. 339(19): p. 1349-57), and 4S (treatment with simvastatin) (*Randomised trial of cholesterol lowering in 4444 patients with coronary heart disease: the Scandinavian Simvastatin Survival Study (4S).* Lancet, 1994. 344(8934): p. 1383-9) studies. In these trials, clinical event risk
 25 was reduced from between 23% and 34% with achieved LDL-C lowering ranging
 30 between 25% and 35%.

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In addition to LDL-lowering, a variety of potential non-lipid lowering effects have been suggested to play a role in cardiovascular risk reduction by statins. These include anti-inflammatory effects on various vascular cell types including foam cell macrophages, improved endothelial responses, inhibition of platelet reactivity thereby decreasing hypercoaguability, and many others (Puddu, P., G.M. Puddu, and A. Muscari, *Current thinking in statin therapy*. Acta Cardiol, 2001. 56(4): p. 225-31, Albert, M.A., et al., *Effect of statin therapy on C-reactive protein levels: the pravastatin inflammation/CRP evaluation (PRINCE): a randomized trial and cohort study*. Jama, 2001. 286(1): p. 64-70, Rosenson, R.S., *Non-lipid-lowering effects of statins on atherosclerosis*. Curr Cardiol Rep, 1999. 1(3): p. 225-32, Dangas, G., et al., *Pravastatin: an antithrombotic effect independent of the cholesterol-lowering effect*. Thromb Haemost, 2000. 83(5): p. 688-92, Crisby, M., *Modulation of the inflammatory process by statins*. Drugs Today (Barc), 2003. 39(2): p. 137-43, Liao, J.K., *Role of statin pleiotropism in acute coronary syndromes and stroke*. Int J Clin Pract Suppl, 2003(134): p. 51-7). However, because hypercholesterolemia is a factor in many of these additional pathophysiologic mechanisms that are reversed by statins, many of these statin benefits may be a consequence of LDL lowering.

Statins as a class of drug are generally well tolerated. The most common side effects include a variety of muscle-related complaints or myopathies. While the incidence of muscle side effects are low, the most serious side effect, myositis with rhabdomyolysis, is life threatening. This adverse effect has been highlighted by the recent withdrawal of cerivastatin when the drug was found to be associated with a relatively high level of rhabdomyolysis-related deaths. In addition, the development of a high dose sustained release formulation of simvastatin was discontinued for rhabdomyolysis-related issues (Davidson, M.H., et al., *The efficacy and six-week tolerability of simvastatin 80 and 160 mg/day*. Am J Cardiol, 1997. 79(1): p. 38-42).

Statins can be divided into two types according to their physicochemical and pharmacokinetic properties. Statins such as lovastatin, simvastatin, atorvastatin, and cerivastatin are hydrophobic in nature and, as such, diffuse across membranes and thus are highly cell permeable. Hydrophilic statins such as pravastatin are more polar, such that they require specific cell surface transporters for cellular uptake (Ziegler, K. and W.

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- Stunkel, *Tissue-selective action of pravastatin due to hepatocellular uptake via a sodium-independent bile acid transporter*. Biochim Biophys Acta, 1992. 1139(3): p. 203-9,
- Yamazaki, M., et al., *Na(+)-independent multispecific anion transporter mediates active transport of pravastatin into rat liver*. Am J Physiol, 1993. 264(1 Pt 1): p. G36-44,
- 5 Komai, T., et al., *Carrier-mediated uptake of pravastatin by rat hepatocytes in primary culture*. Biochem Pharmacol, 1992. 43(4): p. 667-70). The latter statin utilizes a transporter, OATP2, whose tissue distribution is confined to the liver and, therefore, they are relatively hepato-specific inhibitors (Hsiang, B., et al., *A novel human hepatic organic anion transporting polypeptide (OATP2). Identification of a liver-specific human*
- 10 *organic anion transporting polypeptide and identification of rat and human hydroxymethylglutaryl-CoA reductase inhibitor transporters*. J Biol Chem, 1999. 274(52): p. 37161-8). The former statins, not requiring specific transport mechanisms, are available to all cells and they can directly impact a much broader spectrum of cells and tissues. These differences in properties may influence the spectrum of activities that
- 15 each statin possesses. Pravastatin, for instance, has a low myopathic potential in animal models and myocyte cultures compared to other hydrophobic statins (Masters, B.A., et al., *In vitro myotoxicity of the 3-hydroxy-3-methylglutaryl coenzyme A reductase inhibitors, pravastatin, lovastatin, and simvastatin, using neonatal rat skeletal myocytes*. Toxicol Appl Pharmacol, 1995. 131(1): p. 163-74. Nakahara, K., et al., *Myopathy induced by HMG-CoA reductase inhibitors in rabbits: a pathological,*
- 20 *electrophysiological, and biochemical study*. Toxicol Appl Pharmacol, 1998. 152(1): p. 99-106, Reijneveld, J.C., et al., *Differential effects of 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitors on the development of myopathy in young rats*. Pediatr Res, 1996. 39(6): p. 1028-35).
- 25 Cardiovascular mortality in developed countries has decreased sharply in recent decades (Tunstall-Pedoe, H., et al., *Estimation of contribution of changes in coronary care to improving survival, event rates, and coronary heart disease mortality across the WHO MONICA Project populations*. Lancet, 2000. 355(9205): p. 688-700). This is likely due to the development and use of efficacious hypertension, thrombolytic and lipid
- 30 lowering therapies (Kuulasmaa, K., et al., *Estimation of contribution of changes in classic risk factors to trends in coronary-event rates across the WHO MONICA Project*

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populations. *Lancet*, 2000. 355(9205): p. 675-87). Nevertheless, cardiovascular diseases remain the major cause of death in industrialized countries, at least in part due to the presence of highly prevalent risk factors and insufficient treatment (Wong, M.D., et al., *Contribution of major diseases to disparities in mortality*. *N Engl J Med*, 2002. 347(20): p. 1585-92). Even with appropriate therapy, not all patients respond equally well to statin treatment. Despite the overwhelming evidence that statins decrease risk for cardiovascular disease, both in primary and secondary intervention settings, statin therapy clearly only achieves partial risk reduction. While a decrease in risk of 23 to 37% seen in the above trials is substantial and extremely important clinically, the majority of events still are not prevented by statin treatment. This is not surprising given the complexity of cardiovascular disease etiology, which is influenced by genetics, environment, and a variety of additional risk factors including dyslipidemia, age, gender, hypertension, diabetes, obesity, and smoking. It is reasonable to assume that all of these multi-factorial risks modify statin responses and determine the final benefit that each individual achieves from therapy. Furthermore, with the increasing incidence of Type 2 diabetes and obesity in Western countries (Flegal, K.M., et al., *Prevalence and trends in obesity among US adults, 1999-2000*. *Jama*, 2002. 288(14): p. 1723-7; Boyle, J.P., et al., *Projection of diabetes burden through 2050: impact of changing demography and disease prevalence in the U.S.* *Diabetes Care*, 2001. 24(11): p. 1936-40), which are two major risk factors for coronary artery disease, and the emergence of greater cardiovascular risk factors in the developing world (Yusuf, S., et al., *Global burden of cardiovascular diseases: Part II: variations in cardiovascular disease by specific ethnic groups and geographic regions and prevention strategies*. *Circulation*, 2001. 104(23): p. 2855-64; Yusuf, S., et al., *Global burden of cardiovascular diseases: part I: general considerations, the epidemiologic transition, risk factors, and impact of urbanization*. *Circulation*, 2001. 104(22): p. 2746-53), the need for ever more effective treatment of CHD is predicted to steadily increase.

Thus, there is a growing need for ways to better identify people who have the highest chance to benefit from statins, and those who have the lowest risk of developing side-effects. As indicated above, severe myopathies represent a significant risk for a low percentage of the patient population. This would be particularly true for patients that

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may be treated more aggressively with statins in the future. There are currently at least three studies in progress that are investigating whether treatments aimed at lowering LDL-C to levels below current NCEP goals by administering higher statin doses to patients further reduces CHD risk or provides additional cardiovascular benefits

5 (reviewed in Clark, L.T., *Treating dyslipidemia with statins: the risk-benefit profile*. Am Heart J, 2003. 145(3): p. 387-96). It is possible that more aggressive statin therapy than is currently standard practice will become the norm in the future if additional benefit is observed in such trials. More aggressive statin therapy will likely increase the incidence of the above adverse events as well as elevate the cost of treatment. Thus, increased
10 emphasis will be placed on stratifying responder and non-responder patients in order for maximum benefit-risk ratios to be achieved at the lowest cost.

The Third Report of the Expert Panel on Detection, Evaluation and Treatment of High Blood Cholesterol in Adults (ATPIII) contains current recommendations for the management of high serum cholesterol (*Executive Summary of The Third Report of The
15 National Cholesterol Education Program (NCEP) Expert Panel on Detection, Evaluation, And Treatment of High Blood Cholesterol In Adults (Adult Treatment Panel III)*). Jama, 2001. 285(19): p. 2486-97). A meta-analysis of 38 primary and secondary prevention trials found that for every 10% decrease in serum cholesterol, CHD mortality was reduced by 15%. These guidelines took into account additional risk factors beyond
20 serum cholesterol when making recommendations for lipid lowering strategies. After considering additional risk factors and updated information on lipid lowering clinical trials, more patients are classified in the highest risk category of CHD or CHD risk equivalent than before and are recommended to decrease their LDL to less than 100 mg/dl. As a consequence, more aggressive therapy is recommended and drug therapy is
25 recommended for 36.5 million Americans. In implementing these recommendations, cost-effectiveness of treatments is a primary concern. In lower risk populations, the cost of reducing one event may exceed \$125,000 compared with around \$25,000 per event in a high-risk patient group (Singh, B.K. and J.L. Mehta, *Management of dyslipidemia in the primary prevention of coronary heart disease*. Curr Opin Cardiol, 2002. 17(5): p.
30 503-11). The cost of preventing an event in a very low risk patient may exceed \$1 million. In the context of cost-containment, further risk stratification of patients will help

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to avoid unnecessary treatment of patients. In addition to the various clinical endpoints that are currently considered in determining overall risk, the determination of who and who not to treat with statins based on "statin response" genotypes could substantially increase the precision of these determinations in the future.

- 5 Evidence from gene association studies is accumulating to indicate that responses to drugs are, indeed, at least partly under genetic control. As such, pharmacogenetics - the study of variability in drug responses attributed to hereditary factors in different populations - may significantly assist in providing answers toward meeting this challenge (Roses, A.D., *Pharmacogenetics and the practice of medicine*. Nature, 2000. 405(6788):
- 10 p. 857-65, Mooser, V., et al., *Cardiovascular pharmacogenetics in the SNP era*. J Thromb Haemost, 2003. 1(7): p. 1398-1402, Humma, L.M. and S.G. Terra, *Pharmacogenetics and cardiovascular disease: impact on drug response and applications to disease management*. Am. J. Health Syst Pharm, 2002. 59(13): p. 1241-1252). Numerous associations have been reported between selected genotypes, as defined
- 15 by SNPs and other sequence variations and specific responses to cardiovascular drugs. Polymorphisms in several genes have been suggested to influence responses to statins including CETP (Kuivenhoven, J.A., et al., *The role of a common variant of the cholesteryl ester transfer protein gene in the progression of coronary atherosclerosis*. The Regression Growth Evaluation Statin Study Group. N Engl J Med, 1998. 338(2): p. 86-93), beta-fibrinogen (de Maat, M.P., et al., *-455G/A polymorphism of the beta-fibrinogen gene is associated with the progression of coronary atherosclerosis in symptomatic men: proposed role for an acute-phase reaction pattern of fibrinogen*. REGRESS group. Arterioscler Thromb Vasc Biol, 1998. 18(2): p. 265-71), hepatic lipase (Zambon, A., et al., *Common hepatic lipase gene promoter variant determines clinical*
- 25 *response to intensive lipid-lowering treatment*. Circulation, 2001. 103(6): p. 792-8, lipoprotein lipase (Jukema, J.W., et al., *The Asp9 Asn mutation in the lipoprotein lipase gene is associated with increased progression of coronary atherosclerosis*. REGRESS Study Group, Interuniversity Cardiology Institute, Utrecht, The Netherlands. Regression Growth Evaluation Statin Study. Circulation, 1996. 94(8): p. 1913-8), glycoprotein IIIa
- 30 (Bray, P.F., et al., *The platelet PL(A2) and angiotensin-converting enzyme (ACE) D allele polymorphisms and the risk of recurrent events after acute myocardial infarction*. Am J

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Cardiol, 2001. 88(4): p. 347-52), stromelysin-1 (de Maat, M.P., et al., *Effect of the stromelysin-1 promoter on efficacy of pravastatin in coronary atherosclerosis and restenosis*. Am J Cardiol, 1999. 83(6): p. 852-6), and apolipoprotein E (Gerdes, L.U., et al., *The apolipoprotein epsilon4 allele determines prognosis and the effect on prognosis of simvastatin in survivors of myocardial infarction: a substudy of the Scandinavian simvastatin survival study*. Circulation, 2000. 101(12): p. 1366-71, Pedro-Botet, J., et al., *Apolipoprotein E genotype affects plasma lipid response to atorvastatin in a gender specific manner*. Atherosclerosis, 2001. 158(1): p. 183-93).

Some of these variants were shown to effect clinical events while others were associated with changes in surrogate endpoints. The CETP variant alleles B1 and B2 were shown to be correlated with HDL cholesterol levels. Patients with B1B1 and B1B2 genotypes have lower HDL cholesterol and greater progression of angiographically-determined atherosclerosis than B2B2 subjects when on placebo during the pravastatin REGRESS clinical trial. Furthermore, B1B1 and B1B2 had significantly less progression of atherosclerosis when on pravastatin whereas B2B2 patients derived no benefit. Similarly, beta-fibrinogen promoter sequence variants were also associated with disease progression and response to pravastatin in the same study as were Stromelysin-1 promoter variants. In the Cholesterol and Recurrent Events (CARE) trial, a pravastatin secondary intervention study, glycoprotein IIIa variants were also associated with clinical event response to pravastatin. In all of the above cases, genetic subgroups of placebo-treated patients with CHD were identified who had increased risk for major coronary events. Treatment with pravastatin abolished the harmful effects associated with the "riskier" genotype, while having little effect on patients with genotypes that were associated with less risk. Finally, the impact of the apolipoprotein ϵ 4 genotype on prognosis and the response to simvastatin or placebo was investigated in the Scandanavian Simvastatin Survival Study (Pedro-Botet, J., et al., *Apolipoprotein E genotype affects plasma lipid response to atorvastatin in a gender specific manner*. Atherosclerosis, 2001. 158(1): p. 183-93). Patients with at least one apolipoprotein ϵ 4 allele had a higher risk for all cause death than those lacking the allele. As was the case with pravastatin treatment, simvastatin reversed this detrimental effect of the "riskier allele". These results suggest that, in general, high-risk patients with ischemic heart disease derive the greatest benefit

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from statin therapy. However, these initial observations should be repeated in other cohorts to further support the predictive value of these specific genotypes. Although it is likely that additional genes beyond the five examples above impact the final outcome of an individual's response to statins, these five examples serve to illustrate that it is possible to identify genes that associate with statin clinical responses that could be used to predict which patients will benefit from statin treatment and which will not.

SNPs

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor genetic sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). A variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. Additionally, the effects of a variant form may be both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. In many cases, both progenitor and variant forms survive and co-exist in a species population. The coexistence of multiple forms of a genetic sequence gives rise to genetic polymorphisms, including SNPs.

Approximately 90% of all polymorphisms in the human genome are SNPs. SNPs are single base positions in DNA at which different alleles, or alternative nucleotides, exist in a population. The SNP position (interchangeably referred to herein as SNP, SNP site, SNP locus, SNP marker, or marker) is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). An individual may be homozygous or heterozygous for an allele at each SNP position. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP is an amino acid coding sequence.

A SNP may arise from a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the

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replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or vice versa. A SNP may also be a single base insertion or deletion variant referred to as an "indel" (Weber *et al.*, "Human diallelic insertion/deletion polymorphisms", *Am J Hum Genet* 2002 Oct;71(4):854-62).

A synonymous codon change, or silent mutation/SNP (terms such as "SNP", "polymorphism", "mutation", "mutant", "variation", and "variant" are used herein interchangeably), is one that does not result in a change of amino acid due to the degeneracy of the genetic code. A substitution that changes a codon coding for one amino acid to a codon coding for a different amino acid (i.e., a non-synonymous codon change) is referred to as a missense mutation. A nonsense mutation results in a type of non-synonymous codon change in which a stop codon is formed, thereby leading to premature termination of a polypeptide chain and a truncated protein. A read-through mutation is another type of non-synonymous codon change that causes the destruction of a stop codon, thereby resulting in an extended polypeptide product. While SNPs can be bi-, tri-, or tetra- allelic, the vast majority of the SNPs are bi-allelic, and are thus often referred to as "bi-allelic markers", or "di-allelic markers".

As used herein, references to SNPs and SNP genotypes include individual SNPs and/or haplotypes, which are groups of SNPs that are generally inherited together. Haplotypes can have stronger correlations with diseases or other phenotypic effects compared with individual SNPs, and therefore may provide increased diagnostic accuracy in some cases (Stephens *et al. Science* 293, 489-493, 20 July 2001).

Causative SNPs are those SNPs that produce alterations in gene expression or in the expression, structure, and/or function of a gene product, and therefore are most predictive of a possible clinical phenotype. One such class includes SNPs falling within regions of genes encoding a polypeptide product, i.e. cSNPs. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product (i.e., non-synonymous codon changes) and give rise to the expression of a defective or other variant protein. Furthermore, in the case of nonsense mutations, a SNP may lead to premature termination of a polypeptide product. Such variant products can result in a

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pathological condition, e.g., genetic disease. Examples of genes in which a SNP within a coding sequence causes a genetic disease include sickle cell anemia and cystic fibrosis.

Causative SNPs do not necessarily have to occur in coding regions; causative SNPs can occur in, for example, any genetic region that can ultimately affect the expression, structure, and/or activity of the protein encoded by a nucleic acid. Such genetic regions include, for example, those involved in transcription, such as SNPs in transcription factor binding domains, SNPs in promoter regions, in areas involved in transcript processing, such as SNPs at intron-exon boundaries that may cause defective splicing, or SNPs in mRNA processing signal sequences such as polyadenylation signal regions. Some SNPs that are not causative SNPs nevertheless are in close association with, and therefore segregate with, a disease-causing sequence. In this situation, the presence of a SNP correlates with the presence of, or predisposition to, or an increased risk in developing the disease. These SNPs, although not causative, are nonetheless also useful for diagnostics, disease predisposition screening, and other uses.

An association study of a SNP and a specific disorder involves determining the presence or frequency of the SNP allele in biological samples from individuals with the disorder of interest, such as those individuals who respond to statin treatment ("responders") or those individuals who do not respond to statin treatment ("non-responders"), and comparing the information to that of controls (i.e., individuals who do not have the disorder; controls may be also referred to as "healthy" or "normal" individuals) who are preferably of similar age and race. The appropriate selection of patients and controls is important to the success of SNP association studies. Therefore, a pool of individuals with well-characterized phenotypes is extremely desirable.

A SNP may be screened in diseased tissue samples or any biological sample obtained from a diseased individual, and compared to control samples, and selected for its increased (or decreased) occurrence in a specific phenotype, such as response or non-response to statin treatment of cardiovascular disease. Once a statistically significant association is established between one or more SNP(s) and a pathological condition (or other phenotype) of interest, then the region around the SNP can optionally be thoroughly screened to identify the causative genetic locus/sequence(s) (e.g., causative SNP/mutation, gene, regulatory region, etc.) that influences the pathological condition or

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phenotype. Association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families (linkage studies).

Clinical trials have shown that patient response to treatment with pharmaceuticals is often heterogeneous. There is a continuing need to improve pharmaceutical agent design and therapy. In that regard, SNPs can be used to identify patients most suited to therapy with particular pharmaceutical agents such as statins (this is often termed "pharmacogenomics"). Similarly, SNPs can be used to exclude patients from certain treatment due to the patient's increased likelihood of developing toxic side effects or their likelihood of not responding to the treatment. Pharmacogenomics can also be used in pharmaceutical research to assist the drug development and selection process. (Linder et al. (1997), *Clinical Chemistry*, 43, 254; Marshall (1997), *Nature Biotechnology*, 15, 1249; International Patent Application WO 97/40462, Spectra Biomedical; and Schafer et al. (1998), *Nature Biotechnology*, 16, 3).

SUMMARY OF THE INVENTION

The present invention relates to the identification of novel SNPs, unique combinations of such SNPs, and haplotypes of SNPs that are associated with cardiovascular disorders and/or drug response, particularly acute coronary events (e.g., myocardial infarction and stroke) and response to statins for the treatment (including preventive treatment) of cardiovascular disorders such as acute coronary events. The polymorphisms disclosed herein are directly useful as targets for the design of diagnostic reagents and the development of therapeutic agents for use in the diagnosis and treatment of cardiovascular disorders and related pathologies, particularly acute coronary events.

Based on the identification of SNPs associated with cardiovascular disorders, particularly acute coronary events, and/or response to statin treatment, the present invention also provides methods of detecting these variants as well as the design and preparation of detection reagents needed to accomplish this task. The invention specifically provides, for example, novel SNPs in genetic sequences involved in cardiovascular disorders and/or responsiveness to statin treatment, isolated nucleic acid molecules (including, for example, DNA and RNA molecules) containing these SNPs,

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variant proteins encoded by nucleic acid molecules containing such SNPs, antibodies to the encoded variant proteins, computer-based and data storage systems containing the novel SNP information, methods of detecting these SNPs in a test sample, methods of determining the risk of an individual of experiencing a first or recurring acute coronary event, methods for prognosing the severity or consequences of the acute coronary event, methods of treating an individual who has an increased risk of experiencing an acute coronary event, methods of identifying individuals who have an altered (i.e., increased or decreased) likelihood of responding to statin treatment based on the presence or absence of one or more particular nucleotides (alleles) at one or more SNP sites disclosed herein or the detection of one or more encoded variant products (e.g., variant mRNA transcripts or variant proteins), methods of identifying individuals who are more or less likely to respond to a treatment, particularly statin treatment of a cardiovascular disorder such as an acute coronary event (or more or less likely to experience undesirable side effects from a treatment, etc.), methods of screening for compounds useful in the treatment of a disorder associated with a variant gene/protein, compounds identified by these methods, methods of treating disorders mediated by a variant gene/protein, methods of using the novel SNPs of the present invention for human identification, etc.

Since cardiovascular disorders/diseases share certain similar features that may be due to common genetic factors that are involved in their underlying mechanisms, the SNPs identified herein as being particularly associated with acute coronary events and/or statin response may be used as diagnostic/prognostic markers or therapeutic targets for a broad spectrum of cardiovascular diseases such as coronary heart disease (CHD), atherosclerosis, cerebrovascular disease, congestive heart failure, congenital heart disease, and pathologies and symptoms associated with various heart diseases (e.g., angina, hypertension), as well as for predicting responses to a variety of HMG-CoA reductase inhibitors with lipid-lowering activities (statins), and even drugs other than statins that are used to treat cardiovascular diseases. In addition, the SNPs of the present invention are useful for predicting primary acute coronary events, as well as their reoccurrence.

The present invention further provides methods for selecting or formulating a treatment regimen (e.g., methods for determining whether or not to administer statin

treatment to an individual having cardiovascular disease, methods for selecting a particular statin-based treatment regimen such as dosage and frequency of administration of statin, or a particular form/type of statin such as a particular pharmaceutical formulation or compound, methods for administering an alternative, non-statin-based treatment to individuals who are predicted to be unlikely to respond positively to statin treatment, etc.), and methods for determining the likelihood of experiencing toxicity or other undesirable side effects from statin treatment, etc. The present invention also provides methods for selecting individuals to whom a statin or other therapeutic will be administered based on the individual's genotype, and methods for selecting individuals for a clinical trial of a statin or other therapeutic agent based on the genotypes of the individuals (e.g., selecting individuals to participate in the trial who are most likely to respond positively from the statin treatment). Furthermore, the SNPs of the invention are useful for predicting treatment responsiveness at any stage of CHD, including the initial decision for prescribing treatment before the occurrence of the first acute coronary event.

In Tables 1-2, the present invention provides gene information, transcript sequences (SEQ ID NOS: 2-55), encoded amino acid sequences (SEQ ID NOS: 56-109), genomic sequences (SEQ ID NOS: 167-185), transcript-based context sequences (SEQ ID NOS: 110-116) and genomic-based context sequences (SEQ ID NOS: 186-206 & 267) that contain the SNPs of the present invention, and extensive SNP information that includes observed alleles, allele frequencies, populations/ethnic groups in which alleles have been observed, information about the type of SNP and corresponding functional effect, and, for cSNPs, information about the encoded polypeptide product. The transcript sequences (SEQ ID NOS: 2-55), amino acid sequences (SEQ ID NOS: 56-109), genomic sequences (SEQ ID NOS: 167-185), transcript-based SNP context sequences (SEQ ID NOS: 110-116), and genomic-based SNP context sequences (SEQ ID NOS: 186-206 & 267) are also provided in the Sequence Listing.

In a specific embodiment of the present invention, SNPs that occur naturally in the human genome are provided as isolated nucleic acid molecules. These SNPs are associated with cardiovascular disorders, particular acute coronary events, and/or response to statin treatment, such that they can have a variety of uses in the diagnosis

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and/or treatment of cardiovascular disorders and related pathologies and particularly in the treatment of cardiovascular disorders with statins. One aspect of the present invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence in which at least one nucleotide is a SNP disclosed in Tables 3 and/or 4. In an alternative
5 embodiment, a nucleic acid of the invention is an amplified polynucleotide, which is produced by amplification of a SNP-containing nucleic acid template. In another embodiment, the invention provides for a variant protein which is encoded by a nucleic acid molecule containing a SNP disclosed herein.

In yet another embodiment of the invention, a reagent for detecting a SNP in the
10 context of its naturally-occurring flanking nucleotide sequences (which can be, e.g., either DNA or mRNA) is provided. In particular, such a reagent may be in the form of, for example, a hybridization probe or an amplification primer that is useful in the specific detection of a SNP of interest. In an alternative embodiment, a protein detection reagent is used to detect a variant protein that is encoded by a nucleic acid molecule containing a
15 SNP disclosed herein. A preferred embodiment of a protein detection reagent is an antibody or an antigen-reactive antibody fragment.

Various embodiments of the invention also provide kits comprising SNP detection reagents, and methods for detecting the SNPs disclosed herein by employing detection reagents. In a specific embodiment, the present invention provides for a method of
20 identifying an individual having an increased or decreased risk of developing a cardiovascular disorder (e.g. experiencing an acute coronary event) by detecting the presence or absence of one or more SNP alleles disclosed herein. The present invention also provides methods for evaluating whether an individual is likely (or unlikely) to respond to statin treatment of cardiovascular disease by detecting the presence or absence
25 of one or more SNP alleles disclosed herein.

The nucleic acid molecules of the invention can be inserted in an expression vector, such as to produce a variant protein in a host cell. Thus, the present invention also provides for a vector comprising a SNP-containing nucleic acid molecule, genetically-engineered host cells containing the vector, and methods for expressing a
30 recombinant variant protein using such host cells. In another specific embodiment, the host cells, SNP-containing nucleic acid molecules, and/or variant proteins can be used as

targets in a method for screening and identifying therapeutic agents or pharmaceutical compounds useful in the treatment of cardiovascular diseases.

An aspect of this invention is a method for treating cardiovascular disorders, particular acute coronary events, in a human subject wherein said human subject harbors a SNP, gene, transcript, and/or encoded protein identified in Tables 1-2, which method comprises administering to said human subject a therapeutically or prophylactically effective amount of one or more agents (e.g. statins) counteracting the effects of the disorder, such as by inhibiting (or stimulating) the activity of the gene, transcript, and/or encoded protein identified in Tables 1-2.

Another aspect of this invention is a method for identifying an agent useful in therapeutically or prophylactically treating cardiovascular disorders, particular acute coronary events, in a human subject wherein said human subject harbors a SNP, gene, transcript, and/or encoded protein identified in Tables 1-2, which method comprises contacting the gene, transcript, or encoded protein with a candidate agent (e.g., statin) under conditions suitable to allow formation of a binding complex between the gene, transcript, or encoded protein and the candidate agent (such as a statin) and detecting the formation of the binding complex, wherein the presence of the complex identifies said agent.

Another aspect of this invention is a method for treating a cardiovascular disorder in a human subject, which method comprises:

- (i) determining that said human subject harbors a SNP, gene, transcript, and/or encoded protein identified in Tables 1-2, and
- (ii) administering to said subject a therapeutically or prophylactically effective amount of one or more agents (such as a statin) counteracting the effects of the disease.

Various embodiments of the claimed invention relate to a method of indicating whether a human has an increased risk for coronary heart disease (CHD), comprising testing as represented by position 101 of SEQ ID NO:191 or its complement, wherein the presence of G at position 101 of SEQ ID NO:191 or C at position 101 of its complement indicates said human has said increased risk for CHD. The CHD may be myocardial infarction.

Various embodiments of the claimed invention relate to a method of indicating whether a human's risk for coronary heart disease (CHD) is reduced by treatment with an HMG-CoA

reductase inhibitor, the method comprising testing nucleic acid from said human for the presence or absence of a polymorphism as represented by position 101 of SEQ ID NO:191 or its complement, wherein the presence of G at position 101 of SEQ ID NO:191 or C at position 101 of its complement indicates said human has said increased risk for CHD. The CHD may be myocardial infarction. The HMG-CoA reductase inhibitor may be a statin.

Various embodiments of the claimed invention relate to an isolated polynucleotide for use in a method as described above, wherein the polynucleotide specifically hybridizes to at least a portion of SEQ ID NO: 191 or its complement, which portion comprises position 101. Various embodiments of this invention provide a kit for performing a method of this invention, the kit comprising a polynucleotide of this invention, a buffer, and an enzyme.

Many other uses and advantages of the present invention will be apparent to those skilled in the art upon review of the detailed description of the preferred embodiments herein. Solely for clarity of discussion, the invention is described in the sections below by way of non-limiting examples.

SEQUENCE LISTING

The Sequence Listing provides the transcript (SEQ ID NOS: 2-55) and protein sequences (SEQ ID NOS: 56-109) as shown in Table 1, and genomic sequences (SEQ ID NOS: 167-185) as shown in Table 2, for each gene that contains one or more SNPs of the present invention. Also provided in the Sequence Listing are context sequences flanking each SNP, including both transcript-based context sequences as shown in Table 1 (SEQ ID NOS: 110-116) and genomic-based context sequences as shown in Table 2 (SEQ ID NOS: 186-206&267). The context sequences generally provide 100bp upstream (5') and 100bp downstream (3') of each SNP, with the SNP in the middle of the context sequence, for a total of 200bp of context sequence surrounding each SNP.

DESCRIPTION OF TABLE 1 AND TABLE 2

Table 1 and Table 2 disclose the SNP and associated gene/transcript/protein information of the present invention. For each gene, Table 1 and Table 2 each provide a header containing gene/transcript/protein information, followed by a transcript and protein sequence (in Table 1) or genomic sequence (in Table 2), and then SNP information regarding each SNP found in that gene/transcript.

NOTE: SNPs may be included in both Table 1 and Table 2; Table 1 presents the SNPs relative to their transcript sequences and encoded protein sequences, whereas Table

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2 presents the SNPs relative to their genomic sequences (in some instances Table 2 may also include, after the last gene sequence, genomic sequences of one or more intergenic regions, as well as SNP context sequences and other SNP information for any SNPs that lie within these intergenic regions). SNPs can readily be cross-referenced between Tables
5 based on their hCV (or, in some instances, hDV) identification numbers.

The gene/transcript/protein information includes:

- a gene number (1 through n, where n = the total number of genes in the Table)
- a Celera hCG and UID internal identification numbers for the gene
- 10 - a Celera hCT and UID internal identification numbers for the transcript (Table 1 only)
- a public Genbank accession number (e.g., RefSeq NM number) for the transcript (Table 1 only)
- a Celera hCP and UID internal identification numbers for the protein encoded by
15 the hCT transcript (Table 1 only)
- a public Genbank accession number (e.g., RefSeq NP number) for the protein (Table 1 only)
- an art-known gene symbol
- an art-known gene/protein name
- 20 - Celera genomic axis position (indicating start nucleotide position-stop nucleotide position)
- the chromosome number of the chromosome on which the gene is located
- an OMIM (Online Mendelian Inheritance in Man; Johns Hopkins University/NCBI) public reference number for obtaining further information regarding
25 the medical significance of each gene
- alternative gene/protein name(s) and/or symbol(s) in the OMIM entry

NOTE: Due to the presence of alternative splice forms, multiple transcript/protein entries can be provided for a single gene entry in Table 1; i.e., for a single Gene Number, multiple entries may be provided in series that differ in their transcript/protein
30 information and sequences.

Following the gene/transcript/protein information is a transcript sequence and protein sequence (in Table 1), or a genomic sequence (in Table 2), for each gene, as follows:

- transcript sequence (Table 1 only) (corresponding to SEQ ID NOS: 2-55 of the Sequence Listing), with SNPs identified by their IUB codes (transcript sequences can include 5' UTR, protein coding, and 3' UTR regions). (NOTE: If there are differences between the nucleotide sequence of the hCT transcript and the corresponding public transcript sequence identified by the Genbank accession number, the hCT transcript sequence (and encoded protein) is provided, unless the public sequence is a RefSeq transcript sequence identified by an NM number, in which case the RefSeq NM transcript sequence (and encoded protein) is provided. However, whether the hCT transcript or RefSeq NM transcript is used as the transcript sequence, the disclosed SNPs are represented by their IUB codes within the transcript.)
- the encoded protein sequence (Table 1 only) (corresponding to SEQ ID NOS: 56-109 of the Sequence Listing)
- the genomic sequence of the gene (Table 2 only), including 6kb on each side of the gene boundaries (i.e., 6kb on the 5' side of the gene plus 6kb on the 3' side of the gene) (corresponding to SEQ ID NOS: 186-206 & 267 of the Sequence Listing).

After the last gene sequence, Table 2 may include additional genomic sequences of intergenic regions (in such instances, these sequences are identified as "Intergenic region:" followed by a numerical identification number), as well as SNP context sequences and other SNP information for any SNPs that lie within each intergenic region (and such SNPs are identified as "INTERGENIC" for SNP type).

NOTE: The transcript, protein, and transcript-based SNP context sequences are provided in both Table 1 and in the Sequence Listing. The genomic and genomic-based SNP context sequences are provided in both Table 2 and in the Sequence Listing. SEQ ID NOS are indicated in Table 1 for each transcript sequence (SEQ ID NOS: 2-55), protein sequence (SEQ ID NOS: 56-109), and transcript-based SNP context sequence (SEQ ID NOS: 110-116), and SEQ ID NOS are indicated in Table 2 for each genomic sequence (SEQ ID NOS: 167-185), and genomic-based SNP context sequence (SEQ ID NOS: 186-206 & 267).

The SNP information includes:

- context sequence (taken from the transcript sequence in Table 1, and taken from the genomic sequence in Table 2) with the SNP represented by its IUB code, including 100 bp upstream (5') of the SNP position plus 100 bp downstream (3') of the SNP position (the transcript-based SNP context sequences in Table 1 are provided in the Sequence Listing as SEQ ID NOS: 110-116 ; the genomic-based SNP context sequences in Table 2 are provided in the Sequence Listing as SEQ ID NOS: 186-206 & 267.
- Celera hCV internal identification number for the SNP (in some instances, an "hDV" number is given instead of an "hCV" number)
- SNP position [position of the SNP within the given transcript sequence (Table 1) or within the given genomic sequence (Table 2)]
- SNP source (may include any combination of one or more of the following five codes, depending on which internal sequencing projects and/or public databases the SNP has been observed in: "Applera" = SNP observed during the re-sequencing of genes and regulatory regions of 39 individuals, "Celera" = SNP observed during shotgun sequencing and assembly of the Celera human genome sequence, "Celera Diagnostics" = SNP observed during re-sequencing of nucleic acid samples from individuals who have cardiovascular disorders (e.g., experienced an acute coronary event), and/or have undergone statin treatment, "dbSNP" = SNP observed in the dbSNP public database, "HGBASE" = SNP observed in the HGBASE public database, "HGMD" = SNP observed in the Human Gene Mutation Database (HGMD) public database, "HapMap" = SNP observed in the International HapMap Project public database, "CSNP" = SNP observed in an internal Applied Biosystems (Foster City, CA) database of coding SNPs (cSNPs)) (NOTE: multiple "Applera" source entries for a single SNP indicate that the same SNP was covered by multiple overlapping amplification products and the re-sequencing results (e.g., observed allele counts) from each of these amplification products is being provided)
- Population/allele/allele count information in the format of [population1(first_allele,count|second_allele,count)population2(first_allele,count|second_

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allele,count) total (first_allele,total count|second_allele,total count)]. The information in this field includes populations/ethnic groups in which particular SNP alleles have been observed ("cau" = Caucasian, "his" = Hispanic, "chn" = Chinese, and "afr" = African-American, "jpn" = Japanese, "ind" = Indian, "mex" = Mexican, "ain" = "American Indian, "cra" = Celera donor, "no_pop" = no population information available), identified SNP alleles, and observed allele counts (within each population group and total allele counts), where available ["-" in the allele field represents a deletion allele of an insertion/deletion ("indel") polymorphism (in which case the corresponding insertion allele, which may be comprised of one or more nucleotides, is indicated in the allele field on the opposite side of the "|"); "-" in the count field indicates that allele count information is not available]. For certain SNPs from the public dbSNP database, population/ethnic information is indicated as follows (this population information is publicly available in dbSNP): "HISP1" = human individual DNA (anonymized samples) from 23 individuals of self-described HISPANIC heritage; "PAC1" = human individual DNA (anonymized samples) from 24 individuals of self-described PACIFIC RIM heritage; "CAUC1" = human individual DNA (anonymized samples) from 31 individuals of self-described CAUCASIAN heritage; "AFR1" = human individual DNA (anonymized samples) from 24 individuals of self-described AFRICAN/AFRICAN AMERICAN heritage; "P1" = human individual DNA (anonymized samples) from 102 individuals of self-described heritage; "PA130299515"; "SC_12_A" = SANGER 12 DNAs of Asian origin from Coriell cell repositories, 6 of which are male and 6 female; "SC_12_C" = SANGER 12 DNAs of Caucasian origin from Coriell cell repositories from the CEPH/UTAH library. Six male and 6 female; "SC_12_AA" = SANGER 12 DNAs of African-American origin from Coriell cell repositories 6 of which are male and 6 female; "SC_95_C" = SANGER 95 DNAs of Caucasian origin from Coriell cell repositories from the CEPH/UTAH library; and "SC_12_CA" = Caucasians - 12 DNAs from Coriell cell repositories that are from the CEPH/UTAH library. Six male and 6 female.

NOTE: For SNPs of "Applera" SNP source, genes/regulatory regions of 39 individuals (20 Caucasians and 19 African Americans) were re-sequenced and, since each SNP position is represented by two chromosomes in each individual (with the exception

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of SNPs on X and Y chromosomes in males, for which each SNP position is represented by a single chromosome), up to 78 chromosomes were genotyped for each SNP position. Thus, the sum of the African-American ("afr") allele counts is up to 38, the sum of the Caucasian allele counts ("cau") is up to 40, and the total sum of all allele counts is up to 5 78.

(NOTE: semicolons separate population/allele/count information corresponding to each indicated SNP source; i.e., if four SNP sources are indicated, such as "Celera", "dbSNP", "HGBASE", and "HGMD", then population/allele/count information is provided in four groups which are separated by semicolons and listed in the same order 10 as the listing of SNP sources, with each population/allele/count information group corresponding to the respective SNP source based on order; thus, in this example, the first population/allele/count information group would correspond to the first listed SNP source (Celera) and the third population/allele/count information group separated by semicolons would correspond to the third listed SNP source (HGBASE); if population/allele/count 15 information is not available for any particular SNP source, then a pair of semicolons is still inserted as a place-holder in order to maintain correspondence between the list of SNP sources and the corresponding listing of population/allele/count information)

- SNP type (e.g., location within gene/transcript and/or predicted functional effect) ["MIS-SENSE MUTATION" = SNP causes a change in the encoded amino acid 20 (i.e., a non-synonymous coding SNP); "SILENT MUTATION" = SNP does not cause a change in the encoded amino acid (i.e., a synonymous coding SNP); "STOP CODON MUTATION" = SNP is located in a stop codon; "NONSENSE MUTATION" = SNP creates or destroys a stop codon; "UTR 5" = SNP is located in a 5' UTR of a transcript; "UTR 3" = SNP is located in a 3' UTR of a transcript; "PUTATIVE UTR 5" = SNP is 25 located in a putative 5' UTR; "PUTATIVE UTR 3" = SNP is located in a putative 3' UTR; "DONOR SPLICE SITE" = SNP is located in a donor splice site (5' intron boundary); "ACCEPTOR SPLICE SITE" = SNP is located in an acceptor splice site (3' intron boundary); "CODING REGION" = SNP is located in a protein-coding region of the transcript; "EXON" = SNP is located in an exon; "INTRON" = SNP is located in an 30 intron; "hmCS" = SNP is located in a human-mouse conserved segment; "TFBS" = SNP

is located in a transcription factor binding site; "UNKNOWN" = SNP type is not defined;
"INTERGENIC" = SNP is intergenic, i.e., outside of any gene boundary]

- Protein coding information (Table 1 only), where relevant, in the format of
[protein SEQ ID NO:#, amino acid position, (amino acid-1, codon1) (amino acid-2,
5 codon2)]. The information in this field includes SEQ ID NO of the encoded protein
sequence, position of the amino acid residue within the protein identified by the SEQ ID
NO that is encoded by the codon containing the SNP, amino acids (represented by one-
letter amino acid codes) that are encoded by the alternative SNP alleles (in the case of
stop codons, "X" is used for the one-letter amino acid code), and alternative codons
10 containing the alternative SNP nucleotides which encode the amino acid residues (thus,
for example, for missense mutation-type SNPs, at least two different amino acids and at
least two different codons are generally indicated; for silent mutation-type SNPs, one
amino acid and at least two different codons are generally indicated, etc.). In instances
where the SNP is located outside of a protein-coding region (e.g., in a UTR region),
15 "None" is indicated following the protein SEQ ID NO.

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DESCRIPTION OF TABLE 3

Table 3 provides sequences (SEQ ID NOS: 207-266) of primers that have been synthesized and used in the laboratory to carry out allele-specific PCR reactions in order to assay the SNPs disclosed in Tables 4-13 during the course of association studies to verify the association of these SNPs with cardiovascular disorders (particularly acute coronary events such as myocardial infarction and stroke) and statin response.

Table 3 provides the following:

- the column labeled "Marker" provides an hCV identification number for each SNP site
- the column labeled "Alleles" designates the two alternative alleles at the SNP site identified by the hCV identification number that are targeted by the allele-specific primers (the allele-specific primers are shown as "Sequence A" and "Sequence B")
[NOTE: Alleles may be presented in Table 3 based on a different orientation (i.e., the reverse complement) relative to how the same alleles are presented in Tables 1-2].
- the column labeled "Sequence A (allele-specific primer)" provides an allele-specific primer that is specific for an allele designated in the "Alleles" column
- the column labeled "Sequence B (allele-specific primer)" provides an allele-specific primer that is specific for the other allele designated in the "Alleles" column
- the column labeled "Sequence C (common primer)" provides a common primer that is used in conjunction with each of the allele-specific primers (the "Sequence A" primer and the "Sequence B" primer) and which hybridizes at a site away from the SNP position.

All primer sequences are given in the 5' to 3' direction.

Each of the nucleotides designated in the "Alleles" column matches or is the reverse complement of (depending on the orientation of the primer relative to the designated allele) the 3' nucleotide of the allele-specific primer (either "Sequence A" or "Sequence B") that is specific for that allele.

DESCRIPTION OF TABLES 4-13

Tables 4-13 provide results of statistical analyses for SNPs disclosed in Tables 1-2 (SNPs can be cross-referenced between tables based on their hCV identification numbers), and the association of these SNPs with various cardiovascular disease clinical

endpoints or drug response traits. The statistical results shown in Tables 4-13 provide support for the association of these SNPs with cardiovascular disorders, particularly acute coronary events such as myocardial infarction and stroke, and/or the association of these SNPs with response to statin treatment, such as statin treatment administered as a preventive treatment for acute coronary events. For example, the statistical results provided in Tables 4-13 show that the association of these SNPs with acute coronary events and/or response to statin treatment is supported by p-values < 0.05 in an allelic association test.

Table 4 presents statistical associations of SNPs with various trial endpoints. Table 5 presents statistical associations of SNPs with clinical variables such as lab tests at base line and at the end of a trial. Table 6 presents statistical associations of SNPs with cardiovascular endpoints prevention (SNPs predictive of response to statins as a preventive treatment). Table 7 shows the association of SNPs with adverse coronary events such as RMI and stroke in CARE samples. This association of certain SNPs with adverse coronary events could also be replicated by comparing associations in samples between initial analysis and replication (see example section). Table 8 shows association of SNPs predictive of statin response with cardiovascular events prevention under statin treatment, justified by stepwise logistic regression analysis with an adjustment for conventional risk factors such as age, sex, smoking status, baseline glucose levels, body mass index (BMI), history of hypertension, etc. (this adjustment supports independence of the SNP association from conventional risk factors). The statistical results provided in Table 9 demonstrate association of a SNP in the CD6 gene that is predictive of statin response in the prevention of RMI, justified as a significant difference in risk associated with the SNP between placebo and Statin treated strata (Breslow Day p-values < 0.05). Table 9 presents the results observed in samples taken from both the CARE and WOSCOP studies. In both studies the individuals homozygous for the minor allele were statistically different from heterozygous and major allele homozygous individuals in the pravastatin treated group vs. the placebo treated group. Table 10 shows the association of a SNP in the FCAR gene that is predictive of MI risk and response to statin treatment. Individuals who participated in both the CARE and WOSCOPS studies, who did not receive pravastatin treatment and who were

heterozygous or homozygous for the major allele had a significantly higher risk of having an MI vs. individuals who were homozygous for the minor allele. However, individuals in the CARE study who were heterozygous or homozygous for the FCAR major allele were also statistically significantly protected by pravastatin treatment against an adverse coronary event relative to the individuals homozygous for the minor allele.

NOTE: SNPs can be cross-referenced between all tables herein based on the hCV identification number of each SNP.

Table 4 column heading	Definition
Public	Locus Link HUGO approved gene symbol for the gene that contains the tested SNP
Marker	Internal hCV identification number for the tested SNP
Stratum	Subpopulation used for analysis
Phenotype	Disease endpoints (definitions of entries in this column are provided below)
Overall* Chi-square Test: statistic/ p-value	Result of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype (based on placebo patients only)

SNP effect** Chi-square Test: statistic/ p-value	Result of the chi-square test of the SNP effect (based on the logistic regression model for placebo patients only)
Placebo Patients n/total(%) 0 Rare Alleles	"n" is the number of placebo patients with no rare alleles genotype for investigated phenotype. The "total" is the total number of placebo patients with this genotype, and "%" is the percentage of placebo patients with this genotype.
Placebo Patients n/total(%) 1 Rare Allele	"n" is the number of placebo patients with one rare allele genotype for investigated phenotype. The "total" is the total number of placebo patients with this genotype, and "%" is the percentage of placebo patients with this genotype.
Placebo Patients n/total(%) 2 Rare Alleles	"n" is the number of placebo patients with two rare alleles genotype for investigated phenotype. The "total" is the total number of placebo patients with this genotype, and "%" is the percentage of placebo patients with this genotype.
Odd Ratio (95%CI) 2 Rare Alleles vs. 0 Rare Alleles	"Odds ratio" indicates the odds of having this phenotype given that genotype contains two rare alleles of a SNP versus the odds of having this phenotype given a genotype containing no rare alleles. "95%CI" is the 95% confidence interval.
Odd Ratio (95%CI) 1 Rare Alleles vs. 0 Rare Alleles	"Odds ratio" indicates the odds of having this phenotype given that genotype contains one rare allele versus the odds of having this phenotype given a genotype containing no rare alleles. "95%CI" is the 95% confidence interval
Significance Level	"Significance Level" indicates the summary of the result of the "Overall Score Test (chi-square test)" for the logistic regression model and the result of the "chi-square test of the SNP effect". If both p-values are less than 0.05, "<0.05" is indicated. If both p-values are less than 0.005, "<0.005" is indicated.
Table 5 column heading	Definition
Public	Locus Link HUGO approved gene symbol for the gene that contains the tested SNP
Marker	Internal hCV identification number for the tested SNP
Stratum	Subpopulation used for analysis
Phenotype (at Baseline)	Clinical quantitative variables - lab test results at baseline or change from baseline discharge (definitions of entries in this

	column are provided below)
Overall* F-Test: statistic/ p-value	Results of the Overall F-Test for the analysis of variance model in which the quantitative phenotype is a function of SNP genotype (based on placebo patients only)
SNP effect** F-Test: statistic/ p-value	Results of the F-test of the SNP effect (based on the analysis of variance model for placebo patients only)
Placebo Patients Mean (se)# (N) 0 Rare Alleles	"n" is the number of placebo patients with a tested SNP genotype (zero rare alleles) and presented phenotype. "Mean" is the least squares estimate of the mean phenotype result for placebo patients with this genotype. "se" is the least squares estimate of the standard error of the mean phenotype for placebo patients with 0 rare allele genotype
Placebo Patients Mean (se)# (N) 1 Rare Allele	"n" is the number of placebo patients with a tested SNP genotype (one rare allele) and presented phenotype. Mean is the least squares estimate of the mean phenotype result for placebo patients with this genotype. se is the least squares estimate of the standard error of the mean phenotype for placebo patients 1 rare allele genotype
Placebo Patients Mean (se)# (N) 2 Rare Alleles	"n" is the number of placebo patients with a tested SNP genotype (one rare allele) and presented phenotype. Mean is the least squares estimate of the mean phenotype result for placebo patients with this genotype. se is the least squares estimate of the standard error of the mean phenotype for placebo patients 2 rare alleles genotype
Significance Level	"Significance Level" indicates the summary of the result of the "Overall F-Test" for the analysis of variance model and the result of the "F-test of the SNP effect". If both p-values are less than 0.05, "<0.05" is indicated. If both p-values are less than 0.005, "<0.005" is indicated.
Table 6 column heading	Definition
Public	Locus Link HUGO approved gene symbol for the gene that contains the tested SNP
Marker	Internal hCV identification number for the tested SNP
Stratum	Subpopulation used for analysis

Phenotype	Disease endpoints (definitions of entries in this column are provided below)
Overall* Chi-square Test: statistic/ p-value	Results of the Overall Score Test (chi-square test) for the regression model in which the qualitative phenotype is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group
Interaction Effect** Chi-square Test: statistic/ p-value	Results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).
0 Rare Alleles n/total (%) Prava	Results for patients under pravastatin treatment. "n" is the number of pravastatin patients with no rare allele genotype and the investigated phenotype. The "total" is the total number of pravastatin patients with this genotype. "%" is the percentage of pravastatin patients with this genotype who had the investigated phenotype.
0 Rare Alleles n/total (%) Placebo	Results for patients under placebo. "n" is the number of placebo patients with no rare allele genotype and investigated phenotype. "Total" is the total number of placebo patients with the genotype. "%" is the percentage of placebo patients with no rare allele genotype and the investigated phenotype.
1 Rare Allele n/total (%) Prava	Results for patients under pravastatin treatment. "n" is the number of patients under pravastatin with one rare allele genotype and the investigated phenotype. The "total" is the total number of pravastatin patients with the genotype. "%" is the percentage of pravastatin patients with one rare allele genotype and the investigated phenotype.
1 Rare Allele n/total (%) Placebo	Results for patients on placebo. "n" is the number of placebo patients with one rare allele genotype and the investigated phenotype. The "total" is the total number of pravastatin patients with the genotype. "%" is the percentage of pravastatin patients with one rare allele genotype and the investigated phenotype.
2 Rare Alleles n/total (%) Prava	Results for patients under pravastatin treatment. "n" is the number of patients under pravastatin with two rare allele genotype and the investigated phenotype. The "total" is the total number of pravastatin patients with the genotype. "%" is the percentage of pravastatin patients with two rare allele genotypes and the investigated phenotype

2 Rare Alleles n/total (%) Placebo	Results for patients on placebo. "n" is the number of placebo patients with two rare allele genotype and the investigated phenotype. The "total" is the total number of pravastatin patients with the genotype. "%" is the percentage of pravastatin patients with two rare allele genotypes and the investigated phenotype
Prava vs Placebo Odds Ratio (95%CI) 0 Rare Alleles	Odds ratio and its 95% confidence interval for patients with no rare allele genotype, the odd ratios of having the event given pravastatin use versus the odds of having the event on placebo
Prava vs Placebo Odds Ratio (95%CI) 1 Rare Allele	Odds ratio and its 95% confidence interval for patients with one rare allele genotype, the odd ratios of having the event given pravastatin use versus the odds of having the event on placebo
Prava vs Placebo Odds Ratio (95%CI) 2 Rare Alleles	Odds ratio and its 95% confidence interval for patients with two rare alleles genotype, the odd ratio of having the event given pravastatin use versus the odds of having the event on placebo
Significance Level	"Significance Level" indicates the summary of the result of the "Overall Score Test (chi-square test)" for the regression model and the result of the "chi-square test of the interaction". If both p-values are less than 0.05, "<0.05" is indicated. If both p-values are less than 0.005, "<0.005" is indicated.

Table 7 column heading	Definition
Endpoint	Endpoint measured in study
Public	Locus Link HUGO approved gene symbol for the gene that contains the tested SNP
Marker	Internal hCV identification number for the SNP that is tested
Genotype/mode	Effect seen in major homozygous ("Maj. Hom"), minor homozygous ("Min Hom") or heterozygous (Het)/recessive ("Rec") or dominant ("Dom")
Strata	Indicates whether the analysis of the dataset has been stratified by genotypes, such as major homozygote ("Maj Hom"), minor homozygote ("Min Hom"), and heterozygote ("Het")

Confounders	Variables that change the marker risk estimates by $\geq 5\%$
P risk est.	Significance of risk estimated by Wald Test
RR	Relative risk
95%CI	95% confidence interval for relative risk
case	Number of patients (with the corresponding genotype or mode) developed recurrent MI or Stroke during 5 years follow up
Case AF (%)	The allele frequency of patients (with the corresponding genotype or mode) that developed recurrent MI during 6 years follow up
Control	Number of patients (with the corresponding genotype or mode) that had MI
Control AF (%)	The allele frequency of patients (with the corresponding genotype or mode) that had MI
Analysis 1	Statistics are based on initial analysis (see examples).
Analysis 2	Statistics are based on replication analysis (see examples)
Table 8	See Table footnotes and Examples section
Table 9	See Table footnotes and Examples section
Table 10	See Table footnotes and Examples section
Table 11	See Table footnotes and Examples section
Table 12	See Table footnotes and Examples section
Table 13	See Table footnotes and Examples section

Definition of entries in the “Phenotype” column of Table 4:

Phenotype
Definite Nonfatal MI
Fatal CHD/Definite Nonfatal MI
CARE MI: Q-Wave MI
MI (Fatal/Nonfatal)
Fatal Coronary Heart Disease
Total Mortality
Cardiovascular Mortality
Fatal Atherosclerotic Cardiovascular Disease
History of Diabetes
Stroke
Percutaneous Transluminal Coronary Angioplasty
Hosp. for Cardiovascular Disease
Fatal/Nonfatal Cerebrovascular Disease
Hosp. for Unstable Angina
Total Cardiovascular Disease Events
Any Report of Stroke Prior to or During CARE
Any Report of Stroke During CARE
1st Stroke Occurred During CARE
Fatal/Nonfatal MI (def & prob)
History of Congestive Heart Failure (AE)
Nonfatal MI (Probable/Definite)
Nonfatal MI (def & prob)
Fatal/Nonfatal Atherosclerotic CV Disease
Coronary Artery Bypass Graft
Coronary Artery Bypass or Revascularization
Congestive Heart Failure
Hosp. for Peripheral Arterial Disease
History of Coronary Artery Bypass Graft
CARE MI: Non Q-Wave MI
Fatal MI
History of Percutaneous Transluminal Coronary Angioplasty
Catheterization
Total Coronary Heart Disease Events
History of Angina Pectoris
More Than 1 Prior MI
Family History of CV Disease
History of Hypertension
History of Stroke

Definition of entries in the “Phenotype (at Baseline)” column of Table 5:

Phenotype (at Baseline)
Change from Baseline In Urinary Glucose (at LOCF)
Change from Baseline In Urinary Glucose (at LOCF)
Baseline HDL
Baseline Lymphocytes, Absolute (k/cumm)
Baseline HDL

Definition of entries in the "Phenotype" column of Table 6:

Phenotype
Catheterization
Nonfatal MI (Probable/Definite)
Nonfatal MI (def & prob)
Family History of CV Disease
MI (Fatal/Nonfatal)
Definite Nonfatal MI
Fatal/Nonfatal MI (def & prob)
Fatal Coronary Heart Disease
Total Mortality
Total Coronary Heart Disease Events
Cardiovascular Mortality
Fatal Atherosclerotic Cardiovascular Disease
Fatal/Nonfatal Atherosclerotic CV Disease
Hosp. for Cardiovascular Disease
Total Cardiovascular Disease Events
History of Angina Pectoris
Fatal CHD/Definite Nonfatal MI
Coronary Artery Bypass or Revascularization
Coronary Artery Bypass Graft
Hospitalization for Unstable Angina
Percutaneous Transluminal Coronary Angioplasty
Fatal/Nonfatal Cerebrovascular Disease
Stroke

DESCRIPTION OF THE FIGURE

- 5 Figure 1 provides a diagrammatic representation of a computer-based discovery system containing the SNP information of the present invention in computer readable form.

DETAILED DESCRIPTION OF THE INVENTION

- 10 The present invention provides SNPs associated with cardiovascular disorders, particularly acute coronary events such as myocardial infarction and stroke (including

recurrent acute coronary events such as recurrent myocardial infarction), and SNPs that are associated with an individual's responsiveness to therapeutic agents, particularly lipid-lowering compounds such as statins, that are used for the treatment (including preventive treatment) of cardiovascular disorders, particularly treatment of acute coronary events. The present invention further provides nucleic acid molecules containing these SNPs, methods and reagents for the detection of the SNPs disclosed herein, uses of these SNPs for the development of detection reagents, and assays or kits that utilize such reagents. The acute coronary event-associated SNPs and statin response-associated SNPs disclosed herein are useful for diagnosing, screening for, and evaluating an individual's increased or decreased risk of developing cardiovascular disease as well as their responsiveness to drug treatment. Furthermore, such SNPs and their encoded products are useful targets for the development of therapeutic agents.

A large number of SNPs have been identified from re-sequencing DNA from 39 individuals, and they are indicated as "Applera" SNP source in Tables 1-2. Their allele frequencies observed in each of the Caucasian and African-American ethnic groups are provided. Additional SNPs included herein were previously identified during shotgun sequencing and assembly of the human genome, and they are indicated as "Celera" SNP source in Tables 1-2. Furthermore, the information provided in Table 1-2, particularly the allele frequency information obtained from 39 individuals and the identification of the precise position of each SNP within each gene/transcript, allows haplotypes (i.e., groups of SNPs that are co-inherited) to be readily inferred. The present invention encompasses SNP haplotypes, as well as individual SNPs.

Thus, the present invention provides individual SNPs associated with cardiovascular disorders, particularly acute coronary events, and SNPs associated with responsiveness to statin for the treatment of cardiovascular diseases, as well as combinations of SNPs and haplotypes in genetic regions associated with cardiovascular disorders and/or statin response, polymorphic/variant transcript sequences (SEQ ID NOS: 2-55) and genomic sequences (SEQ ID NOS: 167-185) containing SNPs, encoded amino acid sequences (SEQ ID NOS: 56-109), and both transcript-based SNP context sequences (SEQ ID NOS: 110-116) and genomic-based SNP context sequences (SEQ ID NOS: 167-185) (transcript sequences, protein sequences, and

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transcript-based SNP context sequences are provided in Table 1 and the Sequence Listing; genomic sequences and genomic-based SNP context sequences are provided in Table 2 and the Sequence Listing), methods of detecting these polymorphisms in a test sample, methods of determining the risk of an individual of having or developing a cardiovascular disorder such as an acute coronary event, methods of determining response to statin treatment of cardiovascular disease, methods of screening for compounds useful for treating cardiovascular disease, compounds identified by these screening methods, methods of using the disclosed SNPs to select a treatment strategy, methods of treating a disorder associated with a variant gene/protein (i.e., therapeutic methods), and methods of using the SNPs of the present invention for human identification.

Since cardiovascular disorders/diseases share certain similar features that may be due to common genetic factors that are involved in their underlying mechanisms, the SNPs identified herein as being particularly associated with acute coronary events and/or statin response may be used as diagnostic/prognostic markers or therapeutic targets for a broad spectrum of cardiovascular diseases such as coronary heart disease (CHD), atherosclerosis, cerebrovascular disease, congestive heart failure, congenital heart disease, and pathologies and symptoms associated with various heart diseases (e.g., angina, hypertension), as well as for predicting responses to drugs other than statins that are used to treat cardiovascular diseases.

The present invention further provides methods for selecting or formulating a treatment regimen (e.g., methods for determining whether or not to administer statin treatment to an individual having cardiovascular disease, methods for selecting a particular statin-based treatment regimen such as dosage and frequency of administration of statin, or a particular form/type of statin such as a particular pharmaceutical formulation or compound, methods for administering an alternative, non-statin-based treatment to individuals who are predicted to be unlikely to respond positively to statin treatment, etc.), and methods for determining the likelihood of experiencing toxicity or other undesirable side effects from statin treatment, etc. The present invention also provides methods for selecting individuals to whom a statin or other therapeutic will be administered based on the individual's genotype, and methods for selecting individuals for

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a clinical trial of a statin or other therapeutic agent based on the genotypes of the individuals (e.g., selecting individuals to participate in the trial who are most likely to respond positively from the statin treatment).

5 The present invention provides novel SNPs associated with cardiovascular disorders and/or response to statin treatment, as well as SNPs that were previously known in the art, but were not previously known to be associated with cardiovascular disorders and/or statin response. Accordingly, the present invention provides novel compositions and methods based on the novel SNPs disclosed herein, and also provides novel methods of using the known, but previously unassociated, SNPs in methods relating to evaluating
10 an individual's likelihood of having or developing a cardiovascular disorder, predicting the likelihood of an individual experiencing a reoccurrence of a cardiovascular disorder (e.g., experiencing recurrent myocardial infarctions), prognosing the severity of a cardiovascular disorder in an individual, or prognosing an individual's recovery from a cardiovascular disorder, and methods relating to evaluating an individual's likelihood of
15 responding to statin treatment for cardiovascular disease. In Tables 1-2, known SNPs are identified based on the public database in which they have been observed, which is indicated as one or more of the following SNP types: "dbSNP" = SNP observed in dbSNP, "HGBASE" = SNP observed in HGBASE, and "HGMD" = SNP observed in the Human Gene Mutation Database (HGMD). Novel SNPs for which the SNP source is
20 only "Applera" and none other, i.e., those that have not been observed in any public databases and which were also not observed during shotgun sequencing and assembly of the Celera human genome sequence (i.e., "Celera" SNP source), are indicated in Tables 3-4.

Particular SNP alleles of the present invention can be associated with either an
25 increased risk of having a cardiovascular disorder (e.g., experiencing an acute coronary event) or of responding to statin treatment of cardiovascular disease, or a decreased likelihood of having a cardiovascular disorder or of responding to statin treatment of cardiovascular disease. Thus, whereas certain SNPs (or their encoded products) can be assayed to determine whether an individual possesses a SNP allele that is indicative of an
30 increased likelihood of experiencing a coronary event or of responding to statin treatment, other SNPs (or their encoded products) can be assayed to determine whether

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an individual possesses a SNP allele that is indicative of a decreased likelihood of experiencing a coronary event or of responding to statin treatment. Similarly, particular SNP alleles of the present invention can be associated with either an increased or decreased likelihood of having a reoccurrence of a cardiovascular disorder, of fully
5 recovering from a cardiovascular disorder, of experiencing toxic effects from a particular treatment or therapeutic compound, etc. The term "altered" may be used herein to encompass either of these two possibilities (e.g., an increased or a decreased risk/likelihood). SNP alleles that are associated with a decreased risk of having or developing a cardiovascular disorder such as myocardial infarction may be referred to as
10 "protective" alleles, and SNP alleles that are associated with an increased risk of having or developing a cardiovascular disorder may be referred to as "susceptibility" alleles, "risk" alleles, or "risk factors".

Those skilled in the art will readily recognize that nucleic acid molecules may be double-stranded molecules and that reference to a particular site on one strand refers, as
15 well, to the corresponding site on a complementary strand. In defining a SNP position, SNP allele, or nucleotide sequence, reference to an adenine, a thymine (uridine), a cytosine, or a guanine at a particular site on one strand of a nucleic acid molecule also defines the thymine (uridine), adenine, guanine, or cytosine (respectively) at the corresponding site on a complementary strand of the nucleic acid molecule. Thus,
20 reference may be made to either strand in order to refer to a particular SNP position, SNP allele, or nucleotide sequence. Probes and primers, may be designed to hybridize to either strand and SNP genotyping methods disclosed herein may generally target either strand. Throughout the specification, in identifying a SNP position, reference is generally made to the protein-encoding strand, only for the purpose of convenience.

25 References to variant peptides, polypeptides, or proteins of the present invention include peptides, polypeptides, proteins, or fragments thereof, that contain at least one amino acid residue that differs from the corresponding amino acid sequence of the art-known peptide/polypeptide/protein (the art-known protein may be interchangeably referred to as the "wild-type", "reference", or "normal" protein). Such variant
30 peptides/polypeptides/proteins can result from a codon change caused by a nonsynonymous nucleotide substitution at a protein-coding SNP position (i.e., a missense

mutation) disclosed by the present invention. Variant peptides/polypeptides/proteins of the present invention can also result from a nonsense mutation, i.e. a SNP that creates a premature stop codon, a SNP that generates a read-through mutation by abolishing a stop codon, or due to any SNP disclosed by the present invention that otherwise alters the structure, function/activity, or expression of a protein, such as a SNP in a regulatory region (e.g. a promoter or enhancer) or a SNP that leads to alternative or defective splicing, such as a SNP in an intron or a SNP at an exon/intron boundary. As used herein, the terms "polypeptide", "peptide", and "protein" are used interchangeably.

ISOLATED NUCLEIC ACID MOLECULES AND SNP DETECTION REAGENTS & KITS

Tables 1 and 2 provide a variety of information about each SNP of the present invention that is associated with cardiovascular disorders (e.g., acute coronary events such as myocardial infarction and stroke) and/or responsiveness to statin treatment, including the transcript sequences (SEQ ID NOS: 2-55), genomic sequences (SEQ ID NOS: 167-185), and protein sequences (SEQ ID NOS: 56-109) of the encoded gene products (with the SNPs indicated by IUB codes in the nucleic acid sequences). In addition, Tables 1 and 2 include SNP context sequences, which generally include 100 nucleotide upstream (5') plus 100 nucleotides downstream (3') of each SNP position (SEQ ID NOS: 110-116 correspond to transcript-based SNP context sequences disclosed in Table 1, and SEQ ID NOS: 186-206 & 267 correspond to genomic-based context sequences disclosed in Table 2), the alternative nucleotides (alleles) at each SNP position, and additional information about the variant where relevant, such as SNP type (coding, missense, splice site, UTR, etc.), human populations in which the SNP was observed, observed allele frequencies, information about the encoded protein, etc.

Isolated Nucleic Acid Molecules

The present invention provides isolated nucleic acid molecules that contain one or more SNPs disclosed Table 1 and/or Table 2.

Isolated nucleic acid molecules containing one or more SNPs disclosed in at least one of Tables 1-2 may be

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interchangeably referred to throughout the present text as "SNP-containing nucleic acid molecules". Isolated nucleic acid molecules may optionally encode a full-length variant protein or fragment thereof. The isolated nucleic acid molecules of the present invention also include probes and primers (which are described in greater detail below in the section entitled "SNP Detection Reagents"), which may be used for assaying the disclosed SNPs, and isolated full-length genes, transcripts, cDNA molecules, and fragments thereof, which may be used for such purposes as expressing an encoded protein.

As used herein, an "isolated nucleic acid molecule" generally is one that contains a SNP of the present invention or one that hybridizes to such molecule such as a nucleic acid with a complementary sequence, and is separated from most other nucleic acids present in the natural source of the nucleic acid molecule. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule containing a SNP of the present invention, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. A nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered "isolated". Nucleic acid molecules present in non-human transgenic animals, which do not naturally occur in the animal, are also considered "isolated". For example, recombinant DNA molecules contained in a vector are considered "isolated". Further examples of "isolated" DNA molecules include recombinant DNA molecules maintained in heterologous host cells, and purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include in vivo or in vitro RNA transcripts of the isolated SNP-containing DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

Generally, an isolated SNP-containing nucleic acid molecule comprises one or more SNP positions disclosed by the present invention with flanking nucleotide sequences on either side of the SNP positions. A flanking sequence can include nucleotide residues that are naturally associated with the SNP site and/or heterologous nucleotide sequences. Preferably the flanking sequence is up to about 500, 300, 100, 60, 50, 30, 25, 20, 15, 10, 8, or 4 nucleotides (or any other length in-between) on either side of a SNP position, or as long

as the full-length gene or entire protein-coding sequence (or any portion thereof such as an exon), especially if the SNP-containing nucleic acid molecule is to be used to produce a protein or protein fragment.

For full-length genes and entire protein-coding sequences, a SNP flanking sequence
5 can be, for example, up to about 5KB, 4KB, 3KB, 2KB, 1KB on either side of the SNP.
Furthermore, in such instances, the isolated nucleic acid molecule comprises exonic
sequences (including protein-coding and/or non-coding exonic sequences), but may also
include intronic sequences. Thus, any protein coding sequence may be either contiguous or
separated by introns. The important point is that the nucleic acid is isolated from remote and
10 unimportant flanking sequences and is of appropriate length such that it can be subjected to
the specific manipulations or uses described herein such as recombinant protein expression,
preparation of probes and primers for assaying the SNP position, and other uses specific to
the SNP-containing nucleic acid sequences.

An isolated SNP-containing nucleic acid molecule can comprise, for example, a full-
15 length gene or transcript, such as a gene isolated from genomic DNA (e.g., by cloning or
PCR amplification), a cDNA molecule, or an mRNA transcript molecule. Polymorphic
transcript sequences are provided in Table 1 and in the Sequence Listing (SEQ ID NOS: 2-
55), and polymorphic genomic sequences are provided in Table 2 and in the Sequence
Listing (SEQ ID NOS: 167-185). Furthermore, fragments of such full-length genes
20 and transcripts that contain one or more SNPs disclosed herein are also encompassed by the
present invention, and such fragments may be used, for example, to express any part of a
protein, such as a particular functional domain or an antigenic epitope.

Thus, the present invention also encompasses fragments of the nucleic acid
sequences provided in Tables 1-2 (transcript sequences are provided in Table 1 as SEQ ID
25 NOS: 2-55, genomic sequences are provided in Table 2 as SEQ ID NOS: 167-185,
transcript-based SNP context sequences are provided in Table 1 as SEQ ID NO: 110-116,
and genomic-based SNP context sequences are provided in Table 2 as SEQ ID
NO: 186-206 & 267) and their complements. A fragment typically comprises a contiguous
nucleotide sequence at least about 8 or more nucleotides, more preferably at least about 12
30 or more nucleotides, and even more preferably at least about 16 or more nucleotides.
Further, a fragment could comprise at least about 18, 20, 22, 25, 30, 40, 50, 60, 80, 100, 150,

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200, 250 or 500 (or any other number in-between) nucleotides in length. The length of the fragment will be based on its intended use. For example, the fragment can encode epitope-bearing regions of a variant peptide or regions of a variant peptide that differ from the normal/wild-type protein, or can be useful as a polynucleotide probe or primer. Such fragments can be isolated using the nucleotide sequences provided in Table 1 and/or Table 2 for the synthesis of a polynucleotide probe. A labeled probe can then be used, for example, to screen a cDNA library, genomic DNA library, or mRNA to isolate nucleic acid corresponding to the coding region. Further, primers can be used in amplification reactions, such as for purposes of assaying one or more SNPs sites or for cloning specific regions of a gene.

An isolated nucleic acid molecule of the present invention further encompasses a SNP-containing polynucleotide that is the product of any one of a variety of nucleic acid amplification methods, which are used to increase the copy numbers of a polynucleotide of interest in a nucleic acid sample. Such amplification methods are well known in the art, and they include but are not limited to, polymerase chain reaction (PCR) (U.S. Patent Nos. 4,683,195; and 4,683,202; *PCR Technology: Principles and Applications for DNA Amplification*, ed. H.A. Erlich, Freeman Press, NY, NY, 1992), ligase chain reaction (LCR) (Wu and Wallace, *Genomics* 4:560, 1989; Landegren *et al.*, *Science* 241:1077, 1988), strand displacement amplification (SDA) (U.S. Patent Nos. 5,270,184; and 5,422,252), transcription-mediated amplification (TMA) (U.S. Patent No. 5,399,491), linked linear amplification (LLA) (U.S. Patent No. 6,027,923), and the like, and isothermal amplification methods such as nucleic acid sequence based amplification (NASBA), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Natl. Acad. Sci. USA* 87: 1874, 1990). Based on such methodologies, a person skilled in the art can readily design primers in any suitable regions 5' and 3' to a SNP disclosed herein. Such primers may be used to amplify DNA of any length so long that it contains the SNP of interest in its sequence.

As used herein, an "amplified polynucleotide" of the invention is a SNP-containing nucleic acid molecule whose amount has been increased at least two fold by any nucleic acid amplification method performed *in vitro* as compared to its starting amount in a test sample. In other preferred embodiments, an amplified polynucleotide is

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the result of at least ten fold, fifty fold, one hundred fold, one thousand fold, or even ten thousand fold increase as compared to its starting amount in a test sample. In a typical PCR amplification, a polynucleotide of interest is often amplified at least fifty thousand fold in amount over the unamplified genomic DNA, but the precise amount of
5 amplification needed for an assay depends on the sensitivity of the subsequent detection method used.

Generally, an amplified polynucleotide is at least about 16 nucleotides in length. More typically, an amplified polynucleotide is at least about 20 nucleotides in length. In a preferred embodiment of the invention, an amplified polynucleotide is at least about 30
10 nucleotides in length. In a more preferred embodiment of the invention, an amplified polynucleotide is at least about 32, 40, 45, 50; or 60 nucleotides in length. In yet another preferred embodiment of the invention, an amplified polynucleotide is at least about 100, 200, 300, 400, or 500 nucleotides in length. While the total length of an amplified polynucleotide of the invention can be as long as an exon, an intron or the entire gene,
15 where the SNP of interest resides, an amplified product is typically up to about 1,000 nucleotides in length (although certain amplification methods may generate amplified products greater than 1000 nucleotides in length). More preferably, an amplified polynucleotide is not greater than about 600-700 nucleotides in length. It is understood that irrespective of the length of an amplified polynucleotide, a SNP of interest may be
20 located anywhere along its sequence.

In a specific embodiment of the invention, the amplified product is at least about 201 nucleotides in length, comprises one of the transcript-based context sequences or the genomic-based context sequences shown in Tables 1-2. Such a product may have
additional sequences on its 5' end or 3' end or both. In another embodiment, the
25 amplified product is about 101 nucleotides in length, and it contains a SNP disclosed herein. Preferably, the SNP is located at the middle of the amplified product (e.g., at position 101 in an amplified product that is 201 nucleotides in length, or at position 51 in an amplified product that is 101 nucleotides in length), or within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, or 20 nucleotides from the middle of the amplified product (however, as
30 indicated above, the SNP of interest may be located anywhere along the length of the amplified product).

The present invention provides isolated nucleic acid molecules that comprise, consist of, or consist essentially of one or more polynucleotide sequences that contain one or more SNPs disclosed herein, complements thereof, and SNP-containing fragments thereof.

Accordingly, the present invention provides nucleic acid molecules that consist of
5 any of the nucleotide sequences shown in Table 1 and/or Table 2 (transcript sequences are provided in Table 1 as SEQ ID NOS: 2-55, genomic sequences are provided in Table 2 as SEQ ID NOS: 167-185, transcript-based SNP context sequences are provided in Table 1 as SEQ ID NO: 110-116, and genomic-based SNP context sequences are provided in Table 2 as SEQ ID NO: 186-206 & 267), or any nucleic acid molecule that encodes any of
10 the variant proteins provided in Table 1 (SEQ ID NOS: 56-109). A nucleic acid molecule consists of a nucleotide sequence when the nucleotide sequence is the complete nucleotide sequence of the nucleic acid molecule.

The present invention further provides nucleic acid molecules that consist essentially of any of the nucleotide sequences shown in Table 1 and/or Table 2 (transcript sequences
15 are provided in Table 1 as SEQ ID NOS: 2-55, genomic sequences are provided in Table 2 as SEQ ID NOS: 167-185, transcript-based SNP context sequences are provided in Table 1 as SEQ ID NO: 110-116, and genomic-based SNP context sequences are provided in Table 2 as SEQ ID NO: 186-206 & 267), or any nucleic acid molecule that encodes any of the variant proteins provided in Table 1 (SEQ ID NOS: 56-109). A
20 nucleic acid molecule consists essentially of a nucleotide sequence when such a nucleotide sequence is present with only a few additional nucleotide residues in the final nucleic acid molecule.

The present invention further provides nucleic acid molecules that comprise any of the nucleotide sequences shown in Table 1 and/or Table 2 or a SNP-containing fragment
25 thereof (transcript sequences are provided in Table 1 as SEQ ID NOS: 2-55, genomic sequences are provided in Table 2 as SEQ ID NOS: 167-185, transcript-based SNP context sequences are provided in Table 1 as SEQ ID NO: 110-116, and genomic-based SNP context sequences are provided in Table 2 as SEQ ID NO: 186-206 & 267), or any nucleic acid molecule that encodes any of the variant proteins provided in Table 1 (SEQ ID
30 NOS: 56-109). A nucleic acid molecule comprises a nucleotide sequence when the nucleotide sequence is at least part of the final nucleotide sequence of the nucleic acid

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molecule. In such a fashion, the nucleic acid molecule can be only the nucleotide sequence or have additional nucleotide residues, such as residues that are naturally associated with it or heterologous nucleotide sequences. Such a nucleic acid molecule can have one to a few additional nucleotides or can comprise many more additional nucleotides. A brief
5 description of how various types of these nucleic acid molecules can be readily made and isolated is provided below, and such techniques are well known to those of ordinary skill in the art (Sambrook and Russell, 2000, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, NY).

The isolated nucleic acid molecules can encode mature proteins plus additional
10 amino or carboxyl-terminal amino acids or both, or amino acids interior to the mature peptide (when the mature form has more than one peptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, facilitate protein trafficking, prolong or shorten protein half-life, or facilitate manipulation of a protein for assay or production. As generally is the case *in situ*, the additional amino acids
15 may be processed away from the mature protein by cellular enzymes.

Thus, the isolated nucleic acid molecules include, but are not limited to, nucleic acid molecules having a sequence encoding a peptide alone, a sequence encoding a mature peptide and additional coding sequences such as a leader or secretory sequence (e.g., a pre-pro or pro-protein sequence), a sequence encoding a mature peptide with or without
20 additional coding sequences, plus additional non-coding sequences, for example introns and non-coding 5' and 3' sequences such as transcribed but untranslated sequences that play a role in, for example, transcription, mRNA processing (including splicing and polyadenylation signals), ribosome binding, and/or stability of mRNA. In addition, the nucleic acid molecules may be fused to heterologous marker sequences encoding, for
25 example, a peptide that facilitates purification.

Isolated nucleic acid molecules can be in the form of RNA, such as mRNA, or in the form DNA, including cDNA and genomic DNA, which may be obtained, for example, by molecular cloning or produced by chemical synthetic techniques or by a combination thereof (Sambrook and Russell, 2000, Molecular Cloning: A Laboratory
30 Manual, Cold Spring Harbor Press, NY). Furthermore, isolated nucleic acid molecules, particularly SNP detection reagents such as probes and primers, can also be partially or

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completely in the form of one or more types of nucleic acid analogs, such as peptide nucleic acid (PNA) (U.S. Patent Nos. 5,539,082; 5,527,675; 5,623,049; 5,714,331). The nucleic acid, especially DNA, can be double-stranded or single-stranded. Single-stranded nucleic acid can be the coding strand (sense strand) or the complementary non-coding strand (anti-sense strand). DNA, RNA, or PNA segments can be assembled, for example, from fragments of the human genome (in the case of DNA or RNA) or single nucleotides, short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic nucleic acid molecule. Nucleic acid molecules can be readily synthesized using the sequences provided herein as a reference; oligonucleotide and PNA oligomer synthesis techniques are well known in the art (see, e.g., Corey, "Peptide nucleic acids: expanding the scope of nucleic acid recognition", *Trends Biotechnol.* 1997 Jun;15(6):224-9; and Hyrup et al., "Peptide nucleic acids (PNA): synthesis, properties and potential applications", *Bioorg Med Chem.* 1996 Jan;4(1):5-23). Furthermore, large-scale automated oligonucleotide/PNA synthesis (including synthesis on an array or bead surface or other solid support) can readily be accomplished using commercially available nucleic acid synthesizers, such as the Applied Biosystems (Foster City, CA) 3900 High-Throughput DNA Synthesizer or Expedite 8909 Nucleic Acid Synthesis System, and the sequence information provided herein..

The present invention encompasses nucleic acid analogs that contain modified, synthetic, or non-naturally occurring nucleotides or structural elements or other alternative/modified nucleic acid chemistries known in the art. Such nucleic acid analogs are useful, for example, as detection reagents (e.g., primers/probes) for detecting one or more SNPs identified in Table 1 and/or Table 2. Furthermore, kits/systems (such as beads, arrays, etc.) that include these analogs are also encompassed by the present invention. For example, PNA oligomers that are based on the polymorphic sequences of the present invention are specifically contemplated. PNA oligomers are analogs of DNA in which the phosphate backbone is replaced with a peptide-like backbone (Lagriffoul *et al.*, *Bioorganic & Medicinal Chemistry Letters*, 4: 1081-1082 (1994), Petersen *et al.*, *Bioorganic & Medicinal Chemistry Letters*, 6: 793-796 (1996), Kumar *et al.*, *Organic Letters* 3(9): 1269-1272 (2001), WO96/04000). PNA hybridizes to complementary RNA or DNA with higher affinity and specificity than conventional oligonucleotides and

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oligonucleotide analogs. The properties of PNA enable novel molecular biology and biochemistry applications unachievable with traditional oligonucleotides and peptides.

Additional examples of nucleic acid modifications that improve the binding properties and/or stability of a nucleic acid include the use of base analogs such as inosine, intercalators (U.S. Patent No. 4,835,263) and the minor groove binders (U.S. Patent No. 5,801,115). Thus, references herein to nucleic acid molecules, SNP-containing nucleic acid molecules, SNP detection reagents (e.g., probes and primers), oligonucleotides/polynucleotides include PNA oligomers and other nucleic acid analogs. Other examples of nucleic acid analogs and alternative/modified nucleic acid chemistries known in the art are described in *Current Protocols in Nucleic Acid Chemistry*, John Wiley & Sons, N.Y. (2002).

The present invention further provides nucleic acid molecules that encode fragments of the variant polypeptides disclosed herein as well as nucleic acid molecules that encode obvious variants of such variant polypeptides. Such nucleic acid molecules may be naturally occurring, such as paralogs (different locus) and orthologs (different organism), or may be constructed by recombinant DNA methods or by chemical synthesis. Non-naturally occurring variants may be made by mutagenesis techniques; including those applied to nucleic acid molecules, cells, or organisms. Accordingly, the variants can contain nucleotide substitutions, deletions, inversions and insertions (in addition to the SNPs disclosed in Tables 1-2). Variation can occur in either or both the coding and non-coding regions. The variations can produce conservative and/or non-conservative amino acid substitutions.

Further variants of the nucleic acid molecules disclosed in Tables 1-2, such as naturally occurring allelic variants (as well as orthologs and paralogs) and synthetic variants produced by mutagenesis techniques, can be identified and/or produced using methods well known in the art. Such further variants can comprise a nucleotide sequence that shares at least 70-80%, 80-85%, 85-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with a nucleic acid sequence disclosed in Table 1 and/or Table 2 (or a fragment thereof) and that includes a novel SNP allele disclosed in Table 1 and/or Table 2. Further, variants can comprise a nucleotide sequence that encodes a polypeptide that shares at least 70-80%, 80-85%, 85-90%, 91%, 92%, 93%, 94%, 95%,

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96%, 97%, 98%, or 99% sequence identity with a polypeptide sequence disclosed in Table 1 (or a fragment thereof) and that includes a novel SNP allele disclosed in Table 1 and/or Table 2. Thus, an aspect of the present invention that is specifically contemplated are isolated nucleic acid molecules that have a certain degree of sequence variation compared with the sequences shown in Tables 1-2, but that contain a novel SNP allele disclosed herein. In other words, as long as an isolated nucleic acid molecule contains a novel SNP allele disclosed herein, other portions of the nucleic acid molecule that flank the novel SNP allele can vary to some degree from the specific transcript, genomic, and context sequences shown in Tables 1-2, and can encode a polypeptide that varies to some degree from the specific polypeptide sequences shown in Table 1.

To determine the percent identity of two amino acid sequences or two nucleotide sequences of two molecules that share sequence homology, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% or more of the length of a reference sequence is aligned for comparison purposes. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein, amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von

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Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch algorithm (*J. Mol. Biol.* (48):444-453 (1970)) which has been incorporated
5 into the GAP program in the GCG software package, using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package
10 (Devereux, J., *et al.*, *Nucleic Acids Res.* 12(1):387 (1984)), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11-
17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a
15 PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4.

The nucleotide and amino acid sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (*J.*
20 *Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped
25 alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. In addition to BLAST, examples of other search and sequence comparison programs used in the art include, but are not limited to, FASTA
30 (Pearson, *Methods Mol. Biol.* 25, 365-389 (1994)) and KERR (Dufresne *et al.*, *Nat*

Biotechnol 2002 Dec;20(12):1269-71). For further information regarding bioinformatics techniques, see *Current Protocols in Bioinformatics*, John Wiley & Sons, Inc., N.Y.

The present invention further provides non-coding fragments of the nucleic acid molecules disclosed in Table 1 and/or Table 2. Preferred non-coding fragments include, but are not limited to, promoter sequences, enhancer sequences, intronic sequences, 5' untranslated regions (UTRs), 3' untranslated regions, gene modulating sequences and gene termination sequences. Such fragments are useful, for example, in controlling heterologous gene expression and in developing screens to identify gene-modulating agents.

SNP Detection Reagents

In a specific aspect of the present invention, the SNPs disclosed in Table 1 and/or Table 2, and their associated transcript sequences (provided in Table 1 as SEQ ID NOS: 2-55), genomic sequences (provided in Table 2 as SEQ ID NOS: 167-185), and context sequences (transcript-based context sequences are provided in Table 1 as SEQ ID NOS: 110-116; genomic-based context sequences are provided in Table 2 as SEQ ID NOS: 186-206 & 267), can be used for the design of SNP detection reagents. As used herein, a "SNP detection reagent" is a reagent that specifically detects a specific target SNP position disclosed herein, and that is preferably specific for a particular nucleotide (allele) of the target SNP position (i.e., the detection reagent preferably can differentiate between different alternative nucleotides at a target SNP position, thereby allowing the identity of the nucleotide present at the target SNP position to be determined). Typically, such detection reagent hybridizes to a target SNP-containing nucleic acid molecule by complementary base-pairing in a sequence specific manner, and discriminates the target variant sequence from other nucleic acid sequences such as an art-known form in a test sample. An example of a detection reagent is a probe that hybridizes to a target nucleic acid containing one or more of the SNPs provided in Table 1 and/or Table 2. In a preferred embodiment, such a probe can differentiate between nucleic acids having a particular nucleotide (allele) at a target SNP position from other nucleic acids that have a different nucleotide at the same target SNP position. In addition, a detection reagent may hybridize to a specific region 5' and/or 3' to a SNP position, particularly a region corresponding to the context sequences

provided in Table 1 and/or Table 2 (transcript-based context sequences are provided in Table 1 as SEQ ID NOS: 110-116 ; genomic-based context sequences are provided in Table 2 as SEQ ID NOS: 186-206 & 267). Another example of a detection reagent is a primer which acts as an initiation point of nucleotide extension along a complementary strand of a target polynucleotide. The SNP sequence information provided herein is also useful for designing primers, e.g. allele-specific primers, to amplify (e.g., using PCR) any SNP of the present invention.

In one preferred embodiment of the invention, a SNP detection reagent is an isolated or synthetic DNA or RNA polynucleotide probe or primer or PNA oligomer, or a combination of DNA, RNA and/or PNA, that hybridizes to a segment of a target nucleic acid molecule containing a SNP identified in Table 1 and/or Table 2. A detection reagent in the form of a polynucleotide may optionally contain modified base analogs, intercalators or minor groove binders. Multiple detection reagents such as probes may be, for example, affixed to a solid support (e.g., arrays or beads) or supplied in solution (e.g., probe/primer sets for enzymatic reactions such as PCR, RT-PCR, TaqMan assays, or primer-extension reactions) to form a SNP detection kit.

A probe or primer typically is a substantially purified oligonucleotide or PNA oligomer. Such oligonucleotide typically comprises a region of complementary nucleotide sequence that hybridizes under stringent conditions to at least about 8, 10, 12, 16, 18, 20, 22, 25, 30, 40, 50, 55, 60, 65, 70, 80, 90, 100, 120 (or any other number in-between) or more consecutive nucleotides in a target nucleic acid molecule. Depending on the particular assay, the consecutive nucleotides can either include the target SNP position, or be a specific region in close enough proximity 5' and/or 3' to the SNP position to carry out the desired assay.

Other preferred primer and probe sequences can readily be determined using the transcript sequences (SEQ ID NOS: 2-55), genomic sequences (SEQ ID NOS: 167-185), and SNP context sequences (transcript-based context sequences are provided in Table 1 as SEQ ID NOS: 110-116 ; genomic-based context sequences are provided in Table 2 as SEQ ID NOS: 186-206 & 267) disclosed in the Sequence Listing and in Tables 1-2. It will be apparent to one of skill in the art that such primers and probes are directly

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useful as reagents for genotyping the SNPs of the present invention, and can be incorporated into any kit/system format.

In order to produce a probe or primer specific for a target SNP-containing sequence, the gene/transcript and/or context sequence surrounding the SNP of interest is typically examined using a computer algorithm which starts at the 5' or at the 3' end of the nucleotide sequence. Typical algorithms will then identify oligomers of defined length that are unique to the gene/SNP context sequence, have a GC content within a range suitable for hybridization, lack predicted secondary structure that may interfere with hybridization, and/or possess other desired characteristics or that lack other undesired characteristics.

A primer or probe of the present invention is typically at least about 8 nucleotides in length. In one embodiment of the invention, a primer or a probe is at least about 10 nucleotides in length. In a preferred embodiment, a primer or a probe is at least about 12 nucleotides in length. In a more preferred embodiment, a primer or probe is at least about 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides in length. While the maximal length of a probe can be as long as the target sequence to be detected, depending on the type of assay in which it is employed, it is typically less than about 50, 60, 65, or 70 nucleotides in length. In the case of a primer, it is typically less than about 30 nucleotides in length. In a specific preferred embodiment of the invention, a primer or a probe is within the length of about 18 and about 28 nucleotides. However, in other embodiments, such as nucleic acid arrays and other embodiments in which probes are affixed to a substrate, the probes can be longer, such as on the order of 30-70, 75, 80, 90, 100, or more nucleotides in length (see the section below entitled "SNP Detection Kits and Systems").

For analyzing SNPs, it may be appropriate to use oligonucleotides specific for alternative SNP alleles. Such oligonucleotides which detect single nucleotide variations in target sequences may be referred to by such terms as "allele-specific oligonucleotides", "allele-specific probes", or "allele-specific primers". The design and use of allele-specific probes for analyzing polymorphisms is described in, e.g., *Mutation Detection A Practical Approach*, ed. Cotton *et al.* Oxford University Press, 1998; Saiki *et al.*, *Nature* 324, 163-166 (1986); Dattagupta, EP235,726; and Saiki, WO 89/11548.

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While the design of each allele-specific primer or probe depends on variables such as the precise composition of the nucleotide sequences flanking a SNP position in a target nucleic acid molecule, and the length of the primer or probe, another factor in the use of primers and probes is the stringency of the condition under which the hybridization
5 between the probe or primer and the target sequence is performed. Higher stringency conditions utilize buffers with lower ionic strength and/or a higher reaction temperature, and tend to require a more perfect match between probe/primer and a target sequence in order to form a stable duplex. If the stringency is too high, however, hybridization may not occur at all. In contrast, lower stringency conditions utilize buffers with higher ionic
10 strength and/or a lower reaction temperature, and permit the formation of stable duplexes with more mismatched bases between a probe/primer and a target sequence. By way of example and not limitation, exemplary conditions for high stringency hybridization conditions using an allele-specific probe are as follows: Prehybridization with a solution containing 5X standard saline phosphate EDTA (SSPE); 0.5% NaDodSO₄ (SDS) at 55°C,
15 and incubating probe with target nucleic acid molecules in the same solution at the same temperature, followed by washing with a solution containing 2X SSPE, and 0.1% SDS at 55°C or room temperature.

Moderate stringency hybridization conditions may be used for allele-specific primer extension reactions with a solution containing, e.g., about 50mM KCl at about
20 46°C. Alternatively, the reaction may be carried out at an elevated temperature such as 60°C. In another embodiment, a moderately stringent hybridization condition suitable for oligonucleotide ligation assay (OLA) reactions wherein two probes are ligated if they are completely complementary to the target sequence may utilize a solution of about 100mM KCl at a temperature of 46°C.

25 In a hybridization-based assay, allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms (e.g., alternative SNP alleles/nucleotides) in the respective DNA segments from the two individuals. Hybridization conditions should be sufficiently
30 stringent that there is a significant detectable difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles or significantly more strongly to one allele. While a probe may be designed to hybridize to a target sequence that contains a SNP site such that the SNP site aligns anywhere along the sequence of the probe, the probe is preferably designed to hybridize to a segment of the target sequence such that the SNP site aligns
5 with a central position of the probe (e.g., a position within the probe that is at least three nucleotides from either end of the probe). This design of probe generally achieves good discrimination in hybridization between different allelic forms.

In another embodiment, a probe or primer may be designed to hybridize to a segment of target DNA such that the SNP aligns with either the 5' most end or the 3'
10 most end of the probe or primer. In a specific preferred embodiment that is particularly suitable for use in a oligonucleotide ligation assay (U.S. Patent No. 4,988,617), the 3' most nucleotide of the probe aligns with the SNP position in the target sequence.

Oligonucleotide probes and primers may be prepared by methods well known in the art. Chemical synthetic methods include, but are limited to, the phosphotriester
15 method described by Narang *et al.*, 1979, *Methods in Enzymology* 68:90; the phosphodiester method described by Brown *et al.*, 1979, *Methods in Enzymology* 68:109, the diethylphosphoamidate method described by Beaucage *et al.*, 1981, *Tetrahedron Letters* 22:1859; and the solid support method described in U.S. Patent No. 4,458,066.

20 Allele-specific probes are often used in pairs (or, less commonly, in sets of 3 or 4, such as if a SNP position is known to have 3 or 4 alleles, respectively, or to assay both strands of a nucleic acid molecule for a target SNP allele), and such pairs may be identical except for a one nucleotide mismatch that represents the allelic variants at the SNP position. Commonly, one member of a pair perfectly matches a reference form of a target sequence
25 that has a more common SNP allele (i.e., the allele that is more frequent in the target population) and the other member of the pair perfectly matches a form of the target sequence that has a less common SNP allele (i.e., the allele that is rarer in the target population). In the case of an array, multiple pairs of probes can be immobilized on the same support for simultaneous analysis of multiple different polymorphisms.

30 In one type of PCR-based assay, an allele-specific primer hybridizes to a region on a target nucleic acid molecule that overlaps a SNP position and only primes

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amplification of an allelic form to which the primer exhibits perfect complementarity (Gibbs, 1989, *Nucleic Acid Res.* 17 2427-2448). Typically, the primer's 3'-most nucleotide is aligned with and complementary to the SNP position of the target nucleic acid molecule. This primer is used in conjunction with a second primer that hybridizes at a distal site. Amplification proceeds from the two primers, producing a detectable product that indicates which allelic form is present in the test sample. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification or substantially reduces amplification efficiency, so that either no detectable product is formed or it is formed in lower amounts or at a slower pace. The method generally works most effectively when the mismatch is at the 3'-most position of the oligonucleotide (i.e., the 3'-most position of the oligonucleotide aligns with the target SNP position) because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456). This PCR-based assay can be utilized as part of the TaqMan assay, described below.

In a specific embodiment of the invention, a primer of the invention contains a sequence substantially complementary to a segment of a target SNP-containing nucleic acid molecule except that the primer has a mismatched nucleotide in one of the three nucleotide positions at the 3'-most end of the primer, such that the mismatched nucleotide does not base pair with a particular allele at the SNP site. In a preferred embodiment, the mismatched nucleotide in the primer is the second from the last nucleotide at the 3'-most position of the primer. In a more preferred embodiment, the mismatched nucleotide in the primer is the last nucleotide at the 3'-most position of the primer.

In another embodiment of the invention, a SNP detection reagent of the invention is labeled with a fluorogenic reporter dye that emits a detectable signal. While the preferred reporter dye is a fluorescent dye, any reporter dye that can be attached to a detection reagent such as an oligonucleotide probe or primer is suitable for use in the invention. Such dyes include, but are not limited to, Acridine, AMCA, BODIPY, Cascade Blue, Cy2, Cy3, Cy5, Cy7, Dabcyl, Edans, Eosin, Erythrosin, Fluorescein, 6-Fam, Tet, Joe, Hex, Oregon Green, Rhodamine, Rhodol Green, Tamra, Rox, and Texas Red.

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In yet another embodiment of the invention, the detection reagent may be further labeled with a quencher dye such as Tamra, especially when the reagent is used as a self-quenching probe such as a TaqMan (U.S. Patent Nos. 5,210,015 and 5,538,848) or Molecular Beacon probe (U.S. Patent Nos. 5,118,801 and 5,312,728), or other stemless or
5 linear beacon probe (Livak *et al.*, 1995, PCR Method Appl. 4:357-362; Tyagi *et al.*, 1996, Nature Biotechnology 14: 303-308; Nazarenko *et al.*, 1997, Nucl. Acids Res. 25:2516-2521; U.S. Patent Nos. 5,866,336 and 6,117,635).

The detection reagents of the invention may also contain other labels, including but not limited to, biotin for streptavidin binding, hapten for antibody binding, and
10 oligonucleotide for binding to another complementary oligonucleotide such as pairs of zipcodes.

The present invention also contemplates reagents that do not contain (or that are complementary to) a SNP nucleotide identified herein but that are used to assay one or more SNPs disclosed herein. For example, primers that flank, but do not hybridize
15 directly to a target SNP position provided herein are useful in primer extension reactions in which the primers hybridize to a region adjacent to the target SNP position (i.e., within one or more nucleotides from the target SNP site). During the primer extension reaction, a primer is typically not able to extend past a target SNP site if a particular nucleotide (allele) is present at that target SNP site, and the primer extension product can be detected
20 in order to determine which SNP allele is present at the target SNP site. For example, particular ddNTPs are typically used in the primer extension reaction to terminate primer extension once a ddNTP is incorporated into the extension product (a primer extension product which includes a ddNTP at the 3'-most end of the primer extension product, and in which the ddNTP is a nucleotide of a SNP disclosed herein, is a composition that is
25 specifically contemplated by the present invention). Thus, reagents that bind to a nucleic acid molecule in a region adjacent to a SNP site and that are used for assaying the SNP site, even though the bound sequences do not necessarily include the SNP site itself, are also contemplated by the present invention.

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SNP Detection Kits and Systems

A person skilled in the art will recognize that, based on the SNP and associated sequence information disclosed herein, detection reagents can be developed and used to assay any SNP of the present invention individually or in combination, and such detection reagents can be readily incorporated into one of the established kit or system formats which are well known in the art. The terms "kits" and "systems", as used herein in the context of SNP detection reagents, are intended to refer to such things as combinations of multiple SNP detection reagents, or one or more SNP detection reagents in combination with one or more other types of elements or components (e.g., other types of biochemical reagents, containers, packages such as packaging intended for commercial sale, substrates to which SNP detection reagents are attached, electronic hardware components, etc.). Accordingly, the present invention further provides SNP detection kits and systems, including but not limited to, packaged probe and primer sets (e.g., TaqMan probe/primer sets), arrays/microarrays of nucleic acid molecules, and beads that contain one or more probes, primers, or other detection reagents for detecting one or more SNPs of the present invention. The kits/systems can optionally include various electronic hardware components; for example, arrays ("DNA chips") and microfluidic systems ("lab-on-a-chip" systems) provided by various manufacturers typically comprise hardware components. Other kits/systems (e.g., probe/primer sets) may not include electronic hardware components, but may be comprised of, for example, one or more SNP detection reagents (along with, optionally, other biochemical reagents) packaged in one or more containers.

In some embodiments, a SNP detection kit typically contains one or more detection reagents and other components (e.g., a buffer, enzymes such as DNA polymerases or ligases, chain extension nucleotides such as deoxynucleotide triphosphates, and in the case of Sanger-type DNA sequencing reactions, chain terminating nucleotides, positive control sequences, negative control sequences, and the like) necessary to carry out an assay or reaction, such as amplification and/or detection of a SNP-containing nucleic acid molecule. A kit may further contain means for determining the amount of a target nucleic acid, and means for comparing the amount

with a standard, and can comprise instructions for using the kit to detect the SNP-containing nucleic acid molecule of interest. In one embodiment of the present invention, kits are provided which contain the necessary reagents to carry out one or more assays to detect one or more SNPs disclosed herein. In a preferred embodiment of the present invention, SNP
 5 detection kits/systems are in the form of nucleic acid arrays, or compartmentalized kits, including microfluidic/lab-on-a-chip systems.

SNP detection kits/systems may contain, for example, one or more probes, or pairs of probes, that hybridize to a nucleic acid molecule at or near each target SNP position. Multiple pairs of allele-specific probes may be included in the kit/system to simultaneously assay large
 10 numbers of SNPs, at least one of which is a SNP of the present invention. In some kits/systems, the allele-specific probes are immobilized to a substrate such as an array or bead. For example, the same substrate can comprise allele-specific probes for detecting at least 1; 10; 100; 1000; 10,000; 100,000 (or any other number in-between) or substantially all of the SNPs shown in Table 1 and/or Table 2.

15 The terms "arrays", "microarrays", and "DNA chips" are used herein interchangeably to refer to an array of distinct polynucleotides affixed to a substrate, such as glass, plastic, paper, nylon or other type of membrane, filter, chip, or any other suitable solid support. The polynucleotides can be synthesized directly on the substrate, or synthesized separate from the substrate and then affixed to the substrate. In one embodiment, the microarray is prepared and
 20 used according to the methods described in U.S. Patent No. 5,837,832, Chee et al., PCT application W095/11995 (Chee et al.), Lockhart, D. J. et al. (1996; *Nat. Biotech.* 14: 1675-1680) and Schena, M. et al. (1996; *Proc. Natl. Acad. Sci.* 93: 10614-10619). In other embodiments, such arrays are produced by the methods described by Brown et al., U.S. Patent No. 5,807,522.

25 Nucleic acid arrays are reviewed in the following references: Zammattéo et al., "New chips for molecular biology and diagnostics", *Biotechnol Annu Rev.* 2002;8:85-101; Sosnowski et al., "Active microelectronic array system for DNA hybridization, genotyping and pharmacogenomic applications", *Psychiatr Genet.* 2002 Dec;12(4):181-92; Heller, "DNA microarray technology: devices, systems, and applications", *Annu Rev Biomed Eng.*
 30 2002;4:129-53. Epub 2002 Mar 22; Kolchinsky et al., "Analysis of SNPs

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and other genomic variations using gel-based chips", *Hum Mutat.* 2002 Apr;19(4):343-60; and McGall et al., "High-density genechip oligonucleotide probe arrays", *Adv Biochem Eng Biotechnol.* 2002;77:21-42.

Any number of probes, such as allele-specific probes, may be implemented in an array, and each probe or pair of probes can hybridize to a different SNP position. In the case of polynucleotide probes, they can be synthesized at designated areas (or synthesized separately and then affixed to designated areas) on a substrate using a light-directed chemical process. Each DNA chip can contain, for example, thousands to millions of individual synthetic polynucleotide probes arranged in a grid-like pattern and miniaturized (e.g., to the size of a dime). Preferably, probes are attached to a solid support in an ordered, addressable array.

A microarray can be composed of a large number of unique, single-stranded polynucleotides, usually either synthetic antisense polynucleotides or fragments of cDNAs, fixed to a solid support. Typical polynucleotides are preferably about 6-60 nucleotides in length, more preferably about 15-30 nucleotides in length, and most preferably about 18-25 nucleotides in length. For certain types of microarrays or other detection kits/systems, it may be preferable to use oligonucleotides that are only about 7-20 nucleotides in length. In other types of arrays, such as arrays used in conjunction with chemiluminescent detection technology, preferred probe lengths can be, for example, about 15-80 nucleotides in length, preferably about 50-70 nucleotides in length, more preferably about 55-65 nucleotides in length, and most preferably about 60 nucleotides in length. The microarray or detection kit can contain polynucleotides that cover the known 5' or 3' sequence of a gene/transcript or target SNP site, sequential polynucleotides that cover the full-length sequence of a gene/transcript; or unique polynucleotides selected from particular areas along the length of a target gene/transcript sequence, particularly areas corresponding to one or more SNPs disclosed in Table 1 and/or Table 2. Polynucleotides used in the microarray or detection kit can be specific to a SNP or SNPs of interest (e.g., specific to a particular SNP allele at a target SNP site, or specific to particular SNP alleles at multiple different SNP sites), or specific to a polymorphic gene/transcript or genes/transcripts of interest.

Hybridization assays based on polynucleotide arrays rely on the differences in hybridization stability of the probes to perfectly matched and mismatched target sequence variants. For SNP genotyping, it is generally preferable that stringency conditions used in hybridization assays are high enough such that nucleic acid molecules that differ from one another at as little as a single SNP position can be differentiated (e.g., typical SNP hybridization assays are designed so that hybridization will occur only if one particular nucleotide is present at a SNP position, but will not occur if an alternative nucleotide is present at that SNP position). Such high stringency conditions may be preferable when using, for example, nucleic acid arrays of allele-specific probes for SNP detection. Such high stringency conditions are described in the preceding section, and are well known to those skilled in the art and can be found in, for example, *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

In other embodiments, the arrays are used in conjunction with chemiluminescent detection technology. The following patents and patent applications provide additional information pertaining to chemiluminescent detection: U.S. patent applications published as US2005/0019778 and US2005/0026161 describe chemiluminescent approaches for microarray detection; U.S. Patent Nos. 6124478, 6107024, 5994073, 5981768, 5871938, 5843681, 5800999, and 5773628 describe methods and compositions of dioxetane for performing chemiluminescent detection; and U.S. published application US2002/0110828 discloses methods and compositions for microarray controls.

In one embodiment of the invention, a nucleic acid array can comprise an array of probes of about 15-25 nucleotides in length. In further embodiments, a nucleic acid array can comprise any number of probes, in which at least one probe is capable of detecting one or more SNPs disclosed in Table 1 and/or Table 2, and/or at least one probe comprises a fragment of one of the sequences selected from the group consisting of those disclosed in Table 1, Table 2, the Sequence Listing, and sequences complementary thereto, said fragment comprising at least about 8 consecutive nucleotides, preferably 10, 12, 15, 16, 18, 20, more preferably 22, 25, 30, 40, 47, 50, 55, 60, 65, 70, 80, 90, 100, or more consecutive nucleotides (or any other number in-between) and containing (or being complementary to) a novel SNP allele disclosed in Table 1 and/or Table 2. In some embodiments, the nucleotide complementary to the SNP

site is within 5, 4, 3, 2, or 1 nucleotide from the center of the probe, more preferably at the center of said probe.

A polynucleotide probe can be synthesized on the surface of the substrate by using a chemical coupling procedure and an ink jet application apparatus, as described in PCT application
5 W095/251116 (Baldeschweiler et al.). In another aspect, a "gridded" array analogous to a dot (or slot) blot may be used to arrange and link cDNA fragments or oligonucleotides to the surface of a substrate using a vacuum system, thermal, UV, mechanical or chemical bonding procedures. An array, such as those described above, may be produced by hand or by using available devices (slot blot or dot blot apparatus), materials (any suitable solid support), and machines (including robotic
10 instruments), and may contain 8, 24, 96, 384, 1536, 6144 or more polynucleotides, or any other number which lends itself to the efficient use of commercially available instrumentation.

Using such arrays or other kits/systems, the present invention provides methods of identifying the SNPs disclosed herein in a test sample. Such methods typically involve incubating a test sample of nucleic acids with an array comprising one or more probes corresponding to at
15 least one SNP position of the present invention, and assaying for binding of a nucleic acid from the test sample with one or more of the probes. Conditions for incubating a SNP detection reagent (or a kit/system that employs one or more such SNP detection reagents) with a test sample vary. Incubation conditions depend on such factors as the format employed in the assay, the detection methods employed, and the type and nature of the detection reagents used in the assay. One
20 skilled in the art will recognize that any one of the commonly available hybridization, amplification and array assay formats can readily be adapted to detect the SNPs disclosed herein.

A SNP detection kit/system of the present invention may include components that are used to prepare nucleic acids from a test sample for the subsequent amplification and/or detection of a SNP-containing nucleic acid molecule. Such sample preparation components
25 can be used to produce nucleic acid extracts (including DNA and/or RNA), proteins or membrane extracts from any bodily fluids (such as blood, serum, plasma, urine, saliva, phlegm, gastric juices, semen, tears, sweat, etc.), skin, hair, cells (especially nucleated cells), biopsies, buccal swabs or tissue specimens. The test samples used in the

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above-described methods will vary based on such factors as the assay format, nature of the detection method, and the specific tissues, cells or extracts used as the test sample to be assayed. Methods of preparing nucleic acids, proteins, and cell extracts are well known in the art and can be readily adapted to obtain a sample that is compatible with the system utilized. Automated sample preparation systems for extracting nucleic acids from a test sample are commercially available, and examples are Qiagen's BioRobot 9600, Applied Biosystems' PRISM 6700, and Roche Molecular Systems' COBAS AmpliPrep System.

Another form of kit contemplated by the present invention is a compartmentalized kit. A compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include, for example, small glass containers, plastic containers, strips of plastic, glass or paper, or arraying material such as silica. Such containers allow one to efficiently transfer reagents from one compartment to another compartment such that the test samples and reagents are not cross-contaminated, or from one container to another vessel not included in the kit, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another or to another vessel. Such containers may include, for example, one or more containers which will accept the test sample, one or more containers which contain at least one probe or other SNP detection reagent for detecting one or more SNPs of the present invention, one or more containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and one or more containers which contain the reagents used to reveal the presence of the bound probe or other SNP detection reagents. The kit can optionally further comprise compartments and/or reagents for, for example, nucleic acid amplification or other enzymatic reactions such as primer extension reactions, hybridization, ligation, electrophoresis (preferably capillary electrophoresis), mass spectrometry, and/or laser-induced fluorescent detection. The kit may also include instructions for using the kit. Exemplary compartmentalized kits include microfluidic devices known in the art (see, e.g., Weigl et al., "Lab-on-a-chip for drug development", *Adv Drug Deliv Rev.* 2003 Feb 24;55(3):349-77). In such microfluidic devices, the containers may be referred to as, for example, microfluidic "compartments", "chambers", or "channels".

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Microfluidic devices, which may also be referred to as "lab-on-a-chip" systems, biomedical micro-electro-mechanical systems (bioMEMs), or multicomponent integrated systems, are exemplary kits/systems of the present invention for analyzing SNPs. Such systems miniaturize and compartmentalize processes such as probe/target hybridization, nucleic acid amplification, and capillary electrophoresis reactions in a single functional device. Such microfluidic devices typically utilize detection reagents in at least one aspect of the system, and such detection reagents may be used to detect one or more SNPs of the present invention. One example of a microfluidic system is disclosed in U.S. Patent No. 5,589,136, which describes the integration of PCR amplification and capillary electrophoresis in chips. Exemplary microfluidic systems comprise a pattern of microchannels designed onto a glass, silicon, quartz, or plastic wafer included on a microchip. The movements of the samples may be controlled by electric, electroosmotic or hydrostatic forces applied across different areas of the microchip to create functional microscopic valves and pumps with no moving parts. Varying the voltage can be used as a means to control the liquid flow at intersections between the micro-machined channels and to change the liquid flow rate for pumping across different sections of the microchip. See, for example, U.S. Patent Nos. 6,153,073, Dubrow *et al.*, and 6,156,181, Parce *et al.*

For genotyping SNPs, an exemplary microfluidic system may integrate, for example, nucleic acid amplification, primer extension, capillary electrophoresis, and a detection method such as laser induced fluorescence detection. In a first step of an exemplary process for using such an exemplary system, nucleic acid samples are amplified, preferably by PCR. Then, the amplification products are subjected to automated primer extension reactions using ddNTPs (specific fluorescence for each ddNTP) and the appropriate oligonucleotide primers to carry out primer extension reactions which hybridize just upstream of the targeted SNP. Once the extension at the 3' end is completed, the primers are separated from the unincorporated fluorescent ddNTPs by capillary electrophoresis. The separation medium used in capillary electrophoresis can be, for example, polyacrylamide, polyethyleneglycol or dextran. The incorporated ddNTPs in the single nucleotide primer extension products are identified by laser-induced fluorescence detection. Such an exemplary microchip can be used to process, for example, at least 96 to 384 samples, or more, in parallel.

USES OF NUCLEIC ACID MOLECULES

The nucleic acid molecules of the present invention have a variety of uses, especially in predicting an individual's risk for developing a cardiovascular disorder (particularly the risk for experiencing a first or recurrent acute coronary event such as a myocardial infarction or stroke), for prognosing the progression of a cardiovascular disorder in an individual (e.g., the severity or consequences of an acute coronary event), in evaluating the likelihood of an individual who has a cardiovascular disorder of responding to treatment of the cardiovascular disorder with statin, and/or predicting the likelihood that the individual will experience toxicity or other undesirable side effects from the statin treatment, etc. For example, the nucleic acid molecules are useful as hybridization probes, such as for genotyping SNPs in messenger RNA, transcript, cDNA, genomic DNA, amplified DNA or other nucleic acid molecules, and for isolating full-length cDNA and genomic clones encoding the variant peptides disclosed in Table 1 as well as their orthologs.

A probe can hybridize to any nucleotide sequence along the entire length of a nucleic acid molecule provided in Table 1 and/or Table 2. Preferably, a probe of the present invention hybridizes to a region of a target sequence that encompasses a SNP position indicated in Table 1 and/or Table 2. More preferably, a probe hybridizes to a SNP-containing target sequence in a sequence-specific manner such that it distinguishes the target sequence from other nucleotide sequences which vary from the target sequence only by which nucleotide is present at the SNP site. Such a probe is particularly useful for detecting the presence of a SNP-containing nucleic acid in a test sample, or for determining which nucleotide (allele) is present at a particular SNP site (i.e., genotyping the SNP site).

A nucleic acid hybridization probe may be used for determining the presence, level, form, and/or distribution of nucleic acid expression. The nucleic acid whose level is determined can be DNA or RNA. Accordingly, probes specific for the SNPs described herein can be used to assess the presence, expression and/or gene copy number in a given cell, tissue, or organism. These uses are relevant for diagnosis of disorders involving an increase or decrease in gene expression relative to normal levels. *In vitro* techniques for detection of mRNA include, for example, Northern blot hybridizations and *in situ* hybridizations. *In vitro* techniques for detecting DNA include Southern blot

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hybridizations and *in situ* hybridizations (Sambrook and Russell, 2000, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, NY).

Probes can be used as part of a diagnostic test kit for identifying cells or tissues in which a variant protein is expressed, such as by measuring the level of a variant protein-
5 encoding nucleic acid (e.g., mRNA) in a sample of cells from a subject or determining if a polynucleotide contains a SNP of interest.

Thus, the nucleic acid molecules of the invention can be used as hybridization probes to detect the SNPs disclosed herein, thereby determining whether an individual with the polymorphisms is likely or unlikely to develop a cardiovascular disorder such as
10 an acute coronary event, or the likelihood that an individual will respond positively to statin treatment of a cardiovascular disorder. Detection of a SNP associated with a disease phenotype provides a diagnostic tool for an active disease and/or genetic predisposition to the disease.

Furthermore, the nucleic acid molecules of the invention are therefore useful for
15 detecting a gene (gene information is disclosed in Table 2, for example) which contains a SNP disclosed herein and/or products of such genes, such as expressed mRNA transcript molecules (transcript information is disclosed in Table 1, for example), and are thus useful for detecting gene expression. The nucleic acid molecules can optionally be implemented in, for example, an array or kit format for use in detecting gene expression.

20 The nucleic acid molecules of the invention are also useful as primers to amplify any given region of a nucleic acid molecule, particularly a region containing a SNP identified in Table 1 and/or Table 2.

The nucleic acid molecules of the invention are also useful for constructing recombinant vectors (described in greater detail below). Such vectors include expression
25 vectors that express a portion of, or all of, any of the variant peptide sequences provided in Table 1. Vectors also include insertion vectors, used to integrate into another nucleic acid molecule sequence, such as into the cellular genome, to alter *in situ* expression of a gene and/or gene product. For example, an endogenous coding sequence can be replaced via homologous recombination with all or part of the coding region containing one or more
30 specifically introduced SNPs.

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The nucleic acid molecules of the invention are also useful for expressing antigenic portions of the variant proteins, particularly antigenic portions that contain a variant amino acid sequence (e.g., an amino acid substitution) caused by a SNP disclosed in Table 1 and/or Table 2.

5 The nucleic acid molecules of the invention are also useful for constructing vectors containing a gene regulatory region of the nucleic acid molecules of the present invention.

The nucleic acid molecules of the invention are also useful for designing ribozymes corresponding to all, or a part, of an mRNA molecule expressed from a SNP-containing nucleic acid molecule described herein.

10 The nucleic acid molecules of the invention are also useful for constructing host cells expressing a part, or all, of the nucleic acid molecules and variant peptides.

The nucleic acid molecules of the invention are also useful for constructing transgenic animals expressing all, or a part, of the nucleic acid molecules and variant peptides. The production of recombinant cells and transgenic animals having nucleic acid molecules which contain the SNPs disclosed in Table 1 and/or Table 2 allow, for example, effective clinical design of treatment compounds and dosage regimens.

The nucleic acid molecules of the invention are also useful in assays for drug screening to identify compounds that, for example, modulate nucleic acid expression.

20 The nucleic acid molecules of the invention are also useful in gene therapy in patients whose cells have aberrant gene expression. Thus, recombinant cells, which include a patient's cells that have been engineered *ex vivo* and returned to the patient, can be introduced into an individual where the recombinant cells produce the desired protein to treat the individual.

25 SNP Genotyping Methods

The process of determining which specific nucleotide (i.e., allele) is present at each of one or more SNP positions, such as a SNP position in a nucleic acid molecule disclosed in Table 1 and/or Table 2, is referred to as SNP genotyping. The present invention provides methods of SNP genotyping, such as for use in evaluating an individual's risk for developing a cardiovascular disease – particularly an acute coronary event (such as myocardial infarction or stroke) and for evaluating an individual's prognosis for disease

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severity and recovery, for predicting the likelihood that an individual who has previously experienced an acute coronary event will experience one or more recurrent acute coronary events, for implementing a preventive or treatment regimen for an individual based on that individual having an increased susceptibility for developing a cardiovascular disorder (e.g.,
 5 increased risk for experiencing one or more myocardial infarctions or strokes), in evaluating an individual's likelihood of responding to statin treatment for cardiovascular disease, in selecting a treatment regimen (e.g., in deciding whether or not to administer statin treatment to an individual having a cardiovascular disease, or in formulating or selecting a particular statin-based treatment regimen such as dosage and/or frequency of administration of statin
 10 treatment or choosing which form/type of statin to be administered such as a particular pharmaceutical composition or compound, etc.), determining the likelihood of experiencing toxicity or other undesirable side effects from the statin treatment, or selecting individuals for a clinical trial of a statin (e.g., selecting individuals to participate in the trial who are most likely to respond positively from the statin treatment), etc.

15 Nucleic acid samples can be genotyped to determine which allele(s) is/are present at any given genetic region (e.g., SNP position) of interest by methods well known in the art. The neighboring sequence can be used to design SNP detection reagents such as oligonucleotide probes, which may optionally be implemented in a kit format. Exemplary
 20 SNP genotyping methods are described in Chen et al., "Single nucleotide polymorphism genotyping: biochemistry, protocol, cost and throughput", *Pharmacogenomics J.* 2003;3(2):77-96; Kwok et al., "Detection of single nucleotide polymorphisms", *Curr Issues Mol Biol.* 2003 Apr;5(2):43-60; Shi, "Technologies for individual genotyping: detection of genetic polymorphisms in drug targets and disease genes", *Am J Pharmacogenomics.* 2002;2(3):197-205; and Kwok, "Methods for genotyping single nucleotide polymorphisms",
 25 *Annu Rev Genomics Hum Genet* 2001;2:235-58. Exemplary techniques for high-throughput SNP genotyping are described in Marnellos, "High-throughput SNP analysis for genetic association studies", *Curr Opin Drug Discov Devel.* 2003 May;6(3):317-21. Common SNP genotyping methods include, but are not limited to, TaqMan assays, molecular beacon assays, nucleic acid arrays, allele-specific primer extension, allele-specific PCR, arrayed
 30 primer extension, homogeneous primer extension assays, primer extension with detection by mass spectrometry, pyrosequencing, multiplex primer extension sorted on genetic arrays,

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ligation with rolling circle amplification, homogeneous ligation, OLA (U.S. Patent No. 4,988,167), multiplex ligation reaction sorted on genetic arrays, restriction-fragment length polymorphism, single base extension-tag assays, and the Invader assay. Such methods may be used in combination with detection mechanisms such as, for example, luminescence or
5 chemiluminescence detection, fluorescence detection, time-resolved fluorescence detection, fluorescence resonance energy transfer, fluorescence polarization, mass spectrometry, and electrical detection.

Various methods for detecting polymorphisms include, but are not limited to, methods in which protection from cleavage agents is used to detect mismatched bases in
10 RNA/RNA or RNA/DNA duplexes (Myers *et al.*, *Science* 230:1242 (1985); Cotton *et al.*, *PNAS* 85:4397 (1988); and Saleeba *et al.*, *Meth. Enzymol.* 217:286-295 (1992)), comparison of the electrophoretic mobility of variant and wild type nucleic acid molecules (Orita *et al.*, *PNAS* 86:2766 (1989); Cotton *et al.*, *Mutat. Res.* 285:125-144 (1993); and Hayashi *et al.*, *Genet. Anal. Tech. Appl.* 9:73-79 (1992)), and assaying the movement of polymorphic or
15 wild-type fragments in polyacrylamide gels containing a gradient of denaturant using denaturing gradient gel electrophoresis (DGGE) (Myers *et al.*, *Nature* 313:495 (1985)). Sequence variations at specific locations can also be assessed by nuclease protection assays such as RNase and S1 protection or chemical cleavage methods.

In a preferred embodiment, SNP genotyping is performed using the TaqMan
20 assay, which is also known as the 5' nuclease assay (U.S. Patent Nos. 5,210,015 and 5,538,848). The TaqMan assay detects the accumulation of a specific amplified product during PCR. The TaqMan assay utilizes an oligonucleotide probe labeled with a fluorescent reporter dye and a quencher dye. The reporter dye is excited by irradiation at an appropriate wavelength, it transfers energy to the quencher dye in the same probe via a
25 process called fluorescence resonance energy transfer (FRET). When attached to the probe, the excited reporter dye does not emit a signal. The proximity of the quencher dye to the reporter dye in the intact probe maintains a reduced fluorescence for the reporter. The reporter dye and quencher dye may be at the 5' most and the 3' most ends, respectively, or vice versa. Alternatively, the reporter dye may be at the 5' or 3' most
30 end while the quencher dye is attached to an internal nucleotide, or vice versa. In yet another embodiment, both the reporter and the quencher may be attached to internal

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nucleotides at a distance from each other such that fluorescence of the reporter is reduced.

During PCR, the 5' nuclease activity of DNA polymerase cleaves the probe, thereby separating the reporter dye and the quencher dye and resulting in increased fluorescence of the reporter. Accumulation of PCR product is detected directly by monitoring the increase in fluorescence of the reporter dye. The DNA polymerase cleaves the probe between the reporter dye and the quencher dye only if the probe hybridizes to the target SNP-containing template which is amplified during PCR, and the probe is designed to hybridize to the target SNP site only if a particular SNP allele is present.

Preferred TaqMan primer and probe sequences can readily be determined using the SNP and associated nucleic acid sequence information provided herein. A number of computer programs, such as Primer Express (Applied Biosystems, Foster City, CA); can be used to rapidly obtain optimal primer/probe sets. It will be apparent to one of skill in the art that such primers and probes for detecting the SNPs of the present invention are useful in screening for individuals who are susceptible to developing a cardiovascular disorder (e.g., an acute coronary event) or in screening individuals who have a cardiovascular disorder for their likelihood of responding to statin treatment. These probes and primers can be readily incorporated into a kit format. The present invention also includes modifications of the Taqman assay well known in the art such as the use of Molecular Beacon probes (U.S. Patent Nos. 5,118,801 and 5,312,728) and other variant formats (U.S. Patent Nos. 5,866,336 and 6,117,635).

Another preferred method for genotyping the SNPs of the present invention is the use of two oligonucleotide probes in an OLA (see, e.g., U.S. Patent No. 4,988,617). In this method, one probe hybridizes to a segment of a target nucleic acid with its 3' most end aligned with the SNP site. A second probe hybridizes to an adjacent segment of the target nucleic acid molecule directly 3' to the first probe. The two juxtaposed probes hybridize to the target nucleic acid molecule, and are ligated in the presence of a linking agent such as a ligase if there is perfect complementarity between the 3' most nucleotide of the first probe with the SNP site. If there is a mismatch, ligation would not occur.

After the reaction, the ligated probes are separated from the target nucleic acid molecule, and detected as indicators of the presence of a SNP.

The following patents, patent applications, and published international patent applications provide additional information pertaining to techniques for carrying out various types of OLA: U.S. Patent Nos. 6027889, 6268148, 5494810, 5830711, and 6054564 describe OLA strategies for performing SNP detection; WO 97/31256 and WO 00/56927 describe OLA strategies for performing SNP detection using universal arrays, wherein a zipcode sequence can be introduced into one of the hybridization probes, and the resulting product, or amplified product, hybridized to a universal zip code array; WO 01/92579 describes OLA (or LDR) followed by PCR, wherein zipcodes are incorporated into OLA probes, and amplified PCR products are determined by electrophoretic or universal zipcode array readout; U.S. patent applications published as US2005/0053957 and US2006/0141475 describe SNPllex methods and software for multiplexed SNP detection using OLA followed by PCR, wherein zipcodes are incorporated into OLA probes, and amplified PCR products are hybridized with a zipchute reagent, and the identity of the SNP determined from electrophoretic readout of the zipchute. In some embodiments, OLA is carried out prior to PCR (or another method of nucleic acid amplification). In other embodiments, PCR (or another method of nucleic acid amplification) is carried out prior to OLA.

Another method for SNP genotyping is based on mass spectrometry. Mass spectrometry takes advantage of the unique mass of each of the four nucleotides of DNA. SNPs can be unambiguously genotyped by mass spectrometry by measuring the differences in the mass of nucleic acids having alternative SNP alleles. MALDI-TOF (Matrix Assisted Laser Desorption Ionization – Time of Flight) mass spectrometry technology is preferred for extremely precise determinations of molecular mass, such as SNPs. Numerous approaches to SNP analysis have been developed based on mass spectrometry. Preferred mass spectrometry-based methods of SNP genotyping include primer extension assays, which can also be utilized in combination with other approaches, such as traditional gel-based formats and microarrays.

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Typically, the primer extension assay involves designing and annealing a primer to a template PCR amplicon upstream (5') from a target SNP position. A mix of dideoxynucleotide triphosphates (ddNTPs) and/or deoxynucleotide triphosphates (dNTPs) are added to a reaction mixture containing template (e.g., a SNP-containing nucleic acid molecule which has typically been amplified, such as by PCR), primer, and DNA polymerase. Extension of the primer terminates at the first position in the template where a nucleotide complementary to one of the ddNTPs in the mix occurs. The primer can be either immediately adjacent (i.e., the nucleotide at the 3' end of the primer hybridizes to the nucleotide next to the target SNP site) or two or more nucleotides removed from the SNP position. If the primer is several nucleotides removed from the target SNP position, the only limitation is that the template sequence between the 3' end of the primer and the SNP position cannot contain a nucleotide of the same type as the one to be detected, or this will cause premature termination of the extension primer. Alternatively, if all four ddNTPs alone, with no dNTPs, are added to the reaction mixture, the primer will always be extended by only one nucleotide, corresponding to the target SNP position. In this instance, primers are designed to bind one nucleotide upstream from the SNP position (i.e., the nucleotide at the 3' end of the primer hybridizes to the nucleotide that is immediately adjacent to the target SNP site on the 5' side of the target SNP site). Extension by only one nucleotide is preferable, as it minimizes the overall mass of the extended primer, thereby increasing the resolution of mass differences between alternative SNP nucleotides. Furthermore, mass-tagged ddNTPs can be employed in the primer extension reactions in place of unmodified ddNTPs. This increases the mass difference between primers extended with these ddNTPs, thereby providing increased sensitivity and accuracy, and is particularly useful for typing heterozygous base positions. Mass-tagging also alleviates the need for intensive sample-preparation procedures and decreases the necessary resolving power of the mass spectrometer.

The extended primers can then be purified and analyzed by MALDI-TOF mass spectrometry to determine the identity of the nucleotide present at the target SNP position. In one method of analysis, the products from the primer extension reaction are combined with light absorbing crystals that form a matrix. The matrix is then hit with an

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energy source such as a laser to ionize and desorb the nucleic acid molecules into the gas-phase. The ionized molecules are then ejected into a flight tube and accelerated down the tube towards a detector. The time between the ionization event, such as a laser pulse, and collision of the molecule with the detector is the time of flight of that molecule. The time of flight is precisely correlated with the mass-to-charge ratio (m/z) of the ionized molecule. Ions with smaller m/z travel down the tube faster than ions with larger m/z and therefore the lighter ions reach the detector before the heavier ions. The time-of-flight is then converted into a corresponding, and highly precise, m/z . In this manner, SNPs can be identified based on the slight differences in mass, and the corresponding time of flight differences, inherent in nucleic acid molecules having different nucleotides at a single base position. For further information regarding the use of primer extension assays in conjunction with MALDI-TOF mass spectrometry for SNP genotyping, see, e.g., Wise *et al.*, "A standard protocol for single nucleotide primer extension in the human genome using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry", *Rapid Commun Mass Spectrom.* 2003;17(11):1195-202.

The following references provide further information describing mass spectrometry-based methods for SNP genotyping: Bocker, "SNP and mutation discovery using base-specific cleavage and MALDI-TOF mass spectrometry", *Bioinformatics.* 2003 Jul;19 Suppl 1:I44-I53; Storm *et al.*, "MALDI-TOF mass spectrometry-based SNP genotyping", *Methods Mol Biol.* 2003;212:241-62; Jurinke *et al.*, "The use of MassARRAY technology for high throughput genotyping", *Adv Biochem Eng Biotechnol.* 2002;77:57-74; and Jurinke *et al.*, "Automated genotyping using the DNA MassArray technology", *Methods Mol Biol.* 2002;187:179-92.

SNPs can also be scored by direct DNA sequencing. A variety of automated sequencing procedures can be utilized ((1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT International Publication No. WO94/16101; Cohen *et al.*, *Adv. Chromatogr.* 36:127-162 (1996); and Griffin *et al.*, *Appl. Biochem. Biotechnol.* 38:147-159 (1993)). The nucleic acid sequences of the present invention enable one of ordinary skill in the art to readily design sequencing primers for such automated sequencing procedures. Commercial instrumentation, such as the Applied Biosystems

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377, 3100, 3700, 3730, and 3730xl DNA Analyzers (Foster City, CA), is commonly used in the art for automated sequencing.

Other methods that can be used to genotype the SNPs of the present invention include single-strand conformational polymorphism (SSCP), and denaturing gradient gel electrophoresis (DGGE) (Myers *et al.*, *Nature* 313:495 (1985)). SSCP identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita *et al.*, *Proc. Nat. Acad.* Single-stranded PCR products can be generated by heating or otherwise denaturing double stranded PCR products. Single-stranded nucleic acids may refold or form secondary structures that are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products are related to base-sequence differences at SNP positions. DGGE differentiates SNP alleles based on the different sequence-dependent stabilities and melting properties inherent in polymorphic DNA and the corresponding differences in electrophoretic migration patterns in a denaturing gradient gel (Erich, ed., PCR Technology, *Principles and Applications for DNA Amplification*, W.H. Freeman and Co, New York, 1992, Chapter 7).

Sequence-specific ribozymes (U.S. Patent No. 5,498,531) can also be used to score SNPs based on the development or loss of a ribozyme cleavage site. Perfectly matched sequences can be distinguished from mismatched sequences by nuclease cleavage digestion assays or by differences in melting temperature. If the SNP affects a restriction enzyme cleavage site, the SNP can be identified by alterations in restriction enzyme digestion patterns, and the corresponding changes in nucleic acid fragment lengths determined by gel electrophoresis.

SNP genotyping can include the steps of, for example, collecting a biological sample from a human subject (e.g., sample of tissues, cells, fluids, secretions, etc.), isolating nucleic acids (e.g., genomic DNA, mRNA or both) from the cells of the sample, contacting the nucleic acids with one or more primers which specifically hybridize to a region of the isolated nucleic acid containing a target SNP under conditions such that hybridization and amplification of the target nucleic acid region occurs, and determining the nucleotide present at the SNP position of interest, or, in some assays, detecting the presence or absence of an amplification product (assays can be designed so that

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hybridization and/or amplification will only occur if a particular SNP allele is present or absent). In some assays, the size of the amplification product is detected and compared to the length of a control sample; for example, deletions and insertions can be detected by a change in size of the amplified product compared to a normal genotype.

5 SNP genotyping is useful for numerous practical applications, as described below. Examples of such applications include, but are not limited to, SNP-disease association analysis, disease predisposition screening, disease diagnosis, disease prognosis, disease progression monitoring, determining therapeutic strategies based on an individual's genotype ("pharmacogenomics"), developing therapeutic agents based on SNP genotypes
10 associated with a disease or likelihood of responding to a drug, stratifying a patient population for clinical trial for a treatment regimen, predicting the likelihood that an individual will experience toxic side effects from a therapeutic agent, and human identification applications such as forensics.

15 **Analysis of Genetic Association Between SNPs and Phenotypic Traits**

SNP genotyping for disease diagnosis, disease predisposition screening, disease prognosis, determining drug responsiveness (pharmacogenomics), drug toxicity screening, and other uses described herein, typically relies on initially establishing a genetic association between one or more specific SNPs and the particular phenotypic
20 traits of interest.

Different study designs may be used for genetic association studies (*Modern Epidemiology*, Lippincott Williams & Wilkins (1998), 609-622). Observational studies are most frequently carried out in which the response of the patients is not interfered with. The first type of observational study identifies a sample of persons in whom the
25 suspected cause of the disease is present and another sample of persons in whom the suspected cause is absent, and then the frequency of development of disease in the two samples is compared. These sampled populations are called cohorts, and the study is a prospective study. The other type of observational study is case-control or a retrospective study. In typical case-control studies, samples are collected from individuals with the
30 phenotype of interest (cases) such as certain manifestations of a disease, and from individuals without the phenotype (controls) in a population (target population) that

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conclusions are to be drawn from. Then the possible causes of the disease are investigated retrospectively. As the time and costs of collecting samples in case-control studies are considerably less than those for prospective studies, case-control studies are the more commonly used study design in genetic association studies, at least during the exploration and discovery stage.

In both types of observational studies, there may be potential confounding factors that should be taken into consideration. Confounding factors are those that are associated with both the real cause(s) of the disease and the disease itself, and they include demographic information such as age, gender, ethnicity as well as environmental factors. When confounding factors are not matched in cases and controls in a study, and are not controlled properly, spurious association results can arise. If potential confounding factors are identified, they should be controlled for by analysis methods explained below.

In a genetic association study, the cause of interest to be tested is a certain allele or a SNP or a combination of alleles or a haplotype from several SNPs. Thus, tissue specimens (e.g., whole blood) from the sampled individuals may be collected and genomic DNA genotyped for the SNP(s) of interest. In addition to the phenotypic trait of interest, other information such as demographic (e.g., age, gender, ethnicity, etc.), clinical, and environmental information that may influence the outcome of the trait can be collected to further characterize and define the sample set. In many cases, these factors are known to be associated with diseases and/or SNP allele frequencies. There are likely gene-environment and/or gene-gene interactions as well. Analysis methods to address gene-environment and gene-gene interactions (for example, the effects of the presence of both susceptibility alleles at two different genes can be greater than the effects of the individual alleles at two genes combined) are discussed below.

After all the relevant phenotypic and genotypic information has been obtained, statistical analyses are carried out to determine if there is any significant correlation between the presence of an allele or a genotype with the phenotypic characteristics of an individual. Preferably, data inspection and cleaning are first performed before carrying out statistical tests for genetic association. Epidemiological and clinical data of the samples can be summarized by descriptive statistics with tables and graphs. Data validation is preferably performed to check for data completion, inconsistent entries, and

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outliers. Chi-squared tests and t-tests (Wilcoxon rank-sum tests if distributions are not normal) may then be used to check for significant differences between cases and controls for discrete and continuous variables, respectively. To ensure genotyping quality, Hardy-Weinberg disequilibrium tests can be performed on cases and controls separately.

- 5 Significant deviation from Hardy-Weinberg equilibrium (HWE) in both cases and controls for individual markers can be indicative of genotyping errors. If HWE is violated in a majority of markers, it is indicative of population substructure that should be further investigated. Moreover, Hardy-Weinberg disequilibrium in cases only can indicate genetic association of the markers with the disease (*Genetic Data Analysis*, Weir
10 B., Sinauer (1990)).

- To test whether an allele of a single SNP is associated with the case or control status of a phenotypic trait, one skilled in the art can compare allele frequencies in cases and controls. Standard chi-squared tests and Fisher's exact tests can be carried out on a
15 2x2 table (2 SNP alleles x 2 outcomes in the categorical trait of interest). To test whether genotypes of a SNP are associated, chi-squared tests can be carried out on a 3x2 table (3 genotypes x 2 outcomes). Score tests are also carried out for genotypic association to contrast the three genotypic frequencies (major homozygotes, heterozygotes and minor
20 homozygotes) in cases and controls, and to look for trends using 3 different modes of inheritance, namely dominant (with contrast coefficients 2, -1, -1), additive (with contrast coefficients 1, 0, -1) and recessive (with contrast coefficients 1, 1, -2). Odds ratios for minor versus major alleles, and odds ratios for heterozygote and homozygote variants versus the wild type genotypes are calculated with the desired confidence limits, usually 95%.

- In order to control for confounders and to test for interaction and effect modifiers,
25 stratified analyses may be performed using stratified factors that are likely to be confounding, including demographic information such as age, ethnicity, and gender, or an interacting element or effect modifier, such as a known major gene (e.g., APOE for Alzheimer's disease or HLA genes for autoimmune diseases), or environmental factors such as smoking in lung cancer. Stratified association tests may be carried out using
30 Cochran-Mantel-Haenszel tests that take into account the ordinal nature of genotypes with 0, 1, and 2 variant alleles. Exact tests by StatXact may also be performed when

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computationally possible. Another way to adjust for confounding effects and test for interactions is to perform stepwise multiple logistic regression analysis using statistical packages such as SAS or R. Logistic regression is a model-building technique in which the best fitting and most parsimonious model is built to describe the relation between the dichotomous outcome (for instance, getting a certain disease or not) and a set of independent variables (for instance, genotypes of different associated genes, and the associated demographic and environmental factors). The most common model is one in which the logit transformation of the odds ratios is expressed as a linear combination of the variables (main effects) and their cross-product terms (interactions) (Applied Logistic Regression, Hosmer and Lemeshow, Wiley (2000)). To test whether a certain variable or interaction is significantly associated with the outcome, coefficients in the model are first estimated and then tested for statistical significance of their departure from zero.

In addition to performing association tests one marker at a time, haplotype association analysis may also be performed to study a number of markers that are closely linked together. Haplotype association tests can have better power than genotypic or allelic association tests when the tested markers are not the disease-causing mutations themselves but are in linkage disequilibrium with such mutations. The test will even be more powerful if the disease is indeed caused by a combination of alleles on a haplotype (e.g., APOE is a haplotype formed by 2 SNPs that are very close to each other). In order to perform haplotype association effectively, marker-marker linkage disequilibrium measures, both D' and R^2 , are typically calculated for the markers within a gene to elucidate the haplotype structure. Recent studies (Daly et al, *Nature Genetics*, 29, 232-235, 2001) in linkage disequilibrium indicate that SNPs within a gene are organized in block pattern, and a high degree of linkage disequilibrium exists within blocks and very little linkage disequilibrium exists between blocks. Haplotype association with the disease status can be performed using such blocks once they have been elucidated.

Haplotype association tests can be carried out in a similar fashion as the allelic and genotypic association tests. Each haplotype in a gene is analogous to an allele in a multi-allelic marker. One skilled in the art can either compare the haplotype frequencies in cases and controls or test genetic association with different pairs of haplotypes. It has been proposed (Schaid et al, *Am. J. Hum. Genet.*, 70, 425-434, 2002) that score tests can

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be done on haplotypes using the program "haplo.score". In that method, haplotypes are first inferred by EM algorithm and score tests are carried out with a generalized linear model (GLM) framework that allows the adjustment of other factors.

An important decision in the performance of genetic association tests is the determination of the significance level at which significant association can be declared when the p-value of the tests reaches that level. In an exploratory analysis where positive hits will be followed up in subsequent confirmatory testing, an unadjusted p-value < 0.1 (a significance level on the lenient side) may be used for generating hypotheses for significant association of a SNP with certain phenotypic characteristics of a disease. It is preferred that a p-value < 0.05 (a significance level traditionally used in the art) is achieved in order for a SNP to be considered to have an association with a disease. It is more preferred that a p-value < 0.01 (a significance level on the stringent side) is achieved for an association to be declared. When hits are followed up in confirmatory analyses in more samples of the same source or in different samples from different sources, adjustment for multiple testing will be performed as to avoid excess number of hits while maintaining the experiment-wise error rates at 0.05. While there are different methods to adjust for multiple testing to control for different kinds of error rates, a commonly used but rather conservative method is Bonferroni correction to control the experiment-wise or family-wise error rate (*Multiple comparisons and multiple tests*, Westfall et al, SAS Institute (1999)). Permutation tests to control for the false discovery rates, FDR, can be more powerful (Benjamini and Hochberg, Journal of the Royal Statistical Society, Series B 57, 1289-1300, 1995, *Resampling-based Multiple Testing*, Westfall and Young, Wiley (1993)). Such methods to control for multiplicity would be preferred when the tests are dependent and controlling for false discovery rates is sufficient as opposed to controlling for the experiment-wise error rates.

In replication studies using samples from different populations after statistically significant markers have been identified in the exploratory stage, meta-analyses can then be performed by combining evidence of different studies (*Modern Epidemiology*, Lippincott Williams & Wilkins, 1998, 643-673). If available, association results known in the art for the same SNPs can be included in the meta-analyses.

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Since both genotyping and disease status classification can involve errors, sensitivity analyses may be performed to see how odds ratios and p-values would change upon various estimates on genotyping and disease classification error rates.

It has been well known that subpopulation-based sampling bias between cases and controls can lead to spurious results in case-control association studies (Ewens and Spielman, *Am. J. Hum. Genet.* 62, 450-458, 1995) when prevalence of the disease is associated with different subpopulation groups. Such bias can also lead to a loss of statistical power in genetic association studies. To detect population stratification, Pritchard and Rosenberg (Pritchard et al. *Am. J. Hum. Genet.* 1999, 65:220-228) suggested typing markers that are unlinked to the disease and using results of association tests on those markers to determine whether there is any population stratification. When stratification is detected, the genomic control (GC) method as proposed by Devlin and Roeder (Devlin et al. *Biometrics* 1999, 55:997-1004) can be used to adjust for the inflation of test statistics due to population stratification. GC method is robust to changes in population structure levels as well as being applicable to DNA pooling designs (Devlin et al. *Genet. Epidemiol.* 2000, 21:273-284).

While Pritchard's method recommended using 15-20 unlinked microsatellite markers, it suggested using more than 30 biallelic markers to get enough power to detect population stratification. For the GC method, it has been shown (Bacanu et al. *Am. J. Hum. Genet.* 2000, 66:1933-1944) that about 60-70 biallelic markers are sufficient to estimate the inflation factor for the test statistics due to population stratification. Hence, 70 intergenic SNPs can be chosen in unlinked regions as indicated in a genome scan (Kehoe et al. *Hum. Mol. Genet.* 1999, 8:237-245).

Once individual risk factors, genetic or non-genetic, have been found for the predisposition to disease, the next step is to set up a classification/prediction scheme to predict the category (for instance, disease or no-disease) that an individual will be in depending on his genotypes of associated SNPs and other non-genetic risk factors. Logistic regression for discrete trait and linear regression for continuous trait are standard techniques for such tasks (*Applied Regression Analysis*, Draper and Smith, Wiley (1998)). Moreover, other techniques can also be used for setting up classification. Such techniques include, but are not limited to, MART, CART, neural network, and

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discriminant analyses that are suitable for use in comparing the performance of different methods (*The Elements of Statistical Learning*, Hastie, Tibshirani & Friedman, Springer (2002)).

5 Disease Diagnosis and Predisposition Screening

Information on association/correlation between genotypes and disease-related phenotypes can be exploited in several ways. For example, in the case of a highly statistically significant association between one or more SNPs with predisposition to a disease for which treatment is available, detection of such a genotype pattern in an individual may justify immediate administration of treatment, or at least the institution of regular monitoring of the individual. Detection of the susceptibility alleles associated with serious disease in a couple contemplating having children may also be valuable to the couple in their reproductive decisions. In the case of a weaker but still statistically significant association between a SNP and a human disease, immediate therapeutic intervention or monitoring may not be justified after detecting the susceptibility allele or SNP. Nevertheless, the subject can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little or no cost to the individual but would confer potential benefits in reducing the risk of developing conditions for which that individual may have an increased risk by virtue of having the susceptibility allele(s).

20 The SNPs of the invention may contribute to cardiovascular disorders such as acute coronary events, or to responsiveness of an individual to statin treatment, in different ways. Some polymorphisms occur within a protein coding sequence and contribute to disease phenotype by affecting protein structure. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on, for example, replication, transcription, and/or translation. A single SNP may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by multiple SNPs in different genes.

As used herein, the terms “diagnose”, “diagnosis”, and “diagnostics” include, but are not limited to any of the following: detection of a cardiovascular disorders that an individual may presently have, predisposition/susceptibility screening (e.g., determining whether an individual has an increased risk of experiencing an acute coronary event in

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the future, or determining whether an individual has a decreased risk of experiencing an acute coronary event in the future), determining a particular type or subclass of cardiovascular disorder in an individual known to currently have or to have previously experienced a cardiovascular disorder, confirming or reinforcing a previously made
5 diagnosis of a cardiovascular disorder, evaluating an individual's likelihood of responding to statin treatment for cardiovascular disorders, predisposition screening (e.g., evaluating an individual's likelihood of responding to statin treatment if the individual were to develop a cardiovascular disorder in the future), determining a particular type or subclass of responder/non-responder in an individual known to respond or not respond to
10 statin treatment, confirming or reinforcing a previously made classification of an individual as a responder/non-responder to statin treatment, pharmacogenomic evaluation of an individual to determine which therapeutic strategy that individual is most likely to positively respond to or to predict whether a patient is likely to respond to a particular treatment such as statin treatment, predicting whether a patient is likely to experience
15 toxic effects from a particular treatment or therapeutic compound, and evaluating the future prognosis of an individual having a cardiovascular disorder. Such diagnostic uses are based on the SNPs individually or in a unique combination or SNP haplotypes of the present invention.

Haplotypes are particularly useful in that, for example, fewer SNPs can be
20 genotyped to determine if a particular genomic region harbors a locus that influences a particular phenotype, such as in linkage disequilibrium-based SNP association analysis.

Linkage disequilibrium (LD) refers to the co-inheritance of alleles (e.g., alternative nucleotides) at two or more different SNP sites at frequencies greater than would be expected from the separate frequencies of occurrence of each allele in a given
25 population. The expected frequency of co-occurrence of two alleles that are inherited independently is the frequency of the first allele multiplied by the frequency of the second allele. Alleles that co-occur at expected frequencies are said to be in "linkage equilibrium". In contrast, LD refers to any non-random genetic association between allele(s) at two or more different SNP sites, which is generally due to the physical
30 proximity of the two loci along a chromosome. LD can occur when two or more SNPs sites are in close physical proximity to each other on a given chromosome and therefore

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alleles at these SNP sites will tend to remain unseparated for multiple generations with the consequence that a particular nucleotide (allele) at one SNP site will show a non-random association with a particular nucleotide (allele) at a different SNP site located nearby. Hence, genotyping one of the SNP sites will give almost the same information as
 5 genotyping the other SNP site that is in LD.

Various degrees of LD can be encountered between two or more SNPs with the result being that some SNPs are more closely associated (i.e., in stronger LD) than others. Furthermore, the physical distance over which LD extends along a chromosome differs between different regions of the genome, and therefore the degree of physical separation
 10 between two or more SNP sites necessary for LD to occur can differ between different regions of the genome.

For diagnostic purposes and similar uses, if a particular SNP site is found to be useful for, for example, predicting an individual's susceptibility to an acute coronary event or an individual's response to statin treatment, then the skilled artisan would
 15 recognize that other SNP sites which are in LD with this SNP site would also be useful for predicting an individual's response to statin treatment. Various degrees of LD can be encountered between two or more SNPs with the result being that some SNPs are more closely associated (i.e., in stronger LD) than others. Furthermore, the physical distance over which LD extends along a chromosome differs between different regions of the
 20 genome, and therefore the degree of physical separation between two or more SNP sites necessary for LD to occur can differ between different regions of the genome. Thus, polymorphisms (e.g., SNPs and/or haplotypes) that are not the actual disease-causing (causative) polymorphisms, but are in LD with such causative polymorphisms, are also useful. In such instances, the genotype of the polymorphism(s) that is/are in LD with the
 25 causative polymorphism is predictive of the genotype of the causative polymorphism and, consequently, predictive of the phenotype (e.g., responder/non-responder to statin treatment) that is influenced by the causative SNP(s). Therefore, polymorphic markers that are in LD with causative polymorphisms are useful as diagnostic markers, and are particularly useful when the actual causative polymorphism(s) is/are unknown.

30 Examples of polymorphisms that can be in LD with one or more causative polymorphisms (and/or in LD with one or more polymorphisms that have a significant

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statistical association with a condition) and therefore useful for diagnosing the same condition that the causative/associated SNP(s) is used to diagnose, include, for example, other SNPs in the same gene, protein-coding, or mRNA transcript-coding region as the causative/associated SNP, other SNPs in the same exon or same intron as the causative/associated SNP, other SNPs in the same haplotype block as the causative/associated SNP, other SNPs in the same intergenic region as the causative/associated SNP, SNPs that are outside but near a gene (e.g., within 6kb on either side, 5' or 3', of a gene boundary) that harbors a causative/associated SNP, etc. Such useful LD SNPs can be selected from among the SNPs disclosed in Tables 1-2, for example.

Linkage disequilibrium in the human genome is reviewed in: Wall et al., "Haplotype blocks and linkage disequilibrium in the human genome", *Nat Rev Genet.* 2003 Aug;4(8):587-97; Garner et al., "On selecting markers for association studies: patterns of linkage disequilibrium between two and three diallelic loci", *Genet Epidemiol.* 2003 Jan;24(1):57-67; Ardlie et al., "Patterns of linkage disequilibrium in the human genome", *Nat Rev Genet.* 2002 Apr;3(4):299-309 (erratum in *Nat Rev Genet* 2002 Jul;3(7):566); and Remm et al., "High-density genotyping and linkage disequilibrium in the human genome using chromosome 22 as a model"; *Curr Opin Chem Biol.* 2002 Feb;6(1):24-30.

The contribution or association of particular SNPs and/or SNP haplotypes with disease phenotypes, such as susceptibility to acute coronary events or responsiveness to statin treatment, enables the SNPs of the present invention to be used to develop superior diagnostic tests capable of identifying individuals who express a detectable trait, such as predisposition to acute coronary events or responder/non-responder to statin treatment, as the result of a specific genotype, or individuals whose genotype places them at an increased or decreased risk of developing a detectable trait at a subsequent time as compared to individuals who do not have that genotype. As described herein, diagnostics may be based on a single SNP or a group of SNPs. Combined detection of a plurality of SNPs (for example, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 24, 25, 30, 32, 48, 50, 64, 96, 100, or any other number in-between, or more, of the SNPs provided in Table 1 and/or Table 2) typically increases the probability of an accurate

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diagnosis. For example, the presence of a single SNP known to correlate with response to statin treatment might indicate a probability of 20% that an individual will respond to statin treatment, whereas detection of five SNPs, each of which correlates with response to statin treatment, might indicate a probability of 80% that an individual will respond to statin treatment. To further increase the accuracy of diagnosis or predisposition screening, analysis of the SNPs of the present invention can be combined with that of other polymorphisms or other risk factors that correlate with disease risk and response to statin treatment, such as family history.

It will, of course, be understood by practitioners skilled in the treatment or diagnosis of cardiovascular disorders that the present invention generally does not intend to provide an absolute identification of individuals who will or will not experience an acute coronary event or develop another cardiovascular disorder, or those individuals who will or will not respond to statin treatment of cardiovascular disorders, but rather to indicate a certain increased (or decreased) degree or likelihood of developing an acute coronary event or responding to statin treatment based on statistically significant association results. However, this information is extremely valuable as it can, for example, indicate that an individual having a cardiovascular disorder should follow a particular statin-based treatment regimen, or should follow an alternative treatment regimen that does not involve statin. This information can also be used to initiate preventive treatments or to allow an individual carrying one or more significant SNPs or SNP haplotypes to foresee warning signs such as minor clinical symptoms of cardiovascular disease, or to have regularly scheduled physical exams to monitor for cardiovascular disorders in order to identify and begin treatment of the disorder at an early stage. Particularly with diseases that are extremely debilitating or fatal if not treated on time, the knowledge of a potential predisposition to the disease or likelihood of responding to available treatments, even if this predisposition or likelihood is not absolute, would likely contribute in a very significant manner to treatment efficacy.

The diagnostic techniques of the present invention may employ a variety of methodologies to determine whether a test subject has a SNP or a SNP pattern associated with an increased or decreased risk of developing a detectable trait or whether the individual suffers from a detectable trait as a result of a particular

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polymorphism/mutation, including, for example, methods which enable the analysis of individual chromosomes for haplotyping, family studies, single sperm DNA analysis, or somatic hybrids. The trait analyzed using the diagnostics of the invention may be any detectable trait that is commonly observed in cardiovascular disorders or during the course of statin treatment.

Another aspect of the present invention relates to a method of determining whether an individual is at risk (or less at risk) of developing one or more traits or whether an individual expresses one or more traits as a consequence of possessing a particular trait-causing or trait-influencing allele. These methods generally involve obtaining a nucleic acid sample from an individual and assaying the nucleic acid sample to determine which nucleotide(s) is/are present at one or more SNP positions, wherein the assayed nucleotide(s) is/are indicative of an increased or decreased risk of developing the trait or indicative that the individual expresses the trait as a result of possessing a particular trait-causing or trait-influencing allele.

In another embodiment, the SNP detection reagents of the present invention are used to determine whether an individual has one or more SNP allele(s) affecting the level (e.g., the concentration of mRNA or protein in a sample, etc.) or pattern (e.g., the kinetics of expression, rate of decomposition, stability profile, K_m , V_{max} , etc.) of gene expression (collectively, the "gene response" of a cell or bodily fluid). Such a determination can be accomplished by screening for mRNA or protein expression (e.g., by using nucleic acid arrays, RT-PCR, TaqMan assays, or mass spectrometry), identifying genes having altered expression in an individual, genotyping SNPs disclosed in Table 1 and/or Table 2 that could affect the expression of the genes having altered expression (e.g., SNPs that are in and/or around the gene(s) having altered expression, SNPs in regulatory/control regions, SNPs in and/or around other genes that are involved in pathways that could affect the expression of the gene(s) having altered expression, or all SNPs could be genotyped), and correlating SNP genotypes with altered gene expression. In this manner, specific SNP alleles at particular SNP sites can be identified that affect gene expression.

30

Pharmacogenomics and Therapeutics/Drug Development

The present invention provides methods for assessing the pharmacogenomics of a subject harboring particular SNP alleles or haplotypes to a particular therapeutic agent or pharmaceutical compound, or to a class of such compounds. Pharmacogenomics deals
5 with the roles which clinically significant hereditary variations (e.g., SNPs) play in the response to drugs due to altered drug disposition and/or abnormal action in affected persons. See, e.g., Roses, *Nature* 405, 857-865 (2000); Gould Rothberg, *Nature Biotechnology* 19, 209-211 (2001); Eichelbaum, *Clin. Exp. Pharmacol. Physiol.* 23(10-11):983-985 (1996); and Linder, *Clin. Chem.* 43(2):254-266 (1997). The clinical outcomes of these variations
10 can result in severe toxicity of therapeutic drugs in certain individuals or therapeutic failure of drugs in certain individuals as a result of individual variation in metabolism. Thus, the SNP genotype of an individual can determine the way a therapeutic compound acts on the body or the way the body metabolizes the compound. For example, SNPs in drug
metabolizing enzymes can affect the activity of these enzymes, which in turn can affect both
15 the intensity and duration of drug action, as well as drug metabolism and clearance.

The discovery of SNPs in drug metabolizing enzymes, drug transporters, proteins for pharmaceutical agents, and other drug targets has explained why some patients do not obtain the expected drug effects, show an exaggerated drug effect, or experience serious toxicity from standard drug dosages. SNPs can be expressed in the phenotype of the
20 extensive metabolizer and in the phenotype of the poor metabolizer. Accordingly, SNPs may lead to allelic variants of a protein in which one or more of the protein functions in one population are different from those in another population. SNPs and the encoded variant peptides thus provide targets to ascertain a genetic predisposition that can affect treatment modality. For example, in a ligand-based treatment, SNPs may give rise to amino terminal
25 extracellular domains and/or other ligand-binding regions of a receptor that are more or less active in ligand binding, thereby affecting subsequent protein activation. Accordingly, ligand dosage would necessarily be modified to maximize the therapeutic effect within a given population containing particular SNP alleles or haplotypes.

As an alternative to genotyping, specific variant proteins containing variant amino
30 acid sequences encoded by alternative SNP alleles could be identified. Thus, pharmacogenomic characterization of an individual permits the selection of effective

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compounds and effective dosages of such compounds for prophylactic or therapeutic uses based on the individual's SNP genotype, thereby enhancing and optimizing the effectiveness of the therapy. Furthermore, the production of recombinant cells and transgenic animals containing particular SNPs/haplotypes allow effective clinical design and testing of treatment compounds and dosage regimens. For example, transgenic animals can be produced that differ only in specific SNP alleles in a gene that is orthologous to a human disease susceptibility gene.

Pharmacogenomic uses of the SNPs of the present invention provide several significant advantages for patient care, particularly in predicting an individual's predisposition to acute coronary events and other cardiovascular disorders and in predicting an individual's responsiveness to the use of statin for treating cardiovascular disease. Pharmacogenomic characterization of an individual, based on an individual's SNP genotype, can identify those individuals unlikely to respond to treatment with a particular medication and thereby allows physicians to avoid prescribing the ineffective medication to those individuals. On the other hand, SNP genotyping of an individual may enable physicians to select the appropriate medication and dosage regimen that will be most effective based on an individual's SNP genotype. This information increases a physician's confidence in prescribing medications and motivates patients to comply with their drug regimens. Furthermore, pharmacogenomics may identify patients predisposed to toxicity and adverse reactions to particular drugs or drug dosages. Adverse drug reactions lead to more than 100,000 avoidable deaths per year in the United States alone and therefore represent a significant cause of hospitalization and death, as well as a significant economic burden on the healthcare system (Pfof et al., *Trends in Biotechnology*, Aug. 2000.). Thus, pharmacogenomics based on the SNPs disclosed herein has the potential to both save lives and reduce healthcare costs substantially.

Pharmacogenomics in general is discussed further in Rose et al., "Pharmacogenetic analysis of clinically relevant genetic polymorphisms", *Methods Mol Med.* 2003;85:225-37. Pharmacogenomics as it relates to Alzheimer's disease and other neurodegenerative disorders is discussed in Cacabelos, "Pharmacogenomics for the treatment of dementia", *Ann Med.* 2002;34(5):357-79, Maimone et al., "Pharmacogenomics of neurodegenerative diseases", *Eur J Pharmacol.* 2001 Feb

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9;413(1):11-29, and Poirier, "Apolipoprotein E: a pharmacogenetic target for the treatment of Alzheimer's disease", *Mol Diagn.* 1999 Dec;4(4):335-41.

Pharmacogenomics as it relates to cardiovascular disorders is discussed in Siest et al., "Pharmacogenomics of drugs affecting the cardiovascular system", *Clin Chem Lab Med.*

5 2003 Apr;41(4):590-9, Mukherjee et al., "Pharmacogenomics in cardiovascular diseases", *Prog Cardiovasc Dis.* 2002 May-Jun;44(6):479-98, and Mooser et al., "Cardiovascular pharmacogenetics in the SNP era", *J Thromb Haemost.* 2003 Jul;1(7):1398-402.

Pharmacogenomics as it relates to cancer is discussed in McLeod et al., "Cancer pharmacogenomics: SNPs, chips, and the individual patient", *Cancer Invest.*

10 2003;21(4):630-40 and Watters et al., "Cancer pharmacogenomics: current and future applications", *Biochim Biophys Acta.* 2003 Mar 17;1603(2):99-111.

The SNPs of the present invention also can be used to identify novel therapeutic targets for cardiovascular disorders. For example, genes containing the disease-associated variants ("variant genes") or their products, as well as genes or their products
15 that are directly or indirectly regulated by or interacting with these variant genes or their products, can be targeted for the development of therapeutics that, for example, treat the disease or prevent or delay disease onset. The therapeutics may be composed of, for example, small molecules, proteins, protein fragments or peptides, antibodies, nucleic acids, or their derivatives or mimetics which modulate the functions or levels of the target
20 genes or gene products.

The SNP-containing nucleic acid molecules disclosed herein, and their complementary nucleic acid molecules, may be used as antisense constructs to control gene expression in cells, tissues, and organisms. Antisense technology is well established in the art and extensively reviewed in *Antisense Drug Technology: Principles, Strategies, and Applications*, Crooke (ed.), Marcel Dekker, Inc.: New York (2001). An antisense
25 nucleic acid molecule is generally designed to be complementary to a region of mRNA expressed by a gene so that the antisense molecule hybridizes to the mRNA and thereby blocks translation of mRNA into protein. Various classes of antisense oligonucleotides are used in the art, two of which are cleavers and blockers. Cleavers, by binding to target
30 RNAs, activate intracellular nucleases (e.g., RNaseH or RNase L) that cleave the target RNA. Blockers, which also bind to target RNAs, inhibit protein translation through steric

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hindrance of ribosomes. Exemplary blockers include peptide nucleic acids, morpholinos, locked nucleic acids, and methylphosphonates (see, e.g., Thompson, *Drug Discovery Today*, 7 (17): 912-917 (2002)). Antisense oligonucleotides are directly useful as therapeutic agents, and are also useful for determining and validating gene function (e.g.,
 5 in gene knock-out or knock-down experiments).

Antisense technology is further reviewed in: Lavery et al., "Antisense and RNAi: powerful tools in drug target discovery and validation", *Curr Opin Drug Discov Devel.* 2003 Jul;6(4):561-9; Stephens et al., "Antisense oligonucleotide therapy in cancer", *Curr Opin Mol Ther.* 2003 Apr;5(2):118-22; Kurreck, "Antisense technologies. Improvement
 10 through novel chemical modifications", *Eur J Biochem.* 2003 Apr;270(8):1628-44; Dias et al., "Antisense oligonucleotides: basic concepts and mechanisms", *Mol Cancer Ther.* 2002 Mar;1(5):347-55; Chen, "Clinical development of antisense oligonucleotides as anti-cancer therapeutics", *Methods Mol Med.* 2003;75:621-36; Wang et al., "Antisense anticancer oligonucleotide therapeutics", *Curr Cancer Drug Targets.* 2001 Nov;1(3):177-
 15 96; and Bennett, "Efficiency of antisense oligonucleotide drug discovery", *Antisense Nucleic Acid Drug Dev.* 2002 Jun;12(3):215-24.

The SNPs of the present invention are particularly useful for designing antisense reagents that are specific for particular nucleic acid variants. Based on the SNP information disclosed herein, antisense oligonucleotides can be produced that specifically
 20 target mRNA molecules that contain one or more particular SNP nucleotides. In this manner, expression of mRNA molecules that contain one or more undesired polymorphisms (e.g., SNP nucleotides that lead to a defective protein such as an amino acid substitution in a catalytic domain) can be inhibited or completely blocked. Thus, antisense oligonucleotides can be used to specifically bind a particular polymorphic form
 25 (e.g., a SNP allele that encodes a defective protein), thereby inhibiting translation of this form, but which do not bind an alternative polymorphic form (e.g., an alternative SNP nucleotide that encodes a protein having normal function).

Antisense molecules can be used to inactivate mRNA in order to inhibit gene expression and production of defective proteins. Accordingly, these molecules can be
 30 used to treat a disorder, such as a cardiovascular disorder, characterized by abnormal or undesired gene expression or expression of certain defective proteins. This technique can

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involve cleavage by means of ribozymes containing nucleotide sequences complementary to one or more regions in the mRNA that attenuate the ability of the mRNA to be translated. Possible mRNA regions include, for example, protein-coding regions and particularly protein-coding regions corresponding to catalytic activities, substrate/ligand binding, or other functional activities of a protein.

The SNPs of the present invention are also useful for designing RNA interference reagents that specifically target nucleic acid molecules having particular SNP variants. RNA interference (RNAi), also referred to as gene silencing, is based on using double-stranded RNA (dsRNA) molecules to turn genes off. When introduced into a cell, dsRNAs are processed by the cell into short fragments (generally about 21, 22, or 23 nucleotides in length) known as small interfering RNAs (siRNAs) which the cell uses in a sequence-specific manner to recognize and destroy complementary RNAs (Thompson, *Drug Discovery Today*, 7 (17): 912-917 (2002)). Accordingly, an aspect of the present invention specifically contemplates isolated nucleic acid molecules that are about 18-26 nucleotides in length, preferably 19-25 nucleotides in length, and more preferably 20, 21, 22, or 23 nucleotides in length, and the use of these nucleic acid molecules for RNAi. Because RNAi molecules, including siRNAs, act in a sequence-specific manner, the SNPs of the present invention can be used to design RNAi reagents that recognize and destroy nucleic acid molecules having specific SNP alleles/nucleotides (such as deleterious alleles that lead to the production of defective proteins), while not affecting nucleic acid molecules having alternative SNP alleles (such as alleles that encode proteins having normal function). As with antisense reagents, RNAi reagents may be directly useful as therapeutic agents (e.g., for turning off defective, disease-causing genes), and are also useful for characterizing and validating gene function (e.g., in gene knock-out or knock-down experiments).

The following references provide a further review of RNAi: Reynolds et al., "Rational siRNA design for RNA interference", *Nat Biotechnol.* 2004 Mar;22(3):326-30. Epub 2004 Feb 01; Chi et al., "Genomewide view of gene silencing by small interfering RNAs", *PNAS* 100(11):6343-6346, 2003; Vickers et al., "Efficient Reduction of Target RNAs by Small Interfering RNA and RNase H-dependent Antisense Agents", *J. Biol. Chem.* 278: 7108-7118, 2003; Agami, "RNAi and related mechanisms and their potential

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use for therapy", *Curr Opin Chem Biol.* 2002 Dec;6(6):829-34; Lavery et al., "Antisense and RNAi: powerful tools in drug target discovery and validation", *Curr Opin Drug Discov Devel.* 2003 Jul;6(4):561-9; Shi, "Mammalian RNAi for the masses", *Trends Genet* 2003 Jan;19(1):9-12), Shuey et al., "RNAi: gene-silencing in therapeutic intervention", *Drug Discovery Today* 2002 Oct;7(20):1040-1046; McManus et al., *Nat Rev Genet* 2002 Oct;3(10):737-47; Xia et al., *Nat Biotechnol* 2002 Oct;20(10):1006-10; Plasterk et al., *Curr Opin Genet Dev* 2000 Oct;10(5):562-7; Bosher et al., *Nat Cell Biol* 2000 Feb;2(2):E31-6; and Hunter, *Curr Biol* 1999 Jun 17;9(12):R440-2).

A subject suffering from a pathological condition, such as a cardiovascular disorder, ascribed to a SNP may be treated so as to correct the genetic defect (see Kren et al., *Proc. Natl. Acad. Sci. USA* 96:10349-10354 (1999)). Such a subject can be identified by any method that can detect the polymorphism in a biological sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the normal/wild-type nucleotide at the position of the SNP. This site-specific repair sequence can encompass an RNA/DNA oligonucleotide that operates to promote endogenous repair of a subject's genomic DNA. The site-specific repair sequence is administered in an appropriate vehicle, such as a complex with polyethylenimine, encapsulated in anionic liposomes, a viral vector such as an adenovirus, or other pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. A genetic defect leading to an inborn pathology may then be overcome, as the chimeric oligonucleotides induce incorporation of the normal sequence into the subject's genome. Upon incorporation, the normal gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair and therapeutic enhancement of the clinical condition of the subject.

In cases in which a cSNP results in a variant protein that is ascribed to be the cause of, or a contributing factor to, a pathological condition, a method of treating such a condition can include administering to a subject experiencing the pathology the wild-type/normal cognate of the variant protein. Once administered in an effective dosing regimen, the wild-type cognate provides complementation or remediation of the pathological condition.

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The invention further provides a method for identifying a compound or agent that can be used to treat cardiovascular disorders. The SNPs disclosed herein are useful as targets for the identification and/or development of therapeutic agents. A method for identifying a therapeutic agent or compound typically includes assaying the ability of the agent or compound to modulate the activity and/or expression of a SNP-containing nucleic acid or the encoded product and thus identifying an agent or a compound that can be used to treat a disorder characterized by undesired activity or expression of the SNP-containing nucleic acid or the encoded product. The assays can be performed in cell-based and cell-free systems. Cell-based assays can include cells naturally expressing the nucleic acid molecules of interest or recombinant cells genetically engineered to express certain nucleic acid molecules.

Variant gene expression in a patient having a cardiovascular disorder or undergoing statin treatment can include, for example, either expression of a SNP-containing nucleic acid sequence (for instance, a gene that contains a SNP can be transcribed into an mRNA transcript molecule containing the SNP, which can in turn be translated into a variant protein) or altered expression of a normal/wild-type nucleic acid sequence due to one or more SNPs (for instance, a regulatory/control region can contain a SNP that affects the level or pattern of expression of a normal transcript).

Assays for variant gene expression can involve direct assays of nucleic acid levels (e.g., mRNA levels), expressed protein levels, or of collateral compounds involved in a signal pathway. Further, the expression of genes that are up- or down-regulated in response to the signal pathway can also be assayed. In this embodiment, the regulatory regions of these genes can be operably linked to a reporter gene such as luciferase.

Modulators of variant gene expression can be identified in a method wherein, for example, a cell is contacted with a candidate compound/agent and the expression of mRNA determined. The level of expression of mRNA in the presence of the candidate compound is compared to the level of expression of mRNA in the absence of the candidate compound. The candidate compound can then be identified as a modulator of variant gene expression based on this comparison and be used to treat a disorder such as a cardiovascular disorder that is characterized by variant gene expression (e.g., either expression of a SNP-containing nucleic acid or altered expression of a normal/wild-type nucleic acid molecule due to one or

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more SNPs that affect expression of the nucleic acid molecule) due to one or more SNPs of the present invention. When expression of mRNA is statistically significantly greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of nucleic acid expression. When nucleic acid expression is statistically significantly less in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of nucleic acid expression.

The invention further provides methods of treatment, with the SNP or associated nucleic acid domain (e.g., catalytic domain, ligand/substrate-binding domain, regulatory/control region, etc.) or gene, or the encoded mRNA transcript, as a target, using a compound identified through drug screening as a gene modulator to modulate variant nucleic acid expression. Modulation can include either up-regulation (i.e., activation or agonization) or down-regulation (i.e., suppression or antagonization) of nucleic acid expression.

Expression of mRNA transcripts and encoded proteins, either wild type or variant, may be altered in individuals with a particular SNP allele in a regulatory/control element, such as a promoter or transcription factor binding domain, that regulates expression. In this situation, methods of treatment and compounds can be identified, as discussed herein, that regulate or overcome the variant regulatory/control element, thereby generating normal, or healthy, expression levels of either the wild type or variant protein.

The SNP-containing nucleic acid molecules of the present invention are also useful for monitoring the effectiveness of modulating compounds on the expression or activity of a variant gene, or encoded product, in clinical trials or in a treatment regimen. Thus, the gene expression pattern can serve as an indicator for the continuing effectiveness of treatment with the compound, particularly with compounds to which a patient can develop resistance, as well as an indicator for toxicities. The gene expression pattern can also serve as a marker indicative of a physiological response of the affected cells to the compound. Accordingly, such monitoring would allow either increased administration of the compound or the administration of alternative compounds to which the patient has not become resistant. Similarly, if the level of nucleic acid expression falls below a desirable level, administration of the compound could be commensurately decreased.

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In another aspect of the present invention, there is provided a pharmaceutical pack comprising a therapeutic agent (e.g., a small molecule drug, antibody, peptide, antisense or RNAi nucleic acid molecule, etc.) and a set of instructions for administration of the therapeutic agent to humans diagnostically tested for one or more SNPs or SNP
5 haplotypes provided by the present invention.

The SNPs/haplotypes of the present invention are also useful for improving many different aspects of the drug development process. For instance, an aspect of the present invention includes selecting individuals for clinical trials based on their SNP genotype. For example, individuals with SNP genotypes that indicate that they are likely to
10 positively respond to a drug can be included in the trials, whereas those individuals whose SNP genotypes indicate that they are less likely to or would not respond to the drug, or who are at risk for suffering toxic effects or other adverse reactions, can be excluded from the clinical trials. This not only can improve the safety of clinical trials, but also can enhance the chances that the trial will demonstrate statistically significant
15 efficacy. Furthermore, the SNPs of the present invention may explain why certain previously developed drugs performed poorly in clinical trials and may help identify a subset of the population that would benefit from a drug that had previously performed poorly in clinical trials, thereby "rescuing" previously developed drugs, and enabling the drug to be made available to a particular patient population that can benefit from it.

20 SNPs have many important uses in drug discovery, screening, and development. A high probability exists that, for any gene/protein selected as a potential drug target, variants of that gene/protein will exist in a patient population. Thus, determining the impact of gene/protein variants on the selection and delivery of a therapeutic agent should be an integral aspect of the drug discovery and development process. (Jazwinska,
25 *A Trends Guide to Genetic Variation and Genomic Medicine*, 2002 Mar, S30-S36).

Knowledge of variants (e.g., SNPs and any corresponding amino acid polymorphisms) of a particular therapeutic target (e.g., a gene, mRNA transcript, or protein) enables parallel screening of the variants in order to identify therapeutic
30 candidates (e.g., small molecule compounds, antibodies, antisense or RNAi nucleic acid compounds, etc.) that demonstrate efficacy across variants (Rothberg, *Nat Biotechnol* 2001 Mar;19(3):209-11). Such therapeutic candidates would be expected to show equal

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efficacy across a larger segment of the patient population, thereby leading to a larger potential market for the therapeutic candidate.

Furthermore, identifying variants of a potential therapeutic target enables the most common form of the target to be used for selection of therapeutic candidates, thereby helping to ensure that the experimental activity that is observed for the selected candidates reflects the real activity expected in the largest proportion of a patient population (Jazwinska, *A Trends Guide to Genetic Variation and Genomic Medicine*, 2002 Mar; S30-S36).

Additionally, screening therapeutic candidates against all known variants of a target can enable the early identification of potential toxicities and adverse reactions relating to particular variants. For example, variability in drug absorption, distribution, metabolism and excretion (ADME) caused by, for example, SNPs in therapeutic targets or drug metabolizing genes, can be identified, and this information can be utilized during the drug development process to minimize variability in drug disposition and develop therapeutic agents that are safer across a wider range of a patient population. The SNPs of the present invention, including the variant proteins and encoding polymorphic nucleic acid molecules provided in Tables 1-2, are useful in conjunction with a variety of toxicology methods established in the art, such as those set forth in *Current Protocols in Toxicology*, John Wiley & Sons, Inc., N.Y.

Furthermore, therapeutic agents that target any art-known proteins (or nucleic acid molecules, either RNA or DNA) may cross-react with the variant proteins (or polymorphic nucleic acid molecules) disclosed in Table 1, thereby significantly affecting the pharmacokinetic properties of the drug. Consequently, the protein variants and the SNP-containing nucleic acid molecules disclosed in Tables 1-2 are useful in developing, screening, and evaluating therapeutic agents that target corresponding art-known protein forms (or nucleic acid molecules). Additionally, as discussed above, knowledge of all polymorphic forms of a particular drug target enables the design of therapeutic agents that are effective against most or all such polymorphic forms of the drug target.

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Pharmaceutical Compositions and Administration Thereof

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Any of the cardiovascular disease and/or statin response-associated proteins, and encoding nucleic acid molecules, disclosed herein can be used as therapeutic targets (or directly used themselves as therapeutic compounds) for treating cardiovascular disorders and related pathologies, and the present disclosure enables therapeutic compounds (e.g.,
5 small molecules, antibodies, therapeutic proteins, RNAi and antisense molecules, etc.) to be developed that target (or are comprised of) any of these therapeutic targets.

In general, a therapeutic compound will be administered in a therapeutically effective amount by any of the accepted modes of administration for agents that serve similar utilities. The actual amount of the therapeutic compound of this invention, i.e.,
10 the active ingredient, will depend upon numerous factors such as the severity of the disease to be treated, the age and relative health of the subject, the potency of the compound used, the route and form of administration, and other factors.

Therapeutically effective amounts of therapeutic compounds may range from, for example, approximately 0.01-50 mg per kilogram body weight of the recipient per day; preferably about 0.1-20 mg/kg/day. Thus, as an example, for administration to a 70 kg
15 person, the dosage range would most preferably be about 7 mg to 1.4 g per day.

In general, therapeutic compounds will be administered as pharmaceutical compositions by any one of the following routes: oral, systemic (e.g., transdermal, intranasal, or by suppository), or parenteral (e.g., intramuscular, intravenous, or
20 subcutaneous) administration. The preferred manner of administration is oral or parenteral using a convenient daily dosage regimen, which can be adjusted according to the degree of affliction. Oral compositions can take the form of tablets, pills, capsules, semisolids, powders, sustained release formulations, solutions, suspensions, elixirs, aerosols, or any other appropriate compositions.

The choice of formulation depends on various factors such as the mode of drug administration (e.g., for oral administration, formulations in the form of tablets, pills, or capsules are preferred) and the bioavailability of the drug substance. Recently, pharmaceutical formulations have been developed especially for drugs that show poor bioavailability based upon the principle that bioavailability can be increased by
25 increasing the surface area, i.e., decreasing particle size. For example, U.S. Patent No. 4,107,288 describes a pharmaceutical formulation having particles in the size range from
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10 to 1,000 nm in which the active material is supported on a cross-linked matrix of macromolecules. U.S. Patent No. 5,145,684 describes the production of a pharmaceutical formulation in which the drug substance is pulverized to nanoparticles (average particle size of 400 nm) in the presence of a surface modifier and then dispersed in a liquid medium to give a pharmaceutical formulation that exhibits remarkably high bioavailability.

Pharmaceutical compositions are comprised of, in general, a therapeutic compound in combination with at least one pharmaceutically acceptable excipient. Acceptable excipients are non-toxic, aid administration, and do not adversely affect the therapeutic benefit of the therapeutic compound. Such excipients may be any solid, liquid, semi-solid or, in the case of an aerosol composition, gaseous excipient that is generally available to one skilled in the art.

Solid pharmaceutical excipients include starch, cellulose, talc, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, magnesium stearate, sodium stearate, glycerol monostearate, sodium chloride, dried skim milk and the like. Liquid and semisolid excipients may be selected from glycerol, propylene glycol, water, ethanol and various oils, including those of petroleum, animal, vegetable or synthetic origin, e.g., peanut oil, soybean oil, mineral oil, sesame oil, etc. Preferred liquid carriers, particularly for injectable solutions, include water, saline, aqueous dextrose, and glycols.

Compressed gases may be used to disperse a compound of this invention in aerosol form. Inert gases suitable for this purpose are nitrogen, carbon dioxide, etc.

Other suitable pharmaceutical excipients and their formulations are described in Remington's Pharmaceutical Sciences, edited by E. W. Martin (Mack Publishing Company, 18th ed., 1990).

The amount of the therapeutic compound in a formulation can vary within the full range employed by those skilled in the art. Typically, the formulation will contain, on a weight percent (wt %) basis, from about 0.01-99.99 wt % of the therapeutic compound based on the total formulation, with the balance being one or more suitable pharmaceutical excipients. Preferably, the compound is present at a level of about 1-80 wt %.

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Therapeutic compounds can be administered alone or in combination with other therapeutic compounds or in combination with one or more other active ingredient(s). For example, an inhibitor or stimulator of a cardiovascular disorder-associated protein can be administered in combination with another agent that inhibits or stimulates the activity of the same or a different cardiovascular disorder-associated protein to thereby counteract the affects of a cardiovascular disorder.

For further information regarding pharmacology, see *Current Protocols in Pharmacology*, John Wiley & Sons, Inc., N.Y.

10 Human Identification Applications

In addition to their diagnostic and therapeutic uses in cardiovascular disorders and statin treatment of cardiovascular disorders, the SNPs provided by the present invention are also useful as human identification markers for such applications as forensics, paternity testing, and biometrics (see, e.g., Gill, "An assessment of the utility of single nucleotide polymorphisms (SNPs) for forensic purposes", *Int J Legal Med.* 2001;114(4):204-10). Genetic variations in the nucleic acid sequences between individuals can be used as genetic markers to identify individuals and to associate a biological sample with an individual. Determination of which nucleotides occupy a set of SNP positions in an individual identifies a set of SNP markers that distinguishes the individual. The more SNP positions that are analyzed, the lower the probability that the set of SNPs in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked (i.e., inherited independently). Thus, preferred sets of SNPs can be selected from among the SNPs disclosed herein, which may include SNPs on different chromosomes, SNPs on different chromosome arms, and/or SNPs that are dispersed over substantial distances along the same chromosome arm.

Furthermore, among the SNPs disclosed herein, preferred SNPs for use in certain forensic/human identification applications include SNPs located at degenerate codon positions (i.e., the third position in certain codons which can be one of two or more alternative nucleotides and still encode the same amino acid), since these SNPs do not affect the encoded protein. SNPs that do not affect the encoded protein are expected to be under less selective pressure and are therefore expected to be more polymorphic in a

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population, which is typically an advantage for forensic/human identification applications. However, for certain forensics/human identification applications, such as predicting phenotypic characteristics (e.g., inferring ancestry or inferring one or more physical characteristics of an individual) from a DNA sample, it may be desirable to
5 utilize SNPs that affect the encoded protein.

For many of the SNPs disclosed in Tables 1-2 (which are identified as "Applera" SNP source), Tables 1-2 provide SNP allele frequencies obtained by re-sequencing the DNA of chromosomes from 39 individuals (Tables 1-2 also provide allele frequency information for "Celera" source SNPs and, where available, public SNPs from dbEST,
10 HGBASE, and/or HGMD). The allele frequencies provided in Tables 1-2 enable these SNPs to be readily used for human identification applications. Although any SNP disclosed in Table 1 and/or Table 2 could be used for human identification, the closer that the frequency of the minor allele at a particular SNP site is to 50%, the greater the ability of that SNP to discriminate between different individuals in a population since it becomes
15 increasingly likely that two randomly selected individuals would have different alleles at that SNP site. Using the SNP allele frequencies provided in Tables 1-2, one of ordinary skill in the art could readily select a subset of SNPs for which the frequency of the minor allele is, for example, at least 1%, 2%, 5%, 10%, 20%, 25%, 30%, 40%, 45%, or 50%, or any other frequency in-between. Thus, since Tables 1-2 provide allele frequencies based
20 on the re-sequencing of the chromosomes from 39 individuals, a subset of SNPs could readily be selected for human identification in which the total allele count of the minor allele at a particular SNP site is, for example, at least 1, 2, 4, 8, 10, 16, 20, 24, 30, 32, 36, 38, 39, 40, or any other number in-between.

Furthermore, Tables 1-2 also provide population group (interchangeably referred
25 to herein as ethnic or racial groups) information coupled with the extensive allele frequency information. For example, the group of 39 individuals whose DNA was re-sequenced was made-up of 20 Caucasians and 19 African-Americans. This population group information enables further refinement of SNP selection for human identification. For example, preferred SNPs for human identification can be selected from Tables 1-2
30 that have similar allele frequencies in both the Caucasian and African-American populations; thus, for example, SNPs can be selected that have equally high

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discriminatory power in both populations. Alternatively, SNPs can be selected for which there is a statistically significant difference in allele frequencies between the Caucasian and African-American populations (as an extreme example, a particular allele may be observed only in either the Caucasian or the African-American population group but not observed in the other population group); such SNPs are useful, for example, for predicting the race/ethnicity of an unknown perpetrator from a biological sample such as a hair or blood stain recovered at a crime scene. For a discussion of using SNPs to predict ancestry from a DNA sample, including statistical methods, see Frudakis *et al.*, "A Classifier for the SNP-Based Inference of Ancestry", *Journal of Forensic Sciences* 2003; 48(4):771-782.

SNPs have numerous advantages over other types of polymorphic markers, such as short tandem repeats (STRs). For example, SNPs can be easily scored and are amenable to automation, making SNPs the markers of choice for large-scale forensic databases. SNPs are found in much greater abundance throughout the genome than repeat polymorphisms. Population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci. SNPs are mutationally more stable than repeat polymorphisms. SNPs are not susceptible to artefacts such as stutter bands that can hinder analysis. Stutter bands are frequently encountered when analyzing repeat polymorphisms; and are particularly troublesome when analyzing samples such as crime scene samples that may contain mixtures of DNA from multiple sources. Another significant advantage of SNP markers over STR markers is the much shorter length of nucleic acid needed to score a SNP. For example, STR markers are generally several hundred base pairs in length. A SNP, on the other hand, comprises a single nucleotide, and generally a short conserved region on either side of the SNP position for primer and/or probe binding. This makes SNPs more amenable to typing in highly degraded or aged biological samples that are frequently encountered in forensic casework in which DNA may be fragmented into short pieces.

SNPs also are not subject to microvariant and "off-ladder" alleles frequently encountered when analyzing STR loci. Microvariants are deletions or insertions within a repeat unit that change the size of the amplified DNA product so that the amplified product does not migrate at the same rate as reference alleles with normal sized repeat

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units. When separated by size, such as by electrophoresis on a polyacrylamide gel, microvariants do not align with a reference allelic ladder of standard sized repeat units, but rather migrate between the reference alleles. The reference allelic ladder is used for precise sizing of alleles for allele classification; therefore alleles that do not align with the reference allelic ladder lead to substantial analysis problems. Furthermore, when analyzing multi-allelic repeat polymorphisms, occasionally an allele is found that consists of more or less repeat units than has been previously seen in the population, or more or less repeat alleles than are included in a reference allelic ladder. These alleles will migrate outside the size range of known alleles in a reference allelic ladder, and therefore are referred to as "off-ladder" alleles. In extreme cases, the allele may contain so few or so many repeats that it migrates well out of the range of the reference allelic ladder. In this situation, the allele may not even be observed, or, with multiplex analysis, it may migrate within or close to the size range for another locus, further confounding analysis.

SNP analysis avoids the problems of microvariants and off-ladder alleles encountered in STR analysis. Importantly, microvariants and off-ladder alleles may provide significant problems, and may be completely missed, when using analysis methods such as oligonucleotide hybridization arrays, which utilize oligonucleotide probes specific for certain known alleles. Furthermore, off-ladder alleles and microvariants encountered with STR analysis, even when correctly typed, may lead to improper statistical analysis, since their frequencies in the population are generally unknown or poorly characterized, and therefore the statistical significance of a matching genotype may be questionable. All these advantages of SNP analysis are considerable in light of the consequences of most DNA identification cases, which may lead to life imprisonment for an individual, or re-association of remains to the family of a deceased individual.

DNA can be isolated from biological samples such as blood, bone, hair, saliva, or semen, and compared with the DNA from a reference source at particular SNP positions. Multiple SNP markers can be assayed simultaneously in order to increase the power of discrimination and the statistical significance of a matching genotype. For example, oligonucleotide arrays can be used to genotype a large number of SNPs simultaneously. The SNPs provided by the present invention can be assayed in combination with other

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polymorphic genetic markers, such as other SNPs known in the art or STRs, in order to identify an individual or to associate an individual with a particular biological sample.

Furthermore, the SNPs provided by the present invention can be genotyped for inclusion in a database of DNA genotypes, for example, a criminal DNA databank such as the FBI's Combined DNA Index System (CODIS) database. A genotype obtained from a biological sample of unknown source can then be queried against the database to find a matching genotype, with the SNPs of the present invention providing nucleotide positions at which to compare the known and unknown DNA sequences for identity. Accordingly, the present invention provides a database comprising novel SNPs or SNP alleles of the present invention (e.g., the database can comprise information indicating which alleles are possessed by individual members of a population at one or more novel SNP sites of the present invention), such as for use in forensics, biometrics, or other human identification applications. Such a database typically comprises a computer-based system in which the SNPs or SNP alleles of the present invention are recorded on a computer readable medium (see the section of the present specification entitled "Computer-Related Embodiments").

The SNPs of the present invention can also be assayed for use in paternity testing. The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child, with the SNPs of the present invention providing nucleotide positions at which to compare the putative father's and child's DNA sequences for identity. If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the father of the child. If the set of polymorphisms in the child attributable to the father match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match, and a conclusion drawn as to the likelihood that the putative father is the true biological father of the child.

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In addition to paternity testing, SNPs are also useful for other types of kinship testing, such as for verifying familial relationships for immigration purposes, or for cases in which an individual alleges to be related to a deceased individual in order to claim an inheritance from the deceased individual, etc. For further information regarding the utility of SNPs for paternity testing and other types of kinship testing, including methods for statistical analysis, see Krawczak, "Informativity assessment for biallelic single nucleotide polymorphisms", *Electrophoresis* 1999 Jun;20(8):1676-81.

The use of the SNPs of the present invention for human identification further extends to various authentication systems, commonly referred to as biometric systems, which typically convert physical characteristics of humans (or other organisms) into digital data. Biometric systems include various technological devices that measure such unique anatomical or physiological characteristics as finger, thumb, or palm prints; hand geometry; vein patterning on the back of the hand; blood vessel patterning of the retina and color and texture of the iris; facial characteristics; voice patterns; signature and typing dynamics; and DNA. Such physiological measurements can be used to verify identity and, for example, restrict or allow access based on the identification. Examples of applications for biometrics include physical area security, computer and network security, aircraft passenger check-in and boarding, financial transactions, medical records access, government benefit distribution, voting, law enforcement, passports, visas and immigration, prisons, various military applications, and for restricting access to expensive or dangerous items, such as automobiles or guns (see, for example, O'Connor, *Stanford Technology Law Review* and U.S. Patent No. 6,119,096).

Groups of SNPs, particularly the SNPs provided by the present invention, can be typed to uniquely identify an individual for biometric applications such as those described above. Such SNP typing can readily be accomplished using, for example, DNA chips/arrays. Preferably, a minimally invasive means for obtaining a DNA sample is utilized. For example, PCR amplification enables sufficient quantities of DNA for analysis to be obtained from buccal swabs or fingerprints, which contain DNA-containing skin cells and oils that are naturally transferred during contact.

Further information regarding techniques for using SNPs in forensic/human identification applications can be found in, for example, *Current Protocols in Human Genetics*, John Wiley & Sons, N.Y. (2002), 14.1-14.7.

5

**VARIANT PROTEINS, ANTIBODIES,
VECTORS & HOST CELLS, & USES THEREOF**

Variant Proteins Encoded by SNP-Containing Nucleic Acid Molecules

10 The present invention provides SNP-containing nucleic acid molecules, many of which encode proteins having variant amino acid sequences as compared to the art-known (i.e., wild-type) proteins. Amino acid sequences encoded by the polymorphic nucleic acid molecules of the present invention are provided as SEQ ID NOS: 56-109 in Table 1 and the Sequence Listing. These variants will generally be referred to herein as variant
15 proteins/peptides/polypeptides, or polymorphic proteins/peptides/polypeptides of the present invention. The terms "protein", "peptide", and "polypeptide" are used herein interchangeably.

A variant protein of the present invention may be encoded by, for example, a nonsynonymous nucleotide substitution at any one of the cSNP positions disclosed
20 herein. In addition, variant proteins may also include proteins whose expression, structure, and/or function is altered by a SNP disclosed herein, such as a SNP that creates or destroys a stop codon, a SNP that affects splicing, and a SNP in control/regulatory elements, e.g. promoters, enhancers, or transcription factor binding domains.

As used herein, a protein or peptide is said to be "isolated" or "purified" when it is
25 substantially free of cellular material or chemical precursors or other chemicals. The variant proteins of the present invention can be purified to homogeneity or other lower degrees of purity. The level of purification will be based on the intended use. The key feature is that the preparation allows for the desired function of the variant protein, even if in the presence of considerable amounts of other components.

30 As used herein, "substantially free of cellular material" includes preparations of the variant protein having less than about 30% (by dry weight) other proteins (i.e.,

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contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins. When the variant protein is recombinantly produced, it can also be substantially free of culture medium, i.e., culture medium represents less than about 20% of the volume of the protein preparation.

5 The language "substantially free of chemical precursors or other chemicals" includes preparations of the variant protein in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the variant protein having less than about 30% (by dry weight) chemical precursors or other chemicals, less
: 10 than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

An isolated variant protein may be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant host cells), or synthesized using known protein synthesis methods. For example, a nucleic acid molecule
15 containing SNP(s) encoding the variant protein can be cloned into an expression vector, the expression vector introduced into a host cell, and the variant protein expressed in the host cell. The variant protein can then be isolated from the cells by any appropriate purification scheme using standard protein purification techniques. Examples of these techniques are described in detail below (Sambrook and Russell, 2000, Molecular Cloning: A Laboratory
20 Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

The present invention provides isolated variant proteins that comprise, consist of or consist essentially of amino acid sequences that contain one or more variant amino acids encoded by one or more codons which contain a SNP of the present invention.

Accordingly, the present invention provides variant proteins that consist of amino
25 acid sequences that contain one or more amino acid polymorphisms (or truncations or extensions due to creation or destruction of a stop codon, respectively) encoded by the SNPs provided in Table 1 and/or Table 2. A protein consists of an amino acid sequence when the amino acid sequence is the entire amino acid sequence of the protein.

The present invention further provides variant proteins that consist essentially of
30 amino acid sequences that contain one or more amino acid polymorphisms (or truncations or extensions due to creation or destruction of a stop codon, respectively) encoded by the SNPs

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provided in Table 1 and/or Table 2. A protein consists essentially of an amino acid sequence when such an amino acid sequence is present with only a few additional amino acid residues in the final protein.

5 The present invention further provides variant proteins that comprise amino acid sequences that contain one or more amino acid polymorphisms (or truncations or extensions due to creation or destruction of a stop codon, respectively) encoded by the SNPs provided in Table 1 and/or Table 2. A protein comprises an amino acid sequence when the amino acid sequence is at least part of the final amino acid sequence of the protein. In such a fashion, the protein may contain only the variant amino acid sequence or have additional
10 amino acid residues, such as a contiguous encoded sequence that is naturally associated with it or heterologous amino acid residues. Such a protein can have a few additional amino acid residues or can comprise many more additional amino acids. A brief description of how various types of these proteins can be made and isolated is provided below.

The variant proteins of the present invention can be attached to heterologous
15 sequences to form chimeric or fusion proteins. Such chimeric and fusion proteins comprise a variant protein operatively linked to a heterologous protein having an amino acid sequence not substantially homologous to the variant protein. "Operatively linked" indicates that the coding sequences for the variant protein and the heterologous protein are ligated in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the variant protein. In another embodiment, the fusion protein is encoded by a
20 fusion polynucleotide that is synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A variant protein-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the variant protein.

30 In many uses, the fusion protein does not affect the activity of the variant protein. The fusion protein can include, but is not limited to, enzymatic fusion proteins, for example,

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beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions, MYC-tagged, HII-tagged and Ig fusions. Such fusion proteins, particularly poly-His fusions, can facilitate their purification following recombinant expression. In certain host cells (e.g., mammalian host cells), expression and/or secretion of a protein can be increased by using a heterologous
 5 signal sequence. Fusion proteins are further described in, for example, Terpe, "Overview of tag protein fusions: from molecular and biochemical fundamentals to commercial systems", *Appl Microbiol Biotechnol.* 2003 Jan;60(5):523-33. Epub 2002 Nov 07; Graddis et al., "Designing proteins that work using recombinant technologies", *Curr Pharm Biotechnol.* 2002 Dec;3(4):285-97; and Nilsson et al., "Affinity fusion strategies for detection,
 10 purification, and immobilization of recombinant proteins", *Protein Expr Purif.* 1997 Oct;11(1):1-16.

The present invention also relates to further obvious variants of the variant polypeptides of the present invention, such as naturally-occurring mature forms (e.g., alleleic variants), non-naturally occurring recombinantly-derived variants, and orthologs and
 15 paralogues of such proteins that share sequence homology. Such variants can readily be generated using art-known techniques in the fields of recombinant nucleic acid technology and protein biochemistry. It is understood, however, that variants exclude those known in the prior art before the present invention.

Further variants of the variant polypeptides disclosed in Table 1 can comprise an
 20 amino acid sequence that shares at least 70-80%, 80-85%, 85-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with an amino acid sequence disclosed in Table 1 (or a fragment thereof) and that includes a novel amino acid residue (allele) disclosed in Table 1 (which is encoded by a novel SNP allele). Thus, an aspect of the present invention that is specifically contemplated are polypeptides that have a certain
 25 degree of sequence variation compared with the polypeptide sequences shown in Table 1, but that contain a novel amino acid residue (allele) encoded by a novel SNP allele disclosed herein. In other words, as long as a polypeptide contains a novel amino acid residue disclosed herein, other portions of the polypeptide that flank the novel amino acid residue can vary to some degree from the polypeptide sequences shown in Table 1.

30 Full-length pre-processed forms, as well as mature processed forms, of proteins that comprise one of the amino acid sequences disclosed herein can readily be identified

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as having complete sequence identity to one of the variant proteins of the present invention as well as being encoded by the same genetic locus as the variant proteins provided herein.

Orthologs of a variant peptide can readily be identified as having some degree of
5 significant sequence homology/identity to at least a portion of a variant peptide as well as being encoded by a gene from another organism. Preferred orthologs will be isolated from non-human mammals, preferably primates, for the development of human therapeutic targets and agents. Such orthologs can be encoded by a nucleic acid sequence that hybridizes to a variant peptide-encoding nucleic acid molecule under moderate to
10 stringent conditions depending on the degree of relatedness of the two organisms yielding the homologous proteins.

Variant proteins include, but are not limited to, proteins containing deletions, additions and substitutions in the amino acid sequence caused by the SNPs of the present invention. One class of substitutions is conserved amino acid substitutions in which a given
15 amino acid in a polypeptide is substituted for another amino acid of like characteristics. Typical conservative substitutions are replacements, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile; interchange of the hydroxyl residues Ser and Thr; exchange of the acidic residues Asp and Glu; substitution between the amide residues Asn and Gln; exchange of the basic residues Lys and Arg; and replacements among the aromatic
20 residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in, for example, Bowie *et al.*, *Science* 247:1306-1310 (1990).

Variant proteins can be fully functional or can lack function in one or more activities, e.g. ability to bind another molecule, ability to catalyze a substrate, ability to
25 mediate signaling, etc. Fully functional variants typically contain only conservative variations or variations in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one
30 or more non-conservative amino acid substitutions, deletions, insertions, inversions,

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truncations or extensions, or a substitution, insertion, inversion, or deletion of a critical residue or in a critical region.

Amino acids that are essential for function of a protein can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis
 5 (Cunningham *et al.*, *Science* 244:1081-1085 (1989)), particularly using the amino acid sequence and polymorphism information provided in Table 1. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as enzyme activity or in assays such as an *in vitro* proliferative activity. Sites that are critical for binding partner/substrate binding
 10 can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.* *Science* 255:306-312 (1992)).

Polypeptides can contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids. Further, many amino acids,
 15 including the terminal amino acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art. Accordingly, the variant proteins of the present invention also encompass derivatives or analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included,
 20 in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (e.g., polyethylene glycol), or in which additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence for purification of the mature polypeptide or a pro-protein sequence.

Known protein modifications include, but are not limited to, acetylation, acylation,
 25 ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation,
 30 glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation,

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racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

Such protein modifications are well known to those of skill in the art and have been described in great detail in the scientific literature. Several particularly common
5 modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as *Proteins - Structure and Molecular Properties*, 2nd Ed., T.E. Creighton, W. H. Freeman and Company, New York (1993); Wold, F., *Posttranslational Covalent
Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York 1-12 (1983);
10 Seifter *et al.*, *Meth. Enzymol.* 182: 626-646 (1990); and Rattan *et al.*, *Ann. N.Y. Acad. Sci.* 663:48-62 (1992).

The present invention further provides fragments of the variant proteins in which the fragments contain one or more amino acid sequence variations (e.g., substitutions, or truncations or extensions due to creation or destruction of a stop codon) encoded by one or
15 more SNPs disclosed herein. The fragments to which the invention pertains, however, are not to be construed as encompassing fragments that have been disclosed in the prior art before the present invention.

As used herein, a fragment may comprise at least about 4, 8, 10, 12, 14, 16, 18, 20, 25, 30, 50, 100 (or any other number in-between) or more contiguous amino acid residues
20 from a variant protein, wherein at least one amino acid residue is affected by a SNP of the present invention, e.g., a variant amino acid residue encoded by a nonsynonymous nucleotide substitution at a cSNP position provided by the present invention. The variant amino acid encoded by a cSNP may occupy any residue position along the sequence of the fragment. Such fragments can be chosen based on the ability to retain one or more of the
25 biological activities of the variant protein or the ability to perform a function, e.g., act as an immunogen. Particularly important fragments are biologically active fragments. Such fragments will typically comprise a domain or motif of a variant protein of the present invention, e.g., active site, transmembrane domain, or ligand/substrate binding domain. Other fragments include, but are not limited to, domain or motif-containing fragments,
30 soluble peptide fragments, and fragments containing immunogenic structures. Predicted domains and functional sites are readily identifiable by computer programs well known to

those of skill in the art (e.g., PROSITE analysis) (*Current Protocols in Protein Science*, John Wiley & Sons, N.Y. (2002)).

Uses of Variant Proteins

5 The variant proteins of the present invention can be used in a variety of ways, including but not limited to, in assays to determine the biological activity of a variant protein, such as in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another type of immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the variant
10 protein (or its binding partner) in biological fluids; as a marker for cells or tissues in which it is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); as a target for screening for a therapeutic agent; and as a direct therapeutic agent to be administered into a human subject. Any of the variant proteins disclosed herein may be developed into reagent
15 grade or kit format for commercialization as research products. Methods for performing the uses listed above are well known to those skilled in the art (see, e.g., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Sambrook and Russell, 2000, and *Methods in Enzymology: Guide to Molecular Cloning Techniques*, Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987).

20 In a specific embodiment of the invention, the methods of the present invention include detection of one or more variant proteins disclosed herein. Variant proteins are disclosed in Table 1 and in the Sequence Listing as SEQ ID NOS: 56-109. Detection of such proteins can be accomplished using, for example, antibodies, small molecule compounds, aptamers, ligands/substrates, other proteins or protein fragments, or other
25 protein-binding agents. Preferably, protein detection agents are specific for a variant protein of the present invention and can therefore discriminate between a variant protein of the present invention and the wild-type protein or another variant form. This can generally be accomplished by, for example, selecting or designing detection agents that bind to the region of a protein that differs between the variant and wild-type protein, such
30 as a region of a protein that contains one or more amino acid substitutions that is/are encoded by a non-synonymous cSNP of the present invention, or a region of a protein

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that follows a nonsense mutation-type SNP that creates a stop codon thereby leading to a shorter polypeptide, or a region of a protein that follows a read-through mutation-type SNP that destroys a stop codon thereby leading to a longer polypeptide in which a portion of the polypeptide is present in one version of the polypeptide but not the other.

5 In another specific aspect of the invention, the variant proteins of the present invention are used as targets for evaluating an individual's predisposition to developing a cardiovascular disorder, particularly an acute coronary event such as myocardial infarction, or stroke, for treating and/or preventing cardiovascular disorders, or for predicting an individual's response to statin treatment of cardiovascular disorders, etc. Accordingly, the
10 invention provides methods for detecting the presence of, or levels of, one or more variant proteins of the present invention in a cell, tissue, or organism. Such methods typically involve contacting a test sample with an agent (e.g., an antibody, small molecule compound, or peptide) capable of interacting with the variant protein such that specific binding of the agent to the variant protein can be detected. Such an assay can be provided in a single
15 detection format or a multi-detection format such as an array, for example, an antibody or aptamer array (arrays for protein detection may also be referred to as "protein chips"). The variant protein of interest can be isolated from a test sample and assayed for the presence of a variant amino acid sequence encoded by one or more SNPs disclosed by the present invention. The SNPs may cause changes to the protein and the corresponding protein
20 function/activity, such as through non-synonymous substitutions in protein coding regions that can lead to amino acid substitutions, deletions, insertions, and/or rearrangements; formation or destruction of stop codons; or alteration of control elements such as promoters. SNPs may also cause inappropriate post-translational modifications.

One preferred agent for detecting a variant protein in a sample is an antibody
25 capable of selectively binding to a variant form of the protein (antibodies are described in greater detail in the next section). Such samples include, for example, tissues, cells, and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject.

In vitro methods for detection of the variant proteins associated with cardiovascular
30 disorders and/or statin response that are disclosed herein and fragments thereof include, but are not limited to, enzyme linked immunosorbent assays (ELISAs), radioimmunoassays

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(RIA), Western blots, immunoprecipitations, immunofluorescence, and protein arrays/chips (e.g., arrays of antibodies or aptamers). For further information regarding immunoassays and related protein detection methods, see *Current Protocols in Immunology*, John Wiley & Sons, N.Y., and Hage, "Immunoassays", *Anal Chem.* 1999 Jun 15;71(12):294R-304R.

5 Additional analytic methods of detecting amino acid variants include, but are not limited to, altered electrophoretic mobility, altered tryptic peptide digest, altered protein activity in cell-based or cell-free assay, alteration in ligand or antibody-binding pattern, altered isoelectric point, and direct amino acid sequencing.

10 Alternatively, variant proteins can be detected *in vivo* in a subject by introducing into the subject a labeled antibody (or other type of detection reagent) specific for a variant protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

Other uses of the variant peptides of the present invention are based on the class or action of the protein. For example, proteins isolated from humans and their
15 mammalian orthologs serve as targets for identifying agents (e.g., small molecule drugs or antibodies) for use in therapeutic applications, particularly for modulating a biological or pathological response in a cell or tissue that expresses the protein. Pharmaceutical agents can be developed that modulate protein activity.

As an alternative to modulating gene expression, therapeutic compounds can be
20 developed that modulate protein function. For example, many SNPs disclosed herein affect the amino acid sequence of the encoded protein (e.g., non-synonymous cSNPs and nonsense mutation-type SNPs). Such alterations in the encoded amino acid sequence may affect protein function, particularly if such amino acid sequence variations occur in functional protein domains, such as catalytic domains, ATP-binding domains, or ligand/substrate
25 binding domains. It is well established in the art that variant proteins having amino acid sequence variations in functional domains can cause or influence pathological conditions. In such instances, compounds (e.g., small molecule drugs or antibodies) can be developed that target the variant protein and modulate (e.g., up- or down-regulate) protein function/activity.

30 The therapeutic methods of the present invention further include methods that target one or more variant proteins of the present invention. Variant proteins can be

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targeted using, for example, small molecule compounds, antibodies, aptamers, ligands/substrates, other proteins, or other protein-binding agents. Additionally, the skilled artisan will recognize that the novel protein variants (and polymorphic nucleic acid molecules) disclosed in Table 1 may themselves be directly used as therapeutic agents by acting as competitive inhibitors of corresponding art-known proteins (or nucleic acid molecules such as mRNA molecules).

The variant proteins of the present invention are particularly useful in drug screening assays, in cell-based or cell-free systems. Cell-based systems can utilize cells that naturally express the protein, a biopsy specimen, or cell cultures. In one embodiment, cell-based assays involve recombinant host cells expressing the variant protein. Cell-free assays can be used to detect the ability of a compound to directly bind to a variant protein or to the corresponding SNP-containing nucleic acid fragment that encodes the variant protein.

A variant protein of the present invention, as well as appropriate fragments thereof, can be used in high-throughput screening assays to test candidate compounds for the ability to bind and/or modulate the activity of the variant protein. These candidate compounds can be further screened against a protein having normal function (e.g., a wild-type/non-variant protein) to further determine the effect of the compound on the protein activity. Furthermore, these compounds can be tested in animal or invertebrate systems to determine *in vivo* activity/effectiveness. Compounds can be identified that activate (agonists) or inactivate (antagonists) the variant protein, and different compounds can be identified that cause various degrees of activation or inactivation of the variant protein.

Further, the variant proteins can be used to screen a compound for the ability to stimulate or inhibit interaction between the variant protein and a target molecule that normally interacts with the protein. The target can be a ligand, a substrate or a binding partner that the protein normally interacts with (for example, epinephrine or norepinephrine). Such assays typically include the steps of combining the variant protein with a candidate compound under conditions that allow the variant protein, or fragment thereof, to interact with the target molecule, and to detect the formation of a complex between the protein and the target or to detect the biochemical consequence of the interaction with the variant protein and the target, such as any of the associated effects of signal transduction.

Candidate compounds include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam *et al.*, *Nature* 354:82-84 (1991); Houghten *et al.*, *Nature* 354:84-86 (1991)) and combinatorial chemistry-derived molecular libraries made of D- and/or L- configuration amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang *et al.*, *Cell* 72:767-778 (1993)); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')₂, Fab expression library fragments, and epitope-binding fragments of antibodies); and 4) small organic and inorganic molecules (e.g., molecules obtained from combinatorial and natural product libraries).

One candidate compound is a soluble fragment of the variant protein that competes for ligand binding. Other candidate compounds include mutant proteins or appropriate fragments containing mutations that affect variant protein function and thus compete for ligand. Accordingly, a fragment that competes for ligand, for example with a higher affinity, or a fragment that binds ligand but does not allow release, is encompassed by the invention.

The invention further includes other end point assays to identify compounds that modulate (stimulate or inhibit) variant protein activity. The assays typically involve an assay of events in the signal transduction pathway that indicate protein activity. Thus, the expression of genes that are up or down-regulated in response to the variant protein dependent signal cascade can be assayed. In one embodiment, the regulatory region of such genes can be operably linked to a marker that is easily detectable, such as luciferase. Alternatively, phosphorylation of the variant protein, or a variant protein target, could also be measured. Any of the biological or biochemical functions mediated by the variant protein can be used as an endpoint assay. These include all of the biochemical or biological events described herein for these endpoint assay targets, and other functions known to those of ordinary skill in the art.

Binding and/or activating compounds can also be screened by using chimeric variant proteins in which an amino terminal extracellular domain or parts thereof, an entire transmembrane domain or subregions, and/or the carboxyl terminal intracellular domain or parts thereof, can be replaced by heterologous domains or subregions. For example, a

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substrate-binding region can be used that interacts with a different substrate than that which is normally recognized by a variant protein. Accordingly, a different set of signal transduction components is available as an end-point assay for activation. This allows for assays to be performed in other than the specific host cell from which the variant protein is derived.

The variant proteins are also useful in competition binding assays in methods designed to discover compounds that interact with the variant protein. Thus, a compound can be exposed to a variant protein under conditions that allow the compound to bind or to otherwise interact with the variant protein. A binding partner, such as ligand, that normally interacts with the variant protein is also added to the mixture. If the test compound interacts with the variant protein or its binding partner, it decreases the amount of complex formed or activity from the variant protein. This type of assay is particularly useful in screening for compounds that interact with specific regions of the variant protein (Hodgson, *Bio/technology*, 1992, Sept 10(9), 973-80).

To perform cell-free drug screening assays, it is sometimes desirable to immobilize either the variant protein or a fragment thereof, or its target molecule, to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Any method for immobilizing proteins on matrices can be used in drug screening assays. In one embodiment, a fusion protein containing an added domain allows the protein to be bound to a matrix. For example, glutathione-S-transferase/¹²⁵I fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the cell lysates (e.g., ³⁵S-labeled) and a candidate compound, such as a drug candidate, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads can be washed to remove any unbound label, and the matrix immobilized and radiolabel determined directly, or in the supernatant after the complexes are dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of bound material found in the bead fraction quantitated from the gel using standard electrophoretic techniques.

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Either the variant protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Alternatively, antibodies reactive with the variant protein but which do not interfere with binding of the variant protein to its target molecule can be derivatized to the wells of the plate, and the variant protein trapped in the wells by antibody conjugation. Preparations of the target molecule and a candidate compound are incubated in the variant protein-presenting wells and the amount of complex trapped in the well can be quantitated. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the protein target molecule, or which are reactive with variant protein and compete with the target molecule, and enzyme-linked assays that rely on detecting an enzymatic activity associated with the target molecule.

Modulators of variant protein activity identified according to these drug screening assays can be used to treat a subject with a disorder mediated by the protein pathway, such as cardiovascular disease. These methods of treatment typically include the steps of administering the modulators of protein activity in a pharmaceutical composition to a subject in need of such treatment.

The variant proteins, or fragments thereof, disclosed herein can themselves be directly used to treat a disorder characterized by an absence of, inappropriate, or unwanted expression or activity of the variant protein. Accordingly, methods for treatment include the use of a variant protein disclosed herein or fragments thereof.

In yet another aspect of the invention, variant proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J. Biol. Chem.* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300) to identify other proteins that bind to or interact with the variant protein and are involved in variant protein activity. Such variant protein-binding proteins are also likely to be involved in the propagation of signals by the variant proteins or variant protein targets as, for example, elements of a protein-mediated signaling pathway. Alternatively, such variant protein-binding proteins are inhibitors of the variant protein.

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The two-hybrid system is based on the modular nature of most transcription factors, which typically consist of separable DNA-binding and activation domains. Briefly, the assay typically utilizes two different DNA constructs. In one construct, the gene that codes for a variant protein is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a variant protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein that interacts with the variant protein.

Antibodies Directed to Variant Proteins

The present invention also provides antibodies that selectively bind to the variant proteins disclosed herein and fragments thereof. Such antibodies may be used to quantitatively or qualitatively detect the variant proteins of the present invention. As used herein, an antibody selectively binds a target variant protein when it binds the variant protein and does not significantly bind to non-variant proteins, i.e., the antibody does not significantly bind to normal, wild-type, or art-known proteins that do not contain a variant amino acid sequence due to one or more SNPs of the present invention (variant amino acid sequences may be due to, for example, nonsynonymous cSNPs, nonsense SNPs that create a stop codon, thereby causing a truncation of a polypeptide or SNPs that cause read-through mutations resulting in an extension of a polypeptide).

As used herein, an antibody is defined in terms consistent with that recognized in the art: they are multi-subunit proteins produced by an organism in response to an antigen challenge. The antibodies of the present invention include both monoclonal antibodies and polyclonal antibodies, as well as antigen-reactive proteolytic fragments of such antibodies,

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such as Fab, F(ab)₂, and Fv fragments. In addition, an antibody of the present invention further includes any of a variety of engineered antigen-binding molecules such as a chimeric antibody (U.S. Patent Nos. 4,816,567 and 4,816,397; Morrison *et al.*, *Proc. Natl. Acad. Sci. USA*, 81:6851, 1984; Neuberger *et al.*, *Nature* 312:604, 1984), a humanized antibody (U.S. Patent Nos. 5,693,762; 5,585,089; and 5,565,332), a single-chain Fv (U.S. Patent No. 4,946,778; Ward *et al.*, *Nature* 334:544, 1989), a bispecific antibody with two binding specificities (Segal *et al.*, *J. Immunol. Methods* 248:1, 2001; Carter, *J. Immunol. Methods* 248:7, 2001), a diabody, a triabody, and a tetrabody (Todorovska *et al.*, *J. Immunol. Methods*, 248:47, 2001), as well as a Fab conjugate (dimer or trimer), and a minibody.

Many methods are known in the art for generating and/or identifying antibodies to a given target antigen (Harlow, *Antibodies*, Cold Spring Harbor Press, (1989)). In general, an isolated peptide (e.g., a variant protein of the present invention) is used as an immunogen and is administered to a mammalian organism, such as a rat, rabbit, hamster or mouse. Either a full-length protein, an antigenic peptide fragment (e.g., a peptide fragment containing a region that varies between a variant protein and a corresponding wild-type protein), or a fusion protein can be used. A protein used as an immunogen may be naturally-occurring, synthetic or recombinantly produced, and may be administered in combination with an adjuvant, including but not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substance such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and the like.

Monoclonal antibodies can be produced by hybridoma technology (Kohler and Milstein, *Nature*, 256:495, 1975); which immortalizes cells secreting a specific monoclonal antibody. The immortalized cell lines can be created *in vitro* by fusing two different cell types, typically lymphocytes, and tumor cells. The hybridoma cells may be cultivated *in vitro* or *in vivo*. Additionally, fully human antibodies can be generated by transgenic animals (He *et al.*, *J. Immunol.*, 169:595, 2002). Fd phage and Fd phagemid technologies may be used to generate and select recombinant antibodies *in vitro* (Hoogenboom and Chames, *Immunol. Today* 21:371, 2000; Liu *et al.*, *J. Mol. Biol.* 315:1063, 2002). The complementarity-determining regions of an antibody can be

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identified, and synthetic peptides corresponding to such regions may be used to mediate antigen binding (U.S. Patent No. 5,637,677).

Antibodies are preferably prepared against regions or discrete fragments of a variant protein containing a variant amino acid sequence as compared to the corresponding wild-type protein (e.g., a region of a variant protein that includes an amino acid encoded by a nonsynonymous cSNP, a region affected by truncation caused by a nonsense SNP that creates a stop codon, or a region resulting from the destruction of a stop codon due to read-through mutation caused by a SNP). Furthermore, preferred regions will include those involved in function/activity and/or protein/binding partner interaction. Such fragments can be selected on a physical property, such as fragments corresponding to regions that are located on the surface of the protein, e.g., hydrophilic regions, or can be selected based on sequence uniqueness, or based on the position of the variant amino acid residue(s) encoded by the SNPs provided by the present invention. An antigenic fragment will typically comprise at least about 8-10 contiguous amino acid residues in which at least one of the amino acid residues is an amino acid affected by a SNP disclosed herein. The antigenic peptide can comprise, however, at least 12, 14, 16, 20, 25, 50, 100 (or any other number in-between) or more amino acid residues, provided that at least one amino acid is affected by a SNP disclosed herein.

Detection of an antibody of the present invention can be facilitated by coupling (i.e., physically linking) the antibody or an antigen-reactive fragment thereof to a detectable substance. Detectable substances include, but are not limited to, various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

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Antibodies, particularly the use of antibodies as therapeutic agents, are reviewed in: Morgan, "Antibody therapy for Alzheimer's disease", *Expert Rev Vaccines*. 2003 Feb;2(1):53-9; Ross et al., "Anticancer antibodies", *Am J Clin Pathol*. 2003 Apr;119(4):472-85; Goldenberg, "Advancing role of radiolabeled antibodies in the therapy of cancer", *Cancer Immunol Immunother*. 2003 May;52(5):281-96. Epub 2003 Mar 11; Ross et al., "Antibody-based therapeutics in oncology", *Expert Rev Anticancer Ther*. 2003 Feb;3(1):107-21; Cao et al., "Bispecific antibody conjugates in therapeutics", *Adv Drug Deliv Rev*. 2003 Feb 10;55(2):171-97; von Mehren et al., "Monoclonal antibody therapy for cancer", *Annu Rev Med*. 2003;54:343-69. Epub 2001 Dec 03; Hudson et al., "Engineered antibodies", *Nat Med*. 2003 Jan;9(1):129-34; Brekke et al., "Therapeutic antibodies for human diseases at the dawn of the twenty-first century", *Nat Rev Drug Discov*. 2003 Jan;2(1):52-62 (Erratum in: *Nat Rev Drug Discov*. 2003 Mar;2(3):240); Houdebine, "Antibody manufacture in transgenic animals and comparisons with other systems", *Curr Opin Biotechnol*. 2002 Dec;13(6):625-9; Andreakos et al., "Monoclonal antibodies in immune and inflammatory diseases", *Curr Opin Biotechnol*. 2002 Dec;13(6):615-20; Kellermann et al., "Antibody discovery: the use of transgenic mice to generate human monoclonal antibodies for therapeutics", *Curr Opin Biotechnol*. 2002 Dec;13(6):593-7; Pini et al., "Phage display and colony filter screening for high-throughput selection of antibody libraries", *Comb Chem High Throughput Screen*. 2002 Nov;5(7):503-10; Batra et al., "Pharmacokinetics and biodistribution of genetically engineered antibodies", *Curr Opin Biotechnol*. 2002 Dec;13(6):603-8; and Tangri et al., "Rationally engineered proteins or antibodies with absent or reduced immunogenicity", *Curr Med Chem*. 2002 Dec;9(24):2191-9.

25 Uses of Antibodies

Antibodies can be used to isolate the variant proteins of the present invention from a natural cell source or from recombinant host cells by standard techniques, such as affinity chromatography or immunoprecipitation. In addition, antibodies are useful for detecting the presence of a variant protein of the present invention in cells or tissues to determine the pattern of expression of the variant protein among various tissues in an organism and over the course of normal development or disease progression. Further, antibodies can be used to

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detect variant protein *in situ*, *in vitro*, in a bodily fluid, or in a cell lysate or supernatant in order to evaluate the amount and pattern of expression. Also, antibodies can be used to assess abnormal tissue distribution, abnormal expression during development, or expression in an abnormal condition, such as in a cardiovascular disorder or during statin treatment.

5 Additionally, antibody detection of circulating fragments of the full-length variant protein can be used to identify turnover.

Antibodies to the variant proteins of the present invention are also useful in pharmacogenomic analysis. Thus, antibodies against variant proteins encoded by alternative SNP alleles can be used to identify individuals that require modified treatment modalities.

10 Further, antibodies can be used to assess expression of the variant protein in disease states such as in active stages of the disease or in an individual with a predisposition to a disease related to the protein's function, such as a cardiovascular disorder, or during the course of a treatment regime, such as during statin treatment. Antibodies specific for a variant protein encoded by a SNP-containing nucleic acid molecule of the present invention
15 can be used to assay for the presence of the variant protein; such as to predict an individual's response to statin treatment or predisposition/susceptibility to an acute coronary event, as indicated by the presence of the variant protein.

Antibodies are also useful as diagnostic tools for evaluating the variant proteins in conjunction with analysis by electrophoretic mobility, isoelectric point, tryptic peptide
20 digest, and other physical assays well known in the art.

Antibodies are also useful for tissue typing. Thus, where a specific variant protein has been correlated with expression in a specific tissue, antibodies that are specific for this protein can be used to identify a tissue type.

Antibodies can also be used to assess aberrant subcellular localization of a variant
25 protein in cells in various tissues. The diagnostic uses can be applied, not only in genetic testing, but also in monitoring a treatment modality. Accordingly, where treatment is ultimately aimed at correcting the expression level or the presence of variant protein or aberrant tissue distribution or developmental expression of a variant protein, antibodies directed against the variant protein or relevant fragments can be used to monitor therapeutic
30 efficacy.

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The antibodies are also useful for inhibiting variant protein function, for example, by blocking the binding of a variant protein to a binding partner. These uses can also be applied in a therapeutic context in which treatment involves inhibiting a variant protein's function. An antibody can be used, for example, to block or competitively inhibit binding, thus modulating (agonizing or antagonizing) the activity of a variant protein. Antibodies can be prepared against specific variant protein fragments containing sites required for function or against an intact variant protein that is associated with a cell or cell membrane. For *in vivo* administration, an antibody may be linked with an additional therapeutic payload such as a radionuclide, an enzyme, an immunogenic epitope, or a cytotoxic agent. Suitable cytotoxic agents include, but are not limited to, bacterial toxin such as diphtheria, and plant toxin such as ricin. The *in vivo* half-life of an antibody or a fragment thereof may be lengthened by pegylation through conjugation to polyethylene glycol (Leong *et al.*, *Cytokine* 16:106, 2001).

The invention also encompasses kits for using antibodies, such as kits for detecting the presence of a variant protein in a test sample. An exemplary kit can comprise antibodies such as a labeled or labelable antibody and a compound or agent for detecting variant proteins in a biological sample; means for determining the amount, or presence/absence of variant protein in the sample; means for comparing the amount of variant protein in the sample with a standard; and instructions for use.

20

Vectors and Host Cells

The present invention also provides vectors containing the SNP-containing nucleic acid molecules described herein. The term "vector" refers to a vehicle, preferably a nucleic acid molecule, which can transport a SNP-containing nucleic acid molecule. When the vector is a nucleic acid molecule, the SNP-containing nucleic acid molecule can be covalently linked to the vector nucleic acid. Such vectors include, but are not limited to, a plasmid, single or double stranded phage, a single or double stranded RNA or DNA viral vector, or artificial chromosome, such as a BAC, PAC, YAC, or MAC.

A vector can be maintained in a host cell as an extrachromosomal element where it replicates and produces additional copies of the SNP-containing nucleic acid molecules.

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Alternatively, the vector may integrate into the host cell genome and produce additional copies of the SNP-containing nucleic acid molecules when the host cell replicates.

The invention provides vectors for the maintenance (cloning vectors) or vectors for expression (expression vectors) of the SNP-containing nucleic acid molecules. The vectors
5 can function in prokaryotic or eukaryotic cells or in both (shuttle vectors).

Expression vectors typically contain cis-acting regulatory regions that are operably linked in the vector to the SNP-containing nucleic acid molecules such that transcription of the SNP-containing nucleic acid molecules is allowed in a host cell. The SNP-containing nucleic acid molecules can also be introduced into the host cell with a separate nucleic acid
10 molecule capable of affecting transcription. Thus, the second nucleic acid molecule may provide a trans-acting factor interacting with the cis-regulatory control region to allow transcription of the SNP-containing nucleic acid molecules from the vector. Alternatively, a trans-acting factor may be supplied by the host cell. Finally, a trans-acting factor can be produced from the vector itself. It is understood, however, that in some embodiments,
15 transcription and/or translation of the nucleic acid molecules can occur in a cell-free system.

The regulatory sequences to which the SNP-containing nucleic acid molecules described herein can be operably linked include promoters for directing mRNA transcription. These include, but are not limited to, the left promoter from bacteriophage λ , the lac, TRP, and TAC promoters from *E. coli*, the early and late promoters from SV40, the
20 CMV immediate early promoter, the adenovirus early and late promoters, and retrovirus long-terminal repeats.

In addition to control regions that promote transcription, expression vectors may also include regions that modulate transcription, such as repressor binding sites and enhancers. Examples include the SV40 enhancer, the cytomegalovirus immediate early enhancer,
25 polyoma enhancer, adenovirus enhancers, and retrovirus LTR enhancers.

In addition to containing sites for transcription initiation and control, expression vectors can also contain sequences necessary for transcription termination and, in the transcribed region, a ribosome-binding site for translation. Other regulatory control elements for expression include initiation and termination codons as well as polyadenylation
30 signals. A person of ordinary skill in the art would be aware of the numerous regulatory sequences that are useful in expression vectors (see, e.g., Sambrook and Russell, 2000,

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Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

5 A variety of expression vectors can be used to express a SNP-containing nucleic acid molecule. Such vectors include chromosomal, episomal, and virus-derived vectors, for example, vectors derived from bacterial plasmids, from bacteriophage, from yeast episomes, from yeast chromosomal elements, including yeast artificial chromosomes, from viruses such as baculoviruses, papovaviruses such as SV40, Vaccinia viruses, adenoviruses, poxviruses, pseudorabies viruses, and retroviruses. Vectors can also be derived from combinations of these sources such as those derived from plasmid and bacteriophage genetic
10 elements, e.g., cosmids and phagemids. Appropriate cloning and expression vectors for prokaryotic and eukaryotic hosts are described in Sambrook and Russell, 2000, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

15 The regulatory sequence in a vector may provide constitutive expression in one or more host cells (e.g., tissue specific expression) or may provide for inducible expression in one or more cell types such as by temperature, nutrient additive, or exogenous factor, e.g., a hormone or other ligand. A variety of vectors that provide constitutive or inducible expression of a nucleic acid sequence in prokaryotic and eukaryotic host cells are well known to those of ordinary skill in the art.

20 A SNP-containing nucleic acid molecule can be inserted into the vector by methodology well-known in the art. Generally, the SNP-containing nucleic acid molecule that will ultimately be expressed is joined to an expression vector by cleaving the SNP-containing nucleic acid molecule and the expression vector with one or more restriction enzymes and then ligating the fragments together. Procedures for restriction enzyme
25 digestion and ligation are well known to those of ordinary skill in the art.

The vector containing the appropriate nucleic acid molecule can be introduced into an appropriate host cell for propagation or expression using well-known techniques. Bacterial host cells include, but are not limited to, *E. coli*, *Streptomyces*, and *Salmonella typhimurium*. Eukaryotic host cells include, but are not limited to, yeast, insect cells such as
30 *Drosophila*, animal cells such as COS and CHO cells, and plant cells.

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As described herein, it may be desirable to express the variant peptide as a fusion protein. Accordingly, the invention provides fusion vectors that allow for the production of the variant peptides. Fusion vectors can, for example, increase the expression of a recombinant protein, increase the solubility of the recombinant protein, and aid in the purification of the protein by acting, for example, as a ligand for affinity purification. A proteolytic cleavage site may be introduced at the junction of the fusion moiety so that the desired variant peptide can ultimately be separated from the fusion moiety. Proteolytic enzymes suitable for such use include, but are not limited to, factor Xa, thrombin, and enterokinase. Typical fusion expression vectors include pGEX (Smith et al., *Gene* 67:31-40 (1988)), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann et al., *Gene* 69:301-315 (1988)) and pET11d (Studier et al., *Gene Expression Technology: Methods in Enzymology* 185:60-89 (1990)).

Recombinant protein expression can be maximized in a bacterial host by providing a genetic background wherein the host cell has an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Alternatively, the sequence of the SNP-containing nucleic acid molecule of interest can be altered to provide preferential codon usage for a specific host cell, for example, *E. coli* (Wada et al., *Nucleic Acids Res.* 20:2111-2118 (1992)).

The SNP-containing nucleic acid molecules can also be expressed by expression vectors that are operative in yeast. Examples of vectors for expression in yeast (e.g., *S. cerevisiae*) include pYepSec1 (Baldari, et al., *EMBO J.* 6:229-234 (1987)), pMFa (Kurjan et al., *Cell* 30:933-943(1982)), pJRY88 (Schultz et al., *Gene* 54:113-123 (1987)), and pYES2 (Invitrogen Corporation, San Diego, CA).

The SNP-containing nucleic acid molecules can also be expressed in insect cells using, for example, baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf9 cells) include the pAc series (Smith

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et al., *Mol. Cell Biol.* 3:2156-2165 (1983)) and the pVL series (Lucklow et al., *Virology* 170:31-39 (1989)).

In certain embodiments of the invention, the SNP-containing nucleic acid molecules described herein are expressed in mammalian cells using mammalian expression vectors.

5 Examples of mammalian expression vectors include pCDM8 (Seed, B. *Nature* 329:840(1987)) and pMT2PC (Kaufman et al., *EMBO J.* 6:187-195 (1987)).

The invention also encompasses vectors in which the SNP-containing nucleic acid molecules described herein are cloned into the vector in reverse orientation, but operably linked to a regulatory sequence that permits transcription of antisense RNA. Thus, an
10 antisense transcript can be produced to the SNP-containing nucleic acid sequences described herein, including both coding and non-coding regions. Expression of this antisense RNA is subject to each of the parameters described above in relation to expression of the sense RNA (regulatory sequences, constitutive or inducible expression, tissue-specific expression).

The invention also relates to recombinant host cells containing the vectors described
15 herein. Host cells therefore include, for example, prokaryotic cells, lower eukaryotic cells such as yeast, other eukaryotic cells such as insect cells, and higher eukaryotic cells such as mammalian cells.

The recombinant host cells can be prepared by introducing the vector constructs described herein into the cells by techniques readily available to persons of ordinary skill in
20 the art. These include, but are not limited to, calcium phosphate transfection, DEAE-dextran-mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, lipofection, and other techniques such as those described in Sambrook and Russell, 2000, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

25 Host cells can contain more than one vector. Thus, different SNP-containing nucleotide sequences can be introduced in different vectors into the same cell. Similarly, the SNP-containing nucleic acid molecules can be introduced either alone or with other nucleic acid molecules that are not related to the SNP-containing nucleic acid molecules, such as those providing trans-acting factors for expression vectors. When more than one vector is
30 introduced into a cell, the vectors can be introduced independently, co-introduced, or joined to the nucleic acid molecule vector.

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In the case of bacteriophage and viral vectors, these can be introduced into cells as packaged or encapsulated virus by standard procedures for infection and transduction. Viral vectors can be replication-competent or replication-defective. In the case in which viral replication is defective, replication can occur in host cells that provide functions that complement the defects.

Vectors generally include selectable markers that enable the selection of the subpopulation of cells that contain the recombinant vector constructs. The marker can be inserted in the same vector that contains the SNP-containing nucleic acid molecules described herein or may be in a separate vector. Markers include, for example, tetracycline or ampicillin-resistance genes for prokaryotic host cells, and dihydrofolate reductase or neomycin resistance genes for eukaryotic host cells. However, any marker that provides selection for a phenotypic trait can be effective.

While the mature variant proteins can be produced in bacteria, yeast, mammalian cells, and other cells under the control of the appropriate regulatory sequences, cell-free transcription and translation systems can also be used to produce these variant proteins using RNA derived from the DNA constructs described herein.

Where secretion of the variant protein is desired, which is difficult to achieve with multi-transmembrane domain containing proteins such as G-protein-coupled receptors (GPCRs), appropriate secretion signals can be incorporated into the vector. The signal sequence can be endogenous to the peptides or heterologous to these peptides.

Where the variant protein is not secreted into the medium, the protein can be isolated from the host cell by standard disruption procedures, including freeze/thaw, sonication, mechanical disruption, use of lysing agents, and the like. The variant protein can then be recovered and purified by well-known purification methods including, for example, ammonium sulfate precipitation, acid extraction, anion or cationic exchange chromatography, phosphocellulose chromatography, hydrophobic-interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, or high performance liquid chromatography.

It is also understood that, depending upon the host cell in which recombinant production of the variant proteins described herein occurs, they can have various glycosylation patterns, or may be non-glycosylated, as when produced in bacteria. In

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addition, the variant proteins may include an initial modified methionine in some cases as a result of a host-mediated process.

For further information regarding vectors and host cells, see *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y.

5

Uses of Vectors and Host Cells, and Transgenic Animals

Recombinant host cells that express the variant proteins described herein have a variety of uses. For example, the cells are useful for producing a variant protein that can be further purified into a preparation of desired amounts of the variant protein or fragments thereof. Thus, host cells containing expression vectors are useful for variant protein production.

Host cells are also useful for conducting cell-based assays involving the variant protein or variant protein fragments, such as those described above as well as other formats known in the art. Thus, a recombinant host cell expressing a variant protein is useful for assaying compounds that stimulate or inhibit variant protein function. Such an ability of a compound to modulate variant protein function may not be apparent from assays of the compound on the native/wild-type protein, or from cell-free assays of the compound. Recombinant host cells are also useful for assaying functional alterations in the variant proteins as compared with a known function.

Genetically-engineered host cells can be further used to produce non-human transgenic animals. A transgenic animal is preferably a non-human mammal, for example, a rodent, such as a rat or mouse, in which one or more of the cells of the animal include a transgene. A transgene is exogenous DNA containing a SNP of the present invention which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal in one or more of its cell types or tissues. Such animals are useful for studying the function of a variant protein *in vivo*, and identifying and evaluating modulators of variant protein activity. Other examples of transgenic animals include, but are not limited to, non-human primates, sheep, dogs, cows, goats, chickens, and amphibians. Transgenic non-human mammals such as cows and goats can be used to produce variant proteins which can be secreted in the animal's milk and then recovered.

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A transgenic animal can be produced by introducing a SNP-containing nucleic acid molecule into the male pronuclei of a fertilized oocyte, e.g., by microinjection or retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Any nucleic acid molecules that contain one or more SNPs of the present invention can
5 potentially be introduced as a transgene into the genome of a non-human animal.

Any of the regulatory or other sequences useful in expression vectors can form part of the transgenic sequence. This includes intronic sequences and polyadenylation signals, if not already included. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the variant protein in particular cells or tissues.

10 Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described in, for example, U.S. Patent Nos. 4,736,866 and 4,870,009, both by Leder et al., U.S. Patent No. 4,873,191 by Wagner et al., and in Hogan, B., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Similar
15 methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of transgenic mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene can further be bred to other transgenic animals carrying other
20 transgenes. A transgenic animal also includes a non-human animal in which the entire animal or tissues in the animal have been produced using the homologously recombinant host cells described herein.

In another embodiment, transgenic non-human animals can be produced which contain selected systems that allow for regulated expression of the transgene. One example
25 of such a system is the cre/loxP recombinase system of bacteriophage P1 (Lakso et al. *PNAS* 89:6232-6236 (1992)). Another example of a recombinase system is the FLP recombinase system of *S. cerevisiae* (O'Gorman et al. *Science* 251:1351-1355 (1991)). If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are generally needed.
30 Such animals can be provided through the construction of "double" transgenic animals, e.g.,

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by mating two transgenic animals, one containing a transgene encoding a selected variant protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in, for example, Wilmut, I. et al. *Nature* 385:810-813
 5 (1997) and PCT International Publication Nos. WO 97/07668 and WO 97/07669. In brief, a cell (e.g., a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops
 10 to morula or blastocyst and then transferred to pseudopregnant female foster animal. The offspring born of this female foster animal will be a clone of the animal from which the cell (e.g., a somatic cell) is isolated.

Transgenic animals containing recombinant cells that express the variant proteins described herein are useful for conducting the assays described herein in an *in vivo* context.
 15 Accordingly, the various physiological factors that are present *in vivo* and that could influence ligand or substrate binding, variant protein activation, signal transduction, or other processes or interactions, may not be evident from *in vitro* cell-free or cell-based assays. Thus, non-human transgenic animals of the present invention may be used to assay *in vivo* variant protein function as well as the activities of a therapeutic agent or compound that
 20 modulates variant protein function/activity or expression. Such animals are also suitable for assessing the effects of null mutations (i.e., mutations that substantially or completely eliminate one or more variant protein functions).

For further information regarding transgenic animals, see Houdebine, "Antibody manufacture in transgenic animals and comparisons with other systems", *Curr Opin*
 25 *Biotechnol.* 2002 Dec;13(6):625-9; Petters et al., "Transgenic animals as models for human disease", *Transgenic Res.* 2000;9(4-5):347-51; discussion 345-6; Wolf et al., "Use of transgenic animals in understanding molecular mechanisms of toxicity", *J Pharm Pharmacol.* 1998 Jun;50(6):567-74; Echelard, "Recombinant protein production in transgenic animals", *Curr Opin Biotechnol.* 1996 Oct;7(5):536-40; Houdebine, "Transgenic
 30 animal bioreactors", *Transgenic Res.* 2000;9(4-5):305-20; Pirity et al., "Embryonic stem cells, creating transgenic animals", *Methods Cell Biol.* 1998;57:279-93; and Robl et al.,

"Artificial chromosome vectors and expression of complex proteins in transgenic animals",
Theriogenology. 2003 Jan 1;59(1):107-13.

COMPUTER-RELATED EMBODIMENTS

5 The SNPs provided in the present invention may be "provided" in a variety of
mediums to facilitate use thereof. As used in this section, "provided" refers to a
manufacture, other than an isolated nucleic acid molecule, that contains SNP information
of the present invention. Such a manufacture provides the SNP information in a form
that allows a skilled artisan to examine the manufacture using means not directly
10 applicable to examining the SNPs or a subset thereof as they exist in nature or in purified
form. The SNP information that may be provided in such a form includes any of the SNP
information provided by the present invention such as, for example, polymorphic nucleic
acid and/or amino acid sequence information such as SEQ ID NOS: 2-55, SEQ ID
NOS: 56-109, SEQ ID NOS: 167-185, SEQ ID NOS: 110-116, and SEQ ID
15 NOS: 186-206 & 267; information about observed SNP alleles, alternative codons,
populations, allele frequencies, SNP types, and/or affected proteins; or any other
information provided by the present invention in Tables 1-2 and/or the Sequence Listing.

 In one application of this embodiment, the SNPs of the present invention can be
recorded on a computer readable medium. As used herein, "computer readable medium"
20 refers to any medium that can be read and accessed directly by a computer. Such media
include, but are not limited to: magnetic storage media, such as floppy discs, hard disc
storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical
storage media such as RAM and ROM; and hybrids of these categories such as
magnetic/optical storage media. A skilled artisan can readily appreciate how any of the
25 presently known computer readable media can be used to create a manufacture
comprising computer readable medium having recorded thereon a nucleotide sequence of
the present invention. One such medium is provided with the present application,
namely, the present application contains computer readable medium (CD-R) that has
nucleic acid sequences (and encoded protein sequences) containing SNPs
30 provided/recorded thereon in ASCII text format in a Sequence Listing along with
accompanying Tables that contain detailed SNP and sequence information (transcript

sequences are provided as SEQ ID NOS: 2-55, protein sequences are provided as SEQ ID NOS: 56-109, genomic sequences are provided as SEQ ID NOS: 167-185, transcript-based context sequences are provided as SEQ ID NOS: 110-116, and genomic-based context sequences are provided as SEQ ID NOS: 186-206 & 267).

5 As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the SNP information of the present invention.

10 A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide or amino acid sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide/amino acid sequence information of the present invention on computer readable medium. For example, the
15 sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, represented in the form of an ASCII file, or stored in a database application, such as OB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g., text file or database) in order to obtain computer readable
20 medium having recorded thereon the SNP information of the present invention.

By providing the SNPs of the present invention in computer readable form, a skilled artisan can routinely access the SNP information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Examples of publicly available
25 computer software include BLAST (Altschul et al, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag et al, *Comp. Chem.* 17:203-207 (1993)) search algorithms.

The present invention further provides systems, particularly computer-based systems, which contain the SNP information described herein. Such systems may be designed to store and/or analyze information on, for example, a large number of SNP
30 positions, or information on SNP genotypes from a large number of individuals. The SNP information of the present invention represents a valuable information source. The SNP

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information of the present invention stored/analyzed in a computer-based system may be used for such computer-intensive applications as determining or analyzing SNP allele frequencies in a population, mapping disease genes, genotype-phenotype association studies, grouping SNPs into haplotypes, correlating SNP haplotypes with response to particular drugs, or for various other bioinformatic, pharmacogenomic, drug development, or human identification/forensic applications.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the SNP information of the present invention. The minimum hardware means of the computer-based systems of the present invention typically comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. Such a system can be changed into a system of the present invention by utilizing the SNP information provided on the CD-R, or a subset thereof, without any experimentation.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein SNPs of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store SNP information of the present invention, or a memory access means which can access manufactures having recorded thereon the SNP information of the present invention.

As used herein, "search means" refers to one or more programs or algorithms that are implemented on the computer-based system to identify or analyze SNPs in a target sequence based on the SNP information stored within the data storage means. Search means can be used to determine which nucleotide is present at a particular SNP position in the target sequence. As used herein, a "target sequence" can be any DNA sequence containing the SNP position(s) to be searched or queried.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences containing a SNP position in which the sequence(s) is chosen based on a three-dimensional configuration that is formed upon the folding of the target motif. There are a variety of target motifs known in

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the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures, and inducible expression elements (protein binding sequences).

5 A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. An exemplary format for an output means is a display that depicts the presence or absence of specified nucleotides (alleles) at particular SNP positions of interest. Such presentation can provide a rapid, binary scoring system for many SNPs simultaneously.

10 One exemplary embodiment of a computer-based system comprising SNP information of the present invention is provided in Figure 1. Figure 1 provides a block diagram of a computer system 102 that can be used to implement the present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard
15 drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be
20 inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable storage medium 116 once inserted in the removable medium storage device 114.

25 The SNP information of the present invention may be stored in a well-known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. Software for accessing and processing the SNP information (such as SNP scoring tools, search tools, comparing tools, etc.) preferably resides in main memory 108 during execution.

30

EXAMPLES

The following examples are offered to illustrate, but not to limit the claimed invention.

5 **Example 1: Statistical Analysis of SNP Allele Association with Cardiovascular Disorders and Statin Response**

Study design

In order to identify genetic markers associated with acute coronary events (e.g. MI, stroke, unstable angina, congestive heart failure, etc.) or response to statin treatment
 10 for the prevention of coronary events, samples from the Cholesterol and Recurrent Events (CARE) study (a randomized multicentral double-blinded trial on secondary prevention of acute coronary events with pravastatin) (Sacks *et al.*, 1991, *Am. J. Cardiol.* 68: 1436-1446) were genotyped. A well-documented myocardial infarction (MI) was one of the enrollment criteria for entry into the CARE study. Patients were enrolled in the
 15 CARE trial from 80 participating study centers. Men and post-menopausal women were eligible for the trial if they had had an acute MI between 3 and 20 months prior to randomization, were 21 to 75 years of age, and had plasma total cholesterol levels of less than 240 mg/deciliter, LDL cholesterol levels of 115 to 174 mgs/deciliter, fasting triglyceride levels of less than 350 mgs/deciliter, fasting glucose levels of no more than
 20 220 mgs/deciliter, left ventricular ejection fractions of no less than 25 %, and no symptomatic congestive heart failure. Patients were randomized to receive either 40 mg of pravastatin once daily or a matching placebo. The primary endpoint of the trial was death from coronary heart disease and the median duration of follow-up was 5.0 years (range, 4.0 to 6.2 years). Patients enrolled in the CARE study who received placebo had
 25 a 5 year risk of having a recurrent MI (RMI) of 9.5% while those patients enrolled in the study that received pravastatin had a 5 year risk of having a RMI of only 7.2% ($p_{\text{LogRank}}=0.0234$) (25% reduction in risk for RMI in treatment vs. placebo groups, Cox Proportional Hazard Ratio [$HR_{\text{age-adjusted}}$] =0.75 [95% CI: 0.58-0.97, $p=0.0256$]). Secondary endpoints of other related cardiovascular or metabolic disease events, and
 30 changes in clinical variables were also recorded in pravastatin-treated and placebo groups. Examples of secondary endpoints are listed in Tables 6-8. All individuals

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included in the study had signed a written informed consent form and the study protocol was approved by the respective Institutional Review Boards (IRBs).

For genotyping SNPs in CARE patient samples, DNA was extracted from blood samples using conventional DNA extraction methods such as the QIA-amp kit from Qiagen. Allele specific primers were designed for detecting each SNP and they are shown in Table 5. Genotypes were obtained on an ABI PRISM® 7900HT Sequence Detection PCR system (Applied Biosystems, Foster City, CA) by kinetic allele-specific PCR, similar to the method described by Germer et al. (Germer S., Holland M.J., Higuchi R. 2000, *Genome Res.* 10: 258-266).

In the first analysis of samples obtained from patients enrolled in the CARE study, SNP genotype frequencies in a group of 264 patients who had a second MI during the 5 years of CARE follow-up (cases) were compared with the frequencies in the group of 1255 CARE patients who had not experienced second MI (controls). Logistic regression was used to adjust for the major epidemiologic risk factors with the specific emphasis on the interaction between the risk factors and tested SNPs to identify SNPs significantly associated with RMI when patients were stratified by sex, family history, smoking status, body mass index (BMI), ApoE status or hypertension.

To replicate initial findings, a second group of 394 CARE patients were analyzed who had a history of an MI prior to the MI at CARE enrollment (i.e., patients who had experienced a RMI at enrollment) but who had not experienced an MI during trial follow-up (cases), and 1221 of CARE MI patients without second MI were used as controls. No patients from first analysis (cases or controls) were used in this second analysis (cases or controls). There are significant clinical differences between the two analyses e.g., in the first analysis, all MI patients were in a carefully monitored clinical environment prior to their second MI, which could modulate effect of genetic polymorphisms, whereas in the second analysis, only a small portion of patients were treated by lipid lowering drugs prior to second MI. Despite these differences, numerous markers associated with RMI in the first analysis were also found to be associated with RMI in the second analysis (see Table 9).

Additionally, genetic markers identified as associated with acute coronary events or response to statin treatment for the prevention of coronary events in the CARE

samples were also genotyped in a second sample set, the West of Scotland Coronary Prevention Study (WOSCOPS) sample set. The design of the original WOSCOPS cohort and the nested case-control study have been described (Shepherd et. al, N. Eng. J. Med., Nov. 16: 333 (20), pp. 1301-7 1995; Packard et. al. N. Eng. J. Med., Oct. 19: 343 (16), pp. 1148-55, 2000). The objective of the WOSCOPS trial was to assess pravastatin efficacy at reducing risk of primary MI or coronary death among Scottish men with hypercholesterolemia (fasting LDL cholesterol > 155 mg/dl). Participants in the WOSCOPS study were 45-64 years of age and followed for an average of 4.9 years for coronary events. The nested case-control study included as cases all WOSCOPS patients who experienced a coronary event (confirmed nonfatal MI, death from coronary heart disease, or a revascularization procedure; N=580). Controls were 1160 age and smoking status-matched unaffected patients. All individuals included in the study had signed a written informed consent form and the study protocol was approved by IRBs. DNA was extracted and genotyped as described above.

Statistical analysis for association of SNPs with specific clinical endpoints

Qualitative phenotypes of the patients who were genotyped (Table 4) were analyzed using an overall logistic regression model that included an intercept, a parameter for the effect of a genotype containing two rare alleles versus a genotype containing no rare alleles, and a parameter for the effect of a genotype containing one rare allele versus a genotype containing no rare alleles. The test of the overall model is a chi-square test with five degrees of freedom for analyses containing all three genotypes, and four degrees of freedom for analyses containing two genotypes. An example of a SNP associated with increased risk for RMI is hCV529710 (Table 6). hCV529710 is strongly associated with Fatal CHD (Coronary Heart Disease)/Non-fatal MI and Fatal Atherosclerotic Cardiovascular Disease (Relative Risk = 1.5 and 2.3, and p-values <0.05 and <0.005, respectively).

Quantitative phenotypes of the patients who were genotyped (Table 5) were also analyzed using an overall generalized linear model (GLM) that included an intercept, a parameter for the effect of a genotype containing two rare alleles, and a parameter for the

effect of a genotype containing one rare allele. The test of the overall GLM model is an F-test.

Effect sizes for association of SNPs with endpoints were estimated through odds ratios in placebo treated patients only, separately for carriers of each genotype (groups of 0, 1, and 2 minor allele carriers). The effect was considered to be significant if the p-value for testing whether any of the SNP genotype parameters in overall model was < 0.05. An example of a SNP associated with increased risk for a quantitative phenotype such as very low density lipoproteins (VLDL) is hCV22274624 with a p value <0.0005.

Statistical analysis for association of SNPs with pravastatin treatment in cardiovascular events prevention (Table 8) was carried out using an overall logistic regression model that included an intercept, a parameter for the effect of a genotype containing two rare alleles versus a genotype containing no rare alleles, a parameter for the effect of a genotype containing one rare allele versus a genotype containing no rare alleles, a parameter for the effect of use of pravastatin versus the use of placebo, and parameters for the interaction effects between SNP genotypes and pravastatin use. The test of the overall model is a chi-square test with two degrees of freedom for analyses containing all three genotypes, and one degree of freedom for analyses containing two genotypes.

Effect sizes were estimated through odds ratios (pravastatin group versus placebo) for carriers of each genotype (groups of 0, 1, and 2 minor allele carriers). The effect was considered to be significant if p-value for testing whether any of the interactions between SNP genotypes and pravastatin use were < 0.05. An example of a SNP associated with a response to statin treatment in preventing an adverse coronary event is hCV2741051. When the pravastatin group is compared to the control group, individuals with one or two of the rare alleles had odds ratios of 0.43 and 0.26 respectively with a p-value of <0.05. This particular SNP is also associated with a reduced risk of stroke in the pravastatin treated group when one or two rare alleles are present in a patient (odds ratios of 0.21 and 0.23 p<0.05). Odds ratios less than one indicate that the specific SNP allele has a protective effect and odds ratios greater than one indicate that the specific SNP allele has an adverse effect.

Statistical analysis for the association of SNPs with RMI or stroke (Table 7) was also carried out using stepwise logistic regression. Relative risk (RR) and 95% confidence intervals (CI)s – 5-6 years relative risk of a RMI event or stroke given the SNP genotype were calculated by the Wald test. Certain SNPs show association of SNPs with adverse coronary events such as RMI and stroke in CARE samples. This association of certain SNPs with adverse coronary events could also be replicated by comparing associations observed in the first analysis of the CARE samples and the second analysis of the CARE samples (see above). An example of SNPs associated with increased risk for RMI are hCV517658 and hCV 8722981 with RR of 1.34 and 2.01 respectively. RR values <1 are associated with a reduced risk of the indicated outcome and RR values >1 are associated with an increased risk of the indicated outcome. An example of a SNP associated with decreased risk for RMI that replicated between the first and second analysis of the CARE data is hCV761961 that had ORs of 0.5 and 0.5 in the first and second analyses respectively. An example of a SNP associated with increased risk for RMI that replicated in the first and second analyses is hCV8851080 that had ORs of 2.7 and 1.9 in the first and second analyses respectively. An example of a SNP associated with increased risk for stroke that replicated in the first and second analyses of the CARE data is hCV11482766 that had ORs of 3.5 and 3.3 in the first and second analyses respectively.

For statistical analysis of association of SNPs with pravastatin treatment in RMI prevention (Table 8), effect sizes were estimated through genotypic RR, including 95% CIs. Homogeneity of Cochran-Mantel-Haenszel odds ratios was tested across pravastatin and placebo strata using the Wald test. A SNP was considered to have a significant association with response to pravastatin treatment if it exhibited Wald p-value < 0.05 in the allelic association test or in any of the 3 genotypic tests (dominant, recessive, additive). Table 8 shows association of SNPs predictive of statin response with cardiovascular events prevention under statin treatment, with an adjustment for conventional risk factors such as age, sex, smoking status, baseline glucose levels, BMI, history of hypertension, etc. (this adjustment supports independence of the SNP association from conventional risk factors). This table also provides the frequency data for the at risk allele in the columns labeled “Case Y PRIMER ALLELE Nucleotide

Frequency” and “Control Y PRIMER ALLELE Nucleotide Frequency”. Allele frequencies for the cases and controls ≤ 0.49 indicate that the at-risk allele is the minor allele. Allele frequencies ≥ 0.50 indicate that the at-risk allele is the major allele. An example of a SNP associated with increased risk for an adverse cardiovascular event in the placebo group using a dominant genotypic test is hCV25644901. The dominant genotype (GG or GA) had a RR of 1.92 of being associated with an adverse cardiovascular event in the placebo group. However, this same SNP was protective in the statin treated group with a RR of 0.58. An example of a SNP associated with an adverse cardiovascular event in the placebo group using the allelic association test is hCV16044337 with a RR of 1.87 for the homozygous AA genotype. This same genotype was protective in the statin treated group with a RR of 0.56.

The statistical results provided in Table 9 demonstrate association of a SNP in the CD6 gene (hCV2553030) that is predictive of statin response in the prevention of RMI, justified as a significant difference in risk associated with the SNP between placebo and statin treated strata (Breslow Day p-values < 0.05). Table 9 presents the results observed in samples taken from both the CARE and WOSCOP studies. In both studies the individuals homozygous for the minor allele were statistically different from heterozygous and major allele homozygous individuals in the pravastatin treated group vs. the placebo treated group. This SNP was associated with a reduced risk of an adverse coronary event in the CARE and WOSCOPS studies with RR or OR of 0.13 and 0.23 respectively in the two studies. Therefore, SNPs identified as useful for predicting RMI may also be useful for predicting increased risk for developing primary MI.

Table 10 shows the association of a SNP in the FCAR gene (hCV7841642) that is predictive of MI risk and response to statin treatment. Individuals who participated in both the CARE and WOSCOPS studies, who did not receive pravastatin treatment and who were heterozygous or homozygous for the major allele (AG or GG) (OR of 1.58, 1.52, 1.5, 1.47 in the respective studies) had a significantly higher risk of having an MI vs. individuals who were homozygous for the minor allele. However, individuals in the CARE study who were heterozygous or homozygous for the FCAR major allele were also statistically significantly protected by pravastatin treatment against an adverse coronary event relative to the individuals homozygous for the minor allele (OR 0.31,

0.79). Therefore, an allele found to be associated with risk for MI, RMI, stroke, or other adverse cardiovascular event, may also be useful for predicting responsiveness to statin treatment. SNPs associated with treatment response to pravastatin may also be predictive of responsiveness of an individual to other statins as a class.

5 The data presented in Table 6 based on an association of genotypes with pravastatin efficacy of the CARE samples were further analyzed and presented in Table 11. The further analysis was performed to align the data obtained from the analysis of the CARE samples, which was a prospective study, to the analysis of the WOSCOP samples, which was a case/control study. Table 11 also presents an analysis of the
10 association of genotypes with pravastatin efficacy in the WOSCOPs samples. Relative to the analysis performed on the data presented in Table 6, there are two significant differences to determine if the SNP influenced pravastatin efficacy. Data obtained from the CARE samples were separated by study design into two groups, those in the prospective study design group and those in the case/control study design group. The
15 original care study contained 16 protocol defined cardiovascular disease defined endpoints and 150 other phenotypes. The prospective study design presented in Table 11 only looks at two possible end points, those individuals who had a fatal MI, sudden death, or a definite non-fatal MI, or those individuals who had a fatal or non-fatal MI (probable or definite). In the case/control study design, in addition to only looking at cases that fell
20 into the two possible endpoints defined above, cases were only compared to matched controls, ie. controls matched by age, smoking status and did not have any adverse coronary events or died due to other causes. The control groups used to compare the data were also divided into two groups, the "all possible" control group and the "cleaner" control group. The all possible control group consists of all of the controls that were
25 white males and were matched for age and smoking status but had any disease outcome. The cleaner control group were also matched for age and smoking status but were further restricted to only those individuals that had MI as an outcome. Because the participants in the WOSCOPs trial were all white males, only data obtained from white males in the CARE study were analysed. Data from the "all possible" and "cleaner" controls were
30 compared to data obtained from the cases in the prospective study design while only data from "cleaner" controls were compared to cases in the case/control study design. The

data from the case/control cohorts were analysed using conditional logistic regression (as opposed to logistic regression used for the original analysis).

An example of a SNP associated with fatal MI/sudden death/non-fatal MI using data from the CARE study is hCV2442143. Patients with 0 rare alleles (or patients homozygous for the dominant allele) had an OR of 0.42 of being associated with the adverse outcome in the presence of statin treatment. Patients with one or two rare alleles had ORs of 0.78 and 1.16 respectively of being associated with the adverse outcome. However the 95% CI for these two genotypes makes the result not statistically significant.

The data presented in Table 4 based on an association of genotypes with adverse cardiovascular outcomes such as fatal or non-fatal MI were further analyzed and presented in Table 12. Similar to the data presented in Table 11, the analysis was modified to align the data obtained from the CARE samples to data obtained from the WOSCOPs samples. In addition, Table 12 also presents an analysis of the association of genotypes with adverse cardiovascular outcomes observed in the WOSCOPs samples. As above, there are two significant differences. Data obtained from the CARE samples were separated by study design into a prospective or a case/control study design group as defined above. Secondly, as above the control groups were divided into the all possible controls and the cleaner controls. Controls were age matched for age and smoking status with the cases. The all possible controls include individuals as defined above and the cleaner controls also use individuals as defined above. As above, only data obtained from samples from white males were analysed and are presented in Table 12.

An example of a SNP associated with an adverse cardiovascular event such as a fatal MI or non-fatal MI using data from the CARE study is hCV529706. Patients with 2 rare alleles vs. 0 rare alleles had an OR of 2.08 of having the adverse event (p,0.05).

The statistical results provided in Table 13 demonstrate the association of a SNP in the PON1 gene(hCV2548962) with pravastatin efficacy in both the CARE and WOSCOPs sample sets. The analysis was refined as described for both Table 11 and 12. The data show that patients with 2 rare alleles were significantly protected against a fatal or non-fatal MI when treated with pravastatin (ORs 0.28-0.34, p< 0.05).

Example 2: Statistical Analysis of SNP Combinations Associated with RMI and Predictive of Response to Statin Treatment

Multiple markers were identified in the CARE study as associated with the ability of a patient to respond to statin treatment by having a reduced risk of RMI (specifically see Tables 6 and 8). The data presented in those Tables, especially Table 8, indicate that the minor alleles of NPC1 (hCV25472673) and HSPG2 (hCV1603656) and the major allele of ABCA1 (hCV2741051) are protective against RMI in patients that receive statin treatment. The data also show that certain genotypes of the alleles identified in Table 8 are protective against RMI in patients that receive statin treatment. The homozygous minor allele or the heterozygous minor and major allele of the NPC1 gene (CC, CT) and the HSPG2 gene (TT, TC) are protective genotypes (low risk genotypes) against RMI in patients that receive statin treatment. The homozygous major allele of the ABCA1 gene (CC) is a protective genotype (low risk genotype) in patients that receive statin treatment.

The genotype data generated from the DNA of patients who participated in the CARE study was analyzed to determine the effect that pravastatin treatment had on the occurrence of RMI in patients with each of the potential genotypes (low risk, protective or high risk, non-protective) for the ABCA1 gene, the NPC1 gene and the HSPG1 gene independently. The data are presented in Table 14.

Table 14

		Age-Adjusted pravastatin effect (by genotype group)			
N	Label	RR	95% CI		p-value
1366	High risk ABCA1 genotype	0.9567	0.6709	1.3644	0.807
1441	Low risk ABCA1 genotype	0.5883	0.4249	0.8145	0.0014
Total = 2807					
1045	High risk NPC1 genotype	1.0824	0.7265	1.6127	0.6971

1755	Low risk NPC1 genotype	0.5938	0.4388	0.8035	0.0007
Total = 2800					
2375	High risk HSPG2 genotype	0.8097	0.6271	1.0453	0.1053
428	Low risk HSPG2 genotype	0.3934	0.2002	0.7729	0.0068
Total = 2803					

The data show that the low risk genotypes of the ABCA1 gene, the NPC1 gene and the HSPG2 gene are protective against RMI in patients that have received statin treatment.

- 5 The effect of pravastatin treatment on the occurrence of RMI in patients with each of the potential genotypes (protective, low risk genotype or non-protective, high risk genotype) for each of the ABCA1 gene, NPC1 gene, and HSPG2 gene alone, and combinations with the other two genes thereof are presented in Table 15.

Table 15

		Age-adjusted pravastatin effect (by genotype group)			
N	Label	RR	95% CI		p-value
436	High risk, non-protective genotypes	1.7175	0.877	3.3637	0.1148
447	Low risk, protective ABCA1 only	0.8765	0.4848	1.5848	0.6627
701	Low risk, protective NPC1 only	0.8954	0.5543	1.4462	0.6514
83	Low risk, protective HSPG2 only	0.2487	0.0304	2.0372	0.1947
784	Low risk ABCA1 and NPC1 only (pattern 2 genotype)	0.5258	0.3343	0.8271	0.0054
77	Low risk ABCA1 and HSPG2 only	1.0054	0.2593	3.8982	0.9938
144	Low risk NPC1 and HSPG2 only	0.2964	0.0652	1.3482	0.1156
122	Low risk ABCA1, NPC1 and HSPG2 (pattern 3 genotype)	0.2399	0.0704	0.8177	0.0225

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Total =2794	
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The data show that patients that have a combination of the ABCA1 and NPC1 low risk genotypes (pattern 2) or patients that have a combination of the ABCA1, NPC1 and the HSPG2 low risk genotypes (pattern 3) have a significantly reduced risk of RMI if they receive pravastatin treatment relative to those patients who received placebo.

Patients in the CARE trial that had a high risk, non-protective genotype for the ABCA1 gene, the NPC1 gene and the HSPG2 gene, had the low risk ABCA1 genotype only, had the low risk ABCA1 and HSPG2 genotypes only, had the low risk NPC1 genotype only, had the low risk HSPG2 genotype only, or had the low risk NPC1 and HSPG1 genotype are collectively called pattern 0 patients. Patients in the CARE trial that had the pattern 0 genotype and received placebo had a 5 year risk of a RMI of 8.1%. Patients in the trial that had the pattern 2 genotype and received placebo had a 5 year risk of a RMI of 12.5%, or a 64 % increase over those patients that had the pattern 0 genotypes. Patients in the trial that had the pattern 3 genotype and received placebo had a 5 year risk of a RMI of 19.3 % or a 138% increase over those patients that had the pattern 0 genotypes. These data show that patients that do not receive statin treatment and have the pattern 2 or the pattern 3 genotypes have a 64% or a 138% increased risk of a RMI in a 5 year period over patients with a pattern 0 genotype (LogRank p-value = 0.0013).

Patients in the CARE trial with pattern 0 genotypes who did not receive statin treatment had a 5 year risk of a RMI of 8.1%. Patients in the CARE trial with pattern 0 genotypes who did receive pravastatin treatment had a 5 year risk of a RMI of 7.9% (N = 1888, 67.6% of the CARE population, LogRank p-value = 0.9345). Patients in the trial with pattern 2 genotypes, who did not receive statin treatment had a 5 year risk of a RMI of 12.5%. Patients in the trial with pattern 2 genotypes who did receive pravastatin treatment had a 5 year risk of a RMI of 6.8% (HR = 0.53, 95% CI: 0.33-0.85, p = 0.0081, N = 784, 28.1% of the CARE population). This is a 50% reduction in risk over a 5 year period for RMI. Patients in the trial with pattern the 3 genotype, who did not receive statin treatment had a 5 year risk of a RMI of 19.3%. Patients in the trial with the pattern

3 genotype who did receive pravastatin had a 5 year risk of a RMI of 4.6% (HR = 0.2, 95% CI = 0.06-0.8, p = 0.0209, N = 122, 4.4% of the CARE population). This is an 80% reduction in risk over a 5 year period for RMI. These data are summarized in Table 16.

5 Table 16

		RMI	No RMI	Risk	RR _{Statin}	RD _{Statin}
All	Pravastatin	106	1367	0.072	0.76	0.023
	Placebo	137	1303	0.095		
Pattern 0	Pravastatin	78	906	0.079	0.98	0.001
	Placebo	73	831	0.081		
Pattern 2	Pravastatin	25	342	0.068	0.55	0.057
	Placebo	52	365	0.125		
Pattern 3	Pravastatin	3	62	0.046	0.24	0.147
	Placebo	11	46	0.193		

Measures of prognostic value were calculated from the above data. The positive predictive value (PPV) of each genotype pattern can be calculated by dividing the number of individuals with that genotype who received placebo and had a RMI by the total number of individuals who had that genotype and received placebo. The PPV of the pattern 3 genotype is 19.3% and the PPV of the pattern 2 genotype is 12.5%. The negative predictive value (NPV) of each genotype can be calculated by dividing the total number of individuals who had those genotypes, received placebo and did not have a RMI by the total number of individuals who had that genotype and received placebo. The NPV of pattern 0 is 91.9%. From these calculations, the entire population can be broken down into different absolute risk groups. The over all risk of the population to have a RMI after having an MI is 9.5%. However, for individuals with the pattern 0 genotype, the risk of a RMI is reduced to 8.1%. Individuals with pattern 2 and pattern 3 genotypes have a 12.5% and 19.3% risk of a RMI.

Various modifications and variations of the described compositions, methods and systems of the invention will be apparent to those skilled in the art without departing from the scope of the invention. Although the invention has been described in connection with specific preferred embodiments and certain working examples, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, 5 various modifications of the above-described modes for carrying out the invention that are obvious to those skilled in the field of molecular biology, genetics and related fields are intended to be within the scope of the following claims.

TABLE 1

Gene Number: 20
Celera Gene: hCG1647899 - 30000662117559
Celera Transcript: hCT2296986 - 30000662117605
Public Transcript Accession: NM_022046
Celera Protein: hCP1874421 - 30000662117630
Public Protein Accession: NP_071329
Gene Symbol: KLK14
Protein Name: kallikrein 14;KLK-L6
Celera Genomic Axis: GA_x5YUV32VY4T(939936..946866)
Chromosome: Chr19
OMIM number:
OMIM Information:
Transcript Sequence: SEQ ID NO:2 (WO 2005/056837 SEQ ID NO:35)
Protein Sequence: SEQ ID NO:56 (WO 2005/056837 SEQ ID NO:552)

SNP Information

Context: SEQ ID NO:112 (WO 2005/056837 SEQ ID NO:1960):
Celera SNP ID: hCV16044337
SNP Position Transcript: 353
SNP Source: Applera
Population(A allele,Count): african american(C,17|T,19) caucasian(C,20|T,10)
total(C,37|T,29)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:56, 45, (H,CAT) (Y,TAT)

SNP Source: HGBASE;dbSNP
Population(A allele,Count): no_pop(T,-|C,-) ;no_pop(T,-|C,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:56, 45, (H,CAT) (Y,TAT)

Gene Number: 20
Celera Gene: hCG1647899 - 30000662117559
Celera Transcript: hCT1648026 - 30000662117584
Public Transcript Accession: NM_022046
Celera Protein: hCP1611610 - 30000662117628
Public Protein Accession: NP_071329
Gene Symbol: KLK14
Protein Name: kallikrein 14;KLK-L6
Celera Genomic Axis: GA_x5YUV32VY4T(940184..946866)
Chromosome: Chr19
OMIM number:
OMIM Information:
Transcript Sequence: SEQ ID NO:3 (WO 2005/056837 SEQ ID NO:36)
Protein Sequence: SEQ ID NO:57(WO 2005/056837 SEQ ID NO:553)

SNP Information

Context: SEQ ID NO: 113 (WO 2005/056837 SEQ ID NO:1968)
Celera SNP ID: hCV16044337
SNP Position Transcript: 353
SNP Source: Applera

Population(AAllele,Count): african american(C,17|T,19) caucasian(C,20|T,10)
total(C,37|T,29)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:57, 45, (H,CAT) (Y,TAT)
SNP Source: HGBASE;dbSNP
Population(AAllele,Count): no_pop(T,-|C,-) ;no_pop(T,-|C,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:57, 45, (H,CAT) (Y,TAT)

Gene Number: 23
Celera Gene: hCG17143 - 30000662103580
Celera Transcript: hCT8191 - 30000662103581
Public Transcript Accession: NM_002207
Celera Protein: hCP34482 - 30000662101733
Public Protein Accession: NP_002198
Gene Symbol: ITGA9
Protein Name: integrin, alpha 9;ALPHA-RLC;ITGA4L;RLC
Celera Genomic Axis: GA_x5YUV32VV34(37427363..37796112)
Chromosome: Chr3
OMIM number: 603963
OMIM Information: INTEGRIN, ALPHA-9;ITGA9
Transcript Sequence: SEQ ID NO:4 (WO 2005/056837 SEQ ID NO:40)
Protein Sequence: SEQ ID NO:58 (WO 2005/056837 SEQ ID NO:557)

SNP Information

Context: SEQ ID NO:114 (WO 2005/056837 SEQ ID NO:2053)
Celera SNP ID: hCV25644901
SNP Position Transcript: 1965
SNP Source: Applera
Population(AAllele,Count): african american(A,37|G,1) caucasian(A,35|G,3)
total(A,72|G,4)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:58, 632, (Q,CAG) (R,CGG)

Gene Number: 29
Celera Gene: hCG17504 - 30000675938676
Celera Transcript: hCT2343626 - 30000675939209
Public Transcript Accession: NM_000593
Celera Protein: hCP1909032 - 30000675938126
Public Protein Accession: NP_000584
Gene Symbol: TAP1
Protein Name: transporter 1, ATP-binding cassette, sub-family
B (MDR/TAP);ABC17;ABCB2;APT1;D6S114E;PSF1;RING4
Celera Genomic Axis: GA_x5YUV32W6W6(5826227..5834971)
Chromosome: Chr6
OMIM number:
OMIM Information:
Transcript Sequence: SEQ ID NO:5 (WO 2005/056837 SEQ ID NO:56)
Protein Sequence: SEQ ID NO:59 (WO 2005/056837 SEQ ID NO:573)

SNP Information

Context: SEQ ID NO:117 (WO 2005/056837 SEQ ID NO:2413)
Celera SNP ID: hCV549926
SNP Position Transcript: 1262
SNP Source: HGBASE;HGMD;dbSNP
Population(AAllele,Count): no_pop(G,-|A,-) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:61, 286, (I,ATC) (V,GTC)

Gene Number: 29
Celera Gene: hCG17504 - 30000675938676
Celera Transcript: hCT2343627 - 30000675938678
Public Transcript Accession: NM_000593
Celera Protein: hCP1909033 - 30000675938115
Public Protein Accession: NP_000584
Gene Symbol: TAP1
Protein Name: transporter 1, ATP-binding cassette, sub-family B (MDR/TAP);ABCB2;ABCB2;APT1;D6S114E;PSF1;RING4
Celera Genomic Axis: GA_x5YUV32W6W6(5826200..5834972)
Chromosome: Chr6
OMIM number:
OMIM Information:
Transcript Sequence: SEQ ID NO:8 (WO 2005/056837 SEQ ID NO:61)
Protein Sequence: SEQ ID NO:62 (WO 2005/056837 SEQ ID NO:578)

SNP Information

Context: SEQ ID NO:118 (WO 2005/056837 SEQ ID NO:2455)
Celera SNP ID: hCV549926
SNP Position Transcript: 1342
SNP Source: HGBASE;HGMD;dbSNP
Population(AAllele,Count): no_pop(G,-|A,-) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:62, 393, (I,ATC) (V,GTC)

Gene Number: 31
Celera Gene: hCG17514 - 30000675951944
Celera Transcript: hCT1967011 - 30000675951968
Public Transcript Accession: NM_002121
Celera Protein: hCP1779938 - 30000675950563
Public Protein Accession: NP_002112
Gene Symbol: HLA-DPB1
Protein Name: major histocompatibility complex, class II, DP beta 1;HLA-DPB1
Celera Genomic Axis: GA_x5YUV32W6W6(6056837..6073623)
Chromosome: Chr6
OMIM number: 142858
OMIM Information: MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DP BETA-1;HLA-DPB1
Transcript Sequence: SEQ ID NO:9 (WO 2005/056837 SEQ ID NO:64)
Protein Sequence: SEQ ID NO:63 (WO 2005/056837 SEQ ID NO:581)

SNP Information

Context: SEQ ID NO:119 (WO 2005/056837 SEQ ID NO:2480)
 Celera SNP ID: hCV8851080
 SNP Position Transcript: 365
 SNP Source: Applera
 Population(AAllele,Count): african american(A,20|G,6) caucasian(A,10)
 total(A,30|G,6)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:63, 98, (K,AAG) (E,GAG)

SNP Source: HGBASE;HGMD;dbSNP
 Population(AAllele,Count): no_pop(A,-|G,-) ;no_pop(A,-|G,-) ;no_pop(A,-
 |G,-) CEPH(G,16|A,76) total(G,16|A,76)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:63, 98, (K,AAG) (E,GAG)

Gene Number: 31
 Celera Gene: hCG17514 - 30000675951944
 Celera Transcript: hCT1967010 - 30000675951960
 Public Transcript Accession: NM_002121
 Celera Protein: hCP1779913 - 30000675950561
 Public Protein Accession: NP_002112
 Gene Symbol: HLA-DPB1
 Protein Name: major histocompatibility complex, class II, DP
 beta 1;HLA-DPB1
 Celera Genomic Axis: GA_x5YUV32W6W6(6056837..6073623)
 Chromosome: Chr6
 OMIM number: 142858
 OMIM Information: MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DP
 BETA-1;HLA-DPB1
 Transcript Sequence: SEQ ID NO:10 (WO 2005/056837 SEQ ID NO:65)
 Protein Sequence: SEQ ID NO:64 (WO 2005/056837 SEQ ID NO:582)

SNP Information

Context: SEQ ID NO:120 (WO 2005/056837 SEQ ID NO:2573)
 Celera SNP ID: hCV8851080
 SNP Position Transcript: 365
 SNP Source: Applera
 Population(AAllele,Count): african american(A,20|G,6) caucasian(A,10)
 total(A,30|G,6)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:64, 98, (K,AAG) (E,GAG)

SNP Source: HGBASE;HGMD;dbSNP
 Population(AAllele,Count): no_pop(A,-|G,-) ;no_pop(A,-|G,-) ;no_pop(A,-
 |G,-) CEPH(G,16|A,76) total(G,16|A,76)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:64, 98, (K,AAG) (E,GAG)

Gene Number: 31

Celera Gene: hCG17514 - 30000675951944
 Celera Transcript: hCT8565 - 30000675951953
 Public Transcript Accession: NM_002121
 Celera Protein: hCP37473 - 30000675950559
 Public Protein Accession: NP_002112
 Gene Symbol: HLA-DPB1
 Protein Name: major histocompatibility complex, class II, DP
 beta 1;HLA-DP1B
 Celera Genomic Axis: GA_x5YUV32W6W6(6056837..6073623)
 Chromosome: Chr6
 OMIM number: 142858
 OMIM Information: MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DP
 BETA-1;HLA-DPB1
 Transcript Sequence: SEQ ID NO:11 (WO 2005/056837 SEQ ID NO:66)
 Protein Sequence: SEQ ID NO:65 (WO 2005/056837 SEQ ID NO:583)

SNP Information

Context: SEQ ID NO:122 (WO 2005/056837 SEQ ID NO:2666)
 Celera SNP ID: hCV8851080
 SNP Position Transcript: 365
 SNP Source: Applera
 Population(AAllele,Count): african american(A,20|G,6) caucasian(A,10)
 total(A,30|G,6)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:65, 98, (K,AAG) (E,GAG)
 SNP Source: HGBASE;HGMD;dbSNP
 Population(AAllele,Count): no_pop(A,-|G,-) ;no_pop(A,-|G,-) ;no_pop(A,-
 |G,-) CEPH(G,16|A,76) total(G,16|A,76)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:65, 98, (K,AAG) (E,GAG)

Gene Number: 31
 Celera Gene: hCG17514 - 30000675951944
 Celera Transcript: hCT1967009 - 30000675951945
 Public Transcript Accession: NM_002121
 Celera Protein: hCP1779974 - 30000675950557
 Public Protein Accession: NP_002112
 Gene Symbol: HLA-DPB1
 Protein Name: major histocompatibility complex, class II, DP
 beta 1;HLA-DP1B
 Celera Genomic Axis: GA_x5YUV32W6W6(6056837..6073623)
 Chromosome: Chr6
 OMIM number: 142858
 OMIM Information: MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DP
 BETA-1;HLA-DPB1
 Transcript Sequence: SEQ ID NO:12 (WO 2005/056837 SEQ ID NO:67)
 Protein Sequence: SEQ ID NO:66 (WO 2005/056837 SEQ ID NO:584)

SNP Information

Context: SEQ ID NO:121 (WO 2005/056837 SEQ ID NO:2759)
 Celera SNP ID: hCV8851080
 SNP Position Transcript: 365

SNP Source: Applera
 Population(A,Allele,Count): african american(A,20|G,6) caucasian(A,10)
 total(A,30|G,6)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:66, 98, (K,AAG) (E,GAG)

SNP Source: HGBASE;HGMD;dbSNP
 Population(A,Allele,Count): no_pop(A,-|G,-) ;no_pop(A,-|G,-) ;no_pop(A,-
 |G,-) CEPH(G,16|A,76) total(G,16|A,76)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:66, 98, (K,AAG) (E,GAG)

Gene Number: 36
 Celera Gene: hCG1788543 - 30000034442302
 Celera Transcript: hCT2283418 - 30000034442298
 Public Transcript Accession: NM_001082
 Celera Protein: hCP1896156 - 30000034442267
 Public Protein Accession: NP_001073
 Gene Symbol: CYP4F2
 Protein Name: cytochrome P450, subfamily IVF, polypeptide
 2;CPF2
 Celera Genomic Axis: GA_x5YUV32W1A1(7103022..7122995)
 Chromosome: Chr19
 OMIM number: 604426
 OMIM Information: CYTOCHROME P450, SUBFAMILY IVF, POLYPEPTIDE
 2;CYP4F2
 Transcript Sequence: SEQ ID NO:13 (WO 2005/056837 SEQ ID NO:80)
 Protein Sequence: SEQ ID NO:67 (WO 2005/056837 SEQ ID NO:597)

SNP Information

Context: SEQ ID NO:123 (WO 2005/056837 SEQ ID NO:3293)
 Celera SNP ID: hCV16179493
 SNP Position Transcript: 1348
 SNP Source: Applera
 Population(A,Allele,Count): african american(A,2|G,34) caucasian(A,17|G,23)
 total(A,19|G,57)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:67, 433, (M,ATG) (V,GTG)

SNP Source: Celera;HGBASE;dbSNP
 Population(A,Allele,Count): no_pop(A,1|G,6) total(G,6|A,1) ;no_pop(G,-
 |A,-) ;PGA-AFRICAN-PANEL(G,-|A,-) PGA-EUR(EAN-PANEL(G,-|A,-)
 TSC_42_A(A,16|G,60) TSC_42_C(A,27|G,55) TSC_42_AA(A,6|G,78)
 total(G,193|A,49)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:67, 433, (M,ATG) (V,GTG)

Gene Number: 36
 Celera Gene: hCG1788543 - 30000034442302
 Celera Transcript: hCT1827701 - 30000034442304
 Public Transcript Accession: NM_001082
 Celera Protein: hCP1698500 - 30000034442265

Public Protein Accession: NP_001073
Gene Symbol: CYP4F2
Protein Name: cytochrome P450, subfamily IVF, polypeptide
2;CPF2
Celera Genomic Axis: GA_x5YUV32W1A1(7103022..7122995)
Chromosome: Chr19
OMIM number: 604426
OMIM Information: CYTOCHROME P450, SUBFAMILY IVF, POLYPEPTIDE
2;CYP4F2
Transcript Sequence: SEQ ID NO:14 (WO 2005/056837 SEQ ID NO:81)
Protein Sequence: SEQ ID NO:68 (WO 2005/056837 SEQ ID NO:598)

SNP Information

Context: SEQ ID NO:124 (WO 2005/056837 SEQ ID NO:3310)
Celera SNP ID: hCV16179493
SNP Position Transcript: 1348
SNP Source: Applera
Population(A allele,Count): african american(A,2|G,34) caucasian(A,17|G,23)
total(A,19|G,57)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:68, 433, (M,ATG) (V,GTG)

SNP Source: Celera;HGBASE;dbSNP
Population(A allele,Count): no_pop(A,1|G,6) total(G,6|A,1) ;no_pop(G,-
|A,-) ;PGA-AFRICAN-PANEL(G,-|A,-) PGA-EUR(EAN-PANEL(G,-|A,-)
TSC_42_A(A,16|G,60) TSC_42_C(A,27|G,55) TSC_42_AA(A,6|G,78)
total(G,193|A,49)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:68, 433, (M,ATG) (V,GTG)

Gene Number: 36
Celera Gene: hCG1788543 - 30000034442302
Celera Transcript: hCT2283419 - 30000034442305
Public Transcript Accession: NM_001082
Celera Protein: hCP1896158 - 30000034442263
Public Protein Accession: NP_001073
Gene Symbol: CYP4F2
Protein Name: cytochrome P450, subfamily IVF, polypeptide
2;CPF2
Celera Genomic Axis: GA_x5YUV32W1A1(7103022..7122623)
Chromosome: Chr19
OMIM number: 604426
OMIM Information: CYTOCHROME P450, SUBFAMILY IVF, POLYPEPTIDE
2;CYP4F2
Transcript Sequence: SEQ ID NO:15 (WO 2005/056837 SEQ ID NO:82)
Protein Sequence: SEQ ID NO:69 (WO 2005/056837 SEQ ID NO:599)

SNP Information

Context: SEQ ID NO:125 (WO 2005/056837 SEQ ID NO:3333)
Celera SNP ID: hCV16179493
SNP Position Transcript: 1389
SNP Source: Applera

Population(A,Allele,Count): african american(A,2|G,34) caucasian(A,17|G,23)
total(A,19|G,57)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:69, 433, (M,ATG) (V,GTG)

SNP Source: Celera;HGBASE;dbSNP
Population(A,Allele,Count): no_pop(A,1|G,6) total(G,6|A,1) ;no_pop(G,-
|A,-) ;PGA-AFRICAN-PANEL(G,-|A,-) PGA-EUR(EAN-PANEL(G,-|A,-)
TSC_42_A(A,16|G,60) TSC_42_C(A,27|G,55) TSC_42_AA(A,6|G,78)
total(G,193|A,49)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:69, 433, (M,ATG) (V,GTG)

Gene Number: 37
Celera Gene: hCG1789838 - 30000668725918
Celera Transcript: hCT1829098 - 30000668725959
Public Transcript Accession: NM_005502
Celera Protein: hCP1713177 - 30000668725949
Public Protein Accession: NP_005493
Gene Symbol: ABCA1
Protein Name: ATP-binding cassette, sub-family A (ABCA1),
member 1;ABCA1;CEBP;HDLDT1;TGD;Tangier disease
Celera Genomic Axis: GA_x5YUV32VU0F(7758303..7905441)
Chromosome: Chr9
OMIM number: 600046
OMIM Information: ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER
1;ABCA1
Transcript Sequence: SEQ ID NO:16 (WO 2005/056837 SEQ ID NO:83)
Protein Sequence: SEQ ID NO:70 (WO 2005/056837 SEQ ID NO:600)

SNP Information

Context: SEQ ID NO:126 (WO 2005/056837 SEQ ID NO:3344)
Celera SNP ID: hCV2741051
SNP Position Transcript: 969
SNP Source: Applera
Population(A,Allele,Count): african american(A,24|G,14) caucasian(A,14|G,26)
total(A,38|G,40)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:70, 219, (K,AAG) (R,AGG)

SNP Source: Celera;HGBASE;HGMD;dbSNP
Population(A,Allele,Count): no_pop(A,1|G,9)
total(G,9|A,1)Gaucasian(A,78|G,234) Ghinese(A,11|G,47) Japanese(G,6|A,8)
African(G,34|A,66) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-
) HISP1(G,-|A,-) PAC1(G,-|A,-) CAUC1(G,-|A,-) AFR1(G,-|A,-) P1(G,-
|A,-) Cord_blood(G,-|A,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:70, 219, (K,AAG) (R,AGG) 219,
(R,AGG) (K,AAG)

Gene Number: 37
Celera Gene: hCG1789838 - 30000668725918

Celera Transcript: hCT2274784 - 30000668725919
 Public Transcript Accession: NM_005502
 Celera Protein: hCP1872573 - 30000668725943
 Public Protein Accession: NP_005493
 Gene Symbol: ABCA1
 Protein Name: ATP-binding cassette, sub-family A (ABC1), member 1; ABC1; CERP; HDLDT1; TGD; Tangier disease
 Celera Genomic Axis: GA_x5YUV32VU0F(7834987..7905441)
 Chromosome: Chr9
 OMIM number: 600046
 OMIM Information: ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER 1; ABCA1
 Transcript Sequence: SEQ ID NO:17 (WO 2005/056837 SEQ ID NO:84)
 Protein Sequence: SEQ ID NO:71 (WO 2005/056837 SEQ ID NO:601)

SNP Information

Context: SEQ ID NO:127 (WO 2005/056837 SEQ ID NO:3418)
 Celera SNP ID: hCV2741051
 SNP Position Transcript: 969
 SNP Source: Applera
 Population(A allele, Count): african american(A, 24|G, 14) caucasian(A, 14|G, 26)
 total(A, 38|G, 40)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:71, 219, (K, AAG) (R, AGG)

SNP Source: Celera; HGBASE; HGMD; dbSNP
 Population(A allele, Count): no_pop(A, 1|G, 9)
 total(G, 9|A, 1)Gaucasian(A, 78|G, 234) Ghinese(A, 11|G, 47) Japanese(G, 6|A, 8)
 African(G, 34|A, 66) ;no_pop(G, -|A, -) ;no_pop(G, -|A, -) ;no_pop(G, -|A, -)
) HISP1(G, -|A, -) PAC1(G, -|A, -) CAUC1(G, -|A, -) AFR1(G, -|A, -) P1(G, -|A, -)
 Cord_blood(G, -|A, -)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:71, 219, (K, AAG) (R, AGG) 219,
 (R, AGG) (K, AAG)

Gene Number: 37
 Celera Gene: hCG1789838 - 30000668725918
 Celera Transcript: hCT2274785 - 30000668725937
 Public Transcript Accession: NM_005502
 Celera Protein: hCP1872574 - 30000668725946
 Public Protein Accession: NP_005493
 Gene Symbol: ABCA1
 Protein Name: ATP-binding cassette, sub-family A (ABC1), member 1; ABC1; CERP; HDLDT1; TGD; Tangier disease
 Celera Genomic Axis: GA_x5YUV32VU0F(7833011..7905441)
 Chromosome: Chr9
 OMIM number: 600046
 OMIM Information: ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER 1; ABCA1
 Transcript Sequence: SEQ ID NO:18 (WO 2005/056837 SEQ ID NO:85)
 Protein Sequence: SEQ ID NO:72 (WO 2005/056837 SEQ ID NO:602)

SNP Information

Context: SEQ ID NO:128 (WO 2005/056837 SEQ ID NO:3425)
Celera SNP ID: hCV2741051
SNP Position Transcript: 969
SNP Source: Applera
Population(AAllele,Count): african american(A,24|G,14) caucasian(A,14|G,26)
total(A,38|G,40)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:72, 219, (K,AAG) (R,AGG)

SNP Source: Celera;HGBASE;HGMD;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9)
total(G,9|A,1)Gaucasian(A,78|G,234) Ghinese(A,11|G,47) Japanese(G,6|A,8)
African(G,34|A,66) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-
) HISP1(G,-|A,-) PAC1(G,-|A,-) CAUC1(G,-|A,-) AFR1(G,-|A,-) P1(G,-
|A,-) Cord_blood(G,-|A,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:72, 219, (K,AAG) (R,AGG) 219,
(R,AGG) (K,AAG)

Gene Number: 39
Celera Gene: hCG1804187 - 61000125149578
Celera Transcript: hCT1843447 - 61000125149579
Public Transcript Accession:
Celera Protein: hCP1729761 - 197000069364262
Public Protein Accession:
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32W6GH(14166104..14174186)
Chromosome: Chr15
OMIM number: 147370
OMIM Information: INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR;IGF1R
Transcript Sequence: SEQ ID NO:19 (WO 2005/056837 SEQ ID NO:88)
Protein Sequence: SEQ ID NO:73 (WO 2005/056837 SEQ ID NO:605)

SNP Information

Context: SEQ ID NO:110 (WO 2005/056837 SEQ ID NO:3479)
Celera SNP ID: hCV8722981
SNP Position Transcript: 1435
SNP Source: dbSNP
Population(AAllele,Count): no_pop(G,-|A,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:73, 63, (D,GAT) (G,GGT)

Gene Number: 53
Celera Gene: hCG1981506 - 30000675586425
Celera Transcript: hCT2254396 - 30000675586426
Public Transcript Accession: NM_005529
Celera Protein: hCP1855115 - 30000675586296
Public Protein Accession: NP_005520
Gene Symbol: HSPG2

Protein Name: heparan sulfate proteoglycan 2
(perlecan);PLC;SJA;SJS;SJS1
Celera Genomic Axis: GA_x5YUV32W3P1(4948123..5022197)
Chromosome: Chr1
OMIM number: 142461
OMIM Information: HEPARAN SULFATE PROTEOGLYCAN OF BASEMENT
MEMBRANE;HSPG2
Transcript Sequence: SEQ ID NO:20 (WO 2005/056837 SEQ ID NO:153)
Protein Sequence: SEQ ID NO:74 (WO 2005/056837 SEQ ID NO:670)

SNP Information

Context: SEQ ID NO:129 (WO 2005/056837 SEQ ID NO:5243)
Celera SNP ID: hCV1603656
SNP Position Transcript: 10848
SNP Source: Applera
Population(AAllele,Count): african american(A,7|G,27) caucasian(A,2|G,38)
total(A,9|G,65)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:74, 3588, (Q,CAA) (R,CGA)

SNP Source: Celera
Population(AAllele,Count): no_pop(A,4|G,9) total(G,9|A,4)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:74, 3588, (Q,CAA) (R,CGA)

Gene Number: 53
Celera Gene: hCG1981506 - 30000675586425
Celera Transcript: hCT2254394 - 30000675585342
Public Transcript Accession: NM_005529
Celera Protein: hCP1855116 - 30000675586300
Public Protein Accession: NP_005520
Gene Symbol: HSPG2
Protein Name: heparan sulfate proteoglycan 2
(perlecan);PLC;SJA;SJS;SJS1
Celera Genomic Axis: GA_x5YUV32W3P1(4948116..5022197)
Chromosome: Chr1
OMIM number: 142461
OMIM Information: HEPARAN SULFATE PROTEOGLYCAN OF BASEMENT
MEMBRANE;HSPG2
Transcript Sequence: SEQ ID NO:21 (WO 2005/056837 SEQ ID NO:154)
Protein Sequence: SEQ ID NO:75 (WO 2005/056837 SEQ ID NO:671)

SNP Information

Context: SEQ ID NO:130 (WO 2005/056837 SEQ ID NO:5323)
Celera SNP ID: hCV1603656
SNP Position Transcript: 10845
SNP Source: Applera
Population(AAllele,Count): african american(A,7|G,27) caucasian(A,2|G,38)
total(A,9|G,65)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:75, 3587, (Q,CAA) (R,CGA)

SNP Source: Celera
Population(AAllele,Count): no_pop(A,4|G,9) total(G,9|A,4)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:75, 3587, (Q,CAA) (R,CGA)

Gene Number: 53
Celera Gene: hCG1981506 - 30000675586425
Celera Transcript: hCT2254395 - 30000675584686
Public Transcript Accession: NM_005529
Celera Protein: hCP1855117 - 30000675586298
Public Protein Accession: NP_005520
Gene Symbol: HSPG2
Protein Name: heparan sulfate proteoglycan 2
(perlecan);PLC;SJA;SJS;SJS1
Celera Genomic Axis: GA_x5YUV32W3P1(4948116..5022197)
Chromosome: Chr1
OMIM number: 142461
OMIM Information: HEPARAN SULFATE PROTEOGLYCAN OF BASEMENT
MEMBRANE;HSPG2
Transcript Sequence: SEQ ID NO:22 (WO 2005/056837 SEQ ID NO:155)
Protein Sequence: SEQ ID NO:76 (WO 2005/056837 SEQ ID NO:672)

SNP Information

Context: SEQ ID NO:131 (WO 2005/056837 SEQ ID NO:5402)
Celera SNP ID: hCV1603656
SNP Position Transcript: 10784
SNP Source: Applera
Population(AAllele,Count): african american(A,7|G,27) caucasian(A,2|G,38)
total(A,9|G,65)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:76, 2829, (Q,CAA) (R,CGA)

SNP Source: Celera
Population(AAllele,Count): no_pop(A,4|G,9) total(G,9|A,4)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:76, 2829, (Q,CAA) (R,CGA)

Gene Number: 71
Celera Gene: hCG2023324 - 30000669567219
Celera Transcript: hCT2320312 - 30000669567261
Public Transcript Accession: NM_000446
Celera Protein: hCP1873654 - 30000669567241
Public Protein Accession: NP_000437
Gene Symbol: PON3
Protein Name: paraoxonase 3;ESA;PON
Celera Genomic Axis: GA_x5YUV32VYJC(5595311..5687243)
Chromosome: Chr7
OMIM number: 168820
OMIM Information: PARAOXONASE 1;PON1
Transcript Sequence: SEQ ID NO:23 (WO 2005/056837 SEQ ID NO:201)
Protein Sequence: SEQ ID NO:77 (WO 2005/056837 SEQ ID NO:718)

SNP Information

Context: SEQ ID NO:132 (WO 2005/056837 SEQ ID NO:6414)
 Celera SNP ID: hCV2548962
 SNP Position Transcript: 847
 SNP Source: Applera
 Population(AAllele,Count): african american(A,7|G,17) caucasian(A,26)
 total(A,33|G,17)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:77, 105, (Q,CAA) (R,CGA)

SNP Source: Celera;HGBASE;HGMD;dbSNP
 Population(AAllele,Count): no_pop(G,1|A,2) total(G,1|A,2) ;no_pop(G,-
 |A,-) Spanish men(A,158|G,365) Northern Ireland, France,
 Scotland(A,580|G,1420) Individuals(A,190|G,443) Finnish(A,87|G,250)
 ;no_pop(G,-|A,-) ;CEPH(G,17|A,75) PGA-AFRICAN-PANEL(G,-|A,-) PGA-
 EUR(EAN-PANEL(G,-|A,-) total(G,17|A,75) HISP1(G,-|A,-) PAC1(G,-|A,-)
 CAUC1(G,-|A,-) AFR1(G,-|A,-) P1(G,-|A,-) Han(A,1600|G,2400)
 Cau(G,152|A,308) total(G,2552|A,1908)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:77, 105, (Q,CAA) (R,CGA)

Gene Number: 71
 Celera Gene: hCG2023324 - 30000669567219
 Celera Transcript: hCT2320315 - 30000669567245
 Public Transcript Accession: NM_000446
 Celera Protein: hCP1873652 - 30000669567237
 Public Protein Accession: NP_000437
 Gene Symbol: PON3
 Protein Name: paraoxonase 3;ESA;PON
 Celera Genomic Axis: GA_x5YUV32VYJC(5595311..5687243)
 Chromosome: Chr7
 OMIM number: 168820
 OMIM Information: PARAOXONASE 1;PON1
 Transcript Sequence: SEQ ID NO:24 (WO 2005/056837 SEQ ID NO:203)
 Protein Sequence: SEQ ID NO:78 (WO 2005/056837 SEQ ID NO:720)

SNP Information

Context: SEQ ID NO:133 (WO 2005/056837 SEQ ID NO:6436)
 Celera SNP ID: hCV2548962
 SNP Position Transcript: 986
 SNP Source: Applera
 Population(AAllele,Count): african american(A,7|G,17) caucasian(A,26)
 total(A,33|G,17)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:78, 192, (Q,CAA) (R,CGA)

SNP Source: Celera;HGBASE;HGMD;dbSNP
 Population(AAllele,Count): no_pop(G,1|A,2) total(G,1|A,2) ;no_pop(G,-
 |A,-) Spanish men(A,158|G,365) Northern Ireland, France,
 Scotland(A,580|G,1420) Individuals(A,190|G,443) Finnish(A,87|G,250)
 ;no_pop(G,-|A,-) ;CEPH(G,17|A,75) PGA-AFRICAN-PANEL(G,-|A,-) PGA-
 EUR(EAN-PANEL(G,-|A,-) total(G,17|A,75) HISP1(G,-|A,-) PAC1(G,-|A,-)

CAUC1(G,-|A,-) AFR1(G,-|A,-) P1(G,-|A,-) Han(A,1600|G,2400)
Cau(G,152|A,308) total(G,2552|A,1908)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:78, 192, (Q,CAA) (R,CGA)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296537 - 67000129408293
Public Transcript Accession: NM_002000
Celera Protein: hCP1874944 - 197000069408208
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4751053)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:25 (WO 2005/056837 SEQ ID NO:204)
Protein Sequence: SEQ ID NO:79 (WO 2005/056837 SEQ ID NO:721)

SNP Information

Context: SEQ ID NO:134 (WO 2005/056837 SEQ ID NO:6440)
Celera SNP ID: hCV7841642
SNP Position Transcript: 498
SNP Source: Applera
Population(Aallele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:79, 101, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(Aallele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:79, 101, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296543 - 67000129408310
Public Transcript Accession: NM_002000
Celera Protein: hCP1874946 - 197000069408210
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733634..4749113)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:26 (WO 2005/056837 SEQ ID NO:205)
Protein Sequence: SEQ ID NO:80 (WO 2005/056837 SEQ ID NO:722)

SNP Information

Context: SEQ ID NO:135 (WO 2005/056837 SEQ ID NO:6447)
Celera SNP ID: hCV7841642
SNP Position Transcript: 382
SNP Source: Applera
Population(A,Allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:80, 86, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(A,Allele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:80, 86, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296550 - 67000129408302
Public Transcript Accession: NM_002000
Celera Protein: hCP1874945 - 197000069408209
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749113)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:27 (WO 2005/056837 SEQ ID NO:206)
Protein Sequence: SEQ ID NO:81 (WO 2005/056837 SEQ ID NO:723)

SNP Information

Context: SEQ ID NO:136 (WO 2005/056837 SEQ ID NO:6452)
Celera SNP ID: hCV7841642
SNP Position Transcript: 615
SNP Source: Applera
Population(A,Allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:81, 86, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(A,Allele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:81, 86, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296545 - 67000129408108
Public Transcript Accession: NM_002000
Celera Protein: hCP1874926 - 197000069408190

Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4751053)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:28 (WO 2005/056837 SEQ ID NO:207)
Protein Sequence: SEQ ID NO:82 (WO 2005/056837 SEQ ID NO:724)

SNP Information

Context: SEQ ID NO:137 (WO 2005/056837 SEQ ID NO:6458)
Celera SNP ID: hCV7841642
SNP Position Transcript: 534
SNP Source: Applera
Population(A allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:82, 113, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(A allele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:82, 113, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296539 - 67000129408208
Public Transcript Accession: NM_002000
Celera Protein: hCP1874935 - 197000069408199
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4751053)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:29 (WO 2005/056837 SEQ ID NO:208)
Protein Sequence: SEQ ID NO:83 (WO 2005/056837 SEQ ID NO:725)

SNP Information

Context: SEQ ID NO:138 (WO 2005/056837 SEQ ID NO:6465)
Celera SNP ID: hCV7841642
SNP Position Transcript: 615
SNP Source: Applera
Population(A allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:83, 86, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP

Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:83, 86, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296548 - 67000129407927
Public Transcript Accession: NM_002000
Celera Protein: hCP1874908 - 197000069408172
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749726)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:30 (WO 2005/056837 SEQ ID NO:210)
Protein Sequence: SEQ ID NO:84 (WO 2005/056837 SEQ ID NO:727)

SNP Information

Context: SEQ ID NO:139 (WO 2005/056837 SEQ ID NO:6477)
Celera SNP ID: hCV7841642
SNP Position Transcript: 534
SNP Source: Applera
Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:84, 113, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:84, 113, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296541 - 67000129407919
Public Transcript Accession: NM_002000
Celera Protein: hCP1874907 - 197000069408171
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4748324)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:31 (WO 2005/056837 SEQ ID NO:211)
Protein Sequence: SEQ ID NO:85 (WO 2005/056837 SEQ ID NO:728)

SNP Information

Context: SEQ ID NO:140 (WO 2005/056837 SEQ ID NO:6485)
 Celera SNP ID: hCV7841642
 SNP Position Transcript: 498
 SNP Source: Applera
 Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
 total(A,5|G,73)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:85, 101, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
 Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
 |G,-)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:85, 101, (N,AAC) (D,GAC)

Gene Number: 72
 Celera Gene: hCG20262 - 67000129407882
 Celera Transcript: hCT2296534 - 67000129407890
 Public Transcript Accession: NM_002000
 Celera Protein: hCP1874904 - 197000069408168
 Public Protein Accession: NP_001991
 Gene Symbol: FCAR
 Protein Name: Fc fragment of IgA, receptor for;CD89
 Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749726)
 Chromosome: Chr19
 OMIM number: 147045
 OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
 Transcript Sequence: SEQ ID NO:32 (WO 2005/056837 SEQ ID NO:212)
 Protein Sequence: SEQ ID NO:86 (WO 2005/056837 SEQ ID NO:729)

SNP Information

Context: SEQ ID NO:141 (WO 2005/056837 SEQ ID NO:6493)
 Celera SNP ID: hCV7841642
 SNP Position Transcript: 498
 SNP Source: Applera
 Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
 total(A,5|G,73)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:86, 101, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
 Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
 |G,-)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:86, 101, (N,AAC) (D,GAC)

Gene Number: 72
 Celera Gene: hCG20262 - 67000129407882
 Celera Transcript: hCT11338 - 67000129407947
 Public Transcript Accession: NM_002000
 Celera Protein: hCP37971 - 197000069408174

Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749731)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:33 (WO 2005/056837 SEQ ID NO:213)
Protein Sequence: SEQ ID NO:87 (WO 2005/056837 SEQ ID NO:730)

SNP Information

Context: SEQ ID NO:142 (WO 2005/056837 SEQ ID NO:6503)
Celera SNP ID: hCV7841642
SNP Position Transcript: 534
SNP Source: Applera
Population(A allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:87, 113, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(A allele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:87, 113, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296538 - 67000129407883
Public Transcript Accession: NM_002000
Celera Protein: hCP1874903 - 197000069408167
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749726)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:34 (WO 2005/056837 SEQ ID NO:214)
Protein Sequence: SEQ ID NO:88 (WO 2005/056837 SEQ ID NO:731)

SNP Information

Context: SEQ ID NO:143 (WO 2005/056837 SEQ ID NO:6512)
Celera SNP ID: hCV7841642
SNP Position Transcript: 498
SNP Source: Applera
Population(A allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:88, 101, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP

Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:88, 101, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296544 - 67000129408007
Public Transcript Accession: NM_002000
Celera Protein: hCP1874916 - 197000069408180
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749726)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:35 (WO 2005/056837 SEQ ID NO:216)
Protein Sequence: SEQ ID NO:89 (WO 2005/056837 SEQ ID NO:733)

SNP Information

Context: SEQ ID NO:144 (WO 2005/056837 SEQ ID NO:6527)
Celera SNP ID: hCV7841642
SNP Position Transcript: 534
SNP Source: Applera
Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:89, 113, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:89, 113, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296547 - 67000129408016
Public Transcript Accession: NM_002000
Celera Protein: hCP1874917 - 197000069408181
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4748324)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:36 (WO 2005/056837 SEQ ID NO:217)
Protein Sequence: SEQ ID NO:90 (WO 2005/056837 SEQ ID NO:734)

SNP Information

Context: SEQ ID NO:145 (WO 2005/056837 SEQ ID NO:6536)
Celera SNP ID: hCV7841642
SNP Position Transcript: 534
SNP Source: Applera
Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:90, 113, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:90, 113, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296536 - 67000129407975
Public Transcript Accession: NM_002000
Celera Protein: hCP1874913 - 197000069408177
Public Protein Accession: NP_001991
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749731)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Transcript Sequence: SEQ ID NO:37 (WO 2005/056837 SEQ ID NO:218)
Protein Sequence: SEQ ID NO:91 (WO 2005/056837 SEQ ID NO:735)

SNP Information

Context: SEQ ID NO:146 (WO 2005/056837 SEQ ID NO:6545)
Celera SNP ID: hCV7841642
SNP Position Transcript: 498
SNP Source: Applera
Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:91, 101, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:91, 101, (N,AAC) (D,GAC)

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Celera Transcript: hCT2296540 - 67000129407911
Public Transcript Accession: NM_002000

Celera Protein: hCP1874905 - 197000069408169
 Public Protein Accession: NP_001991
 Gene Symbol: FCAR
 Protein Name: Fc fragment of IgA, receptor for;CD89
 Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4749726)
 Chromosome: Chr19
 OMIM number: 147045
 OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
 Transcript Sequence: SEQ ID NO:38 (WO 2005/056837 SEQ ID NO:219)
 Protein Sequence: SEQ ID NO:92 (WO 2005/056837 SEQ ID NO:736)

SNP Information

Context: SEQ ID NO:147 (WO 2005/056837 SEQ ID NO:6554)
 Celera SNP ID: hCV7841642
 SNP Position Transcript: 498
 SNP Source: Applera
 Population(A allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
 total(A,5|G,73)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:92, 101, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
 Population(A allele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
 |G,-)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:92, 101, (N,AAC) (D,GAC)

Gene Number: 72
 Celera Gene: hCG20262 - 67000129407882
 Celera Transcript: hCT2296546 - 67000129408187
 Public Transcript Accession: NM_002000
 Celera Protein: hCP1874933 - 197000069408197
 Public Protein Accession: NP_001991
 Gene Symbol: FCAR
 Protein Name: Fc fragment of IgA, receptor for;CD89
 Celera Genomic Axis: GA_x5YUV32VY4T(4733437..4748324)
 Chromosome: Chr19
 OMIM number: 147045
 OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
 Transcript Sequence: SEQ ID NO:39 (WO 2005/056837 SEQ ID NO:220)
 Protein Sequence: SEQ ID NO:93 (WO 2005/056837 SEQ ID NO:737)

SNP Information

Context: SEQ ID NO:148 (WO 2005/056837 SEQ ID NO:6563)
 Celera SNP ID: hCV7841642
 SNP Position Transcript: 534
 SNP Source: Applera
 Population(A allele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
 total(A,5|G,73)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:93, 113, (N,AAC) (D,GAC)

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:93, 113, (N,AAC) (D,GAC)

Gene Number: 112
Celera Gene: hCG23557 - 30000672836692
Celera Transcript: hCT14664 - 30000672836718
Public Transcript Accession: NM_003053
Celera Protein: hCP40951 - 30000672836608
Public Protein Accession: NP_003044
Gene Symbol: SLC18A1
Protein Name: solute carrier family 18 (vesicular monoamine),
member 1;CGAT;VAT1;VMAT1
Celera Genomic Axis: GA_x5YUV32VUUD(23750742..23789095)
Chromosome: Chr8
OMIM number: 193002
OMIM Information: SOLUTE CARRIER FAMILY 18, MEMBER 1;SLC18A1
Transcript Sequence: SEQ ID NO:40 (WO 2005/056837 SEQ ID NO:341)
Protein Sequence: SEQ ID NO:94 (WO 2005/056837 SEQ ID NO:858)

SNP Information

Context: SEQ ID NO:149 (WO 2005/056837 SEQ ID NO:9441)
Celera SNP ID: hCV2715953
SNP Position Transcript: 1441
SNP Source: Applera
Population(AAllele,Count): african american(C,36) caucasian(C,35|G,5)
total(C,71|G,5)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:94, 392, (L,CTC) (V,GTC)

SNP Source: Celera
Population(AAllele,Count): Caucasian(C,30|G,282) Chinese(C,1|G,59)
Japanese(G,20) African(C,1|G,99) total(G,460|C,32) no_pop(G,2|C,11)
total(G,2|C,11)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:94, 392, (L,CTC) (V,GTC) 392,
(L,CTC) (V,GTC)

Gene Number: 112
Celera Gene: hCG23557 - 30000672836692
Celera Transcript: hCT2273323 - 30000672836693
Public Transcript Accession: NM_003053
Celera Protein: hCP1885376 - 30000672836607
Public Protein Accession: NP_003044
Gene Symbol: SLC18A1
Protein Name: solute carrier family 18 (vesicular monoamine),
member 1;CGAT;VAT1;VMAT1
Celera Genomic Axis: GA_x5YUV32VUUD(23750742..23789095)
Chromosome: Chr8
OMIM number: 193002

OMIM Information: SOLUTE CARRIER FAMILY 18, MEMBER 1;SLC18A1
Transcript Sequence: SEQ ID NO:41 (WO 2005/056837 SEQ ID NO:342)
Protein Sequence: SEQ ID NO:95 (WO 2005/056837 SEQ ID NO:859)

SNP Information

Context: SEQ ID NO:150 (WO 2005/056837 SEQ ID NO:9457)
Celera SNP ID: hCV2715953
SNP Position Transcript: 1345
SNP Source: Applera
Population(AAllele,Count): african american(C,36) caucasian(C,35|G,5)
total(C,71|G,5)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:95, 360, (L,CTC) (V,GTC)

SNP Source: Celera
Population(AAllele,Count): Caucasian(C,30|G,282) Chinese(C,1|G,59)
Japanese(A,0|G,20) African(C,1|G,99) total(G,460|C,32)
no_pop(G,2|C,11) total(G,2|C,11)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:95, 360, (I,ATC) (L,CTC) (V,GTC)
360, (L,CTC) (V,GTC)

Gene Number: 117
Celera Gene: hCG25215 - 208000034985688
Celera Transcript: hCT16340 - 208000034985689
Public Transcript Accession: NM_000014
Celera Protein: hCP42149 - 208000034985656
Public Protein Accession: NP_000005
Gene Symbol: A2M
Protein Name: alpha-2-macroglobulin
Celera Genomic Axis: GA_x5YUV32W234(3872415..3920901)
Chromosome: Chr12
OMIM number: 103950
OMIM Information: ALPHA-2-MACROGLOBULIN;A2M
Transcript Sequence: SEQ ID NO:42 (WO 2005/056837 SEQ ID NO:356)
Protein Sequence: SEQ ID NO:96 (WO 2005/056837 SEQ ID NO:873)

SNP Information

Context: SEQ ID NO:151 (WO 2005/056837 SEQ ID NO:9769)
Celera SNP ID: hCV517658
SNP Position Transcript: 3350
SNP Source: Applera
Population(AAllele,Count): african american(A,14|G,4) caucasian(A,18|G,6)
total(A,32|G,10)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:96, 1000, (I,ATC) (V,GTC)

SNP Source: Applera
Population(AAllele,Count): african american(A,26|G,8) caucasian(A,26|G,10)
total(A,52|G,18)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:96, 1000, (I,ATC) (V,GTC)

SNP Source: Celera;HGBASE;dbSNP
Population(AAllele,Count): no_pop(G,4|A,17) total(G,4|A,17)
;Caucasians(G,0|A,0) ;no_pop(G,-|A,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:96, 1000, (I,ATC) (V,GTC)

Gene Number: 137
Celera Gene: hCG33048 - 84000314084586
Celera Transcript: hCT2304954 - 84000314084653
Public Transcript Accession: NM_005336
Celera Protein: hCP1808961 - 197000064951602
Public Protein Accession: NP_005327
Gene Symbol: HDLBP
Protein Name: high density lipoprotein binding protein
(vigilin);HBP;VGL
Celera Genomic Axis: GA_x5YUV32VWPT(46750109..46839155)
Chromosome: Chr2
OMIM number: 142695
OMIM Information: HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN;HDLBP
Transcript Sequence: SEQ ID NO:43 (WO 2005/056837 SEQ ID NO:401)
Protein Sequence: SEQ ID NO:97 (WO 2005/056837 SEQ ID NO:918)

SNP Information

Context: SEQ ID NO:152 (WO 2005/056837 SEQ ID NO:10680)
Celera SNP ID: hCV22274624
SNP Position Transcript: 1442
SNP Source: Applera
Population(AAllele,Count): african american(A,29|G,7) caucasian(A,27|G,13)
total(A,56|G,20)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:97, 418, (N,AAT) (S,AGT)

SNP Source: dbSNP
Population(AAllele,Count): no_pop(G,-|A,-) CEPH(G,18|A,74)
total(G,18|A,74)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:97, 418, (N,AAT) (S,AGT)

Gene Number: 137
Celera Gene: hCG33048 - 84000314084586
Celera Transcript: hCT1966929 - 84000314084619
Public Transcript Accession: NM_005336
Celera Protein: hCP1780807 - 197000064951601
Public Protein Accession: NP_005327
Gene Symbol: HDLBP
Protein Name: high density lipoprotein binding protein
(vigilin);HBP;VGL
Celera Genomic Axis: GA_x5YUV32VWPT(46750947..46796058)
Chromosome: Chr2
OMIM number: 142695
OMIM Information: HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN;HDLBP

Transcript Sequence: SEQ ID NO:44 (WO 2005/056837 SEQ ID NO:402)
Protein Sequence: SEQ ID NO:98 (WO 2005/056837 SEQ ID NO:919)

SNP Information

Context: SEQ ID NO:153 (WO 2005/056837 SEQ ID NO:10714)
Celera SNP ID: hCV22274624
SNP Position Transcript: 1664
SNP Source: Applera
Population(AAllele,Count): african american(A,29|G,7) caucasian(A,27|G,13)
total(A,56|G,20)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:98, 418, (N,AAT) (S,AGT)

SNP Source: dbSNP
Population(AAllele,Count): no_pop(G,-|A,-) CEPH(G,18|A,74)
total(G,18|A,74)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:98, 418, (N,AAT) (S,AGT)

Gene Number: 137
Celera Gene: hCG33048 - 84000314084586
Celera Transcript: hCT24241 - 84000314084587
Public Transcript Accession: NM_005336
Celera Protein: hCP46402 - 197000064951600
Public Protein Accession: NP_005327
Gene Symbol: HDLBP
Protein Name: high density lipoprotein binding protein
(vigilin);HBP;VGL
Celera Genomic Axis: GA_x5YUV32VWPT(46750947..46796072)
Chromosome: Chr2
OMIM number: 142695
OMIM Information: HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN;HDLBP
Transcript Sequence: SEQ ID NO:45 (WO 2005/056837 SEQ ID NO:403)
Protein Sequence: SEQ ID NO:99 (WO 2005/056837 SEQ ID NO:920)

SNP Information

Context: SEQ ID NO:154 (WO 2005/056837 SEQ ID NO:10738)
Celera SNP ID: hCV22274624
SNP Position Transcript: 1431
SNP Source: Applera
Population(AAllele,Count): african american(A,29|G,7) caucasian(A,27|G,13)
total(A,56|G,20)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:99, 418, (N,AAT) (S,AGT)

SNP Source: dbSNP
Population(AAllele,Count): no_pop(G,-|A,-) CEPH(G,18|A,74)
total(G,18|A,74)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:99, 418, (N,AAT) (S,AGT)

Gene Number: 149
 Celera Gene: hCG37187 - 146000220350063
 Celera Transcript: hCT28417 - 146000220350064
 Public Transcript Accession: NM_000271
 Celera Protein: hCP47700 - 197000069426589
 Public Protein Accession: NP_000262
 Gene Symbol: NPC1
 Protein Name: Niemann-Pick disease, type C1;NPC
 Celera Genomic Axis: GA_x5YUV32W66L(2595858..2650984)
 Chromosome: Chr18
 OMIM number:
 OMIM Information:
 Transcript Sequence: SEQ ID NO:46 (WO 2005/056837 SEQ ID NO:435)
 Protein Sequence: SEQ ID NO:100 (WO 2005/056837 SEQ ID NO:952)

SNP Information

Context: SEQ ID NO:155 (WO 2005/056837 SEQ ID NO:11381)
 Celera SNP ID: hCV25472673
 SNP Position Transcript: 767
 SNP Source: Applera
 Population(AAllele,Count): african american(A,35|G,3) caucasian(A,21|G,17)
 total(A,56|G,20)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:100, 215, (H,CAT) (R,CGT)

SNP Source: Celera;dbSNP
 Population(AAllele,Count): no_pop(G,1|A,8) total(G,1|A,8) ;no_pop(G,-
 |A,-)
 SNP Type: MISSENSE MUTATION
 Protein Coding: SEQ ID NO:100, 215, (H,CAT) (R,CGT)

Gene Number: 156
 Celera Gene: hCG38633 - 226000018878110
 Celera Transcript: hCT29876 - 226000018878111
 Public Transcript Accession: NM_000134
 Celera Protein: hCP48455 - 197000069464429
 Public Protein Accession: NP_000125
 Gene Symbol: FABP2
 Protein Name: fatty acid binding protein 2,
 intestinal;FABPI;FABPI, I-FABP
 Celera Genomic Axis: GA_x5YUV32VYAM(769337..774251)
 Chromosome: Chr4
 OMIM number: 134640
 OMIM Information: FATTY ACID-BINDING PROTEIN 2;FABP2
 Transcript Sequence: SEQ ID NO:47 (WO 2005/056837 SEQ ID NO:449)
 Protein Sequence: SEQ ID NO:101 (WO 2005/056837 SEQ ID NO:966)

SNP Information

Context: SEQ ID NO:156 (WO 2005/056837 SEQ ID NO:11659)
 Celera SNP ID: hCV761961
 SNP Position Transcript: 224
 SNP Source: Applera

Population(AAllele,Count): african american(A,7|G,27) caucasian(A,5|G,29)
total(A,12|G,56)

SNP Type: MISSENSE MUTATION

Protein Coding: SEQ ID NO:101, 55, (T,ACT) (A,GCT)

SNP Source: HGBASE;HGMD;dbSNP

Population(AAllele,Count): Oji-Cree with type 2 diabetes, Northern Ontario,
Canada(A,150|G,850) Caucasian,Canada(G,165|A,496) Keewatin Inuit,
Northern Ontario, Canada(G,122|A,227) total(G,1137|A,873) ;no_pop(G,-
|A,-) ;no_pop(G,-|A,-)

SNP Type: MISSENSE MUTATION

Protein Coding: SEQ ID NO:101, 55, (T,ACT) (A,GCT)

Gene Number: 162

Celera Gene: hCG401141 - 104000116851304

Celera Transcript: hCT401143 - 104000116851305

Public Transcript Accession: NM_006988

Celera Protein: hCP801069 - 197000064955866

Public Protein Accession: NP_008919

Gene Symbol: ADAMTS1

Protein Name: a disintegrin-like and metalloprotease
(reprolysin type) with thrombospondin type 1 motif, 1;C3-C5;KIAA1346;METH1

Celera Genomic Axis: GA_x5YUV32W8NG(19815538..19824668)

Chromosome: Chr21

OMIM number: 605174

OMIM Information: A DISINTEGRIN-LIKE AND METALLOPROTEINASE WITH
THROMBOSPONDIN TYPE 1 MOTIF, 1;ADAMTS1

Transcript Sequence: SEQ ID NO:48 (WO 2005/056837 SEQ ID NO:462)

Protein Sequence: SEQ ID NO:102 (WO 2005/056837 SEQ ID NO:979)

SNP Information

Context: SEQ ID NO:157 (WO 2005/056837 SEQ ID NO:11916)

Celera SNP ID: hCV529706

SNP Position Transcript: 1140

SNP Source: HGBASE;dbSNP

Population(AAllele,Count): no_pop(G,-|C,-) ;no_pop(G,-|C,-)

CEPH(G,39|C,53) total(G,39|C,53)

SNP Type: MISSENSE MUTATION

Protein Coding: SEQ ID NO:102, 227, (P,CCT) (A,GCT)

Context: SEQ ID NO:158 (WO 2005/056837 SEQ ID NO:11935)

Celera SNP ID: hCV529710

SNP Position Transcript: 415

SNP Source: HGBASE;dbSNP

Population(AAllele,Count): no_pop(G,-|C,-) ;no_pop(G,-|C,-)

NCBI|NIHP|R(G,2|C,6) total(G,2|C,6) CEPH(G,22|C,70) total(G,22|C,70)

SNP Type: UTR 5

Protein Coding: SEQ ID NO:102, None

Gene Number: 162

Celera Gene: hCG401141 - 104000116851304

Celera Transcript: hCT2296407 - 104000116851318

Public Transcript Accession: NM_006988
Celera Protein: hCP1813226 - 197000064955867
Public Protein Accession: NP_008919
Gene Symbol: ADAMTS1
Protein Name: a disintegrin-like and metalloprotease
(reprolysin type) with thrombospondin type 1 motif, 1;C3-C5;KIAA1346;METH1
Celera Genomic Axis: GA_x5YUV32W8NG(19815538..19824413)
Chromosome: Chr21
OMIM number: 605174
OMIM Information: A DISINTEGRIN-LIKE AND METALLOPROTEINASE WITH
THROMBOSPONDIN TYPE 1 MOTIF, 1;ADAMTS1
Transcript Sequence: SEQ ID NO:49 (WO 2005/056837 SEQ ID NO:463)
Protein Sequence: SEQ ID NO:103 (WO 2005/056837 SEQ ID NO:980)

SNP Information

Context: SEQ ID NO:159 (WO 2005/056837 SEQ ID NO:11936)
Celera SNP ID: hCV529706
SNP Position Transcript: 1140
SNP Source: HGBASE;dbSNP
Population(AAllele,Count): no_pop(G,-|C,-) ;no_pop(G,-|C,-)
CEPH(G,39|C,53) total(G,39|C,53)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:103, 227, (P,CCT) (A,GCT)

Context: SEQ ID NO:160 (WO 2005/056837 SEQ ID NO:11955)
Celera SNP ID: hCV529710
SNP Position Transcript: 415
SNP Source: HGBASE;dbSNP
Population(AAllele,Count): no_pop(G,-|C,-) ;no_pop(G,-|C,-)
NCBI|NIHP|R(G,2|C,6) total(G,2|C,6) CEPH(G,22|C,70) total(G,22|C,70)
SNP Type: UTR 5
Protein Coding: SEQ ID NO:103, None

Gene Number: 166
Celera Gene: hCG40393 - 30000674330026
Celera Transcript: hCT1958535 - 30000674330070
Public Transcript Accession: NM_006725
Celera Protein: hCP1762318 - 30000674329043
Public Protein Accession: NP_006716
Gene Symbol: CD6
Protein Name: CD6 antigen;TP120
Celera Genomic Axis: GA_x5YUV32VYAU(6448144..6496988)
Chromosome: Chr11
OMIM number: 186720
OMIM Information: CD6 ANTIGEN;CD6
Transcript Sequence: SEQ ID NO:50 (WO 2005/056837 SEQ ID NO:475)
Protein Sequence: SEQ ID NO:104 (WO 2005/056837 SEQ ID NO:992)

SNP Information

Context: SEQ ID NO:161 (WO 2005/056837 SEQ ID NO:12367)
Celera SNP ID: hCV2553030
SNP Position Transcript: 791

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(T,4|C,10) Caucasian(T,90|C,220)
Chinese(T,1|C,59) Japanese(T,0|C,20) African(T,3|C,97)
total(C,396|T,94) ;no_pop(C,-|T,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:104, 217, (T,ACG) (M,ATG)

Gene Number: 166
Celera Gene: hCG40393 - 30000674330026
Celera Transcript: hCT2309439 - 30000674330556
Public Transcript Accession: NM_006725
Celera Protein: hCP1902644 - 30000674329048
Public Protein Accession: NP_006716
Gene Symbol: CD6
Protein Name: CD6 antigen;TP120
Celera Genomic Axis: GA_x5YUV32VYAU(6448144..6495928)
Chromosome: Chr11
OMIM number: 186720
OMIM Information: CD6 ANTIGEN;CD6
Transcript Sequence: SEQ ID NO:51 (WO 2005/056837 SEQ ID NO:476)
Protein Sequence: SEQ ID NO:105 (WO 2005/056837 SEQ ID NO:993)

SNP Information

Context: SEQ ID NO:162 (WO 2005/056837 SEQ ID NO:12376)
Celera SNP ID: hCV2553030
SNP Position Transcript: 791
SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(T,4|C,10) Caucasian(T,90|C,220)
Chinese(T,1|C,59) Japanese(T,0|C,20) African(T,3|C,97)
total(C,396|T,94) ;no_pop(C,-|T,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:105, 217, (T,ACG) (M,ATG)

Gene Number: 166
Celera Gene: hCG40393 - 30000674330026
Celera Transcript: hCT1958534 - 30000674330108
Public Transcript Accession: NM_006725
Celera Protein: hCP1762321 - 30000674329044
Public Protein Accession: NP_006716
Gene Symbol: CD6
Protein Name: CD6 antigen;TP120
Celera Genomic Axis: GA_x5YUV32VYAU(6448144..6496988)
Chromosome: Chr11
OMIM number: 186720
OMIM Information: CD6 ANTIGEN;CD6
Transcript Sequence: SEQ ID NO:52 (WO 2005/056837 SEQ ID NO:477)
Protein Sequence: SEQ ID NO:106 (WO 2005/056837 SEQ ID NO:994)

SNP Information

Context: SEQ ID NO:163 (WO 2005/056837 SEQ ID NO:12385)
Celera SNP ID: hCV2553030

SNP Position Transcript: 791
SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(T,4|C,10) Caucasian(T,90|C,220)
Chinese(T,1|C,59) Japanese(T,0|C,20) African(T,3|C,97)
total(C,396|T,94) ;no_pop(C,-|T,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:106, 217, (T,ACG) (M,ATG)

Gene Number: 166
Celera Gene: hCG40393 - 30000674330026
Celera Transcript: hCT1971576 - 30000674330027
Public Transcript Accession: NM_006725
Celera Protein: hCP1784138 - 30000674329041
Public Protein Accession: NP_006716
Gene Symbol: CD6
Protein Name: CD6 antigen;TP120
Celera Genomic Axis: GA_x5YUV32VYAU(6448144..6496988)
Chromosome: Chr11
OMIM number: 186720
OMIM Information: CD6 ANTIGEN;CD6
Transcript Sequence: SEQ ID NO:53 (WO 2005/056837 SEQ ID NO:478)
Protein Sequence: SEQ ID NO:107 (WO 2005/056837 SEQ ID NO:995)

SNP Information

Context: SEQ ID NO:164 (WO 2005/056837 SEQ ID NO:12393)
Celera SNP ID: hCV2553030
SNP Position Transcript: 791
SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(T,4|C,10) Caucasian(T,90|C,220)
Chinese(T,1|C,59) Japanese(T,0|C,20) African(T,3|C,97)
total(C,396|T,94) ;no_pop(C,-|T,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:107, 217, (T,ACG) (M,ATG)

Gene Number: 166
Celera Gene: hCG40393 - 30000674330026
Celera Transcript: hCT31651 - 30000674330141
Public Transcript Accession: NM_006725
Celera Protein: hCP50172 - 30000674329046
Public Protein Accession: NP_006716
Gene Symbol: CD6
Protein Name: CD6 antigen;TP120
Celera Genomic Axis: GA_x5YUV32VYAU(6448144..6496988)
Chromosome: Chr11
OMIM number: 186720
OMIM Information: CD6 ANTIGEN;CD6
Transcript Sequence: SEQ ID NO:54 (WO 2005/056837 SEQ ID NO:479)
Protein Sequence: SEQ ID NO:108 (WO 2005/056837 SEQ ID NO:996)

SNP Information

Context: SEQ ID NO:165 (WO 2005/056837 SEQ ID NO:12402)

Celera SNP ID: hCV2553030
SNP Position Transcript: 791
SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(T,4|C,10) Caucasian(T,90|C,220)
Chinese(T,1|C,59) Japanese(T,0|C,20) African(T,3|C,97)
total(C,396|T,94) ;no_pop(C,-|T,-)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:108, 217, (T,ACG) (M,ATG)

Gene Number: 168
Celera Gene: hCG41331 - 84000315067311
Celera Transcript: hCT32601 - 84000315067312
Public Transcript Accession: NM_000482
Celera Protein: hCP51233 - 197000069365036
Public Protein Accession: NP_000473
Gene Symbol: APOA4
Protein Name: apolipoprotein A-IV
Celera Genomic Axis: GA_x5YUV32VVY5(26718133..26720736)
Chromosome: Chr11
OMIM number: 107690
OMIM Information: APOLIPOPROTEIN A-IV;APOA4
Transcript Sequence: SEQ ID NO:55 (WO 2005/056837 SEQ ID NO:488)
Protein Sequence: SEQ ID NO:109 (WO 2005/056837 SEQ ID NO:1005)

SNP Information

Context: SEQ ID NO:166 (WO 2005/056837 SEQ ID NO:12550)
Celera SNP ID: hCV11482766
SNP Position Transcript: 553
SNP Source: Applera
Population(AAllele,Count): african american(A,32|G,4) caucasian(A,35|G,3)
total(A,67|G,7)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:109, 147, (N,AAC) (S,AGC)

SNP Source: HGBASE;dbSNP
Population(AAllele,Count): 40 Africans; 32 white Americans; 2 CEPH
individuals(A,22|G,125) 80 chromosomes from Harare, Zimbabwe; 64
chromosomes from Tecumseh, Michigan; 4 chromosomes from CEPH individuals.
Population size refers to number of chromosomes studied(A,44|G,251)
total(G,376|A,66) ;CEPH(G,4|A,88) total(G,4|A,88) no_pop(G,-|A,-)
JBIC-allele(G,509|A,991) total(G,509|A,991) HYP3(G,22|A,126)
total(G,22|A,126)PA129964589(G,18|A,126) total(G,18|A,126)
SNP Type: MISSENSE MUTATION
Protein Coding: SEQ ID NO:109, 147, (N,AAC) (S,AGC)

TABLE 2

Gene Number: 11
 Celera Gene: hCG1640727 - 61000125148997
 Gene Symbol: LOC51049
 Protein Name: insulin-like growth factor 1 receptor;JTK13
 Celera Genomic Axis: GA_x5YUV32W6GH(14096498..14417517)
 Chromosome: Chr15
 OMIM number: 147370
 OMIM Information: INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR;IGF1R
 Genomic Sequence SEQ ID NO:167 (WO 2005/056837 SEQ ID NO:13204)

SNP Information

Context SEQ ID NO:186 (WO 2005/056837 SEQ ID NO:16597)
 Celera SNP ID: hCV8722981
 SNP Position Genomic: 72457
 SNP Source: dbSNP
 Population(AAllele,Count): no_pop(C,-|T,-)
 SNP Type: INTRON;MISSENSE

Gene Number: 19
 Celera Gene: hCG1644130 - 30000035058841
 Gene Symbol: HLA-DPA1
 Protein Name: major histocompatibility complex, class II, DP
 alpha 1;HLA-DP1A;HLADP;HLASB
 Celera Genomic Axis: GA_x5YUV32W6W6(6039880..6067732)
 Chromosome: Chr6
 OMIM number: 142858
 OMIM Information: MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DP
 BETA-1;HLA-DPB1
 Genomic Sequence SEQ ID NO:168 (WO 2005/056837 SEQ ID NO:13212)

SNP Information

Context SEQ ID NO:187 (WO 2005/056837 SEQ ID NO:17869)
 Celera SNP ID: hCV8851080
 SNP Position Genomic: 5997
 SNP Source: Applera
 Population(AAllele,Count): african american(C,6|T,20) caucasian(T,10)
 total(C,6|T,30)
 SNP Type: MISSENSE

SNP Source: HGBASE;HGMD;dbSNP
 Population(AAllele,Count): no_pop(T,-|C,-) ;no_pop(T,-|C,-) ;(T,-|C,-)
 CEPH(C,16|T,76) total(C,16|T,76)
 SNP Type: MISSENSE

Gene Number: 20
 Celera Gene: hCG1647899 - 30000662117559
 Gene Symbol:
 Protein Name:
 Celera Genomic Axis: GA_x5YUV32VY4T(933937..952867)

Chromosome: Chr19
OMIM number:
OMIM Information:
Genomic Sequence SEQ ID NO:169 (WO 2005/056837 SEQ ID NO:13213)

SNP Information

Context SEQ ID NO:188 (WO 2005/056837 SEQ ID NO:18287)
Celera SNP ID: hCV16044337
SNP Position Genomic: 8589
SNP Source: Applera
Population(A allele,Count): african american(C,17|T,19) caucasian(C,20|T,10)
total(C,37|T,29)
SNP Type: MISSENSE;TFBS

SNP Source: HGBASE;dbSNP
Population(A allele,Count): no_pop(T,-|C,-) ;no_pop(T,-|C,-)
SNP Type: MISSENSE;TFBS

Gene Number: 23
Celera Gene: hCG17143 - 30000662103580
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32VV34(37421364..37802113)
Chromosome: Chr3
OMIM number: 603963
OMIM Information: INTEGRIN, ALPHA-9;ITGA9
Genomic Sequence SEQ ID NO:170 (WO 2005/056837 SEQ ID NO: 13216)

SNP Information

Context SEQ ID NO:189 (WO 2005/056837 SEQ ID NO:19736)
Celera SNP ID: hCV25644901
SNP Position Genomic: 207434
SNP Source: Applera
Population(A allele,Count): african american(A,37|G,1) caucasian(A,35|G,3)
total(A,72|G,4)
SNP Type: hmCS;MISSENSE

Gene Number: 29
Celera Gene: hCG17504 - 30000675938676
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32W6W6(5820200..5840973)
Chromosome: Chr6
OMIM number:
OMIM Information:
Genomic Sequence SEQ ID NO:171 (WO 2005/056837 SEQ ID NO:13222)

SNP Information

Context SEQ ID NO:190 (WO 2005/056837 SEQ ID NO:21389)
Celera SNP ID: hCV549926

SNP Position Genomic: 8986
SNP Source: HGBASE;HGMD;dbSNP
Population(AAllele,Count): no_pop(G,-|A,-) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-)
SNP Type: hmCS;INTRON;MISSENSE;NONSENSE MUTATION;TFBS

Gene Number: 36
Celera Gene: hCG1788543 - 30000034442302
Gene Symbol: CYP4F2
Protein Name: cytochrome P450, family 4, subfamily F, polypeptide 2;CPF2
Celera Genomic Axis: GA_x5YUV32W1A1(7097023..7128996)
Chromosome: Chr19
OMIM number: 604426
OMIM Information: CYTOCHROME P450, SUBFAMILY IVF, POLYPEPTIDE 2;CYP4F2
Genomic Sequence SEQ ID NO:172 (WO 2005/056837 SEQ ID NO:13229)

SNP Information

Context SEQ ID NO:191 (WO 2005/056837 SEQ ID NO:23746)
Celera SNP ID: hCV16179493
SNP Position Genomic: 24377
SNP Source: Applera
Population(AAllele,Count): african_american(A,2|G,34) caucasian(A,17|G,23) total(A,19|G,57)
SNP Type: MISSENSE;TFBS

SNP Source: Celera;HGBASE;dbSNP
Population(AAllele,Count): no_pop(A,1|G,6) total(G,6|A,1) ;no_pop(G,-|A,-) ;PGA-AFRICAN-PANEL(G,-|A,-) PGA-EUR(EAN-PANEL(G,-|A,-) TSC_42_A(A,16|G,60) TSC_42_C(A,27|G,55) TSC_42_AA(A,6|G,78) total(G,193|A,49)
SNP Type: MISSENSE;TFBS

Gene Number: 37
Celera Gene: hCG1789838 - 30000668725918
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32VU0F(7752304..7911442)
Chromosome: Chr9
OMIM number: 600046
OMIM Information: ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER 1;ABCA1
Genomic Sequence SEQ ID NO:173 (WO 2005/056837 SEQ ID NO:13230)

SNP Information

Context SEQ ID NO:192 (WO 2005/056837 SEQ ID NO:24301)
Celera SNP ID: hCV2741051
SNP Position Genomic: 75565
SNP Source: Applera

Population(AAllele,Count): african american(A,24|G,14) caucasian(A,14|G,26)
total(A,38|G,40)
SNP Type: hmCS;MISSENSE

SNP Source: Celera;HGBASE;HGMD;dbSNP
Population(AAllele,Count): (A,1|G,9) total(G,9|A,1)Gaucasian(A,78|G,234)
Ghinese(A,11|G,47) Japanese(G,6|A,8) African(G,34|A,66) ; (G,-|A,-)
; (G,-|A,-) ; ; (G,-|A,-) HISP1(G,-|A,-) PAG1(G,-|A,-) GAUG1(G,-|A,-)
AFR1(G,-|A,-) P1(G,-|A,-) Gord_blood(G,-|A,-)
SNP Type: hmCS;MISSENSE

Gene Number: 53
Celera Gene: hCG1981506 - 30000675586425
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32W3P1(4942117..5028198)
Chromosome: Chr1
OMIM number: 142461
OMIM Information: HEPARAN SULFATE PROTEOGLYCAN OF BASEMENT
MEMBRANE;HSPG2
Genomic Sequence SEQ ID NO:174 (WO 2005/056837 SEQ ID NO: 13246)

SNP Information

Context SEQ ID NO:194 (WO 2005/056837 SEQ ID NO: 29100)
Celera SNP ID: hCV1603656
SNP Position Genomic: 68776
SNP Source: Applera
Population(AAllele,Count): african american(A,7|G,27) caucasian(A,2|G,38)
total(A,9|G,65)
SNP Type: hmCS;MISSENSE;TFBS

SNP Source: Celera
Population(AAllele,Count): no_pop(A,4|G,9) total(G,9|A,4)
SNP Type: hmCS;MISSENSE;TFBS

Gene Number: 71
Celera Gene: hCG2023324 - 30000669567219
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32VYJC(5582533..5693244)
Chromosome: Chr7
OMIM number: 168820
OMIM Information: PARAOXONASE 1;PON1
Genomic Sequence SEQ ID NO:175 (WO 2005/056837 SEQ ID NO: 13264)

SNP Information

Context SEQ ID NO:195 (WO 2005/056837 SEQ ID NO: 33505)
Celera SNP ID: hCV2548962
SNP Position Genomic: 94248
SNP Source: Applera

Population(AAllele,Count): african american(A,7|G,17) caucasian(A,26)
total(A,33|G,17)
SNP Type: hmCS;MISSENSE

SNP Source: Celera;HGBASE;HGMD;dbSNP
Population(AAllele,Count): no_pop(G,1|A,2) total(G,1|A,2) ;(G,-|A,-)
Spanish men(A,158|G,365) Northern Ireland, France, Scotland(A,580|G,1420)
Individuals(A,190|G,443) Finnish(A,87|G,250) ;(G,-|A,-)
;CEPH(G,17|A,75) PGA-AFRICAN-PANEL(G,-|A,-) PGA-EUR(EAN-PANEL(G,-|A,-)
total(G,17|A,75) HISP1(G,-|A,-) PAC1(G,-|A,-) CAUC1(G,-|A,-)
AFR1(G,-|A,-) P1(G,-|A,-) Han(A,1600|G,2400) Cau(G,152|A,308)
total(G,2552|A,1908)
SNP Type: hmCS;MISSENSE

Gene Number: 72
Celera Gene: hCG20262 - 67000129407882
Gene Symbol: FCAR
Protein Name: Fc fragment of IgA, receptor for;CD89
Celera Genomic Axis: GA_x5YUV32VY4T(4727438..4757054)
Chromosome: Chr19
OMIM number: 147045
OMIM Information: Fc FRAGMENT OF IgA, RECEPTOR FOR;FCAR
Genomic Sequence SEQ ID NO:176 (WO 2005/056837 SEQ ID NO: 13265)

SNP Information

Context SEQ ID NO:196 (WO 2005/056837 SEQ ID NO: 33891)
Celera SNP ID: hCV7841642
SNP Position Genomic: 17363
SNP Source: Applera
Population(AAllele,Count): african american(A,2|G,36) caucasian(A,3|G,37)
total(A,5|G,73)
SNP Type: INTRON;MISSENSE

SNP Source: Celera;dbSNP
Population(AAllele,Count): no_pop(A,1|G,9) total(G,9|A,1) ;no_pop(A,-
|G,-)
SNP Type: INTRON;MISSENSE

Gene Number: 112
Celera Gene: hCG23557 - 30000672836692
Gene Symbol:
Protein Name:
Celera Genomic Axis: GA_x5YUV32VUUD(23744743..23795096)
Chromosome: Chr8
OMIM number: 193002
OMIM Information: SOLUTE CARRIER FAMILY 18, MEMBER 1;SLC18A1
Genomic Sequence SEQ ID NO:177 (WO 2005/056837 SEQ ID NO: 13305)

SNP Information

Context SEQ ID NO:197 (WO 2005/056837 SEQ ID NO: 51065)
Celera SNP ID: hCV2715953

SNP Position Genomic: 41162
SNP Source: Applera
Population(AAllele,Count): african american(C,36) caucasian(C,35|G,5)
total(C,71|G,5)
SNP Type: hmCS;MISSENSE

SNP Source: Celera
Population(AAllele,Count): Caucasian(C,30|G,282) Chinese(C,1|G,59)
Japanese(G,20) African(C,1|G,99) total(G,460|C,32) (G,2|C,11)
total(G,2|C,11)
SNP Type: hmCS;MISSENSE

Gene Number: 117
Celera Gene: hCG25215 - 208000034985688
Gene Symbol: A2M
Protein Name: alpha-2-macroglobulin
Celera Genomic Axis: GA_x5YUV32W234(3866416..3926902)
Chromosome: Chr12
OMIM number: 103950
OMIM Information: ALPHA-2-MACROGLOBULIN;A2M
Genomic Sequence SEQ ID NO:178 (WO 2005/056837 SEQ ID NO: 13310)

SNP Information

Context SEQ ID NO:198 (WO 2005/056837 SEQ ID NO: 51941)
Celera SNP ID: hCV517658
SNP Position Genomic: 42522
SNP Source: Applera
Population(AAllele,Count): african american(A,14|G,4) caucasian(A,18|G,6)
total(A,32|G,10)
SNP Type: hmCS;MISSENSE;SILENT MUTATION;TFBS

SNP Source: Applera
Population(AAllele,Count): african american(A,26|G,8) caucasian(A,26|G,10)
total(A,52|G,18)
SNP Type: hmCS;MISSENSE;SILENT MUTATION;TFBS

SNP Source: Celera;HGBASE;dbSNP
Population(AAllele,Count): no_pop(G,4|A,17) total(G,4|A,17)
;Caucasians(G,0|A,0) ; (G,-|A,-)
SNP Type: hmCS;MISSENSE;SILENT MUTATION;TFBS

Gene Number: 137
Celera Gene: hCG33048 - 84000314084586
Gene Symbol: HDLBP
Protein Name: high density lipoprotein binding protein
(vigilin);HBP;VGL
Celera Genomic Axis: GA_x5YUV32VWPT(46744110..46845156)
Chromosome: Chr2
OMIM number: 142695
OMIM Information: HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN;HDLBP
Genomic Sequence SEQ ID NO:179 (WO 2005/056837 SEQ ID NO: 13330)

SNP Information

Context SEQ ID NO:199 (WO 2005/056837 SEQ ID NO: 56926)
 Celera SNP ID: hCV22274624
 SNP Position Genomic: 68488
 SNP Source: Applera
 Population(A allele,Count): african american(A,29|G,7) caucasian(A,27|G,13)
 total(A,56|G,20)
 SNP Type: hmCS;MISSENSE;SILENT MUTATION

SNP Source: dbSNP
 Population(A allele,Count): (G,-|A,-) CEPH(G,18|A,74) total(G,18|A,74)
 SNP Type: hmCS;MISSENSE;SILENT MUTATION

Gene Number: 149
 Celera Gene: hCG37187 - 146000220350063
 Gene Symbol: NPC1
 Protein Name: Niemann-Pick disease, type C1;NPC
 Celera Genomic Axis: GA_x5YUV32W66L(2589859..2656985)
 Chromosome: Chr18
 OMIM number:
 OMIM Information:
 Genomic Sequence SEQ ID NO:180 (WO 2005/056837 SEQ ID NO: 13342)

SNP Information

Context SEQ ID NO:200 (WO 2005/056837 SEQ ID NO: 59198)
 Celera SNP ID: hCV25472673
 SNP Position Genomic: 32166
 SNP Source: Applera
 Population(A allele,Count): african american(A,35|G,3) caucasian(A,21|G,17)
 total(A,56|G,20)
 SNP Type: hmCS;MISSENSE

SNP Source: Celera;dbSNP
 Population(A allele,Count): no_pop(G,1|A,8) total(G,1|A,8) ;no_pop(G,-
 |A,-)
 SNP Type: hmCS;MISSENSE

Gene Number: 156
 Celera Gene: hCG38633 - 226000018878110
 Gene Symbol: FABP2
 Protein Name: fatty acid binding protein 2,
 intestinal;FABPI;FABPI, I-FABP
 Celera Genomic Axis: GA_x5YUV32VYAM(763338..780252)
 Chromosome: Chr4
 OMIM number: 134640
 OMIM Information: FATTY ACID-BINDING PROTEIN 2;FABP2
 Genomic Sequence SEQ ID NO:181 (WO 2005/056837 SEQ ID NO: 13349)

SNP Information

Context SEQ ID NO:201 (WO 2005/056837 SEQ ID NO: 60653)

Celera SNP ID: hCV761961
SNP Position Genomic: 7418
SNP Source: Applera
Population(A,7|G,27) caucasian(A,5|G,29)
total(A,12|G,56)
SNP Type: hmCS;MISSENSE

SNP Source: HGBASE;HGMD;dbSNP
Population(A,150|G,850) Caucasian,Canada(G,165|A,496) Keewatin Inuit,
Northern Ontario, Canada(G,122|A,227) total(G,1137|A,873) ; (G,-|A,-)
; (G,-|A,-)
SNP Type: hmCS;MISSENSE

Gene Number: 162
Celera Gene: hCG401141 - 104000116851304
Gene Symbol: ADAMTS1
Protein Name: a disintegrin-like and metalloprotease
(reprolysin type) with thrombospondin type 1 motif, 1;C3-C5;KIAA1346;METH1
Celera Genomic Axis: GA_x5YUV32W8NG(19809539..19830669)
Chromosome: Chr21
OMIM number: 605174
OMIM Information: A DISINTEGRIN-LIKE AND METALLOPROTEINASE WITH
THROMBOSPONDIN TYPE 1 MOTIF, 1;ADAMTS1
Genomic Sequence SEQ ID NO:182 (WO 2005/056837 SEQ ID NO: 13355)

SNP Information

Context SEQ ID NO:203 (WO 2005/056837 SEQ ID NO: 61571)
Celera SNP ID: hCV529706
SNP Position Genomic: 7139
SNP Source: HGBASE;dbSNP
Population(A,39|C,53) no_pop(G,-|C,-) ;no_pop(G,-|C,-)
CEPH(G,39|C,53) total(G,39|C,53)
SNP Type: MISSENSE

Context SEQ ID NO:204 (WO 2005/056837 SEQ ID NO: 61580)
Celera SNP ID: hCV529710
SNP Position Genomic: 6414
SNP Source: HGBASE;dbSNP
Population(A,2|C,6) no_pop(G,-|C,-) ; (G,-|C,-)
NCBI|NIHP|R(G,2|C,6) total(G,2|C,6) CEPH(G,22|C,70) total(G,22|C,70)
SNP Type: UTR 5

Gene Number: 166
Celera Gene: hCG40393 - 30000674330026
Gene Symbol: CD6
Protein Name: CD6 ANTIGEN;CD6
Celera Genomic Axis: GA_x5YUV32VYAU(6442145..6502989)
Chromosome: Chr11
OMIM number: 186720
OMIM Information: CD6 ANTIGEN;CD6
Genomic Sequence SEQ ID NO:183 (WO 2005/056837 SEQ ID NO: 13359)

SNP Information

Context SEQ ID NO:205(WO 2005/056837 SEQ ID NO: 62578)
 Celera SNP ID: hCV2553030
 SNP Position Genomic: 43168
 SNP Source: Celera;dbSNP
 Population(AAllele,Count): no_pop(T,4|C,10) Caucasian(T,90|C,220)
 Chinese(T,1|C,59) Japanese(T,0|C,20) African(T,3|C,97)
 total(C,396|T,94) ; (C,-|T,-)
 SNP Type: hmCS;MISSENSE;TFBS

Gene Number: 168
 Celera Gene: hCG41331 - 84000315067311
 Gene Symbol: APOA4
 Protein Name: apolipoprotein A-IV
 Celera Genomic Axis: GA_x5YUV32VY5(26712134..26726737)
 Chromosome: Chr11
 OMIM number: 107690
 OMIM Information: APOLIPOPROTEIN A-IV;APOA4
 Genomic Sequence SEQ ID NO:184 (WO 2005/056837 SEQ ID NO: 13361)

SNP Information

Context SEQ ID NO:267 (WO 2005/056837 SEQ ID NO: 62978)
 Celera SNP ID: hCV11482766
 SNP Position Genomic: 7688
 SNP Source: Applera
 Population(AAllele,Count): african american(A,32|G,4) caucasian(A,35|G,3)
 total(A,67|G,7)
 SNP Type: hmCS;MISSENSE;REPEATS;SILENT MUTATION

SNP Source: HGBASE;dbSNP
 Population(AAllele,Count): 40 Africans; 32 white Americans; 2 CEPH
 individuals(A,22|G,125) 80 chromosomes from Harare, Zimbabwe; 64
 chromosomes from Tecumseh, Michigan; 4 chromosomes from CEPH individuals.
 Population size refers to number of chromosomes studied(A,44|G,251)
 total(G,376|A,66) ;CEPH(G,4|A,88) total(G,4|A,88) (G,-|A,-) JBIC-
 allele(G,509|A,991) total(G,509|A,991) HYP3(G,22|A,126)
 total(G,22|A,126) PA129964589(G,18|A,126) total(G,18|A,126)
 SNP Type: hmCS;MISSENSE;REPEATS;SILENT MUTATION

Gene Number: 287
 Celera Gene: hCG28255 - 11000596131988
 Gene Symbol: ASAH1
 Protein Name: N-acylsphingosine amidohydrolase (acid
 ceramidase) 1;AC;ASAH;FLJ21558;N-acylsphingosine amidohydrolase;PHP32
 Celera Genomic Axis: GA_x5L2HTU51L1(5362800..5403444)
 Chromosome: 8
 OMIM number: 228000
 OMIM Information: FARBER LIPOGRANULOMATOSIS
 Genomic Sequence SEQ ID NO:185 (WO 2005/056837 SEQ ID NO: 13480)

SNP Information

Context SEQ ID NO:206 (WO 2005/056837 SEQ ID NO: 79133)
Celera SNP ID: hCV2442143
SNP Position Genomic: 19671
SNP Source: Celera;HGBASE;dbSNP
Population(AAllele,Count): Caucasian(G,3|A,2) Hispanic(A,2)
total(G,3|A,4) ;no_pop(G,-|A,-) ;no_pop(G,-|A,-)
SNP Type: SILENT MUTATION;MISSENSE MUTATION

TABLE 3

<u>Marker</u>	<u>Alleles</u>	<u>Sequence A (allele-specific primer)</u>	<u>Sequence B (allele-specific primer)</u>	<u>Sequence C (common primer)</u>
hCV11482766	C/T	GCGCACCAGGTCAG (SEQ ID NO: 207) (WO 2005/056837 SEQ ID NO:85103)	GCGCACCAGGTCAA (SEQ ID NO:208) (WO 2005/056837 SEQ ID NO:85104)	CCACGTTCTGGTCGATCTT (SEQ ID NO:209) (WO 2005/056837 SEQ ID NO: 85105)
hCV1603656	C/T	GCTGCCCTCAGTCCG (SEQ ID NO:210) (WO 2005/056837 SEQ ID NO: 85205)	TGCTGCCCTCAGTCCA (SEQ ID NO:211) (WO 2005/056837 SEQ ID NO:85206)	GGGCACTGCCAATCTTAG (SEQ ID NO:212) (WO 2005/056837 SEQ ID NO: 85207)
hCV16044337	A/G	TCCGGGTGCACGTATA (SEQ ID NO:213) (WO 2005/056837 SEQ ID NO: 85214)	CGGGTGCACGTATG (SEQ ID NO:214) (WO 2005/056837 SEQ ID NO: 85215)	TGGAGAGTGTTTGCTCATCTAC (SEQ ID NO:215) (WO 2005/056837 SEQ ID NO: 85216)
hCV16179493	C/T	GGGTCCGGCCACAC (SEQ ID NO:216) (WO 2005/056837 SEQ ID NO: 85253)	GGGTCCGGCCACAT (SEQ ID NO:217) (WO 2005/056837 SEQ ID NO: 85254)	GGGCCCCCTCAGTGAAG (SEQ ID NO:218) (WO 2005/056837 SEQ ID NO: 85255)
hCV22274624	C/T	CCCTACAGAGGATGTCAG (SEQ ID NO:219) (WO 2005/056837 SEQ ID NO: 85319)	CCCTACAGAGGATGTCAA (SEQ ID NO:220) (WO 2005/056837 SEQ ID NO: 85320)	CAGAGCCTCCCTTGTCAC (SEQ ID NO:221) (WO 2005/056837 SEQ ID NO: 85321)
hCV2442143	C/T	ATTTAAGCATCATAGCATACCAC (SEQ ID NO:222) (WO 2005/056837 SEQ ID NO: 85328)	ATTTAAGCATCATAGCATACCAT (SEQ ID NO:223) (WO 2005/056837 SEQ ID NO: 85329)	TGGTACACCAATAATCTTGACTTAC (SEQ ID NO:224) (WO 2005/056837 SEQ ID NO: 85330)
hCV25472673	C/T	TGGGCTCCATCCCAC (SEQ ID NO:225) (WO 2005/056837 SEQ ID NO: 85340)	TGGGCTCCATCCCAC (SEQ ID NO:226) (WO 2005/056837 SEQ ID NO: 85341)	CCAATTCCTTTCTTCTTCAGTT (SEQ ID NO:227) (WO 2005/056837 SEQ ID NO: 85342)

TABLE 3 (continued)

<u>Marker</u>	<u>Alleles</u>	<u>Sequence A (allele-specific primer)</u>	<u>Sequence B (allele-specific primer)</u>	<u>Sequence C (common primer)</u>
hCV2548962	C/T	CAAATACATCTCCAGGATC (SEQ ID NO:228) (WO 2005/056837 SEQ ID NO: 85349)	CAATACATCTCCAGGATT (SEQ ID NO:229) (WO 2005/056837 SEQ ID NO: 85350)	GTTTAAATGCAGTTTGAATGATAT (SEQ ID NO:230) (WO 2005/056837 SEQ ID NO: 85351)
hCV2553030	C/T	CCGGCTTGCACTTCAC (SEQ ID NO:231) (WO 2005/056837 SEQ ID NO: 85352)	CCGGCTTGCACTTCAT (SEQ ID NO:232) (WO 2005/056837 SEQ ID NO: 85353)	CTTTGTGGCCGCAGTAGT (SEQ ID NO:233) (WO 2005/056837 SEQ ID NO: 85354)
hCV25644901	A/G	CAGACCTGCAGCTTCA (SEQ ID NO:234) (WO 2005/056837 SEQ ID NO: 85424)	AGACCTGCAGCTTCG (SEQ ID NO:235) (WO 2005/056837 SEQ ID NO: 85425)	TGTAACCCATCAACTCTGTTTATC (SEQ ID NO:236) (WO 2005/056837 SEQ ID NO: 85426)
hCV2715953	C/G	CATTGGGGCCAATGAC (SEQ ID NO:237) (WO 2005/056837 SEQ ID NO: 85466)	ATTGGGGCCAATGAG (SEQ ID NO:238) (WO 2005/056837 SEQ ID NO: 85467)	ATGCATTTTCATGTGAAAACCTCT (SEQ ID NO:239) (WO 2005/056837 SEQ ID NO: 85468)
hCV2741051	C/T	GCAGCCAGTTTCTCCC (SEQ ID NO:240) (WO 2005/056837 SEQ ID NO: 85469)	TGCAGCCAGTTTCTCCT (SEQ ID NO:241) (WO 2005/056837 SEQ ID NO: 85470)	CATGAAATGCTTCCAGGTATT (SEQ ID NO:242) (WO 2005/056837 SEQ ID NO: 85471)
hCV517658	T/C	AATGGCCTTGGACTTGAT (SEQ ID NO:243) (WO 2005/056837 SEQ ID NO: 85529)	AATGGCCTTGGACTTGAC (SEQ ID NO:244) (WO 2005/056837 SEQ ID NO: 85530)	CTCTGCCCATGCAAAACAC (SEQ ID NO:245) (WO 2005/056837 SEQ ID NO: 85531)
hCV529706	C/G	GCGAGGACGAAGGGG (SEQ ID NO:246) (WO 2005/056837 SEQ ID NO: 85532)	GCGAGGACGAAGGGC (SEQ ID NO:247) (WO 2005/056837 SEQ ID NO: 85533)	GGAGGATGAATGGACAGACAA (SEQ ID NO:248) (WO 2005/056837 SEQ ID NO: 85534)

TABLE 3 (continued)

<u>Marker</u>	<u>Alleles</u>	<u>Sequence A (allele-specific primer)</u>	<u>Sequence B (allele-specific primer)</u>	<u>Sequence C (common primer)</u>
hCV529710	C/G	CCGACCCGAACTAAAGG (SEQ ID NO:249) (WO 2005/056837 SEQ ID NO: 85535)	CCGACCCGAACTAAAGC (SEQ ID NO:250) (WO 2005/056837 SEQ ID NO: 85536)	CGCGTTCCCATGTC (SEQ ID NO:251) (WO 2005/056837 SEQ ID NO: 85537)
hCV549926	C/T	ACCATGGTCACCCTGG (SEQ ID NO:252) (WO 2005/056837 SEQ ID NO: 85538)	CACCATGGTCACCCTGA (SEQ ID NO:253) (WO 2005/056837 SEQ ID NO: 85539)	GGACTGAAAGCAATGTGAGAG (SEQ ID NO:254) (WO 2005/056837 SEQ ID NO: 85540)
hCV761961	C/T	CACAGTCAAAGAATCAAGCG (SEQ ID NO:255) (WO 2005/056837 SEQ ID NO: 85592)	TCACAGTCAAAGAATCAAGCA (SEQ ID NO:256) (WO 2005/056837 SEQ ID NO: 85593)	AAATTCCTTACCCTGAGTTCAGTTC (SEQ ID NO:257) (WO 2005/056837 SEQ ID NO: 85594)
hCV7841642	A/G	ACCAGCTCCAGGGTGT (SEQ ID NO:258) (WO 2005/056837 SEQ ID NO: 85604)	ACCAGCTCCAGGGTGTC (SEQ ID NO:259) (WO 2005/056837 SEQ ID NO: 85605)	TGAAGTTTGGGAATGAGACTGAT (SEQ ID NO:260) (WO 2005/056837 SEQ ID NO: 85606)
hCV8722981	C/T	GCGCTGGTTTGAGG (SEQ ID NO:261) (WO 2005/056837 SEQ ID NO: 85634)	GCGCTGGTTTGAGAG (SEQ ID NO:262) (WO 2005/056837 SEQ ID NO: 85635)	TGGCACAGGCAGTATTAAGTAG (SEQ ID NO:263) (WO 2005/056837 SEQ ID NO: 85636)
hCV8851080	A/G	GGCACTGCCCGCTT (SEQ ID NO:264) (WO 2005/056837 SEQ ID NO: 85655)	GGCACTGCCCGCTC (SEQ ID NO:265) (WO 2005/056837 SEQ ID NO: 85656)	CGCTTCCTGGAGAGATACATC (SEQ ID NO:266) (WO 2005/056837 SEQ ID NO: 85657)

TABLE 4

Significant Associations Between SNP Genotypes and Qualitative Phenotypes

<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>	Overall*		SNP Effect**	
				Chi-Square statistic	Test p-value	Chi-Square statistic	Test p-value
ADAMTS1	hCV529706	All Patients	Fatal CHD/Definite Non-fatal MI	7.3723	0.0251	6.5765	0.0103
ADAMTS1	hCV529706	All Patients	Fatal Coronary Heart Disease	7.4845	0.0237	7.1633	0.0074
ADAMTS1	hCV529706	All Patients	Total Mortality	12.4705	0.002	12.0029	0.0005
ADAMTS1	hCV529706	All Patients	Cardiovascular Mortality	10.455	0.0054	9.947	0.0016
ADAMTS1	hCV529706	All Patients	Fatal Atherosclerotic Cardiovascular Disease	10.455	0.0054	9.947	0.0016
APOA4	hCV11482766	All Patients	Fatal/Non-fatal Cerebrovascular Disease	7.0664	0.0292	6.169	0.013
APOA4	hCV11482766	All Patients	Any Report of Stroke During CARE	9.6951	0.0078	7.46	0.0063
APOA4	hCV11482766	All Patients	1st Stroke Occurred During CARE	11.7036	0.0029	9.2108	0.0024
HDLBP	hCV22274624	All Patients	Hosp. for Unstable Angina	6.3052	0.0427	5.2308	0.0222
HSPG2	hCV1603656	All Patients	Hosp. for Unstable Angina	7.3564	0.0253	5.9731	0.0145
HSPG2	hCV1603656	All Patients	History of Angina Pectoris	16.9406	0.0002	10.423	0.0012
IGF1R	hCV8722981	All Patients	Fatal CHD/Definite Non-fatal MI	12.0129	0.0025	8.8843	0.0029
IGF1R	hCV8722981	All Patients	Fatal Coronary Heart Disease	11.536	0.0031	5.1641	0.0231
IGF1R	hCV8722981	All Patients	Fatal/Non-fatal MI (def & prob)	7.2529	0.0266	4.8925	0.027
IGF1R	hCV8722981	All Patients	Cardiovascular Mortality	10.1906	0.0061	4.8293	0.028

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype (based on placebo patients only).

** Results of the chi-square test of the SNP effect (based on the logistic regression model for placebo patients only).

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes				Placebo Patients n/total (%)	Odds Ratio (95% CI)				
Public	Marker	Stratum	Phenotype	0 Rare Alleles	1 Rare Alleles	2 Rare Alleles	1 Rare Allele vs. 0 Rare Alleles	Significance level	
ADAMTS1	hCV5297 06	All Patients	Fatal CHD/Definite Non-fatal MI	92/872 (10.6%)	78/511 (15.3%)	14/90 (15.6%)	1.53 (1.10 to 2.11)	1.56 (0.82 to 2.79)	p < 0.05
ADAMTS1	hCV5297 06	All Patients	Fatal Coronary Heart Disease	24/872 (2.8%)	29/511 (5.7%)	4/90 (4.4%)	2.13 (1.23 to 3.72)	1.64 (0.48 to 4.38)	p < 0.05
ADAMTS1	hCV5297 06	All Patients	Total Mortality	40/872 (4.6%)	48/511 (9.4%)	6/90 (6.7%)	2.16 (1.40 to 3.34)	1.49 (0.55 to 3.36)	p < 0.005
ADAMTS1	hCV5297 06	All Patients	Cardiovascular Mortality	26/872 (3.0%)	34/511 (6.7%)	4/90 (4.4%)	2.32 (1.38 to 3.94)	1.51 (0.44 to 4.00)	p < 0.005
ADAMTS1	hCV5297 06	All Patients	Fatal Atherosclerotic Cardiovascular Disease	26/872 (3.0%)	34/511 (6.7%)	4/90 (4.4%)	2.32 (1.38 to 3.94)	1.51 (0.44 to 4.00)	p < 0.005
APOA4	hCV1148 2766	All Patients	Fatal/Non-fatal Cerebrovascular Disease	72/1106 (6.5%)	23/347 (6.6%)	5/25 (20.0%)	1.02 (0.62 to 1.63)	3.59 (1.17 to 9.17)	p < 0.05
APOA4	hCV1148 2766	All Patients	Any Report of Stroke During CARE	43/1106 (3.9%)	12/347 (3.5%)	4/25 (16.0%)	0.89 (0.44 to 1.65)	4.71 (1.33 to 13.04)	p < 0.05
APOA4	hCV1148 2766	All Patients	1st Stroke Occurred During CARE	36/1106 (3.3%)	12/347 (3.5%)	4/25 (16.0%)	1.07 (0.53 to 2.01)	5.66 (1.59 to 15.83)	p < 0.005
HDLBP	hCV2227 4624	All Patients	Hosp. for Unstable Angina	157/802 (19.6%)	91/545 (16.7%)	12/114 (10.5%)	0.82 (0.62 to 1.09)	0.48 (0.25 to 0.87)	p < 0.05
HSPG2	hCV1603 656	All Patients	Hosp. for Unstable Angina	217/1246 (17.4%)	42/223 (18.8%)	5/10 (50.0%)	1.10 (0.76 to 1.57)	4.74 (1.31 to 17.18)	p < 0.05
HSPG2	hCV1603 656	All Patients	History of Angina Pectoris	248/1246 (19.9%)	38/223 (17.0%)	7/10 (70.0%)	0.83 (0.56 to 1.19)	9.39 (2.59 to 43.80)	p < 0.005
IGF1R	hCV8722 981	All Patients	Fatal CHD/Definite Non-fatal MI	169/1418 (11.9%)	15/59 (25.4%)	1/2 (50.0%)	2.52 (1.33 to 4.53)	7.39 (0.29 to 187.30)	p < 0.005
IGF1R	hCV8722 981	All Patients	Fatal Coronary Heart Disease	54/1418 (3.8%)	2/59 (3.4%)	1/2 (50.0%)	0.89 (0.14 to 2.95)	25.26 (0.99 to 643.88)	p < 0.05
IGF1R	hCV8722 981	All Patients	Fatal/Non-fatal MI (def & prob)	190/1418 (13.4%)	14/59 (23.7%)	1/2 (50.0%)	2.01 (1.05 to 3.64)	6.46 (0.26 to 163.75)	p < 0.05
IGF1R	hCV8722 981	All Patients	Cardiovascular Mortality	60/1418 (4.2%)	3/59 (5.1%)	1/2 (50.0%)	1.21 (0.29 to 3.41)	22.68 (0.89 to 576.45)	p < 0.05

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes							
Public	Marker	Stratum	Phenotype	Overall*		SNP Effect**	
				Chi-Square Test statistic	p-value	Chi-Square Test statistic	p-value
NPC1	hCV25472673	All Patients	Hosp. for Cardiovascular Disease	14.1028	0.0009	13.6581	0.0002
NPC1	hCV25472673	All Patients	Total Coronary Heart Disease Events	6.9104	0.0316	6.8509	0.0089
NPC1	hCV25472673	All Patients	Total Cardiovascular Disease Events	13.7798	0.001	13.0217	0.0003
NPC1	hCV25472673	All Patients	Fatal/Non-fatal Atherosclerotic CV Disease	9.3597	0.0093	9.2405	0.0024
PON1	hCV2548962	All Patients	History of Stroke	7.762	0.0206	6.2747	0.0122
PON1	hCV2548962	All Patients	Any Report of Stroke During CARE	18.3981	0.0001	15.8161	<.0001
PON1	hCV2548962	All Patients	1st Stroke Occurred During CARE	15.5223	0.0004	13.6541	0.0002

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype (based on placebo patients only).

** Results of the chi-square test of the SNP effect (based on the logistic regression model for placebo patients only).

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes				Placebo Patients n/total (%)				Odds Ratio (95% CI)			
Public	Marker	Stratum	Phenotype	0 Rare Alleles	1 Rare Alleles	2 Rare Alleles	2 Rare Alleles vs. 0 Rare Alleles	1 Rare Allele vs. 0 Rare Alleles	Significance level		
NPC1	hCV254 72673	All Patients	Hosp. for Cardiovascular Disease	244/560 (43.6%)	323/697 (46.3%)	122/208 (58.7%)	1.12 (0.89 to 1.40)	1.84 (1.33 to 2.54)	p < 0.0005		
NPC1	hCV254 72673	All Patients	Total Coronary Heart Disease Events	180/560 (32.1%)	242/697 (34.7%)	88/208 (42.3%)	1.12 (0.89 to 1.42)	1.55 (1.12 to 2.15)	p < 0.05		
NPC1	hCV254 72673	All Patients	Total Cardiovascular Disease Events	254/560 (45.4%)	330/697 (47.3%)	125/208 (60.1%)	1.08 (0.87 to 1.35)	1.81 (1.32 to 2.51)	p < 0.0005		
NPC1	hCV254 72673	All Patients	Fatal/Non-fatal Atherosclerotic CV Disease	204/560 (36.4%)	274/697 (39.3%)	101/208 (48.6%)	1.13 (0.90 to 1.42)	1.65 (1.19 to 2.27)	p < 0.005		
PON1	hCV254 8962	All Patients	History of Stroke	28/753 (3.7%)	8/579 (1.4%)	2/133 (1.5%)	0.36 (0.15 to 0.77)	0.40 (0.06 to 1.34)	p < 0.05		
PON1	hCV254 8962	All Patients	Any Report of Stroke During CARE	16/753 (2.1%)	39/579 (6.7%)	4/133 (3.0%)	3.33 (1.88 to 6.18)	1.43 (0.40 to 3.97)	p < 0.0005		
PON1	hCV254 8962	All Patients	1st Stroke Occurred During CARE	14/753 (1.9%)	34/579 (5.9%)	4/133 (3.0%)	3.29 (1.79 to 6.40)	1.64 (0.46 to 4.65)	p < 0.0005		

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes					
<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>	Overall*	SNP Effect**
ADAMTS1	hCV529710	All Patients	Fatal CHD/Definite Nonfatal MI	Chi-Square Test <u>statistic</u> 7.5605	Chi-Square Test <u>statistic</u> 6.7732
ADAMTS1	hCV529710	All Patients	Fatal Coronary Heart Disease	<u>p-value</u> 0.0228	<u>p-value</u> 0.0093
ADAMTS1	hCV529710	All Patients	Total Mortality	7.3045	6.9927
ADAMTS1	hCV529710	All Patients	Cardiovascular Mortality	12.1574	11.7126
ADAMTS1	hCV529710	All Patients	Fatal Atherosclerotic Cardiovascular Disease	0.0023	0.0006
ADAMTS1	hCV529710	All Patients	History of Diabetes	10.2172	9.7327
ADAMTS1	hCV529710	All Patients	MI (Fatal/Nonfatal)	0.006	0.0018
ADAMTS1	hCV529710	All Patients	Definite Nonfatal MI	10.2172	9.7327
ASAH1	hCV2442143	All Patients	Fatal CHD/Definite Nonfatal MI	0.0307	0.0086
ASAH1	hCV2442143	All Patients	Fatal/Nonfatal MI (def & prob)	0.0378	0.0138
ASAH1	hCV2442143	All Patients		7.1575	6.9682
ASAH1	hCV2442143	All Patients		0.0279	0.0083
ASAH1	hCV2442143	All Patients		7.3794	7.0385
ASAH1	hCV2442143	All Patients		0.025	0.008
ASAH1	hCV2442143	All Patients		6.1285	5.639
ASAH1	hCV2442143	All Patients		0.0467	0.0176

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype (based on placebo patients only).

** Results of the chi-square test of the SNP effect (based on the logistic regression model for placebo patients only).

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes

Placebo Patients
n/total (%)

Odds Ratio (95% CI)

Public ADAM TS1	Marker hCV529 710	Stratum All Patients	Phenotype Fatal CHD/Definite Nonfatal MI	0 Rare Alleles		1 Rare Alleles		2 Rare Alleles		2 Rare Alleles vs. 0 Rare Alleles		1 Rare Allele vs. 0 Rare Alleles		Significance level
				92/873 (10.5%)	24/873 (2.7%)	79/516 (15.3%)	29/516 (5.6%)	4/90 (15.6%)	14/90 (4.4%)	1.56 (0.82 to 2.80)	1.53 (1.11 to 2.12)			
ADAM TS1	hCV529 710	All Patients	Fatal Coronary Heart Disease	24/873 (10.5%)	24/873 (2.7%)	29/516 (15.3%)	29/516 (5.6%)	4/90 (15.6%)	4/90 (4.4%)	1.65 (0.48 to 4.38)	2.11 (1.21 to 3.69)		p < 0.05	
ADAM TS1	hCV529 710	All Patients	Total Mortality	40/873 (4.6%)	40/873 (4.6%)	48/516 (9.3%)	48/516 (9.3%)	6/90 (6.7%)	6/90 (6.7%)	1.49 (0.55 to 3.36)	2.14 (1.38 to 3.31)		p < 0.005	
ADAM TS1	hCV529 710	All Patients	Cardiovascular Mortality	26/873 (3.0%)	26/873 (3.0%)	34/516 (6.6%)	34/516 (6.6%)	4/90 (4.4%)	4/90 (4.4%)	1.52 (0.44 to 4.00)	2.30 (1.37 to 3.91)		p < 0.005	
ADAM TS1	hCV529 710	All Patients	Fatal Atherosclerotic Cardiovascular Disease	26/873 (3.0%)	26/873 (3.0%)	34/516 (6.6%)	34/516 (6.6%)	4/90 (4.4%)	4/90 (4.4%)	1.52 (0.44 to 4.00)	2.30 (1.37 to 3.91)		p < 0.005	
ADAM TS1	hCV529 710	All Patients	History of Diabetes	112/873 (12.8%)	112/873 (12.8%)	93/516 (18.0%)	93/516 (18.0%)	13/90 (14.4%)	13/90 (14.4%)	1.15 (0.59 to 2.07)	1.49 (1.11 to 2.01)		p < 0.05	
ASAH1	hCV244 2143	All Patients	MI (Fatal/Nonfatal)	64/397 (16.1%)	64/397 (16.1%)	108/735 (14.7%)	108/735 (14.7%)	34/343 (9.9%)	34/343 (9.9%)	0.57 (0.36 to 0.89)	0.90 (0.64 to 1.26)		p < 0.05	
ASAH1	hCV244 2143	All Patients	Definite Nonfatal MI	47/397 (11.8%)	47/397 (11.8%)	72/735 (9.8%)	72/735 (9.8%)	21/343 (6.1%)	21/343 (6.1%)	0.49 (0.28 to 0.82)	0.81 (0.55 to 1.20)		p < 0.05	
ASAH1	hCV244 2143	All Patients	Fatal CHD/Definite Nonfatal MI	59/397 (14.9%)	59/397 (14.9%)	96/735 (13.1%)	96/735 (13.1%)	29/343 (8.5%)	29/343 (8.5%)	0.53 (0.33 to 0.84)	0.86 (0.61 to 1.23)		p < 0.05	
ASAH1	hCV244 2143	All Patients	Fatal/Nonfatal MI (def & prob)	63/397 (15.9%)	63/397 (15.9%)	107/735 (14.6%)	107/735 (14.6%)	34/343 (9.9%)	34/343 (9.9%)	0.58 (0.37 to 0.90)	0.90 (0.65 to 1.27)		p < 0.05	

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes					
<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>	Overall*	SNP Effect**
CD6	hCV2553030	All Patients	Congestive Heart Failure	Chi-Square Test <u>statistic</u> 7.2236 <u>p-value</u> 0.027	Chi-Square Test <u>statistic</u> 4.9062 <u>p-value</u> 0.0268
CD6	hCV2553030	All Patients	Hosp. for Peripheral Arterial Disease	7.4666	6.4999
CD6	hCV2553030	All Patients	History of Coronary Artery Bypass Graft	10.2377	10.0806
CD6	hCV2553030	All Patients	CARE MI: Non Q-Wave MI	6.7337	5.7915
CYP4F2	hCV16179493	All Patients	Fatal Coronary Heart Disease	9.3585	8.497
CYP4F2	hCV16179493	All Patients	Total Mortality	9.4509	6.6827
CYP4F2	hCV16179493	All Patients	Congestive Heart Failure	7.5512	4.7724
CYP4F2	hCV16179493	All Patients	Hosp. for Unstable Angina	8.1794	3.8637
CYP4F2	hCV16179493	All Patients	Cardiovascular Mortality	9.0692	8.0291
CYP4F2	hCV16179493	All Patients	Fatal Atherosclerotic Cardiovascular Disease	9.0692	8.0291

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype (based on placebo patients only).

** Results of the chi-square test of the SNP effect (based on the logistic regression model for placebo patients only).

TABLE 4 (continued)**Significant Associations Between SNP Genotypes and Qualitative Phenotypes**Placebo
Patients
n/total (%)

Odds Ratio (95% CI)

<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>	<u>0 Rare Alleles</u>	<u>1 Rare Alleles</u>	<u>2 Rare Alleles</u>	<u>2 Rare Alleles vs. 0 Rare Alleles</u>	<u>1 Rare Allele vs. 0 Rare Alleles</u>	<u>Significance level</u>
CD6	hCV255 3030	All Patients	Congestive Heart Failure	56/888 (6.3%)	47/512 (9.2%)	10/76 (13.2%)	2.25 (1.04 to 4.44)	1.50 (1.00 to 2.25)	p < 0.05
CD6	hCV255 3030	All Patients	Hosp. for Peripheral Arterial Disease	22/888 (2.5%)	14/512 (2.7%)	6/76 (7.9%)	3.37 (1.21 to 8.12)	1.11 (0.55 to 2.16)	p < 0.05
CD6	hCV255 3030	All Patients	History of Coronary Artery Bypass Graft	210/888 (23.6%)	161/512 (31.4%)	19/76 (25.0%)	1.08 (0.61 to 1.82)	1.48 (1.16 to 1.89)	p < 0.005
CD6	hCV255 3030	All Patients	CARE MI: Non Q-Wave MI	69/888 (7.8%)	51/512 (10.0%)	12/75 (16.0%)	2.26 (1.12 to 4.26)	1.31 (0.90 to 1.92)	p < 0.05
CYP4 F2	hCV161 79493	All Patients	Fatal Coronary Heart Disease	39/720 (5.4%)	14/629 (2.2%)	4/125 (3.2%)	0.58 (0.17 to 1.47)	0.40 (0.21 to 0.72)	p < 0.005
CYP4 F2	hCV161 79493	All Patients	Total Mortality	60/720 (8.3%)	30/629 (4.8%)	4/125 (3.2%)	0.36 (0.11 to 0.90)	0.55 (0.35 to 0.86)	p < 0.05
CYP4 F2	hCV161 79493	All Patients	Congestive Heart Failure	68/720 (9.4%)	39/629 (6.2%)	5/125 (4.0%)	0.40 (0.14 to 0.92)	0.63 (0.42 to 0.95)	p < 0.05
CYP4 F2	hCV161 79493	All Patients	Hosp. for Unstable Angina	138/720 (19.2%)	95/629 (15.1%)	31/125 (24.8%)	1.39 (0.88 to 2.15)	0.75 (0.56 to 1.00)	p < 0.05
CYP4 F2	hCV161 79493	All Patients	Cardiovascular Mortality	43/720 (6.0%)	17/629 (2.7%)	4/125 (3.2%)	0.52 (0.15 to 1.31)	0.44 (0.24 to 0.76)	p < 0.005
CYP4 F2	hCV161 79493	All Patients	Fatal Atherosclerotic Cardiovascular Disease	43/720 (6.0%)	17/629 (2.7%)	4/125 (3.2%)	0.52 (0.15 to 1.31)	0.44 (0.24 to 0.76)	p < 0.005

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes							
Public	Marker	Stratum	Phenotype	Overall*		SNP Effect**	
				Chi-Square Test statistic	p-value	Chi-Square Test statistic	p-value
KLK14	hCV16044337	All Patients	MI (Fatal/Nonfatal)	11.9595	0.0025	11.623	0.0007
KLK14	hCV16044337	All Patients	Nonfatal MI (Probable/Definite)	10.3731	0.0056	9.8772	0.0017
KLK14	hCV16044337	All Patients	Definite Nonfatal MI	8.8701	0.0119	8.2722	0.004
KLK14	hCV16044337	All Patients	Fatal MI	11.2134	0.0037	8.3119	0.0039
KLK14	hCV16044337	All Patients	Coronary Artery Bypass Graft	6.4727	0.0393	6.2691	0.0123
KLK14	hCV16044337	All Patients	Fatal CHD/Definite Nonfatal MI	11.2734	0.0036	10.8986	0.001
KLK14	hCV16044337	All Patients	Nonfatal MI (def & prob)	11.0705	0.0039	10.1263	0.0015
KLK14	hCV16044337	All Patients	Fatal/Nonfatal MI (def & prob)	12.3831	0.002	12.0168	0.0005
KLK14	hCV16044337	All Patients	History of Diabetes	7.2874	0.0262	7.1207	0.0076
KLK14	hCV16044337	All Patients	Family History of CV Disease	7.7839	0.0204	7.6659	0.0056

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype (based on placebo patients only).

** Results of the chi-square test of the SNP effect (based on the logistic regression model for placebo patients only).

TABLE 4 (continued)

Significant Associations Between SNP Genotypes and Qualitative Phenotypes				Placebo Patients n/total (%)	Odds Ratio (95% CI)					Significance level
Public	Marker	Stratum	Phenotype	0 Rare Alleles	1 Rare Alleles	2 Rare Alleles	1 Rare Allele vs. 0 Rare Alleles			
				81/685 (11.8%)	89/629 (14.1%)	35/156 (22.4%)	1.23 (0.89 to 1.70)			
KLK14	hCV1604 4337	All Patients	MI (Fatal/Nonfatal)	81/685 (11.8%)	89/629 (14.1%)	35/156 (22.4%)	1.23 (0.89 to 1.70)	p < 0.005		
KLK14	hCV1604 4337	All Patients	Nonfatal MI (Probable/Definite)	79/685 (11.5%)	81/629 (12.9%)	33/156 (21.2%)	1.13 (0.81 to 1.58)	p < 0.005		
KLK14	hCV1604 4337	All Patients	Definite Nonfatal MI	57/685 (8.3%)	58/629 (9.2%)	25/156 (16.0%)	1.12 (0.76 to 1.64)	p < 0.005		
KLK14	hCV1604 4337	All Patients	Fatal MI	2/685 (0.3%)	9/629 (1.4%)	5/156 (3.2%)	4.96 (1.27 to 32.60)	p < 0.005		
KLK14	hCV1604 4337	All Patients	Coronary Artery Bypass Graft	57/685 (8.3%)	79/629 (12.6%)	15/156 (9.6%)	1.58 (1.11 to 2.27)	p < 0.05		
KLK14	hCV1604 4337	All Patients	Fatal CHD/Definite Nonfatal MI	73/685 (10.7%)	79/629 (12.6%)	32/156 (20.5%)	1.20 (0.86 to 1.69)	p < 0.005		
KLK14	hCV1604 4337	All Patients	Nonfatal MI (def & prob)	75/685 (10.9%)	74/629 (11.8%)	32/156 (20.5%)	1.08 (0.77 to 1.53)	p < 0.005		
KLK14	hCV1604 4337	All Patients	Fatal/Nonfatal MI (def & prob)	80/685 (11.7%)	88/629 (14.0%)	35/156 (22.4%)	1.23 (0.89 to 1.70)	p < 0.005		
KLK14	hCV1604 4337	All Patients	History of Diabetes	91/685 (13.3%)	93/629 (14.8%)	34/156 (21.8%)	1.13 (0.83 to 1.55)	p < 0.05		
KLK14	hCV1604 4337	All Patients	Family History of CV Disease	294/685 (42.9%)	258/629 (41.0%)	48/156 (30.8%)	0.92 (0.74 to 1.15)	p < 0.05		

TABLE 5

Significant Associations Between SNP Genotypes and Quantitative Phenotypes

<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype (at Baseline)</u>	<u>Overall F-Test</u>		<u>SNP Effect F-Test</u>	
				<u>statistic</u>	<u>p-value</u>	<u>statistic</u>	<u>p-value</u>
HDLBP	hCV22274624	All Patients	Ln(Triglycerides)	5.55	0.004	5.5479	0.004
HDLBP	hCV22274624	All Patients	VLDL	8	0.0004	7.9953	0.0004

<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype (at Baseline)</u>	<u>Placebo Patients mean (se)# (N)</u>		<u>Significance Level</u>	
				<u>0 Rare Alleles</u>	<u>1 Rare Allele</u>	<u>2 Rare Alleles</u>	
HDLBP	hCV22274624	All Patients	Ln(Triglycerides)	4.955 (0.014) (N= 802)	4.998 (0.016) (N= 545)	5.073 (0.036) (N= 114)	p < 0.005
HDLBP	hCV22274624	All Patients	VLDL	25.969 (0.564) (N= 802)	27.873 (0.685) (N= 544)	32.000 (1.497) (N= 114)	p < 0.0005

* Results of the Overall F-Test for the analysis of variance model in which the quantitative phenotype is a function of SNP genotype (based on placebo patients only).

** Results of the F-test of the SNP effect (based on the analysis of variance model for placebo patients only).

Least squares estimates of the mean and its standard error based on the analysis of variance model.

TABLE 6

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy					Overall*		Interaction Effect**	
<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>		<u>Chi-Square</u>	<u>Test</u>	<u>Chi-Square</u>	<u>inter_pvalue</u>
ABCA1	hCV2741051	All Patients	Fatal/Non-fatal Cerebrovascular Disease		19.4858	0.0016	7.5666	0.0227
ABCA1	hCV2741051	All Patients	Any Report of Stroke During CARE		20.2702	0.0011	8.3498	0.0154
ABCA1	hCV2741051	All Patients	1st Stroke Occurred During CARE		19.1074	0.0018	7.1772	0.0276
NPC1	hCV25472673	All Patients	Fatal CHD/Definite Non-fatal MI		16.7713	0.005	6.9147	0.0315
NPC1	hCV25472673	All Patients	Hosp. for Cardiovascular Disease		33.7727	<.0001	16.8966	0.0002
NPC1	hCV25472673	All Patients	Total Coronary Heart Disease Events		23.8979	0.0002	12.324	0.0021
NPC1	hCV25472673	All Patients	Total Cardiovascular Disease Events		36.5639	<.0001	18.2781	0.0001
NPC1	hCV25472673	All Patients	Fatal/Non-fatal Atherosclerotic CV Disease		28.4984	<.0001	15.5441	0.0004
PON1	hCV2548962	All Patients	Total Coronary Heart Disease Events		16.8056	0.0049	6.2165	0.0447
PON1	hCV2548962	All Patients	Any Report of Stroke During CARE		34.8995	<.0001	7.1404	0.0281
PON1	hCV2548962	All Patients	1st Stroke Occurred During CARE		28.2289	<.0001	6.8104	0.0332

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

** Results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy									
Public	Marker	Stratum	Phenotype	0 Rare Alleles		1 Rare Allele		2 Rare Alleles	
				n/total (%)		n/total (%)		n/total (%)	
				Prava	Placebo	Prava	Placebo	Prava	Placebo
ABCA1	hCV2741 051	All Patients	Fatal/Non-fatal Cerebrovascular Disease	51/730 (7.0%)	53/746 (7.1%)	18/651 (2.8%)	38/615 (6.2%)	3/127 (2.4%)	9/107 (8.4%)
ABCA1	hCV2741 051	All Patients	Any Report of Stroke During CARE	27/730 (3.7%)	30/746 (4.0%)	5/651 (0.8%)	22/615 (3.6%)	2/127 (1.6%)	7/107 (6.5%)
ABCA1	hCV2741 051	All Patients	1st Stroke Occurred During CARE	26/730 (3.6%)	27/746 (3.6%)	5/651 (0.8%)	18/615 (2.9%)	2/127 (1.6%)	7/107 (6.5%)
NPC1	hCV2547 2673	All Patients	Fatal CHD/Definite Non-fatal MI	65/596 (10.9%)	61/560 (10.9%)	56/664 (8.4%)	86/697 (12.3%)	19/242 (7.9%)	36/208 (17.3%)
NPC1	hCV2547 2673	All Patients	Hosp. for Cardiovascular Disease	262/596 (44.0%)	244/560 (43.6%)	255/664 (38.4%)	323/697 (46.3%)	88/242 (36.4%)	122/208 (58.7%)
NPC1	hCV2547 2673	All Patients	Total Coronary Heart Disease Events	193/596 (32.4%)	180/560 (32.1%)	186/664 (28.0%)	242/697 (34.7%)	59/242 (24.4%)	88/208 (42.3%)
NPC1	hCV2547 2673	All Patients	Total Cardiovascular Disease Events	274/596 (46.0%)	254/560 (45.4%)	259/664 (39.0%)	330/697 (47.3%)	90/242 (37.2%)	125/208 (60.1%)
NPC1	hCV2547 2673	All Patients	Fatal/Non-fatal Atherosclerotic CV Disease	221/596 (37.1%)	204/560 (36.4%)	213/664 (32.1%)	274/697 (39.3%)	68/242 (28.1%)	101/208 (48.6%)
PON1	hCV2548 962	All Patients	Total Coronary Heart Disease Events	217/736 (29.5%)	266/753 (35.3%)	190/625 (30.4%)	189/579 (32.6%)	33/144 (22.9%)	54/133 (40.6%)
PON1	hCV2548 962	All Patients	Any Report of Stroke During CARE	13/736 (1.8%)	16/753 (2.1%)	14/625 (2.2%)	39/579 (6.7%)	7/144 (4.9%)	4/133 (3.0%)
PON1	hCV2548 962	All Patients	1st Stroke Occurred During CARE	13/736 (1.8%)	14/753 (1.9%)	13/625 (2.1%)	34/579 (5.9%)	7/144 (4.9%)	4/133 (3.0%)

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy				Prava vs. Placebo			Significance Level	
Public	Marker	Stratum	Phenotype	Odds Ratio (95% CI)				
				0 Rare Alleles	1 Rare Alleles	2 Rare Alleles		
ABCA1	hCV2741051	All Patients	Fatal/Non-fatal Cerebrovascular Disease	0.98 (0.66 to 1.46)	0.43 (0.18 to 1.01)	0.26 (0.06 to 1.15)	p < 0.05	
ABCA1	hCV2741051	All Patients	Any Report of Stroke During CARE	0.92 (0.54 to 1.56)	0.21 (0.06 to 0.75)	0.23 (0.04 to 1.38)		p < 0.05
ABCA1	hCV2741051	All Patients	1st Stroke Occurred During CARE	0.98 (0.57 to 1.70)	0.26 (0.07 to 0.96)	0.23 (0.04 to 1.40)		
NPC1	hCV25472673	All Patients	Fatal CHD/Definite Non-fatal MI	1.00 (0.69 to 1.45)	0.65 (0.33 to 1.30)	0.41 (0.18 to 0.94)	p < 0.05	
NPC1	hCV25472673	All Patients	Hosp. for Cardiovascular Disease	1.02 (0.81 to 1.28)	0.72 (0.47 to 1.11)	0.40 (0.24 to 0.68)		p < 0.0005
NPC1	hCV25472673	All Patients	Total Coronary Heart Disease Events	1.01 (0.79 to 1.29)	0.73 (0.46 to 1.15)	0.44 (0.25 to 0.77)		
NPC1	hCV25472673	All Patients	Total Cardiovascular Disease Events	1.03 (0.81 to 1.29)	0.71 (0.46 to 1.09)	0.39 (0.23 to 0.67)	p < 0.0005	
NPC1	hCV25472673	All Patients	Fatal/Non-fatal Atherosclerotic CV Disease	1.03 (0.81 to 1.31)	0.73 (0.47 to 1.13)	0.41 (0.24 to 0.71)		p < 0.0005
PON1	hCV2548962	All Patients	Total Coronary Heart Disease Events	0.77 (0.62 to 0.95)	0.90 (0.59 to 1.37)	0.44 (0.23 to 0.81)		
PON1	hCV2548962	All Patients	Any Report of Stroke During CARE	0.83 (0.40 to 1.73)	0.32 (0.09 to 1.18)	1.65 (0.30 to 9.06)	p < 0.05	
PON1	hCV2548962	All Patients	1st Stroke Occurred During CARE	0.95 (0.44 to 2.03)	0.34 (0.09 to 1.33)	1.65 (0.29 to 9.33)		p < 0.05

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy					Overall*		Interaction Effect**	
<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>		Chi-Square <u>statistic</u>	p-value	Chi-Square <u>statistic</u>	<u>inter_pvalue</u>
CD6	hCV2553030	All Patients	Hosp. for Cardiovascular Disease		20.6003	0.001	6.0367	0.0489
CD6	hCV2553030	All Patients	Total Cardiovascular Disease Events		21.3941	0.0007	6.0879	0.0476
CD6	hCV2553030	All Patients	History of Angina Pectoris		12.5002	0.0285	11.4198	0.0033
CYP4F2	hCV16179493	All Patients	Catheterization		16.4595	0.0056	9.206	0.01
CYP4F2	hCV16179493	All Patients	Fatal Coronary Heart Disease		14.8471	0.011	11.1566	0.0038
CYP4F2	hCV16179493	All Patients	Total Mortality		13.9492	0.0159	8.7397	0.0127
CYP4F2	hCV16179493	All Patients	Cardiovascular Mortality		12.7875	0.0255	7.6593	0.0217
CYP4F2	hCV16179493	All Patients	Fatal Atherosclerotic Cardiovascular Disease		13.275	0.0209	8.1604	0.0169

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

** Results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy									
Public	Marker	Stratum	Phenotype	0 Rare Alleles		1 Rare Allele		2 Rare Alleles	
				Prava	Placebo	Prava	Placebo	Prava	Placebo
CD6	hCV25530 30	All	Hosp. for Cardiovascular Disease	351/845	415/888	220/551	236/512	36/115	42/76
		Patients		(41.5%)	(46.7%)	(39.9%)	(46.1%)	(31.3%)	(55.3%)
CD6	hCV25530 30	All	Total Cardiovascular Disease Events	365/845	425/888	222/551	245/512	38/115	43/76
		Patients		(43.2%)	(47.9%)	(40.3%)	(47.9%)	(33.0%)	(56.6%)
CD6	hCV25530 30	All	History of Angina Pectoris	180/845	181/888	125/551	91/512	14/115	22/76
		Patients		(21.3%)	(20.4%)	(22.7%)	(17.8%)	(12.2%)	(28.9%)
CYP4F2	hCV16179 493	All	Catheterization	76/724	100/720	55/639	77/629	24/144	9/125
		Patients		(10.5%)	(13.9%)	(8.6%)	(12.2%)	(16.7%)	(7.2%)
CYP4F2	hCV16179 493	All	Fatal Coronary Heart Disease	18/724	39/720	27/639	14/629	3/144	4/125
		Patients		(2.5%)	(5.4%)	(4.2%)	(2.2%)	(2.1%)	(3.2%)
CYP4F2	hCV16179 493	All	Total Mortality	34/724	60/720	42/639	30/629	6/144	4/125
		Patients		(4.7%)	(8.3%)	(6.6%)	(4.8%)	(4.2%)	(3.2%)
CYP4F2	hCV16179 493	All	Cardiovascular Mortality	24/724	43/720	28/639	17/629	3/144	4/125
		Patients		(3.3%)	(6.0%)	(4.4%)	(2.7%)	(2.1%)	(3.2%)
CYP4F2	hCV16179 493	All	Fatal Atherosclerotic Cardiovascular Disease	23/724	43/720	28/639	17/629	3/144	4/125
		Patients		(3.2%)	(6.0%)	(4.4%)	(2.7%)	(2.1%)	(3.2%)

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy					Prava vs. Placebo Odds Ratio (95% CI)			Significance Level
Public	Marker	Stratum	Phenotype	0 Rare Alleles	1 Rare Alleles	2 Rare Alleles		
CD6	hCV25530 30	All Patients	Hosp. for Cardiovascular Disease	0.81 (0.67 to 0.98)	0.78 (0.53 to 1.14)	0.37 (0.19 to 0.72)	p < 0.05	
CD6	hCV25530 30	All Patients	Total Cardiovascular Disease Events	0.83 (0.69 to 1.00)	0.74 (0.50 to 1.08)	0.38 (0.19 to 0.74)	p < 0.05	
CD6	hCV25530 30	All Patients	History of Angina Pectoris	1.06 (0.84 to 1.33)	1.36 (0.84 to 2.18)	0.34 (0.15 to 0.78)	p < 0.005	
CYP4F2	hCV16179 493	All Patients	Catheterization	0.73 (0.53 to 1.00)	0.68 (0.36 to 1.25)	2.58 (1.00 to 6.65)	p < 0.05	
CYP4F2	hCV16179 493	All Patients	Fatal Coronary Heart Disease	0.45 (0.25 to 0.79)	1.94 (0.65 to 5.74)	0.64 (0.11 to 3.69)	p < 0.005	
CYP4F2	hCV16179 493	All Patients	Total Mortality	0.54 (0.35 to 0.84)	1.40 (0.62 to 3.20)	1.32 (0.31 to 5.62)	p < 0.05	
CYP4F2	hCV16179 493	All Patients	Cardiovascular Mortality	0.54 (0.32 to 0.90)	1.65 (0.61 to 4.47)	0.64 (0.12 to 3.55)	p < 0.05	
CYP4F2	hCV16179 493	All Patients	Fatal Atherosclerotic Cardiovascular Disease	0.52 (0.31 to 0.87)	1.65 (0.61 to 4.50)	0.64 (0.12 to 3.56)	p < 0.05	

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy					Overall*		Interaction Effect**	
<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>		Chi-Square Test		Chi-Square	
KLK14	hCV16044337	All Patients	MI (Fatal/Nonfatal)		statistic	p-value	statistic	inter_pvalue
KLK14	hCV16044337	All Patients	Nonfatal MI (Probable/Definite)		27.4658	<.0001	8.606	0.0135
KLK14	hCV16044337	All Patients	Definite Nonfatal MI		25.1331	0.0001	8.1765	0.0168
KLK14	hCV16044337	All Patients	Coronary Artery Bypass Graft		18.9026	0.002	6.7602	0.034
KLK14	hCV16044337	All Patients	Fatal CHD/Definite Nonfatal MI		18.8672	0.002	8.7354	0.0127
KLK14	hCV16044337	All Patients	Nonfatal MI (def & prob)		23.3389	0.0003	9.6221	0.0081
KLK14	hCV16044337	All Patients	Fatal/Nonfatal MI (def & prob)		23.6296	0.0003	7.6653	0.0217
TAP1	hCV549926	All Patients	Fatal CHD/Definite Non-fatal MI		28.3799	<.0001	8.3321	0.0155
					16.2424	0.0062	6.4831	0.0391

* Results of the Overall Score Test (chi-square test) for the logistic regression model in which the qualitative phenotype is a function of SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

** Results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy		Stratum		Phenotype		0 Rare Alleles		1 Rare Allele		2 Rare Alleles	
						n/total (%)		n/total (%)		n/total (%)	
Public	Marker	All	Patients	MI (Fatal/Nonfatal)		Prava	Placebo	Prava	Placebo	Prava	Placebo
KLK14	hCV16044337	All	Patients	MI (Fatal/Nonfatal)		70/693	81/685	67/657	89/629	11/160	35/156
						(10.1%)	(11.8%)	(10.2%)	(14.1%)	(6.9%)	(22.4%)
KLK14	hCV16044337	All	Patients	Nonfatal MI (Probable/Definite)		67/693	79/685	62/657	81/629	10/160	33/156
						(9.7%)	(11.5%)	(9.4%)	(12.9%)	(6.3%)	(21.2%)
KLK14	hCV16044337	All	Patients	Definite Nonfatal MI		49/693	57/685	47/657	58/629	7/160	25/156
						(7.1%)	(8.3%)	(7.2%)	(9.2%)	(4.4%)	(16.0%)
KLK14	hCV16044337	All	Patients	Coronary Artery Bypass Graft		60/693	57/685	41/657	79/629	9/160	15/156
						(8.7%)	(8.3%)	(6.2%)	(12.6%)	(5.6%)	(9.6%)
KLK14	hCV16044337	All	Patients	Fatal CHD/Definite Nonfatal MI		66/693	73/685	65/657	79/629	9/160	32/156
						(9.5%)	(10.7%)	(9.9%)	(12.6%)	(5.6%)	(20.5%)
KLK14	hCV16044337	All	Patients	Nonfatal MI (def & prob)		63/693	75/685	60/657	74/629	10/160	32/156
						(9.1%)	(10.9%)	(9.1%)	(11.8%)	(6.3%)	(20.5%)
KLK14	hCV16044337	All	Patients	Fatal/Nonfatal MI (def & prob)		68/693	80/685	66/657	88/629	11/160	35/156
						(9.8%)	(11.7%)	(10.0%)	(14.0%)	(6.9%)	(22.4%)
TAP1	hCV549926	All	Patients	Fatal CHD/Definite Non-fatal MI		104/1042	117/1013	34/414	58/407	2/49	9/42
						(10.0%)	(11.5%)	(8.2%)	(14.3%)	(4.1%)	(21.4%)

TABLE 6 (continued)

Significant Interactions Between SNP Genotypes and Pravastatin Efficacy				Prava vs. Placebo Odds Ratio (95% CI)			Significance Level
<u>Public</u>	<u>Marker</u>	<u>Stratum</u>	<u>Phenotype</u>	<u>0 Rare Alleles</u>	<u>1 Rare Alleles</u>	<u>2 Rare Alleles</u>	
KLK14	hCV16044337	All Patients	MI (Fatal/Nonfatal)	0.84 (0.60 to 1.18)	0.69 (0.37 to 1.29)	0.26 (0.10 to 0.62)	p < 0.05
KLK14	hCV16044337	All Patients	Nonfatal MI (Probable/Definite)	0.82 (0.58 to 1.16)	0.70 (0.37 to 1.34)	0.25 (0.10 to 0.62)	p < 0.05
KLK14	hCV16044337	All Patients	Definite Nonfatal MI	0.84 (0.56 to 1.25)	0.76 (0.36 to 1.59)	0.24 (0.08 to 0.70)	p < 0.05
KLK14	hCV16044337	All Patients	Coronary Artery Bypass Graft	1.04 (0.71 to 1.53)	0.46 (0.23 to 0.95)	0.56 (0.20 to 1.60)	p < 0.05
KLK14	hCV16044337	All Patients	Fatal CHD/Definite Nonfatal MI	0.88 (0.62 to 1.25)	0.76 (0.40 to 1.47)	0.23 (0.09 to 0.60)	p < 0.05
KLK14	hCV16044337	All Patients	Nonfatal MI (def & prob)	0.81 (0.57 to 1.16)	0.75 (0.39 to 1.46)	0.26 (0.10 to 0.66)	p < 0.05
KLK14	hCV16044337	All Patients	Fatal/Nonfatal MI (def & prob)	0.82 (0.58 to 1.16)	0.69 (0.36 to 1.30)	0.26 (0.10 to 0.63)	p < 0.05
TAP1	hCV549926	All Patients	Fatal CHD/Definite Non-fatal MI	0.85 (0.64 to 1.12)	0.54 (0.29 to 1.01)	0.16 (0.03 to 0.82)	p < 0.05

TABLE 7

RMI_Logistic Regression

Endpoint	Public	Marker	Genotype/mode	Strata	Confounder	P risk est ^a	RR ^b	95% CI ^c
RMI(fatal MI, confirmed non-fatal MI)	A2M	hCV517658	Het(CT)	All	statin, hx_smoke*	0.026	1.34	1.04-1.71
RMI(fatal MI, confirmed non-fatal MI)	IGF1R	hCV8722981	Het(TC)	All	statin	0.0039	2.01	1.26-3.06

Endpoint	Public	Marker	Genotype/mode	Strata	Confounder	case ^d	Case AF(%) ^e
RMI(fatal MI, confirmed non-fatal MI)	A2M	hCV517658	Het(CT)	All	statin, hx_smoke*	130	51.8
RMI(fatal MI, confirmed non-fatal MI)	IGF1R	hCV8722981	Het(TC)	All	statin	17	6.7

Endpoint	Public	Marker	Genotype/mode	Strata	Confounder	control ^f	Control AF(%) ^g
RMI(fatal MI, confirmed non-fatal MI)	A2M	hCV517658	Het(CT)	All	statin, hx_smoke*	1137	44.8
RMI(fatal MI, confirmed non-fatal MI)	IGF1R	hCV8722981	Het(TC)	All	statin	80	3.1

* History of smoking

^a Significance of risk estimated by Wald test

^b Relative risk

^c 95% confidence interval for relative risk

^d Number of patients (with the corresponding genotype or mode) developed recurrent MI during 5 years of follow up

^e The allele frequency of patients (with the corresponding genotype or mode) developed recurrent MI during 6 years of follow up

^f Number of patients (with the corresponding genotype or mode) had MI

^g The allele frequency of patients (with the corresponding genotype or mode) had MI

TABLE 7 (continued)

RMI Replication Between CAREand PreCARE Sample Sets						Analysis 1 of CARE samples					
Endpoint	Pubic	Marker	Genotype/ mode	Strata	P risk est ^a	OR ^b	95%CI ^c	case ^d	Case AF(%) ^e	control ^f	Control AF(%) ^g
RMI(fatal MI, confirmed non-fatal MI)	FABP2	hCV7619 61	Dom(TC+T T)	AGE_T 1	0.01	0.50	0.3-0.9	19	40.8	110	25.2
RMI(fatal MI, confirmed non-fatal MI)	HLA-DPB1	hCV8851 080	Rec(GG)	AGE_T 3	0.037	2.70	1.1-6.7	10	11.1	11	4.4

						Analysis 2 of CARE Samples					
Endpoint	Pubic	Marker	Genotype/ mode	Strata	P risk est ^a	OR ^b	95%CI ^c	case ^d	Case AF(%) ^e	control ^f	Control AF(%) ^g
RMI(fatal MI, confirmed non-fatal MI)	FABP2	hCV7619 61	Dom(TC+T T)	AGE_T 1	0.01	0.5	0.3-0.9	21	26.6	187	41.7
RMI(fatal MI, confirmed non-fatal MI)	HLA-DPB1	hCV8851 080	Rec(GG)	AGE_T 3	0.039	1.9	1.0-3.6	19	10.7	25	5.8

^a Significance of risk estimated by Wald test

^b Odds ratio

^c 95% confidence interval for odds ratio

^d Number of patients (with the corresponding genotype or mode) developed recurrent MI during 5 years of follow up

^e The allele frequency of patients (with the corresponding genotype or mode) developed recurrent MI during 6 years of follow up

^f Number of patients (with the corresponding genotype or mode) had MI

^g The allele frequency of patients (with the corresponding genotype or mode) had MI

AGE_T1 indicate that Age<55

AGE_T13 indicate that age>=64

HYP_Y indicate that patients had history of hypertension

TABLE 7 (continued)

Stroke Replication between CARE and PreCARE Sample Sets

				Analysis 1 of CARE samples				
Endpoint	Public	Marker	Genotype/ mode	Strata	P risk est ^a	OR ^b	95%CI ^c	case ^d AF(%) ^e control ^f Control AF(%) ^g
Stroke	APOA4	hCV11482766	Rec(CC)	all	0.016	3.5	1.4-9.1	6 4.23 16 1.24

				Analysis 2 of CARE Samples				
Endpoint	Public	Marker	Genotype/ mode	Strata	P risk est ^a	OR ^b	95%CI ^c	case ^d AF(%) ^e control ^f Control AF(%) ^g
Stroke	APOA4	hCV11482766	Rec(CC)	all	0.05	3.3	1.1-9.8	4 5 20 1.59

^a Significance of risk estimated by Wald test
^b Odds ratio
^c 95% confidence interval for odds ratio
^d Number of patients (with the corresponding genotype or mode) developed recurrent MI during 5 years of follow up
^e The allele frequency of patients (with the corresponding genotype or mode) developed recurrent MI during 6 years of follow up
^f Number of patients (with the corresponding genotype or mode) had MI
^g The allele frequency of patients (with the corresponding genotype or mode) had MI

TABLE 8

Risk of cardiovascular disease events associated with Pravastatin by genotypes

Gene symbol	hCV	Case Y PRIMER ALLELE Nucleotide Freq*	Control Y PRIMER ALLELE Nucleotide Freq**	Stratum	Group	ptrend ^a	N ^{aff} ^b	N ^{unaf} ^c	RR ^d	RR 95%CI ^e	P ^{risk est} ^f	P ^{int} ^g	Covars ^h
ITGA9	hCV25644901	0.08	0.04	Placebo	dom(GA+GG)vs. ref(AA)		24	105	1.92	(1.29-2.86)	0.0013	0.0093	none
					ref (AA)		121	1129	1.00				
				Statin	dom(GA+GG)vs. ref(AA)		6	123	0.58	(0.26-1.31)	0.1904		
					ref (AA)		103	1192	1.00				
KLK14	hCV16044337	0.62	0.69	Placebo	hom(AA) vs. ref(GG)	0.0096	23	117	1.87	(1.19-2.92)	0.0063	0.0188	none
					het(GA) vs. ref(GG)		64	521	1.24	(0.89-1.75)	0.2073		
					ref(GG)		57	591	1.00				
				Statin	hom(AA) vs. ref(GG)	0.3371	6	128	0.56	(0.25-1.28)	0.1678		
					het(GA) vs. ref(GG)		50	570	1.01	(0.69-1.46)	0.9629		
					ref(GG)		53	610	1.00				

a P value for trend
b Number of patients developed recurrent MI during 5 years of follow up
c Number of patients had MI
d Relative risk for RMI
e 95% confidence interval for relative risk
f Significance of risk estimated by Wald test
g P vale for interaction
h Confounders
* Y primer nucleotide frequency for cases*
* Y primer nucleotide frequency for controls**

TABLE 8 (continued)

Risk of cardiovascular disease events associated with Pravastatin by genotypes

Gene symbol	hCV	Case Y PRIMER ALLELE Nucleoti de Freq*	Control Y PRIMER ALLELE Nucleotide Freq**	Stratum	Group	ptrend ^a	N aff ^b	N unaf ^c	RR ^d	RR 95%CI ^e	P _{risk est} ^f	P _{int} ^g	Covars ^h
SLC18A 1	hCV2715 953	0.88	0.92	Placebo	hom(CC) vs. ref(GG)		4	17	1.9 2	(0.78- 4.71)	0.1560	0.02 74	none
					het(GC) vs. ref (GG)	0.0714	26	175	1.3 0	(0.87- 1.94)	0.1950		
					ref(GG)		115	1042	1.0 0				
					hom(CC) vs. ref(GG)		0	12			0.9995		
					het(GC) vs. ref (GG)	0.1356	14	229	0.7 2	(0.42- 1.23)	0.2295		
FCAR	hCV7841 642	0.90	0.93	Placebo	ref(GG)		93	1063	1.0 0			0.04 63	none
					hom (AA)vs. ref(GG)		1	11	0.8 5	(0.13- 5.59)	0.8656		
					het(GA) vs. ref(GG)	0.0687	28	159	1.5 3	(1.05- 2.24)	0.0302		
					ref(GG)		116	1067	1.0 0				
					hom (AA)vs. ref(GG)		1	8	1.3 8	(0.22- 8.83)	0.7350		
				Statin	het(GA) vs. ref(GG)	0.2107	9	178	0.6 0	(0.31- 1.16)	0.1283		
					ref(GG)		99	1129	1.0 0				

a P value for trend
b Number of patients developed recurrent MI during 5 years of follow up
c Number of patients had MI
d Relative risk for RMI
e 95% confidence interval for relative risk
f Significance of risk estimated by Wald test
g P vale for interaction
h Confounders
* Y primer nucleotide frequency for cases*
* Y primer nucleotide frequency for controls**

TABLE 8 (continued)

Risk of cardiovascular disease events associated with Pravastatin by genotypes															
Gene symbol	hCV	Case Y		Control Y	Stratum	Group	ptrend ^a	N aff ^b	N unaf ^c	RR ^d	RR 95%CI ^e	P ^f _{risk est}	P ^g _{int}	Covars ^h	
		PRIMER ALLELE Nucleotide Freq [*]	PRIMER ALLELE Nucleotide Freq ^{**}												
ABCA1	hCV27 41051	0.21	0.28	Placebo	hom(TT) vs. ref(CC)	0.0149	6	84	0.54	(0.24-1.16)	0.1188	0.0369	none		
					het(TC) vs. ref(CC)									0.0338	
					ref(CC)										
		Statin	hom(TT) vs. ref(CC)	0.5954	9	99	1.14	(0.57-2.19)	0.6981						
			het(TC) vs. ref(CC)							0.6440					
			ref(CC)												
HSPG2	hCV16 03656	0.10	0.08	Placebo	hom(TT) vs. ref(CC)	0.1704	2	6	2.46	(0.60-6.24)	0.1954	0.0334	hx_smoke		
					het (TC)vs. ref(CC)									0.3189	
					ref(CC)										
		Statin	hom(TT) vs. ref(CC)	0.1033	0	11	N/A	0.9771							
			het (TC)vs. ref(CC)						0.1607						
			ref(CC)							1.00					

a P value for trend
b Number of patients developed recurrent MI during 5 years of follow up
c Number of patients had MI
d Relative risk for RMI
e 95% confidence interval for relative risk
f Significance of risk estimated by Wald test
g P vale for interaction
h Confounders
* Y primer nucleotide frequency for cases*
* Y primer nucleotide frequency for controls**

TABLE 8 (continued)

Risk of cardiovascular disease events associated with Pravastatin by genotypes

Gene symbol	hCV	Case Y PRIMER ALLELE Nucleotide Freq*	Control Y PRIMER ALLELE Nucleotide Freq**	Stratum	Group	ptrend ^a	N ^{aff} ^b	N ^{unaf} ^c	RR ^d	RR 95%CI ^e	P ^f _{risk est}	P ^g _{int}	Covars ^h		
NPC1	hCV254 72673	0.53	0.62	Placebo	hom(CC) vs. ref(TT)	0.0037	33	173	1.9 6	(1.28- 2.91)	0.0023	0.009 3	none		
					het(TC) vs. ref(TT)										
					ref(TT)										
				Statin	hom(CC) vs. ref(TT)	0.4107	18	215	0.8 7	(0.51- 1.45)	0.6102				
					het(TC) vs. ref(TT)										
					ref(TT)										
				Maj Hom(TT)	Statin		48	495	1.0 8	(0.72- 1.60)	0.6973				
					Placebo										
					Statin										
				Het(TC)	Placebo		70	602	1.0 0		0.013				
					Statin										
					Placebo										
				Min Hom(CC)	Statin		18	215	0.4 8	(0.27- 0.83)	0.008				
					Placebo										
							33	173	1.0 0						

a P value for trend

b Number of patients developed recurrent MI during 5 years of follow up

c Number of patients had MI

d Relative risk for RMI

e 95% confidence interval for relative risk

f Significance of risk estimated by Wald test

g P vale for interaction

h Confounders

* Y primer nucleotide frequency for cases*

* Y primer nucleotide frequency for controls**

TABLE 10

Risk of cardiovascular disease events associated with FCAR genotype in untreated arms, CARE and WOSCOPS

Endpoint	Gene	Marker	FCARgenotype	N		Unadjusted		
RMI	FCAR	hCV7841642		RMI ^a	MI ^b	OR	95% CI	P ‡
	CARE		AA	1	11	0.84	(0.11-6.54)	0.87
			AG	28	159	1.62	(1.04-2.53)	0.034
			AA+AG	29	170	1.57	(1.01-2.43)	0.044
			GG	116	1067	1	(ref)	

Endpoint	Gene	Marker	FCARgenotype	Adjusted for Age, Smoking status, Gender *		Adjusted for Age, Smoking status, Gender, hypertension, BMI, diabetes, baseline LDL and HDL ^{*, †}	
RMI	FCAR	hCV7841642		OR	95% CI	OR	95% CI
	CARE		AA	0.74	(0.09-5.89)	0.86	(0.11-6.71)
			AG	1.58	(1.01-2.48)	1.58	(1.02-2.46)
			AA+AG	1.52	(0.98-2.37)	1.58	(1.02-2.46)
			GG	1	(ref)	1	(ref)

CARE indicates Cholesterol and Recurrent Events trial; WOSCOPS, West of Scotland Coronary Prevention Study; RMI; BMI, body-mass index (kg/m2); LDL, low-density lipoprotein; HDL, high-density lipoprotein; OR, odds ratio; CI, confidence interval

* Adjusted for age (continuous for CARE, 5-year age groups for WOSCOPS), smoking (never, former, current) and gender (all male in WOSCOPS)

† Further adjusted for history of hypertension, BMI (continuous), history of diabetes, baseline LDL level (continuous), and baseline HDL level (continuous)

‡ Wald test

§ Conditional logistic regression used to account for matching of WOSCOPS cases and controls (all male) on smoking and age

|| Major homozygote (AspAsp) was used as reference

^a Patients developed recurrent MI during 5 years follow up

^b Patients had MI before entry but didn't developed current MI during 6 years follow up

^c Patients had MI

^d Patients had no MI

TABLE 10 (continued)

Risk of cardiovascular disease events associated with FCAR genotype in untreated arms, CARE and WOSCOPS						
Endpoint	Gene	Marker	FCARgenotype		N	
			RMI ^a	MI ^b	OR	Unadjusted 95% CI
MI	WOSCOPS §		Cs ^c	Cn ^d		P ‡
	AA		1	3		
	AG		54	70		
	AA+AG		55	73		
	GG		233	456		

Endpoint	Gene	Marker	FCARgenotype		Adjusted for Age, Smoking status, Gender *		Adjusted for Age, Smoking status, Gender, hypertension, BMI, diabetes, baseline LDL and HDL [*] , †	
			OR	95% CI	P ‡	OR	95% CI	P ‡
MI	WOSCOPS §		0.67	(0.07-6.52)	0.73	0.68	(0.07-6.75)	0.75
	AA		1.5	(1.01-2.22)	0.043	1.49	(1.00-2.22)	0.05
	AG		1.47	(1.00-2.16)	0.053	1.46	(0.98-2.16)	0.061
	AA+AG		1	(ref)		1	(ref)	

CARE indicates Cholesterol and Recurrent Events trial; WOSCOPS, West of Scotland Coronary Prevention Study; RMI: BMI, body-mass index (kg/m2); LDL, low-density lipoprotein; HDL, high-density lipoprotein; OR, odds ratio; CI, confidence interval
* Adjusted for age (continuous for CARE, 5-year age groups for WOSCOPS), smoking (never, former, current) and gender (all male in WOSCOPS)
† Further adjusted for history of hypertension, BMI (continuous), history of diabetes, baseline LDL level (continuous), and baseline HDL level (continuous)
‡ Wald test
§ Conditional logistic regression used to account for matching of WOSCOPS cases and controls (all male) on smoking and age
|| Major homozygote (AspAsp) was used as reference

^a Patients developed recurrent MI during 5 years follow up
^b Patients had MI before entry but didn't developed current MI during 6 years follow up
^c Patients had MI
^d Patients had no MI

TABLE 11

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Overall* Chi-Square Test</u>		<u>Interaction Effect** Chi-Square Test</u>	
							<u>Statistic</u>	<u>p-value</u>	<u>Statistic</u>	<u>p-value</u>
A2M	hCV517658	CARE	Case/Control	F&NF MI	All Possible	WM	15.24	0.0094	6.84	0.0327
A2M	hCV517658	CARE	Case/Control	F&NF MI	Cleaner	WM	17.54	0.0036	6.16	0.046
ADAMTS1	hCV529706	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	12.79	0.0254	6.44	0.0399
ADAMTS1	hCV529710	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	13.42	0.0197	6.54	0.038
ASAH1	hCV2442143	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	15.62	0.008	6.23	0.0445
CD6	hCV2553030	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	11.51	0.0422	6.86	0.0323
CD6	hCV2553030	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	15.89	0.0072	7.8	0.0202
CD6	hCV2553030	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	12.22	0.0318	12.46	0.002
CD6	hCV2553030	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	16.02	0.0068	13.78	0.001

* For the CARE prospective study: results of the Overall Score Test (chi-square test) for the logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

For case/control studies: results of the Overall Score Test (chi-square test) for the conditional logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group and cases and controls have been matched on age and smoking status.

** For the CARE prospective study: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

For the case/control studies: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the conditional logistic regression model).

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

Public	Marker	Study	Study Design	Case Definition	Control Group Definition**	Stratum	0 Rare Alleles n/total (%)		1 Rare Allele n/total (%)		2 Rare Alleles n/total (%)	
							Pravastatin Patients	Placebo Patients	Pravastatin Patients	Placebo Patients	Pravastatin Patients	Placebo Patients
A2M	hCV51 7658	CARE	Case/Control	F&NF MI	All Possible	WM	42/525 (8.0%)	64/479 (13.4%)	72/540 (13.3%)	72/544 (13.2%)	11/144 (7.6%)	20/138 (14.5%)
A2M	hCV51 7658	CARE	Case/Control	F&NF MI	Cleaner	WM	42/355 (11.8%)	64/318 (20.1%)	72/380 (18.9%)	72/351 (20.5%)	11/101 (10.9%)	20/86 (23.3%)
ADAMT S1	hCV52 9706	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	65/470 (13.8%)	67/434 (15.4%)	42/305 (13.8%)	51/258 (19.8%)	4/50 (8.0%)	12/42 (28.6%)
ADAMT S1	hCV52 9710	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	65/471 (13.8%)	67/435 (15.4%)	43/307 (14.0%)	52/258 (20.2%)	4/50 (8.0%)	12/42 (28.6%)
ASAH1	hCV24 42143	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	21/201 (10.4%)	43/196 (21.9%)	62/414 (15.0%)	67/364 (18.4%)	29/220 (13.2%)	21/181 (11.6%)
CD6	hCV25 53030	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	68/668 (10.2%)	73/697 (10.5%)	43/470 (9.1%)	48/432 (11.1%)	1/92 (1.1%)	10/64 (15.6%)
CD6	hCV25 53030	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	68/449 (15.1%)	73/434 (16.8%)	43/323 (13.3%)	48/272 (17.6%)	1/63 (1.6%)	10/37 (27.0%)
CD6	hCV25 53030	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	68/656 (10.4%)	73/683 (10.7%)	43/465 (9.2%)	48/426 (11.3%)	1/91 (1.1%)	10/62 (16.1%)
CD6	hCV25 53030	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	68/442 (15.4%)	73/427 (17.1%)	43/320 (13.4%)	48/270 (17.8%)	1/62 (1.6%)	10/37 (27.0%)

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

Pravastatin vs. Placebo Odds Ratio (95% CI)							Significance Level			
Public	Marker	Study	Study Design	Case Definition	Control Group Definition ***	Stratum				
A2M	hCV517 658	CARE	Case/Control	F&NF MI	All Possible	WM	Patients with 0 Rare Alleles	Patients with 1 Rare Allele	Patients with 2 Rare Alleles	P<=0.05
A2M	hCV517 658	CARE	Case/Control	F&NF MI	Cleaner	WM	0.55 (0.36 to 0.83)	1.04 (0.73 to 1.48)	0.47 (0.21 to 1.02)	P<=0.05
ADAMT S1	hCV529 706	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	0.53 (0.34 to 0.81)	0.93 (0.65 to 1.35)	0.38 (0.17 to 0.86)	P<=0.05
ADAMT S1	hCV529 710	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	0.91 (0.62 to 1.32)	0.64 (0.40 to 1.01)	0.20 (0.06 to 0.68)	P<=0.05
ASAH1	hCV244 2143	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.91 (0.63 to 1.33)	0.63 (0.40 to 0.99)	0.20 (0.06 to 0.69)	P<=0.05
CD6	hCV255 3030	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.42 (0.24 to 0.73)	0.78 (0.29 to 2.13)	1.16 (0.38 to 3.50)	P<=0.05
CD6	hCV255 3030	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	0.97 (0.68 to 1.37)	0.81 (0.38 to 1.69)	0.06 (0.01 to 0.52)	P<=0.05
CD6	hCV255 3030	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.88 (0.62 to 1.27)	0.72 (0.33 to 1.54)	0.04 (0.00 to 0.39)	P<=0.05
CD6	hCV255 3030	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	0.97 (0.68 to 1.38)	0.80 (0.51 to 1.23)	0.06 (0.01 to 0.44)	P<=0.05
CD6	hCV255 3030	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	0.92 (0.64 to 1.32)	0.68 (0.43 to 1.08)	0.04 (0.01 to 0.36)	P<=0.05

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Overall* Chi-Square Test</u>		<u>Interaction Effect** Chi-Square Test</u>	
							<u>Statistic</u>	<u>p-value</u>	<u>Statistic</u>	<u>p-value</u>
FCAR	hCV7841642	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	13.17	0.0218	6.22	0.0445
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	17.43	0.0037	8.78	0.0124
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	18.02	0.0029	7.27	0.0264
KLK14	hCV16044337	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	17.18	0.0042	9.22	0.01
KLK14	hCV16044337	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	18.67	0.0022	7.63	0.022
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	11.68	0.0394	6.39	0.0409
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	21.8	0.0006	11.02	0.004
NPC1	hCV25472673	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	19.06	0.0019	9.81	0.0074

* For the CARE prospective study: results of the Overall Score Test (chi-square test) for the logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

For case/control studies: results of the Overall Score Test (chi-square test) for the conditional logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group and cases and controls have been matched on age and smoking status.

** For the CARE prospective study: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

For the case/control studies: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the conditional logistic regression model).

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition**</u>	<u>Stratum</u>	<u>0 Rare Alleles n/total (%)</u>		<u>1 Rare Allele n/total (%)</u>		<u>2 Rare Alleles n/total (%)</u>	
							<u>Pravastatin Patients</u>	<u>Placebo Patients</u>	<u>Pravastatin Patients</u>	<u>Placebo Patients</u>	<u>Pravastatin Patients</u>	<u>Placebo Patients</u>
FCAR	hCV784 1642	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	103/734 (14.0%)	104/637 (16.3%)	8/96 (8.3%)	26/103 (25.2%)	1/8 (12.5%)	1/4 (25.0%)
KLK14	hCV160 44337	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	52/560 (9.3%)	50/560 (8.9%)	54/556 (9.7%)	57/511 (11.2%)	6/114 (5.3%)	23/115 (20.0%)
KLK14	hCV160 44337	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	52/366 (14.2%)	50/342 (14.6%)	54/401 (13.5%)	57/323 (17.6%)	6/67 (9.0%)	23/76 (30.3%)
KLK14	hCV160 44337	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	52/550 (9.5%)	50/549 (9.1%)	54/549 (9.8%)	57/502 (11.4%)	6/113 (5.3%)	23/113 (20.4%)
KLK14	hCV160 44337	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	52/359 (14.5%)	50/339 (14.7%)	54/397 (13.6%)	57/318 (17.9%)	6/67 (9.0%)	23/75 (30.7%)
NPC1	hCV254 72673	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	48/462 (10.4%)	37/436 (8.5%)	46/552 (8.3%)	65/575 (11.3%)	18/208 (8.7%)	28/173 (16.2%)
NPC1	hCV254 72673	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	48/302 (15.9%)	37/282 (13.1%)	46/381 (12.1%)	65/360 (18.1%)	18/146 (12.3%)	28/95 (29.5%)
NPC1	hCV254 72673	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	48/299 (16.1%)	37/279 (13.3%)	46/376 (12.2%)	65/356 (18.3%)	18/143 (12.6%)	28/93 (30.1%)

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition</u> ***	<u>Stratum</u>	<u>Pravastatin vs. Placebo Odds Ratio (95% CI)</u>			<u>Significance Level</u>
							<u>Patients with 0 Rare Alleles</u>	<u>Patients with 1 Rare Allele</u>	<u>Patients with 2 Rare Alleles</u>	
FCAR	hCV7841642	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.84 (0.62 to 1.12)	0.27 (0.10 to 0.73)	0.43 (0.02 to 9.77)	P<=0.05
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	1.04 (0.69 to 1.57)	0.86 (0.38 to 1.92)	0.22 (0.07 to 0.72)	P<=0.05
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.97 (0.64 to 1.47)	0.73 (0.32 to 1.67)	0.23 (0.07 to 0.76)	P<=0.05
KLK14	hCV16044337	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	1.02 (0.68 to 1.54)	0.85 (0.57 to 1.27)	0.23 (0.09 to 0.60)	P<=0.05
KLK14	hCV16044337	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	0.98 (0.64 to 1.50)	0.74 (0.49 to 1.12)	0.23 (0.09 to 0.62)	P<=0.05
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	1.25 (0.80 to 1.96)	0.71 (0.29 to 1.74)	0.49 (0.18 to 1.35)	P<=0.05
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	1.25 (0.79 to 1.99)	0.62 (0.25 to 1.55)	0.34 (0.12 to 0.96)	P<=0.005
NPC1	hCV25472673	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	1.21 (0.76 to 1.94)	0.65 (0.43 to 0.98)	0.34 (0.17 to 0.67)	P<=0.05

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Overall* Chi-Square Test</u>		<u>Interaction Effect** Chi-Square Test</u>	
							<u>Statistic</u>	<u>p-value</u>	<u>Statistic</u>	<u>p-value</u>
ABCA1	hCV2741051	CARE	Prospective	F&NF MI	All Possible	WM	13.87	0.0165	7.96	0.0187
ABCA1	hCV2741051	CARE	Prospective	F&NF MI	Cleaner	WM	16.34	0.0059	6.38	0.0411
ABCA1	hCV2741051	CARE	Case/Control	F&NF MI	All Possible	WM	13.37	0.0202	7.64	0.0219
ABCA1	hCV2741051	CARE	Case/Control	F&NF MI	Cleaner	WM	15.31	0.0091	6.25	0.044
CD6	hCV2553030	CARE	Prospective	F&NF MI	All Possible	WM	12.37	0.0301	6.35	0.0418
CD6	hCV2553030	CARE	Prospective	F&NF MI	Cleaner	WM	17.24	0.0041	7.6	0.0224
CD6	hCV2553030	CARE	Case/Control	F&NF MI	All Possible	WM	12.41	0.0295	8.44	0.0147
CD6	hCV2553030	CARE	Case/Control	F&NF MI	Cleaner	WM	17.04	0.0044	10.19	0.0061
FCAR	hCV7841642	CARE	Case/Control	F&NF MI	All Possible	WM	11.78	0.038	6.15	0.0461

* For the CARE prospective study: results of the Overall Score Test (chi-square test) for the logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

For case/control studies: results of the Overall Score Test (chi-square test) for the conditional logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group and cases and controls have been matched on age and smoking status.

** For the CARE prospective study: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

For the case/control studies: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the conditional logistic regression model).

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

Public	Marker	Study	Study Design	Case Definition	Control Group Definition ***	Stratum	0 Rare Alleles n/total (%)		1 Rare Allele n/total (%)		2 Rare Alleles n/total (%)	
							Pravastatin Patients	Placebo Patients	Pravastatin Patients	Placebo Patients	Pravastatin Patients	Placebo Patients
ABCA1	hCV27 41051	CARE	Prospective	F&NF MI	All Possible	WM	56/625 (9.0%)	96/628 (15.3%)	59/517 (11.4%)	56/487 (11.5%)	12/94 (12.8%)	6/80 (7.5%)
ABCA1	hCV27 41051	CARE	Prospective	F&NF MI	Cleaner	WM	56/414 (13.5%)	96/414 (23.2%)	59/375 (15.7%)	56/304 (18.4%)	12/65 (18.5%)	6/54 (11.1%)
ABCA1	hCV27 41051	CARE	Case/Control	F&NF MI	All Possible	WM	56/612 (9.2%)	96/616 (15.6%)	59/509 (11.6%)	56/478 (11.7%)	12/93 (12.9%)	6/77 (7.8%)
ABCA1	hCV27 41051	CARE	Case/Control	F&NF MI	Cleaner	WM	56/405 (13.8%)	96/410 (23.4%)	59/371 (15.9%)	56/298 (18.8%)	12/64 (18.8%)	6/53 (11.3%)
CD6	hCV25 53030	CARE	Prospective	F&NF MI	All Possible	WM	77/668 (11.5%)	89/697 (12.8%)	48/470 (10.2%)	59/432 (13.7%)	2/92 (2.2%)	10/64 (15.6%)
CD6	hCV25 53030	CARE	Prospective	F&NF MI	Cleaner	WM	77/458 (16.8%)	89/450 (19.8%)	48/328 (14.6%)	59/283 (20.8%)	2/64 (3.1%)	10/37 (27.0%)
CD6	hCV25 53030	CARE	Case/Control	F&NF MI	All Possible	WM	77/654 (11.8%)	89/682 (13.0%)	48/463 (10.4%)	59/425 (13.9%)	2/91 (2.2%)	10/62 (16.1%)
CD6	hCV25 53030	CARE	Case/Control	F&NF MI	Cleaner	WM	77/449 (17.1%)	89/442 (20.1%)	48/324 (14.8%)	59/280 (21.1%)	2/63 (3.2%)	10/37 (27.0%)
FCAR	hCV78 41642	CARE	Case/Control	F&NF MI	All Possible	WM	115/1045 (11.0%)	127/997 (12.7%)	11/160 (6.9%)	30/162 (18.5%)	1/8 (12.5%)	1/12 (8.3%)

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

							Pravastatin vs. Placebo Odds Ratio (95% CI)			
<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Patients with 0 Rare Alleles</u>	<u>Patients with 1 Rare Allele</u>	<u>Patients with 2 Rare Alleles</u>	<u>Significance Level</u>
ABCA1	hCV274 1051	CARE	Prospective	F&NF MI	All Possible	WM	0.55 (0.38 to 0.77)	0.99 (0.49 to 2.00)	1.80 (0.55 to 5.89)	P<=0.05
ABCA1	hCV274 1051	CARE	Prospective	F&NF MI	Cleaner	WM	0.52 (0.36 to 0.74)	0.83 (0.40 to 1.71)	1.81 (0.54 to 6.11)	P<=0.05
ABCA1	hCV274 1051	CARE	Case/Control	F&NF MI	All Possible	WM	0.55 (0.38 to 0.78)	0.98 (0.66 to 1.46)	1.71 (0.61 to 4.83)	P<=0.05
ABCA1	hCV274 1051	CARE	Case/Control	F&NF MI	Cleaner	WM	0.52 (0.36 to 0.76)	0.82 (0.54 to 1.24)	1.81 (0.62 to 5.28)	P<=0.05
CD6	hCV255 3030	CARE	Prospective	F&NF MI	All Possible	WM	0.89 (0.64 to 1.23)	0.72 (0.36 to 1.43)	0.12 (0.02 to 0.63)	P<=0.05
CD6	hCV255 3030	CARE	Prospective	F&NF MI	Cleaner	WM	0.82 (0.59 to 1.15)	0.65 (0.32 to 1.33)	0.09 (0.02 to 0.47)	P<=0.05
CD6	hCV255 3030	CARE	Case/Control	F&NF MI	All Possible	WM	0.89 (0.64 to 1.23)	0.71 (0.47 to 1.07)	0.12 (0.02 to 0.55)	P<=0.05
CD6	hCV255 3030	CARE	Case/Control	F&NF MI	Cleaner	WM	0.84 (0.59 to 1.18)	0.63 (0.41 to 0.97)	0.09 (0.02 to 0.42)	P<=0.05
FCAR	hCV784 1642	CARE	Case/Control	F&NF MI	All Possible	WM	0.84 (0.64 to 1.10)	0.33 (0.16 to 0.69)	1.78 (0.09 to 33.90)	P<=0.05

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Overall* Chi-Square Test</u>		<u>Interaction Effect** Chi-Square Test</u>	
							<u>Statistic</u>	<u>p-value</u>	<u>Statistic</u>	<u>p-value</u>
KLK14	hCV160444337	CARE	Prospective	F&NF MI	All Possible	WM	20.37	0.0011	7.7	0.0212
KLK14	hCV160444337	CARE	Prospective	F&NF MI	Cleaner	WM	21.38	0.0007	6.24	0.0442
KLK14	hCV160444337	CARE	Case/Control	F&NF MI	All Possible	WM	20.43	0.001	7.96	0.0186
KLK14	hCV160444337	CARE	Case/Control	F&NF MI	Cleaner	WM	22.24	0.0005	6.75	0.0343
NPC1	hCV25472673	CARE	Prospective	F&NF MI	Cleaner	WM	24.23	0.0002	10.08	0.0065
NPC1	hCV25472673	CARE	Case/Control	F&NF MI	Cleaner	WM	21.33	0.0007	8.55	0.0139
TAP1	hCV549926	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	13.9	0.0163	7.13	0.0283
TAP1	hCV549926	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	14.3	0.0138	6.22	0.0447
TAP1	hCV549926	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	13.04	0.023	9.44	0.0089
TAP1	hCV549926	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	12.88	0.0245	8.15	0.017

* For the CARE prospective study: results of the Overall Score Test (chi-square test) for the logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

For case/control studies: results of the Overall Score Test (chi-square test) for the conditional logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group and cases and controls have been matched on age and smoking status.

** For the CARE prospective study: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

For the case/control studies: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the conditional logistic regression model).

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition**</u>	<u>Stratum</u>	<u>0 Rare Alleles n/total (%)</u>		<u>1 Rare Allele n/total (%)</u>		<u>2 Rare Alleles n/total (%)</u>	
							<u>Pravastatin Patients</u>	<u>Placebo Patients</u>	<u>Pravastatin Patients</u>	<u>Placebo Patients</u>	<u>Pravastatin Patients</u>	<u>Placebo Patients</u>
KLK14	hCV160 44337	CARE	Prospective	F&NF MI	All Possible	WM	60/560 (10.7%)	61/560 (10.9%)	57/556 (10.3%)	68/511 (13.3%)	9/114 (7.9%)	27/115 (23.5%)
KLK14	hCV160 44337	CARE	Prospective	F&NF MI	Cleaner	WM	60/374 (16.0%)	61/353 (17.3%)	57/404 (14.1%)	68/334 (20.4%)	9/70 (12.9%)	27/80 (33.8%)
KLK14	hCV160 44337	CARE	Case/Control	F&NF MI	All Possible	WM	60/548 (10.9%)	61/548 (11.1%)	57/547 (10.4%)	68/501 (13.6%)	9/113 (8.0%)	27/113 (23.9%)
KLK14	hCV160 44337	CARE	Case/Control	F&NF MI	Cleaner	WM	60/365 (16.4%)	61/349 (17.5%)	57/399 (14.3%)	68/328 (20.7%)	9/70 (12.9%)	27/79 (34.2%)
NPC1	hCV254 72673	CARE	Prospective	F&NF MI	Cleaner	WM	53/307 (17.3%)	45/290 (15.5%)	51/386 (13.2%)	81/376 (21.5%)	22/150 (14.7%)	31/98 (31.6%)
NPC1	hCV254 72673	CARE	Case/Control	F&NF MI	Cleaner	WM	53/304 (17.4%)	45/287 (15.7%)	51/378 (13.5%)	81/370 (21.9%)	22/147 (15.0%)	31/96 (32.3%)
TAP1	hCV549 926	CARE	Prospective	F MI/SD/N F MI	All Possible	WM	83/848 (9.8%)	81/829 (9.8%)	28/349 (8.0%)	42/329 (12.8%)	1/36 (2.8%)	8/33 (24.2%)
TAP1	hCV549 926	CARE	Prospective	F MI/SD/N F MI	Cleaner	WM	83/576 (14.4%)	81/505 (16.0%)	28/237 (11.8%)	42/214 (19.6%)	1/25 (4.0%)	8/24 (33.3%)
TAP1	hCV549 926	CARE	Case/Control	F MI/SD/N F MI	All Possible	WM	83/832 (10.0%)	81/817 (9.9%)	28/347 (8.1%)	42/319 (13.2%)	1/36 (2.8%)	8/33 (24.2%)
TAP1	hCV549 926	CARE	Case/Control	F MI/SD/N F MI	Cleaner	WM	83/566 (14.7%)	81/501 (16.2%)	28/236 (11.9%)	42/209 (20.1%)	1/25 (4.0%)	8/24 (33.3%)

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 11 (continued)

Statistically Significant Interactions Between SNP Genotypes and Pravastatin Efficacy for Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

Public	Marker	Study	Study Design	Case Definition	Control Group Definition ***	Stratum	Pravastatin vs. Placebo Odds Ratio (95% CI)			Significance Level
							Patients with 0 Rare Alleles	Patients with 1 Rare Allele	Patients with 2 Rare Alleles	
KLK14	hCV1604 4337	CARE	Prospective	F&NF MI	All Possible	WM	0.98 (0.67 to 1.43)	0.74 (0.35 to 1.58)	0.28 (0.10 to 0.79)	P<=0.05
KLK14	hCV1604 4337	CARE	Prospective	F&NF MI	Cleaner	WM	0.91 (0.62 to 1.35)	0.64 (0.29 to 1.40)	0.29 (0.10 to 0.85)	P<=0.05
KLK14	hCV1604 4337	CARE	Case/Control	F&NF MI	All Possible	WM	0.96 (0.66 to 1.41)	0.75 (0.51 to 1.09)	0.28 (0.12 to 0.63)	P<=0.05
KLK14	hCV1604 4337	CARE	Case/Control	F&NF MI	Cleaner	WM	0.92 (0.62 to 1.37)	0.65 (0.44 to 0.97)	0.28 (0.12 to 0.65)	P<=0.05
NPC1	hCV2547 2673	CARE	Prospective	F&NF MI	Cleaner	WM	1.14 (0.74 to 1.75)	0.55 (0.24 to 1.30)	0.37 (0.14 to 0.99)	P<=0.05
NPC1	hCV2547 2673	CARE	Case/Control	F&NF MI	Cleaner	WM	1.09 (0.70 to 1.69)	0.58 (0.39 to 0.86)	0.37 (0.20 to 0.70)	P<=0.05
TAP1	hCV5499 26	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	1.00 (0.73 to 1.38)	0.60 (0.28 to 1.27)	0.09 (0.01 to 0.82)	P<=0.05
TAP1	hCV5499 26	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.88 (0.63 to 1.23)	0.55 (0.25 to 1.19)	0.08 (0.01 to 0.79)	P<=0.05
TAP1	hCV5499 26	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	0.98 (0.71 to 1.36)	0.61 (0.37 to 1.01)	0.08 (0.01 to 0.70)	P<=0.05
TAP1	hCV5499 26	CARE	Case/Control	F MI/SD/NF MI	Cleaner	WM	0.89 (0.63 to 1.25)	0.56 (0.33 to 0.94)	0.08 (0.01 to 0.72)	P<=0.05

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = White Males

For study, "W" = WOSCOPS

TABLE 12

Statistically Significant Associations Between SNP Genotypes and Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

							Overall* Chi-Square Test		SNP Effect	
<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Statistic</u>	<u>p-value</u>	<u>Statistic</u>	<u>p-value</u>
ADAMTS1	hCV529706	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	6.5	0.0388	12.25	0.0156
ADAMTS1	hCV529710	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	5.99	0.0499	5.85	0.0536
ASAH1	hCV2442143	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	7.17	0.0278	7	0.0302
ITGA9	hCV25644901	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	11.24	0.0008	10.71	0.0011
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	12.02	0.0025	11.5	0.0032
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	7.63	0.022	7.47	0.0239
CD6	hCV2553030	W	Case/Control	F&NF MI	All Possible	WM	7.21	0.0272	9.82	0.0435
HSPG2	hCV1603656	W	Case/Control	F&NF MI	All Possible	WM	10.29	0.0058	9.7	0.0458
TAP1	hCV549926	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	8.24	0.0163	7.77	0.0206
TAP1	hCV549926	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	7.02	0.0299	11.77	0.0191

* For the CARE prospective study design: results of the Overall Score Test (chi-square test) for the logistic regression model in which the phenotype (case definition) is a function of SNP genotype (based on placebo patients only).
For the case/control study designs: results of the Overall Score Test (chi-square test) for the conditional logistic regression model in which the phenotype (case definition) is a function of SNP genotype (based on placebo patients only) and cases and controls were matched on age and current smoking status.

** Results of the chi-square test of the SNP effect based on the logistic regression model in which the phenotype (case definition) is a function of SNP genotype (based on placebo patients only).
Results of the chi-square test of the SNP effect based on the conditional logistic regression model in which the phenotype (case definition) is a function of SNP genotype (based on placebo patients only) and cases and controls were matched on age and current smoking status.

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI
For case definition, "F&NF MI" = Fatal & Nonfatal MI
For stratum, "WM" = WM
For study, "W" = W

TABLE 12 (continued)

Statistically Significant Associations Between SNP Genotypes and Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>Placebo Patients</u>		
							<u>n/total (%)</u>		
							<u>0 Rare Alleles</u>	<u>1 Rare Allele</u>	<u>2 Rare Alleles</u>
ADAMTS1	hCV529706	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	67/695 (9.6%)	51/406 (12.6%)	12/67 (17.9%)
ADAMTS1	hCV529710	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	67/439 (15.3%)	52/263 (19.8%)	12/42 (28.6%)
ASAH1	hCV2442143	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	43/196 (21.9%)	67/364 (18.4%)	21/181 (11.6%)
ITGA9	hCV25644901	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	107/665 (16.1%)	24/76 (31.6%)	0/0 (0.0%)
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	50/560 (8.9%)	57/511 (11.2%)	23/115 (20.0%)
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	37/436 (8.5%)	65/575 (11.3%)	28/173 (16.2%)
CD6	hCV2553030	W	Case/Control	F&NF MI	All Possible	WM	148/479 (30.9%)	67/288 (23.3%)	17/43 (39.5%)
HSPG2	hCV1603656	W	Case/Control	F&NF MI	All Possible	WM	191/665 (28.7%)	33/133 (24.8%)	6/7 (85.7%)
TAP1	hCV549926	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	81/829 (9.8%)	42/329 (12.8%)	8/33 (24.2%)
TAP1	hCV549926	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	81/817 (9.9%)	42/319 (13.2%)	8/33 (24.2%)

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = WM

For study, "W" = W

TABLE 12 (continued)

Statistically Significant Associations Between SNP Genotypes and Two CVD Case Definitions: Fatal MI / Sudden Death / Definite Non-fatal MI and Fatal / Non-fatal MI

							Odds Ratio (95% CI)		
<u>Public</u>	<u>Marker</u>	<u>Study</u>	<u>Study Design</u>	<u>Case Definition</u>	<u>Control Group Definition***</u>	<u>Stratum</u>	<u>2 Rare Alleles vs. 0 Rare Alleles</u>	<u>1 Rare Allele vs. 0 Rare Alleles</u>	<u>Significance Level</u>
ADAMTS1	hCV529706	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	2.08 (1.04 to 4.16)	1.47 (0.99 to 2.19)	P<=0.05
ADAMTS1	hCV529710	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	2.22 (1.05 to 4.46)	1.37 (0.91 to 2.04)	P<=0.05
ASAH1	hCV2442143	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM	0.47 (0.26 to 0.81)	0.80 (0.52 to 1.24)	P<=0.05
ITGA9	hCV25644901	CARE	Prospective	F MI/SD/NF MI	Cleaner	WM		2.41 (1.40 to 4.03)	P<=0.005
KLK14	hCV16044337	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	2.55 (1.46 to 4.34)	1.28 (0.86 to 1.92)	P<=0.005
NPC1	hCV25472673	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	2.08 (1.22 to 3.52)	1.37 (0.90 to 2.12)	P<=0.05
CD6	hCV2553030	W	Case/Control	F&NF MI	All Possible	WM	1.43 (0.74 to 2.75)	0.68 (0.48 to 0.95)	P<=0.05
HSPG2	hCV1603656	W	Case/Control	F&NF MI	All Possible	WM	13.24 (1.58 to 111.11)	0.85 (0.55 to 1.31)	P<=0.05
TAP1	hCV549926	CARE	Prospective	F MI/SD/NF MI	All Possible	WM	2.96 (1.21 to 6.50)	1.35 (0.90 to 2.00)	P<=0.05
TAP1	hCV549926	CARE	Case/Control	F MI/SD/NF MI	All Possible	WM	2.73 (1.17 to 6.39)	1.36 (0.91 to 2.05)	P<=0.05

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

For case definition, "F MI/SD/NF MI" = Fatal MI/Sudden Death/Definite Nonfatal MI

For case definition, "F&NF MI" = Fatal & Nonfatal MI

For stratum, "WM" = WM

For study, "W" = W

TABLE 13

PON1 hCV2548962: Consistent Interaction between PON1 Genotype and Pravastatin Efficacy within Both CARE and WOSCOPS

Public	Marker	Study	Study Design	Case Definition	Control Group Definition ***	Stratum	Overall* Chi-Square Test		Interaction Effect** Chi-Square Test	
							Statistic	p-value	Statistic	p-value
PON1	hCV2548962	CARE	Prospective	Total CHD Events	All Possible	White Males	21.92	0.0005	11.61	0.0030
PON1	hCV2548962	CARE	Prospective	Fatal & Nonfatal MI	Cleaner	White Males	13.00	0.0234	3.69	0.1583
PON1	hCV2548962	CARE	Case/Control	Fatal & Nonfatal MI	Cleaner	White Males	13.79	0.0170	5.15	0.0763
PON1	hCV2548962	WOSCOPS	Case/Control	Fatal & Nonfatal MI	Cleaner	White Males	15.66	0.0079	4.69	0.0958

* For the CARE prospective study: results of the Overall Score Test (chi-square test) for the logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group.

* For case/control studies: results of the Overall Score Test (chi-square test) for the conditional logistic regression model in which the phenotype (case definition) is a function of the SNP genotype, treatment group, and the interaction between SNP genotype and treatment group and cases and controls have been matched on age and smoking status.

** For the CARE prospective study: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the logistic regression model).

**For the case/control studies: results of the chi-square test of the interaction between SNP genotype and treatment group (based on the conditional logistic regression model).

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

TABLE 13 (continued)

PON1 hCV2548962: Consistent Interaction between PON1 Genotype and Pravastatin Efficacy within Both CARE and WOSCOPS

Public	Marker	Study	Study Design	Case Definition	Control Group Definition ***	Stratum	0 Rare Alleles n/total (%)		1 Rare Allele n/total (%)		2 Rare Alleles n/total (%)	
							Pravastatin Patients	Placebo Patients	Pravastatin Patients	Placebo Patients	Pravastatin Patients	Placebo Patients
PON1	hCV25 48962	CARE	Prospective	Total CHD Events	All Possible	White Males	183/613 (29.9%)	223/627 (35.6%)	151/504 (30.0%)	143/458 (31.2%)	18/107 (16.8%)	42/100 (42.0%)
PON1	hCV25 48962	CARE	Prospective	Fatal & Nonfatal MI	Cleaner	White Males	67/423 (15.8%)	75/398 (18.8%)	50/340 (14.7%)	64/303 (21.1%)	9/80 (11.3%)	18/64 (28.1%)
PON1	hCV25 48962	CARE	Case/Control	Fatal & Nonfatal MI	Cleaner	White Males	67/416 (16.1%)	75/394 (19.0%)	50/335 (14.9%)	64/297 (21.6%)	9/79 (11.4%)	18/64 (28.1%)
PON1	hCV25 48962	WOSCO PS	Case/Control	Fatal & Nonfatal MI	Cleaner	White Males	88/344 (25.6%)	112/386 (29.0%)	65/282 (23.1%)	98/293 (33.5%)	9/53 (17.0%)	22/59 (37.3%)

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

Likelihood-ratio tests and Chi-square tests were used to determine whether effects (either of SNP genotype or of the interaction between SNP genotype and treatment) were statistically significant. P-values for CARE and WOSCOPS were combined using the method of Fisher (1954). Results for CARE and WOSCOPS were determined to be consistent when (1) the combined p-value for the 2 studies is ≤ 0.05 , (2) the odds ratios are concordant, and (3) study-specific p-values for the effect (interaction or association) are both ≤ 0.10 . Odd ratios are defined to be concordant if both of the 95% confidence intervals (for both odds ratios) are entirely below 1.0 or if both of the entire 95% confidence intervals are entirely above 1.0.

NA = Not Applicable

TABLE 13 (continued)

PON1 hCV2548962: Consistent Interaction between PON1 Genotype and Pravastatin Efficacy within Both CARE and WOSCOPS

Public	Marker	Study	Study Design	Case Definition	Control Group Definition**	Stratum	Pravastatin vs. Placebo Odds Ratio (95% CI)			CARE & WOSCOPS Combined#		Significance Level
							Patients with 0 Rare Alleles	Patients with 1 Rare Allele	Patients with 2 Rare Alleles	Statistic	p-value	
PON1	hCV2548962	CARE	Prospective	Total CHD Events	All Possible	White Males	0.77 (0.61 to 0.98)	0.94 (0.58 to 1.54)	0.28 (0.13 to 0.60)	NA		
PON1	hCV2548962	CARE	Prospective	Fatal & Nonfatal MI	Cleaner	White Males	0.81 (0.56 to 1.16)	0.64 (0.31 to 1.36)	0.32 (0.11 to 0.95)	NA		
PON1	hCV2548962	CARE	Case/Control	Fatal & Nonfatal MI	Cleaner	White Males	0.84 (0.58 to 1.22)	0.63 (0.42 to 0.95)	0.29 (0.12 to 0.71)	9.84	0.0432	p<0.05
PON1	hCV2548962	WOSCOPS	Case/Control	Fatal & Nonfatal MI	Cleaner	White Males	0.84 (0.60 to 1.16)	0.58 (0.40 to 0.84)	0.34 (0.14 to 0.82)			

*** All Possible Controls include all controls with genotype data. Cleaner controls include controls with genotype data but with no other CVD-related events during the trial.

Likelihood-ratio tests and Chi-square tests were used to determine whether effects (either of SNP genotype or of the interaction between SNP genotype and treatment) were statistically significant. P-values for CARE and WOSCOPS were combined using the method of Fisher (1954). Results for CARE and WOSCOPS were determined to be consistent when (1) the combined p-value for the 2 studies is ≤ 0.05 , (2) the odds ratios are concordant, and (3) study-specific p-values for the effect (interaction or association) are both ≤ 0.10 . Odd ratios are defined to be concordant if both of the 95% confidence intervals (for both odds ratios) are entirely below 1.0 or if both of the entire 95% confidence intervals are entirely above 1.0.

NA = Not Applicable

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __4__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __4__

NOTE: For additional volumes please contact the Canadian Patent Office.

What is claimed is:

1. A method of indicating whether a human has an increased risk for myocardial infarction (MI), comprising testing nucleic acid from said human for the presence or absence of a polymorphism as represented by position 101 of SEQ ID NO:191 or its complement, wherein the presence of G at position 101 of SEQ ID NO:191 or C at position 101 of its complement indicates said human has said increased risk for MI.
2. The method of claim 1, wherein said nucleic acid is in a biological sample from said human.
3. The method of claim 2, wherein said biological sample is blood, saliva, or buccal cells.
4. The method of claim 2 or 3, further comprising preparing a nucleic acid extract from said biological sample prior to said testing.
5. The method of any one of claims 1 to 4, wherein said testing comprises nucleic acid amplification.
6. The method of claim 5, wherein said nucleic acid amplification is carried out by polymerase chain reaction.
7. The method of any one of claims 1 to 4, wherein said testing is performed using one or more of sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, single-stranded conformation polymorphism analysis, and denaturing gradient gel electrophoresis (DGGE).
8. The method of any one of claims 1 to 4, wherein said testing is performed using an allele-specific method.
9. The method of claim 8, wherein said allele-specific method detects said G or said C.

10. The method of claim 8 or 9, wherein said allele-specific method is allele-specific probe hybridization, allele-specific primer extension, or allele-specific amplification.

11. The method of claim 8, 9 or 10, wherein said allele-specific method is carried out using at least one allele-specific primer having a nucleotide sequence comprising SEQ ID NO:216 or SEQ ID NO:217.

12. The method of any one of claims 1 to 11, comprising using computer software to indicate said increased risk for MI due to the presence of said G or said C.

13. The method of any one of claims 1 to 11, wherein the absence of G at position 101 of SEQ ID NO:191 or C at position 101 of its complement indicates no said increased risk for MI.

14. The method of claim 13, comprising using computer software to indicate said no increased risk for MI due to the absence of said G or said C.

15. The method of any one of claims 1 to 14, wherein said human is homozygous for said G or said C.

16. The method of any one of claims 1 to 14, wherein said human is heterozygous for said G or said C.

17. The method of any one of claims 1 to 16, which is an automated method.

18. A method of indicating whether a human's risk for myocardial infarction (MI) is reduced by treatment with a statin, the method comprising testing nucleic acid from said human for the presence or absence of a polymorphism as represented by position 101 of SEQ ID NO:191 or its complement, wherein the presence of G at position 101 of SEQ ID NO:191 or C at position 101 of its complement indicates said human's risk for MI is reduced by treatment with said statin.

19. The method of claim 18, wherein said nucleic acid is in a biological sample from said human.

20. The method of claim 19, wherein said biological sample is blood, saliva, or buccal cells.
21. The method of claim 19 or 20, further comprising preparing a nucleic acid extract from said biological sample prior to said testing.
22. The method of any one of claims 18 to 21, wherein said testing comprises nucleic acid amplification.
23. The method of claim 22, wherein said nucleic acid amplification is carried out by polymerase chain reaction.
24. The method of any one of claims 18 to 21, wherein said testing is performed using one or more of sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, single-stranded conformation polymorphism analysis, and denaturing gradient gel electrophoresis (DGGE).
25. The method of any one of claims 18 to 21, wherein said testing is performed using an allele-specific method.
26. The method of claim 25, wherein said allele-specific method detects said G or said C.
27. The method of claim 25 or 26, wherein said allele-specific method is allele-specific probe hybridization, allele-specific primer extension, or allele-specific amplification.
28. The method of claim 25, 26 or 27, wherein said allele-specific method is carried out using at least one allele-specific primer having a nucleotide sequence comprising SEQ ID NO:216 or SEQ ID NO:217.
29. The method of any one of claims 18 to 28, comprising using computer software to indicate, due to the presence of said G or said C, a reduction of said human's risk for MI by treatment with a statin.

30. The method of any one of claims 18 to 28, wherein the absence of G at position 101 of SEQ ID NO:191 or C at position 101 of its complement indicates said human's risk for MI is not reduced by treatment with said statin.

31. The method of claim 30, comprising using computer software to indicate, due to said absence of said G or said C, no reduction of said human's risk for MI by treatment with said statin.

32. The method of any one of claims 18 to 29, wherein said human is homozygous for said G or said C.

33. The method of any one of claims 18 to 29, wherein said human is heterozygous for said G or said C.

34. The method of any one of claims 18 to 33, which is an automated method.

35. The method of any one of claims 18 to 34, wherein said statin is a hydrophilic statin.

36. The method of any one of claims 18 to 34, wherein said statin is a hydrophobic statin.

37. The method of any one of claims 19 to 34, wherein said statin is pravastatin, atorvastatin, simvastatin, cerivastatin, lovastatin, or a combination thereof.

38. An isolated polynucleotide for use in a method of indicating whether a human has an increased risk for myocardial infarction (MI) as defined in claim 10 or for use in a method of indicating whether a human's risk for MI is reduced by treatment with a statin as defined in claim 27, wherein the polynucleotide specifically hybridizes to at least a portion of SEQ ID NO:191 or its complement, which portion comprises position 101.

39. The polynucleotide of claim 38, wherein position 101 of SEQ ID NO:191 is G and position 101 of its complement is C.

40. The polynucleotide of claim 38 or 39, which is 8-70 nucleotides in length.

41. The polynucleotide of claim 38, 39 or 40, for use as an allele-specific probe.
42. The polynucleotide of claim 38, 39 or 40, for use as an allele-specific primer.
43. A kit for performing a method of indicating whether a human has an increased risk for myocardial infarction (MI) as defined in claim 10 or for performing a method of indicating whether a human's risk for MI is reduced by treatment with a statin as defined in claim 27, the kit comprising a polynucleotide as defined in any one of claims 38 to 42, a buffer, and an enzyme.

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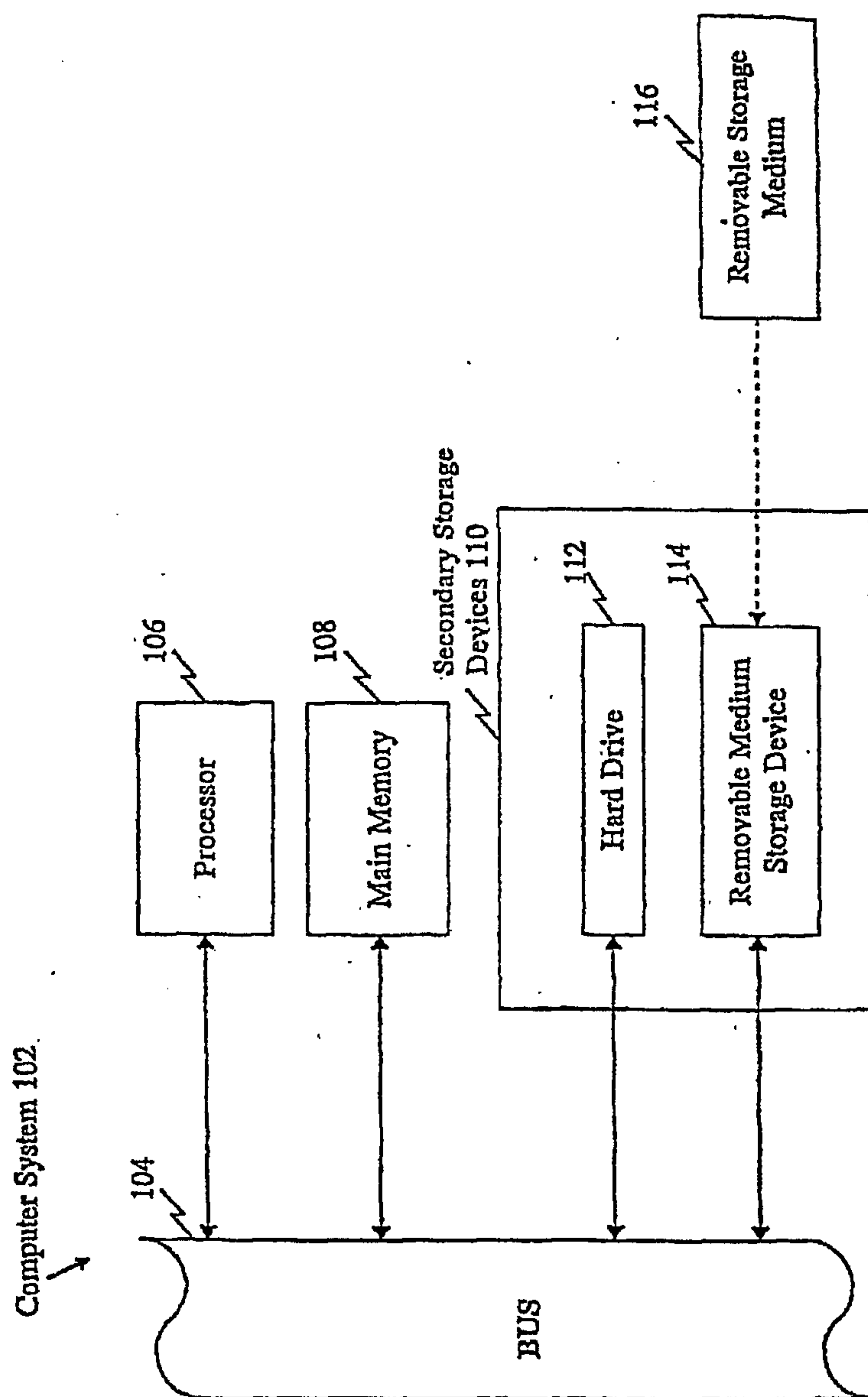


FIGURE 1

Computer System 102

