GENETIC MARKERS FOR RISK MANAGEMENT OF CARDIAC ARRHYTHMIA

BACKGROUND OF THE INVENTION

Cardiac arrhythmia is a group of medical conditions, in which the electrical activity of the heart is irregular, or is slower or faster than normal. Some arrhythmias are life-threatening, and can cause cardiac arrest or sudden death. Others cause, or predispose to, other aggravating symptoms or disease, including stroke. Fibrillation is a serious form of arrhythmia, in which the heart muscle presents with irregular or quivering motion due to lack of unity in the function of contractile cells. Fibrillation can affect the atrium (Atrial Fibrillation (AF) or Atrial Flutter (AFl)), or the ventricle (Ventricular Fibrillation (VF)).

Atrial fibrillation (AF) is an abnormal heart rhythm (cardiac arrhythmia) which involves the two small, upper heart chambers (the atria). Heart beats in a normal heart begin after electricity generated in the atria by the sinoatrial node spreads through the heart and causes contraction of the heart muscle and pumping of blood. In AF, the regular electrical impulses of the sinoatrial node are replaced by disorganized, rapid electrical impulses which result in irregular heart beats.

Atrial fibrillation is the most common cardiac arrhythmia. The risk of developing atrial fibrillation increases with age — AF affects four percent of individuals in their 80s. An individual may spontaneously alternate between AF and a normal rhythm (*paroxysmal atrial fibrillation*) or may continue with AF as the dominant cardiac rhythm without reversion to the normal rhythm (*chronic atrial fibrillation*). Atrial fibrillation is often asymptomatic, but may result in symptoms of palpitations, fainting, chest pain, or even heart failure. These symptoms are especially common when atrial fibrillation results in a heart rate which is either too fast or too slow. In addition, the erratic motion of the atria leads to blood stagnation (stasis) which increases the risk of blood clots that may travel from the heart to the brain and other areas. Thus, AF is an important risk factor for stroke, the most feared complication of atrial fibrillation.

The symptoms of atrial fibrillation may be treated with medications which slow the heart rate. Several medications as well as electrical cardioversion may be used to convert AF to a normal heart rhythm. Surgical and catheter-based therapies may also be used to prevent atrial fibrillation in certain individuals. People with AF are often given blood thinners such as warfarin to protect them from strokes.

Any patient with 2 or more identified episodes of atrial fibrillation is said to have recurrent atrial fibrillation. This is further classified into paroxysmal and persistent based on when the episode terminates without therapy. Atrial fibrillation is said to be paroxysmal when it terminates spontaneously within 7 days, most commonly within 24 hours. Persistent or chronic atrial fibrillation is AF established for more than seven days. Differentiation of paroxysmal from chronic or established AF is based on the history of recurrent episodes and the duration of the current episode of AF (Levy S., *J Cardiovasc Electrophysiol.* 8 Suppl, S78-82 (1998)).

Lone atrial fibrillation (LAF) is defined as atrial fibrillation in the absence of clinical or echocardiographic findings of cardiopulmonary disease.

Atrial fibrillation is usually accompanied by symptoms related to either the rapid heart rate or embolization. Rapid and irregular heart rates may be perceived as palpitations, exercise intolerance, and occasionally produce angina and congestive symptoms of shortness of breath or edema. Sometimes the arrhythmia will be identified with the onset of a stroke or a transient ischemic attack (TIA). It is not uncommon to identify atrial fibrillation on a routine physical examination or electrocardiogram (ECG/EKG), as it may be asymptomatic in some cases. *Paroxysmal* atrial fibrillation is the episodic occurrence of the arrhythmia and may be difficult to diagnose. Episodes may occur with sleep or with exercise, and their episodic nature may require prolonged ECG monitoring (e.g. a Holter monitor) for diagnosis.

Atrial fibrillation is diagnosed on an electrocardiogram, an investigation performed routinely whenever irregular heart beat is suspected. Characteristic findings include absence of P waves, unorganized electrical activity in their place and irregularity of R-R interval due to irregular conduction of impulses to the ventricles. If paroxysmal AF is suspected, episodes may be documented with the use of Holter monitoring (continuous ECG recording for 24 hours or longer).

While many cases of AF have no definite cause, it may be the result of various other problems (see below). Hence, renal function and electrolytes are routinely determined, as well as thyroid-stimulating hormone and a blood count. A chest X-ray is generally performed. In acute-onset AF associated with chest pain, cardiac troponins or other markers of damage to the heart muscle may be ordered. Coagulation studies (INR/aPTT) are usually performed, as anticoagulant medication may be commenced. A transesophageal echocardiogram may be indicated to identify any intracardiac thrombus (Fuster V., *et al.*, Circulation.;104, 2118-2150 (2001)).

Atrial Flutter (AFl) is characterized by an abnormal fast heart rhythm in the atria. Patients who present with atrial flutter commonly also experience Atrial Fibrillation and

vice versa (Waldo, A., *Progr Cardiovasc Disease,* **48**:41-56 (2005)). Mechanistically and biologically, AF and AFl are thus likely to be highly related.

AF (and AFl) is linked to several cardiac causes, but may occur in otherwise normal hearts. Known associations include: High blood pressure, Mitral stenosis (e.g. due to rheumatic heart disease or mitral valve prolapse), Mitral regurgitation, Heart surgery, Coronary artery disease, Hypertrophic cardiomyopathy, Excessive alcohol consumption ("binge drinking" or "holiday heart"), Hyperthyroidism, Hyperstimulation of the vagus nerve, usually by having large meals ("binge eating"), Lung pathology (such as pneumonia, lung cancer, pulmonary embolism, Sarcoidosis), Pericarditis, Intense emotional turmoil, and Congenital heart disease.

The normal electrical conduction system of the heart allows the impulse that is generated by the sinoatrial node (SA node) of the heart to be propagated to and stimulate the myocardium (muscle of the heart). When the myocardium is stimulated, it contracts. It is the ordered stimulation of the myocardium that allows efficient contraction of the heart, thereby allowing blood to be pumped to the body. In atrial fibrillation, the regular impulses produced by the sinus node to provide rhythmic contraction of the heart are overwhelmed by the rapid randomly generated discharges produced by larger areas of atrial tissue. An organized electrical impulse in the atrium produces atrial contraction; the lack of such an impulse, as in atrial fibrillation, produces stagnant blood flow, especially in the atrial appendage and predisposes to clotting. The dislodgement of a clot from the atrium results in an embolus, and the damage produced is related to where the circulation takes it. An embolus to the brain produces the most feared complication of atrial fibrillation, stroke, while an embolus may also lodge in the mesenteric circulation (the circulation supplying the abdominal organs) or digit, producing organ-specific damage.

Treatment of atrial fibrillation is directed by two main objectives: (i) prevent temporary circulatory instability; (ii) prevent stroke. The most common methods for achieving the former includes rate and rhythm control, while anticoagulation is usually the desired method for the latter (Prystowsky E.N., *Am J Cardiol.*;85, 3D-11D (2000); van Walraven C, *et al., Jama.* 288, 2441-2448 (2002)). Common methods for rate control, i.e. for reducing heart rate to normal, include beta blockers (*e.g.,* metotprolol), cardiac glycosides (*e.g.,* digoxin) and calcium channel blockers (*e.g.,* verapamil). All these medications work by slowing down the generation of pulses from the atria, and the conduction from the atria to the ventricles. Other drugs commonly used include quinidine, flecainide, propafenone, disopyramide, sotalol and amiodarone. Rhythm control can be achieved by electrical cardioversion, i.e. by applying DC electrical shock, or by chemical cardioversion, using drugs such as amiodarione, propafenone and flecainide.

Preventive measures for stroke include anticoagulants. Representative examples of anticoagulant agents are Dalteparin (*e.g.,* Fragmin), Danaparoid (*e.g.,* Orgaran), Enoxaparin (*e.g.,* Lovenox), Heparin (various), Tinzaparin (*e.g.,* Innohep), Warfarin (*e.g.,* Coumadin). Some patients with lone atrial fibrillation are sometimes treated with aspirin or clopidogrel. There is evidence that aspirin and clopidogrel are effective when used together, but the combination is still inferior to warfarin (Connolly S., *et al. Lancet.*;367, 1903-1912 (2006)).(*2*) The new anticoagulant ximelagatran has been shown to prevent stroke with equal efficacy as warfarin, without the difficult monitoring process associated with warfarin and with possibly fewer adverse haemorrhagic events. Unfortunately, ximegalatran and other similar anticoagulant drugs (commonly referred to as direct thrombin inhibitors), have yet to be widely licensed.

Determining who should and should not receive anti-coagulation with warfarin is not straightforward. The CHADS2 score is the best validated method of determining risk of stroke (and therefore who should be anticoagulated). The UK NICE guidelines have instead opted for an algorithm approach. The underlying problem is that if a patient has a yearly risk of stroke that is less than 2%, then the risks associated with taking warfarin outweigh the risk of getting a stroke (Gage B.F. *et al. Stroke* 29, 1083-1091 (1998))

Atrial fibrillation can sometimes be controlled with treatment. The natural tendency of atrial fibrillation, however, is to become a chronic condition. Chronic AF leads to an increased risk of death. Patients with atrial fibrillation are at significantly increased chance of stroke.

Atrial fibrillation is common among older adults. In developed countries, the number of patients with atrial fibrillation is likely to increase during the next 50 years, due to the growing proportion of elderly individuals (Go A.S. *et al., Jama.*, 285, 2370-2375 (2001))(*3*). In the Framingham study the lifetime risk for development of AF is 1 in 4 for men and women 40 years of age and older. Lifetime risks for AF are high (1 in 6). According to data from the National Hospital Discharge Survey (1996-2001) on cases that included AF as a primary discharge diagnosis found that 45% of the patients are male, and that the mean age for men was 66.8 years and 74.6 for women. The racial breakdown for admissions was found to be 71.2 % white, 5.6% black,2% other races, and 20% not specified. Furthermore, African American patients were, on average, much younger than other races. The incidence in men ranged from 20.58/100,000 persons per year for patients ages 15-44 years to 1203/100,000 persons per years for those ages 85 and older. From 1996-2001, hospitalizations with AF as the first listed diagnosis, increased by 34%.

Stroke is a common and serious disease. Each year in the United States more than 600,000 individuals suffer a stroke and more than 160,000 die from stroke-related causes (Sacco, R.L. *et al., Stroke* 28, 1507-17 (1997)). Furthermore, over 300,000 individuals

present with Transient Ischemic Attack, a mild form of stroke, every year in the US. In western countries stroke is the leading cause of severe disability and the third leading cause of death (Bonita, R., *Lancet* 339, 342-4 (1992)). The lifetime risk of those who reach the age of 40 exceeds 10%.

The clinical phenotype of stroke is complex but is broadly divided into ischemic (accounting for 80-90%) and hemorrhagic stroke (10-20%) (Caplan, L.R. *Caplan´s Stroke: A Clinical Approach*, 1-556 (Butterworth-Heinemann, 2000)). Ischemic stroke is further subdivided into large vessel occlusive disease (referred to here as carotid stroke), usually due to atherosclerotic involvement of the common and internal carotid arteries, small vessel occlusive disease, thought to be a non-atherosclerotic narrowing of small end-arteries within the brain, and cardiogenic stroke due to blood clots arising from the heart usually on the background of atrial fibrillation or ischemic (atherosclerotic) heart disease (Adams, H.P., Jr. *et al., Stroke* 24, 35-41 (1993)). Therefore, it appears that stroke is not one disease but a heterogeneous group of disorders reflecting differences in the pathogenic mechanisms (Alberts, M.J. *Genetics of Cerebrovascular Disease*, 386 (Futura Publishing Company, Inc., New York, 1999); Hassan, A. & Markus, H.S. *Brain* 123, 1784-812 (2000)). However, all forms of stroke share risk factors such as hypertension, diabetes, hyperlipidemia, and smoking (Sacco, R.L. *et al., Stroke* 28, 1507-17 (1997); Leys, D. *et al., J. Neurol.* 249, 507-17 (2002)). Family history of stroke is also an independent risk factor suggesting the existence of genetic factors that may interact with environmental factors (Hassan, A. & Markus, H.S. *Brain* 123, 1784-812 (2000); Brass, L.M. & Alberts, M.J. *Baillieres Clin. Neurol.* 4, 221-45 (1995)).

The genetic determinants of the common forms of stroke are still largely unknown. There are examples of mutations in specific genes that cause rare Mendelian forms of stroke such as the *Notch3* gene in CADASIL (cerebral autosomal dominant arteriopathy with subcortical infarctions and leukoencephalopathy) (Tournier-Lasserve, E. *et al., Nat. Genet.* 3, 256-9 (1993); Joutel, A. *et al., Nature* 383, 707-10 (1996)), *Cystatin C* in the Icelandic type of hereditary cerebral hemorrhage with amyloidosis (Palsdottir, A. *et al., Lancet* 2, 603-4 (1988)), *APP* in the Dutch type of hereditary cerebral hemorrhage (Levy, E. *et al., Science* 248, 1124-6 (1990)) and the *KRIT1* gene in patients with hereditary cavernous angioma (Gunel, M. *et al., Proc. Natl. Acad. Sci. USA* 92, 6620-4 (1995); Sahoo, T. *et al., Hum. Mol. Genet.* 8, 2325-33 (1999)). None of these rare forms of stroke occur on the background of atherosclerosis, and therefore, the corresponding genes are not likely to play roles in the common forms of stroke which most often occur with atherosclerosis.

It is very important for the health care system to develop strategies to prevent stroke. Once a stroke happens, irreversible cell death occurs in a significant portion of the brain supplied by the blood vessel affected by the stroke. Unfortunately, the neurons that

die cannot be revived or replaced from a stem cell population. Therefore, there is a need to prevent strokes from happening in the first place. Although we already know of certain clinical risk factors that increase stroke risk (listed above), there is an unmet medical need to define the genetic factors involved in stroke to more precisely define stroke risk. Further, if predisposing alleles are common in the general population and the specificity of predicting a disease based on their presence is low, additional loci such as protective loci are needed for meaningful prediction of disposition of the disease state. There is also a great need for therapeutic agents for preventing the first stroke or further strokes in individuals who have suffered a previous stroke or transient ischemic attack.

AF is an independent risk factor for stroke, increasing risk about 5-fold. The risk for stroke attributable to AF increases with age. AF is responsible for about 15-20% of all strokes. AF is also an independent risk factor for stroke recurrence and stroke severity. A recent report showed people who had AF and were not treated with anticoagulants had a 2.1-fold increase in risk for recurrent stroke and a 2.4 fold increase in risk for recurrent severe stroke. People who have stroke caused by AF have been reported as 2.23 times more likely to be bedridden compared to those who have strokes from other causes.

There is a need for an understanding of the susceptibility factors leading to increased predisposition for AF and stroke. Identification of at-risk variants for AF can, for example, be useful for assessing which individuals are at particularly high risk for AF and subsequent stroke. Furthermore, preventive treatment can be administered to individuals suffering from AF and who are carriers of at-risk susceptibility variants for AF and/or stroke. Finally, identification of at-risk variants for AF and/or stroke can lead to the identification of new targets for drug therapy, as well as the development of novel therapeutic measures.

SUMMARY OF THE INVENTION

The present invention relates to the discovery that certain genetic markers have been shown to be associated with cardiac arrhythmia, in particular atrial fibrillation and atrial flutter, and stroke. This discovery can be utilized in a variety of methods, procedures, apparatus, media and kits, as described herein, relating to methods and procedures of diagnosis and/or determination of a susceptibility, methods of genotyping associated variants, methods of predicting response to therapeutic agents, methods of predicting prognosis, methods of monitoring progress of treatment, and systems and kits for use in such methods.

One aspect of the invention relates to a method of determining a susceptibility to cardiac arrhythmia or stroke in a human individual, the method comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample from the individual, wherein the at least one polymorphic marker is selected from the polymorphic markers set forth in Table 5, and markers in linkage disequilibrium therewith, wherein determination of the presence or absence of the at least one allele is indicative of a susceptibility to cardiac arrhythmia or stroke in the individual. In one embodiment, the at least one polymorphic marker is located within the LD block C04, set forth in SEQ ID NO:50 herein. In another embodiment, the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith. In one embodiment, the at least one marker is selected from marker rs2220427 (SEQ ID NO:1) and marker rs10033464 (SEQ ID NO:41), and markers in linkage disequilibrium therewith. In another embodiment, the at least one polymorphic marker is selected from the markers set forth in Table 19. In one embodiment, the method further comprises a step of assessing at least one haplotype comprising at least two polymorphic markers in the individual.

In another aspect, the invention relates to a method of determining a susceptibility to cardiac arrhythmia or stroke in a human individual, comprising determining whether at least one at-risk allele in at least one polymorphic marker is present in a genotype dataset derived from the individual, wherein the at least one polymorphic marker is selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith, and wherein determination of the presence of the at least one at-risk allele is indicative of increased susceptibility to cardiac arrhythmia or stroke in the individual.

The genotype dataset comprises in one embodiment information about marker identity, and the allelic status of the individual for the at least one polymorphic marker, i.e. information about the identity of the two alleles carried by the individual for the marker and/or information about whether an individual is a carrier of a particular at-risk allele for the at least one polymorphic marker. The genotype dataset may comprise allelic information about one or more marker, including two or more markers, three or more markers, five or more markers, one hundred or more markers, etc. In some embodiments, the genotype dataset comprises genotype information from a whole-genome assessment of the individual including hundreds of thousands of markers, or even one million or more markers.

The invention, in another aspect, relates to a procedure comprising a step of analyzing a nucleic acid from a human individual to determine the presence or absence of at least one allele of at least one polymorphic marker or haplotype associated with the genomic sequence with sequence as set forth in SEQ ID NO:50; and a step of determining the status of a genetic indicator of cardiac arrhythmia or stroke in the individual from the

presence or absence of the at least one marker or haplotype. Thus the genotype and/or haplotype status of the individual is used as in indicator of cardiac arrhythmia, including atrial fibrillation and atrial flutter, as well as stroke, in the individual.

The invention also relates to a method of assessing a susceptibility to cardiac arrhythmia or stroke in a human individual, comprising screening a nucleic acid from the individual for at least one polymorphic marker or haplotype in SEQ ID NO:50 that correlates with increased occurrence of cardiac arrhythmia or stroke in a human population; wherein determination of the presence of an at-risk marker allele in the at least one polymorphism or an at-risk haplotype in the nucleic acid identifies the individual as having elevated susceptibility to cardiac arrhythmia and/or stroke, and wherein the absence of the at least one at-risk marker allele or at-risk haplotype in the nucleic acid identifies the individual as not having the elevated susceptibility.

The procedure or methods of the invention in one embodiment entail at least one polymorphic marker or haplotype comprising a contiguous nucleic acid fragment of LD block C04 as set forth in SEQ ID NO:50, or the complement thereof, wherein the fragment is less than 500 nucleotides in size and specifically hybridizes to a complimentary segment of LD block C04. In one embodiment, the fragment is more than 15 nucleotides and less than 400 nucleotides in size, and wherein the fragment specifically hybridizes to a complimentary segment of LD block C04 as set forth in SEQ ID NO:50.

In alternative embodiments, the susceptibility conferred by the polymorphic markers or haplotypes is decreased susceptibility, i.e. the markers and haplotypes of the invention confer decreased risk of an individual develops cardiac arrhythmia, including atrial fibrillation and atrial flutter, and/or stroke. In one such embodiment, the decreased susceptibility is characterized by an odds ratio (OR) or relative risk (RR) of less than 0.8. In another embodiment, the decreased susceptibility is characterized by an odds ratio (OR) of less than 0.7. In another embodiment, the decreased susceptibility is characterized by an OR or RR of less than 0.6. In another embodiment, the decreased susceptibility is characterized by OR or RR of less than 0.5. Other embodiments relate to other values for OR or RR including values of 0.9, 0.85, 0.75, 0.65, 0.55, etc.

Another aspect of the invention relates to a method of identification of a marker for use in assessing susceptibility to symptoms associated with cardiac arrhythmia and/or stroke in a human individual, the method comprising at least one polymorphic marker within SEQ ID NO:50, or at least one polymorphic marker in linkage disequilibrium with at least one marker within SEQ ID NO:50, determining the genotype status of a sample of individuals diagnosed with cardiac arrhythmia and/or stroke and the genotype status of a sample of control individuals, wherein a significant difference in frequency of at least one allele in at least one polymorphism in individuals diagnosed with cardiac arrhythmia and/or

stroke as compared with the frequency of the at least one allele in the control sample is indicative of the at least one polymorphism being useful for assessing susceptibility to cardiac arrhythmia and/or stroke. In one embodiment, an increase in frequency of the at least one allele in the at least one polymorphism in individuals diagnosed with cardiac arrhythmia and/or stroke, as compared with the frequency of the at least one allele in the control sample, is indicative of the at least one polymorphism being useful for assessing increased susceptibility to cardiac arrhythmia. In another embodiment, a decrease in frequency of the at least one allele in the at least one polymorphism in individuals diagnosed with cardiac arrhythmia and/or stroke, as compared with the frequency of the at least one allele in the control sample, is indicative of the at least one polymorphism being useful for assessing decreased susceptibility to, or protection against, cardiac arrhythmia and/or stroke. In preferred embodiments, the significant difference in frequency is characterized by a statistical measure. In one embodiment, the statistical measure is a P-value. In particular embodiments, a significant P-value is less than 0.05, less than 0.01, less than 0.001, less than 0.0001, less than 0.00001, less than 0.000001, less than 0.0000001 or less than 0.00000001. In other embodiments, the significant difference is characterized by an odds ratio (OR) or relative risk (RR) with particular confidence interval (CE) values.

In another aspect, the invention relates to a method of genotyping a nucleic acid sample obtained from a human individual, comprising determining the presence or absence of at least one allele of at least one polymorphic marker predictive of increased risk of cardiac arrhythmia and/or stroke in the sample, wherein the at least one marker is selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith, and wherein determination of the presence or absence of the at least one allele of the at least one polymorphic marker is predictive of increased risk of cardiac arrhythmia and/or stroke in the individual. In one embodiment, genotyping is performed using a process selected from allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, nucleic acid sequencing, 5'-exonuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation analysis. In a preferred embodiment, the process comprises allele-specific probe hybridization. The process of genotyping preferably comprises amplifying a segment of a nucleic acid that comprises the at least one polymorphic marker, by Polymerase Chain Reaction (PCR), using a nucleotide primer pair flanking the at least one polymorphic marker. In a preferred method of genotyping, the following steps are performed:

1. contacting copies of the nucleic acid with a detection oligonucleotide probe and an enhancer oligonucleotide probe under conditions for specific hybridization of the oligonucleotide probe with the nucleic acid;wherein

a) the detection oligonucleotide probe is from 5-100 nucleotides in length and specifically hybridizes to a first segment of the nucleic acid whose nucleotide sequence is given by SEQ ID NO:50 that comprises at least one polymorphic site;

b) the detection oligonucleotide probe comprises a detectable label at its 3' terminus and a quenching moiety at its 5' terminus;

c) the enhancer oligonucleotide is from 5-100 nucleotides in length and is complementary to a second segment of the nucleotide sequence that is 5' relative to the oligonucleotide probe, such that the enhancer oligonucleotide is located 3' relative to the detection oligonucleotide probe when both oligonucleotides are hybridized to the nucleic acid; and

d) a single base gap exists between the first segment and the second segment, such that when the oligonucleotide probe and the enhancer oligonucleotide probe are both hybridized to the nucleic acid, a single base gap exists between the oligonucleotides;

2. treating the nucleic acid with an endonuclease that will cleave the detectable label from the 3' terminus of the detection probe to release free detectable label when the detection probe is hybridized to the nucleic acid; and

measuring free detectable label, wherein the presence of the free detectable label indicates that the detection probe specifically hybridizes to the first segment of the nucleic acid, and indicates the sequence of the polymorphic site as the complement of the detection probe.

A further aspect of the invention relates to a method of determining a susceptibility to cardiac arrhythmia or stroke in a human individual, the method comprising determining the identity of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one marker is selected from the group of markers associated with the PITX2 gene, wherein the presence of the at least one allele is indicative of a susceptibility to cardiac arrhythmia or stroke in the individual.

Some embodiments of the invention relate to a further step of assessing at least one additional biomarker for atrial fibrillation, atrial flutter or stroke, wherein combining the genetic information from the markers provides risk assessment for atrial fibrillation, atrial flutter or stroke. In some of these embodiments, the biomarker is a genetic marker or haplotype, i.e. genetic risk factors shown to be, or contemplated to be, related to increased or decreased risk of atrial fibrillation, atrial flutter or stroke. In other embodiments the biomarker is a protein biomarker. The protein biomarker is in some embodiments selected from fibrin D-dimer, prothrombin activation fragment 1.2 (F1.2),

thrombin-antithrombin III complexes (TAT), fibrinopeptide A (FPA), lipoprotein-associated phospholipase A2 (lp-PLA2), beta-thromboglobulin, platelet factor 4, P-selectin, von Willebrand Factor, pro-natriuretic peptide (BNP), matrix metalloproteinase-9 (MMP-9), PARK7, nucleoside diphosphate kinase (NDKA), tau, neuron-specific enolase, B-type neurotrophic growth factor, astroglial protein S-100b, glial fibrillary acidic protein, C-reactive protein, seum amyloid A, marix metalloproteinase-9, vascular and intracellular cell adhesion molecules, tumor necrosis factor alpha, and interleukins, including interleukin-1, -6, and -8). In one embodiment, the at least one biomarker includes progenitor cells. In particular embodiments, more than one biomarker is determined. In a preferred embodiment, the biomarker is measured in plasma from the individual. Other embodiments further relate to combining non-genetic information to make risk assessment, diagnosis, or prognosis of atrial fibrillation, atrial flutter or stroke in the individual. The non-genetic information can comprise age, age at onset of disease, gender, ethnicity, previous disease diagnosis, e.g., diagnosis of cardiag arrhythmia (e.g., atrial fibrillation) and stroke, medical history of the individual, family history of disease, biochemical measurements, and clinical measurements (e.g., blood pressure, serum lipid levels). Analysis of such combined information from various genetic markers, or genetic markers plus non-genetic markers is possible by methods known to those skilled in the art. In one embodiment, analysis is performed calculating overall risk by logistic regression.

The invention further relates to a method of diagnosing increased susceptibility of stroke in a human individual, comprising the steps of (a) determining whether the individual has experienced symptoms associated with Atrial Fibrillation, Atrial Flutter or a Transient Ischemic Attack; (b) determining whether a nucleic acid sample from the individual comprises at least one copy of an at-risk allele of at least one polymorphic marker selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith; wherein the presence of symptoms associated with Atrial Fibrillation, Atrial Flutter and/or Transient Ischemic Attack and the presence of the at least one copy of the at-risk allele is indicative of increased susceptibility of stroke.

The invention in a further aspect relates to a method of assessing an individual for probability of response to a therapeutic agent for preventing and/or ameliorating symptoms associated with cardiac arrhythmia and/or stroke, comprising: determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith, wherein determination of the presence of the at least one allele of the at least one marker is indicative of a probability of a positive response to the therapeutic agent for cardiac arrhythmia and/or stroke.

In one embodiment, the therapeutic agent is an anticoagulant, an anti-arrhythmic agent, a hear rate control agent, a cardioversion agent, or a heart rhythm control agent. In another embodiment, the therapeutic agent is selected from warfarin, heparin, low molecular weight heparins, factor Xa inhibitors, and thrombin inhibitors, sodium channel blockers, beta blockers, potassium channel blockers, and calcium channel blockers.

In another embodiment, the therapeutic agent is selected from warfaring, ximelagatran, heparin, enoxaparin, dalteparin, tinzaparin, ardeparin, nadroparin, reviparin, fondaparinux, idraparinux, lepirudin, bivalirudin, argatroban, danaparoid, disopyramide, moricizine, procainamide, quinidine, lidocaine, mexiletine, tocainide, phenytoin, encainide, flecainide, propafenone, ajmaline, cibenzoline, detajmium, esmolol, propranolol, metoprolol, alprenolol, atenolol, carvedilol, bisoprolol, acebutolol, nadolol, pindololol, labetalol, oxprenotol, penbutolol, timolol, betaxolol, cartelol, sotalol, levobunolol, amiodarone, azimilide, bretylium, dofetilide, tedisamil, ibutilide, sematilide, N-acetyl procainamide, nifekalant hydrochloride, vernakalant, ambasilide, verpamil, mibefradil, diltiazem, digoxin, adenosine, ibutilide, amiodarone, procainamide, profafenone and flecainide.

Yet another aspect of the invention relates to a method of predicting prognosis of an individual diagnosed with, cardiac arrhythmia and/or stroke, the method comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the the markers set forth in Table 9, and markers in linkage disequilibrium therewith, wherein determination of the presence of the at least one allele is indicative of a worse prognosis of the cardiac arrhythmia and/or stroke in the individual.

Methods of monitoring progress of a treatment of an individual undergoing treatment for cardiac arrhythmia and/or stroke are also within scope of the invention, the methods comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith, wherein determination of the presence of the at least one allele is indicative of the treatment outcome of the individual.

In particular embodiments of the invention, e.g. in the various methods, uses, procedures, apparatus and kits of the invention, the cardiac arrhythmia phenotype is further characterized as being atrial fibrillation or atrial flutter. The inventors have determined that the risk conferred by the AF at-risk variants described herein is greater for individual with early age at onset than for individuals with late age at onset. Thus in one embodiment, the atrial fibrillation or atrial flutter is further characterized by an age of

onset in the individual of less than 80 years. In another embodiment, the atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 70 years. In yet another embodiment, the atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 60 years. Other age cutoffs are possible in alternative embodiments of the invention, and are also contemplated, including, but not limited to, age cutoff of less than 75 years, less than 65 years, and less than 55 years. Furthermore, age at onset or diagnosis above age 55, 60, 65, 70, 75 or 80 are also contemplated and within scope of the invention, as are age ranges within which diagnosis or symptoms or onset of the disease occurs, including, but not limited to, age 50-80, age 55-75, age 60-80, age 65-75, etc.

In certain embodiments of the invention, the stroke is further characterized as ischemic stroke. In other embodiments, the stroke phenotype may be characterized as one or more of the ischemic stroke sub-phenotypes large artery atherosclerosis (LAA), cardioembolic stroke (CES) and small vessel disease (SVD).

In particular embodiments of the invention, linkage disequilibrium (LD) is defined by a specific quantitative cutoff. As described in detail herein, linkage disequilibrium can be quantitatively determined by measures such as r^2 and |D'|. As a consequence, certain embodiments of the invention relate to markers in linkage disequilibrium by a measure within a certain range specified by particular values of r^2 and/or |D'|. In one such embodiment, LD is characterized by numerical values for r^2 of greater than 0.1. In another embodiment, LD is characterized by numerical values for r^2 of greater than 0.1. In another embodiment, LD is characterized by numerical values for r^2 of greater than 0.5. In yet another embodiment, LD is characterized by numerical values for r^2 of greater than 0.8. Other cutoff values for r^2 are also contemplated, as described in more detail herein. In certain embodiments, LD is characterized by certain cutoff values for r^2 and/or |D'|. In one such embodiment, LD is characterized by values for r^2 and/or |D'| of greater than 0.2 and 0.8, respectively. Other combination and permutations of these or other measures of LD are possible to practice the invention, and are also contemplated and within scope of the invention.

The procedures, uses, or methods of the invention in some embodiments further comprise a step of administering to an individual determined to be at increased risk for developing cardiac arrhythmia or stroke a composition comprising at least one therapeutic agent effective to treat or prevent cardiac arrhythmia or stroke, or prevent symptoms associated with cardiac arrhythmia or stroke. Thus, the invention can be used to determine whether an individual is suitable for a particular treatment module.

Kits for use in the various methods and procedures described herein are also within scope of the invention. Thus, in one aspect, the invention relates to a kit for assessing

susceptibility to cardiac arrhythmia and/or stroke in a human individual, the kit comprising reagents for selectively detecting at least one allele of at least one polymorphic marker in the genome of the individual, wherein the polymorphic marker is selected from the group consisting of the polymorphic markers within the segment whose sequence is set forth in SEQ ID NO:50, and markers in linkage disequilibrium therewith, and wherein the presence of the at least one allele is indicative of a susceptibility to cardiac arrhythmia and/or stroke.

In one embodiment, the at least one polymorphic marker is selected from the markers set forth in Table 5. In another embodiment, the at least one polymorphic marker is selected from the group of markers set forth in Table 9, and markers in linkage disequilibrium therewith. In another embodiment, the at least one polymorphic marker is selected from marker rs2220427 (SEQ ID NO:1) and rs10033464 (SEQ ID NO:41), and markers in linkage disequilibrium therewith. In one preferred embodiment, the at least one polymorphic marker is selected from the markers set forth in Table 19. In another preferred embodiment, the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51). In one embodiment, the reagents comprise at least one contiguous oligonucleotide that hybridizes to a fragment of the genome of the individual comprising the at least one polymorphic marker, a buffer and a detectable label.

In another embodiment, the reagents comprise at least one pair of oligonucleotides that hybridize to opposite strands of a genomic nucleic acid segment obtained from the subject, wherein each oligonucleotide primer pair is designed to selectively amplify a fragment of the genome of the individual that includes one polymorphic marker, and wherein the fragment is at least 30 base pairs in size. The at least one oligonucleotide is in preferred embodiments completely complementary to the genome of the individual. In one embodiment, the oligonucleotide is about 18 to about 50 nucleotides in length. In another embodiment, the oligonucleotide is 20-30 nucleotides in length. In one preferred embodiment, the kit comprises:

a. a detection oligonucleotide probe that is from 5-100 nucleotides in length;

b. an enhancer oligonucleotide probe that is from 5-100 nucleotides in length; and

c. an endonuclease enzyme;

wherein the detection oligonucleotide probe specifically hybridizes to a first segment of the nucleic acid whose nucleotide sequence is given by SEQ ID NO: 2 that comprises at least

one polymorphic site; wherein the detection oligonucleotide probe comprises a detectable label at its 3′ terminus and a quenching moiety at its 5′ terminus; wherein the enhancer oligonucleotide is from 5-100 nucleotides in length and is complementary to a second segment of the nucleotide sequence that is 5′ relative to the oligonucleotide probe, such that the enhancer oligonucleotide is located 3′ relative to the detection oligonucleotide probe when both oligonucleotides are hybridized to the nucleic acid; wherein a single base gap exists between the first segment and the second segment, such that when the oligonucleotide probe and the enhancer oligonucleotide probe are both hybridized to the nucleic acid, a single base gap exists between the oligonucleotides; and wherein treating the nucleic acid with the endonuclease will cleave the detectable label from the 3' terminus of the detection probe to release free detectable label when the detection probe is hybridized to the nucleic acid.

The polymorphic markers described herein as predictive of risk of cardiac arrhythmia (e.g., AF and Atrial flutter) and stroke are useful as diagnostic markers. In aspect, the invention therefore relates to the use of an oligonucleotide probe in the manufacture of a diagnostic reagent for diagnosing and/or assessing susceptibility to cardiac arrhythmia and/or stroke in a human individual, wherein the probe hybridizes to a segment of a nucleic acid whose nucleotide sequence is given by SEQ ID NO:50 that comprises at least one polymorphic site, wherein the fragment is 15-500 nucleotides in length.

In one such embodiment, the polymorphic site is selected from the polymorphic markers set forth in Table 5, and polymorphisms in linkage disequilibrium therewith. In another embodiment, the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51),

Computer-readable medium for storing information about disease-associated markers as described herein are also within scope of the present invention. In one such aspect, the invention relates to a computer-readable medium on which is stored an identifier for at least one polymorphic marker; an indicator of the frequency of at least one allele of said at least one polymorphic marker in a plurality of individuals diagnosed with atrial fibrillation, atrial flutter and/or stroke; and an indicator of the frequency of the least one allele of said at least one polymorphic markers in a plurality of reference individuals; wherein the at least one polymorphic marker is selected from the polymorphic markers set forth in Table 5, and polymorphisms in linkage disequilibrium therewith. In a preferred embodiment, the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51).

The invention also related to an apparatus for determining a genetic indicator for cardiac arrhythmia and/or stroke in a human individual, comprising: a computer readable memory; and a routine stored on the computer readable memory; wherein the routine is adapted to be executed on a processor to analyze genotype and/or haplotype data for at least one human individual with respect to at least one polymorphic marker selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith, and generate an output based on the marker or haplotype data, wherein the output comprises a risk measure of the at least one marker or haplotype as a genetic indicator of cardiac arrhythmia and/or stroke for the human individual. In a preferred embodiment, the routine further comprises determining an indicator of the frequency of at least one allele of at least one polymorphic marker and/or at least one haplotype in a plurality of individuals diagnosed with cardiac arrhythmia and/or stroke, and an indicator of the frequency of at the least one allele of at least one polymorphic marker or at least one haplotype in a plurality of reference individuals, and calculating a risk measure for the at least one allele and/or haplotype based thereupon; and wherein a risk measure for the individual is calculated based on a comparison of the at least one marker and/or haplotype status for the individual to the calculated risk for the at least one marker and/or haplotype information for the plurality of individuals diagnosed with atrial fibrillation, atrial flutter and/or stroke. In certain embodiments, the risk measure is characterized by an Odds Ratio (OR) or a Relative Risk (RR), as described in more detail herein.

The polymorphic markers discovered in the present invention as predictive of a susceptibility of cardiac arrhythmia and stroke, as described, as well as markers in linkage disequilibrium therewith, are all useful for practicing the various aspects of the present invention. Thus, although particular polymorphic markers were used by the present inventors do detect an association of a particular region on chromosome 4 to cardiac arrhythmia (e.g, atrial fibrillation and atrial flutter) and stroke, it is equally useful to assess markers in strong linkage disequilibrium with those markers. As a consequence, in one embodiment of the methods, uses, kits, procedures, apparatus and media of the invention, the at least one polymorphic marker or haplotype useful in the methods or procedure of the invention comprises at least one of the markers set forth in Table 5 (e.g., Table 5A and Table 5B) and markers in linkage disequilibrium therewith. In another embodiment, the at least one polymorphic marker or haplotype comprises at least one of the markers set forth in Table 9, and markers in linkage disequilibrium therewith. In one embodiment, the at least one polymorphic marker or haplotype comprises at least one of the markers set forth in Table 5. In another embodiment, the at least one polymorphic marker or haplotype comprises at least one of the markers set forth in Table 9. In another embodiment, the at least one polymorphic marker is selected from the markers set forth in Table 4. In one embodiment, the at least one marker is selected from marker rs2220427 (SEQ ID NO:1) and marker rs10033464 (SEQ ID NO:41), and markers in linkage disequilibrium therewith.

In another embodiment, the at least one polymorphic marker is selected from the markers set forth in Table 19.

In one embodiment, the at least one marker or haplotype comprises at least one of markers D4S406 (SEQ ID NO:45), rs2723296 (SEQ ID NO:35), rs16997168 (SEQ ID NO:36), rs2723316 (SEQ ID NO:37), rs6419178 (SEQ ID NO:38), rs1448817 (SEQ ID NO:39), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs13105878 (SEQ ID NO: 40), rs10033464 (SEQ ID NO:41), rs13141190 (SEQ ID NO:42), rs3853444 (SEQ ID NO:43), and rs4576077 (SEQ ID NO:44). In another embodiment, the at least one marker or haplotype comprises at least one of the markers D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51), In yet another embodiment, the at least one marker is selected from rs10033464, rs2200733, rs13143308 and rs2220427, and markers in linkage disequilibrium therewith.

In a further embodiment, the presence of alleles -2, -4 and/or -8 of marker D4S406, allele G of marker rs2723296, allele T of marker rs16997168, allele T of marker rs2723316, allele A of marker rs6419178, allele G of marker rs1448817, allele A of marker rs2634073, allele T of marker rs2200733, allele T of marker rs2220427, allele C of marker rs13105878, allele T of marker rs10033464, allele A of marker rs13141190, allele A of marker rs3853444, and/or allele T of marker rs4576077 is indicative of increased susceptibility of cardiac arrhythmia or stroke in the individual.

In particular embodiments of the invention, the susceptibility conferred by the at-risk variant (i.e. a particular allele at a polymorphic marker (e.g, a SNP) or a particular haplotype) is increased susceptibility, i.e. the markers and haplotypes of the invention confer increased risk of an individual develops cardiac arrhtythmia, including atrial fibrillation and atrial flutter, and stroke. Susceptibility is typically characterized by the measure Odds Ratio (OR) or, alternatively, by a Relative Risk (RR). In one embodiment, the increased susceptibility is characterized by an odds ratio (OR) of at least 1.3. In another embodiment, the increased susceptibility is characterized by an odds ratio (OR) of at least 1.4. In another embodiment, the increased susceptibility characterized by an odds ratio (OR) of at least 1.5. In another embodiment, the increased susceptibility characterized by an odds ratio (OR) or relative risk (RR) of at least 1.6. In yet another embodiment, the increased susceptibility characterized by an odds ratio (OR) or relative risk (RR) of at least 1.8. Other embodiments relate to other values for OR, or comparable values for RR including values of 1.25, 1.35, 1.45, 1.55, etc.

Certain embodiments of the invention relate to individuals of a particular ethnicity or ancestry. In one such embodiment, the human individual has ancestry selected from

black African ethnicity, Asian ethnicity, Caucasian ethnicity, Hispanic ethnicity, and Arabic ethnicity. In particular embodiments, the ethnicity is self-reported. In other embodiments, ancestry is determined by the assessment of particular ethnicity-specific genetic markers.

BRIEF DESCRIPTION OF THE FIGURES

The foregoing and other objects, features and advantages of the invention will be apparent from the following more particular description of preferred embodiments of the invention.

FIG. 1 Shows a plot of linkage disequilibrium (LD) in the region comprising variants of the present invention for the CEPH population (HapMap data). The LD block C04 (111,954,811 - 112,104,250 on Chromosome 4, NCBI Build 35 positions) is indicated on the Figure by a black box. The plot shows two measures of LD, i.e. D' in the upper and left part of Figure 1 and r^2 in the lower and right part of the figure.

FIG. 2 Shows a schematic of the haplotype structure at the associated region within the LD block. The areas of the dark (left) circles are proportional to the haplotype frequencies of the haplotypes in Iceland and the areas of the light (right) circles are proportional to the haplotype frequencies in Hong Kong. The intermediary haplotype, shown in the middle of the graph, no longer exists with certainty in either of the two populations (its estimated frequency is less than 0.2% which is indistinguishable from genotyping errors).

FIG .3 Is an overview of a 200kb genomic neighborhood of rs2200733 and rs10033464. It includes predicted ESTs, the locations of the three main classes of equivalent SNPs in the CEU HapMap samples and an overview of the LD structure of the region in the various ethnic HapMap samples.

FIG 4. Shows Northern Blot analysis of PITX2 expression in human heart and aorta..

The PITX2 cDNA clone HU3_p983E0327D was used as a probe and detected 1.8, 2 and 3 kb transcripts and 2.2 and 3 kb PITX2 transcripts in left atrium and aorta respectively. Lane 1: Fetal heart, lane 2: Whole heart, lane 3: Aorta, lane 4: Apex of the heart, lane 5: Left atrium, lane 6: Right atrium, lane 7: Left ventricle lane 8: Right ventricle. Blot probed with PITX2 cDNA clone (HU3_p983E0327D).

DETAILED DESCRIPTION OF THE INVENTION

A description of preferred embodiments of the invention follows.

Definitions

The following terms shall, in the present context, have the meaning as indicated:

Atrial fibrillation (AF), as described herein, refers to AF as commonly defined according to established medical criteria. AF classified by ICD-10 in class I48 and by ICD-9 in class 427.3

Atrial flutter (AFl), as described herein, refers to AFl as commonly defined according to established medical criteria. Afl is classified ICD-10 class I48 and by ICD-9 in class 427.32.

A "polymorphic marker", sometime referred to as a "marker", as described herein, refers to a genomic polymorphic site. Each polymorphic marker has at least two sequence variations characteristic of particular alleles at the polymorphic site. Thus, genetic association to a polymorphic marker implies that there is association to at least one specific allele of that particular polymorphic marker. The marker can comprise any allele of any variant type found in the genome, including SNPs, microsatellites, insertions, deletions, duplications and translocations.

An "allele" refers to the nucleotide sequence of a given locus (position) on a chromosome. A polymorphic marker allele thus refers to the composition (i.e., sequence) of the marker on a chromosome. Genomic DNA from an individual contains two alleles for any given polymorphic marker, representative of each copy of the marker on each chromosome.

A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules) is referred to herein as a "polymorphic site".

A "Single Nucleotide Polymorphism" or "SNP" is a DNA sequence variation occurring when a single nucleotide at a specific location in the genome differs between members of a species or between paired chromosomes in an individual. Most SNP polymorphisms have two alleles. Each individual is in this instance either homozygous for one allele of the polymorphism (i.e. both chromosomal copies of the individual have the same nucleotide at the SNP location), or the individual is heterozygous (i.e. the two sister chromosomes of the individual contain different nucleotides). The SNP nomenclature as reported herein refers

to the official Reference SNP (rs) ID identification tag as assigned to each unique SNP by the National Center for Biotechnological Information (NCBI).

A "variant", as described herein, refers to a segment of DNA that differs from the reference DNA. A "marker" or a "polymorphic marker", as defined herein, is a variant. Alleles that differ from the reference are referred to as "variant" alleles.

A "microsatellite" is a polymorphic marker that has multiple small repeats of bases that are 2-8 nucleotides in length (such as CA repeats) at a particular site, in which the number of repeat lengths varies in the general population. An "indel" is a common form of polymorphism comprising a small insertion or deletion that is typically only a few nucleotides long.

A "haplotype," as described herein, refers to a segment of genomic DNA that is characterized by a specific combination of alleles arranged along the segment. For diploid organisms such as humans, a haplotype comprises one member of the pair of alleles for each polymorphic marker or locus . In a certain embodiment, the haplotype can comprise two or more alleles, three or more alleles, four or more alleles, or five or more alleles.

The term "susceptibility", as described herein, encompasses both increased susceptibility and decreased susceptibility. Thus, particular polymorphic markers and/or haplotypes of the invention may be characteristic of increased susceptibility (i.e., increased risk) of atrial fibrillation or stroke, as characterized by a relative risk (RR) or odds ratio (OR) of greater than one. Alternatively, the markers and/or haplotypes of the invention are characteristic of decreased susceptibility (i.e., decreased risk) of atrial fibrillation or stroke, as characterized by a relative risk of less than one.

A "nucleic acid sample" is a sample obtained from an individuals that contains nucleic acid. In certain embodiments, i.e. the detection of specific polymorphic markers and/or haplotypes, the nucleic acid sample comprises genomic DNA. Such a nucleic acid sample can be obtained from any source that contains genomic DNA, including as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs.

The term "atrial fibrillation and/or stroke therapeutic agent" refers to an agent that can be used to ameliorate or prevent symptoms associated with atrial fibrillation (AF), atrial flutter (AFl) or stroke, as described in more detail herein.

The term "cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke -associated nucleic acid", as described herein, refers to a nucleic acid that has been found to be associated to cardiac arrhythmia, *e.g.,* atrial fibrillation (AF), atrial flutter (AFl) or stroke. This includes, but is not limited to, the markers and haplotypes described herein

and markers and haplotypes in strong linkage disequilibrium (LD) therewith. In one embodiment, an atrial fibrillation, atrial flutter or stroke-associated nucleic acid refers to the LD-block C04 found to be associated with atrial fibrillation and stroke. In another embodiment, the atrial fibrillation, atrial flutter or stroke-associated nucleic acid refers to the PITX2 gene.

The term "LD Block C04", as described herein, refers to the Linkage Disequilibrium (LD) block on Chromosome 4 between position 111,954,811 and 112,104,250 of NCBI (National Center for Biotechnology Information) Build 35, with the genomic sequence as set forth in SEQ ID NO:50.

The term "fragment", as described herein, refers to a segment of a nucleic acid or protein sequence. Fragments are of size smaller than their reference point, i.e. a fragment of a reference nucleic acid molecule that is 1000 nucleotides in size is smaller than 1000 nucleotides in size. Nucleic acid fragments of the invention are commonly more than 5 nucleotides in size and typically more than 15 nucleotides in size, with an upper limit as defined by either their reference nucleotide or by the practical utility of the nucleotide fragment. For example, nucleotide fragments useful as hybridization probes in some embodiments of the invention are more than 15 nucleotides and less than about 500 nucleotides in size. Other size ranges will apply for other nucleotide fragments and protein or peptide fragments of the invention.

The term "PITX2", as described herein, refers to the paired-like homeodomain transcription factor 2 gene on chromosome 4q25. This gene is also referred to as pituitary homeobox 2 (PTX2), rieg bicoid-related homeobox transcription factor 1 (RIEG1), solurshin, and all-1 responsive gene 1 (ARP1).

The present invention relates to the observation that certain polymorphic markers on chromosome 4q25 of the human genome have been found to be associated with cardiac arrhythmia an stroke. In particular embodiments of the invention, polymorphic markers at chromosome 4q25 are associated with the cardiac arrhythmias Atrial fibrillation (AF) and Atrial flutter (AFl), and stroke. These observation have important and unforeseen implications for the development of diagnostic and therapeutics methods, uses, kits and systems, as described in further detail herein.

In a genome-wide scan for genetic variants conferring susceptibility to AF, several markers on chromosome 4q25 were found to be associated with AF. The most significant association was found for markers rs2220427 and rs2220733, both of which gave p-values close to 10^{-9} (Table 2) for AF, and smaller, but nominally significant association to stroke

(Table 3). A large number of markers were identified as perfect surrogates for these markers, including the microsatellite marker D4S406 (Table 1) and a number of SNP markers (Table 4).

Further refinement of the results revealed that the association signal appears to center, in genetic terms, to markers of rs2200733 and rs10033464 (Table 7) and markers in linkage disequilibrium with those markers (including, but not limited to, the SNP markers listed in Table 9).

The original observation in the Icelandic population was replicated in an independent Icelandic AF/AFl cohort, in a Swedish AF cohort, and in a US AF cohort (Table 7). When combined with the Icelandic samples, the association to rs2200733 was unequivocal (OR = 1.72, $P = 3.3 \times 10^{-41}$), and the significance of rs10033464 was well beyond the threshold of genome-wide significance (OR = 1.39, $P = 6.9 \times 10^{-11}$). Assuming the multiplicative model, the population attributable risk (PAR) of the two variants combined is approximately 20% in populations of European ancestry. Furthermore, the association replicated in a Chinese AF cohort from Hong Kong (Table 7).

The inventors have also found that age at diagnosis of AF/AFl for the Icelandic samples correlates with the two SNPs rs2200733 and rs10033464. Thus, diagnosis occurs 2.28 years earlier per T allele of rs2200733 and 1.10 years earlier per T allele of rs10033464 (joint $P = 1.29 \times 10^{-6}$). This effect is manifested by the association of the two variants being strongest in those diagnosed at a younger age, although the risk remains significant even in those diagnosed after reaching 80 years of age (Table 8). A similar age at onset effect is observed in the US cohort (Table 8).

The inventors have also observed a strong association between the variants and AFl, that appears to be even stronger than for AF. Thus is revealed by the association to the subset (N=116) of the Icelandic patients that have a diagnosis of AFl (OR = 2.60, 95% confidence interval (CI) = 1.83-3.68, $P = 7.5 \times 10^{-8}$ for rs2200733, OR = 1.94, 95% CI = 1.26-3.00, $P = .0028$ for rs10033464). In fact, for rs2200733, the OR for these definite AFl cases is significantly higher than that for the cases with an AF phenotype ($P = 0.0026$), and close to significantly higher for rs10033464 ($P = .084$). These results that both AF and AFl have significant genetic risk factors that are illustrated by the association to SNPs rs2200733 and rs10033464.

The inventors have furthermore established that the variants associating with AF/AFl also associated with stroke, in particular ischemic stroke (Table 21). Marker rs2200733 replicated significantly in Ischemic stroke and in the Ischemic stroke (IS) subphenotype cardioembolic stroke (CES). Both this marker and marker rs10033464 were found, after genotyping additional Icelandic IS cases and controls (total 1,943

cases/25,708 controls) and four large IS case/control replication sets (4,294 cases/3,709 controls), to associate most strongly with the CES, of which AF is the primary cause, (rs2200733: OR=1.53, $P=1.5\times10^{-12}$; rs10033464: OR=1.27, $P=5.9\times10^{-4}$) (Table 21).

There is no known gene present in the LD block containing rs2200733 and rs10033464 (Figure 3). The LD block contains one spliced EST (DA725631) and two single-exon ESTs (DB324364 and AF017091). RT-PCR of cDNA libraries from various tissues did not detect the expression of these ESTs (Table 16). The *PITX2* gene located in the adjacent upstream LD block is the gene closest to the risk variants. Several markers within the LD block containing *PITX2* gene are correlated to the markers showing association to AF and Afl, as shown in Table 18. It is therefore possible that variants within the *PITX2* gene are the underlying causative variants. Alternatively, it is possible that the variants of the present invention, as described herein, affect the function, stability, expression, post-translational modification, splicing, message stability of *PITX2*, or by other means affect the gene so as to predispose to the symptoms associated with atrial fibrillation, atrial flutter and/or stroke. The protein encoded by this gene, the paired-like homeodomain transcription factor 2, is an interesting candidate for AF/AFl as it is known to play an important role in cardiac development by directing asymmetric morphogenesis of the heart (Franco, D., Trends Cardiovasc Med 13: 157-63 (2003)). Furthermore, in a mouse knockout model Pitx2 has been shown to suppress a default pathway for sinoatrial node formation in the left atrium. There is very little mRNA expression of *PITX2* in all easily accessible tissues, such as blood and adipose tissue, hampering the study of correlation between genotypes and expression levels. The next gene upstream of *PITX2* is *ENPEP*, an aminopeptidase responsible for the breakdown of angiotensin II in the vascular endothelium. This gene is expressed more widely, but the variants associated with AF showed no correlation to its expression in blood or adipose tissue. No other annotated genes are located within a 400kb region upstream and 1.5 Mb regions downstream of the associated variants.

Assessment for markers and haplotypes

The genomic sequence within populations is not identical when individuals are compared. Rather, the genome exhibits sequence variability between individuals at many locations in the genome. Such variations in sequence are commonly referred to as polymorphisms, and there are many such sites within each genome For example, the human genome exhibits sequence variations which occur on average every 500 base pairs. The most common sequence variant consists of base variations at a single base position in the genome, and such sequence variants, or polymorphisms, are commonly called Single Nucleotide Polymorphisms ("SNPs"). These SNPs are believed to have occurred in a single

mutational event, and therefore there are usually two possible alleles possible at each SNPsite; the original allele and the mutated allele. Due to natural genetic drift and possibly also selective pressure, the original mutation has resulted in a polymorphism characterized by a particular frequency of its alleles in any given population. Many other types of sequence variants are found in the human genome, including microsatellites, insertions, deletions, inversions and copy number variations. A polymorphic microsatellite has multiple small repeats of bases (such as CA repeats, TG on the complimentary strand) at a particular site in which the number of repeat lengths varies in the general population. In general terms, each version of the sequence with respect to the polymorphic site represents a specific allele of the polymorphic site. These sequence variants can all be referred to as polymorphisms, occurring at specific polymorphic sites characteristic of the sequence variant in question. In general terms, polymorphisms can comprise any number of specific alleles. Thus in one embodiment of the invention, the polymorphism is characterized by the presence of two or more alleles in any given population. In another embodiment, the polymorphism is characterized by the presence of three or more alleles. In other embodiments, the polymorphism is characterized by four or more alleles, five or more alleles, six or more alleles, seven or more alleles, nine or more alleles, or ten or more alleles. All such polymorphisms can be utilized in the methods and kits of the present invention, and are thus within the scope of the invention.

In some instances, reference is made to different alleles at a polymorphic site without choosing a reference allele. Alternatively, a reference sequence can be referred to for a particular polymorphic site. The reference allele is sometimes referred to as the "wild-type" allele and it usually is chosen as either the first sequenced allele or as the allele from a "non-affected" individual (*e.g.,* an individual that does not display a trait or disease phenotype).

Alleles for SNP markers as referred to herein refer to the bases A, C, G or T as they occur at the polymorphic site in the SNP assay employed. The allele codes for SNPs used herein are as follows: 1= A, 2=C, 3=G, 4=T. The person skilled in the art will however realise that by assaying or reading the opposite DNA strand, the complementary allele can in each case be measured. Thus, for a polymorphic site (polymorphic marker) characterized by an A/G polymorphism, the assay employed may be designed to specifically detect the presence of one or both of the two bases possible, i.e. A and G. Alternatively, by designing an assay that is designed to detect the opposite strand on the DNA template, the presence of the complementary bases T and C can be measured. Quantitatively (for example, in terms of relative risk), identical results would be obtained from measurement of either DNA strand (+ strand or – strand).

Typically, a reference sequence is referred to for a particular sequence. Alleles that differ from the reference are sometimes referred to as "variant" alleles. A variant

sequence, as used herein, refers to a sequence that differs from the reference sequence but is otherwise substantially similar. Alleles at the polymorphic genetic markers described herein are variants. Additional variants can include changes that affect a polypeptide. Sequence differences, when compared to a reference nucleotide sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence,. Such sequence changes can alter the polypeptide encoded by the nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a disease or trait can be a synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of an encoded polypeptide. It can also alter DNA to increase the possibility that structural changes, such as amplifications or deletions, occur at the somatic level. The polypeptide encoded by the reference nucleotide sequence is the "reference" polypeptide with a particular reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as "variant" polypeptides with variant amino acid sequences. A sequence or a reference sequence can either represent the (+) or (-) direction of double stranded DNA. Such sequences are related as being the reverse complement of one another, as well known to the skilled person.

A haplotype refers to a segment of DNA that is characterized by a specific combination of alleles arranged along the segment. For diploid organisms such as humans, a haplotype comprises one member of the pair of alleles for each polymorphic marker or locus . In a certain embodiment, the haplotype can comprise two or more alleles, three or more alleles, four or more alleles, or five or more alleles, each allele corresponding to a specific polymorphic marker along the segment. Haplotypes can comprise a combination of various polymorphic markers, *e.g.*, SNPs and microsatellites, having particular alleles at the polymorphic sites. The haplotypes thus comprise a combination of alleles at various genetic markers.

Detecting specific polymorphic markers and/or haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites. For example,

standard techniques for genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescence-based techniques (Chen, X. *et al., Genome Res. 9(5)*: 492-98 (1999)), utilizing PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. Specific methodologies available for SNP genotyping include, but are not limited to, TaqMan genotyping assays and SNPlex platforms (Applied Biosystems), mass spectrometry (*e.g.,* MassARRAY system from Sequenom), minisequencing methods, real-time PCR, Bio-Plex system (BioRad), CEQ and SNPstream systems (Beckman), Molecular Inversion Probe array technology (*e.g.,* Affymetrix GeneChip), and BeadArray Technologies (*e.g.,* Illumina GoldenGate and Infinium assays). By these or other methods available to the person skilled in the art, one or more alleles at polymorphic markers, including microsatellites, SNPs or other types of polymorphic markers, can be identified.

In certain methods described herein, an individual who is at an increased susceptibility (i.e., increased risk) for any specific disease or trait under study, is an individual in whom at least one specific allele at one or more polymorphic marker or haplotype conferring increased susceptibility for the disease or trait is identified (i.e., at-risk marker alleles or haplotypes). In one aspect, the at-risk marker or haplotype is one that confers a significant increased risk (or susceptibility) of the disease or trait. In one embodiment, significance associated with a marker or haplotype is measured by a relative risk (RR). In another embodiment, significance associated with a marker or haplotye is measured by an odds ratio (OR). In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant increased risk is measured as a risk (relative risk and/or odds ratio) of at least 1.2, including but not limited to: at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, 1.8, at least 1.9, at least 2.0, at least 2.5, at least 3.0, at least 4.0, and at least 5.0. In a particular embodiment, a risk (relative risk and/or odds ratio)of at least 1.2 is significant. In another particular embodiment, a risk of at least 1.3 is significant. In yet another embodiment, a risk of at least 1.4 is significant. In a further embodiment, a relative risk of at least about 1.5 is significant. In another further embodiment, a significant increase in risk is at least about 1.7 is significant. However, other cutoffs are also contemplated, e.g. at least 1.15, 1.25, 1.35, and so on, and such cutoffs are also within scope of the present invention. In other embodiments, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 150%, 200%, 300%, and 500%. In one particular embodiment, a significant increase in risk is at least 20%. In other embodiments, a significant increase in risk is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90% and at least 100%. Other cutoffs or ranges as deemed suitable by the person skilled in the art to characterize the invention are however also contemplated, and those are also within scope of the present invention.

An at-risk polymorphic marker or haplotype of the present invention is one where at least one allele of at least one marker or haplotype is more frequently present in an individual at risk for the disease or trait (e.g., cardiac arrhythmia or stroke) (affected), compared to the frequency of its presence in a comparison group (control), and wherein the presence of the marker or haplotype is indicative of susceptibility to the disease or trait. The control group may in one embodiment be a population sample, i.e. a random sample from the general population. In another embodiment, the control group is represented by a group of individuals who are disease-free. Such disease-free control may in one embodiment be characterized by the absence of one or more specific disease-associated symptoms. In another embodiment, the disease-free control group is characterized by the absence of one or more disease-specific risk factors. Such risk factors are in one embodiment at least one environmental risk factor. Representative environmental factors are natural products, minerals or other chemicals which are known to affect, or contemplated to affect, the risk of developing the specific disease or trait. Other environmental risk factors are risk factors related to lifestyle, including but not limited to food and drink habits, geographical location of main habitat, and occupational risk factors. In another embodiment, the risk factors are at least one genetic risk factor.

As an example of a simple test for correlation would be a Fisher-exact test on a two by two table. Given a cohort of chromosomes, the two by two table is constructed out of the number of chromosomes that include both of the markers or haplotypes, one of the markers or haplotypes but not the other and neither of the markers or haplotypes.

In other embodiments of the invention, an individual who is at a decreased susceptibility (i.e., at a decreased risk) for the disease or trait is an individual in whom at least one specific allele at one or more polymorphic marker or haplotype conferring decreased susceptibility for the disease or trait is identified. The marker alleles and/or haplotypes conferring decreased risk are also said to be protective. In one aspect, the protective marker or haplotype is one that confers a significant decreased risk (or susceptibility) of the disease or trait. In one embodiment, significant decreased risk is measured as a relative risk of less than 0.9, including but not limited to less than 0.9, less than 0.8, less than 0.7, less than 0.6, less than 0.5, less than 0.4, less than 0.3, less than 0.2 and less than 0.1. In one particular embodiment, significant decreased risk is less than 0.7. In another embodiment, significant decreased risk is less than 0.5. In yet another embodiment, significant decreased risk is less than 0.3. In another embodiment, the decrease in risk (or susceptibility) is at least 20%, including but not limited to at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% and at least 98%. In one particular embodiment, a significant decrease in risk is at least about 30%. In another embodiment, a significant decrease in risk at least about 50%. In another embodiment, the decrease in risk

is at least about 70%. Other cutoffs or ranges as deemed suitable by the person skilled in the art to characterize the invention are however also contemplated, and those are also within scope of the present invention.

The person skilled in the art will appreciate that for markers with two alleles present in the population being studied, and wherein one allele is found in increased frequency in a group of individuals with a trait or disease in the population, compared with controls, the other allele of the marker will be found in decreased frequency in the group of individuals with the trait or disease, compared with controls. In such a case, one allele of the marker (the one found in increased frequency in individuals with the trait or disease) will be the at-risk allele, while the other allele will be a protective allele.

Linkage Disequilibrium

The natural phenomenon of recombination, which occurs on average once for each chromosomal pair during each meiotic event, represents one way in which nature provides variations in sequence (and biological function by consequence). It has been discovered that recombination does not occur randombly in the genome; rather, there are large variations in the frequency of recombination rates, resulting in small regions of high recombination frequency (also called recombination hotspots) and larger regions of low recombination frequency, which are commonly referred to as Linkage Disequilibrium (LD) blocks (Myers, S. *et al., Biochem Soc Trans* 34:526-530 (2006); Jeffreys, A.J., *et al.,Nature Genet* 29:217-222 (2001); May, C.A., *et al., Nature Genet* 31:272-275(2002)).

Linkage Disequilibrium (LD) refers to a non-random assortment of two genetic elements. For example, if a particular genetic element (*e.g.*, an allele of a polymorphic marker, or a haplotype) occurs in a population at a frequency of 0.25 (25%) and another element occurs at a frequency of 0.25 (25%), then the predicted occurrance of a person's having both elements is 0.125 (12.5%), assuming a random distribution of the elements. However, if it is discovered that the two elements occur together at a frequency higher than 0.125, then the elements are said to be in linkage disequilibrium, since they tend to be inherited together at a higher rate than what their independent frequencies of occurrence (*e.g.,* allele or haplotype frequencies) would predict. Roughly speaking, LD is generally correlated with the frequency of recombination events between the two elements. Allele or haplotype frequencies can be determined in a population by genotyping individuals in a population and determining the frequency of the occurence of each allele or haplotype in the population. For populations of diploids, *e.g.*, human populations, individuals will typically have two alleles for each genetic element (*e.g.*, a marker, haplotype or gene).

Many different measures have been proposed for assessing the strength of linkage disequilibrium (LD). Most capture the strength of association between pairs of biallelic sites. Two important pairwise measures of LD are r^2 (sometimes denoted Δ^2) and |D'|. Both measures range from 0 (no disequilibrium) to 1 ('complete' disequilibrium), but their interpretation is slightly different. |D'| is defined in such a way that it is equal to 1 if just two or three of the possible haplotypes are present, and it is <1 if all four possible haplotypes are present. Therefore, a value of |D'| that is <1 indicates that historical recombination may have occurred between two sites (recurrent mutation can also cause |D'| to be <1, but for single nucleotide polymorphisms (SNPs) this is usually regarded as being less likely than recombination). The measure r^2 represents the statistical correlation between two sites, and takes the value of 1 if only two haplotypes are present.

The r^2 measure is arguably the most relevant measure for association mapping, because there is a simple inverse relationship between r^2 and the sample size required to detect association between susceptibility loci and SNPs. These measures are defined for pairs of sites, but for some applications a determination of how strong LD is across an entire region that contains many polymorphic sites might be desirable (*e.g.*, testing whether the strength of LD differs significantly among loci or across populations, or whether there is more or less LD in a region than predicted under a particular model). Measuring LD across a region is not straightforward, but one approach is to use the measure r, which was developed in population genetics. Roughly speaking, r measures how much recombination would be required under a particular population model to generate the LD that is seen in the data. This type of method can potentially also provide a statistically rigorous approach to the problem of determining whether LD data provide evidence for the presence of recombination hotspots. For the methods and procedures described herein, a significant r^2 value can be at least 0.1 such as at least 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45, 0.5, 0.55, 0.6, 0.65, 0.7, 0.75, 0.8, 0.85, 0.9, 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99 or 1.0. In one preferred embodiment, the significant r^2 value can be at least 0.2. Alternatively, linkage disequilibrium as described herein, refers to linkage disequilibrium characterized by values of |D'| of at least 0.2, such as 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.85, 0.9, 0.95, 0.96, 0.97, 0.98, 0.99. Thus, linkage disequilibrium represents a correlation between alleles of distinct markers. It is measured by correlation coefficient or |D'| (r^2 up to 1.0 and |D'| up to 1.0). Linkage disequilibrium can be determined in a single human population, as defined herein, or it can be determined in a collection of samples comprising individuals from more than one human population. In one embodiment of the invention, LD is determined in a sample from one or more of the HapMap populations (caucasian, african, japanese, chinese), as defined (http://www.hapmap.org). In one such embodiment, LD is determined in the CEU population of the HapMap samples. In another embodiment, LD is determined in the YRI

population. In yet another embodiment, LD is determined in samples from the Icelandic population.

If all polymorphisms in the genome were identical at the population level, then every single one of them would need to be investigated in association studies. However, due to linkage disequilibrium between polymorphisms, tightly linked polymorphisms are strongly correlated, which reduces the number of polymorphisms that need to be investigated in an association study to observe a significant association. Another consequence of LD is that many polymorphisms may give an association signal due to the fact that these polymorphisms are strongly correlated.

Genomic LD maps have been generated across the genome, and such LD maps have been proposed to serve as framework for mapping disease-genes (Risch, N. & Merkiangas, K, *Science* 273:1516-1517 (1996); Maniatis, N., *et al., Proc Natl Acad Sci USA* 99:2228-2233 (2002); Reich, DE *et al, Nature* 411:199-204 (2001)).

It is now established that many portions of the human genome can be broken into series of discrete haplotype blocks containing a few common haplotypes; for these blocks, linkage disequilibrium data provides little evidence indicating recombination (see, *e.g.,* Wall., J.D. and Pritchard, J.K., *Nature Reviews Genetics 4*:587-597 (2003); Daly, M. *et al., Nature Genet. 29*:229-232 (2001); Gabriel, S.B. *et al., Science 296*:2225-2229 (2002); Patil, N. *et al., Science 294*:1719-1723 (2001); Dawson, E. *et al., Nature 418*:544-548 (2002); Phillips, M.S. *et al., Nature Genet. 33*:382-387 (2003)).

There are two main methods for defining these haplotype blocks: Blocks can be defined as regions of DNA that have limited haplotype diversity (see, *e.g.,* Daly, M. *et al., Nature Genet. 29*:229-232 (2001); Patil, N. *et al., Science 294*:1719-1723 (2001); Dawson, E. *et al., Nature 418*:544-548 (2002); Zhang, K. *et al., Proc. Natl. Acad. Sci. USA 99*:7335-7339 (2002)), or as regions between transition zones having extensive historical recombination, identified using linkage disequilibrium (see, *e.g.,* Gabriel, S.B. *et al., Science 296*:2225-2229 (2002); Phillips, M.S. *et al., Nature Genet. 33*:382-387 (2003); Wang, N. *et al., Am. J. Hum. Genet. 71*:1227-1234 (2002); Stumpf, M.P., and Goldstein, D.B., *Curr. Biol. 13*:1-8 (2003)). More recently, a fine-scale map of recombination rates and corresponding hotspots across the human genome has been generated (Myers, S., *et al., Science* 310:321-32324 (2005); Myers, S. *et al., Biochem Soc Trans* 34:526530 (2006)). The map reveals the enormous variation in recombination across the genome, with recombination rates as high as 10-60 cM/Mb in hotspots, while closer to 0 in intervening regions, which thus represent regions of limited haplotype diversity and high LD. The map can therefore be used to define haplotype blocks/LD blocks as regions flanked by recombination hotspots. As used herein, the terms "haplotype block" or "LD

block" includes blocks defined by any of the above described characteristics, or other alternative methods used by the person skilled in the art to define such regions.

Haplotype blocks can be used to map associations between phenotype and haplotype status, using single markers or haplotypes comprising a plurality of markers. The main haplotypes can be identified in each haplotype block, and then a set of "tagging" SNPs or markers (the smallest set of SNPs or markers needed to distinguish among the haplotypes) can then be identified. These tagging SNPs or markers can then be used in assessment of samples from groups of individuals, in order to identify association between phenotype and haplotype. If desired, neighboring haplotype blocks can be assessed concurrently, as there may also exist linkage disequilibrium among the haplotype blocks.

It has thus become apparent that for any given observed association to a polymorphic marker in the genome, it is likely that additional markers in the genome also show association. This is a natural consequence of the uneven distribution of LD across the genome, as observed by the large variation in recombination rates. The markers used to detect association thus in a sense represent "tags" for a genomic region (i.e., a haplotype block or LD block) that is associating with a given disease or trait, and as such are useful for use in the methods and kits of the present invention. One or more causative (functional) variants or mutations may reside within the region found to be associating to the disease or trait. Such variants may confer a higher relative risk (RR) or odds ratio (OR) than observed for the tagging markers used to detect the association. The present invention thus refers to the markers used for detecting association to the disease, as described herein, as well as markers in linkage disequilibrium with the markers. Thus, in certain embodiments of the invention, markers that are in LD with the markers and/or haplotypes of the invention, as described herein, may be used as surrogate markers. The surrogate markers have in one embodiment relative risk (RR) and/or odds ratio (OR) values smaller than for the markers or haplotypes initially found to be associating with the disease, as described herein. In other embodiments, the surrogate markers have RR or OR values greater than those initially determined for the markers initially found to be associating with the disease, as described herein. An example of such an embodiment would be a rare, or relatively rare (< 10% allelic population frequency) variant in LD with a more common variant (> 10% population frequency) initially found to be associating with the disease, such as the variants described herein. Identifying and using such markers for detecting the association discovered by the inventors as described herein can be performed by routine methods well known to the person skilled in the art, and are therefore within the scope of the present invention.

It is possible that certain polymorphic markers in linkage disequilibrium with the markers shown herein to be associated with cardiac arrhythmia (e.g., atrial fibrillation and atrial flutter) and stroke are located outside the physical boundaries of the LD block C04

as defined herein by the sequence set forth in SEQ ID NO:50. This is a consequence of the historical recombination rates in the region in question, which may have led to a region of strong LD (the LD block), with residual markers outside the block in LD with markers within the block. Such markers are also within scope of the present invention, as they are also useful for practicing the invention by virtue of their genetic relationship with the markers shown herein to be associated with cardiac arrhythmia and stroke. Examples of such markers are shown in Table 18 (rs7668322 (SEQ ID NO:46), rs2197815 (SEQ ID NO:47), rs6831623 (SEQ ID NO:48), rs2595110 (SEQ ID NO:49))

Determination of haplotype frequency

The frequencies of haplotypes in patient and control groups can be estimated using an expectation-maximization algorithm (Dempster A. *et al.*, *J. R. Stat. Soc. B*, 39:1-38 (1977)). An implementation of this algorithm that can handle missing genotypes and uncertainty with the phase can be used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an alternative hypothesis is tested, where a candidate at-risk-haplotype, which can include the markers described herein, is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the same in both groups. Likelihoods are maximized separately under both hypotheses and a corresponding 1-df likelihood ratio statistic is used to evaluate the statistical significance.

To look for at-risk and protective markers and haplotypes within a linkage region, for example, association of all possible combinations of genotyped markers is studied, provided those markers span a practical region. The combined patient and control groups can be randomly divided into two sets, equal in size to the original group of patients and controls. The marker and haplotype analysis is then repeated and the most significant p-value registered is determined. This randomization scheme can be repeated, for example, over 100 times to construct an empirical distribution of p-values. In a preferred embodiment, a p-value of <0.05 is indicative of an significant marker and/or haplotype association.

Haplotype Analysis

One general approach to haplotype analysis involves using likelihood-based inference applied to NEsted MOdels (Gretarsdottir S., *et al.*, *Nat. Genet. 35*:131-38 (2003)). The method is implemented in the program NEMO, which allows for many polymorphic markers, SNPs and microsatellites. The method and software are specifically

designed for case-control studies where the purpose is to identify haplotype groups that confer different risks. It is also a tool for studying LD structures. In NEMO, maximum likelihood estimates, likelihood ratios and p-values are calculated directly, with the aid of the EM algorithm, for the observed data treating it as a missing-data problem.

Even though likelihood ratio tests based on likelihoods computed directly for the observed data, which have captured the information loss due to uncertainty in phase and missing genotypes, can be relied on to give valid p-values, it would still be of interest to know how much information had been lost due to the information being incomplete. The information measure for haplotype analysis is described in Nicolae and Kong (Technical Report 537, Department of Statistics, University of Statistics, University of Chicago; *Biometrics*, 60(2):368-75 (2004)) as a natural extension of information measures defined for linkage analysis, and is implemented in NEMO.

For single marker association to a disease, the Fisher exact test can be used to calculate two-sided p-values for each individual allele. Usually, all p-values are presented unadjusted for multiple comparisons unless specifically indicated. The presented frequencies (for microsatellites, SNPs and haplotypes) are allelic frequencies as opposed to carrier frequencies. To minimize any bias due the relatedness of the patients who were recruited as families for the linkage analysis, first and second-degree relatives can be eliminated from the patient list. Furthermore, the test can be repeated for association correcting for any remaining relatedness among the patients, by extending a variance adjustment procedure described in Risch, N. & Teng, J. (*Genome Res.*, 8:1273-1288 (1998)), DNA pooling (*ibid*) for sibships so that it can be applied to general familial relationships, and present both adjusted and unadjusted p-values for comparison. The differences are in general very small as expected. To assess the significance of single-marker association corrected for multiple testing we can carry out a randomization test using the same genotype data. Cohorts of patients and controls can be randomized and the association analysis redone multiple times (*e.g.*, up to 500,000 times) and the p-value is the fraction of replications that produced a p-value for some marker allele that is lower than or equal to the p-value we observed using the original patient and control cohorts.

For both single-marker and haplotype analyses, relative risk (RR) and the population attributable risk (PAR) can be calculated assuming a multiplicative model (haplotype relative risk model) (Terwilliger, J.D. & Ott, J., *Hum. Hered. 42*:337-46 (1992) and Falk, C.T. & Rubinstein, P, *Ann. Hum. Genet. 51 (Pt 3)*:227-33 (1987)), i.e., that the risks of the two alleles/haplotypes a person carries multiply. For example, if RR is the risk of A relative to a, then the risk of a person homozygote AA will be RR times that of a heterozygote Aa and RR^2 times that of a homozygote aa. The multiplicative model has a nice property that simplifies analysis and computations — haplotypes are independent, *i.e.*, in Hardy-Weinberg equilibrium, within the affected population as well as within the

control population. As a consequence, haplotype counts of the affecteds and controls each have multinomial distributions, but with different haplotype frequencies under the alternative hypothesis. Specifically, for two haplotypes, h_i and h_j, risk(h_i)/risk(h_j) = (f_i/p_i)/(f_j/p_j), where f and p denote, respectively, frequencies in the affected population and in the control population. While there is some power loss if the true model is not multiplicative, the loss tends to be mild except for extreme cases. Most importantly, p-values are always valid since they are computed with respect to null hypothesis.

Linkage Disequilibrium Using NEMO

LD between pairs of markers can be calculated using the standard definition of D' and r^2 (Lewontin, R., *Genetics 49*:49-67 (1964); Hill, W.G. & Robertson, A. *Theor. Appl. Genet. 22*:226-231 (1968)). Using NEMO, frequencies of the two marker allele combinations are estimated by maximum likelihood and deviation from linkage equilibrium is evaluated by a likelihood ratio test. The definitions of D' and r^2 are extended to include microsatellites by averaging over the values for all possible allele combination of the two markers weighted by the marginal allele probabilities. When plotting all marker combination to elucidate the LD structure in a particular region, we plot D' in the upper left corner and the p-value in the lower right corner. In the LD plots the markers can be plotted equidistant rather than according to their physical location, if desired.

Risk assessment and Diagnostics

As described herein, certain polymorphic markers and haplotypes comprising such markers are found to be useful for risk assessment of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) or stroke. Risk assessment can involve the use of the markers for diagnosing a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) or stroke. Particular alleles of polymorphic markers are found more frequently in individuals with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) or stroke, than in individuals without diagnosis of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) or stroke. Therefore, these marker alleles have predictive value for detecting cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke, or a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) or stroke, in an individual. Tagging markers within haplotype blocks or LD blocks comprising at-risk markers, such as the markers of the present invention, can be used as surrogates for other markers and/or haplotypes within the haplotype block or LD block. Markers with values of r^2 equal to 1 are perfect surrogates for the at-risk variants, i.e. genotypes for one marker perfectly predicts

genotypes for the other. Markers with smaller values of r^2 than 1 can also be surrogates for the at-risk variant, or alternatively represent variants with relative risk values as high or possibly even higher than the at-risk variant. The at-risk variant identified may not be the functional variant itself, but is in this instance in linkage disequilibrium with the true functional variant. The present invention encompasses the assessment of such surrogate markers for the markers as disclosed herein. Such markers are annotated, mapped and listed in public databases, as well known to the skilled person, or can alternatively be readily identified by sequencing the region or a part of the region identified by the markers of the present invention in a group of individuals, and identify polymorphisms in the resulting group of sequences. As a consequence, the person skilled in the art can readily and without undue experimentation genotype surrogate markers in linkage disequilibrium with the markers and/or haplotypes as described herein. The tagging or surrogate markers in LD with the at-risk variants detected, also have predictive value for detecting association to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke or a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) or stroke, in an individual. These tagging or surrogate markers that are in LD with the markers of the present invention can also include other markers that distinguish among haplotypes, as these similarly have predictive value for detecting susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke.

The markers and haplotypes of the invention, *e.g.,* the markers presented in Tables 5 and 9, as well as markers in linkage disequilibrium therewith,, may be useful for risk assessment and diagnostic purposes for, either alone or in combination. Thus, even in cases where the increase in risk by individual markers is relatively modest, i.e. on the order of 10-30%, the association may have significant implications. Thus, relatively common variants may have significant contribution to the overall risk (Population Attributable Risk is high), or combination of markers can be used to define groups of individual who, based on the combined risk of the markers, is at significant combined risk of developing the disease.

Thus, in one embodiment of the invention, a plurality of variants (markers and/or haplotypes) is used for overall risk assessment. These variants are in one embodiment selected from the variants as disclosed herein. Other embodiments include the use of the variants of the present invention in combination with other variants known to be useful for diagnosing a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke. In such embodiments, the genotype status of a plurality of markers and/or haplotypes is determined in an individual, and the status of the individual compared with the population frequency of the associated variants, or the frequency of the variants in clinically healthy subjects, such as age-matched and sex-matched subjects. Methods known in the art, such as multivariate analyses or joint risk analyses, may subsequently

be used to determine the overall risk conferred based on the genotype status at the multiple loci. Assessment of risk based on such analysis may subsequently be used in the methods and kits of the invention, as described herein.

As described in the above, the haplotype block structure of the human genome has the effect that a large number of variants (markers and/or haplotypes) in linkage disequilibrium with the variant originally associated with a disease or trait may be used as surrogate markers for assessing association to the disease or trait. The number of such surrogate markers will depend on factors such as the historical recombination rate in the region, the mutational frequency in the region (i.e., the number of polymorphic sites or markers in the region), and the extent of LD (size of the LD block) in the region. These markers are usually located within the physical boundaries of the LD block or haplotype block in question as defined using the methods described herein, or by other methods known to the person skilled in the art. However, sometimes marker and haplotype association is found to extend beyond the physical boundaries of the haplotype block as defined. Such markers and/or haplotypes may in those cases be also used as surrogate markers and/or haplotypes for the markers and/or haplotypes physically residing within the haplotype block as defined. As a consequence, markers and haplotypes in LD (typically characterized by r^2 greater than 0.1, such as r^2 greater than 0.2, including r^2 greater than 0.3, also including r^2 greater than 0.4) with the markers and haplotypes of the present invention are also within the scope of the invention, even if they are physically located beyond the boundaries of the haplotype block as defined. This includes markers that are described herein (*e.g.*, Tables 5 and 9), but may also include other markers that are in strong LD (characterized by r^2 greater than 0.1 or 0.2 and/or $|D'| > 0.8$) with one or more of the markers listed in Tables 5 and 9.

For the SNP markers described herein, the opposite allele to the allele found to be in excess in patients (at-risk allele) is found in decreased frequency in cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke patients.. These markers and haplotypes in LD and/or comprising such markers, are thus protective for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. i.e. they confer a decreased risk or susceptibility of individuals carrying these markers and/or haplotypes developing cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke..

Certain variants of the present invention, including certain haplotypes comprise, in some cases, a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Detecting haplotypes can be accomplished by methods known in the art and/or described herein for detecting sequences at polymorphic sites. Furthermore, correlation between certain haplotypes or sets of markers and disease phenotype can be verified using standard techniques. A representative example of a simple test for correlation would be a Fisher-exact test on a two by two table.

In specific embodiments, a marker or haplotype found to be associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke., (*e.g.*, markers as listed in Table 5 (Tables 5A and 5B), Table 9 and/or Table 19, and markers in linkage disequilibrium therewith) is one in which the marker allele or haplotype is more frequently present in an individual at risk for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke (affected), compared to the frequency of its presence in a healthy individual (control), wherein the presence of the marker allele or haplotype is indicative of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. or a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke.. In other embodiments, at-risk markers in linkage disequilibrium with one or more markers found to be associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. (*e.g.*, marker alleles as listed in Tables 5A and 5B, and markers in linkage disequilibrium therewith) are tagging markers that are more frequently present in an individual at risk for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke (affected), compared to the frequency of their presence in a healthy individual (control), wherein the presence of the tagging markers is indicative of increased susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. In a further embodiment, at-risk markers alleles (i.e. conferring increased susceptibility) in linkage disequilibrium with one or more markers found to be associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. (*e.g.*, marker alleles as listed in Tables 5A and 5B and markers in linkage disequilibrium therewith), are markers comprising one or more allele that is more frequently present in an individual at risk for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke compared to the frequency of their presence in a healthy individual (control), wherein the presence of the markers is indicative of increased susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke.

Study population

In a general sense, the methods and kits of the invention can be utilized from samples containing genomic DNA from any source, i.e. any individual. In preferred embodiments, the individual is a human individual. The individual can be an adult, child, or fetus. The present invention also provides for assessing markers and/or haplotypes in individuals who are members of a target population. Such a target population is in one embodiment a population or group of individuals at risk of developing the disease, based on other genetic factors, biomarkers, biophysical parameters (*e.g.*, weight, BMD, blood pressure), or general health and/or lifestyle parameters (*e.g.*, history of disease or related diseases, previous diagnosis of disease, family history of disease).

The invention provides for embodiments that include individuals from specific age subgroups, such as those over the age of 40, over age of 45, or over age of 50, 55, 60, 65, 70, 75, 80, or 85. Other embodiments of the invention pertain to other age groups, such as individuals aged less than 85, such as less than age 80, less than age 75, or less than age 70, 65, 60, 55, 50, 45, 40, 35, or age 30. Other embodiments relate to individuals with age at onset of the disease in any of the age ranges described in the above. It is also contemplated that a range of ages may be relevant in certain embodiments, such as age at onset at more than age 45 but less than age 60. Other age ranges are however also contemplated, including all age ranges bracketed by the age values listed in the above.

Other embodiments related to individuals with age at onset of the disease at particular age or age range. Thus, it is known that predisposing factors, genetic and non-genetic, can affect at what age an individual develops a disease. For cardiovascular disorders, including cardiac arrhythmias and stroke, common risk factors can influence if, and at what age, an individual develops the disease. Some embodiments of the invention therefore relate to age at onset or age at diagnosis of cardiac arrhythmia (*e.g.,* atrial fibrillation and/or atrial flutter) or stroke in a certain age range. In one embodiment, the individuals at risk for developing cardiac arrhythmia (*e.g.,* atrial fibrillation and/or atrial flutter) or stroke have age at onset or age at diagnosis over the age of 40. In other embodiments, the individuals have age at onset or age at diagnosis over age of 45, or over age of 50, 55, 60, 65, 70, 75, 80, or 85. Other embodiments of the invention pertain to individuals who have an age at onset or age at diagnosis at age less than 85, such as less than age 80, less than age 75, or less than age 70, 65, 60, 55, 50, 45, 40, 35, or age 30. One preferred embodiment includes individuals diagnosed with atrial fibrillation or atrial flutter or stroke below age 80. Another preferred embodiment relates to individuals diagnosed with atrial fibrillation or atrial flutter or stroke below age 70. Another preferred embodiment, relates to individuals diagnosed with atrial fibrillation or atrial flutter or stroke below age 60. Yet another preferred embodiment relates to individuals diagnosed with atrial fibrillation or atrial flutter or stroke below age 50. Other embodiments relate to individuals with age at onset of the disease in specific age ranges, described in the above. It is also contemplated that a range of ages may be relevant in certain embodiments, such as age at onset at more than age 45 but less than age 60, age at onset at age more than 60 and less than age 70, age at onset at age more than 70 and less than 80, or age at onset at age more than 60 and less than 80. Other age ranges are however also contemplated, including all age ranges bracketed by the age values listed in the above.

The invention furthermore relates to individuals of either sex, males or females. It also provides for embodiments that relate to human subjects that are from one or more human population including, but not limited to, Bantu, Mandenk, Yoruba, San, Mbuti

Pygmy, Orcadian, Adygel, Russian, Sardinian, Tuscan, Mozabite, Bedouin, Druze, Palestinian, Balochi, Brahui, Makrani, Sindhi, Pathan, Burusho, Hazara, Uygur, Kalash, Han, Dai, Daur, Hezhen, Lahu, Miao, Oroqen, She, Tujia, Tu, Xibo, Yi, Mongolan, Naxi, Cambodian, Japanese, Yakut, Melanesian, Papuan, Karitianan, Surui, Colmbian, Maya and Pima. The invention also relates to European populations, American populations, Eurasian populations, Asian populations, Central/South Asian populations, East Asian populations, Middle Eastern populations, African populations, Hispanic populations, and Oceanian populations. European populations include, but are not limited to, Swedish, Norwegian, Finnish, Russian, Danish, Icelandic, Irish, Kelt, English, Scottish, Dutch, Belgian, French, German, Spanish, Portuguese, Italian, Polish, Bulgarian, Slavic, Serbian, Bosnian, Chech, Greek and Turkish populations.

In one preferred embodiment, the invention relates to populations that include black African ancestry such as populations comprising persons of African descent or lineage. Black African ancestry may be determined by self reporting as African-Americans, Afro-Americans, Black Americans, being a member of the black race or being a member of the negro race. For example, African Americans or Black Americans are those persons living in North America and having origins in any of the black racial groups of Africa. In another example, self-reported persons of black African ancestry may have at least one parent of black African ancestry or at least one grandparent of black African ancestry.

The racial contribution in individual subjects may also be determined by genetic analysis. Genetic analysis of ancestry may be carried out using unlinked microsatellite markers such as those set out in Smith *et al.* (*Am J Hum Genet* **74**, 1001-13 (2004)).

In certain embodiments, the invention relates to markers and/or haplotypes identified in specific populations, as described in the above. The person skilled in the art will appreciate that measures of linkage disequilibrium (LD) may give different results when applied to different populations. This is due to different population history of different human populations as well as differential selective pressures that may have led to differences in LD in specific genomic regions. It is also well known to the person skilled in the art that certain markers, e.g. SNP markers, are polymorphic in one population but not in another. The person skilled in the art will however apply the methods available and as taught ??herein to practice the present invention in any given human population. This may include assessment of polymorphic markers in the LD region of the present invention, so as to identify those markers that give strongest association within the specific population. Thus, the at-risk variants of the present invention may reside on different haplotype background and in different frequencies in various human populations. However, utilizing methods known in the art and the markers of the present invention, the invention can be practiced in any given human population.

Utility of Genetic Testing

The person skilled in the art will appreciate and understand that the variants described herein in general do not, by themselves, provide an absolute identification of individuals who will develop cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. The variants described herein do however indicate increased and/or decreased likelihood that individuals carrying the at-risk or protective variants of the invention will develop symptoms associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke This information is however extremely valuable in itself, as outlined in more detail in the below, as it can be used to, for example, initiate preventive measures at an early stage, perform regular physical and/or mental exams to monitor the progress and/or appearance of symptoms, or to schedule exams at a regular interval to identify the condition in question, so as to be able to apply treatment at an early stage.

The knowledge about a genetic variant that confers a risk of developing cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke offers the opportunity to apply a genetic test to distinguish between individuals with increased risk of developing the disease (i.e. carriers of the at-risk variant) and those with decreased risk of developing the disease (i.e. carriers of the protective variant). The core values of genetic testing, for individuals belonging to both of the above mentioned groups, are the possibilities of being able to diagnose cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke, or a predisposition to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke at an early stage and provide information to the clinician about prognosis of cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke in order to be able to apply the most appropriate treatment.

Individuals with a family history of cardiac arrhythmia *(e.g.,* atrial fibrillation or atrial flutter) and/or stroke and carriers of at-risk variants may benefit from genetic testing since the knowledge of the presence of a genetic risk factor, or evidence for increased risk of being a carrier of one or more risk factors, may provide increased incentive for implementing a healthier lifestyle, by avoiding or minimizing known environmental risk factors for cardiovascular diseases related to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke. Genetic testing of cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke patients may furthermore give valuable information about the primary cause of the disease and can aid the clinician in selecting the best treatment options and medication for each individual.

The present invention furthermore relates to risk assessment for cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and/or stroke, including determining

whether an individual is at risk for developing cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. The polymorphic markers of the present invention can be used alone or in combination, as well as in combination with other factors, including other genetic risk factors or biomarkers, for risk assessment of an individual for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. Many factors known to affect the predisposition of an individual towards developing risk of cardiovascular disease are susceptibility factors for cardiac arrhythmias (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke, and are known to the person skilled in the art and can be utilized in such assessment. These include, but are not limited to, age, gender, smoking status, physical activity, waist-to-hip circumference ratio, family history of cardiac arrhythmia (in particular atrial fibrillation and/or atrial flutter) and/or stroke , previously diagnosed cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke, obesity, hypertriglyceridemia, low HDL cholesterol, hypertension, elevated blood pressure, cholesterol levels, HDL cholesterol, LDL cholesterol, triglycerides, apolipoprotein AI and B levels, fibrinogen, ferritin, C-reactive protein and leukotriene levels. Particular biomarkers that have been associated with Atrial fibrillation/Atrial flutter and stroke are discussed in Allard et al. (*Clin Chem* 51:2043-2051 (2005) and Becker (*J Thromb Thrombolys* 19:71-75 (2005)). These include, but are not limited to, fibrin D-dimer, prothrombin activation fragment 1.2 (F1.2), thrombin-antithrombin III complexes (TAT), fibrinopeptide A (FPA), lipoprotein-associated phospholipase A2 (lp-PLA2), beta-thromboglobulin, platelet factor 4, P-selectin, von Willebrand Factor, pro-natriuretic peptide (BNP), matrix metalloproteinase-9 (MMP-9), PARK7, nucleoside diphosphate kinase (NDKA), tau, neuron-specific enolase, B-type neurotrophic growth factor, astroglial protein S-100b, glial fibrillary acidic protein, C-reactive protein, seum amyloid A, marix metalloproteinase-9, vascular and intracellular cell adhesion molecules, tumor necrosis factor alpha, and interleukins, including interleukin-1, -6, and -8). Circulating progenitor cells have also been implicated as being useful biomarkers for AF. In particular embodiments, more than one biomarker is determined for an individual, and combined with results of a determination of at least one polymorphic marker as described herein. Preferably, biomarker is measured in plasma or serum from the individual. Alternatively, the biomarker is deterrmined in other suitable tissues containing measurable amounts of the biomarker, and such embodiments are also within scope of the invention.

Methods known in the art can be used for overall risk assessment, including multivariate analyses or logistic regression.

Atrial fibrillation is a disease of great significance both to the individual patient and to the health care system as a whole. It can be a permanent condition but may also be paroxysmal and recurrent in which case it can be very challenging to diagnose. The most devastating complication of atrial fibrillation and atrial flutter is the occurrence of

debilitating stroke. Importantly the risk of stroke is equal in permanent and paroxysmal atrial fibrillation. It has repeatedly been shown that therapy with warfarin anticoagulation can significantly reduce the risk of first or further episodes of stroke in the setting of atrial fibrillation. Therefor, anticoagulation with warfarin is standard therapy for almost all patients with atrial fibrillation for stroke-prevention, whether they have the permanent or paroxysmal type. The only patients for whom warfarin is not strongly recommended are those younger than 65 years old who are considered low-risk, i.e., they have no organic heart disease, including, neither hypertension no coronary artery disease, no previous history of stroke or transient ischemic attacks and no diabetes. This group has a lower risk of stroke and stroke-prevention with aspirin is recommended.

Due to the nature of paroxysmal atrial fibrillation it can be very difficult to diagnose. When the patient seeks medical attention due to disease-related symptoms, such as palpitations, chest pain, shortness of breath, dizziness, heart failure, transient ischemic attacks or even stroke, normal heart rhythm may already be restored precluding diagnosis of the arrhythmia. In these cases cardiac rhythm monitoring is frequently applied in the attempt to diagnose the condition. The cardiac rhythm is commonly monitored continuously for 24 to 48 hours. Unfortunately atrial fibrillation episodes are unpredictable and frequently missed by this approach. The opportunity to diagnose the arrhythmia, institute recommended therapy, and possibly prevent a debilitating first or recurrent stroke may be missed with devastating results to the patient. Prolonged and more complex cardiac rhythm monitoring measures are available and applied occasionally when the suspicion of atrial fibrillation is very strong. These tests are expensive, the diagnostic yield with current approach is often low, and they are used sparingly for this indication. In these circumstances additional risk stratification with genetic testing may be extremely helpful. Understanding that the individual in question carries either an at-risk or a protective genetic variant can be an invaluable contribution to diagnostic and/or treatment decision making. This way, in some cases, unnecessary testing and therapy may be avoided, and in other cases, with the help of more aggressive diagnostic approach, the arrhythmia may be diagnosed and/or proper therapy initiated and later complications of disease diminished.

METHODS OF THE INVENTION

Methods for risk assessment of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke are described herein and are encompassed by the invention. The invention also encompasses methods of assessing an individual for probability of response to a therapeutic agent for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke, as well as methods for predicting the effectiveness of a therapeutic agent to treat

patients with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. Kits for assaying a sample from a subject to detect susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke are also encompassed by the invention.

Diagnostic and screening assays of the invention

In certain embodiments, the present invention pertains to methods of diagnosing, or aiding in the diagnosis of, cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke or a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke, by detecting particular alleles at genetic markers that appear more frequently in cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke subjects or subjects who are susceptible to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. In a particular embodiment, the invention is a method of diagnosing a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke by detecting at least one allele of at least one polymorphic marker (*e.g.*, the markers described herein). The present invention describes methods whereby detection of particular alleles of particular markers or haplotypes is indicative of a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke. Such prognostic or predictive assays can also be used to determine prophylactic treatment of a subject prior to the onset of symptoms of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke.

The present invention pertains in some embodiments to methods of clinical applications of diagnosis, *e.g.*, diagnosis performed by a medical professional, which may include an assessment or determination of genetic risk variants, and their interpretation. In other embodiments, the invention pertains to methods of risk assessment (or diagnosis) performed by a layman or a non-medical professional. Recent technological advances in genotyping technologies, including high-throughput genotyping of SNP markers, such as Molecular Inversion Probe array technology (*e.g.*, Affymetrix GeneChip), and BeadArray Technologies (*e.g.*, Illumina GoldenGate and Infinium assays) have made it possible for individuals to have their own genome assessed for large number of variations simultaneously, or up to one million SNPs. The resulting genotype information, made available to the individual, can be compared to information from the public scientific litterature about disease or trait risk associated with various SNPs. The diagnostic application of disease-associated alleles as described herein, can thus be performed either by a health professional based on results of a clinical test or by a layman, or non-medical professional, including an individual providing service for performing an assessment of SNPs throught SNP genotyping, either on an individual SNP basis or by large-scale high-throughput methods such as array technologies. In other words, the diagnosis or

assessment of a susceptibility based on genetic risk can be made by health professionals, genetic counselors, genotype services providers or by the layman, based on information about his/her genotype and publications on various risk factors. In the present context, the term "diagnosing", and "diagnose a susceptibility", is meant to refer to any available diagnostic method, including those mentioned above.

In addition, in certain other embodiments, the present invention pertains to methods of diagnosing, or aiding in the diagnosis of, a decreased susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke by detecting particular genetic marker alleles or haplotypes that appear less frequently in cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke patients than in individual not diagnosed with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke or in the general population.

As described and exemplified herein, particular marker alleles or haplotypes (e.g. the markers and haplotypes as listed in Table 5 (Tables 5A and 5B) and markers in linkage disequilibrium therewith, *e.g.*, the markers listed in Tables 4 and/or 9 markers in linkage disequilibrium therewith, *e.g.*, the markers as set forth in Table 19) are associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. In one embodiment, the marker allele or haplotype is one that confers a significant risk or susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. In another embodiment, the invention relates to a method of diagnosing a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke in a human individual, the method comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the group consisting of the polymorphic markers listed in Tables 5A and 5B, and markers in linkage disequilibrium therewith. In another embodiment, the invention pertains to methods of diagnosing a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke in a human individual, by screening for at least one marker allele or haplotype as listed in Tables 5A and5B or markers in linkage disequilibrium therewith. In another embodiment, the marker allele or haplotype is more frequently present in a subject having, or who is susceptible to, cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke (affected), as compared to the frequency of its presence in a healthy subject (control, such as population controls). In certain embodiments, the significance of association of the at least one marker allele or haplotype is characterized by a p value < 0.05. In other embodiments, the significance of association is characterized by smaller p-values, such as < 0.01, <0.001, <0.0001, <0.00001, <0.000001, <0.0000001, <0.00000001 or <0.000000001.

In these embodiments, the presence of the at least one marker allele or haplotype is indicative of a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. These diagnostic methods involve detecting the presence or absence of at least one marker allele or haplotype that is associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. The haplotypes described herein include combinations of alleles at various genetic markers (*e.g.*, SNPs, microsatellites). The detection of the particular genetic marker alleles that make up the particular haplotypes can be performed by a variety of methods described herein and/or known in the art. For example, genetic markers can be detected at the nucleic acid level (*e.g.*, by direct nucleotide sequencing or by other means known to the skilled in the art) or at the amino acid level if the genetic marker affects the coding sequence of a protein encoded by a cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke -associated nucleic acid (*e.g.*, by protein sequencing or by immunoassays using antibodies that recognize such a protein). The marker alleles or haplotypes of the present invention correspond to fragments of a genomic DNA sequence associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and/or stroke. Such fragments encompass the DNA sequence of the polymorphic marker or haplotype in question, but may also include DNA segments in strong LD (linkage disequilibrium) with the marker or haplotype. In one embodiment, such segments comprises segments in LD with the marker or haplotype as determined by a value of r^2 greater than 0.2 and/or $|D'| > 0.8$.

In one embodiment, diagnosis of a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke can be accomplished using hybridization methods, such as Southern analysis, Northern analysis, and/or *in situ* hybridizations (see Current Protocols in Molecular Biology, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements). A biological sample from a test subject or individual (a "test sample") of genomic DNA, RNA, or cDNA is obtained from a subject suspected of having, being susceptible to, or predisposed for cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke (the "test subject"). The subject can be an adult, child, or fetus. The test sample can be from any source that contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined. The presence of a specific marker allele can be indicated by sequence-specific hybridization of a nucleic acid probe specific for the particular allele. The presence of more than specific marker allele or a specific haplotype can be indicated by using several sequence-specific nucleic acid probes, each being specific for a particular allele. In one embodiment, a haplotype can be indicated by a single nucleic acid probe that is specific for the specific haplotype (i.e., hybridizes specifically to a DNA strand comprising the specific

marker alleles characteristic of the haplotype). A sequence-specific probe can be directed to hybridize to genomic DNA, RNA, or cDNA. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe that hybridizes to a complementary sequence. One of skill in the art would know how to design such a probe so that sequence specific hybridization will occur only if a particular allele is present in a genomic sequence from a test sample.

To diagnose a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, a hybridization sample is formed by contacting the test sample containing an atrial fibrillation and /or stroke -associated nucleic acid, such as a genomic DNA sample, with at least one nucleic acid probe. A non-limiting example of a probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe that is capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length that is sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. The nucleotide acid probe may be up to 1000 or more nucleotides in length, including up to 500 nucleotides, 400 nucleotide, 300 nucleotides, 200 nucleotides or 100 nucleotides. Certain embodiments include nucleotide probes that are from 15 to 1000 nucleotides in length. Other embodiments pertain to use of nucleotide probes that are from 15 to 500 nucleotides in length, or from 15 to 400 nucleotides in length, or from 20 to 400 nucleotides in length. Other size ranges of the nucleotide probes of the invention are contemplated, as well known to the skilled person. In one embodiment, the nucleic acid probe can comprise all or a portion of the nucleotide sequence of LD Block C04, as described herein, optionally comprising at least one allele of a marker described herein, or at least one haplotype described herein, or the probe can be the complementary sequence of such a sequence. In a particular embodiment, the nucleic acid probe is a portion of the nucleotide sequence of LD Block C04 as set forth in SEQ ID NO:50 or , as described herein, optionally comprising at least one allele of a marker described herein, or at least one allele of one polymorphic marker or haplotype comprising at least one polymorphic marker described herein, or the probe can be the complementary sequence of such a sequence. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization can be performed by methods well known to the person skilled in the art (see, *e.g.*, Current Protocols in Molecular Biology, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements). In one embodiment, hybridization refers to specific hybridization, i.e., hybridization with no mismatches (exact hybridization). In one embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the nucleic acid in the test sample, then the sample contains the allele that is complementary to the nucleotide that is present in the nucleic acid probe. The process can be repeated for any markers of the present invention, or markers that make up a haplotype of the present invention, or multiple probes can be used concurrently to detect more than one marker alleles at a time. It is also possible to design a single probe containing more than one marker alleles of a particular haplotype (*e.g.,* a probe containing alleles complementary to 2, 3, 4, 5 or all of the markers that make up a particular haplotype). Detection of the particular markers of the haplotype in the sample is indicative that the source of the sample has the particular haplotype (*e.g.,* a haplotype) and therefore is susceptible to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke.

In another hybridization method, Northern analysis (see Current Protocols in Molecular Biology, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) is used to identify the presence of a polymorphism associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. For Northern analysis, a test sample of RNA is obtained from the subject by appropriate means. As described herein, specific hybridization of a nucleic acid probe to RNA from the subject is indicative of a particular allele complementary to the probe. For representative examples of use of nucleic acid probes, see, for example, U.S. Patent Nos. 5,288,611 and 4,851,330.

Additionally, or alternatively, a peptide nucleic acid (PNA) probe can be used in addition to, or instead of, a nucleic acid probe in the hybridization methods described herein. A PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P., *et al.*, *Bioconjug. Chem. 5*:3-7 (1994)). The PNA probe can be designed to specifically hybridize to a molecule in a sample suspected of containing one or more of the marker alleles or haplotypes that are associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. Hybridization of the PNA probe is thus diagnostic for cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke or a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke.

In one embodiment of the invention, a test sample containing genomic DNA obtained from the subject is collected and the polymerase chain reaction (PCR) is used to amplify a fragment comprising one ore more markers or haplotypes of the present invention. As described herein, identification of a particular marker allele or haplotype associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, can be accomplished using a variety of methods (*e.g.,* sequence analysis, analysis by restriction digestion, specific hybridization, single stranded conformation polymorphism

assays (SSCP), electrophoretic analysis, etc.). In another embodiment, diagnosis is accomplished by expression analysis using quantitative PCR (kinetic thermal cycling). This technique can, for example, utilize commercially available technologies, such as TaqMan® (Applied Biosystems, Foster City, CA) . The technique can assess the presence of an alteration in the expression or composition of a polypeptide or splicing variant(s) that is encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. Further, the expression of the variant(s) can be quantified as physically or functionally different.

In another method of the invention, analysis by restriction digestion can be used to detect a particular allele if the allele results in the creation or elimination of a restriction site relative to a reference sequence. Restriction fragment length polymorphism (RFLP) analysis can be conducted, *e.g.,* as described in Current Protocols in Molecular Biology, *supra*. The digestion pattern of the relevant DNA fragment indicates the presence or absence of the particular allele in the sample.

Sequence analysis can also be used to detect specific alleles or haplotypes associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke (e.g. the polymorphic markers of Table 5 (Tables 5A and 5B), Table 9 and/or Table 19). Therefore, in one embodiment, determination of the presence or absence of a particular marker alleles or haplotypes comprises sequence analysis of a test sample of DNA or RNA obtained from a subject or individual. PCR or other appropriate methods can be used to amplify a portion of a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, and the presence of a specific allele can then be detected directly by sequencing the polymorphic site (or multiple polymorphic sites in a haplotype) of the genomic DNA in the sample.

Allele-specific oligonucleotides can also be used to detect the presence of a particular allele in a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, (e.g. the polymorphic markers of Table 5 (Tables 5A and 5B), Table 9 and/or Table 19), through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al., Nature*, 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-500 base pairs, approximately 15-400 base pairs, approximately 15-200 base pairs, approximately 15-100 base pairs, approximately 15-50 base pairs, or approximately 15-30 base pairs, that specifically hybridizes to a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, and which contains a specific allele at a polymorphic site (*e.g.,* a marker or haplotype as described herein). An allele-specific oligonucleotide probe that is specific for one or more particular a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and

/or stroke can be prepared using standard methods (see, *e.g.,* Current Protocols in Molecular Biology, *supra*). PCR can be used to amplify the desired region. The DNA containing the amplified region can be dot-blotted using standard methods (*see, e.g.,* Current Protocols in Molecular Biology, *supra*), and the blot can be contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified region can then be detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the subject is indicative of a specific allele at a polymorphic site associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke (see, *e.g.,* Gibbs, R. *et al., Nucleic Acids Res., 17*:2437-2448 (1989) and WO 93/22456).

With the addition of such analogs as locked nucleic acids (LNAs), the size of primers and probes can be reduced to as few as 8 bases. LNAs are a novel class of bicyclic DNA analogs in which the 2' and 4' positions in the furanose ring are joined via an O-methylene (oxy-LNA), S-methylene (thio-LNA), or amino methylene (amino-LNA) moiety. Common to all of these LNA variants is an affinity toward complementary nucleic acids, which is by far the highest reported for a DNA analog. For example, particular all oxy-LNA nonamers have been shown to have melting temperatures (T_m) of 64°C and 74°C when in complex with complementary DNA or RNA, respectively, as opposed to 28°C for both DNA and RNA for the corresponding DNA nonamer. Substantial increases in T_m are also obtained when LNA monomers are used in combination with standard DNA or RNA monomers. For primers and probes, depending on where the LNA monomers are included (*e.g.,* the 3' end, the 5' end, or in the middle), the T_m could be increased considerably.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from a subject, can be used to identify polymorphisms in a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke (e.g. the polymorphic markers of Tables 5A and 5B and markers in linkage disequilibrium therewith). For example, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art (see, *e.g.,* U.S. Patent No. 5,143,854, PCT Patent Publication Nos. WO 90/15070 and 92/10092). These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods, or by other methods known to the person skilled in the art (see, *e.g.,* Fodor, S. *et al., Science, 251*:767-773 (1991); Pirrung *et al.,* U.S. Patent No. 5,143,854 (see also published PCT Application No. WO 90/15070); and Fodor. S. *et al.,* published PCT Application No. WO 92/10092 and U.S. Patent No. 5,424,186, the entire teachings of each of which are incorporated by reference herein). Techniques for the synthesis of these arrays using

mechanical synthesis methods are described in, *e.g.,* U.S. Patent No. 5,384,261; the entire teachings of which are incorporated by reference herein. In another example, linear arrays can be utilized. Additional descriptions of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patent Nos. 5,858,659 and 5,837,832, the entire teachings of both of which are incorporated by reference herein.

Other methods of nucleic acid analysis that are available to those skilled in the art can be used to detect a particular allele at a polymorphic site associated with atrial fibrillation and /or stroke (e.g. the polymorphic markers of Table 5 (Tables 5A and 5B), Table 9 and/or Table 19). Representative methods include, for example, direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA, 81*: 1991-1995 (1988); Sanger, F., *et al., Proc. Natl. Acad. Sci. USA, 74*:5463-5467 (1977); Beavis, *et al.*, U.S. Patent No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V., *et al., Proc. Natl. Acad. Sci. USA, 86*:232-236 (1989)), mobility shift analysis (Orita, M., *et al., Proc. Natl. Acad. Sci. USA, 86*:2766-2770 (1989)), restriction enzyme analysis (Flavell, R., *et al., Cell*, 15:25-41 (1978); Geever, R., *et al., Proc. Natl. Acad. Sci. USA, 78*:5081-5085 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton, R., *et al., Proc. Natl. Acad. Sci. USA, 85*:4397-4401 (1985)); RNase protection assays (Myers, R., *et al., Science, 230*:1242-1246 (1985); use of polypeptides that recognize nucleotide mismatches, such as *E. coli* mutS protein; and allele-specific PCR.

In another embodiment of the invention, diagnosis of cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke or a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke can be made by examining expression and/or composition of a polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke in those instances where the genetic marker(s) or haplotype(s) of the present invention result in a change in the composition or expression of the polypeptide. Thus, diagnosis of a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke can be made by examining expression and/or composition of one of these polypeptides, or another polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, in those instances where the genetic marker or haplotype of the present invention results in a change in the composition or expression of the polypeptide. The haplotypes and markers of the present invention that show association to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke may play a role through their effect on one or more of these nearby genes (e.g., the PITX2 gene). Possible mechanisms affecting these genes include, *e.g.,* effects on transcription, effects on RNA splicing, alterations in relative amounts of alternative splice forms of

mRNA, effects on RNA stability, effects on transport from the nucleus to cytoplasm, and effects on the efficiency and accuracy of translation.

Thus, in another embodiment, the variants (markers or haplotypes) of the invention showing association to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke affect the expression of a nearby gene. It is well known that regulatory element affecting gene expression may be located tenths or even hundreds of kilobases away from the promoter region of a gene. By assaying for the presence or absence of at least one allele of at least one polymorphic marker of the present invention, it is thus possible to assess the expression level of such nearby genes. It is thus contemplated that the detection of the markers or haplotypes of the present invention can be used for assessing expression for one or more genes that are linked to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke.

A variety of methods can be used for detecting protein expression levels, including enzyme linked immunosorbent assays (ELISA), Western blots, immunoprecipitations and immunofluorescence. A test sample from a subject is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke. An alteration in expression of a polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke can be, for example, an alteration in the quantitative polypeptide expression (i.e., the amount of polypeptide produced). An alteration in the composition of a polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant polypeptide or of a different splicing variant). In one embodiment, diagnosis of a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke is made by detecting a particular splicing variant encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared to the expression or composition of the polypeptide in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from a subject who is not affected by, and/or who does not have a susceptibility to, cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke. In one embodiment, the control sample is from a subject that does not possess a marker allele or haplotype as described herein. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in

the test sample, as compared with the control sample, can be indicative of a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, can be indicative of a specific allele in the instance where the allele alters a splice site relative to the reference in the control sample. Various means of examining expression or composition of a polypeptide encoded by a nucleic acid are known to the person skilled in the art and can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.,* David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see, *e.g.,* Current Protocols in Molecular Biology, particularly chapter 10, *supra*).

For example, in one embodiment, an antibody (*e.g.,* an antibody with a detectable label) that is capable of binding to a polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke can be used. Antibodies can be polyclonal or monoclonal. An intact antibody, or a fragment thereof (*e.g.,* Fv, Fab, Fab', $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a labeled secondary antibody (*e.g.,* a fluorescently-labeled secondary antibody) and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin.

In one embodiment of this method, the level or amount of polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke in a test sample is compared with the level or amount of the polypeptide in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the nucleic acid, and is diagnostic for a particular allele or haplotype responsible for causing the difference in expression. Alternatively, the composition of the polypeptide in a test sample is compared with the composition of the polypeptide in a control sample. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample.

In another embodiment, the diagnosis of a susceptibility to cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke is made by detecting at least one marker or haplotypes of the present invention (*e.g.,* associated alleles of the markers listed in Tables 5A and 5B, and markers in linkage disequilibrium therewith), in

combination with an additional protein-based, RNA-based or DNA-based assay. The methods of the invention can also be used in combination with an analysis of a subject's family history and risk factors (*e.g.*, environmental risk factors, lifestyle risk factors).

Kits

Kits useful in the methods and procedures of the invention comprise components useful in any of the methods described herein, including for example, hybridization probes, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies that bind to an altered polypeptide encoded by a nucleic acid of the invention as described herein (*e.g.*, a genomic segment comprising at least one polymorphic marker and/or haplotype of the present invention) or to a non-altered (native) polypeptide encoded by a nucleic acid of the invention as described herein, means for amplification of a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, means for analyzing the nucleic acid sequence of a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, means for analyzing the amino acid sequence of a polypeptide encoded by a nucleic acid associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, etc. The kits can for example include necessary buffers, nucleic acid primers for amplifying nucleic acids of the invention (*e.g.*, one or more of the polymorphic markers as described herein), and reagents for allele-specific detection of the fragments amplified using such primers and necessary enzymes (*e.g.*, DNA polymerase). Additionally, kits can provide reagents for assays to be used in combination with the methods of the present invention, *e.g.*, reagents for use with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke diagnostic assays.

In one embodiment, the invention is a kit for assaying a sample from a subject to detect the presence of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke or a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke in a subject, wherein the kit comprises reagents necessary for selectively detecting at least one allele of at least one polymorphism of the present invention in the genome of the individual. In a particular embodiment, the reagents comprise at least one contiguous oligonucleotide that hybridizes to a fragment of the genome of the individual comprising at least one polymorphism of the present invention. In another embodiment, the reagents comprise at least one pair of oligonucleotides that hybridize to opposite strands of a genomic segment obtained from a subject, wherein each oligonucleotide primer pair is designed to selectively amplify a fragment of the genome of the individual that includes at least one polymorphism, wherein the polymorphism is selected from the group consisting of the polymorphisms as listed in Tables 5A and 5B and polymorphic

markers in linkage disequilibrium therewith. In yet another embodiment the fragment is at least 20 base pairs in size. Such oligonucleotides or nucleic acids (*e.g.*, oligonucleotide primers) can be designed using portions of the nucleic acid sequence flanking polymorphisms (*e.g.*, SNPs or microsatellites) that are indicative of cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke. In another embodiment, the kit comprises one or more labeled nucleic acids capable of allele-specific detection of one or more specific polymorphic markers or haplotypes associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, and reagents for detection of the label. Suitable labels include, *e.g.*, a radioisotope, a fluorescent label, an enzyme label, an enzyme co-factor label, a magnetic label, a spin label, an epitope label.

In particular embodiments, the polymorphic marker or haplotype to be detected by the reagents of the kit comprises one or more markers, two or more markers, three or more markers, four or more markers or five or more markers selected from the group consisting of the markers in Tables 5A and 5B. In another embodiment, the marker or haplotype to be detected comprises the markers listed in Tables 5A and 5B. In another embodiment, the marker or haplotype to be detected comprises the markers listed in Tables 4 and 9. In another embodiment, the marker or haplotype to be detected comprises at least one marker from the group of markers in strong linkage disequilibrium, as defined by values of r^2 greater than 0.2, to at least one of the group of markers consisting of the markers listed in Tables 5A and 5B. In another embodiment, the marker or haplotype to be detected comprises at least one marker from the markers in strong linkage disequilibrium, as defined by values of r^2 greater than 0.2, to at least one of the group of markers consisting of the markers listed in Tables 4 and 9. In another embodiment, the marker or haplotype to be detected comprises marker rs2220427 (SEQ ID NO:1) or marker rs1033464 (SEQ ID NO:41), or markers in linkage disequilibrium therewith. In another embodiment, the marker or haplotype to be detected comprises at least one of the markers set forth in Table 19. In another embodiment, the marker or haplotype to be detected comprises markers D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51) and markers in linkage disequilibrium therewith. In yet another embodiment, the marker or haplotype comprises the at-risk alleles -2, -4 and/or -8 in marker D4S406, allele A of marker rs2634073, allele T of marker rs2200733, allele T of marker rs2220427, allele T of marker rs10033464, and/or allele G of marker rs13143308. In one such embodiment, linkage disequilibrium is defined by values of r^2 greater than 0.1. In another such embodiment, linkage disequilibrium is defined by values of r^2 greater than 0.2.

In one preferred embodiment, the kit for detecting the markers of the invention comprises a detection oligonucleotide probe, that hybridizes to a segment of template DNA

containing a SNP polymorphisms to be detected, an enhancer oligonucleotide probe and an endonuclease. As explained in the above, the detection oligonucleotide probe comprises a fluorescent moiety or group at its 3' terminus and a quencher at its 5' terminus, and an enhancer oligonucleotide, is employed, as described by Kutyavin *et al.* (*Nucleic Acid Res.* **34:**e128 (2006)). The fluorescent moiety can be Gig Harbor Green or Yakima Yellow, or other suitable fluorescent moieties. The detection probe is designed to hybridize to a short nucleotide sequence that includes the SNP polymorphism to be detected. Preferably, the SNP is anywhere from the terminal residue to -6 residues from the 3' end of the detection probe. The enhancer is a short oligonucleotide probe which hybridizes to the DNA template 3' relative to the detection probe. The probes are designed such that a single nucleotide gap exists between the detection probe and the enhancer nucleotide probe when both are bound to the template. The gap creates a synthetic abasic site that is recognized by an endonuclease, such as Endonuclease IV. The enzyme cleaves the dye off the fully complementary detection probe, but cannot cleave a detection probe containing a mismatch. Thus, by measuring the fluorescence of the released fluorescent moiety, assessment of the presence of a particular allele defined by nucleotide sequence of the detection probe can be performed.

The detection probe can be of any suitable size, although preferably the probe is relatively short. In one embodiment, the probe is from 5-100 nucleotides in length. In another embodiment, the probe is from 10-50 nucleotides in length, and in another embodiment, the probe is from 12-30 nucleotides in length. Other lengths of the probe are possible and within scope of the skill of the average person skilled in the art.

In a preferred embodiment, the DNA template containing the SNP polymorphism is amplified by Polymerase Chain Reaction (PCR) prior to detection, and primers for such amplification are included in the reagent kit. In such an embodiment, the amplified DNA serves as the template for the detection probe and the enhancer probe.

Certain embodiments of the detection probe, the enhancer probe, and/or the primers used for amplification of the template by PCR include the use of modified bases, including modified A and modified G. The use of modified bases can be useful for adjusting the melting temperature of the nucleotide molecule (probe and/or primer) to the template DNA, for example for increasing the melting temperature in regions containing a low percentage of G or C bases, in which modified A with the capability of forming three hydrogen bonds to its complementary T can be used, or for decreasing the melting temperature in regions containing a high percentage of G or C bases, for example by using modified G bases that form only two hydrogen bonds to their complementary C base in a double stranded DNA molecule. In a preferred embodiment, modified bases are used in the design of the detection nucleotide probe. Any modified base known to the skilled person can be selected in these methods, and the selection of suitable bases is well within

the scope of the skilled person based on the teachings herein and known bases available from commercial sources as known to the skilled person.

In one of such embodiments, the presence of the marker or haplotype is indicative of a susceptibility (increased susceptibility or decreased susceptibility) to atrial fibrillation and/or stroke. In another embodiment, the presence of the marker or haplotype is indicative of response to atrial fibrillation and/or stroke therapeutic agent. In another embodiment, the presence of the marker or haplotype is indicative of atrial fibrillation and /or stroke prognosis. In yet another embodiment, the presence of the marker or haplotype is indicative of progress of atrial fibrillation and/or stroke treatment. Such treatment may include intervention by surgery, medication or by other means (*e.g.,* lifestyle changes).

Therapeutic agents

Variants of the present invention (*e.g.,* the markers and/or haplotypes of the invention, *e.g.,* the markers listed in Tables 5A and 5B and/or Table 19) can be used to identify novel therapeutic targets for cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. For example, genes containing, or in linkage disequilibrium with, variants (markers and/or haplotypes) associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, or their products, as well as genes or their products that are directly or indirectly regulated by or interact with these variant genes or their products, can be targeted for the development of therapeutic agents to treat cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, or prevent or delay onset of symptoms associated with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke. Therapeutic agents may comprise one or more of, for example, small non-protein and non-nucleic acid molecules, proteins, peptides, protein fragments, nucleic acids (DNA, RNA), PNA (peptide nucleic acids), or their derivatives or mimetics which can modulate the function and/or levels of the target genes or their gene products.

The nucleic acids and/or variants of the invention, or nucleic acids comprising their complementary sequence, may be used as antisense constructs to control gene expression in cells, tissues or organs. The methodology associated with antisense techniques is well known to the skilled artisan, and is described and reviewed in *AntisenseDrug Technology: Principles, Strategies, and Applications,* Crooke, ed., Marcel Dekker Inc., New York (2001). In general, antisense nucleic acid molecules are designed to be complementary to a region of mRNA expressed by a gene, so that the antisense molecule hybridizes to the mRNA, thus blocking translation of the mRNA into protein. Several classes of antisense oligonucleotide are known to those skilled in the art, including cleavers and blockers. The

former bind to target RNA sites, activate intracellular nucleases (*e.g.*, RnaseH or Rnase L), that cleave the target RNA. Blockers bind to target RNA, inhibit protein translation by steric hindrance of the ribosomes. Examples of blockers include nucleic acids, morpholino compounds, locked nucleic acids and methylphosphonates (Thompson, *Drug Discovery Today*, 7:912-917 (2002)). Antisense oligonucleotides are useful directly as therapeutic agents, and are also useful for determining and validating gene function, for example by gene knock-out or gene knock-down experiments. Antisense technology is further described in Lavery *et al.*, *Curr. Opin. Drug Discov. Devel.* 6:561-569 (2003), Stephens *et al.*, *Curr. Opin. Mol. Ther.* 5:118-122 (2003), Kurreck, *Eur. J. Biochem.* 270:1628-44 (2003), Dias *et al.*, *Mol. Cancer Ter.* 1:347-55 (2002), Chen, *Methods Mol. Med.* 75:621-636 (2003), Wang *et al.*, *Curr. Cancer Drug Targets* 1:177-96 (2001), and Bennett, *Antisense Nucleic Acid Drug.Dev.* 12:215-24 (2002)

The variants described herein can be used for the selection and design of antisense reagents that are specific for particular variants. Using information about the variants described herein, antisense oligonucleotides or other antisense molecules that specifically target mRNA molecules that contain one or more variants of the invention can be designed. In this manner, expression of mRNA molecules that contain one or more variant of the present invention (markers and/or haplotypes) can be inhibited or blocked. In one embodiment, the antisense molecules are designed to specifically bind a particular allelic form (i.e., one or several variants (alleles and/or haplotypes)) of the target nucleic acid, thereby inhibiting translation of a product originating from this specific allele or haplotype, but which do not bind other or alternate variants at the specific polymorphic sites of the target nucleic acid molecule.

As antisense molecules can be used to inactivate mRNA so as to inhibit gene expression, and thus protein expression, the molecules can be used to treat a disease or disorder, such as cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke. The methodology can 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. Such mRNA regions include, for example, protein-coding regions, in particular protein-coding regions corresponding to catalytic activity, substrate and/or ligand binding sites, or other functional domains of a protein.

The phenomenon of RNA interference (RNAi) has been actively studied for the last decade, since its original discovery in *C. elegans* (Fire *et al.*,*Nature* 391:806-11 (1998)), and in recent years its potential use in treatment of human disease has been actively pursued (reviewed in Kim & Rossi, *Nature Rev. Genet.* 8:173-204 (2007)). RNA interference (RNAi), also called gene silencing, is based on using double-stranded RNA molecules (dsRNA) to turn off specific genes. In the cell, cytoplasmic double-stranded RNA molecules (dsRNA) are processed by cellular complexes into small interfering RNA (siRNA).

The siRNA guide the targeting of a protein-RNA complex to specific sites on a target mRNA, leading to cleavage of the mRNA (Thompson, *Drug Discovery Today,* 7:912-917 (2002)). The siRNA molecules are typically about 20, 21, 22 or 23 nucleotides in length. Thus, one aspect of the invention relates to isolated nucleic acid molecules, and the use of those molecules for RNA interference, i.e. as small interfering RNA molecules (siRNA). In one embodiment, the isolated nucleic acid molecules are 18-26 nucleotides in length, preferably 19-25 nucleotides in length, more preferably 20-24 nucleotides in length, and more preferably 21, 22 or 23 nucleotides in length.

Another pathway for RNAi-mediated gene silencing originates in endogenously encoded primary microRNA (pri-miRNA) transcripts, which are processed in the cell to generate precursor miRNA (pre-miRNA). These miRNA molecules are exported from the nucleus to the cytoplasm, where they undergo processing to generate mature miRNA molecules (miRNA), which direct translational inhibition by recognizing target sites in the 3′ untranslated regions of mRNAs, and subsequent mRNA degradation by processing P-bodies (reviewed in Kim & Rossi, *Nature Rev. Genet.* 8:173-204 (2007)).

Clinical applications of RNAi include the incorporation of synthetic siRNA duplexes, which preferably are approximately 20-23 nucleotides in size, and preferably have 3′ overlaps of 2 nucleotides. Knockdown of gene expression is established by sequence-specific design for the target mRNA. Several commercial sites for optimal design and synthesis of such molecules are known to those skilled in the art.

Other applications provide longer siRNA molecules (typically 25-30 nucleotides in length, preferably about 27 nucleotides), as well as small hairpin RNAs (shRNAs; typically about 29 nucleotides in length). The latter are naturally expressed, as described in Amarzguioui *et al.* (*FEBS Lett.* 579:5974-81 (2005)). Chemically synthetic siRNAs and shRNAs are substrates for *in vivo* processing, and in some cases provide more potent gene-silencing than shorter designs (Kim *et al., Nature Biotechnol.* 23:222-226 (2005); Siolas *et al., Nature Biotechnol.* 23:227-231 (2005)). In general siRNAs provide for transient silencing of gene expression, because their intracellular concentration is diluted by subsequent cell divisions. By contrast, expressed shRNAs mediate long-term, stable knockdown of target transcrips, for as long as transcription of the shRNA takes place (Marques *et al., Nature Biotechnol.* 23:559-565 (2006); Brummelkamp *et al., Science* 296: 550-553 (2002)).

Since RNAi molecules, including siRNA, miRNA and shRNA, act in a sequence-dependent manner, the variants of the present invention (*e.g.*, the markers and haplotypes associated with LD block C04, *e.g.*, the markers listed in Tables 5A and 5B) can be used to design RNAi reagents that recognize specific nucleic acid molecules comprising specific alleles and/or haplotypes (*e.g.*, the alleles and/or haplotypes of the present

invention), while not recognizing nucleic acid molecules comprising other alleles or haplotypes. These RNAi reagents can thus recognize and destroy the target nucleic acid molecules. As with antisense reagents, RNAi reagents can be useful as therapeutic agents (i.e., for turning off disease-associated genes or disease-associated gene variants), but may also be useful for characterizing and validating gene function (*e.g.*, by gene knock-out or gene knock-down experiments).

Delivery of RNAi may be performed by a range of methodologies known to those skilled in the art. Methods utilizing non-viral delivery include cholesterol, stable nucleic acid-lipid particle (SNALP), heavy-chain antibody fragment (Fab), aptamers and nanoparticles. Viral delivery methods include use of lentivirus, adenovirus and adeno-associated virus. The siRNA molecules are in some embodiments chemically modified to increase their stability. This can include modifications at the 2' position of the ribose, including 2'-O-methylpurines and 2'-fluoropyrimidines, which provide resistance to Rnase activity. Other chemical modifications are possible and known to those skilled in the art.

The following references provide a further summary of RNAi, and possibilities for targeting specific genes using RNAi: Kim & Rossi, *Nat. Rev. Genet.* 8:173-184 (2007), Chen & Rajewsky, *Nat. Rev. Genet.* 8: 93-103 (2007), Reynolds, *et al., Nat. Biotechnol.* 22:326-330 (2004), Chi *et al., Proc. Natl. Acad. Sci. USA* 100:6343-6346 (2003), Vickers *et al., J. Biol. Chem.* 278:7108-7118 (2003), Agami, *Curr. Opin. Chem. Biol.* 6:829-834 (2002), Lavery, *et al., Curr. Opin. Drug Discov. Devel.* 6:561-569 (2003), Shi, *Trends Genet.* 19:9-12 (2003), Shuey *et al., Drug Discov. Today* 7:1040-46 (2002), McManus *et al., Nat. Rev. Genet.* 3:737-747 (2002), Xia *et al., Nat. Biotechnol.* 20:1006-10 (2002), Plasterk *et al., curr. Opin. Genet. Dev.* 10:562-7 (2000), Bosher *et al., Nat. Cell Biol.* 2:E31-6 (2000), and Hunter, *Curr. Biol.* 9:R440-442 (1999).

A genetic defect leading to increased predisposition or risk for development of a disease, including cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, or a defect causing the disease, may be corrected permanently by administering to a subject carrying the defect a nucleic acid fragment that incorporates a repair sequence that supplies the normal/wild-type nucleotide(s) at the site of the genetic defect. Such site-specific repair sequence may concompass an RNA/DNA oligonucleotide that operates to promote endogenous repair of a subject's genomic DNA. The administration of the repair sequence may be performed by an appropriate vehicle, such as a complex with polyethelenimine, encapsulated in anionic liposomes, a viral vector such as an adenovirus vector, or other pharmaceutical compositions suitable for promoting intracellular uptake of the administered nucleic acid. The genetic defect may then be overcome, since the chimeric oligonucleotides induce the incorporation of the normal sequence into the genome of the subject, leading to expression of the normal/wild-type gene product. The

replacement is propagated, thus rendering a permanent repair and alleviation of the symptoms associated with the disease or condition.

The present invention provides methods for identifying compounds or agents that can be used to treat cardiac arrhythmia, *e.g.* atrial fibrillation and atrial flutter, and stroke. Thus, the variants of the invention are useful as targets for the identification and/or development of therapeutic agents. Such methods may include assaying the ability of an agent or compound to modulate the activity and/or expression of a nucleic acid that includes at least one of the variants (markers and/or haplotypes) of the present invention, or the encoded product of the nucleic acid. This in turn can be used to identify agents or compounds that inhibit or alter the undesired activity or expression of the encoded nucleic acid product. Assays for performing such experiments can be performed in cell-based systems or in cell-free systems, as known to the skilled person. Cell-based systems include cells naturally expressing the nucleic acid molecules of interest, or recombinant cells that have been genetically modified so as to express a certain desired nucleic acid molecule.

Variant gene expression in a patient can be assessed by expression of a variant-containing nucleic acid sequence (for example, a gene containing at least one variant of the present invention, which can be transcribed into RNA containing the at least one variant, and in turn translated into protein), or by altered expression of a normal/wild-type nucleic acid sequence due to variants affecting the level or pattern of expression of the normal transcripts, for example variants in the regulatory or control region of the gene. Assays for gene expression include direct nucleic acid assays (mRNA), assays for expressed protein levels, or assays of collateral compounds involved in a pathway, for example a signal pathway. Furthermore, the expression of genes that are up- or down-regulated in response to the signal pathway can also be assayed. One embodiment includes operably linking a reporter gene, such as luciferase, to the regulatory region of the gene(s) of interest.

Modulators of gene expression can in one embodiment be identified when a cell is contacted with a candidate compound or agent, and the expression of mRNA is determined. The expression level of mRNA in the presence of the candidate compound or agent is compared to the expression level in the absence of the compound or agent. Based on this comparison, candidate compounds or agents for treating disorders such as atrial fibrillation, atrial flutter and stroke can be identified as those modulating the gene expression of the variant gene. When expression of mRNA or the encoded protein is statistically significantly greater in the presence of the candidate compound or agent than in its absence, then the candidate compound or agent is identified as a stimulator or up-regulator of expression of the nucleic acid. When nucleic acid expression or protein level is statistically significantly less in the presence of the candidate compound or agent than in

its absence, then the candidate compound is identified as an inhibitor or down-regulator of the nucleic acid expression.

The invention further provides methods of treatment using a compound identified through drug (compound and/or agent) screening as a gene modulator (i.e. stimulator and/or inhibitor of gene expression).

In a further aspect of the present invention, a pharmaceutical pack (kit) is provided, the pack comprising a therapeutic agent and a set of instructions for administration of the therapeutic agent to humans diagnostically tested for one or more variants of the present invention, as disclosed herein. The therapeutic agent can be a small molecule drug, an antibody, a peptide, an antisense or RNAi molecule, or other therapeutic molecules. In one embodiment, an individual identified as a carrier of at least one variant of the present invention is instructed to take a prescribed dose of the therapeutic agent. In one such embodiment, an individual identified as a homozygous carrier of at least one variant of the present invention is instructed to take a prescribed dose of the therapeutic agent. In another embodiment, an individual identified as a non-carrier of at least one variant of the present invention is instructed to take a prescribed dose of the therapeutic agent.

Methods of assessing probability of response to therapeutic agents, methods of monitoring progress of treatment and methods of treatment

As is known in the art, individuals can have differential responses to a particular therapy (*e.g.,* a therapeutic agent or therapeutic method). Pharmacogenomics addresses the issue of how genetic variations (*e.g.,* the variants (markers and/or haplotypes) of the present invention) affect drug response, due to altered drug disposition and/or abnormal or altered action of the drug . Thus, the basis of the differential response may be genetically determined in part. Clinical outcomes due to genetic variations affecting drug response may result in toxicity of the drug in certain individuals (*e.g.,* carriers or non-carriers of the genetic variants of the present invention), or therapeutic failure of the drug. Therefore, the variants of the present invention may determine the manner in which a therapeutic agent and/or method acts on the body, or the way in which the body metabolizes the therapeutic agent.

Accordingly, in one embodiment, the presence of a particular allele at a polymorphic site or haplotype is indicative of a different, e.g. a different response rate, to a particular treatment modality. This means that a patient diagnosed with cardiac arrhythmia (*e.g.,* atrial fibrillation or atrial flutter) and /or stroke, and carrying a certain

allele at a polymorphic or haplotype of the present invention (*e.g.*, the at-risk and protective alleles and/or haplotypes of the invention) would respond better to, or worse to, a specific therapeutic, drug and/or other therapy used to treat the disease. Therefore, the presence or absence of the marker allele or haplotype could aid in deciding what treatment should be used for a the patient. For example, for a newly diagnosed patient, the presence of a marker or haplotype of the present invention may be assessed (*e.g.*, through testing DNA derived from a blood sample, as described herein). If the patient is positive for a marker allele or haplotype at (that is, at least one specific allele of the marker, or haplotype, is present), then the physician recommends one particular therapy, while if the patient is negative for the at least one allele of a marker, or a haplotype, then a different course of therapy may be recommended (which may include recommending that no immediate therapy, other than serial monitoring for progression of the disease, be performed). Thus, the patient's carrier status could be used to help determine whether a particular treatment modality should be administered. The value lies within the possibilities of being able to diagnose the disease at an early stage, to select the most appropriate treatment, and provide information to the clinician about prognosis/aggressiveness of the disease in order to be able to apply the most appropriate treatment.

Treatment of Atrial Fibrillation and Atrial flutter is generally directed by two main objectives: (i) to prevent stroke and (ii) to treat symptoms.

(i) Stroke Prevention

Anticoagulation is the therapy of choice for stroke prevention in atrial fibrillation and is indicated for the majority of patients with this arrhythmia. The only patients for whom anticoagulation is not strongly recommended are those younger than 65 years old who are considered low-risk, i.e., they have no organic heart disease, no hypertension, no previous history of stroke or transient ischemic attacks and no diabetes. This group as a whole has a lower risk of stroke and stroke prevention with aspirin is generally recommended. For all other patients, anticoagulation is indicated whether the atrial fibrillation is permanent, recurrent paroxysmal or recurrent persistent. It cannot be generalized how patients who present with their first episode of paroxysmal atrial fibrillation should be treated and the decision needs to be individualized for each patient. Anticoagulation is also indicated even when the patient with atrial fibrillation is felt to be maintained in sinus rhythm with antiarrhythmic therapy (rhythm controlled) since this type of therapy does not affect stroke risk.

Anticoagulants. Anticoagulation is recommended in atrial fibrillation, as detailed above, for prevention of cardioembolism and stroke. The most widely studied oral anticoagulant is warfarin and this medication is universally recommended for chronic oral anticoagulation in atrial fibrillation. Warfarin has few side effects aside from the risk of bleeding but requires regular and careful monitoring of blood values during therapy (to measure the effect of the anticoagulation). The oral anticoagulant ximelagatran showed promise in stroke prevention in patients with atrial fibrillation and had the advantage of not requiring regular monitoring like warfarin. Ximelagatran was found however to cause unexplained liver injury and was withdrawn from the market in 2006. Several agents are available for intravenous and/or subcutaneous therapy, including heparin and the low molecular weight heparins (e.g. enoxaparin, dalteparin, tinzaparin, ardeparin, nadroparin and reviparin). These medications are recommended when rapid initiation of anticoagulation is necessary or if oral anticoagulation therapy has to be interrupted in high risk patients or for longer than one week in other patients for example due to a series of procedures. Other parenteral anticoagulants are available but not specifically recommended as therapy in atrial fibrillation; e.g., the factor Xa inhibitors fondaparinux and idraparinux, the thrombin-inhibitors lepirudin, bivalirudin and argatroban as well as danaparoid.

(ii) Symptom Control. Medical and surgical therapy applied to control symptoms of atrial fibrillation is tailored to the individual patient and consists of heart rate and/or rhythm control with medications, radiofrequency ablation and/or surgery.

Antiarrhythmic medications. In general terms, antiarrhythmic agents are used to suppress abnormal rhythms of the heart that are characteristic of cardiac arrhythmias, including atrial fibrillation and atrial flutter. One classification of antiarrhythmic agents is the Vaughan Williams classification, in which five main categories of antiarrhythmic agents are defined. Class I agents are fast sodium channel blockers and are subclassified based on kinetics and strenght of blockade as well as their effect on repolarization. Class Ia includes disopyramide, moricizine, procainamide and quinidine. Class Ib agents are lidocaine, mexiletine, tocainide, and phenytoin. Class Ic agents are encainide, flecainide, propafenone, ajmaline, cibenzoline and detajmium. Class II agents are beta blockers, they block the effects of catecholamines at beta-adrenergic receptors. Examples of beta blockers are esmolol, propranolol, metoprolol, alprenolol, atenolol, carvedilol, bisoprolol, acebutolol, nadolol, pindolol, labetalol, oxprenotol, penbutolol, timolol, betaxolol, cartelol, sotalol and levobunolol. Class III agents have mixed properties but are collectively potassium channel blockers and prolong repolarization. Medications in this category are amiodarone, azimilide, bretylium, dofetilide, tedisamil, ibutilide, sematilide, sotalol, N-acetyl procainamide, nifekalant hydrochloride, vernakalant and ambasilide. Class IV agents are calcium channel blockers and include verapamil, mibefradil and diltiazem.

Finally, class V consists of miscellaneous antiarrhythmics and includes digoxin and adenosine.

Heart rate control, Pharmacologic measures for maintenance of heart rate control include beta blockers, calcium channel blockers and digoxin. All these medications slow the electrical conduction through the atrioventricular node and slow the ventricular rate response to the rapid atrial fibrillation. Some antiarrhythmics used primarily for rhythm control (see below) also slow the atrioventricular node conduction rate and thus the ventricular heart rate response. These include some class III and Ic medications such as amiodarone, sotalol and flecainide.

Cardioversion. Cardioversion of the heart rhythm from atrial fibrillation or atrial flutter to sinus rhythm can be achieved electrically, with synchronized direct-current cardioversion, or with medications such as ibutilide, amiodarone, procainamide, propafenone and flecainide.

Heart rhythm control

Medications used for maintenance of sinus rhythm, i.e. rhythm control, include mainly antiarrhythmic medications from classes III, Ia and Ic. Examples are sotalol, amiodarone and dofetilide from class III, disopyramide, procainamide and quinidine from class Ia and flecinide and propafenone from class Ic. Treatment with these antiarrhythmic medications is complicated, can be hazardous, and should be directed by physicians specifically trained to use these medications. Many of the antiarrhythmics have serious side effects and should only be used in specific populations. For example, class Ic medications should not be used in patients with coronary artery disease and even if they can suppress atrial fibrillation, they can actually promote rapid ventricular response in atrial flutter. Class Ia medications can be used as last resort in patients without structural heart diseases. Sotalol (as most class III antiarrhythmics) can cause significant prolongation of the QT interval, specifically in patients with renal failure, and promote serious ventricular arrhythmias. Both sotalol and dofetilide as well as the Ia medications need to be initiated on an inpatient basis to monitore the QT interval. Although amiodarone is usually well tolerated and is widely used, amiodarone has many serious side effects with long-term therapy.

How genetic testing may directly affect choice of treatment

When individuals present with their first (diagnosed) episode of paroxysmal atrial fibrillation and either spontaneously convert to sinus rhythm or undergo electrical or chemical cardioversion less than 48 hours into the episode, the decision to initiate, or not

to initiate, anticoagulation therapy, is individualized based on the risk profile of the patient in question and the managing physicians preference. This can be a difficult choice to make since committing the patient to anticoagulation therapy has a major impact on the patients life. Often the choice is made to withhold anticoagulation in such a situation and this may be of no significant consequence to the patient. On the other hand the patient may later develop a stroke and the opportunity of prevention may thus have been missed. In such circumstances, knowing that the patient is a carrier of the at-risk variant may be of great significance and support initiation of anticoagulation treatment.

Individuals who are diagnosed with atrial fibrillation under the age of 65 and are otherwise considered low risk for stroke, i.e. have no organic heart disease, no hypertension, no diabetes and no previous history of stroke, are generally treated with aspirin only for stroke-prevention and not anticoagulation. If such a patient is found to be carrier for the at-risk variants described herein, this could be considered support for initiating anticoagulation earlier than otherwise recommended. This would be a reasonable consideration since the results of stroke from atrial fibrillation can be devastating.

Ischemic stroke is generally classified into five subtypes based on suspected cause; large artery atherosclerosis, small artery occlusion, cardioembolism (majority due to atrial fibrillation), stroke of other determined cause and stroke of undetermined cause (either no cause found or more than 1 plausible cause). Importantly, strokes due to cardioembolism have the highest recurrence, are most disabling and are associated with the lowest survival. It is therefore imperative not to overlook atrial fibrillation as the major cause of stroke, particularly since treatment measures vary based on the subtype. Therefore, if an individual is diagnosed with stroke or a transient ischemic attack and a plausible cause is not identified despite standard work-up, knowing that the patient is a carrier of the at-risk variant may be of great value and support either initiation of anticoagulation treatment or more aggressive diagnostic testing in the attempt to diagnose atrial fibrillation.

Furthermore, the markers of the present invention can be used to increase power and effectiveness of clinical trials. Thus, individuals who are carriers of at least one at-risk variant of the present invention, i.e. individuals who are carriers of at least one allele of at least one polymorphic marker conferring increased risk of developing cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke may be more likely to respond to a particular treatment modality, e.g., as described in the above. In one embodiment, individuals who carry at-risk variants for gene(s) in a pathway and/or metabolic network for which a particular treatment (*e.g.*, small molecule drug) is targeting, are more likely to be responders to the treatment. In another embodiment, individuals who carry at-risk variants for a gene, which expression and/or function is altered by the at-risk variant, are more likely to be responders to a treatment modality targeting that gene, its expression or its gene product. This application can improve the safety of clinical trials, but can also

enhance the chance that a clinical trial will demonstrate statistically significant efficacy, which may be limited to a certain sub-group of the population. Thus, one possible outcome of such a trial is that carriers of certain genetic variants, *e.g.*, the markers and haplotypes of the present invention, are statistically significantly likely to show positive response to the therapeutic agent, i.e. experience alleviation of symptoms associated with cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke when taking the therapeutic agent or drug as prescribed.

In a further aspect, the markers and haplotypes of the present invention can be used for targeting the selection of pharmaceutical agents for specific individuals. Personalized selection of treatment modalities, lifestyle changes or combination of the two, can be realized by the utilization of the at-risk variants of the present invention. Thus, the knowledge of an individual's status for particular markers of the present invention, can be useful for selection of treatment options that target genes or gene products affected by the at-risk variants of the invention. Certain combinations of variants may be suitable for one selection of treatment options, while other gene variant combinations may target other treatment options. Such combination of variant may include one variant, two variants, three variants, or four or more variants, as needed to determine with clinically reliable accuracy the selection of treatment module.

Computer-implemented applications

The present invention also relates to computer-implemented applications of the polymorphic markers and haplotypes described herein to be associated with cardiac arrhythmia (e.g., atrial fibrillation and atrial flutter) and stroke. Such applications can be useful for storing, manipulating or otherwise analyzing genotype data that is useful in the methods of the invention. One example pertains to storing genotype information derived from an individual on readable media, so as to be able to provide the genotype information to a third party (*e.g.*, the individual), or for deriving information from the genotype data, *e.g.*, by comparing the genotype data to information about genetic risk factors contributing to increased susceptibility to cardiac arrhythmia (e.g., atrial fibrillation and atrial flutter) and stroke, and reporting results based on such comparison.

One such aspect relates to computer-readable media. In general terms, such medium has capabilities of storing (i) identifier information for at least one polymorphic marker or a haplotye; (ii) an indicator of the frequency of at least one allele of said at least one marker, or the frequency of a haplotype, in individuals with cardiac arrhythmia (e.g., atrial fibrillation and atrial flutter) and/or stroke; and an indicator of the frequency of at least one allele of said at least one marker, or the frequency of a haplotype, in a reference

population. The reference population can be a disease-free population of individuals. Alternatively, the reference population is a random sample from the general population, and is thus representative of the population at large. The frequency indicator may be a calculated frequency, a count of alleles and/or haplotype copies, or normalized or otherwise manipulated values of the actual frequencies that are suitable for the particular medium.

Additional information about the individual can be stored on the medium, such as ancestry information, information about sex, physical attributes or characteristics (including height and weight), biochemical measurements (such as blood pressure, blood lipid levels, fasting glucose levels, insulin response measurements), biomarker results, or other useful information that is desirable to store or manipulate in the context of the genotype status of a particular individual.

The invention furthermore relates to an apparatus that is suitable for determination or manipulation of genetic data useful for determining a susceptibility to cardiac arrhythmia (e.g., atrial fibrillation and atrial flutter) and stroke in a human individual. Such an apparatus can include a computer-readable memory, a routine for manipulating data stored on the computer-readable memory, and a routine for generating an output that includes a measure of the genetic data. Such measure can include values such as allelic or haplotype frequencies, genotype counts, sex, age, phenotype information, values for odds ratio (OR) or relative risk (RR), population attributable risk (PAR), or other useful information that is either a direct statistic of the original genotype data or based on calculations based on the genetic data.

The above-described applications can all be practiced with the markers and haplotypes of the invention that have in more detail been described with respect to methods of assessing susceptibility to cardiac arrhythmia (e.g., atrial fibrillation and atrial flutter) and stroke. Thus, these applications can in general be reduced to practice using markers listed in Tables 5, Table 4, Table 9, and Table 19, and markers in linkage disequilibrium therewith. In one embodiment, the markers or haplotypes are present within the genomic segment whose sequences is set forth in SEQ ID NO:50. In another embodimetn, the markers or haplotypes comprise at least one marker selected from the markers set forth in Table 19. In another embodiment, the markers and haplotypes comprise at least one marker selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51), optionally including markers in linkage disequilibrium therewith. In one such embodiment, linkage disequilibrium is defined by numerical values for r^2 of greater than 0.1. In another such embodiment, linkage disequilibrium is defined by numerical values for r^2 of greater than 0.2. In another embodiment, the marker or haplotype comprises at least one allele selected from alleles -

2, -4 and/or -8 in marker D4S406, allele A of marker rs2634073, allele T of marker rs2200733, allele T of marker rs2220427, allele T of marker rs10033464, and/or allele G of marker rs13143308

Nucleic acids and polypeptides

The nucleic acids and polypeptides described herein can be used in methods an kits of the present invention, as described in the above.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.,* as in an RNA library). For example, an isolated nucleic acid of the invention can be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material can be purified to essential homogeneity, for example as determined by polyacrylamide gel electrophoresis (PAGE) or column chromatography (*e.g.,* HPLC). An isolated nucleic acid molecule of the invention can comprise at least about 50%, at least about 80% or at least about 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 250 kb, 200 kb, 150 kb, 100 kb, 75 kb, 50 kb, 25 kb, 10 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of the nucleotides that flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells or heterologous organisms, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Such isolated nucleotide sequences are useful, for example, in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences

(*e.g.,* from other mammalian species), for gene mapping (*e.g.,* by *in situ* hybridization with chromosomes), or for detecting expression of the gene in tissue (*e.g.,* human tissue), such as by Northern blot analysis or other hybridization techniques.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.,* nucleic acid molecules that specifically hybridize to a nucleotide sequence containing a polymorphic site associated with a marker or haplotype described herein). In one embodiment, the invention includes variants that hybridize under high stringency hybridization and wash conditions (*e.g.*, for selective hybridization) to a nucleotide sequence that comprises the nucleotide sequence of LD Block C04 (SEQ ID NO:50). Such nucleic acid molecules can be detected and/or isolated by allele- or sequence-specific hybridization (*e.g.,* under high stringency conditions). Stringency conditions and methods for nucleic acid hybridizations are well known to the skilled person (see, *e.g., Current Protocols in Molecular Biology*, Ausubel, F. *et al*, John Wiley & Sons, (1998), and Kraus, M. and Aaronson, S., *Methods Enzymol.*, 200:546-556 (1991), the entire teachings of which are incorporated by reference herein.

The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.,* gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%, of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A non-limiting example of such a mathematical algorithm is described in Karlin, S. and Altschul, S., *Proc. Natl. Acad. Sci. USA, 90*:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0), as described in Altschul, S. *et al., Nucleic Acids Res., 25*:3389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.,* NBLAST) can be used. See the website on the world wide web at ncbi.nlm.nih.gov. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.,* W=5 or W=20).

Other examples include the algorithm of Myers and Miller, CABIOS (1989), ADVANCE and ADAM as described in Torellis, A. and Robotti, C., *Comput. Appl. Biosci. 10*:3-5 (1994); and FASTA described in Pearson, W. and Lipman, D., *Proc. Natl. Acad. Sci. USA, 85*:2444-48 (1988). In another embodiment, the percent identity between two

amino acid sequences can be accomplished using the GAP program in the GCG software package (Accelrys, Cambridge, UK).

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleic acid that comprises, or consists of, the nucleotide sequence of LD Block C04 (SEQ ID NO:50), or a nucleotide sequence comprising, or consisting of, the complement of the nucleotide sequence of LD Block C04 (SEQ ID NO:50), wherein the nucleotide sequence comprises at least one polymorphic allele contained in the markers and haplotypes described herein. The nucleic acid fragments of the invention are at least about 15, at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200, 500, 1000, 10,000 or more nucleotides in length.

The nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of a nucleic acid molecule. In addition to DNA and RNA, such probes and primers include polypeptide nucleic acids (PNA), as described in Nielsen, P. *et al.*, *Science 254*:1497-1500 (1991). A probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and in certain embodiments about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule. In one embodiment, the probe or primer comprises at least one allele of at least one polymorphic marker or at least one haplotype described herein, or the complement thereof. In particular embodiments, a probe or primer can comprise 100 or fewer nucleotides; for example, in certain embodiments from 6 to 50 nucleotides, or, for example, from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical, at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical, to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. In another embodiment, the probe or primer is capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, a radioisotope, a fluorescent label, an enzyme label, an enzyme co-factor label, a magnetic label, a spin label, an epitope label.

The nucleic acid molecules of the invention, such as those described above, can be identified and isolated using standard molecular biology techniques well known to the skilled person. The amplified DNA can be labeled (*e.g.*, radiolabeled) and used as a probe for screening a cDNA library derived from human cells. The cDNA can be derived from mRNA and contained in a suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art-recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. Using these or similar methods, the

polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers that are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke or a susceptibility to cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample (*e.g.*, subtractive hybridization). The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using immunization techniques, and/or as an antigen to raise anti-DNA antibodies or elicit immune responses.

Antibodies

Polyclonal antibodies and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided which bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain antigen-binding sites that specifically bind an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and $F(ab')_2$ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or a fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using

immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4: 72 (1983)), the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss,1985, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.*, (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981)). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *Surf*ZAP™ Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9: 1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246: 1275-1281 (1989); and Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. The antibody can be coupled to a detectable substance to facilitate its detection. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-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 ^{3}H.

Antibodies may also be useful in pharmacogenomic analysis. In such embodiments, antibodies against variant proteins encoded by nucleic acids according to the invention, such as variant proteins that are encoded by nucleic acids that contain at least one polymorphic marker of the invention, can be used to identify individuals that require modified treatment modalities.

Antibodies can furthermore be useful for assessing expression of variant proteins in disease states, such as in active stages of a disease, or in an individual with a predisposition to a disease related to the function of the protein, in particular cardiac arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke. Antibodies specific for a variant protein of the present invention that is encoded by a nucleic acid that comprises at least one polymorphic marker or haplotype as described herein can be used to screen for the presence of the variant protein, for example to screen for a predisposition to cardiac

arrhythmia (*e.g.*, atrial fibrillation or atrial flutter) and /or stroke as indicated by the presence of the variant protein.

Antibodies can be used in other methods. Thus, antibodies are useful as diagnostic tools for evaluating proteins, such as variant proteins of the invention, in conjunction with analysis by electrophoretic mobility, isoelectric point, tryptic or other protease digest, or for use in other physical assays known to those skilled in the art. Antibodies may also be used in tissue typing. In one such embodiment, a specific variant protein has been correlated with expression in a specific tissue type, and antibodies specific for the variant protein can then be used to identify the specific tissue type.

Subcellular localization of proteins, including variant proteins, can also be determined using antibodies, and can be applied to assess aberrant subcellular localization of the protein in cells in various tissues. Such use can be applied in genetic testing, but also in monitoring a particular treatment modality. In the case where treatment is aimed at correcting the expression level or presence of the variant protein or aberrrant tissue distribution or developmental expression of the variant protein, antibodies specific for the variant protein or fragments thereof can be used to monitor therapeutic efficacy.

Antibodies are further useful for inhibiting variant protein function, for example by blocking the binding of a variant protein to a binding molecule or partner. Such uses can also be applied in a therapeutic context in which treatment involves inhibiting a variant protein's function. An antibody can be for example be used to block or competitively inhibit binding, thereby modulating (i.e., agonizing or antagonizing) the activity of the protein. Antibodies can be prepared against specific protein fragments containing sites required for specific function or against an intact protein that is associated with a cell or cell membrane. For administration *in vivo*, an antibody may be linked with an additional therapeutic payload, such as radionuclide, an enzyme, an immunogenic epitope, or a cytotoxic agent, including bacterial toxins (diphteria or plant toxins, such as ricin). The *in vivo* half-life of an antibody or a fragment thereof may be increased by pegylation through conjugation to polyethylene glycol.

The present invention further relates to kits for using antibodies in the methods described herein. This includes, but is not limited to, kits for detecting the presence of a variant protein in a test sample. One preferred embodiment comprises antibodies such as a labelled or labelable antibody and a compound or agent for detecting variant proteins in a biological sample, means for determining the amount or the presence and/or absence of variant protein in the sample, and means for comparing the amount of variant protein in the sample with a standard, as well as instructions for use of the kit.

The present invention will now be exemplified by the following non-limiting example.

EXEMPLIFICATION

Example 1. Identification of at-risk variants for Atrial Fibrillation on chromosome 4.

The following contains description of the identification of susceptibility factors found to be associated with atrial fibrillation and stroke through single-point analysis of SNP markers.

Methods. The study was approved by the Data Protection Commission of Iceland and the National Bioethics Committee.

Icelandic AF cohort. The patients were all diagnosed with AF at the Landspitali University Hospital in Reykjavik, Iceland, from 1987 to 2003. Diagnoses were confirmed by a 12 lead electrocardiogram demonstrating no P waves and irregularly irregular R-R intervals. All ECGs were manually read by a cardiologist.

Icelandic Stroke cohort. The stroke cohort was derived from two major hospitals in Iceland and the Icelandic Heart Association. Patients with hemorrhagic stroke represented 6% of all patients (patients with the Icelandic type of hereditary cerebral hemorrhage with amyloidosis and patients with subarachnoid hemorrhage were excluded). Ischemic stroke accounted for 67% of the total patients and TIAs 27%. The distribution of stroke suptypes in this study is similar to that reported in other Caucasian populations (Mohr, J.P., *et al., Neurology, 28*:754-762 (1978); L. R. Caplan, *In Stroke, A Clinical Approach* (Butterworth-Heinemann, Stoneham, MA, ed 3, (1993)).

Genotyping. A genome-wide scan of 437 Icelandic individuals diagnosed with Atrial Fibrillation (AF) and 7406 population controls was performed using Infinium HumanHap300 SNP chips from Illumina for assaying approximately 317,000 single nucleotide polymorphisms (SNPs) on a single chip (Illumina, San Diego, CA, USA). SNP genotyping for replication in other case-control cohorts was carried using the Centaurus platform

(Nanogen). A total of 347 individuals diagnosed with Stroke and 7497 controls was also performed for SNPs within the LD Block found to be associated with Atrial Fibrillation.

Statistical Methods for Association Analysis. For single marker association to atrial fibrillation or stroke, we used a likelihood ratio test to calculate a two-sided p-value for each allele. We calculated relative risk (RR) *and population attributable risk (PAR) assuming a multiplicative model (C. T. Falk, P.* Rubinstein, *Ann Hum Genet* 51 (Pt 3), 227 (1987); J. D. Terwilliger, J. Ott, *Hum Hered* 42, 337 (1992)). For the CEPH Caucasian HapMap data, we calculated LD between pairs of SNPs using the standard definition of D' (R. C. Lewontin, *Genetics* 50, 757 (1964)) and R^2 W. G. Hill, A. Robertson, *Genetics* 60, 615 (Nov, 1968). When plotting all SNP combinations to elucidate the LD structure in a particular region, we plotted D' in the upper left corner and p-values in the lower right corner. In the LD plots we present, the markers are plotted equidistantly rather than according to their physical positions.

RESULTS

Genome-wide association study

We successfully genotyped 437 Icelandic Atrial Fibriallation patients and 7406 population control individuals using the Illumina 330K chip. Association analysis was performed for single SNPs. The most significant association was found for markers rs2220427 and rs2220733, both of which give p-values close to 10^{-9}. The value for rs2220427 is significant after correcting for the number of tests performed, i.e. the association is significant at the genome-wide level.

There is an apparent excess of homozygotes in affected individuals. We reject both the multiplicative model (P=.002) and the recessive model (P=.001). The best fitting model gives risk 1.46 to heterozygous carriers and 5.17 to homozygous carriers. The (uncorrected) P-value comparing this full model to the null model of no association is 5.43e-11. These data show that individuals with two copies of the at-risk allele are at greater risk than expected based on a simple multiplicative model.

Fitting an age at onset model for all genotypes gives a P-value of 4.84e-5. Heterozygotes are estimated to have onset 1.4090 years earlier than non-carriers and homozygote carriers are estimated to have onset 9.6126 years earlier than non-carriers. This shows a significant effect of age at onset – individuals carrying the at-risk variant are at significant risk of developing AF at a younger age than individuals who are non-carriers of the at-risk allele.

Investigating markers in the vicinity of rs2220427, we realized that the microsatellite marker D4S406 can be used as a surrogate marker for rs2220427. In particular, alleles -2, -4 and -8 (with respect to the CEPH reference) were found to be sufficient to tag the SNP based on haplotype frequencies:

Table 1. *Relationship between rs2220427 and D4S406*

Frequency	Haplotype			
	MS allele		SNP Allele	
7.55E-05	-2	D4S406	2	rs2220427
0.000109727	16	D4S406	4	rs2220427
0.000148065	-6	D4S406	4	rs2220427
0.000149685	20	D4S406	2	rs2220427
0.000149756	-4	D4S406	2	rs2220427
0.000210154	8	D4S406	4	rs2220427
0.000225802	-8	D4S406	2	rs2220427
0.000227036	4	D4S406	4	rs2220427
0.000299371	18	D4S406	2	rs2220427
0.000899281	0	D4S406	4	rs2220427
0.00203518	-4	D4S406	4	rs2220427
0.00673851	-6	D4S406	2	rs2220427
0.0245484	2	D4S406	2	rs2220427
0.0394983	-2	D4S406	4	rs2220427
0.0422112	14	D4S406	2	rs2220427
0.0594303	0	D4S406	2	rs2220427
0.0762831	-8	D4S406	4	rs2220427
0.0855451	6	D4S406	2	rs2220427
0.0949753	12	D4S406	2	rs2220427
0.100105	16	D4S406	2	rs2220427
0.145942	4	D4S406	2	rs2220427
0.155838	8	D4S406	2	rs2220427
0.164354	10	D4S406	2	rs2220427

Thus, for individuals typed for the D4S406 marker but not rs222047, merging the -2, -4 and -8 alleles leads to a very good estimate of the frequency of the 4 allele of the SNP. We analyzed an Icelandic replication cohort for AF, comprised of 1269 cases and 69,070 controls, in this fashion. The results are quite dramatic in that the association is accompanied by a p-value of 2.94e-14 and a relative risk (multiplicative model) of 1.53. Thus, our initial finding has been replicated in an independent Icelandic cohort.

Table 2. *Association of AF patients to Chromosome 4 (LD Block C04) . Shown are values for RR under the multiplicative model.*

p-value	Relative Risk	Aff freq	Con freq	Allele	Marker
0.16839039	0.8473	0.902746	0.916352	3	rs10033464
0.16839039	1.1802	0.097254	0.083648	4	rs10033464
0.24275346	0.8746	0.098398	0.110939	1	rs13105878
0.24275346	1.1433	0.901602	0.889061	2	rs13105878
4.89E-06	1.3816	0.441648	0.364078	1	rs13141190
4.89E-06	0.7238	0.558352	0.635922	3	rs13141190
1.25E-06	0.6905	0.677346	0.752498	1	rs1448817
1.25E-06	1.4483	0.322654	0.247502	3	rs1448817
0.00995996	0.7903	0.811213	0.844653	2	rs16997168
0.00995996	1.2654	0.188787	0.155347	4	rs16997168
1.07E-09	0.5601	0.811213	0.884688	2	rs2200733
1.07E-09	1.7855	0.188787	0.115312	4	rs2200733
7.78E-10	0.557	0.810345	0.884673	2	rs2220427
7.78E-10	1.7953	0.189655	0.115327	4	rs2220427
9.75E-08	1.5803	0.236239	0.163692	1	rs2634073
9.75E-08	0.6328	0.763761	0.836308	3	rs2634073
0.96927011	0.9968	0.768879	0.769444	1	rs2723296
0.96927011	1.0032	0.231121	0.230556	3	rs2723296
0.03281713	0.8529	0.665904	0.700311	2	rs2723316
0.03281713	1.1724	0.334096	0.299689	4	rs2723316
0.01803327	1.1855	0.635632	0.595393	1	rs3853444
0.01803327	0.8435	0.364368	0.404607	3	rs3853444
0.40105752	0.9214	0.146789	0.15734	2	rs4576077
0.40105752	1.0853	0.853211	0.84266	4	rs4576077
0.93269621	1.0084	0.145309	0.144275	1	rs6419178
0.93269621	0.9917	0.854691	0.855725	3	rs6419178

Table 3. *Association of Stroke to markers within LD Block C04 (SEQ ID NO:50)*

p-value	Relative Risk	Aff freq	Con freq	Allele	Marker
0.37701852	0.8872	0.90634	0.916022	3	rs10033464
0.37701852	1.1272	0.09366	0.083978	4	rs10033464
0.2838194	0.8717	0.097983	0.110807	1	rs13105878
0.2838194	1.1472	0.902017	0.889193	2	rs13105878
0.01534596	1.2123	0.412104	0.366378	1	rs13141190
0.01534596	0.8249	0.587896	0.633622	3	rs13141190
0.04856224	0.8418	0.716138	0.7498	1	rs1448817
0.04856224	1.1879	0.283862	0.2502	3	rs1448817
0.14450185	0.8599	0.822767	0.843717	2	rs16997168
0.14450185	1.1629	0.177233	0.156283	4	rs16997168
0.00374992	0.724	0.84438	0.882271	2	rs2200733
0.00374992	1.3812	0.15562	0.117729	4	rs2200733
0.0025713	0.7141	0.842566	0.882274	2	rs2220427
0.0025713	1.4003	0.157434	0.117726	4	rs2220427
0.01664881	1.2682	0.201729	0.166154	1	rs2634073
0.01664881	0.7885	0.798271	0.833846	3	rs2634073
0.58350156	0.9511	0.760807	0.769811	1	rs2723296
0.58350156	1.0514	0.239193	0.230189	3	rs2723296
0.03150475	0.8367	0.661383	0.700107	2	rs2723316
0.03150475	1.1952	0.338617	0.299893	4	rs2723316
0.16517516	1.1172	0.622832	0.596462	1	rs3853444
0.16517516	0.8951	0.377168	0.403538	3	rs3853444
0.24301926	0.8797	0.14121	0.157473	2	rs4576077
0.24301926	1.1367	0.85879	0.842527	4	rs4576077
0.19773377	1.1482	0.161383	0.143543	1	rs6419178
0.19773377	0.8709	0.838617	0.856457	3	rs6419178

Table 4. *Markers in perfect linkage disequilibrium (r^2 = 1.0) with rs2220427 in the CEU population in the International HapMap data set (Individuals of European descent). Also shown are correlation with samples from Yuroba (Nigeria), and Asia (China and Japan) – cohort description is further documented on http://www.hapmap.org.*

SNP	Allele	CEU_R2	CEU_frq	YRI_R2	YRI_frq	ASIA_R2	ASIA_frq
rs17042059	1	1	0.117647	0.500382	0.117647	0.473183	0.30814
rs4529121	1	1	0.116667	0.604601	0.1	0.539766	0.337079
rs4543199	2	1	0.116667	0.502036	0.116667	0.539766	0.337079
rs10019689	1	1	0.116667	0.128175	0.341667	0.664071	0.388889
rs4626276	2	1	0.116667	0.603474	0.10084	0.537439	0.333333
rs17042076	2	1	0.117647	0.128175	0.341667	0.664071	0.388889
rs11098089	2	1	0.117647	0.549368	0.108333	0.539766	0.337079
rs11930528	4	1	0.11017	0.120773	0.321429	0.662926	0.377907
rs17042098	1	1	0.116667	0.669219	0.092437	0.64297	0.355556
rs17042102	1	1	0.091743	NA	NA	0.580822	0.302632
rs17042121	3	1	0.116667	0.736119	0.141667	0.639142	0.353933
rs10516563	3	1	0.109244	0.846743	0.128205	0.636329	0.364706
rs4605724	1	1	0.116667	0.748252	0.083333	0.645257	0.359551
rs2350269	4	1	0.11017	0.495806	0.098214	0.628257	0.346154
rs6533527	1	1	0.116667	0.425151	0.133333	0.804123	0.421348
rs17042144	2	1	0.119658	0.727891	0.077586	NA	NA
rs1906618	2	1	0.115044	NA	NA	NA	NA
rs1906617	2	1	0.116667	0.541206	0.183333	0.977348	0.454545
rs12646447	2	1	0.119658	1	0.108333	1	0.444444
rs12646754	4	1	0.119658	0.681842	0.11017	1	0.425
rs2129981	1	1	0.116667	1	0.108333	1	0.444444
rs12639654	4	1	0.116667	0.139505	0.016667	1	0.438202
rs6817105	2	1	0.117647	0.27862	0.299145	1	0.440476
rs17042171	1	1	0.109244	0.281063	0.302521	1	0.425287
rs1906591	1	1	0.116667	1	0.108333	1	0.444444
rs1906592	3	1	0.109244	0.283489	0.3	1	0.446429
rs2200732	2	1	0.112069	0.272544	0.308334	1	0.449438
rs2200733	4	1	0.116667	0.276161	0.301724	1	0.445783
rs4611994	2	1	0.116667	0.272544	0.308334	1	0.449438
rs4540107	1	1	0.116667	0.27862	0.305085	1	0.44382
rs1906593	4	1	0.117647	0.285134	0.301724	1	0.438202
rs1906596	2	1	0.121739	0.255864	0.330275	0.97478	0.448718

Table 5.

A. *SNP markers within LD Block C04 (Between 111,954,811 and 112,104,250 on C04; NCBI Build 35; SEQ ID NO:50).*

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs1448824	111954811	1	A/G	-
rs1947189	111955221	411	A/G	-
rs1947188	111955479	669	C/G	-
rs1992927	111956353	1543	C/T	-
rs1470619	111957122	2312	A/G	-
rs1448823	111958486	3676	A/G	-
rs4834327	111958676	3866	A/T	+
rs1448822	111958702	3892	C/T	-
rs2044674	111959075	4265	A/G	-
rs28445748	111959470	4660	A/T	+
rs2595116	111959591	4781	C/T	-
rs2595115	111959725	4915	A/C	-
rs13120244	111961948	7138	A/G	+
rs2723296	111962087	7277	A/G	+
rs2723297	111962201	7391	A/T	+
rs10021211	111962246	7436	C/T	+
rs17042011	111962331	7521	C/T	+
rs2595114	111962791	7981	C/G	-
rs2595113	111962792	7982	C/G	-
rs2595112	111963368	8558	C/G	-
rs6831623	111964677	9867	C/T	+
rs6854883	111964919	10109	C/T	+
rs2255793	111965457	10647	A/G	+
rs2723298	111966089	11279	C/T	+
rs12505886	111966218	11408	A/T	+
rs28718263	111966220	11410	A/T	+
rs12501913	111966355	11545	A/C	+
rs13126974	111966385	11575	A/T	+
rs36194761	111966385	11575	A/T	+
rs28473341	111966486	11676	C/T	+
rs36160675	111967780	12970	G/T	+
rs13147139	111968764	13954	A/G	+
rs13147489	111968795	13985	C/T	+
rs13147299	111968812	14002	A/C	+
rs13147726	111968923	14113	C/T	+
rs13147730	111968926	14116	C/T	+
rs13147552	111968949	14139	A/G	+
rs13123918	111968996	14186	A/T	+
rs35610510	111970561	15751	C/T	+
rs36162200	111971480	16670	G/T	+
rs11098086	111971997	17187	C/T	+
rs4034950	111972120	17310	A/G	-
rs11724067	111972144	17334	A/G	+
rs2723299	111972436	17626	A/G	+
rs2723300	111972512	17702	A/G	+
rs13138211	111972606	17796	A/G	+
rs2595075	111973312	18502	C/T	-
rs2723301	111973731	18921	C/G	+
rs2595074	111974709	19899	A/T	-
rs2723302	111974736	19926	C/G	+
rs2723303	111974741	19931	A/G	+
rs2218698	111975356	20546	G/T	-
rs2218697	111975357	20547	C/T	-
rs2595073	111975436	20626	A/G	-
rs2723307	111975800	20990	A/T	+
rs1584430	111976043	21233	C/G	-

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs1584429	111976151	21341	C/G	-
rs1900828	111976526	21716	C/T	-
rs7672226	111976785	21975	C/T	+
rs1839189	111976971	22161	C/T	-
rs1579946	111977724	22914	A/G	-
rs12509115	111977892	23082	A/G	+
rs1579945	111978096	23286	A/T	-
rs7661383	111979181	24371	A/C	+
rs2122078	111979201	24391	A/G	-
rs2122077	111979254	24444	C/T	-
rs2723311	111979626	24816	A/G	+
rs7667461	111979738	24928	A/G	+
rs1448799	111980386	25576	C/T	-
rs1448798	111980789	25979	C/T	-
rs12650829	111980880	26070	A/G	+
rs2723312	111980956	26146	A/G	+
rs1900827	111981343	26533	A/G	-
rs6815628	111981980	27170	C/T	+
rs6838131	111981993	27183	A/G	+
rs6838139	111982000	27190	A/C	+
rs6838295	111982012	27202	C/T	+
rs4582211	111982043	27233	A/G	+
rs4353966	111982088	27278	A/T	+
rs6838536	111982144	27334	C/T	+
rs1375302	111983068	28258	C/T	+
rs1375303	111983069	28259	A/G	+
rs7699114	111983094	28284	C/T	+
rs2197814	111983098	28288	A/C	+
rs2218700	111983340	28530	A/G	+
rs969642	111983529	28719	C/T	+
rs17042020	111984067	29257	A/C	+
rs2595099	111984371	29561	A/C	+
rs4371683	111984371	29561	A/C	+
rs2595093	111984960	30150	C/T	-
rs17625509	111984998	30188	A/G	+
rs2723313	111985093	30283	A/G	+
rs2723314	111985111	30301	G/T	+
rs2595092	111985112	30302	A/G	-
rs2595091	111985223	30413	C/G	-
rs1375301	111985458	30648	A/G	-
rs2245595	111985715	30905	C/T	+
rs2595088	111985958	31148	C/T	-
rs981150	111986232	31422	C/T	-
rs16997168	111986643	31833	C/T	+
rs6812840	111986654	31844	A/T	+
rs16997169	111986685	31875	C/T	+
rs4527540	111986742	31932	C/T	+
rs2595078	111987397	32587	A/G	+
rs11098087	111987538	32728	C/T	+
rs6843456	111988165	33355	C/T	+
rs998101	111988219	33409	A/G	-
rs13120535	111989691	34881	A/G	+
rs17042026	111989978	35168	A/G	+
rs6840960	111991045	36235	C/T	+
rs2122079	111991108	36298	C/T	+
rs2166961	111991365	36555	C/T	+
rs2723316	111991891	37081	C/T	+
rs2595079	111992019	37209	A/G	+
rs7665126	111992019	37209	A/G	+
rs2595080	111992042	37232	A/G	+

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs12646859	111992237	37427	G/T	+
rs10222783	111992430	37620	C/T	+
rs12498380	111992563	37753	C/T	+
rs2595081	111992761	37951	C/T	+
rs2595082	111992896	38086	G/T	+
rs2723317	111993104	38294	A/G	+
rs6419178	111993104	38294	A/G	+
rs13110876	111993625	38815	A/G	+
rs2595083	111993625	38815	A/G	+
rs7690164	111994069	39259	C/T	+
rs2595084	111994163	39353	A/G	+
rs2595085	111994377	39567	C/G	+
rs2595086	111994385	39575	C/T	+
rs2723318	111994576	39766	G/T	+
rs17042050	111994805	39995	C/T	+
rs9998222	111995088	40278	A/G	+
rs2723319	111995233	40423	A/T	+
rs2595087	111995380	40570	C/T	+
rs17042052	111995521	40711	A/T	+
rs28558677	111995664	40854	G/T	+
rs6812731	111995691	40881	A/C	+
rs2723320	111997050	42240	C/T	+
rs12644107	111997588	42778	C/T	+
rs28482179	111998237	43427	C/T	+
rs28759131	111998559	43749	C/T	+
rs1448817	111998657	43847	A/G	+
rs28526075	111998725	43915	A/G	+
rs17042059	111998790	43980	A/G	+
rs10014075	112000023	45213	G/T	+
rs10026140	112000455	45645	G/T	+
rs13351232	112000455	45645	G/T	+
rs7666806	112000477	45667	G/T	+
rs10028327	112000489	45679	G/T	+
rs12650941	112002415	47605	A/T	+
rs28650220	112002617	47807	C/T	+
rs13113361	112002671	47861	G/T	+
rs13113522	112002686	47876	G/T	+
rs4529121	112003159	48349	A/G	+
rs6831284	112003582	48772	G/T	+
rs10009621	112003846	49036	C/T	+
rs10021534	112003945	49135	C/T	+
rs10032150	112004222	49412	A/G	+
rs10024267	112004571	49761	C/T	+
rs10012705	112004726	49916	C/T	+
rs11943627	112005073	50263	C/T	+
rs4543199	112005744	50934	C/T	+
rs28410055	112006340	51530	A/G	+
rs7693227	112006532	51722	C/T	+
rs6852197	112006679	51869	A/G	+
rs12647316	112006855	52045	C/T	+
rs12647393	112006886	52076	G/T	+
rs10019645	112007248	52438	G/T	+
rs10019689	112007473	52663	A/C	+
rs4626276	112007593	52783	A/C	+
rs10022067	112007672	52862	C/T	+
rs4469143	112007678	52868	C/G	+
rs6836206	112007902	53092	C/T	+
rs13150693	112008086	53276	G/T	+
rs11737632	112008416	53606	C/T	+
rs5011975	112008427	53617	A/G	+

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs6811511	112008429	53619	A/C	+
rs4383676	112008437	53627	A/G	+
rs28392642	112009161	54351	C/T	+
rs17631468	112009386	54576	A/G	+
rs17042076	112009942	55132	C/T	+
rs4434326	112010480	55670	C/T	+
rs17042081	112010815	56005	G/T	+
rs4833436	112011350	56540	C/T	+
rs7679623	112011519	56709	A/C	+
rs11098088	112011728	56918	C/T	+
rs4530699	112011761	56951	A/T	+
rs11098089	112011830	57020	A/C	+
rs17042088	112012418	57608	C/T	+
rs12648785	112013496	58686	A/G	+
rs12639820	112013644	58834	C/T	+
rs10001807	112013708	58898	A/G	+
rs10024486	112013722	58912	G/T	+
rs12648889	112013890	59080	C/G	+
rs28376747	112013925	59115	A/G	+
rs11098090	112014012	59202	C/T	+
rs11944778	112014571	59761	A/G	+
rs7436333	112014951	60141	A/C	+
rs4307025	112015107	60297	A/T	+
rs4447925	112015252	60442	C/T	+
rs28523292	112015772	60962	C/T	+
rs28635581	112015858	61048	C/T	+
rs28508237	112016004	61194	C/T	+
rs28521134	112016167	61357	C/T	+
rs17042093	112017716	62906	C/G	+
rs11930438	112017749	62939	C/T	+
rs28542185	112017795	62985	C/T	+
rs11930528	112017798	62988	G/T	+
rs13121382	112020177	65367	G/T	+
rs7439625	112021082	66272	A/T	+
rs28501998	112021318	66508	A/T	+
rs10016838	112021718	66908	C/T	+
rs17042098	112021762	66952	A/G	+
rs10005076	112021953	67143	C/T	+
rs10027473	112022056	67246	A/G	+
rs2634073	112023387	68577	A/G	-
rs1906611	112023520	68710	A/G	-
rs1906610	112023521	68711	C/T	-
rs28446238	112024025	69215	A/C	+
rs1906609	112024055	69245	A/C	-
rs34916665	112025294	70484	G/T	+
rs17042102	112026230	71420	A/G	+
rs17042104	112026555	71745	C/T	+
rs10015819	112026628	71818	C/T	+
rs2634071	112026824	72014	A/G	-
rs10007386	112028021	73211	C/T	+
rs10007547	112028050	73240	A/G	+
rs12647522	112028465	73655	C/T	+
rs1906614	112028900	74090	A/G	-
rs2723335	112029230	74420	A/G	+
rs17042112	112029281	74471	C/T	+
rs17042115	112029414	74604	A/G	+
rs10013510	112029527	74717	C/G	+
rs11939057	112029755	74945	C/T	+
rs2634076	112029877	75067	A/G	-
rs2723293	112031377	76567	A/G	+

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs28494131	112032777	77967	C/T	+
rs2634075	112033582	78772	A/G	-
rs13121715	112034239	79429	G/T	+
rs2634074	112034645	79835	A/T	-
rs17042121	112034705	79895	A/G	+
rs10516563	112035326	80516	G/T	+
rs17042125	112035883	81073	A/G	+
rs13136439	112036254	81444	G/T	+
rs13114686	112036503	81693	C/T	+
rs36166388	112037782	82972	A/G	+
rs2450934	112038532	83722	A/C	-
rs36138049	112040474	85664	A/C	+
rs36168695	112040495	85685	A/G	+
rs36129850	112040548	85738	A/G	+
rs12513264	112041966	87156	C/T	+
rs2882365	112041975	87165	A/G	+
rs36139649	112042072	87262	C/T	+
rs4033107	112042072	87262	C/T	+
rs36176419	112042092	87282	A/G	+
rs4033108	112042092	87282	A/G	+
rs4450997	112042160	87350	A/C	+
rs2350268	112042213	87403	A/G	+
rs4613627	112042225	87415	A/C	+
rs4033109	112042227	87417	C/T	+
rs4833443	112042247	87437	C/T	+
rs2723336	112042258	87448	C/T	-
rs4033111	112042302	87492	A/G	+
rs1807360	112042333	87523	C/T	-
rs4605724	112042685	87875	A/C	+
rs6856879	112043066	88256	A/T	+
rs6834418	112043172	88362	C/T	+
rs2466455	112043219	88409	A/G	-
rs6857810	112043220	88410	A/G	+
rs2634079	112043541	88731	C/G	-
rs28366840	112043710	88900	A/T	+
rs2350269	112044728	89918	C/T	+
rs7665409	112045070	90260	C/T	+
rs6533527	112045118	90308	A/C	+
rs12649717	112045283	90473	A/C	+
rs6822831	112045374	90564	A/G	+
rs35916701	112046074	91264	C/T	+
rs6829419	112046178	91368	C/T	+
rs2723334	112046356	91546	A/G	-
rs2634078	112046528	91718	C/T	-
rs12512819	112046597	91787	C/T	+
rs17042144	112047270	92460	C/T	+
rs2171594	112047908	93098	A/G	-
rs6842887	112048170	93360	A/G	+
rs2171593	112048375	93565	G/T	-
rs7690874	112048681	93871	A/G	+
rs17042145	112049101	94291	G/T	+
rs17042146	112049106	94296	C/T	+
rs9998815	112049904	95094	C/G	+
rs7683336	112051207	96397	C/T	+
rs17042150	112051452	96642	A/T	+
rs10016842	112051810	97000	C/T	+
rs10005432	112052219	97409	A/G	+
rs1906620	112052624	97814	C/T	-
rs1906619	112052670	97860	C/T	-
rs1906618	112053026	98216	C/T	-

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs1906617	112053418	98608	C/T	-
rs6847935	112054255	99445	A/T	+
rs6831873	112055138	100328	C/T	+
rs1906616	112055172	100362	C/T	-
rs6837901	112055712	100902	C/T	+
rs2723333	112056695	101885	C/T	-
rs12646447	112056930	102120	C/T	+
rs6820568	112057435	102625	C/T	+
rs1906615	112059402	104592	A/C	-
rs2634077	112061112	106302	A/G	-
rs7689774	112061114	106304	G/T	+
rs12646754	112061176	106366	C/T	+
rs35807830	112061497	106687	G/T	+
rs2129983	112061684	106874	C/T	-
rs2129982	112061747	106937	C/T	-
rs2129981	112061803	106993	A/C	-
rs6854111	112062140	107330	A/T	+
rs12639654	112062899	108089	C/T	+
rs4515229	112062985	108175	A/G	+
rs2129984	112063010	108200	C/T	+
rs6817105	112063372	108562	C/T	+
rs12503217	112063765	108955	C/T	+
rs2634070	112064016	109206	A/C	+
rs17042171	112065891	111081	A/C	+
rs7434417	112066042	111232	A/G	+
rs1906591	112066493	111683	A/G	+
rs1906592	112066608	111798	G/T	+
rs12510087	112066632	111822	A/G	+
rs7661554	112067221	112411	A/G	+
rs34796144	112067333	112523	A/C	+
rs2200732	112067646	112836	C/T	+
rs2200733	112067773	112963	C/T	+
rs17042175	112068571	113761	A/T	+
rs4611994	112068645	113835	C/T	+
rs4540107	112068706	113896	A/C	+
rs1906593	112069526	114716	C/T	+
rs4371684	112069651	114841	A/G	+
rs1906594	112069739	114929	A/G	+
rs1906595	112069788	114978	G/T	+
rs1906596	112069840	115030	C/T	+
rs6838775	112069908	115098	G/T	+
rs2129977	112070036	115226	A/G	+
rs2129978	112070158	115348	A/C	+
rs1906597	112070190	115380	G/T	+
rs1906598	112070229	115419	C/T	+
rs1906599	112070290	115480	C/T	+
rs1906600	112070480	115670	C/T	+
rs1906601	112070883	116073	C/T	+
rs1906602	112070927	116117	C/T	+
rs1906603	112071040	116230	C/T	+
rs28645285	112071426	116616	A/G	+
rs2171590	112071435	116625	C/T	+
rs6852357	112071939	117129	C/T	+
rs13143308	112072023	117213	G/T	+
rs2220427	112072493	117683	C/T	+
rs17632693	112072538	117728	C/T	+
rs11935917	112072850	118040	A/G	+
rs4833456	112073911	119101	C/T	+
rs12644625	112074117	119307	C/T	+
rs4400058	112074277	119467	A/G	+

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs1906604	112074452	119642	A/G	+
rs1906605	112074796	119986	C/T	+
rs13126975	112075129	120319	A/T	+
rs6837490	112075447	120637	C/T	+
rs6843082	112075671	120861	A/G	+
rs13105878	112075751	120941	A/C	+
rs6533528	112076843	122033	A/G	+
rs7692272	112076857	122047	G/T	+
rs2171591	112077012	122202	A/G	+
rs17042195	112077142	122332	C/G	+
rs11931959	112077289	122479	A/G	+
rs17042198	112077582	122772	G/T	+
rs10033464	112078365	123555	G/T	+
rs2171592	112078392	123582	C/T	+
rs13121924	112078423	123613	A/G	+
rs2129979	112078601	123791	G/T	+
rs2350539	112078814	124004	G/T	+
rs1906606	112080996	126186	A/C	+
rs7672570	112081189	126379	C/T	+
rs4834418	112081408	126598	A/G	+
rs723364	112082075	127265	C/G	-
rs723363	112082105	127295	A/G	-
rs7697491	112083422	128612	A/T	+
rs13125644	112083505	128695	A/G	+
rs2350294	112084449	129639	A/G	-
rs2350293	112084451	129641	A/G	-
rs3855819	112084767	129957	C/G	-
rs2220428	112085064	130254	A/G	+
rs2220429	112085089	130279	A/C	+
rs11727566	112085934	131124	A/T	+
rs13141190	112086218	131408	A/G	+
rs4032976	112086371	131561	A/G	-
rs3866829	112086379	131569	A/C	-
rs7671348	112086408	131598	A/G	+
rs3866830	112086598	131788	C/G	-
rs6811267	112086942	132132	C/T	+
rs3853440	112087213	132403	C/T	-
rs3853441	112087344	132534	A/G	-
rs3853442	112087632	132822	C/T	-
rs3853443	112087733	132923	A/G	-
rs4124158	112087798	132988	C/T	+
rs4124159	112087847	133037	A/G	+
rs12506083	112088016	133206	A/C	+
rs34809282	112088051	133241	A/G	+
rs7683219	112088051	133241	A/G	+
rs7683618	112088259	133449	A/C	+
rs7683625	112088269	133459	A/G	+
rs7662050	112088325	133515	C/T	+
rs36183416	112088804	133994	C/T	+
rs4447926	112088804	133994	C/T	+
rs4594787	112088813	134003	A/G	+
rs10390275	112089009	134199	A/T	+
rs36179422	112089009	134199	A/T	+
rs10006659	112089030	134220	G/T	+
rs36181695	112089078	134268	A/G	+
rs7440730	112089078	134268	A/G	+
rs10006881	112089277	134467	C/T	+
rs36149087	112089277	134467	C/T	+
rs6533530	112089540	134730	C/T	+
rs6533531	112089569	134759	G/T	+

Marker ID	Pos Build 35	Pos in SEQ ID NO:50	Type	Strand
rs3866831	112089718	134908	C/T	-
rs4269241	112089833	135023	A/G	+
rs4032975	112089842	135032	A/C	-
rs4032974	112090140	135330	A/G	-
rs4124160	112090452	135642	A/G	+
rs3866832	112091304	136494	C/G	-
rs3853444	112091740	136930	A/G	-
rs7662345	112091766	136956	A/G	+
rs2350545	112092258	137448	C/T	-
rs17042215	112092562	137752	C/T	+
rs2003121	112093023	138213	C/T	+
rs880309	112093143	138333	A/G	+
rs9991046	112093346	138536	G/T	+
rs17042216	112094463	139653	C/T	+
rs17570669	112094486	139676	A/T	+
rs17042218	112094520	139710	A/G	+
rs17042223	112094922	140112	C/T	+
rs3866833	112095138	140328	C/T	-
rs17042224	112096509	141699	G/T	+
rs13130446	112096760	141950	C/T	+
rs10516564	112096896	142086	A/G	+
rs7686320	112097215	142405	A/T	+
rs7686499	112097282	142472	C/T	+
rs17042230	112097319	142509	C/T	+
rs4124161	112097459	142649	C/T	+
rs4576077	112098061	143251	C/T	+
rs4260600	112098098	143288	C/T	+
rs12644093	112098445	143635	A/G	+
rs4124162	112098593	143783	A/G	+
rs7674295	112099042	144232	A/G	+
rs11938968	112100356	145546	A/G	+
rs28601812	112101457	146647	A/C	+
rs4032983	112101551	146741	G/T	+
rs3866834	112101617	146807	A/G	+
rs6852021	112101716	146906	A/G	+
rs28580491	112102583	147773	C/T	+
rs13110989	112102671	147861	G/T	+
rs3866835	112102983	148173	C/T	-
rs4124163	112103203	148393	A/G	+
rs3866836	112103244	148434	A/G	+
rs17042238	112103458	148648	A/G	+
rs4124164	112104250	149440	C/T	+

B. *Microsatellite markers within LD Block C04 (Between 111,954,811 and 112,104,250 on C04; NCBI Build 35; SEQ ID NO:50).*

Marker	Start position	End position	Forward primer	Reverse Primer
D4S193	112062811	112062911	ACAACCCCATTTGTGAAGAC	TTTATAGAAAATTTAGCATGGA
D4S2940	112070055	112070267	CTAAGTTGTGCAGCCATGAA	TGGAACCACTTTTGCAGTAA
D4S406	112076047	112076292	CTGGTTTTAAGGCATGTTTG	TCCTCAGGGAGGTCTAATCA

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Table 6. Key to sequences presented in sequence listing.

SEQ ID NO	Marker ID
1	rs2220427
2	rs17042059
3	rs4529121
4	rs4543199
5	rs10019689
6	rs4626276
7	rs17042076
8	rs11098089
9	rs11930528
10	rs17042098
11	rs17042102
12	rs17042121
13	rs10516563
14	rs4605724
15	rs2350269
16	rs6533527
17	rs17042144
18	rs1906618
19	rs1906617
20	rs12646447
21	rs12646754
22	rs2129981
23	rs12639654
24	rs6817105
25	rs17042171
26	rs1906591
27	rs2200732
28	rs2200733
29	rs4611994
30	rs4540107
31	rs1906593
32	rs1906596
33	rs2634073
34	rs1906592
35	rs2723296
36	rs16997168
37	rs2723316
38	rs6419178
39	rs1448817
40	rs13105878
41	rs10033464
42	rs13141190
43	rs3853444
44	rs4576077
45	D4S406
46	rs7668322
47	rs2197815
48	rs6831623
49	rs2595110
50	LD Block C04
51	rs13143308

Example 2. Characterization of AF risk variants

The following contains further description of the identification of variants conferring risk for atrial fibrillation on chromosome 4q25

Atrial fibrillation (AF) is the most common sustained cardiac arrhythmia in man and is characterized by chaotic electrical activity of the atria[1]. It affects one in ten individuals over eighty, causes significant morbidity, and is an independent predictor of mortality[2]. Recent studies have provided evidence of a genetic contribution to AF[3-5]. Mutations in potassium channel genes have been associated with familial AF[6-10] but account for only a small fraction of all AF cases[11, 12]. We performed a genome-wide association scan, followed by replication studies in three populations of European descent and a Chinese population from Hong Kong and find a strong association between two sequence variants on chromosome 4q25 to AF. Approximately 35% of individuals of European descent have at least one of the variants and the risk of AF increases by 1.72 and 1.39 per copy. The association to the stronger variant was replicated in the Chinese population, where it is carried by 75% of individuals and risk of AF is increased by 1.42 per copy. A stronger association was observed in individuals with typical atrial flutter (AFl). Both variants are adjacent to *PITX2*, which is known to play a critical role in left-right asymmetry of the heart[13-15].We conducted a genome-wide association study using the Illumina Hap300 BeadChip on an Icelandic population with AF and/or AFl. 316,515 SNPs satisfying our quality criteria were tested individually for association to AF/AFl in a sample of 550 patients and 4,476 controls from Iceland. Three strongly correlated SNPs, all located within a single linkage disequilibrium (LD) block on chromosome 4q25, were the only SNPs found to be genome-wide significant after accounting for the 316,515 SNPs tested ($P < 0.05/316,515 = 1.58 \times 10^{-7}$): rs2200733 (OR = 1.75; $P = 1.6 \times 10^{-10}$), rs2220427 (OR = 1.75; $P = 1.9 \times 10^{-10}$) and rs2634073 (OR = 1.60; $P = 2.1 \times 10^{-9}$). These results and all other results based on the Icelandic population were adjusted for the relatedness of individuals. The two most significant SNPs, rs2200733 and rs2220427, are perfect proxies for one another in the CEPH CEU HapMap[16] dataset and are close to being perfect proxies for one another in the Icelandic dataset ($D' = 1$, $r^2 = .999$), therefore, only rs2200733 will be referred to in the following discussion. The correlation of rs2634073 to rs2200733 is weaker in the Icelandic dataset ($D' = .95$, $r^2 = .605$). Upon further study of the Illumina Hap300 SNPs in the vicinity of the first three SNPs and conditioning on the association to rs2200733, an association to a new SNP, rs10033464, was identified (OR = 1.42; $P = .0024$). After accounting for the association to rs2200733 and rs10033464, the association to rs2634073 was no longer significant ($P = 0.30$). Henceforth, all association results for rs2200733 T and rs10033464 T, including those presented in Table 7, are based on comparison to the wild type haplotype which carries neither of the two at risk alleles, rather than comparison to the major alleles of each SNP separately. Specifically, odds-

ratios for rs2200733 T and rs10033464 T are each computed conditionally and could be interpreted as the estimated relative risk of each variant compared to the wild-type. The at risk alleles T of rs2200733 and T of rs10033464 have estimated population allelic frequencies of 12.05% and 8.53% in Iceland, respectively, and are never observed together on the same chromosome, in the Icelandic dataset or in the CEU HapMap dataset. A third SNP, rs13143308, which has a minor allele that corresponds completely to chromosomes carrying either the T allele of rs2200733 or the T allele of rs10033464, was identified through the CEU HapMap dataset. Figure 2 demonstrates the haplotype structure over the key SNPs of the associated region. Sets of SNPs, that are perfect proxies (i.e., perfect surrogates, r2 = 1.0 to the tagging SNP) of each of these three key SNPs in the CEU HapMap samples, are provided in Table 9 and relative locations displayed in Figure 3. We emphasize that the SNPs named should be considered representatives of the haplotypes defined by the SNPs which they are equivalent to and are primarily chosen for the sake of convenience.

A microsatellite marker, D4S406, located in the same LD block as the two SNPs was identified. In Iceland, three of the four shortest alleles of D4S406 (-8, -4, and -2) combine to form a near perfect surrogate for the T allele of rs2200733 (D' = .995, r^2 = .98) and the two shortest remaining alleles (-6 and 0) form a good surrogate of the T allele of rs10033464 (D' = .98, r^2 = .75) (Table 10). None of the remaining (longer) alleles of D4S406 are associated to AF/AFl after accounting for the effect of the short alleles. For the replication of the original observation in Iceland the D4S406 genotypes were used to provide information when SNP genotypes were not available.

In an attempt to replicate our original discovery we analyzed an additional Icelandic samples consisting of 2,251 AF/AFl patients and 13,238 controls (Table 7). The association of both SNPs to AF/AFl was replicated in these samples (OR = 1.64, $P = 2.7 \times 10^{-23}$ for rs2200733, OR = 1.40, $P = 8.2 \times 10^{-8}$ for rs10033464) and both achieve genome-wide significance in the combined Icelandic samples (OR=1.68, $P = 1.9 \times 10^{-30}$ for rs2200733, OR = 1.38, $P = 9.4 \times 10^{-9}$ for rs10033464). We also typed all the 18 Hap300 Illumina SNPs in the region around our signal in 404 of the additional AF cases and 2,036 of the additional controls. None of these SNPs remained significant after accounting for the association to rs2200733 and rs10033464 (Table 11).

In further attempts to replicate our results, we tested these variants for an association to AF in two populations of European ancestry, one from Sweden, consisting of 143 cases and 738 controls, and the other from the United States (U.S.), consisting of 636 cases and 804 controls (Table 7). The association to rs2200733 was strongly replicated in both populations (OR = 2.01, P = 0.00027 in Sweden, OR = 1.84, $P = 9.8 \times 10^{-10}$ in the U.S.). The association to rs10033464 is weaker, but was nonetheless replicated in the Swedish population (OR = 1.65, P = 0.0087) and was nearly significant in the U.S.

population (OR = 1.30, P = 0.052). When combined with the Icelandic samples, the association to rs2200733 was unequivocal (OR = 1.72, $P = 3.3 \times 10^{-41}$), and the significance of rs10033464 was well beyond the threshold of genome-wide significance (OR = 1.39, $P = 6.9 \times 10^{-11}$). Assuming the multiplicative model, the population attributable risk (PAR) of the two variants combined is approximately 20% in populations of European ancestry.

Finally, we attempted to replicate these signals in a Han Chinese population from Hong Kong consisting of 333 cases and 2,836 controls. The association to rs2200733 T was significantly replicated (OR = 1.42, P = 0.00064), but the association to rs10033464 T was not significant, although in the right direction (OR = 1.08, P = 0.55) (Table 7). Interestingly, the T allele of rs2200733 is much more frequent in the Chinese (allelic frequency in controls: 0.528) than in those of European descent (allelic frequency in controls: 0.098-0.139) (Figure 2) which is reflected in a greater joint PAR of approximately 35%, even though the estimated risk is less. The LD block containing the two variants is more fragmented in the Chinese CHB and Japanese JPT HapMap samples than in the CEU HapMap samples (Figure 3). We therefore analysed several markers in the Hong Kong population which were in perfect LD with rs2200733 in the CEU samples, but in imperfect LD in the CHB and JPT samples (Table 12). These markers had weaker apparent association to AF than rs2200733, suggesting that the functional variants driving the association is located in the approximately 20kb region around the original rs2200733 variant and defined by the SNPs that remain equivalent to rs2200733 in the CHB and JPT samples (coloured red in figure 3).

For the initial Icelandic discovery samples, rs2200733 had a significantly higher OR than rs10033464 (P = 0.041). This held true in the replication samples, and overall there is a significant difference in the risks associated with the two variants (P = 0.00019 in the combined European samples and P = 0.0099 in Hong Kong). When genotype-specific odds ratios were studied, some deviation away from the multiplicative model is detectable in the combined dataset (P = 0.018 for European samples, see Table 13). Estimated risks of heterozygous carriers relative to non-carriers were similar, but homozygous carriers of rs2200733 T and rs10033464 T have estimated risks that were, respectively, higher and lower than that predicted by a multiplicative model. A similar trend was seen in the Hong Kong samples; although the sample size is too small to have power to detect such deviations with significance. In the combined populations of European descent the observed OR for individuals homozygous for rs2200733 T was 3.64 as compared to individuals homozygous for the wild type haplotype and 1.77 for the Chinese population demonstrating that these variants are important components in any predictive modeling of AF.

The age at diagnosis of AF/AFl for the Icelandic samples correlates with the two SNPs (diagnosis occurs 2.28 years earlier per T allele of rs2200733 and 1.10 years earlier per T

allele of rs10033464, joint $P = 1.29x10^{-6}$). The effect of the age at diagnosis was also evaluated by measuring the strength of association while stratifying by age at diagnosis. The association of the two variants is strongest in those diagnosed at a younger age, although the risk remains significant even in those diagnosed after reaching 80 years of age (Table 8). Information on age at diagnosis of AF was not available for the Swedish samples. The U.S. samples were comprised of two main groups, younger patients with either lone AF or AF and hypertension (HTN), and older AF cases who are mostly hemorrhagic and ischemic stroke patients. In both populations there is a clear trend towards a stronger association in younger AF cases than in older cases. Our analysis of the data did not suggest any differential association by sex (Table 8).

AF1 often accompanies AF, but can occur in isolation[17]. Interestingly we observed a strong association between the variants and the small subset (N=116) of the AF1 Icelandic patients (OR = 2.60, 95% confidence interval (CI) = 1.83-3.68, $P = 7.5x10^{-8}$ for rs2200733, OR = 1.94, 95% CI = 1.26-3.00, $P = .0028$ for rs10033464). Indeed, for rs2200733, the OR for these definite AFl cases is significantly higher than that for the cases with an AF phenotype ($P = 0.0026$), and close to significantly higher for rs10033464 ($P = .084$). Our results suggest that while these traits share genetic risk factors, AFl is less influenced by phenocopies than AF.

Neither variant showed a association to obesity, hypertension or myocardial infarction in the Icelandic samples, all known risk factors for AF (observed OR < 1.1 in all instances, Table 14). Although these negative results do not exclude the possibility that the new variants associate with these phenotypes, they do suggest, along with the high risk in U.S. lone AF and earlier age at onset in carriers, that the new variants are not affecting risk of AF through these known risk factors.

There is no known gene present in the LD block containing rs2200733 and rs10033464 (Figure 3). The LD block contains one spliced EST (DA725631) and two single-exon ESTs (DB324364 and AF017091). RT-PCR of cDNA libraries from various tissues did not detect the expression of these ESTs (Table 16). The *PITX2* gene located in the adjacent upstream LD block is the gene closest to the risk variants. Several markers within the LD block containing the PITX2 gene are correlated to the markers showing association to AF and Afl, as shown in Table 18. The protein encoded by this gene, the paired-like homeodomain transcription factor 2, is an interesting candidate for AF/AFl as it is known to play an important role in cardiac development by directing asymmetric morphogenesis of the heart[13]. In a mouse knockout model Pitx2 was shown to suppress a default pathway for sinoatrial node formation in the left atrium[14, 15]. There is very little mRNA expression of *PITX2* in all easily accessible tissues, such as blood and adipose tissue, hampering the study of correlation between genotypes and expression levels. The next gene upstream of *PITX2* is *ENPEP*, an aminopeptidase responsible for the breakdown

of angiotensin II in the vascular endothelium[18]. This gene is expressed more widely, but the variants associated with AF showed no correlation to its expression in blood or adipose tissue. No other annotated genes are located within a 400kb region upstream and 1.5 Mb regions downstream of the associated variants.

In summary, we have identified two variants on chromosome 4q25 that are strongly associated with AF in three distinct populations of European descent. The stronger variant also replicates well in a Chinese population where it is much more common and has higher PAR than in populations of European descent. This association is particularly compelling in younger patients and in those with lone AF, but is also present in older patients with more commonly encountered forms of AF. Although the mechanism for this association is unknown, our results provide a foundation for further studies on the molecular underpinnings of AF.

METHODS

Subjects

The Icelandic cases consisted of all patients diagnosed with AF and/or AFl at the two largest hospitals in the country from 1987 to 2005. The Swedish cases were recruited from 1996 to 2002 as a part of an ongoing genetic epidemiology study, the South Stockholm Ischemic Stroke Study. The U.S. cases were a mixture of stroke patients with a AF diagnosis and younger consecutive patients with lone AF or AF with a coexisting diagnosis of hypertension. The Hong Kong cases were a collection of stroke and diabetes patients with an AF diagnosis. The AF diagnosis was confirmed by a twelve lead electrocardiogram in all study populations.

The Icelandic controls were chosen at random from individuals who have participated in other genetic studies at deCODE, excluding first-degree relatives of patients and controls (Table 15). The Swedish controls were recruited from the same region as patients from blood donors (in 2001) and healthy volunteers (1990-1994). The U.S. controls were recruited from a large primary care practice and from patients participating in a hemorrhagic stroke study. The Hong Kong controls were individuals without an AF diagnosis.

Icelandic study population

This study initially included the all patients consenting to participation, which were diagnosed with AF and/or AFl (ICD 10 diagnosis I48 and ICD 9 diagnosis 427.3) at Landspitali University Hospital in Reykjavik, the only tertiary referral centre in Iceland, and at Akureyri Regional Hospital, the second largest hospital in the country, from 1987 to 2005. All diagnoses were confirmed by a twelve lead electrocardiogram (EKG) which was manually read by a cardiologist. All cases were included, regardless of whether the patients had clinical symptoms or not, except those diagnosed only immediately after open cardiac surgery.

A set of 550 cases were successfully genotyped according to our quality control criteria in a genome-wide SNP genotyping effort, using the Infinium II assay method and the Sentrix HumanHap300 BeadChip (Illumina, San Diego, CA, USA). The mean age at diagnosis for this initial group of 550 patients (370 males and 180 females) was 72.5 (SD = 11.0) years and the range was from 34.7-96.2 years. The validation group of 2,273 patients (1,359 males and 913 females) had a mean age at diagnosis of 70.5 (SD = 13.0) and the range was from 16.8-100.6. The AF/AFl free controls (2,201 males and 2,275 females at the initial genome-wide screening with mean age 61.5 (SD = 15.8) and 5,654 males and 7,597 females at the validation stage with mean age 61.9 (SD = 18.4)) used in this study consisted of controls randomly selected from the Icelandic genealogical database and individuals from other ongoing related genetic studies at deCODE. Controls having first-degree relatives (siblings, parents or offspring) with AF/AFl, or a first-degree control relative, were excluded from the analysis.

Icelandic MI, obesity and hypertension populations

Individuals who suffered an MI were identified from a registry of over 10,000 individuals who: a) had an MI before the age of 75 in Iceland in the years 1981 to 2002 and satisfy the MONICA criteria 9 (REF II), or had MI discharge diagnosis from the major hospitals in Reykjavik in the years 2003 and 2005. MI diagnoses of all individuals in the registry follow strict diagnostic criteria based on signs, symptoms, electrocardiograms, cardiac enzymes and necropsy findings'. Genotype information was available for 2,462 males and 1,114 females, mean age 72.6 (SD = 11.7). Body mass index (BMI) was measured for individuals participating in the cardiovascular atrial fibrillation and /or stroke (CVD) genetics program at deCODE (either patients with CVD, their first degree relatives or spouses). For the purpose of this study subjects with BMI > 35 were defined as obese. Genotype information was available for 555 males and 1,046 females, mean age 53.2 (SD = 16.1). Hypertensive patients included those who had attended the ambulatory

hypertension clinic at the Landspitali, University Hospital in Iceland and/or had been given the diagnosis on discharge from the hospital. The diagnosis was verified by confirming that they were taking antihypertensivemedications as a treatment for hypertension. Genotype information was available for 1,293 males and 1,327 females, mean age 71.5 (SD = 12.5). The study was approved by the Data Protection Commission of Iceland and the National Bioethics Committee of Iceland. Written informed consent was obtained from all patients, relatives and controls.

Swedish study population

Patients with ischemic stroke or TIA attending the stroke unit or the stroke outpatient clinic at Karolinska University Hospital, Huddinge unit in Stockholm, Sweden were recruited from 1996 to 2002 as part of an ongoing genetic epidemiology study, the South Stockholm Ischemic Stroke Study (SSISS). The study was approved by the Bioethics Committee of Karolinska Institutet (Dnr 286/96 and 08/02). AF diagnosis in the Swedish samples was based on a twelve lead EKG. The fraction of males in the Swedish AF cases was 46.2% and the mean age at stroke diagnosis for the Swedish AF cases was 74.4 (SD=8.7).

The Swedish controls used in this study are population-based controls recruited from the same region in central Sweden as the patients, representing the general population in this area. The individuals were either blood donors (recruited in 2001) or healthy volunteers (collected in 1990-1994) recruited by the clinical chemistry department at the Karolinska University Hospital to represent a normal reference population. The fraction of males in the Swedish controls was 59.7% and the mean age at recruitment for the Swedish controls was 43.1 (SD=12.3).

U.S. study population

U.S. subjects were enrolled in ongoing case-control and cohort studies at Massachusetts General Hospital (MGH) between January 1998 and July 2006. All aspects of these studies have been approved by the local Institutional Review Board. Subjects enrolled in the case-control study consisted of patients hospitalized with acute ischemic or hemorrhagic stroke confirmed by CT or MRI, admitted to a single acute care hospital. Of the 328 hemorrhagic stroke patients recruited 78 were diagnosed with AF and were used as cases for the current study, the remaining 250 were used as controls. 170 ischemic stroke patients had an AF diagnosis and were treated as cases but no ischemic stroke patients were treated as controls. Patients were excluded for primary subarachnoid

hemorrhage and for intracerebral hemorrhage secondary to head trauma, tumor, vascular malformation, or vasculitis. 624 stroke-free controls were recruited from a large, primary care practice (>18 000 patients) serving the hospital catchment area as well as the hospital's Anticoagulation Management Service. 70 of the 624 individuals collected as controls were diagnosed with AF and treated cases for the purposes of the current study. 50.9% of all individuals used as controls were males and their mean age was 67.4 (SD=12.3). All subjects or an accompanying informant provided informed consent for participation in genetic studies and were interviewed prospectively regarding medical history, medications, social and family history. Presence or absence of atrial fibrillation was prospectively documented through interview and from review of medical records.

The second part of the U.S. subjects consisted of consecutive patients with lone AF or AF with coexisting diagnosis of hypertension referred to the arrhythmia service who provided written informed consent for participation in genetic. Inclusion criteria were AF documented by EKG, and an age less than or equal to 65 years. The exclusion criteria were structural heart atrial fibrillation and /or stroke as assessed by echocardiography, rheumatic heart atrial fibrillation and /or stroke, hyperthyroidism, myocardial infarction, or congestive heart failure. Each patient underwent a physical examination and a standardized interview to identify past medical conditions, medications, symptoms and possible triggers for initiation of AF. All patients were evaluated by twelve lead EKG, echocardiogram, and laboratory studies. EKGs and echocardiograms were interpreted using standard criteria.

Hong Kong Study population

All subjects in the Hong Kong study population were of southern Han Chinese ancestry residing in Hong Kong. The cases consisted of 217 individuals (49.1% male, mean age 68.1 (SD=9.6)) selected from the Prince of Wales Hospital Diabetes Registry[23] and 116 subjects (30.2% male, mean age 76.1 (SD=10.9)) from the Stroke Registry[24]. All subjects were diagnosed to have atrial fibrillation by EKG. The controls consisted of 2,836 subjects without evidence of AF. Informed consent was obtained for each participating subject. This study was approved by the Clinical Research Ethics Committee of the Chinese University of Hong Kong.

Illumina genome-wide genotyping

All Icelandic case- and control-samples were assayed with the Infinium HumanHap300 SNP chips (Illumina, SanDiego, CA, USA), containing 317 503 haplotype

tagging SNPs derived from phase I of the International HapMap project. Of the SNPs assayed on the chip, 162 SNPs generated no genotypes, and an additional 178 SNPs had yield lower than 90%. Forty-eight SNPs were monomorphic and 107 others nearly monomorphic (i.e. the minor allele frequency in the combined cohort of patients and controls was less than 0.001). An additional 475 SNPs showed very significant distortion from Hardy-Weinberg equilibrium in the controls ($p < 1x10^{-10}$). Lastly, a few markers (n=18) were determined to have genotyping problems after investigation of particular regions and possible signals in several different on-going genome-wide association studies in house. Thus, the final analyses presented in the text utilizes 316,515 SNPs. Any samples with a call rate below 98% were excluded from the analysis.

Single SNP- and Microsatellite Genotyping.

SNP genotyping was carried out by the Centaurus (Nanogen) platform[25]. The quality of each Centaurus SNP assay was evaluated by genotyping each assay in the CEU and/or YRI HapMap samples and comparing the results with the HapMap data. Assays with >1.5% mismatch rate were not used and a linkage disequilibrium (LD) test was used for markers known to be in LD.

Association analysis

An attempt was made to genotype all participating individuals for rs2200733, rs4611994 (a perfect proxy for rs2200733), rs13143308, and rs6843082 (a perfect proxy for rs13143308). For each of the SNPs, yield was higher than 90% in every group. In addition genotypes for the D4S406 microsatellite were available for all Icelandic and Swedish subjects. Because of the redundancy in genotyping, observed genotypes reduced the amount of information lost due to missing genotypes through a likelihood approach we have used before[26]. This ensured that results presented in the tables were always based on the same number of individuals, allowing meaningful comparisons of results. As data on rs10033464 was only directly available in the initial Icelandic discovery samples and in the HapMap project the rs2200733 C rs13143308 T haplotype was used to tag this SNP. This tagging was perfect in both the initial discovery samples and the CEPH CEU HapMap samples.

A likelihood procedure described in a previous , and implemented in the NEMO software, was used for the association analyses. We tested the association of an allele to each phenotype using a standard likelihood ratio statistic, which, if the subjects were unrelated, would have asymptotically a chi-square distribution, with one degree of

freedom, under the null hypothesis. Allele-specific OR was calculated assuming a multiplicative model for the two chromosomes of an individual[4]. Results from multiple case-control groups were combined using a Mantel-Haenszel model[5] in which the groups were allowed to have different allelic population frequencies, haplotypes and genotypes but were assumed to have common relative risks. There was no significant deviation from Hardy-Weinberg equilibrium (HWE) in any control group.

In Tables 7 and 8, *P* values for both rs2200733 and rs10033464 were computed based on comparison to the wild type rs2200733 C, rs13143308 G, rs10033464 G haplotype carrying neither of the at risk alleles. The corresponding conditional odds ratio for rs2200733 T is defined as [f(rs2200733 T)/f(WT)]/[p(rs2200733 T)/p(WT)] where WT denotes the wild-type haplotype, and f(.) and p(.) denote frequencies in cases and controls respectively. Under the multiplicative model and when the controls could be considered as population controls, this conditional odds ratio is the appropriate estimate of the relative risk of rs2200733 T versus the wild-type. Conditional odd-ratio for rs13143308 T is similarly defined and has a similar interpretation.

Correction for relatedness and Genomic Control.

Some of the individuals in the Icelandic case-control groups were related to each other, causing the aforementioned chi-square test statistic to have a mean >1 and median > 0.675[26]. We estimated the inflation factor by using a previously described procedure where we simulated genotypes through the genealogy of 731,175 Icelanders[30]. For the initial discovery samples, where genotypes for the 316,515 genome-wide scan SNPs were available, we also estimated the inflation factor by using genomic controls and calculating the average of the 316,515 chi-square statistics, and by computing the median of the 316,515 chi-square statistics and dividing it by 0.675[26] as describe previously[31, 32]. For these initial samples the inflation factors, estimated by our genealogy method and the two genomic control methods gave similar inflation factor estimates; 1.047, 1.058 and 1.054 respectively . The P values and confidence intervals presented are based on adjusting by the inflation factor estimated by the genealogy method.

PCR screening of cDNA libraries.

To confirm the expression of the spliced ESTs (DA725631, DB324364 and AF017091) within the LD block we screened commercially available cDNA libraries and libraries generated at deCODE. The commercial libraries screened were heart (Clontech-639304), aorta (Clontech-639325) bone marrow (Clontech 7416-1), testis (Clontech 7414-1) and

whole brain (BD S0598) Marathon Ready cDNA libraries. In addition cDNA libraries were constructed for whole blood and EBV-transformed human lymphoblastoid cells. Total RNA was isolated from the lymphoblastoid cell lines and whole blood, using the RNeasy RNA isolation kit from Qiagen (Cat. 75144) and the RNeasy RNA isolation from whole blood kit (Cat. 52304), respectively. cDNA libraries were prepared at deCODE using High Capacity cDNA Archive Kit with random primers (Applied Biosystems PN 4322171).

PCR screening was carried out using the Advantage® 2 PCR Enzyme RT _PCR System (Clontech) according to manufacturers instructions and using PCR primers from Operon Biotechnologies. The PCR reactions were done in 10 µl volume at a final concentration of 3,5µM of forward and reverse primers (Table 16), 2mM dNTP, 1x Advantage 2 PCR buffer and 0.5µl of cDNA library.

Northern Blot analysis.

Commercial multiple tissue poly-A Northern blots were obtained from Clontech (Human Cardiovascular system, Cat. 636825).

Probes used:

i) The PITX2 cDNA clone (HU3_p983E0327D), obtained from RZPD Deutsches Ressourcenzentrum für Genomforschung GmbH, Germany http://www.rzpd.de/products/genomecube.shtml) (sequence verified, data not shown);

ii) cDNA clone that corresponded to exons 1-12 of the ENPEP transcripts obtained from RT-PCR experiments. The ENPEP clone was sequence verified:

TCCTGCTCCAGCTTGTGGATATTTTGCAAAAAAGCTCTCCATCTGCCACAGTTGCAGTTCAGTGTTG
AATGGCTCTGCTATTGTGACAATTCGGCCAAGGTTTCTGTTATTGAGTGTATATCTGTTGACTAGAT
AGTCCCAGTTGAGTTGTATCCAATTCCAGGCCATGTTCTTCCCATAGCTGTTATATGAGATATATCG
AATGACTGTAAACACATCCTGAGTTTTAATAAGGTTCGTGTCCTTGAGCAAATCCAAATACCTTGAC
AAAAGAGTAACGTTCTTCACTGATGCTAATCCATACAGCAGTTTTTCTTTTTCTTGAGCTAATGAAGT
TTTCTGGTATTGCTCAAGAGTGTAGTTCCATGAAATCTCATTGCCAGAGTTCTGCATCCCATACCGA
TACACCAGAAGCCTGAGATTTACGGGAAGGCTTACAGTCCCATTTAGCCACTGCTCAAATAACGAG
GAAGCATTGTTCAAGGCTTCTCTGTCTCCCATCTTGCACGCAAACCCTAACACGGAGGAACGGAGT
AACTTTGTGACATGGTCTCCAGCATCATTCCATCCCAGAGAATCTGCAATAGGCTTCACTTGACCTT
GGAAGTATTCCTCAATCATAGGATATAGCTCTTTATCATCTTCAAACATGCTAATGATGTAGGTTACA
GCTGAAATTACTCTCTGCCATGGTAAAAAATTCTCTTCCCTTTTGAGATACTTGGTCAAGTTCAAAG
CCACCTTATAATCTAGAAGTTGAGCTCTTGCCAAGGCAAAAGCATCATCAATAAGACTTGCACGATC
TGCTGAAGAAAATGTCTTGTGGTTCAAGGAGAGCGCTGTAGCTATCGAGTCCCAAGTTGCTACTTC
ATAATTTACACGATAAAACCCAATATGATCTGGGTTTATTTTGAGAAAAGCATTTCCACTAGGATTA
GAGGAGTTCAAAGTGATTCCTTCTTTTTCTGACCTATTAAATAACACACTGCTTGTTATATTATCTTC
AGTCCATTTAACTGGGATATTCCATGTATAACCAAGATCTGAAGGGGGCTGAGAAGGGTTAGCTCT
TGGGTCCAACAAAAAGCGTTTCTGTGTGATGTTCTTGACACCGTTCACGTTAAGCACAGGATAACC
CATCTgGTCTGGTCCAGGTGTCCATTACTTCTTTCACTGGTAGCCTACTTGCCTCTTCCAGTGCTGC
CCAAAAAT

cDNA fragments were radiolabelled with [α-^{32}P]dCTP (specific activity6000Ci/mmol), using the Megaprime labeling kit (GE Healthcare Cat. RPN 1607) and unincorporated nucleotides removed from the reaction using ProbeQuant G-50 microcolumns (GE Healthcare Cat. 27-5335-01). Membranes were pre-hybridized in Rapid-hyb buffer (GE Healthcare Cat. RPN 1635) for at least 30 minutes and subsequently hybridized with 100-300ng of the labelled cDNA probe. Hybridizations were performed in Rapid-hyb buffer at 65°C overnight. The labelled probes were heated for 5 minutes at 95°C before addition to the filters in the pre-hybridization solution. After hybridization, the membranes were washed at low stringency in 2x SSC, 0.05% SDS at room temperature for 30-40 minutes followed by two high stringency washes in 0.1x SSC, 0.1% SDS at 50°C for 40 minutes. The blots were immediately sealed and exposed to Kodak BioMax MR X-ray film (Cat. 8715187).

Surveying for candidate regulatory variants in the AF region

The UCSC browser was used to extracted positions of SNPs and conserved transcription factor binding sites (TFBS) for a 172.5 kb region around the SNPs associated with AF (hg release 17, chromosome 4, 111,942,401-112,114,901). The two tables were cross referenced and SNPs that landed in binding sites were further interrogated for LD with rs2220427 or rs6843082 in the HapMap data. This was done for releases 16, 17 and 18 of the human genome, but the results are reported in hg 17 coordinates. This yielded 3 SNPs that land in conserved binding sites for known transcription factors (Table 17). Note, this analysis only detects a limited sample of functional candidates as i) the AF haplotypes have not been sequenced fully, ii) several candidate SNPs are not typed in Hapmap and it is unknown whether they sit on the AF haplotypes, iii) polymorphisms in less conserved regions could be functional.

Evolutionary conservation of three TFBS

Utilizing the Multiz alignment in the UCSC genome enabled an assessment of the evolutionary conservation of the regions affected by these SNPs. In all three cases is the core part of the TF binding sites intact, but the positions affected are preserved to a different degree. The SOX5 affected by rs12510087 is least conserved in mammals but the second one (affected by rs2220427) is strikingly preserved (with the exception of Opossum it is maintained in all species to the chicken). The rs17042171 mutation is in last position in the core GGAAAA motif of the NFAT binding site. The conservation indicates that a G is preferred at this location, resulting in a GGAAAG motif.

Correlation between genotype and expression of ENPEP

Blood was collected in the morning, between 8 and 10 am, after overnight fasting (from 9 pm) and RNA extracted within 2 hours from phlebotomy from 1,002 individuals. RNA isolation was performed using the RNeasy Midi Kit (QIAGEN GmbH, Hilden, Germany). Subcutaneous fat samples (5-10 cm^3) were removed through a 3 cm incision at the bikini line (always from the same site to avoid site-specific variation) after local anesthesia using 10ml of lidocaine-adrenalin (1%) from 673 individuals. Purification of the total RNA was performed with the RNeasy Mini Kit (QIAGEN GmbH, Hilden, Germany).

Integrity of the total RNA was assessed through analysis on the Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, U.S., CA). Each labelled RNA sample including reference pools, 1,765 samples in total, was hybridized to a Human 25K array manufactured by Agilent Technologies. Array images were processed as described previously to obtain background noise, single-channel intensity and associated measurement error estimates[11]. Expression changes between two samples were quantified as mean logarithm (log_{10}) expression ratio (MLR), i.e. expression ratios compared to background corrected intensity values for the two channels for each spot on the array[12]. The hybridizations went through standard QC process, i.e. signal to noise ratio, reproducibility and accuracy at spike-in compounds, comparing Cy3 to Cy5 intensities.

Neither associated SNP was correlated to the expression of ENPEP adjusted for age and sex in blood (P = 0.90 and P = 0.82 for rs2200733 and rs10033464, respectively) or adipose tissue (P = 0.23 and P = 0.37 for rs2200733 and rs10033464, respectively)

Table 7. *Analysis of the association of rs2200733 and rs10033464 on chromosome 4q25 to AF/AFI.*

Sample	rs2200733 T[a]			rs10033464 T[a,b]				
(N cases/ N controls)	Freq.[c]	OR (95% CI)	*P*	Freq.[c]	OR (95% CI)	*P*	Comp-arison *P*[d]	Joint PAR
Iceland[e]								
Discovery (550/4,476)	0.191 0.114	1.84 (1.54-2.21)	$2.0x10^{-11}$	0.110 0.080	1.42 (1.13-1.77)	0.0024	0.041	0.216
Replication (2,251/13,238)	0.166 0.108	1.64 (1.49-1.81)	$2.7x10^{-23}$	0.108 0.080	1.40 (1.24-1.58)	$8.2x10^{-8}$	0.028	0.176
Combined (2,801/17,714)	0.171 0.110	1.68 (1.53-1.83)	$1.9x10^{-30}$	0.108 0.080	1.40 (1.25-1.55)	$9.4x10^{-9}$	0.0025	0.180
Other European ancestry								
Sweden (143/738)	0.179 0.098	2.01 (1.38-2.93)	0.00027	0.172 0.111	1.65 (1.14-2.41)	0.0087	0.41	0.272
U.S. (636/804)	0.229 0.139	1.84 (1.51-2.23)	$9.8x10^{-10}$	0.105 0.083	1.30 (1.00-1.69)	0.052	0.026	0.232
Combined[f]	- -	1.88 (1.58-2.23)	$1.2x10^{-12}$	- -	1.41 (1.13-1.75)	0.0019	0.027	0.237
All European ancestry								
Combined[f]	- -	1.72 (1.59-1.86)	$3.3x10^{-41}$	- -	1.39 (1.26-1.53)	$6.9x10^{-11}$	0.00019	0.206
Hong Kong								
Hong Kong (333/2,836)	0.605 0.528	1.42 (1.16-1.73)	0.00064	0.190 0.218	1.08 (0.84-1.39)	0.55	0.0099	0.346

Each row contains the results from a joint analysis of two variants, rs2200733 T and rs10033464 T[b]. The numbers of cases and controls (N) are shown for each case-control study and for each variant the allelic frequencies of the variant in cases and controls, the OR with a 95% CI and two- sided P values, are shown. In addition a P value for comparing the effect of the two variants and their joint population attributable risk (PAR) is reported. For example, the first row indicates that, for the initial Icelandic discovery samples, rs2200733 T has an estimated odds ratio (OR) of 1.84 (95% CI (1.54-2.21), P = $4.1x10^{-11}$) vs the wild type (rs2200733 C, rs13143308 G, rs10033464 G haplotype), and rs10033464 T has an estimated OR of 1.42 (95% CI (1.13-1.77), P = 0.0024) vs the wild type.

[a] *Results of comparing rs2200733 T and rs10033464 T to the wild type rs2200733 C, rs13143308 G, rs10033464 G haplotype.*

[b] *In the Swedish and the U.S. samples rs10033464 T was tagged by the rs2200733 C, rs13143308 T haplotype*

[c] *The frequency in cases (above) and controls (below)*

[d] *P value for comparing the ORs of rs2200733 T and rs10033464 T.*

[e] *The association analysis was adjusted for the relatedness of some of the individuals.*

[f] *For the combined study populations of European decent, the PAR was calculated by using the average, unweighted control frequency of the populations, while the OR and the P value were estimated using the Mantel-Haenszel model.*

Table 8. *Association by age at diagnosis in Iceland and by AF sub-phenotype in the U.S.*

Sample (N cases/ N controls)	Male %	Age ±SD	rs2200733[a] OR (95% CI)	rs10033464[a,b] OR (95% CI)	*P*	Sex *P*
Iceland[c]						
Diagn. ≤ 60 (510/17,714)	**77.8**	**50.7 ±8.4**	2.12 (1.77-2.54)	1.69 (1.34-2.12)	$6.3x10^{-18}$	**0.82**
Diagn. 60-70 (654/17,714)	**66.2**	**65.6 ±2.9**	1.88 (1.60-2.21)	1.44 (1.18-1.77)	$6.7x10^{-15}$	**0.58**
Diagn. 70-80 (958/17,714)	**58.9**	**75.0 ±2.8**	1.60 (1.39-1.84)	1.23 (1.03-1.47)	$7.5x10^{-11}$	**0.96**
Diagn. > 80 (679/17,714)	**47.4**	**85.6 ±4.2**	1.20 (1.01-1.43)	1.31 (1.08-1.60)	0.0044	**0.36**
U.S.						
Lone AF (251/804)	**81.7**	**46.1 ±11.5**	2.32 (1.80-2.99)	1.68 (1.19-2.37)	$1.2x10^{-10}$	**0.46**
AF/HTN (67/804)	**74.6**	**54.5 ±10.2**	2.23 (1.43-3.48)	1.66 (0.90-3.04)	0.0010	**0.54**
Other AF (318/804)	**52.8**	**75.2 ±11.3**	1.44 (1.12-1.84)	0.97 (0.69-1.37)	0.015	**0.85**

Each row contains the results from a joint analysis of two variants, rs2200733 T and rs10033464 T[a]. The numbers of cases and controls (N), the percentage of male cases, and the mean age (± SD) for cases, are shown for each case-control study. The OR, with a 95% CI, and P values are shown for each variant. In addition a joint P value for the combined effect of the two variants, and a joint P value for testing if there is a difference of the allelic frequency of the variants between the sexes within each sub-group of patients.

[a] *Results of comparing rs2200733 T and rs10033464 T to the wild type rs2200733 C, rs13143308 G, rs10033464 G haplotype.*

[b] *In the U.S. samples rs10033464 T was tagged by the rs2200733 C, rs13143308 T haplotype.*

[c] *The association analysis was adjusted for the relatedness of some of the individuals.*

Table 9. *SNPs equivalent to rs10033464, rs13143308 and rs2200733 in CEU HapMap data*

SNP	Tagging SNP	Build 35 location	SEQ ID NO:50 location
rs12503217	rs10033464	112063765	108955
rs12510087	rs10033464	112066632	111822
rs6852357	rs10033464	112071939	117129
rs4400058	rs10033464	112074277	119467
rs10033464	rs10033464	112078365	123555
rs2171592	rs10033464	112078392	123582
rs2350539	rs10033464	112078814	124004
rs1906606	rs10033464	112080996	126186
rs723364	rs10033464	112082075	127265
rs2220429	rs10033464	112085089	130279
rs4032976	rs10033464	112086371	131561
rs3853440	rs10033464	112087213	132403
rs3853441	rs10033464	112087344	132534
rs3853442	rs10033464	112087632	132822
rs3853443	rs10033464	112087733	132923
rs4124158	rs10033464	112087798	132988
rs4124159	rs10033464	112087847	133037
rs12506083	rs10033464	112088016	133206
rs4032975	rs10033464	112089842	135032
rs4032974	rs10033464	112090140	135330
rs2634074	rs13143308	112034645	79835
rs2466455	rs13143308	112043219	88409
rs2723334	rs13143308	112046356	91546
rs1906616	rs13143308	112055172	100362
rs1906615	rs13143308	112059402	104592
rs2129983	rs13143308	112061684	106874
rs2129982	rs13143308	112061747	106937
rs1906599	rs13143308	112070290	115480
rs13143308	rs13143308	112072023	117213
rs6843082	rs13143308	112075671	120861
rs17042059	rs2200733	111998790	43980
rs4529121	rs2200733	112003159	48349
rs4543199	rs2200733	112005744	50934
rs12647316	rs2200733	112006855	52045
rs10019689	rs2200733	112007473	52663
rs4626276	rs2200733	112007593	52783
rs17042076	rs2200733	112009942	55132
rs11098089	rs2200733	112011830	57020
rs17042088	rs2200733	112012418	57608
rs11930528	rs2200733	112017798	62988
rs17042098	rs2200733	112021762	66952
rs17042102	rs2200733	112026230	71420
rs17042121	rs2200733	112034705	79895
rs10516563	rs2200733	112035326	80516
rs4605724	rs2200733	112042685	87875
rs2350269	rs2200733	112044728	89918
rs6533527	rs2200733	112045118	90308
rs17042144	rs2200733	112047270	92460
rs1906618	rs2200733	112053026	98216
rs1906617	rs2200733	112053418	98608
rs12646447	rs2200733	112056930	102120
rs12646754	rs2200733	112061176	106366
rs2129981	rs2200733	112061803	106993

SNP	Tagging SNP	Build 35 location	SEQ ID NO:50 location
rs12639654	rs2200733	112062899	108089
rs6817105	rs2200733	112063372	108562
rs17042171	rs2200733	112065891	111081
rs1906591	rs2200733	112066493	111683
rs1906592	rs2200733	112066608	111798
rs2200732	rs2200733	112067646	112836
rs2200733	rs2200733	112067773	112963
rs4611994	rs2200733	112068645	113835
rs4540107	rs2200733	112068706	113896
rs1906593	rs2200733	112069526	114716
rs1906596	rs2200733	112069840	115030
rs2220427	rs2200733	112072493	117683

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Table 10. *Haplotype structure (haplotypes with estimated frequency > 0.1%) over key SNPs and the D4S406 microsatellite in Iceland*

Frequency	D4S406	rs2200733	rs13143308	rs10033464
0.0800	-8	T	T	G
0.00647	-6	C	T	T
0.00225	-4	T	T	G
0.0415	-2	T	T	G
0.00108	0	T	T	G
0.0592	0	C	T	T
0.00679	2	C	T	T
0.0169	2	C	G	G
0.00923	4	C	T	T
0.135	4	C	G	G
0.0853	6	C	G	G
0.1587	8	C	G	G
0.163	10	C	G	G
0.0928	12	C	G	G
0.0398	14	C	G	G
0.101	16	C	G	G

Table 11. *Association to all Hap300 Illumina SNPs in a 200kb region around rs2200733 and rs10033464 in an extended set of Icelandic AF/AFI cases and controls. Results have not been adjusted for relatedness of individuals.*

						Adjusting for rs2220427		Also adjusting for rs10033464	
SNP	Location	All.	Freq	OR	*P* value	OR	*P* value	OR	*P* value
rs4834295	111892810	G	0.817	1.0	0.27	1.0	0.39	1.03	0.63
rs2278782	111899758	C	0.883	1.0	0.79	0.9	0.70	0.99	0.93
rs2595110	111902927	T	0.637	1.0	0.13	1.0	1.0	1.01	0.89
rs976568	111908325	A	0.743	1.0	0.83	0.9	0.62	0.97	0.58
rs2197815	111924481	T	0.030	1.1	0.34	1.1	0.34	0.97	0.84
rs2723286	111940938	A	0.231	1.0	0.26	1.0	0.50	1.03	0.59
rs2723296	111962087	G	0.229	1.0	0.38	1.0	0.60	1.03	0.67
rs1699716	111986643	T	0.153	1.3	$4.7x10^{-5}$	0.9	0.59	0.95	0.53
rs2723316	111991891	T	0.297	1.2	$1.9x10^{-5}$	1.0	0.59	0.95	0.40
rs6419178	111993104	A	0.143	1.1	0.17	1.0	0.25	0.98	0.77
rs1448817	111998657	G	0.252	1.4	$4.2x10^{-}$	1.1	0.035	1.06	0.46
rs2634073	112023387	A	0.167	1.6	$2.4x10^{-}$	1.2	0.039	0.90	0.48
rs2200733	112067773	T	0.119	1.7	$7.6x10^{-}$	-	-	-	-
rs2220427	112072493	T	0.120	1.7	$5.6x10^{-}$	-	-	-	-
rs1310587	112075751	C	0.888	1.0	0.33	0.9	0.89	0.95	0.56
rs1003346	112078365	T	0.082	1.2	0.013	1.3	$5.1x10^{-4}$	-	-
rs1314119	112086218	A	0.368	1.3	$2.0x10^{-}$	1.1	0.0067	1.08	0.29
rs3853444	112091740	A	0.604	1.1	0.053	1.0	0.45	1.06	0.24

Table 12. *Association study of SNPs which are equivalent to rs2200733 in CEU HapMap samples in the Chinese samples from Hong Kong.*

SNP	Location	All.	Freq	OR	*P* value	HapMap D'	HapMap R^2
rs11930528	112017798	T	0.472	1.27	0.011	0.91	0.66
rs17042121	112034705	G	0.418	1.32	0.0029	0.97	0.64
rs6533527	112045118	A	0.518	1.37	0.0014	0.95	0.79
rs1906617	112053418	C	0.524	1.35	0.0026	1.00	0.98
rs12639654	112062899	T	0.519	1.39	0.0012	1.00	1.00
rs2200733	112067773	T	0.516	1.42	$6.4x10^{-4}$	-	-
rs4611994	112068645	C	0.518	1.39	0.0012	1.00	1.00

The LD values reported are to rs2200733 in the combined CHB and JPT HapMap samples

Table 13. *Association to AF/AFl by genotype*

	Allelic RR		Genotype RR						
	1	2	00	01	02	11	12	22	P value
Iceland	1.68	1.38	1	1.55	1.36	3.42	2.47	1.58	0.12
Sweden	2.01	1.65	1	1.66	1.72	5.86	3.10	2.04	0.68
U.S.	1.84	1.30	1	1.63	1.40	4.86	2.31	0.90	0.25
Combined	1.71	1.38	1	1.56	1.37	3.64	2.44	1.43	0.018
Hong Kong	1.42	1.07	1	1.15	0.95	1.77	1.34	0.97	0.87

The three possible haplotypes are coded as
0 = rs2200733 C, rs13143308 G, rs10033464 G
1 = rs2200733 T, rs13143308 T, rs10033464 G
2 = rs2200733 C, rs13143308 T, rs10033464 T

Table 14. *Association of various phenotypes, considered risk factors for AF to risk variants.*

Phenotype	T rs2200733		T rs10033464	
(N cases/N controls)	OR	*P* value	OR	*P* value
Hypertension (2,620/19,862)	1.08	0.11	1.05	0.37
Myocardial infarction (3,576/19,542)	1.05	0.26	1.04	0.49
Obesity – BMI > 35 (1,601/21,593)	0.96	0.51	1.00	1.00

Table 15. *A summary of the source of the Icelandic controls. Note that individuals may come from multiple project and that some individuals may have been collected as relatives of probands.*

Source Project	Count	Frequency of T rs2200733	Frequency of T rs10033464
Discovery Controls			
Addiction	376	0.096	0.082
Anxiety	337	0.110	0.088
Breast Cancer	876	0.116	0.085
Colon Cancer	370	0.119	0.070
Infectious Disease	297	0.109	0.096
MI	454	0.104	0.076
Population Controls	389	0.099	0.077
Prostate Cancer	713	0.123	0.081
Schizophrenia	291	0.110	0.091
Type II Diabetes	551	0.102	0.078
Replication Controls			
Breast Cancer	228	0.122	0.074
Type II Diabetes	340	0.097	0.082
Alzheimer	459	0.107	0.061
Osteoarthritis	1,175	0.107	0.081
PAD	479	0.096	0.083
COPD	326	0.125	0.082
Stroke	414	0.092	0.069
Osteoporosis	1,155	0.109	0.072
MI	390	0.112	0.075
Hypertension	210	0.118	0.101
Depression	152	0.128	0.061
Asthma	538	0.106	0.076
Parkinson	173	0.102	0.058
Population Controls	305	0.105	0.097
Ankylosing Spondylitis	155	0.095	0.077
Sleep Apnea	422	0.118	0.074
AMD	442	0.101	0.067
Rheumatoid Arthritis	430	0.100	0.094
Lung Cancer	237	0.106	0.084
FCH	265	0.112	0.057
Longevity	392	0.09	0.077
Benign Prostatic Hyperplasia	245	0.101	0.058
Pre-eclampsia	262	0.129	0.083
Enuresis	249	0.104	0.087
Migrane	590	0.112	0.085
Myopia	353	0.123	0.085
Thyroid Cancer	104	0.121	0.097
ADHD	123	0.119	0.089
Prostate Cancer	580	0.117	0.073
Anxiety	546	0.121	0.096
Obesity	162	0.081	0.092
Endometriosis	258	0.106	0.084
Kidney Cancer	174	0.099	0.100
Melanoma	283	0.088	0.089
Addiction	201	0.138	0.098
Psoriasis	392	0.136	0.079
IBD	356	0.093	0.102

Table 16. *Primers used for ESTs screening of cDNA libraries*

ESTs*	Forward primer	Reverse primer
DA725631	AGTGGAGGCTGCCAGACTTC	TGCACCACTCATCACCAACA
DB324364	CCGAGGATGTCTTTAGTCTGCAA	ATCATACAGCAGGAATGCAAACA
AF017091	TGAGATTCCACATCCAACATCTTT	TGGCAAACTTGATATTGTTCTTG

**EST names are from NCBI BUILD 35*

Table 17. *SNPs that land in conserved TFBS in the region associated with AF.*

SNP	Location	Strand	Ancestral	Polym.	TFBS	TF start	TF end
rs17042171	112065890	+	C	A/C	NFAT	112065889	112065900
rs12510087	112066631	+	A	A/G	SOX5	112066632	112066641
rs2220427	112072492	+	C	C/T	SOX5	112072483	112072493

Strand indicates the strand in genome alignment that the mutation lands in.
Polym. is the two alleles of the polymorphism at this site.

Table 18. Markers in or near the PITX2 gene in LD with markers in the LD block C04. Shown are markers in or near PITX2 (marker 1) and their correlation to markers in LD block C04 (marker 2).

Marker 1	Marker 2	D'	r2	p-value
rs7668322	rs10033464	0.46291	0.133423	0.000953
rs2197815	rs10033464	0.660377	0.300172	2.55E-06
rs6831623	rs2200733	1	0.02834	0.025473
rs2595110	rs2200733	0.699643	0.02996	0.067245

Table 19. *Markers in linkage disequilibrium with marker rs2220427 and markerrs10033464 by values for r^2 of greater than 0.1. LD was calculated based on the HapMap CEU population sample.*

Marker 1	anchor	D'	r2	P-value	Pos in B35	Pos in SEQ ID NO:50
rs9994891	rs2220427	1	0.128329	0.002914	111149057	
rs11568995	rs2220427	1	0.128329	0.002914	111255189	
rs4698804	rs2220427	1	0.128329	0.002914	111297649	
rs721413	rs2220427	1	0.128329	0.002914	111305212	
rs10488883	rs2220427	1	0.128329	0.002914	111305486	
rs6854883	rs2220427	0.788889	0.510189	4.17E-09	111964919	10109
rs2255793	rs2220427	1	0.245283	9.27E-09	111965457	10647
rs2723298	rs2220427	1	0.274924	8.39E-09	111966089	11279
rs2723300	rs2220427	1	0.236507	1.40E-08	111972512	17702
rs2723307	rs2220427	1	0.176558	2.98E-07	111975800	20990
rs1584429	rs2220427	1	0.245283	9.27E-09	111976151	21341
rs1448799	rs2220427	1	0.245283	9.27E-09	111980386	25576
rs1448798	rs2220427	1	0.245283	9.27E-09	111980789	25979
rs1900827	rs2220427	1	0.246741	8.60E-08	111981343	26533
rs2197814	rs2220427	1	0.240506	1.20E-08	111983098	28288
rs969642	rs2220427	1	0.245283	9.27E-09	111983529	28719
rs2595093	rs2220427	0.830131	0.513828	1.59E-10	111984960	30150
rs2245595	rs2220427	1	0.252078	6.90E-09	111985715	30905
rs2595088	rs2220427	1	0.254302	1.99E-08	111985958	31148
rs981150	rs2220427	1	0.245283	9.27E-09	111986232	31422
rs16997168	rs2220427	0.819277	0.507451	2.11E-10	111986643	31833
rs16997169	rs2220427	1	0.245283	9.27E-09	111986685	31875
rs4527540	rs2220427	1	0.245283	9.27E-09	111986742	31932
rs17042026	rs2220427	0.833488	0.554106	1.23E-11	111989978	35168
rs2723316	rs2220427	1	0.245283	9.27E-09	111991891	37081
rs2595081	rs2220427	0.832621	0.549261	3.07E-11	111992761	37951
rs2595085	rs2220427	1	0.242283	1.16E-08	111994377	39567
rs2723318	rs2220427	1	0.236507	1.40E-08	111994576	39766
rs1448817	rs2220427	1	0.296277	9.75E-10	111998657	43847
rs17042059	rs2220427	1	1	1.62E-20	111998790	43980
rs4529121	rs2220427	1	1	1.43E-20	112003159	48349
rs10032150	rs2220427	1	0.296277	9.75E-10	112004222	49412
rs4543199	rs2220427	1	1	1.43E-20	112005744	50934
rs12647316	rs2220427	1	1	1.43E-20	112006855	52045
rs12647393	rs2220427	1	0.917379	1.57E-15	112006886	52076
rs10019689	rs2220427	1	1	1.43E-20	112007473	52663
rs4626276	rs2220427	1	1	1.43E-20	112007593	52783
rs17042076	rs2220427	1	1	1.62E-20	112009942	55132
rs11098089	rs2220427	1	1	1.62E-20	112011830	57020
rs17042088	rs2220427	1	1	1.62E-20	112012418	57608
rs11944778	rs2220427	0.91509	0.811642	4.20E-12	112014571	59761
rs4307025	rs2220427	1	0.296277	9.75E-10	112015107	60297
rs11930528	rs2220427	1	1	1.42E-19	112017798	62988
rs17042098	rs2220427	1	1	1.43E-20	112021762	66952
rs2634073	rs2220427	1	0.523052	1.42E-12	112023387	68577
rs17042102	rs2220427	1	1	2.07E-16	112026230	71420
rs2634071	rs2220427	1	0.528302	2.16E-13	112026824	72014
rs2634074	rs2220427	1	0.433962	5.12E-12	112034645	79835
rs17042121	rs2220427	1	1	1.43E-20	112034705	79895
rs10516563	rs2220427	1	1	1.43E-20	112035326	80516
rs4605724	rs2220427	1	1	1.43E-20	112042685	87875
rs2466455	rs2220427	1	0.491956	5.72E-12	112043219	88409
rs2350269	rs2220427	1	1	1.42E-19	112044728	89918
rs6533527	rs2220427	1	1	1.43E-20	112045118	90308

Marker 1	anchor	D'	r2	P-value	Pos in B35	Pos in SEQ ID NO:50
rs2723334	rs2220427	1	0.433962	5.12E-12	112046356	91546
rs17042144	rs2220427	1	1	1.43E-20	112047270	92460
rs1906618	rs2220427	1	1	2.67E-19	112053026	98216
rs1906617	rs2220427	1	1	1.43E-20	112053418	98608
rs6847935	rs2220427	1	0.921053	1.10E-18	112054255	99445
rs1906616	rs2220427	1	0.433962	5.12E-12	112055172	100362
rs12646447	rs2220427	1	1	1.84E-20	112056930	102120
rs1906615	rs2220427	1	0.433962	5.12E-12	112059402	104592
rs12646754	rs2220427	1	1	2.08E-20	112061176	106366
rs2129983	rs2220427	1	0.428571	6.61E-12	112061684	106874
rs2129982	rs2220427	1	0.433962	5.12E-12	112061747	106937
rs2129981	rs2220427	1	1	1.43E-20	112061803	106993
rs12639654	rs2220427	1	1	1.43E-20	112062899	108089
rs6817105	rs2220427	1	1	1.62E-20	112063372	108562
rs17042171	rs2220427	1	1	1.43E-20	112065891	111081
rs1906591	rs2220427	1	1	1.43E-20	112066493	111683
rs1906592	rs2220427	1	1	1.26E-19	112066608	111798
rs2200732	rs2220427	1	1	1.85E-19	112067646	112836
rs2200733	rs2220427	1	1	1.43E-20	112067773	112963
rs4611994	rs2220427	1	1	1.43E-20	112068645	113835
rs4540107	rs2220427	1	1	1.43E-20	112068706	113896
rs1906593	rs2220427	1	1	1.62E-20	112069526	114716
rs1906596	rs2220427	1	1	2.68E-20	112069840	115030
rs1906599	rs2220427	1	0.433962	5.12E-12	112070290	115480
rs13143308	rs2220427	1	0.438445	5.36E-12	112072023	117213
rs6843082	rs2220427	1	0.433962	5.12E-12	112075671	120861
rs11931959	rs2220427	1	0.249653	7.85E-09	112077289	122479
rs13121924	rs2220427	1	0.156089	9.36E-07	112078423	123613
rs2129979	rs2220427	1	0.256789	5.78E-09	112078601	123791
rs723363	rs2220427	1	0.156089	9.36E-07	112082105	127295
rs7697491	rs2220427	1	0.154058	1.07E-06	112083422	128612
rs13141190	rs2220427	1	0.156089	9.36E-07	112086218	131408
rs6533530	rs2220427	1	0.156089	9.36E-07	112089540	134730
rs6533531	rs2220427	1	0.156089	9.36E-07	112089569	134759
rs3866831	rs2220427	1	0.156089	9.36E-07	112089718	134908
rs3866832	rs2220427	0.857992	0.109603	0.000186	112091304	136494
rs11098083	rs10033464	0.407276	0.12964	0.00205	111855920	
rs11721423	rs10033464	0.365905	0.11129	0.003321	111858873	
rs10005945	rs10033464	0.433962	0.101848	0.004763	111860013	
rs7668322	rs10033464	0.46291	0.133423	0.000953	111906200	
rs2197815	rs10033464	0.660377	0.300172	2.55E-06	111924481	
rs6831623	rs10033464	1	0.511236	3.33E-10	111964677	9867
rs7661383	rs10033464	0.637611	0.21478	0.000011	111979181	24371
rs7667461	rs10033464	0.637611	0.21478	0.000011	111979738	24928
rs1900827	rs10033464	0.735008	0.134278	0.000368	111981343	26533
rs998101	rs10033464	0.635887	0.20914	0.000014	111988219	33409
rs12646859	rs10033464	0.719793	0.271646	0.000191	111992237	37427
rs12498380	rs10033464	0.60232	0.178165	0.000097	111992563	37753
rs7690164	rs10033464	0.496308	0.148782	0.005455	111994069	39259
rs11098090	rs10033464	0.551083	0.169161	0.000104	112014012	59202
rs2634073	rs10033464	0.640189	0.223694	8.35E-06	112023387	68577
rs2634071	rs10033464	0.637611	0.21478	0.000011	112026824	72014
rs2634074	rs10033464	1	0.433962	5.12E-12	112034645	79835
rs2466455	rs10033464	1	0.428256	1.77E-09	112043219	88409
rs2723334	rs10033464	1	0.433962	5.12E-12	112046356	91546
rs1906616	rs10033464	1	0.433962	5.12E-12	112055172	100362
rs1906615	rs10033464	1	0.433962	5.12E-12	112059402	104592

Marker 1	anchor	D'	r2	P-value	Pos in B35	Pos in SEQ ID NO:50
rs2129983	rs10033464	1	0.428571	6.61E-12	112061684	106874
rs2129982	rs10033464	1	0.433962	5.12E-12	112061747	106937
rs12503217	rs10033464	1	1	1.43E-20	112063765	108955
rs12510087	rs10033464	1	1	1.43E-20	112066632	111822
rs1906599	rs10033464	1	0.433962	5.12E-12	112070290	115480
rs6852357	rs10033464	1	1	1.43E-20	112071939	117129
rs13143308	rs10033464	1	0.421583	2.22E-11	112072023	117213
rs4833456	rs10033464	1	0.923858	6.67E-19	112073911	119101
rs4400058	rs10033464	1	1	1.43E-20	112074277	119467
rs6843082	rs10033464	1	0.433962	5.12E-12	112075671	120861
rs2171592	rs10033464	1	1	1.43E-20	112078392	123582
rs13121924	rs10033464	1	0.156089	9.36E-07	112078423	123613
rs2350539	rs10033464	1	1	1.43E-20	112078814	124004
rs1906606	rs10033464	1	1	1.43E-20	112080996	126186
rs723364	rs10033464	1	1	1.43E-20	112082075	127265
rs723363	rs10033464	1	0.156089	9.36E-07	112082105	127295
rs7697491	rs10033464	1	0.154058	1.07E-06	112083422	128612
rs2220429	rs10033464	1	1	1.43E-20	112085089	130279
rs13141190	rs10033464	1	0.156089	9.36E-07	112086218	131408
rs4032976	rs10033464	1	1	1.62E-20	112086371	131561
rs3853440	rs10033464	1	1	1.62E-20	112087213	132403
rs3853441	rs10033464	1	1	1.43E-20	112087344	132534
rs3853442	rs10033464	1	1	1.43E-20	112087632	132822
rs3853443	rs10033464	1	1	1.43E-20	112087733	132923
rs4124158	rs10033464	1	1	1.10E-17	112087798	132988
rs4124159	rs10033464	1	1	1.43E-20	112087847	133037
rs12506083	rs10033464	1	1	1.43E-20	112088016	133206
rs6533530	rs10033464	1	0.156089	9.36E-07	112089540	134730
rs6533531	rs10033464	1	0.156089	9.36E-07	112089569	134759
rs3866831	rs10033464	1	0.156089	9.36E-07	112089718	134908
rs4032975	rs10033464	1	1	7.06E-20	112089842	135032
rs4032974	rs10033464	1	1	1.43E-20	112090140	135330
rs3866832	rs10033464	1	0.148936	1.44E-06	112091304	136494
rs7654080	rs10033464	1	0.151515	0.002495	112585323	

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Example 3. Association of Chromosome 4 variants to Ischemic stroke

Stroke is a common cause of death and the leading cause of adult disability in Western societies. It is now also becoming a major health problem in low-income and middle-income countries due to population ageing and changes in modifiable risk factors for cardiovascular diseases[1]. Stroke is not a single disease but a highly complex syndrome consisting of a group of heterogeneous disorders with many genetic and environmental risk factors[2,3]. Studies on twins, family history and animal models[4-8] provide evidence for genetic contribution to the common forms of stroke but no major risk variant has yet been identified showing consistent results across populations.

Ischemic strokes (IS), accounting for the majority of cerebral insults (>80%), result from thrombosis or embolism leading to obstruction of cerebral arteries. Various pathophysiological mechanisms can cause IS but the most common ones are large artery atherosclerosis (LAA), cardioembolic stroke (CES) and small vessel disease (SVD)[9].

Methods

Study populations.

Iceland: Icelandic stroke patients were recruited from a registry of over 4,000 individuals diagnosed with ischemic stroke or TIA at the only university hospital in Reykjavik, the Landspitali University Hospital, during the years 1993 to 2006. Stroke patients have been enrolled over the last nine years through the cardiovascular disease (CVD) genetics program at deCODE. Stroke diagnosis was clinically confirmed by neurologists (see below). The discovery cohort included 1,661 patients and when analysing the SNPs on 4q25 we used an additional set of 282 patients (mean age±SD: 77.2±11.3 years, 45% females). We used 25,708 controls (mean age±SD: 59.2±21.1 years, 59% females) from various genetic programs under study at Decode, including: abdominal aneurysm (250), atrial fibrillation (1,150), addiction (750), Alzheimer (350), anxiety (200), asthma (1300), COPD (850), colon cancer (200), deep vein thrombosis (550), dyslexia (200), infection diseases (250), longevity (400), lung cancer (750), myocardial infarction (2,400), migraine (1,100), peripheral artery disease (1,200), polycystic ovary syndrome (1,200), pre-eclampsia (700), prostate cancer (400), psoriasis (750), rheumatic arthritis (550), restless leg syndrome (350), and type 2 diabetes (400).

The study was approved by the Data Protection Commission of Iceland (DPC) and the National Bioethics Committee of Iceland. All participants gave informed consent.

Sweden: Swedish patients with ischemic stroke attending the stroke unit or the stroke outpatient clinic at Karolinska University Hospital, Huddinge unit in Stockholm, Sweden, were recruited from 1996 to 2002 as part of an ongoing genetic epidemiology study, the South Stockholm Ischemic Stroke Study (SSISS) (mean age±SD: 67.3±11.8 years, 44% females). The Swedish controls used in this study are population-based controls recruited from the same region in central Sweden as the patients, representing the general population in this area. The individuals were either blood donors recruited at the Huddinge or Karolinska University Hospitals or healthy volunteers (recruited in 1990-1994) recruited by the Clinical Chemistry Department at the Karolinska University Hospital to represent a normal reference population (mean age±SD: 46.8±15.9 years for controls from Huddinge hospital, 41% females, age information not available for blood donors recruited at the Karolinska hospital). The study was approved by the Bioethics Committee of Karolinska Institutet.

South-Germany: The German population, herein referred to as Germany-S, consisted of IS patients consecutively recruited during the period 2001-2006 at the stroke unit of the Department of Neurology, Klinikum Grosshadern, University of Munich, Germany (mean age±SD: 65.3±13.7 years, 38% females). The control group consisted of age and gender matched individuals without a history of cardiovascular disease (mean age±SD: 62.7±10.9 years, 38% females). These were selected from the KORA S4 study, a community based epidemiological project near Munich [23]. The study was approved by the local ethics committee and informed consent was obtained from all individuals (or relatives or legal guardians).

Westphalia region, Germany: The second German population, referred to as Germany-W, recruited ischemic stroke patients through hospitals participating in the regional Westphalian Stroke Register, located in the west of the country, during the period 2000-2003 (mean age±SD: 70.4±12.6 years, 53% females). Population controls without a self-reported history of stroke were drawn from the cross-sectional, prospective, population based Dortmund Health Study[24], conducted in the same region, and subsequently frequency matched to the cases (mean age±SD: 52.3±13.7 years, 53% females). Both studies were approved by the ethics committee of the University of Munster. All participants gave their informed consent.

SE-England, United Kingdom. Ischemic stroke patients of European descent attending a cerebrovascular service were recruited 1995-2002. All cases were phenotyped by one experienced stroke neurologist with review of original imaging (mean age±SD: 64.6±12.7 years, 41% females). Community controls free of symptomatic cerebrovascular disease were also recruited by sampling family doctor lists from the same geographical region as the patients. Sampling was stratified to provide a similar distribution of age and gender as in the patient group (mean age±SD: 64.8±8.6 years, 41% females). The study

was approved by local research ethics committees and informed consent was obtained from all participants.

Phenotyping. Only patients with ischemic but not with hemorrhagic strokes were included in the study. All patients had clinically relevant diagnostic work-up performed, including brain imaging with computed tomography (CT) or/and magnetic resonance imaging (MRI) as well as ancillary diagnostic investigations including duplex ultrasonography of the carotid and vertebral arteries, echocardiography, Holter monitoring, MR-angiography, CT-angiography and blood tests. Patients with clinically confirmed Transient Ischemic Attack (TIA) were included in the Ischemic stroke group from Iceland, Germany-S and Sweden. Patients were classified into etiologic subtypes according to the Trial of Org 10172 in Acute Stroke Treatment (TOAST) [25]. This classification includes six categories: (1) large-artery occlusive disease (large vessel disease), (2) cardioembolism (cardiogenic stroke), (3) small vessel disease (lacunar stroke), (4) other determined etiology, (5) etiology unknown despite diagnostic efforts, or (6) more than one etiology. Patients classified into the TOAST categories 4-6 were excluded from the stroke population from Germany-W. In Iceland, patients were classified as having large-artery occlusive disease if stenosis was ≥ 70% which is a stricter criterion than usually used i.e. ≥ 50%. Classification of stroke patients into subtypes according to the Trial of Org 10172 in Acute Stroke Treatment (TOAST) classification system[25] in the Icelandic discovery and the four replication sample sets is listed in Table 1.

Illumina genome-wide genotyping. All Icelandic cases and control samples were assayed with the Infinium HumanHap300 SNP chips (Illumina), containing 317,503 tagging SNPs derived from phase 1 of the International HapMap project. OF the SNPs assayed on the chip, 6,622 SNPs were excluded because they showed either (i) a call rate lower than 95% in cases or controls, (ii) minor allele frequency less than 1% in the population or (iii) significant distortion from Hardy-Weinberg equilibrium in the contols ($P<1\times10^{-10}$). Any sample with yield <98% were excluded from the analysis. In the final analysis 310,881 SNPs were used.

Single SNP Genotyping. Single-SNP genotyping for all 121 SNP was carried out at deCODE genetics in Reykjavik, Iceland using the Centaurus (Nanogen) platform [26]. The quality of each SNP assay was evaluated by comparing the genotyping of the CEU HapMap samples with the publicly available HapMap data. All SNPs passed mismatch tests, linkage disequilibrium (LD) tests and were in Hardy-Weinberg equilibrium.

Association analysis. For association analysis a standard likelihood ratio statistics was used, as implemented in the NEMO software created at deCODE[27], to calculate two-sided P values and odds ratio (OR) for each individual allele, assuming a multiplicative model for

risk, i.e., that the risk of the two alleles a person carries multiply. Allelic frequencies, rather than carrier frequencies are presented for the markers.

At the locus on chromosome 4q25, we analysed 3 SNPs, rs2200733, rs10033464 and rs13143308. The third SNP, rs13143308, is in high LD with both rs2200733 and rs10033464 (D'=0.99 for both) and has a minor allele that corresponds completely to chromosomes carrying either rs2200733 allele T or rs10033464 allele T. It was genotyped in all populations using a Centaurus assay, and was used to infer genotypes for those individuals who had missing data for either rs2200733 or rs10033464 on the Illumina Infinium platform. In Table 21 and Supplementary Table 22, *P* values and OR for both risk alleles rs2200733-T and rs10033464-T were computed on the basis of comparison with the wild-type rs2200733 allele C, rs13143308 allele G, rs10033464 allele G haplotype, which contains neither of the at-risk alleles[11].

For the Icelandic study groups, *P* values are given after adjustment for the relatedness of the subjects and other possible population stratification using the method of genomic control[10]. The inflation factors for the chi-squared statistics are estimated to be 1.07, 1.04, 1.06 and 1.02 for the genome-wide association analysis of the IS, CES, LAA of SVD patient groups respectively. With the additional cases and controls typed for the 4q locus, we estimated the inflation factors using simulations as previously described[28]. The resulting inflation factors are 1.09, 1.03, 1.06, 1.05, 1.01, 1.00, 1.01 and 1.00, for the groups IS, CES, IS excl CES, LVD, SVD, other, unknown and more than one cause, respectively.

Due to the large number of controls used, the effective samples size after adjusting for the relatedness of the cases and controls corresponds to testing 2,690 IS patients and 2,690 controls. The corresponding effective sample sizes for the CES, LAA and SVD patients are 710, 417 and 467, respectively.

Results from multiple case-control groups were combined using a Mantel-Haenszel model in which the groups were allowed to have different population frequencies for alleles, haplotypes and genotypes but were assumed to have a common relative risk[29]

Results

The association of variants within the LD Block C04 region to Ischemic Stroke was investigated. In order to investigate further the contribution of the two AF risk variants on 4q25, rs2200733 and rs10033464, to the risk of developing Ischemic Stroke and its subtypes, large artery atherosclerosis (LAA), cardioembolic stroke (CES) and small vessel disease (SVD), we genotyped marker rs2200733 and marker rs10033464 in Icelandic

samples, and for replication purposes we also analyzed replication data sets in cohorts from South-Germany (1,181 cases and 1,189 controls, Germany-S), Sweden (1,032 cases and 1,387 controls), Westphalia region in Germany (1,388 cases and 1,106 controls, Germany-W), and United Kingdom (654 cases/676 controls, UK). The phenotype classification of the study cohorts is shown in Table 20.

Table 20. TOAST subclassification of genotyped stroke cases, n (%)

	Discovery group	Replication groups			
	Iceland	Germany-S	Sweden	Germany-W	United Kingdom
Ischemic stroke	1943	1183	1066	1391	654
TOAST subtyping:	1443	1183	1061	1389	654
Cardioembolism	385 (45)	297 (38)	185 (37)	554 (40)	78 (18)
Large artery atherosclerosis	229 (27)	372 (47)	230 (46)	560 (40)	232 (55)
Small vessel disease	246 (29)	118 (15)	82 (16)	275 (20)	114 (27)
other cause	42	67	56	not recruited	3
more than one cause	34		42	not recruited	40
unknown cause	507	329	466	not recruited	187

TOAST= Trial of Org 10172 in Acute Stroke Treatment.

Additional patients (282) and controls (14,893) from Iceland were also genotyped for these particular SNPs. The association test was done by comparing each SNP with the wild-type haplotype (see Methods). As shown in Table 21, rs2200733 conferred an increased risk of Ischemic Stroke in all sample sets, and the association with Ischemic Stroke was highly significant with a combined OR=1.26 ($P = 8.8\times10^{-11}$). For rs10033464, the association with Ischemic Stroke was not significant (OR=1.03, P=0.45). Both SNPs however, associated significantly with Cardiembolic Stroke and this risk was significantly greater than in the Ischemic Stroke group as a whole (rs2200733: OR=1.53, $P=1.5\times10^{-12}$; rs10033464: OR=1.27, $P=5.9\times10^{-4}$). This is as expected given the known contribution of Atrial Fibrillation to this subphenotype. By removing patients with Cardioembolic Stroke from the Ischemic Stroke group, the observed effect for both SNPs was weaker in the remaining Ischemic Stroke patients, but remained significant for the stronger variant (rs2200733: OR=1.18, $P=1.5\times10^{-5}$, rs10033464: OR=0.96, P=0.39). Apart from Cardioembolic Stroke, Large Artery Atherosclerosis and stroke of undetermined cause were the only subphenotypes showing significant association with rs2200733 (OR=1.22, $P=1.5\times10^{-3}$, Table 2 and OR=1.18, P=0.01). These results suggest that a significant portion of strokes classified as either cryptogenic stroke or large artery atherosclerosis may be due to undiagnosed, intermittent AF.

Table 21. Association between rs2200733 (allele T) and rs1033464 (allele T) and Ischemic stroke. Association results for rs2200733 allele T and rs10033464 allele T for ischemic stroke and the subphenotypes; cardioembolic stroke, large artery atherosclerosis and small vessel disease, in five study populations. Also presented are the results for ischemic stroke after excluding patients with cardioembolism. Results for each phenotype are also included after combining the study populations using a Mantel-Haenszel model (All groups). Number of controls (m) and cases (n) is shown in parenthesis, the allelic frequencies in each group, the OR with a 95% CI and two-sided *P* value for comparison to the wild type haplotype (see Supplementary Methods). The results for the Icelandic population are adjusted for relatedness of the individuals.

Phenotype	rs2200733-T frequency				rs10033464-T frequency			
Study population (m/n)	**Controls**	**Cases**	**OR (95% CI)**	***P***	**Controls**	**Cases**	**OR (95% CI)**	***P***
Ischemic stroke								
Iceland (25708/1943)	0.119	0.142	1.23 (1.11-1.36)	4.7×10^{-5}	0.082	0.085	1.07 (0.95-1.21)	0.28
Germany-S (1186/1183)	0.118	0.138	1.19 (1.00-1.41)	0.05	0.093	0.083	0.90 (0.73-1.10)	0.31
Germany-W (1107/1391)	0.114	0.146	1.34 (1.13-1.58)	7.0×10^{-4}	0.092	0.096	1.10 (0.91-1.33)	0.34
Sweden (740/1066)	0.098	0.121	1.27 (1.02-1.58)	0.03	0.113	0.111	1.01 (0.81-1.24)	0.96
UK (676/654)	0.087	0.119	1.43 (1.11-1.74)	0.0056	0.090	0.088	1.02 (0.78-1.33)	0.90
All groups (29417/6237)	0.107	0.133	1.26 (1.17-1.35)	8.8×10^{-11}	0.094	0.093	1.03 (0.95-1.12)	0.45
Cardioembolism								
Iceland (25708/385)	0.119	0.164	1.50 (1.22-1.85)	1.1×10^{-4}	0.082	0.105	1.39 (1.09-1.79)	0.009
Germany-S (1186/297)	0.118	0.175	1.61 (1.25-2.08)	2.5×10^{-4}	0.093	0.096	1.11 (0.81-1.52)	0.502
Germany-W (1107/554)	0.114	0.161	1.52 (1.23-1.88)	1.0×10^{-4}	0.092	0.104	1.22 (0.95-1.56)	0.113
Sweden (740/185)	0.098	0.149	1.67 (1.18-2.36)	4.0×10^{-3}	0.113	0.133	1.28 (0.90-1.82)	0.162
UK (676/78)	0.087	0.090	1.08 (0.60-1.95)	0.79	0.090	0.122	1.42 (0.83-2.43)	0.198
All groups (29417/1499)	0.107	0.148	1.53 (1.36-1.72)	1.5×10^{-12}	0.094	0.112	1.27 (1.11-1.45)	5.9×10^{-4}
Ischemic stroke excl Cardioembolism								
Iceland (25708/1558)	0.119	0.136	1.17 (1.05-1.31)	0.01	0.082	0.081	1.00 (0.87-1.14)	0.95
Germany-S (1186/886)	0.118	0.125	1.06 (0.87-1.28)	0.57	0.093	0.078	0.83 (0.67-1.04)	0.11
Germany-W (1107/837)	0.114	0.136	1.22 (1.01-1.48)	0.04	0.092	0.091	1.02 (0.82-1.28)	0.84
Sweden (740/881)	0.098	0.115	1.19 (0.95-1.50)	0.13	0.113	0.106	0.95 (0.76-1.19)	0.66
UK (676/576)	0.087	0.123	1.48 (1.14-1.91)	0.003	0.090	0.083	0.96 (0.73-1.28)	0.80
All groups (29417/4738)	0.107	0.127	1.18 (1.10-1.28)	1.5×10^{-5}	0.094	0.088	0.96 (0.88-1.05)	0.39

Large artery atherosclerosis								
Iceland (25708/229)	0.119	0.157	1.41 (1.08-1.86)	0.012	0.082	0.096	1.25 (0.89-1.74)	0.19
Germany-S (1186/372)	0.118	0.117	0.96 (0.75-1.25)	0.78	0.093	0.071	0.74 (0.54-1.00)	0.05
Germany-W (1107/560)	0.114	0.140	1.28 (1.03-1.59)	0.03	0.092	0.100	1.14 (0.89-1.46)	0.30
Sweden (740/230)	0.098	0.094	0.94 (0.65-1.34)	0.72	0.113	0.096	0.82 (0.58-1.17)	0.27
UK (676/232)	0.087	0.138	1.66 (1.19-2.31)	3.0×10^{-3}	0.090	0.071	0.82 (0.55-1.23)	0.34
All groups (29417/1623)	0.107	0.129	1.22 (1.08-1.38)	1.5×10^{-3}	0.094	0.087	0.96 (0.83-1.11)	0.57
Small vessel disease								
Iceland (25708/246)	0.119	0.112	0.94 (0.71-1.24)	0.64	0.082	0.085	1.03 (0.75-1.42)	0.86
Germany-S (1186/118)	0.118	0.145	1.23 (0.83-1.83)	0.30	0.093	0.063	0.68 (0.40-1.14)	0.14
Germany-W (1107/275)	0.114	0.126	1.10 (0.83-1.47)	0.51	0.092	0.075	0.81 (0.57-1.14)	0.22
Sweden (740/82)	0.098	0.110	1.11 (0.66-1.88)	0.70	0.113	0.091	0.80 (0.46-1.37)	0.42
UK (676/114)	0.087	0.101	1.18 (0.73-1.91)	0.50	0.090	0.087	0.99 (0.60-1.63)	0.97
All groups (29417/835)	0.107	0.119	1.07 (0.91-1.26)	0.39	0.094	0.080	0.88 (0.73-1.05)	0.16

Table 22. Association results for rs2200733 allele T and rs10033464 allele T for the TOAST subphenotypes; other cause, more than one cause and unknown cause in three or four study populations. Results for each phenotype are also included after combining the study populations using a Mantel-Haenszel model (All groups). Number of controls (m) and cases (n) is shown in parenthesis, the allelic frequencies in each group, the OR with a 95% CI and two-sided *P* value for comparison to the wild type haplotype (see Supplementary Methods). The results for the Icelandic population are adjusted for relatedness of the individuals.

Phenotype	rs2200733-T frequency				rs10033464-T frequency			
Study population (m/n)	**Controls**	**Cases**	**OR (95% CI)**	***P***	**Controls**	**Cases**	**OR (95% CI)**	***P***
Other cause								
Iceland (25708/42)	0.119	0.155	1.32 (0.72-2.45)	0.37	0.082	0.060	0.73 (0.31-1.75)	0.48
Germany-S (1186/67)	0.118	0.119	1.03 (0.60-1.77)	0.91	0.093	0.105	1.14 (0.64-2.04)	0.66
Sweden (740/56)	0.098	0.125	1.36 (0.74-2.50)	0.32	0.113	0.134	1.26 (0.70-2.26)	0.44
All groups (27634/168)	0.111	0.133	1.19 (0.85-1.66)	0.32	0.096	0.099	1.06 (0.74-1.54)	0.74
More than one cause								
Iceland (25708/34)	0.119	0.088	0.68 (0.31-1.52)	0.35	0.082	0.044	0.49 (0.17-1.39)	0.18
Sweden (740/42)	0.098	0.112	1.27 (0.61-2.66)	0.52	0.113	0.187	1.84 (0.99-3.41)	0.05
UK (676/40)	0.087	0.213	2.89 (1.54-5.39)	8.9×10^{-4}	0.090	0.088	1.15 (0.51-2.61)	0.74
All groups (27124/116)	0.101	0.138	1.48 (0.99-2.21)	0.06	0.095	0.106	1.21 (0.78-1.88)	0.41
Unknown cause								
Iceland (25708/507)	0.119	0.135	1.15 (0.95-1.38)	0.15	0.082	0.073	0.89 (0.70-1.13)	0.35
Germany-S (1186/329)	0.118	0.129	1.10 (0.85-1.44)	0.46	0.093	0.087	0.94 (0.69-1.28)	0.70
Sweden (740/466)	0.098	0.126	1.32 (1.01-1.71)	0.04	0.113	0.104	0.94 (0.72-1.23)	0.65
UK (760/187)	0.087	0.102	1.20 (0.81-1.78)	0.35	0.090	0.096	1.10 (0.74-1.64)	0.63
All groups (28310/1489)	0.105	0.123	1.18 (1.04-1.34)	0.01	0.095	0.090	0.94 (0.82-1.08)	0.41

As discussed in the above (Example 2), the risk alleles of rs2200733 and rs10033464 correlate significantly with the age of diagnosis of Atrial Fibrillation. A non-significant trend in the same direction was observed in our study for the age at diagnosis of Cardioembolic Stroke (0.62 years per copy of T rs2200733, P=0.33, and 0.29 years per copy of T rs10033464, P=0.71, Table 23), suggesting that the observed age effect on AF may apply to Cardioembolic Stroke also, albeit being a weaker effect.

Table 23. Linear regression of age at diagnosis on the number of risk alleles of rs2200733 allele T and rs10033464 allele T. Shown are the regression coefficients and the corresponding two-sided P-values obtained using the age at diagnostics as a response (in years) and the number of at risk alleles as predictor variables. The sex was included as a covariate factor in all tests, and also the population in the test for all groups combined. Numbers of cases used in the analysis are shown in parenthesis (n).

	rs2200733-T	rs2200733-T	rs10033464-T	rs10033464-T
Ischemic	**reg.coeff**	**P**	**reg.coeff**	**P**
Iceland (1830)	0.11	0.85	-0.35	0.62
Germany-S (1174)	0.29	0.73	0.85	0.43
Sweden (780)	0.56	0.56	1.11	0.23
Germany-W (1352)	0.17	0.80	1.21	0.14
UK (654)	0.24	0.83	0.47	0.71
All Groups (5790)	0.40	0.25	0.68	0.10
Cardioembolic	**reg.coeff**	**P**	**reg.coeff**	**P**
Iceland (356)	-1.52	0.16	-0.29	0.85
Germany-S (296)	-1.72	0.21	-2.53	0.18
Sweden (173)	-2.09	0.20	0.81	0.62
Germany-W (1352)	-0.04	1.00	0.82	0.53
UK (78)	7.11	0.084	-5.29	0.16
All Groups (1441)	-0.62	0.33	-0.29	0.71

Discussion

Through this study on 1661 Icelandic IS patients and 10815 controls and the follow-up replication in large and well characterized European Ischemic Stroke case/control sample sets we identified and validated a risk variant on chromosome 4q25, tagged by rs2200733, that associates with Iscemic Stroke. In our study, as expected, these variants associated most strongly with the subphenotype Cardioembolic Stroke, which is a major complication of Atrial Fibrillation. The risk that is observed in Ischemic Stroke patients without Cardioembolic Stroke is possibly due to an underdiagnosis of Atrial Fibrillation and thereby Cardioembolic Stroke, since Atrial Fibrillation is often asymptomatic or intermittent and can consequently be difficult to detect in stroke patients.

Up to 30% of Ischemic Stroke are caused by cardioembolism(*5, 6*) of which a large proportion occurs in the presence of Atrial Fibrillation(*7, 8*). Atrial Fibrillation is the most common sustained cardiac arrhythmia of man and its prevalence increases with age, affecting approximately 10% of those over 80 years of age (*3, 9*). As such, AF is one of the most powerful independent risk factors for stroke and on a population level, AF is associated with a fourfold to fivefold increase in the risk of stroke(*3, 7, 8, 10*). Moreover, Caridembolic Stroke is generally severe, reflected by greater disability, higher rates of stroke recurrence and higher mortality than in other subtypes of strokes (*6, 11*). Early detection of those at risk for AF is important in order to reduce the risk of suffering a future stroke. Clinical trials on stroke prevention in patients with AF have shown that anticoagulant medications (e.g. warfarin) reduce the risk of stroke substantially(*7, 12*) and is much more effective than anti-platelet agents such as aspirin and clopidogrel. Our results strongly suggest that a significant portion of stroke patients have undiagnosed atrial fibrillation and are classified either as cryptogenic stroke or as large vessel stroke. Such patients may have asymptomatic, intermittent AF that is not detected during routine workup of 24 to 48 hours of cardiac monitoring. This is supported by two studies of post-stroke patients who underwent another 4 to 7 days of ambulatory cardiac monitoring; the rates of intermittent AF previously undiagnosed were 5.6 and 14.3%(*13, 14*). Stroke patients with asymptomatic or intermittent AF would be inadequately treated if misdiagnosed instead as e.g. cryptogenic stroke or large vessel stroke since such patients are placed on an anti-platelet agent instead of warfarin. Therefore, these markers for AF may help determine which patient might benefit from prolonged cardiac monitoring as an outpatient to document the presence or absence of AF. Prospective studies are needed to determine whether these findings can be translated into better prevention or treatment for stroke.

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CLAIMS

1. A method of determining a susceptibility to cardiac arrhythmia or stroke in a human individual, the method comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample from the individual, wherein the at least one polymorphic marker is selected from the polymorphic markers set forth in Table 5, and markers in linkage disequilibrium therewith,

and wherein determination of the presence or absence of the at least one allele is indicative of a susceptibility to cardiac arrhythmia or stroke in the individual.

2. A method of determining a susceptibility to cardiac arrhythmia or stroke in a human individual, comprising determining whether at least one at-risk allele in at least one polymorphic marker is present in a genotype dataset derived from the individual, wherein the at least one polymorphic marker is selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith, and wherein determination of the presence of the at least one at-risk allele is indicative of increased susceptibility to cardiac arrhythmia or stroke in the individual.

3. The method of Claim 1 or 2, wherein the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith.

4. The method of any of the preceding Claims, wherein the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51), and markers in linkage disequilibrium therewith.

5. The method of any of the preceding Claims, wherein the presence of alleles -2, -4 and/or -8 in marker D4S406, allele A of marker rs2634073, allele T of marker rs2200733, allele T of marker rs2220427, allele T of marker rs10033464, and/or allele G of marker rs13143308 is indicative of increased susceptibility of cardiac arrhythmia or stroke in the individual.

6. The method of any of the preceding Claims, wherein the susceptibility is increased susceptibility characterized by an odds ratio (OR) of at least 1.3.

7. The method of any of the preceding Claims, wherein the susceptibility is increased susceptibility characterized by an odds ratio (OR) of at least 1.4.

8. The method of any of the preceding Claims, wherein the susceptibility is increased susceptibility characterized by an odds ratio (OR) of at least 1.5.

9. The method of any of the preceding Claims, wherein the susceptibility is increased susceptibility characterized by an odds ratio (OR) of at least 1.6.

10. The method of any of the preceding Claims, wherein the susceptibility is increased susceptibility characterized by an odds ratio (OR) of at least 1.8.

11. A method of assessing a susceptibility to cardiac arrhythmia or stroke in a human individual, comprising screening a nucleic acid from the individual for at least one polymorphic marker allele or haplotype in SEQ ID NO:50 that correlates with increased occurrence of cardiac arrhythmia or stroke in a human population;

wherein determination of the presence of an at-risk marker allele in the at least one polymorphism or an at-risk haplotype in the nucleic acid identifies the individual as having elevated susceptibility to cardiac arrhythmia and/or stroke, and

wherein the absence of the at least one at-risk marker allele or at-risk haplotype in the nucleic acid identifies the individual as not having the elevated susceptibility.

12. The method of Claim 11, wherein the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith.

13. The method of Claim 11, wherein the at least one polymorphic marker is selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith.

14. The method of any of the Claims 11-13, wherein the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51),

15. The method of any of the Claims 11-14, wherein the presence of alleles -2, -4 and/or -8 in marker D4S406, allele A of marker rs2634073, allele T of marker rs2200733, allele T of marker rs2220427, allele T of marker rs10033464, and/or allele G of marker rs13143308 is indicative of increased susceptibility of cardiac arrhythmia or stroke in the individual.

16. A method of identification of a marker for use in assessing susceptibility to cardiac arrhthmia and/or stroke in human individuals, the method comprising

a. identifying at least one polymorphic marker within SEQ ID NO:50, or at least one polymorphic marker in linkage disequilibrium with at least one marker within SEQ ID NO:50;

b. determining the genotype status of a sample of individuals diagnosed with cardiac arrhythmia and/or stroke; and

c. determining the genotype status of a sample of control individuals;

wherein a significant difference in frequency of at least one allele in at least one polymorphism in individuals diagnosed with cardiac arrhtyhmia and/or stroke as compared with the frequency of the at least one allele in the control sample is indicative of the at least one polymorphism being useful for assessing susceptibility to cardiac arrhythmia and/or stroke.

17. The method of Claim 16, wherein an increase in frequency of the at least one allele in the at least one polymorphism in individuals diagnosed with cardiac arrhythmia and/or stroke, as compared with the frequency of the at least one allele in the control sample, is indicative of the at least one polymorphism being useful for assessing increased susceptibility to cardiac arrhythmia.

18. The method of Claim 16, wherein a decrease in frequency of the at least one allele in the at least one polymorphism in individuals diagnosed with cardiac arrhythmia and/or stroke, as compared with the frequency of the at least one allele in the control sample, is indicative of the at least one polymorphism being useful for assessing decreased susceptibility to, or protection against, cardiac arrhythmia and/or stroke.

19. The method of any of the Claims 16-18, wherein the significant difference in frequency is characterized by a statistical measure.

20. A method of genotyping a nucleic acid sample obtained from a human individual, comprising determining the presence or absence of at least one allele of at least one polymorphic marker predictive of increased risk of cardiac arrhythmia and/or stroke in the sample, wherein the at least one marker is selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith, and wherein determination of the presence or absence of the at least one allele of the at least one polymorphic marker is predictive of increased risk of cardiac arrhythmia and/or stroke in the individual.

21. The method of Claim 20, wherein genotyping comprises amplifying a segment of a nucleic acid that comprises the at least one polymorphic marker, by Polymerase Chain Reaction (PCR), using a nucleotide primer pair flanking the at least one polymorphic marker.

22. The method of Claim 20 or 21, wherein genotyping is performed using a process selected from allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, nucleic acid sequencing, 5'-exonuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation analysis.

23. The method of Claim 22, wherein the process comprises allele-specific probe hybridization.

24. The method of any of the Claims 20-23, comprising:

1. contacting copies of the nucleic acid with a detection oligonucleotide probe and an enhancer oligonucleotide probe under conditions for specific hybridization of the oligonucleotide probe with the nucleic acid;

wherein

e) the detection oligonucleotide probe is from 5-100 nucleotides in length and specifically hybridizes to a first segment of the nucleic acid whose nucleotide sequence is given by SEQ ID NO:50 that comprises at least one polymorphic site;

f) the detection oligonucleotide probe comprises a detectable label at its 3' terminus and a quenching moiety at its 5' terminus;

g) the enhancer oligonucleotide is from 5-100 nucleotides in length and is complementary to a second segment of the nucleotide sequence that is 5' relative to the oligonucleotide probe, such that the enhancer oligonucleotide is located 3' relative to the detection oligonucleotide probe when both oligonucleotides are hybridized to the nucleic acid; and

h) a single base gap exists between the first segment and the second segment, such that when the oligonucleotide probe and the enhancer oligonucleotide probe are both hybridized to the nucleic acid, a single base gap exists between the oligonucleotides;

2. treating the nucleic acid with an endonuclease that will cleave the detectable label from the 3' terminus of the detection probe to release free detectable label when the detection probe is hybridized to the nucleic acid; and

3. measuring free detectable label, wherein the presence of the free detectable label indicates that the detection probe specifically hybridizes to the first segment of the nucleic acid, and indicates the sequence of the polymorphic site as the complement of the detection probe.

25. The method of Claim 24, wherein the copies of the nucleic acid are provided by amplification by Polymerase Chain Reaction (PCR)

26. A method of determining a susceptibility to cardiac arrhythmia or stroke in a human individual, the method comprising determining the identity of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one marker is selected from the group of markers associated with the PITX2 gene, wherein the presence of the at least one allele is indicative of a susceptibility to cardiac arrhythmia or stroke in the individual.

27. The method according to Claim 16, wherein the at least one marker is selected from rs7668322 (SEQ ID NO:46), rs2197815 (SEQ ID NO:47), rs6831623 (SEQ ID NO:48) and rs259110 (SEQ ID NO:49), and markers in linkage disequilibrium therewith.

28. The method of Claim 26 or 27, wherein the susceptibility is increased susceptibility.

29. The method of Claim 26 or 27, wherein the susceptibility is decreased susceptibility.

30. The method of any of the preceding Claims, wherein the cardiac arrhythmia is atrial fibrillation or atrial flutter.

31. The method of Claim 30, wherein atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 80 years.

32. The method of Claim 30, wherein atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 70 years.

33. The method of Claim 30, wherein atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 60 years.

34. The method of any of the preceding Claims, wherein the stroke is ischemic stroke.

35. The method of any of the preceding Claims, wherein linkage disequilibrium is characterized by numerical values for r2 of greater than 0.2.

36. A method of assessing an individual for probability of response to a therapeutic agent for preventing and/or ameliorating symptoms associated with cardiac arrythmia and/or stroke, comprising: determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith, wherein determination of the presence of the at least one allele of the at least one marker is indicative of a probability of a positive response to the therapeutic agent for cardiac arrhythmia and/or stroke.

37. The method according to Claim 36, wherein the therapeutic agent is an anticoagulant, an anti-arrhythmic agent, a hear rate control agent, a cardioversion agent, or a heart rhythm control agent.

38. The method according to Claim 36 or 37, wherein the therapeutic agent is selected from warfarin, heparin, low molecular weight heparins, factor Xa inhibitors, thrombin inhibitors, sodium channel blockers, beta blockers, potassium channel blockers, and calcium channel blockers.

39. The method according to any of the Claims 36 – 38, whereint the therapeutic agent is selected from warfarin, ximelagatran, heparin, enoxaparin, dalteparin, tinzaparin, ardeparin, nadroparin, reviparin, fondaparinux, idraparinux, lepirudin, bivalirudin, argatroban, danaparoid, disopyramide, moricizine, procainamide, quinidine, lidocaine, mexiletine, tocainide, phenytoin, encainide, flecainide, propafenone, ajmaline, cibenzoline, detajmium, esmolol, propranolol, metoprolol, alprenolol, atenolol, carvedilol, bisoprolol, acebutolol, nadolol, pindololol, labetalol, oxprenotol, penbutolol, timolol, betaxolol, cartelol, sotalol, levobunolol, amiodarone, azimilide, bretylium, dofetilide, tedisamil, ibutilide, sematilide, N-acetyl procainamide, nifekalant hydrochloride, vernakalant, ambasilide, verpamil, mibefradil, diltiazem, digoxin, adenosine, ibutilide, amiodarone, procainamide, profafenone and flecainide.

40. A method of predicting prognosis of an individual diagnosed with, cardiac arrhythmia and/or stroke, the method comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the the markers set forth in Table 9, and markers in linkage disequilibrium therewith, wherein determination of the presence of the at least one

allele is indicative of a worse prognosis of the cardiac arrhythmia and/or stroke in the individual.

41. A method of monitoring progress of a treatment of an individual undergoing treatment for cardiac arrhythmia and/or stroke, the method comprising determining the presence or absence of at least one allele of at least one polymorphic marker in a nucleic acid sample obtained from the individual, wherein the at least one polymorphic marker is selected from the markers set forth in Table 9, and markers in linkage disequilibrium therewith, wherein determination of the presence of the at least one allele is indicative of the treatment outcome of the individual.

42. The method of any of the Claims 36 – 41, wherein the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51).

43. The method of any of the Claims 36 - 41, wherein linkage disequilibrium is characterized by numerical values of r^2 of at least 0.2.

44. The method of any of the Claims 36 - 43, wherein the cardiac arrhythmia is atrial fibrillation or atrial flutter.

45. The method of any of the Claims 36 - 44, wherein atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 80 years.

46. The method of any of the Claims 36 - 44, wherein atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 70 years.

47. The method of any of the Claims 36 - 44, wherein atrial fibrillation or atrial flutter is further characterized by an age of onset in the individual of less than 60 years.

48. The method of any of the Claims 36 - 44, wherein the stroke is ischemic stroke.

49. The method of any of the preceding Claims, further comprising assessing at least one biomarker for atrial fibrillation, atrial flutter and/or stroke in a sample from the individual.

50. The method of any of the preceding Claims, further comprising analyzing non-genetic information to make risk assessment, diagnosis, or prognosis of the individual.

51. The method of Claim 50, wherein the non-genetic information is selected from age, age at onset of disease, gender, ethnicity, socioeconomic status, previous disease diagnosis, medical history of subject, family history of atrial fibrillation, atrial flutter and/or stroke, biochemical measurements, and clinical measurements.

52. The method of any of the Claims 49 - 51, further comprising calculating overall risk by logistic regression.

53. A kit for assessing susceptibility to cardiac arrhythmia and/or stroke in a human individual, the kit comprising reagents for selectively detecting at least one allele of at least one polymorphic marker in the genome of the individual, wherein the polymorphic marker is selected from the group consisting of the polymorphic markers within the segment whose sequence is set forth in SEQ ID NO:50, and markers in linkage disequilibrium therewith, and wherein the presence of the at least one allele is indicative of a susceptibility to cardiac arrhythmia and/or stroke.

54. The kit of Claim 53, wherein the at least one polymorphic marker is selected from the markers set forth in Table 5.

55. The kit of Claim 53 or 54, wherein the at least one polymorphic marker is selected from the group of markers set forth in Table 9, and markers in linkage disequilibrium therewith.

56. The kit of any of the Claims 53 - 55, wherein the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51),

57. The kit of any of the Claims 53 - 56, wherein the cardiac arrhythmia is atrial fibrillation or atrial flutter.

58. The kit of any of the Claims 53 – 57, wherein the stroke is ischemic stroke.

59. The kit of any of the Claims 53 – 58, wherein linkage disequilibrium is characterized by numerical values of r^2 of greater than 0.2.

60. The kit of any of the Claims 53 - 59, wherein the reagents comprise at least one contiguous oligonucleotide that hybridizes to a fragment of the genome of the individual comprising the at least one polymorphic marker, a buffer and a detectable label.

61. The kit of any of the Claims 53 - 60, wherein the reagents comprise at least one pair of oligonucleotides that hybridize to opposite strands of a genomic nucleic acid

segment obtained from the subject, wherein each oligonucleotide primer pair is designed to selectively amplify a fragment of the genome of the individual that includes one polymorphic marker, and wherein the fragment is at least 30 base pairs in size.

62. The kit of Claim 60 or 61, wherein the at least one oligonucleotide is completely complementary to the genome of the individual.

63. The kit of any of the Claims 60 - 62, wherein the oligonucleotide is about 18 to about 50 nucleotides in length.

64. The kit of any of the Claims 60 - 63, wherein the oligonucleotide is 20-30 nucleotides in length.

65. The kit of any of the Claims 53 - 64, wherein the kit comprises:

a. a detection oligonucleotide probe that is from 5-100 nucleotides in length;

b. an enhancer oligonucleotide probe that is from 5-100 nucleotides in length; and

c. an endonuclease enzyme;

wherein the detection oligonucleotide probe specifically hybridizes to a first segment of the nucleic acid whose nucleotide sequence is given by SEQ ID NO: 50 that comprises at least one polymorphic site; and

wherein the detection oligonucleotide probe comprises a detectable label at its 3' terminus and a quenching moiety at its 5' terminus;

wherein the enhancer oligonucleotide is from 5-100 nucleotides in length and is complementary to a second segment of the nucleotide sequence that is 5' relative to the oligonucleotide probe, such that the enhancer oligonucleotide is located 3' relative to the detection oligonucleotide probe when both oligonucleotides are hybridized to the nucleic acid;

wherein a single base gap exists between the first segment and the second segment, such that when the oligonucleotide probe and the enhancer oligonucleotide probe are both hybridized to the nucleic acid, a single base gap exists between the oligonucleotides; and

wherein treating the nucleic acid with the endonuclease will cleave the detectable label from the 3' terminus of the detection probe to release free detectable label when the detection probe is hybridized to the nucleic acid.

66. Use of an oligonucleotide probe in the manufacture of a diagnostic reagent for diagnosing and/or assessing susceptibility to cardiac arrhythmia and/or stroke in a human individual, wherein the probe hybridizes to a segment of a nucleic acid whose nucleotide sequence is given by SEQ ID NO:50 that comprises at least one polymorphic site, wherein the fragment is 15-500 nucleotides in length.

67. The use according to Claim 66, wherein the polymorphic site is selected from the polymorphic markers set forth in Table 5, and polymorphisms in linkage disequilibrium therewith.

68. The use according to Claim 66 or 67, wherein the at least one polymorphic site is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51),

69. The use of any of the Claims 66 - 68, wherein the cardiac arrhythmia is atrial fibrillation or atrial flutter.

70. The use of any of the Claims 66 – 69, wherein the stroke is ischemic stroke.

71. The use of any of the Claims 66 – 70, wherein linkage disequilibrium is defined by numerical values of r^2 of at least 0.2 and/or values of |D'| of at least 0.8.

72. A computer-readable medium on which is stored:

a. an identifier for at least one polymorphic marker;

b. an indicator of the frequency of at least one allele of said at least one polymorphic marker in a plurality of individuals diagnosed with atrial fibrillation, atrial flutter and/or stroke; and

c. an indicator of the frequency of the least one allele of said at least one polymorphic markers in a plurality of reference individuals;

wherein the at least one polymorphic marker is selected from the polymorphic markers set forth in Table 5, and polymorphisms in linkage disequilibrium therewith.

73. The medium according to Claim 72, wherein the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733

(SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51),

74. The medium of Claim 72 or 73, wherein the stroke is ischemic stroke.

75. An apparatus for determining a genetic indicator for cardiac arrhythmia and/or stroke in a human individual, comprising:

a computer readable memory; and

a routine stored on the computer readable memory;

wherein the routine is adapted to be executed on a processor to analyze genotype and/or haplotype data for at least one human individual with respect to at least one polymorphic marker selected from the markers set forth in Table 5, and markers in linkage disequilibrium therewith, and generate an output based on the marker or haplotype data, wherein the output comprises a risk measure of the at least one marker or haplotype as a genetic indicator of cardiac arrhythmia and/or stroke for the human individual.

76. The apparatus of Claim 75, wherein the routine further comprises determining an indicator of the frequency of at least one allele of at least one polymorphic marker and/or at least one haplotype in a plurality of individuals diagnosed with cardiac arrhythmia and/or stroke, and an indicator of the frequency of at the least one allele of at least one polymorphic marker or at least one haplotype in a plurality of reference individuals, and calculating a risk measure for the at least one allele and/or haplotype based thereupon;

and wherein a risk measure for the individual is calculated based on a comparison of the at least one marker and/or haplotype status for the individual to the calculated risk for the at least one marker and/or haplotype information for the plurality of individuals diagnosed with atrial fibrillation, atrial flutter and/or stroke.

77. The apparatus of Claim 75 or 76, wherein the at least one polymorphic marker is selected from D4S406 (SEQ ID NO:45), rs2634073 (SEQ ID NO:33), rs2200733 (SEQ ID NO:28), rs2220427 (SEQ ID NO:1), rs10033464 (SEQ ID NO:41), and rs13143308 (SEQ ID NO:51).

78. The apparatus of any of the Claims 75 - 77, wherein the risk measure is characterized by an Odds Ratio (OR) or a Relative Risk (RR).

79. The apparatus or medium of any of the Claims 75 – 78, wherein linkage disequilibrium is characterized by values of r^2 of greater than 0.2.