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(71) Applicant *(for all designated States except US)*: **SYNERGENZ BIOSCIENCE LIMITED**; Sea Meadow House, PO Box 116, Road Town, Tortola (VG).

(71) Applicant and
(72) Inventor: **YOUNG, Robert, Peter** [NZ/NZ]; 73 St Stephens Avenue, Parnell, Auckland (NZ).

(74) Agents: **ADAMS, Matthew, D** et al.; A J Park, 6th Floor Huddart Parker Building, PO Box 949, Wellington 6015 (NZ).

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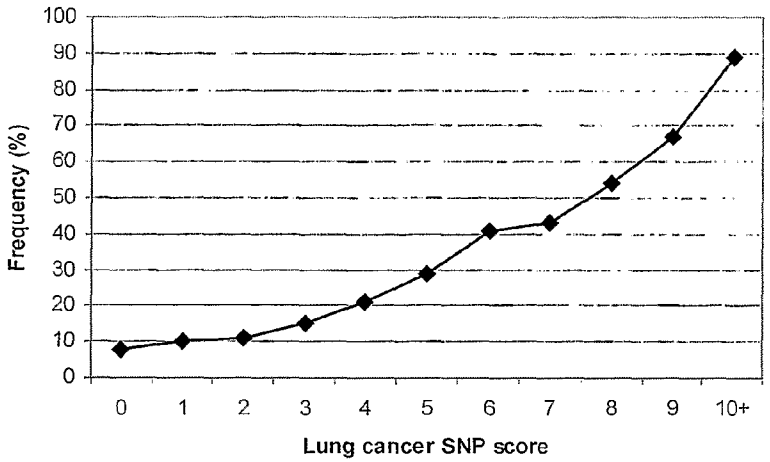
(54) **Title:** METHODS AND COMPOSITIONS FOR ASSESSMENT OF PULMONARY FUNCTION AND DISORDERS



(57) **Abstract:** The present invention provides methods for the assessment of risk of developing lung cancer in smokers and non-smokers using analysis of genetic polymorphisms. The present invention also relates to the use of genetic polymorphisms in assessing a subject's risk of developing lung cancer, and the suitability of a subject for an intervention in respect of lung cancer. Nucleotide probes and primers, kits, and microarrays suitable for such assessment are also provided.

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"METHODS AND COMPOSITIONS FOR ASSESSMENT OF PULMONARY FUNCTION AND DISORDERS"

FIELD OF THE INVENTION

The present invention is concerned with methods for assessment of pulmonary function and/or disorders, and in particular for assessing risk of developing lung cancer in smokers and non-smokers using analysis of genetic polymorphisms.

BACKGROUND OF THE INVENTION

Lung cancer is the second most common cancer and has been attributed primarily to cigarette smoking. Other factors contributing to the development of lung cancer include occupational exposure, genetic factors, radon exposure, exposure to other aero-pollutants and possibly dietary factors (Alberg AJ, et al., 2003). Non-smokers are estimated to have a one in 400 risk of lung cancer (0.25%). Smoking increases this risk by approximately 40 fold, such that smokers have a one in 10 risk of lung cancer (10%) and in long-term smokers the life-time risk of lung cancer has been reported to be as high 10-15% (Schwartz AG. 2004). Genetic factors are thought to play some part as evidenced by a weak familial tendency (among smokers) and the fact that only the minority of smokers get lung cancer. It is generally accepted that the majority of this genetic tendency comes from low penetrant high frequency polymorphisms, that is, polymorphisms which are common in the general population that in context of chronic smoking exposure contribute collectively to cancer development (Schwartz AG. 2004, Wu X et al., 2004). Several epidemiological studies have reported that impaired lung function (Anthonisen NR. 1989, Skillrud DM. 1986, Tockman MS et al., 1987, Kuller LH, et al., 1990, Nomura A, et al., 1991) or symptoms of obstructive lung disease (Mayne ST, et al., 1999) are independent risk factors for lung cancer and are possibly more relevant than smoking exposure dose.

Despite advances in the treatment of airways disease, current therapies do not significantly alter the natural history of lung cancer, which may include metastasis and progressive loss of lung function causing respiratory failure and death. Although cessation of smoking may be expected to reduce this decline in lung function, it is probable that if this is not achieved at an early stage, the loss is considerable and symptoms of worsening breathlessness likely cannot be averted. Analogous to the discovery of serum cholesterol and its link to coronary artery disease, there is a need to

better understand the factors that contribute to lung cancer so that tests that identify at risk subjects can be developed and that new treatments can be discovered to reduce the adverse effects of lung cancer. The early diagnosis of lung cancer or of a propensity to developing lung cancer enables a broader range of prophylactic or therapeutic treatments to be employed than can be employed in the treatment of late stage lung cancer. Such prophylactic or early therapeutic treatment is also more likely to be successful, achieve remission, improve quality of life, and/or increase lifespan.

To date, a number of biomarkers useful in the diagnosis and assessment of propensity towards developing various pulmonary disorders have been identified. These include, for example, single nucleotide polymorphisms including the following: A-82G in the promoter of the gene encoding human macrophage elastase (MMP12); T→C within codon 10 of the gene encoding transforming growth factor beta (TGFß); C+760G of the gene encoding superoxide dismutase 3 (SOD3); T-1296C within the promoter of the gene encoding tissue inhibitor of metalloproteinase 3 (TIMP3); and polymorphisms in linkage disequilibrium with these polymorphisms, as disclosed in PCT International Application PCT/NZ02/00106 (published as WO 02/099134 and incorporated herein in its entirety).

It would be desirable and advantageous to have additional biomarkers which could be used to assess a subject's risk of developing pulmonary disorders such as lung cancer, or a risk of developing lung cancer-related impaired lung function, particularly if the subject is a smoker.

It is primarily to such biomarkers and their use in methods to assess risk of developing such disorders that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention is primarily based on the finding that certain polymorphisms are found more often in subjects with lung cancer than in control subjects. Analysis of these polymorphisms reveals an association between polymorphisms and the subject's risk of developing lung cancer.

Thus, according to one aspect there is provided a method of determining a subject's risk of developing lung cancer comprising analysing a sample from said subject for the presence or absence of one or more polymorphisms selected from the group consisting of:

Ser307Ser G/T (rs1056503) in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4),

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43 (CYP3A43),

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2 (BCL2),

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3 (ITGB3),

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1 (DAT1),

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1 (TNFR1),

C/Del (rs1799732) in the gene encoding Dopamine receptor D2 (DRD2),

C/T (rs763110) in the gene encoding Fas ligand (FasL), or

C/T (rs5743836) in the gene encoding Toll-like receptor 9 (TLR9),

wherein the presence or absence of said polymorphism is indicative of the subject's risk of developing lung cancer.

This polymorphism can be detected directly or by detection of one or more polymorphisms which are in linkage disequilibrium with one or more of said polymorphisms.

Linkage disequilibrium (LD) is a phenomenon in genetics whereby two or more mutations or polymorphisms are in such close genetic proximity that they are co-inherited. This means that in genotyping, detection of one polymorphism as present infers the presence of the other. (Reich DE et al; Linkage disequilibrium in the human genome, Nature 2001, 411:199-204.)

The lung cancer may be non–small cell lung cancer including adenocarcinoma and squamous cell carcinoma, or small cell lung cancer, or may be a carcinoid tumor, a lymphoma, or a metastatic cancer.

The method can additionally comprise analysing a sample from said subject for the presence or absence of one or more further polymorphisms selected from the group consisting of:

R19W A/G (rs10115703) in the gene encoding Cerberus 1 (Cer 1);

K3326X A/T (rs11571833) in the breast cancer 2 early onset gene (BRCA2);

V433M A/G (rs2306022) in the gene encoding Integrin alpha-11;

E375G T/C (rs7214723) in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1); or

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73 (P73).

Again, detection of the one or more further polymorphisms may be carried out directly or by detection of polymorphisms in linkage disequilibrium with the one or more further polymorphisms.

The presence of one or more polymorphisms selected from the group consisting of:

the E375G T/C TT genotype in the gene encoding CAMKK1;
the -81 C/T (rs 2273953) CC genotype the gene encoding P73;
the A/C (rs2279115) AA genotype in the gene encoding BCL2;
the +3100 A/G (rs2317676) AG or GG genotype in the gene encoding ITGB3;
the C/Del (rs1799732) CDel or DelDel genotype in the gene encoding DRD2; or
the C/T (rs763110) TT genotype in the gene encoding FasL,

may be indicative of a reduced risk of developing lung cancer.

The presence of one or more polymorphisms selected from the group consisting of:

the R19W A/G AA or GG genotype in the gene encoding Cer 1;
the Ser307Ser G/T GG or GT genotype in the XRCC4 gene;
the K3326X A/T AT or TT genotype in the BRCA2 gene;
the V433M A/G AA genotype in the gene encoding Integrin alpha-11;
the A/T c74delA AT or TT genotype in the gene encoding CYP3A43;
the -3714 G/T (rs6413429) GT or TT genotype in the gene encoding DAT1;
the A/G (rs1139417) AA genotype in the gene encoding TNFR1; or
the C/T (rs5743836) CC genotype in the gene encoding TLR9,

may be indicative of an increased risk of developing lung cancer.

The methods of the invention are particularly useful in smokers (both current and former).

It will be appreciated that the methods of the invention identify two categories of polymorphisms – namely those associated with a reduced risk of developing lung cancer (which can be termed "protective polymorphisms") and those associated with an increased risk of developing lung cancer (which can be termed "susceptibility polymorphisms").

Therefore, the present invention further provides a method of assessing a subject's risk of developing lung cancer, said method comprising:

determining the presence or absence of at least one protective polymorphism associated with a reduced risk of developing lung cancer; and

in the absence of at least one protective polymorphism, determining the presence or absence of at least one susceptibility polymorphism associated with an increased risk of developing lung cancer;

wherein the presence of one or more of said protective polymorphisms is indicative of a reduced risk of developing lung cancer, and the absence of at least one protective polymorphism in combination with the presence of at least one susceptibility polymorphism is indicative of an increased risk of developing lung cancer.

Preferably, the at least one protective polymorphism selected from the group consisting of:

the E375G T/C TT genotype in the gene encoding CAMKK1;

the -81 C/T (rs 2273953) CC genotype the gene encoding P73;

the A/C (rs2279115) AA genotype in the gene encoding BCL2;

the +3100 A/G (rs2317676) AG or GG genotype in the gene encoding ITGB3;

the C/Del (rs1799732) CDel or DelDel genotype in the gene encoding DRD2; or

the C/T (rs763110) TT genotype in the gene encoding Fas ligand.

The at least one susceptibility polymorphism may be selected from the group consisting of:

the R19W A/G AA or GG genotype in the gene encoding Cer 1;

the Ser307Ser G/T GG or GT genotype in the XRCC4 gene;

the K3326X A/T AT or TT genotype in the BRCA2 gene;

the V433M A/G AA genotype in the gene encoding Integrin alpha-11;

the A/T c74delA AT or TT genotype in the gene encoding CYP3A43;

the -3714 G/T (rs6413429) GT or TT genotype in the gene encoding DAT1;

the A/G (rs1139417) AA genotype in the gene encoding TNFR1; or

the C/T (rs5743836) CC genotype in the gene encoding TLR9.

In a preferred form of the invention the presence of two or more protective polymorphisms is indicative of a reduced risk of developing lung cancer.

In a further preferred form of the invention the presence of two or more susceptibility polymorphisms is indicative of an increased risk of developing lung cancer.

In still a further preferred form of the invention the presence of two or more protective polymorphims irrespective of the presence of one or more susceptibility polymorphisms is indicative of reduced risk of developing lung cancer.

In another aspect, the invention provides a method of determining a subject's risk of developing lung cancer, said method comprising obtaining the result of one or more genetic tests of a sample from said subject, and analysing the result for the presence or absence of of one or more polymorphisms selected from the group consisting of:

Ser307Ser G/T in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene;

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43,

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2,

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3,

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1,

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1,

C/Del (rs1799732) in the gene encoding Dopamine receptor D2,

C/T (rs763110) in the gene encoding Fas ligand,

C/T (rs5743836) in the gene encoding Toll-like receptor 9,

or one or more polymorphisms in linkage disequilibrium with this polymorphism;

wherein a result indicating the presence or absence of one or more of said polymorphisms is indicative of the subject's risk of developing lung cancer.

The method can additionally comprise obtaining the result of one or more genetic tests of a sample from said subject, and analysing the result for the presence or absence of one or more further polymorphisms selected from the group consisting of:

R19W A/G in the gene encoding Cerberus 1;

K3326X A/T in the breast cancer 2 early onset gene;

V433M A/G in the gene encoding Integrin alpha-11;

E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1; or

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73.

Again, the presence or absence may be determined directly or by determining the presence or absence of polymorphisms in linkage disequilibrium with the one or more further polymorphisms.

In a further aspect there is provided a method of determining a subject's risk of developing lung cancer comprising the analysis of two or more polymorphisms selected from the group consisting of:

R19W A/G in the gene encoding Cerberus 1;

Ser307Ser G/T in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene;

K3326X A/T in the breast cancer 2 early onset gene;

V433M A/G in the gene encoding Integrin alpha-11; or

E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1;

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43,

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2,

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3,

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1,

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1,

C/Del (rs1799732) in the gene encoding Dopamine receptor D2,

C/T (rs763110) in the gene encoding Fas ligand,

C/T (rs5743836) in the gene encoding Toll-like receptor 9,

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73, or

one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

V433M A/G (rs2306022) in the gene encoding ITGA11;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

-511 A/G (rs 16944) in the gene encoding Interleukin 1B;

V433M A/G (rs2306022) in the gene encoding ITGA11;

Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

R19W A/G (rs 10115703) in the gene encoding Cerberus 1;

-3714 G/T (rs6413429) in the gene encoding DAT1;

A/G (rs1139417) in the gene encoding TNFR1;

C/T (rs5743836) in the gene encoding TLR9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

-751 G/T (rs 13181) in the promoter of the gene encoding XPD;

Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;

C/T (rs763110) in the gene encoding FasL;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In various embodiments, any one or more of the above methods comprises the step of analysing the amino acid present at a position mapping to codon 19 of the gene encoding Cer 1.

The presence of tryptophan at said position is indicative of an increased risk of developing lung cancer.

The presence of arginine at said position is indicative of reduced risk of developing lung cancer.

In various embodiments, any one or more of the above methods comprises the step of analysing the amino acid present at a position mapping to codon 3326 in the BRCA2 gene.

The presence of lysine at said position is indicative of reduced risk of developing lung cancer.

The presence of a truncated gene product of 3325 amino acids is indicative of an increased risk of developing lung cancer.

In various embodiments, any one or more of the above methods comprises the step of analysing the amino acid present at a position mapping to codon 433 in the gene encoding Integrin alpha-11.

The presence of methionine at said position is indicative of an increased risk of developing lung cancer.

The presence of valine at said position is indicative of reduced risk of developing lung cancer.

In various embodiments, any one or more of the above methods comprises the step of analysing the amino acid present at a position mapping to codon 375 in the gene encoding CAMKK1.

The presence of glycine at said position is indicative of an increased risk of developing lung cancer.

The presence of glutamate at said position is indicative of reduced risk of developing lung cancer.

In a preferred form of the invention the methods as described herein are performed in conjunction with an analysis of one or more risk factors, including one or more epidemiological risk factors, associated with a risk of developing lung cancer. Such epidemiological risk factors include but are not limited to smoking or exposure to tobacco smoke, age, sex, and familial history of lung cancer.

In a further aspect, the invention provides for the use of at least one polymorphism in the assessment of a subject's risk of developing lung cancer, wherein the at least one polymorphism is selected from the group consisting of;

Ser307Ser G/T in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene;

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43,

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2,

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3,

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1,

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1,

C/Del (rs1799732) in the gene encoding Dopamine receptor D2,

C/T (rs763110) in the gene encoding Fas ligand, or

C/T (rs5743836) in the gene encoding Toll-like receptor 9,

or one or more polymorphisms in linkage disequilibrium with said polymorphism.

Optionally, said use may be in conjunction with the use of at least one further polymorphism selected from the group consisting of:

R19W A/G in the gene encoding Cerberus 1 (Cer 1);

K3326X A/T in the breast cancer 2 early onset gene (BRCA2);

V433M A/G in the gene encoding Integrin alpha-11;

E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73;

or one or more polymorphisms which are in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

V433M A/G (rs2306022) in the gene encoding ITGA11;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

-511 A/G (rs 16944) in the gene encoding Interleukin 1B;

V433M A/G (rs2306022) in the gene encoding ITGA11;

Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

R19W A/G (rs 10115703) in the gene encoding Cerberus 1;

-3714 G/T (rs6413429) in the gene encoding DAT1;

A/G (rs1139417) in the gene encoding TNFR1;

C/T (rs5743836) in the gene encoding TLR9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

-751 G/T (rs 13181) in the promoter of the gene encoding XPD;

Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;

C/T (rs763110) in the gene encoding FasL;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In another aspect the invention provides a set of nucleotide probes and/or primers for use in the preferred methods of the invention herein described. Preferably, the nucleotide probes and/or primers are those which span, or are able to be used to span, the polymorphic regions of the genes. Also provided are one or more nucleotide probes and/or primers comprising the sequence of any one of the probes and/or primers herein described, including any one comprising the sequence of any one of SEQ.ID.NO. 1 to 72, more preferably any one of SEQ.ID.NO. 1 to 10 or any one of SEQ.ID.NO. 26 to 43.

In yet a further aspect, the invention provides a nucleic acid microarray for use in the methods of the invention, which microarray comprises a substrate presenting nucleic acid sequences capable of hybridizing to nucleic acid sequences which encode one or more of the susceptibility or protective polymorphisms described herein or sequences complimentary thereto.

In another aspect, the invention provides an antibody microarray for use in the methods of the invention, which microarray comprises a substrate presenting antibodies capable of binding to a product of expression of a gene the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism as described herein.

In a further aspect the present invention provides a method treating a subject having an increased risk of developing lung cancer comprising the step of replicating, genotypically or phenotypically, the presence and/or functional effect of a protective polymorphism in said subject.

In yet a further aspect, the present invention provides a method of treating a subject having an increased risk of developing lung cancer, said subject having a detectable susceptibility polymorphism which either upregulates or downregulates expression of a gene such that the physiologically active concentration of the expressed gene product is outside a range which is normal for the age and sex of the subject, said method comprising the step of restoring the physiologically active concentration of said

product of gene expression to be within a range which is normal for the age and sex of the subject.

In yet a further aspect, the present invention provides a method for screening for compounds that modulate the expression and/or activity of a gene, the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism, said method comprising the steps of:

contacting a candidate compound with a cell comprising a susceptibility or protective polymorphism which has been determined to be associated with the upregulation or downregulation of expression of a gene; and

measuring the expression of said gene following contact with said candidate compound,

wherein a change in the level of expression after the contacting step as compared to before the contacting step is indicative of the ability of the compound to modulate the expression and/or activity of said gene.

Preferably, said cell is a human lung cell which has been pre-screened to confirm the presence of said polymorphism.

Preferably, said cell comprises a susceptibility polymorphism associated with upregulation of expression of said gene and said screening is for candidate compounds which downregulate expression of said gene.

Alternatively, said cell comprises a susceptibility polymorphism associated with downregulation of expression of said gene and said screening is for candidate compounds which upregulate expression of said gene.

In another embodiment, said cell comprises a protective polymorphism associated with upregulation of expression of said gene and said screening is for candidate compounds which further upregulate expression of said gene.

Alternatively, said cell comprises a protective polymorphism associated with downregulation of expression of said gene and said screening is for candidate compounds which further downregulate expression of said gene.

In another aspect, the present invention provides a method for screening for compounds that modulate the expression and/or activity of a gene, the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism, said method comprising the steps of:

contacting a candidate compound with a cell comprising a gene, the expression of which is upregulated or downregulated when associated with a susceptibility or

protective polymorphism but which in said cell the expression of which is neither upregulated nor downregulated; and

measuring the expression of said gene following contact with said candidate compound,

wherein a change in the level of expression after the contacting step as compared to before the contacting step is indicative of the ability of the compound to modulate the expression and/or activity of said gene.

Preferably, expression of the gene is downregulated when associated with a susceptibility polymorphism once said screening is for candidate compounds which in said cell, upregulate expression of said gene.

Preferably, said cell is a human lung cell which has been pre-screened to confirm the presence, and baseline level of expression, of said gene.

Alternatively, expression of the gene is upregulated when associated with a susceptibility polymorphism and said screening is for candidate compounds which, in said cell, downregulate expression of said gene.

In another embodiment, expression of the gene is upregulated when associated with a protective polymorphism and said screening is for compounds which, in said cell, upregulate expression of said gene.

Alternatively, expression of the gene is downregulated when associated with a protective polymorphism and said screening is for compounds which, in said cell, downregulate expression of said gene.

In yet a further aspect, the present invention provides a method of assessing the likely responsiveness of a subject at risk of developing or suffering from lung cancer to a prophylactic or therapeutic treatment, which treatment involves restoring the physiologically active concentration of a product of gene expression to be within a range which is normal for the age and sex of the subject, which method comprises detecting in said subject the presence or absence of a susceptibility polymorphism which when present either upregulates or downregulates expression of said gene such that the physiological active concentration of the expressed gene product is outside said normal range, wherein the detection of the presence of said polymorphism is indicative of the subject likely responding to said treatment.

In still a further aspect, the present invention provides a method of assessing a subject's suitability for an intervention that is diagnostic of or therapeutic for a disease, the method comprising:

a) providing a net score for said subject, wherein the net score is or has been determined by:

i) providing the result of one or more genetic tests of a sample from the subject, and analysing the result for the presence or absence of protective polymorphisms and for the presence or absence of susceptibility polymorphisms, wherein said protective and susceptibility polymorphisms are associated with said disease,

ii) assigning a positive score for each protective polymorphism and a negative score for each susceptibility polymorphism or vice versa;

iii) calculating a net score for said subject by representing the balance between the combined value of the protective polymorphisms and the combined value of the susceptibility polymorphisms present in the subject sample;

and

b) providing a distribution of net scores for disease sufferers and non-sufferers wherein the net scores for disease sufferers and non-sufferers are or have been determined in the same manner as the net score determined for said subject;

c) determining whether the net score for said subject lies within a threshold on said distribution separating individuals deemed suitable for said intervention from those for whom said intervention is deemed unsuitable;

wherein a net score within said threshold is indicative of the subject's suitability for the intervention, and wherein a net score outside the threshold is indicative of the subject's unsuitability for the intervention.

The value assigned to each protective polymorphism may be the same or may be different. The value assigned to each susceptibility polymorphism may be the same or may be different, with either each protective polymorphism having a negative value and each susceptibility polymorphism having a positive value, or vice versa.

In one embodiment, the intervention is a diagnostic test for said disease.

In another embodiment, the intervention is a therapy for said disease, more preferably a preventative therapy for said disease.

Preferably, the disease is lung cancer, more preferably the disease is lung cancer and the protective and susceptibility polymorphisms are selected from the group consisting of:

the -133 G/C polymorphism in the Interleukin-18 gene;

the -1053 C/T polymorphism in the CYP 2E1 gene;

the Arg197Gln polymorphism in the NAT2 gene;

the -511 G/A polymorphism in the Interleukin 1B gene;

the Ala 9 Thr polymorphism in the Anti-chymotrypsin gene;

the S allele polymorphism in the Alpha1-antitrypsin gene;

the -251 A/T polymorphism in the Interleukin-8 gene;

the Lys 751 gln polymorphism in the XPD gene;

the +760 G/C polymorphism in the SOD3 gene;

the Phe257Ser polymorphism in the REV gene;

the Z alelle polymorphism in the Alpha1-antitrypsin gene;

the R19W A/G polymorphism in the Cerberus 1 (Cer 1) gene;

the Ser307Ser G/T polymorphism in the XRCC4 gene;

the K3326X A/T polymorphism in the BRCA2 gene;

the V433M A/G polymorphism in the Integrin alpha-11 gene;

the E375G T/C polymorphism in the CAMKK1 gene;

the A/T c74delA polymorphism in the gene encoding cytochrome P450 polypeptide CYP3A43,

the A/C (rs2279115) polymorphism in the gene encoding B-cell CLL/lymphoma 2,

the A/G at +3100 in the 3'UTR (rs2317676) polymorphism of the gene encoding Integrin beta 3,

the -3714 G/T (rs6413429) polymorphism in the gene encoding Dopamine transporter 1,

the A/G (rs1139417) polymorphism in the gene encoding Tumor necrosis factor receptor 1,

the C/Del (rs1799732) polymorphism in the gene encoding Dopamine receptor D2,

the C/T (rs763110) polymorphism in the gene encoding Fas ligand,

the C/T (rs5743836) polymorphism in the gene encoding Toll-like receptor 9,

the -81 C/T (rs 2273953) polymorphism in the 5' UTR of the gene encoding Tumor protein P73,

or one or more polymorphisms in linkage disequilibrium with one or more of said polymorphisms.

More preferably, said intervention is a CT scan for lung cancer.

Still more preferably, the method is as described herein with reference to the examples and/or figures.

In a further aspect, the present invention provides a kit for assessing a subject's risk of developing lung cancer, said kit comprising a means of analysing a sample from said subject for the presence or absence of one or more polymorphisms disclosed herein.

BRIEF DESCRIPTION OF FIGURES

Figure 1: depicts a graph showing the likelihood of having lung cancer plotted against the SNP score derived from the 5 SNP panel shown in Table 16 herein.

Figure 2: depicts a graph showing the log odds of having lung cancer plotted against the SNP score derived from the 5 SNP panel shown in Table 16 herein.

Figure 3 depicts a graph showing the likelihood of having lung cancer plotted against the SNP score derived from an 11 SNP panel (11 SNP panel A) comprising SNPs 1 – 11 in Table 18 herein.

Figure 4 depicts a receiver-operator curve analysis of sensitivity and specificity for the 11 SNP panel A.

Figure 5 depicts a graph showing the distribution of frequencies of control smokers and lung cancer subjects plotted against SNP score derived from the 11 SNP panel A.

Figure 6 depicts a graph showing the likelihood of having lung cancer plotted against the SNP score derived from a 16 SNP panel comprising SNPs 1 – 16 in Table 18 herein.

Figure 7 depicts a receiver-operator curve analysis of sensitivity and specificity for the 16 SNP panel.

Figure 8 depicts a graph showing the distribution of frequencies of control smokers and lung cancer subjects plotted against SNP score derived from the 16 SNP panel.

Figure 9 depicts a graph showing the log odds of having lung cancer plotted against the SNP score derived from the 9 SNP panel described herein.

Figure 10 depicts a receiver-operator curve analysis of sensitivity and specificity for the 9 SNP panel.

Figure 11 depicts a graph showing the distribution of frequencies of control smokers and lung cancer subjects plotted against SNP score derived from the 9 SNP panel.

Figure 12 depicts a graph showing the likelihood of having one of the four common types of lung cancer plotted against the SNP score, as described in Example 5.

Figure 13a depicts a graph showing the frequency of lung cancer plotted against the SNP score derived from the 19 SNP panel described in Example 6 herein.

Figure 13b depicts a graph showing the odds ratio of lung cancer according to the SNP score derived from the 19 SNP panel described in Example 6 herein.

Figure 14 depicts a graph showing the distribution of frequencies of control smokers and lung cancer subjects plotted against SNP score derived from the 19 SNP panel described in Example 6 herein.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

Using case-control studies the frequencies of several genetic variants (polymorphisms) of candidate genes in smokers who have developed lung cancer and blood donor controls have been compared. The majority of these candidate genes have confirmed (or likely) functional effects on gene expression or protein function. Specifically the frequencies of polymorphisms between blood donor controls, resistant smokers and those with lung cancer (subdivided into those with early onset and those with normal onset) have been compared. The present invention demonstrates that there are both protective and susceptibility polymorphisms present in selected candidate genes of the patients tested.

In one embodiment described herein 8 susceptibility genetic polymorphisms and 6 protective genetic polymorphism are identified. These are as follows:

Gene and SNP	rs number	Genotype	Phenotype	OR	P value
Cerberus 1 (Cer 1) R19W A/G	rs10115703	AA/AG	susceptiblility	1.7	0.02
XRCC4 Ser307Ser G/T	rs1056503	GG/GT	susceptiblility	1.3	0.04
BRCA2 K3326X A/T	rs11571833	AT/TT	susceptiblility	2.5	0.04
Integrin alpha-11 V433M A/G	rs2306022	AA	susceptiblility	4.3	0.002
CAMKK1 E375G T/C	rs7214723	TT	protective	0.76	0.13
P73	rs2273953	CC	protective	0.46	<0.001

CYP3A43 C74 delA		AT/TT	susceptiblility	1.74	0.05
BCL2	rs2279115	AA	protective	0.69	0.05
ITGB3	rs2317676	AG/GG	protective	0.57	0.02
DAT1	rs6413429	GT/TT	susceptibility	1.6	0.05
TNFR1	rs1139417	AA	susceptibility	1.5	0.02
DRD2	rs1799732	CDel/DelDel	protective	0.61	0.02
FasL	rs763110	TT	protective	0.61	0.05
TLR9	rs5743836	CC	susceptibility	3.1	0.03

A susceptibility genetic polymorphism is one which, when present, is indicative of an increased risk of developing lung cancer. In contrast, a protective genetic polymorphism is one which, when present, is indicative of a reduced risk of developing lung cancer.

As used herein, the phrase "risk of developing lung cancer" means the likelihood that a subject to whom the risk applies will develop lung cancer, and includes predisposition to, and potential onset of the disease. Accordingly, the phrase "increased risk of developing lung cancer" means that a subject having such an increased risk possesses an hereditary inclination or tendency to develop lung cancer. This does not mean that such a person will actually develop lung cancer at any time, merely that he or she has a greater likelihood of developing lung cancer compared to the general population of individuals that either does not possess a polymorphism associated with increased lung cancer or does possess a polymorphism associated with decreased lung cancer risk. Subjects with an increased risk of developing lung cancer include those with a predisposition to lung cancer, such as a tendency or predilection regardless of their lung function at the time of assessment, for example, a subject who is genetically inclined to lung cancer but who has normal lung function, those at potential risk, including subjects with a tendency to mildly reduced lung function who are likely to go on to suffer lung cancer if they keep smoking, and subjects with potential onset of lung cancer, who have a tendency to poor lung function on spirometry etc., consistent with lung cancer at the time of assessment.

Similarly, the phrase "decreased risk of developing lung cancer" means that a subject having such a decreased risk possesses an hereditary disinclination or reduced tendency to develop lung cancer. This does not mean that such a person will not develop lung cancer at any time, merely that he or she has a decreased likelihood of developing lung cancer compared to the general population of individuals that either

does possess one or more polymorphisms associated with increased lung cancer, or does not possess a polymorphism associated with decreased lung cancer.

It will be understood that in the context of the present invention the term "polymorphism" means the occurrence together in the same population at a rate greater than that attributable to random mutation (usually greater than 1%) of two or more alternate forms (such as alleles or genetic markers) of a chromosomal locus that differ in nucleotide sequence or have variable numbers of repeated nucleotide units. See www.ornl.gov/sci/techresources/Human_Genome/publicat/97pr/09gloss.html#p. Accordingly, the term "polymorphisms" is used herein contemplates genetic variations, including single nucleotide substitutions, insertions and deletions of nucleotides, repetitive sequences (such as microsatellites), and the total or partial absence of genes (eg. null mutations). As used herein, the term "polymorphisms" also includes genotypes and haplotypes. A genotype is the genetic composition at a specific locus or set of loci. A haplotype is a set of closely linked genetic markers present on one chromosome which are not easily separable by recombination, tend to be inherited together, and may be in linkage disequilibrium. A haplotype can be identified by patterns of polymorphisms such as SNPs. Similarly, the term "single nucleotide polymorphism" or "SNP" in the context of the present invention includes single base nucleotide subsitutions and short deletion and insertion polymorphisms.

A reduced or increased risk of a subject developing lung cancer may be diagnosed by analysing a sample from said subject for the presence of a polymorphism selected from the group consisting of:

R19W A/G (rs10115703) in the gene encoding Cerberus 1 (Cer 1);

Ser307Ser G/T (rs1056503) in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4);

K3326X A/T (rs11571833) in the breast cancer 2 early onset gene (BRCA2);

V433M A/G (rs2306022) in the gene encoding Integrin alpha-11;

E375G T/C (rs7214723) in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43 (CYP3A43);

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2 (BCL2);

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3 (ITGB3);

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1 (DAT1);

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1 (TNFR1);

C/Del (rs1799732) in the gene encoding Dopamine receptor D2 (DRD2);

C/T (rs763110) in the gene encoding Fas ligand (FasL); or

C/T (rs5743836) in the gene encoding Toll-like receptor 9 (TLR9)

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73 (P73);

or one or more polymorphisms which are in linkage disequilibrium with any one or more of the above group.

These polymorphisms can also be analysed in combinations of two or more, or in combination with other polymorphisms indicative of a subject's risk of developing lung cancer inclusive of the remaining polymorphisms listed above.

Expressly contemplated are combinations of the above polymorphisms with polymorphisms as described in PCT International application PCT/NZ02/00106, published as WO 02/099134, or as described in PCT International application PCT/NZ2006/000125, published as WO2006/123955, or those polymorphisms recited herein in Table 18.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

V433M A/G (rs2306022) in the gene encoding ITGA11;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

In one embodiment of the methods and uses of the present invention each of the following polymorphisms are selected:

Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

-511 A/G (rs 16944) in the gene encoding Interleukin 1B;

V433M A/G (rs2306022) in the gene encoding ITGA11;

Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

R19W A/G in the gene encoding Cerberus 1 (rs 10115703);

-3714 G/T (rs6413429) in the gene encoding DAT1 (rs6413429);

A/G (rs1139417) in the gene encoding TNFR1;

C/T (rs5743836) in the gene encoding TLR9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

-751 G/T (rs 13181) in the promoter of the gene encoding XPD;

Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;

C/T (rs763110) in the gene encoding FasL;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

Assays which involve combinations of polymorphisms, including those amenable to high throughput, such as those utilising microarrays, are preferred.

Statistical analyses, particularly of the combined effects of these polymorphisms, show that the genetic analyses of the present invention can be used to determine the risk quotient of any smoker and in particular to identify smokers at greater risk of developing lung cancer. Such combined analysis can be of combinations of susceptibility polymorphisms only, of protective polymorphisms only, or of combinations of both. Analysis can also be step-wise, with analysis of the presence or absence of protective polymorphisms occurring first and then with analysis of susceptibility polymorphisms proceeding only where no protective polymorphisms are present.

Thus, through systematic analysis of the frequency of these polymorphisms in well defined groups of smokers and non-smokers, as described herein, it is possible to implicate certain proteins in the development of lung cancer and improve the ability to identify which smokers are at increased risk of developing lung cancer -related impaired lung function and lung cancer for predictive purposes.

The present results show for the first time that the minority of smokers who develop lung cancer do so because they have one or more of the susceptibility polymorphisms and few or none of the protective polymorphisms defined herein. It is thought that the presence of one or more suscetptible polymorphisms, together with the

damaging irritant and oxidant effects of smoking, combine to make this group of smokers highly susceptible to developing lung cancer. Additional risk factors, such as familial history, age, weight, pack years, etc., will also have an impact on the risk profile of a subject, and can be assessed in combination with the genetic analyses described herein.

The one or more polymorphisms can be detected directly or by detection of one or more polymorphisms which are in linkage disequilibrium with said one or more polymorphisms. As discussed above, linkage disequilibrium is a phenomenon in genetics whereby two or more mutations or polymorphisms are in such close genetic proximity that they are co-inherited. This means that in genotyping, detection of one polymorphism as present infers the presence of the other. (Reich DE et al; Linkage disequilibrium in the human genome, Nature 2001, 411:199-204.)

It will be apparent that polymorphsisms in linkage disequilibrium with one or more other polymorphism associated with increased or decreased risk of developing lung cancer will also provide utility as biomarkers for risk of developing lung cancer. The data presented herein shows that the frequency for SNPs in linkage disequilibrium is very similar. Accordingly, these genetically linked SNPs can be utilized in combined polymorphism analyses to derive a level of risk comparable to that calculated from the original SNP.

It will therefore be apparent that one or more polymorphisms in linkage disequilibrium with the polymorphisms specified herein can be identified, for example, using public data bases. Examples of such polymorphisms reported to be in linkage disequilibrium with the polymorphisms specified herein are presented herein in Table 26.

It will also be apparent that frequently a variety of nomenclatures may exist for any given polymorphism or for any given gene. For example, the polymorphism Arg 312 Gln in the gene encoding superoxide dismutase 3 (SOD3) is believed to have been referred to variously as Arg 213 Gly, +760 G/C, and Arg 231 Gly (rs1799895). In another example, the gene referred to herein as the breast cancer 2 early onset gene is also variously referred to as BRCC2, Breast Cancer 2 Gene, Breast Cancer Type 2, Breast Cancer Type 2 Susceptibility Gene, Breast cancer type 2 susceptibility protein, FACD, FAD, FAD1, FANCB, FANCD1, and Hereditary Breast Cancer 2. When referring to a susceptibility or protective polymorphism as herein described, such alternative nomenclatures are also contemplated by the present invention.

The methods of the invention are primarily directed to the detection and identification of the above polymorphisms associated with lung cancer, which are all single nucleotide polymorphisms. In general terms, a single nucleotide polymorphism (SNP) is a single base change or point mutation resulting in genetic variation between individuals. SNPs occur in the human genome approximately once every 100 to 300 bases, and can occur in coding or non-coding regions. Due to the redundancy of the genetic code, a SNP in the coding region may or may not change the amino acid sequence of a protein product. A SNP in a non-coding region can, for example, alter gene expression by, for example, modifying control regions such as promoters, transcription factor binding sites, processing sites, ribosomal binding sites, and affect gene transcription, processing, and translation.

SNPs can facilitate large-scale association genetics studies, and there has recently been great interest in SNP discovery and detection. SNPs show great promise as markers for a number of phenotypic traits (including latent traits), such as for example, disease propensity and severity, wellness propensity, and drug responsiveness including, for example, susceptibility to adverse drug reactions. Knowledge of the association of a particular SNP with a phenotypic trait, coupled with the knowledge of whether an individual has said particular SNP, can enable the targeting of diagnostic, preventative and therapeutic applications to allow better disease management, to enhance understanding of disease states and to ultimately facilitate the discovery of more effective treatments, such as personalised treatment regimens.

Indeed, a number of databases have been constructed of known SNPs, and for some such SNPs, the biological effect associated with a SNP. For example, the NCBI SNP database "dbSNP" is incorporated into NCBI's Entrez system and can be queried using the same approach as the other Entrez databases such as PubMed and GenBank. This database has records for over 1.5 million SNPs mapped onto the human genome sequence. Each dbSNP entry includes the sequence context of the polymorphism (i.e., the surrounding sequence), the occurrence frequency of the polymorphism (by population or individual), and the experimental method(s), protocols, and conditions used to assay the variation, and can include information associating a SNP with a particular phenotypic trait.

At least in part because of the potential impact on health and wellness, there has been and continues to be a great deal of effort to develop methods that reliably and rapidly identify SNPs. Initially, this was no trivial task, at least in part because of the

complexity of human genomic DNA, with a haploid genome of 3 x 10^9 base pairs, and the associated sensitivity and discriminatory requirements.

Genotyping approaches to detect SNPs well-known in the art include DNA sequencing, methods that require allele specific hybridization of primers or probes, allele specific incorporation of nucleotides to primers bound close to or adjacent to the polymorphisms (often referred to as "single base extension", or "minisequencing"), allele-specific ligation (joining) of oligonucleotides (ligation chain reaction or ligation padlock probes), allele-specific cleavage of oligonucleotides or PCR products by restriction enzymes (restriction fragment length polymorphisms analysis or RFLP) or chemical or other agents, resolution of allele-dependent differences in electrophoretic or chromatographic mobilities, by structure specific enzymes including invasive structure specific enzymes, or mass spectrometry. Analysis of amino acid variation is also possible where the SNP lies in a coding region and results in an amino acid change.

DNA sequencing allows the direct determination and identification of SNPs. The benefits in specificity and accuracy are generally outweighed for screening purposes by the difficulties inherent in whole genome, or even targeted subgenome, sequencing.

Mini-sequencing involves allowing a primer to hybridize to the DNA sequence adjacent to the SNP site on the test sample under investigation. The primer is extended by one nucleotide using all four differentially tagged fluorescent dideoxynucleotides (A, C, G, or T), and a DNA polymerase. Only one of the four nucleotides (homozygous case) or two of the four nucleotides (heterozygous case) is incorporated. The base that is incorporated is complementary to the nucleotide at the SNP position.

A number of methods currently used for SNP detection involve site-specific and/or allele-specific hybridisation. These methods are largely reliant on the discriminatory binding of oligonucleotides to target sequences containing the SNP of interest. The techniques of Affymetrix (Santa Clara, Calif.) and Nanogen Inc. (San Diego, Calif.) are particularly well-known, and utilize the fact that DNA duplexes containing single base mismatches are much less stable than duplexes that are perfectly base-paired. The presence of a matched duplex is detected by fluorescence.

The majority of methods to detect or identify SNPs by site-specific hybridisation require target amplification by methods such as PCR to increase sensitivity and specificity (see, for example U.S. Pat. No. 5,679,524, PCT publication WO 98/59066, PCT publication WO 95/12607). US Application 20050059030 (incorporated herein in

its entirety) describes a method for detecting a single nucleotide polymorphism in total human DNA without prior amplification or complexity reduction to selectively enrich for the target sequence, and without the aid of any enzymatic reaction. The method utilises a single-step hybridization involving two hybridization events: hybridization of a first portion of the target sequence to a capture probe, and hybridization of a second portion of said target sequence to a detection probe. Both hybridization events happen in the same reaction, and the order in which hybridisation occurs is not critical.

US Application 20050042608 (incorporated herein in its entirety) describes a modification of the method of electrochemical detection of nucleic acid hybridization of Thorp et al. (U.S. Pat. No. 5,871,918). Briefly, capture probes are designed, each of which has a different SNP base and a sequence of probe bases on each side of the SNP base. The probe bases are complementary to the corresponding target sequence adjacent to the SNP site. Each capture probe is immobilized on a different electrode having a non-conductive outer layer on a conductive working surface of a substrate. The extent of hybridization between each capture probe and the nucleic acid target is detected by detecting the oxidation-reduction reaction at each electrode, utilizing a transition metal complex. These differences in the oxidation rates at the different electrodes are used to determine whether the selected nucleic acid target has a single nucleotide polymorphism at the selected SNP site.

The technique of Lynx Therapeutics (Hayward, Calif.) using MEGATYPE™ technology can genotype very large numbers of SNPs simultaneously from small or large pools of genomic material. This technology uses fluorescently labeled probes and compares the collected genomes of two populations, enabling detection and recovery of DNA fragments spanning SNPs that distinguish the two populations, without requiring prior SNP mapping or knowledge.

A number of other methods for detecting and identifying SNPs exist. These include the use of mass spectrometry, for example, to measure probes that hybridize to the SNP. This technique varies in how rapidly it can be performed, from a few samples per day to a high throughput of 40,000 SNPs per day, using mass code tags. A preferred example is the use of mass spectrometric determination of a nucleic acid sequence which comprises the polymorphisms of the invention, for example, as shown herein in the Examples. Such mass spectrometric methods are known to those skilled in the art, and the genotyping methods of the invention are amenable to adaptation for the mass

spectrometric detection of the polymorphisms of the invention, for example, the polymorphisms of the invention as shown in Table 16 herein.

SNPs can also be determined by ligation-bit analysis. This analysis requires two primers that hybridize to a target with a one nucleotide gap between the primers. Each of the four nucleotides is added to a separate reaction mixture containing DNA polymerase, ligase, target DNA and the primers. The polymerase adds a nucleotide to the 3'end of the first primer that is complementary to the SNP, and the ligase then ligates the two adjacent primers together. Upon heating of the sample, if ligation has occurred, the now larger primer will remain hybridized and a signal, for example, fluorescence, can be detected. A further discussion of these methods can be found in U.S. Pat. Nos. 5,919,626; 5,945,283; 5,242,794; and 5,952,174.

US Patent 6,821,733 (incorporated herein in its entirety) describes methods to detect differences in the sequence of two nucleic acid molecules that includes the steps of: contacting two nucleic acids under conditions that allow the formation of a four-way complex and branch migration; contacting the four-way complex with a tracer molecule and a detection molecule under conditions in which the detection molecule is capable of binding the tracer molecule or the four-way complex; and determining binding of the tracer molecule to the detection molecule before and after exposure to the four-way complex. Competition of the four-way complex with the tracer molecule for binding to the detection molecule indicates a difference between the two nucleic acids.

Protein- and proteomics-based approaches are also suitable for polymorphism detection and analysis. Polymorphisms which result in or are associated with variation in expressed proteins can be detected directly by analysing said proteins. This typically requires separation of the various proteins within a sample, by, for example, gel electrophoresis or HPLC, and identification of said proteins or peptides derived therefrom, for example by NMR or protein sequencing such as chemical sequencing or more prevalently mass spectrometry. Proteomic methodologies are well known in the art, and have great potential for automation. For example, integrated systems, such as the ProteomIQ™ system from Proteome Systems, provide high throughput platforms for proteome analysis combining sample preparation, protein separation, image acquisition and analysis, protein processing, mass spectrometry and bioinformatics technologies.

The majority of proteomic methods of protein identification utilise mass spectrometry, including ion trap mass spectrometry, liquid chromatography (LC) and

LC/MSn mass spectrometry, gas chromatography (GC) mass spectroscopy, Fourier transform-ion cyclotron resonance-mass spectrometer (FT-MS), MALDI-TOF mass spectrometry, and ESI mass spectrometry, and their derivatives. Mass spectrometric methods are also useful in the determination of post-translational modification of proteins, such as phosphorylation or glycosylation, and thus have utility in determining polymorphisms that result in or are associated with variation in post-translational modifications of proteins.

Associated technologies are also well known, and include, for example, protein processing devices such as the "Chemical Inkjet Printer" comprising piezoelectric printing technology that allows in situ enzymatic or chemical digestion of protein samples electroblotted from 2-D PAGE gels to membranes by jetting the enzyme or chemical directly onto the selected protein spots. After in-situ digestion and incubation of the proteins, the membrane can be placed directly into the mass spectrometer for peptide analysis.

A large number of methods reliant on the conformational variability of nucleic acids have been developed to detect SNPs.

For example, Single Strand Conformational Polymorphism (SSCP, Orita *et al.*, PNAS 1989 86:2766-2770) is a method reliant on the ability of single-stranded nucleic acids to form secondary structure in solution under certain conditions. The secondary structure depends on the base composition and can be altered by a single nucleotide substitution, causing differences in electrophoretic mobility under nondenaturing conditions. The various polymorphs are typically detected by autoradiography when radioactively labelled, by silver staining of bands, by hybridisation with detectably labelled probe fragments or the use of fluorescent PCR primers which are subsequently detected, for example by an automated DNA sequencer.

Modifications of SSCP are well known in the art, and include the use of differing gel running conditions, such as for example differing temperature, or the addition of additives, and different gel matrices. Other variations on SSCP are well known to the skilled artisan, including,RNA-SSCP, restriction endonuclease fingerprinting-SSCP, dideoxy fingerprinting (a hybrid between dideoxy sequencing and SSCP), bi-directional dideoxy fingerprinting (in which the dideoxy termination reaction is performed simultaneously with two opposing primers), and Fluorescent PCR-SSCP (in which PCR products are internally labelled with multiple fluorescent dyes, may be

digested with restriction enzymes, followed by SSCP, and analysed on an automated DNA sequencer able to detect the fluorescent dyes).

Other methods which utilise the varying mobility of different nucleic acid structures include Denaturing Gradient Gel Electrophoresis (DGGE), Temperature Gradient Gel Electrophoresis (TGGE), and Heteroduplex Analysis (HET). Here, variation in the dissociation of double stranded DNA (for example, due to base-pair mismatches) results in a change in electrophoretic mobility. These mobility shifts are used to detect nucleotide variations.

Denaturing High Pressure Liquid Chromatography (HPLC) is yet a further method utilised to detect SNPs, using HPLC methods well-known in the art as an alternative to the separation methods described above (such as gel electophoresis) to detect, for example, homoduplexes and heteroduplexes which elute from the HPLC column at different rates, thereby enabling detection of mismatch nucleotides and thus SNPs.

Yet further methods to detect SNPs rely on the differing susceptibility of single stranded and double stranded nucleic acids to cleavage by various agents, including chemical cleavage agents and nucleolytic enzymes. For example, cleavage of mismatches within RNA:DNA heteroduplexes by RNase A, of heteroduplexes by, for example bacteriophage T4 endonuclease YII or T7 endonuclease I, of the 5' end of the hairpin loops at the junction between single stranded and double stranded DNA by cleavase I, and the modification of mispaired nucleotides within heteroduplexes by chemical agents commonly used in Maxam-Gilbert sequencing chemistry, are all well known in the art.

Further examples include the Protein Translation Test (PTT), used to resolve stop codons generated by variations which lead to a premature termination of translation and to protein products of reduced size, and the use of mismatch binding proteins. Variations are detected by binding of, for example, the MutS protein, a component of *Escherichia coli* DNA mismatch repair system, or the human hMSH2 and GTBP proteins, to double stranded DNA heteroduplexes containing mismatched bases. DNA duplexes are then incubated with the mismatch binding protein, and variations are detected by mobility shift assay. For example, a simple assay is based on the fact that the binding of the mismatch binding protein to the heteroduplex protects the heteroduplex from exonuclease degradation.

Those skilled in the art will know that a particular SNP, particularly when it occurs in a regulatory region of a gene such as a promoter, can be associated with altered expression of a gene. Altered expression of a gene can also result when the SNP is located in the coding region of a protein-encoding gene, for example where the SNP is associated with codons of varying usage and thus with tRNAs of differing abundance. Such altered expression can be determined by methods well known in the art, and can thereby be employed to detect such SNPs. Similarly, where a SNP occurs in the coding region of a gene and results in a non-synonomous amino acid substitution, such substitution can result in a change in the function of the gene product. Similarly, in cases where the gene product is an RNA, such SNPs can result in a change of function in the RNA gene product. Any such change in function, for example as assessed in an activity or functionality assay, can be employed to detect such SNPs.

The above methods of detecting and identifying SNPs are amenable to use in the methods of the invention.

Of course, in order to detect and identify SNPs in accordance with the invention, a sample containing material to be tested is obtained from the subject. The sample can be any sample potentially containing the target SNPs (or target polypeptides, as the case may be) and obtained from any bodily fluid (blood, urine, saliva, etc) biopsies or other tissue preparations.

DNA or RNA can be isolated from the sample according to any of a number of methods well known in the art. For example, methods of purification of nucleic acids are described in Tijssen; Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization with nucleic acid probes Part 1: Theory and Nucleic acid preparation, Elsevier, New York, N.Y. 1993, as well as in Maniatis, T., Fritsch, E. F. and Sambrook, J., Molecular Cloning Manual 1989.

To assist with detecting the presence or absence of polymorphisms/SNPs, nucleic acid probes and/or primers can be provided. Such probes have nucleic acid sequences specific for chromosomal changes evidencing the presence or absence of the polymorphism and are preferably labeled with a substance that emits a detectable signal when combined with the target polymorphism.

The nucleic acid probes can be genomic DNA or cDNA or mRNA, or any RNA-like or DNA-like material, such as peptide nucleic acids, branched DNAs, and the like. The probes can be sense or antisense polynucleotide probes. Where target polynucleotides are double-stranded, the probes may be either sense or antisense

strands. Where the target polynucleotides are single-stranded, the probes are complementary single strands.

The probes can be prepared by a variety of synthetic or enzymatic schemes, which are well known in the art. The probes can be synthesized, in whole or in part, using chemical methods well known in the art (Caruthers et al., *Nucleic Acids Res., Symp. Ser.,* 215-233 (1980)). Alternatively, the probes can be generated, in whole or in part, enzymatically.

Nucleotide analogs can be incorporated into probes by methods well known in the art. The only requirement is that the incorporated nucleotide analog must serve to base pair with target polynucleotide sequences. For example, certain guanine nucleotides can be substituted with hypoxanthine, which base pairs with cytosine residues. However, these base pairs are less stable than those between guanine and cytosine. Alternatively, adenine nucleotides can be substituted with 2,6-diaminopurine, which can form stronger base pairs than those between adenine and thymidine.

Additionally, the probes can include nucleotides that have been derivatized chemically or enzymatically. Typical chemical modifications include derivatization with acyl, alkyl, aryl or amino groups.

The probes can be immobilized on a substrate. Preferred substrates are any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which the polynucleotide probes are bound. Preferably, the substrates are optically transparent.

Furthermore, the probes do not have to be directly bound to the substrate, but rather can be bound to the substrate through a linker group. The linker groups are typically about 6 to 50 atoms long to provide exposure to the attached probe. Preferred linker groups include ethylene glycol oligomers, diamines, diacids and the like. Reactive groups on the substrate surface react with one of the terminal portions of the linker to bind the linker to the substrate. The other terminal portion of the linker is then functionalized for binding the probe.

The probes can be attached to a substrate by dispensing reagents for probe synthesis on the substrate surface or by dispensing preformed DNA fragments or clones on the substrate surface. Typical dispensers include a micropipette delivering solution to the substrate with a robotic system to control the position of the micropipette with

respect to the substrate. There can be a multiplicity of dispensers so that reagents can be delivered to the reaction regions simultaneously.

Nucleic acid microarrays are preferred. Such microarrays (including nucleic acid chips) are well known in the art (see, for example US Patent Nos 5,578,832; 5,861,242; 6,183,698; 6,287,850; 6,291,183; 6,297,018; 6,306,643; and 6,308,170, each incorporated by reference).

Alternatively, antibody microarrays can be produced. The production of such microarrays is essentially as described in Schweitzer & Kingsmore, "Measuring proteins on microarrays", *Curr Opin Biotechnol* 2002; 13(1): 14-9; Avseekno et al., "Immobilization of proteins in immunochemical microarrays fabricated by electrospray deposition", *Anal Chem* 2001 15; 73(24): 6047-52; Huang, "Detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13.

The present invention also contemplates the preparation of kits for use in accordance with the present invention. Suitable kits include various reagents for use in accordance with the present invention in suitable containers and packaging materials, including tubes, vials, and shrink-wrapped and blow-molded packages.

Materials suitable for inclusion in an exemplary kit in accordance with the present invention comprise one or more of the following: gene specific PCR primer pairs (oligonucleotides) that anneal to DNA or cDNA sequence domains that flank the genetic polymorphisms of interest, reagents capable of amplifying a specific sequence domain in either genomic DNA or cDNA without the requirement of performing PCR; reagents required to discriminate between the various possible alleles in the sequence domains amplified by PCR or non-PCR amplification (e.g., restriction endonucleases, oligonucleotide that anneal preferentially to one allele of the polymorphism, including those modified to contain enzymes or fluorescent chemical groups that amplify the signal from the oligonucleotide and make discrimination of alleles more robust); reagents required to physically separate products derived from the various alleles (e.g. agarose or polyacrylamide and a buffer to be used in electrophoresis, HPLC columns, SSCP gels, formamide gels or a matrix support for MALDI-TOF).

It will be appreciated that the methods of the invention can be performed in conjunction with an analysis of other risk factors known to be associated with lung cancer. Such risk factors include epidemiological risk factors associated with an increased risk of developing lung cancer. Such risk factors include, but are not limited

to smoking and/or exposure to tobacco smoke, age, sex and familial history. These risk factors can be used to augment an analysis of one or more polymorphisms as herein described when assessing a subject's risk of developing lung cancer.

It is recognised that individual SNPs may confer weak risk of susceptibility or protection to a disease or phenotype of interest. These modest effects from individual SNPs are typically measured as odds ratios in the order of 1-3. The specific phenotype of interest may be a disease, such as lung cancer, or an intermediate phenotype based on a pathological, biochemical or physiological abnormality (for example, impaired lung function). As shown herein, when specific genotypes from individual SNPs are assigned a numerical value reflecting their phenotypic effect (for example, a positive value for susceptibility SNPs and a negative value for protective SNPs), the combined effects of these SNPs can be derived from an algorithm that calculates an overall score. Again as shown herein in a case-control study design, this SNP score is linearly related to the frequency of disease (or likelihood of having disease) – see for example Figures 3 and 4.

The SNP score provides a means of comparing people with different scores and their odds of having disease in a simple dose-response relationship. In this analysis, the people with the lowest SNP score are the referent group (Odds ratio=1) and those with greater SNP scores have a correspondingly greater odds (or likelihood) of having the disease – again in a linear fashion. The Applicants believe, without wishing to be bound by any theory, that the extent to which combining SNPs optimises these analyses is dependent, at least in part, on the strength of the effect of each SNP individually in a univariate analysis (independent effect) and/or multivariate analysis (effect after adjustment for effects of other SNPs or non-genetic factors) and the frequency of the genotype from that SNP (how common the SNP is). However, the effect of combining certain SNPs may also be in part related to the effect that those SNPs have on certain pathophysiological pathways that underlie the phenotype or disease of interest.

The Applicants have found that combining certain SNPs may increase the accuracy of the determination of risk or likelihood of disease in an unpredictable fashion. Specifically, when the distribution of SNP scores for the cases and controls are plotted according to their frequency, the ability to segment those with and without disease (or risk of disease) can be improved according to the specific combination of SNPs that are analysed. See, for example, the distributions for the 11 SNP panel A (Figure 6) and for the 16 SNP panel (Figure 8). It appears that this effect is not solely

dependent on the number of relevant SNPs that are analysed in combination, nor the magnitude of their individual effects, nor their frequencies in the cases or controls. It further appears that the ability to improve this segmentation of the population into high and low risk is not due to any specific ratio of susceptibility or protective SNPs. The Applicants believe, without wishing to be bound by any theory, that the greater separation of the population in to high and low risk may at least partly be a function of identifying SNPs that confer a susceptibility or protective phenotype in important but independent pathophysiological pathways.

This observation has clinical utility in helping to define a threshold or cut-off level in the SNP score that will define a subgroup of the population to undergo an intervention. Such an intervention may be a diagnostic intervention, such as imaging test, other screening or diagnostic test (eg biochemical or RNA based test), or may be a therapeutic intervention, such as a chemopreventive therapy (for example, cisplatin or etoposide for small cell lung cancer), radiotherapy, or a preventive lifestyle modification (stopping smoking for lung cancer). In defining this clinical threshold, people can be prioritised to a particular intervention in such a way to minimise costs or minimise risks of that intervention (for example, the costs of image-based screening or expensive preventive treatment or risk from drug side-effects or risk from radiation exposure). In determining this threshold, one might aim to maximise the ability of the test to detect the majority of cases (maximise sensitivity) but also to minimise the number of people at low risk that require, or may be are otherwise eligible for, the intervention of interest.

Receiver-operator curve (ROC) analyses analyze the clinical performance of a test by examining the relationship between sensitivity and false positive rate (i.e., 1-specificity) for a single variable in a given population. In an ROC analysis, the test variable may be derived from combining several factors. Either way, this type of analysis does not consider the frequency distribution of the test variable (for example, the SNP score) in the population and therefore the number of people who would need to be screened in order to identify the majority of those at risk but minimise the number who need to be screened or treated. The Applicants have found that this frequency distribution plot may be dependent on the particular combination of SNPs under consideration and it appears it may not be predicted by the effect conferred by each SNP on its own nor from its performance characteristics (sensitivity and specificity) in an ROC analysis.

The data presented herein shows that determining a specific combination of SNPs can enhance the ability to segment or subgroup people into intervention and non-intervention groups in order to better prioritise these interventions. Such an approach is useful in identifying which smokers might be best prioritised for interventions, such as CT screening for lung cancer. Such an approach could also be used for initiating treatments or other screening or diagnostic tests. As will be appreciated, this has important cost implications to offering such interventions.

Accordingly, the present invention also provides a method of assessing a subject's suitability for an intervention diagnostic of or therapeutic for a disease, the method comprising:

a) providing a net score for said subject, wherein the net score is or has been determined by:

i) providing the result of one or more genetic tests of a sample from the subject, and analysing the result for the presence or absence of protective polymorphisms and for the presence or absence of susceptibility polymorphisms, wherein said protective and susceptibility polymorphisms are associated with said disease,

ii) assigning a positive score for each protective polymorphism and a negative score for each susceptibility polymorphism or vice versa;

iii) calculating a net score for said subject by representing the balance between the combined value of the protective polymorphisms and the combined value of the susceptibility polymorphisms present in the subject sample;

and

b) providing a distribution of net scores for disease sufferers and non-sufferers wherein the net scores for disease sufferers and non-sufferers are or have been determined in the same manner as the net score determined for said subject;

c) determining whether the net score for said subject lies within a threshold on said distribution separating individuals deemed suitable for said intervention from those for whom said intervention is deemed unsuitable;

wherein a net score within said threshold is indicative of the subject's suitability for the intervention, and wherein a net score outside the threshold is indicative of the subject's unsuitability for the intervention.

The value assigned to each protective polymorphism may be the same or may be different. The value assigned to each susceptibility polymorphism may be the same or

may be different, with either each protective polymorphism having a negative value and each susceptibility polymorphism having a positive value, or vice versa.

The intervention may be a diagnostic test for the disease, such as a blood test or a CT scan for lung cancer. Alternatively, the intervention may be a therapy for the disease, such as chemotherapy or radiotherapy, including a preventative therapy for the disease, such as the provision of motivation to the subject to stop smoking.

As described herein, a distribution of SNP scores for lung cancer sufferers and resistant smoker controls (non-sufferers) can be established using the methods of the invention. For example, a distribution of SNP scores derived from the 16 SNP panel consisting of the protective and susceptibility polymorphisms selected from the group consisting of the -133 G/C polymorphism in the Interleukin-18 gene, the -1053 C/T polymorphism in the CYP 2E1 gene, the Arg197gln polymorphism in the Nat2 gene, the -511 G/A polymorphism in the Interleukin 1B gene, the Ala 9 Thr polymorphism in the Anti-chymotrypsin gene, the S allele polymorphism in the Alpha1-antitrypsin gene, the -251 A/T polymorphism in the Interleukin-8 gene, the Lys 751 gln polymorphism in the XPD gene, the +760 G/C polymorphism in the SOD3 gene, the Phe257Ser polymorphism in the REV gene, the Z alelle polymorphism in the Alpha1-antitrypsin gene, the R19W A/G polymorphism in the Cerberus 1 (Cer 1) gene, the Ser307Ser G/T polymorphism in the XRCC4 gene, the K3326X A/T polymorphism in the BRCA2 gene, the V433M A/G polymorphism in the Integrin alpha-11 gene, and the E375G T/C polymorphism in the CAMKK1 gene, among lung cancer sufferers and non-sufferers is described herein. As shown herein, a threshold SNP score can be determined that separates people into intervention and non-intervention groups, so as to better prioritise those individuals suitable for such interventions.

The predictive methods of the invention allow a number of therapeutic interventions and/or treatment regimens to be assessed for suitability and implemented for a given subject. The simplest of these can be the provision to the subject of motivation to implement a lifestyle change, for example, where the subject is a current smoker, the methods of the invention can provide motivation to quit smoking.

The manner of therapeutic intervention or treatment will be predicated by the nature of the polymorphism(s) and the biological effect of said polymorphism(s). For example, where a susceptibility polymorphism is associated with a change in the expression of a gene, intervention or treatment is preferably directed to the restoration of normal expression of said gene, by, for example, administration of an agent capable

of modulating the expression of said gene. Where a polymorphism is associated with decreased expression of a gene, therapy can involve administration of an agent capable of increasing the expression of said gene, and conversely, where a polymorphism is associated with increased expression of a gene, therapy can involve administration of an agent capable of decreasing the expression of said gene. Methods useful for the modulation of gene expression are well known in the art. For example, in situations where a polymorphism is associated with upregulated expression of a gene, therapy utilising, for example, RNAi or antisense methodologies can be implemented to decrease the abundance of mRNA and so decrease the expression of said gene. Alternatively, therapy can involve methods directed to, for example, modulating the activity of the product of said gene, thereby compensating for the abnormal expression of said gene.

Where a susceptibility polymorphism is associated with decreased gene product function or decreased levels of expression of a gene product, therapeutic intervention or treatment can involve augmenting or replacing of said function, or supplementing the amount of gene product within the subject for example, by administration of said gene product or a functional analogue thereof. For example, where a polymorphism is associated with decreased enzyme function, therapy can involve administration of active enzyme or an enzyme analogue to the subject. Similarly, where a polymorphism is associated with increased gene product function, therapeutic intervention or treatment can involve reduction of said function, for example, by administration of an inhibitor of said gene product or an agent capable of decreasing the level of said gene product in the subject. For example, where a SNP allele or genotype is associated with increased enzyme function, therapy can involve administration of an enzyme inhibitor to the subject.

Likewise, when a protective polymorphism is associated with upregulation of a particular gene or expression of an enzyme or other protein, therapies can be directed to mimic such upregulation or expression in an individual lacking the resistive genotype, and/or delivery of such enzyme or other protein to such individual Further, when a protective polymorphism is associated with downregulation of a particular gene, or with diminished or eliminated expression of an enzyme or other protein, desirable therapies can be directed to mimicking such conditions in an individual that lacks the protective genotype.

The relationship between the various polymorphisms identified above and the susceptibility (or otherwise) of a subject to lung cancer also has application in the design and/or screening of candidate therapeutics. This is particularly the case where the association between a susceptibility or protective polymorphism is manifested by either an upregulation or downregulation of expression of a gene. In such instances, the effect of a candidate therapeutic on such upregulation or downregulation is readily detectable.

For example, in one embodiment existing human lung organ and cell cultures are screened for polymorphisms as set forth above. (For information on human lung organ and cell cultures, *see, e.g.*: Bohinski et al. (1996) *Molecular and Cellular Biology* **14**:5671-5681; Collettsolberg et al. (1996) *Pediatric Research* **39**:504; Hermanns et al. (2004) *Laboratory Investigation* **84**:736-752; Hume et al. (1996) *In Vitro Cellular & Developmental Biology-Animal* **32**:24-29; Leonardi et al. (1995) **38**:352-355; Notingher et al. (2003) Biopolymers (Biospectroscopy) **72**:230-240; Ohga et al. (1996) *Biochemical and Biophysical Research Communications* **228**:391-396; each of which is hereby incorporated by reference in its entirety.) Cultures representing susceptibility and protective genotype groups are selected, together with cultures which are putatively "normal" in terms of the expression of a gene which is either upregulated or downregulated where a protective polymorphism is present.

Samples of such cultures are exposed to a library of candidate therapeutic compounds and screened for any or all of: (a) downregulation of susceptibility genes that are normally upregulated in susceptibility polymorphisms; (b) upregulation of susceptibility genes that are normally downregulated in susceptibility polymorphisms; (c) downregulation of protective genes that are normally downregulated or not expressed (or null forms are expressed) in protective polymorphisms; and (d) upregulation of protective genes that are normally upregulated in protective polymorphisms. Compounds are selected for their ability to alter the regulation and/or action of susceptibility genes and/or protective genes in a culture having a susceptibility polymorphisms.

Similarly, where the polymorphism is one which when present results in a physiologically active concentration of an expressed gene product outside of the normal range for a subject (adjusted for age and sex), and where there is an available prophylactic or therapeutic approach to restoring levels of that expressed gene product to within the normal range, individual subjects can be screened to determine the

likelihood of their benefiting from that restorative approach. Such screening involves detecting the presence or absence of the polymorphism in the subject by any of the methods described herein, with those subjects in which the polymorphism is present being identified as individuals likely to benefit from treatment.

The methods of the invention are primarily directed at assessing risk of developing lung cancer. Lung cancer can be divided into two main types based on histology – non-small cell (approximately 80% of lung cancer cases) and small-cell (roughly 20% of cases) lung cancer. This histological division also reflects treatment strategies and prognosis.

The non-small cell lung cancers (NSCLC) are generally considered collectively because their prognosis and management is roughly identical. For non-small cell lung cancer, prognosis is poor. The most common types of NSCLC are adenocarcinoma, which accounts for 50% to 60% of NSCLC, squamous cell carcinoma, and large cell carcinoma.

Adenocarcinoma typically originates near the gas-exchanging surface of the lung. Most cases of the adenocarcinoma are associated with smoking. However, adenocarcinoma is the most common form of lung cancer among non-smokers. A subtype of adenocarcinoma, the bronchioalveolar carcinoma, is more common in female non-smokers.

Squamous cell carcinoma, accounting for 20% to 25% of NSCLC, generally originates in the larger breathing tubes. This is a slower growing form of NSCLC.

Large cell carcinoma is a fast-growing form that grows near the surface of the lung. An initial diagnosis of large cell carcinoma is frequently reclassified to squamous cell carcinoma or adenocarcinoma on further investigation.

For small cell lung cancer (SCLC), prognosis is also poor. It tends to start in the larger breathing tubes and grows rapidly becoming quite large. It is initially more sensitive to chemotherapy, but ultimately carries a worse prognosis and is often metastatic at presentation. SCLC is strongly associated with smoking.

Other types of lung cancer include carcinoid lung cancer, adenoid cystic carcinoma, cylindroma, mucoepidermoid carcinoma, and metastatic cancers which originate in other parts of the body and metatisize to the lungs. Generally, these cancers are identified by the site of origin, i.e., a breast cancer metastasis to the lung is still known as breast cancer. Conversely, the adrenal glands, liver, brain, and bone are the most common sites of metastasis from primary lung cancer itself.

Due to the poor prognosis for lung cancer sufferors, early detection is of paramount importance. However, the screening methodologies currently widely available have been reported to be largely ineffective. Regular chest radiography and sputum examination programs were not effective in reducing mortality from lung cancer, leading the authors to conclude that the current evidence did not support screening for lung cancer with chest radiography or sputum cytology, and that frequent chest x-ray screening might be harmful. (See Manser RL, et al., Screening for lung cancer. *Cochrane Database of Systematic Reviews* 2004, Issue 1. Art. No.: CD001991. DOI: 10.1002/14651858.CD001991.pub2.).

Computed tomography (CT) scans can uncover tumors not yet visible on an X-ray. CT scanning is now being actively evaluated as a screening tool for lung cancer in high risk patients. In a study of over 31,000 high-risk patients, 85% of the 484 detected lung cancers were stage I and were considered highly treatable (see Henschke CI, et al., Survival of patients with stage I lung cancer detected on CT screening. N Engl J Med., 355(17):1763-71, (2006).

In contrast, a recent study in which 3,200 current or former smokers were screened for 4 years and offered 3 or 4 CT scans reported increased diagnoses of lung cancer and increased surgeries, but no significant differences between observed and expected numbers of advanced cancers or deaths (see Bach PB, et al., Computed Tomography Screening and Lung Cancer Outcomes, JAMA., 297:953-961 (2007)).

It should be noted that screening studies have only been done in high risk populations, such as smokers and workers with occupational exposure to certain substances. A more definitive appraisal of the efficacy of screening using CT may need await the results of ongoing randomized trials in the U.S. and Europe. This is important when one considers that repeated radiation exposure from screening could actually induce carcinogenesis in a small percentage of screened subjects, so this risk should be mitigated by a (relatively) high prevalence of lung cancer in the population being screened. This high prevalence can be achieved by prescreening prior to CT scanning by, for example, the methods described herein.

The invention will now be described in more detail, with reference to the following non-limiting examples.

EXAMPLE 1

Case Association Study

Introduction

Case-control association studies allow the careful selection of a control group where matching for important risk factors is critical. In this study, smokers diagnosed with lung cancer and smokers without lung cancer with normal lung function were compared. This unique control group is highly relevant as it is impossible to pre-select smokers with zero risk of lung cancer – i.e., those who although smokers will never develop lung cancer. Smokers with a high pack year history and normal lung function were used as a "low risk" group of smokers, as the Applicants believe it is not possible with current knowledge to identify a lower risk group of smokers. The Applicants believe, without wishing to be bound by any theory, that this approach allows for a more rigorous comparison of low penetrant, high frequency polymorphisms that may confer an increased risk of developing lung cancer. The Applicants also believe, again without wishing to be bound by any theory, that there may be polymorphisms that confer a degree of protection from lung cancer which may only be evident if a smoking cohort with normal lung function is utilised as a comparator group. Thus smokers with lung cancer would be expected to have a lower frequency of these polymorphisms compared to smokers with normal lung function and no diagnosed lung cancer.

Methods

Subject recruitment

Subjects of European decent who had smoked a minimum of fifteen pack years and diagnosed with lung cancer were recruited. Subjects met the following criteria: diagnosed with lung cancer based on radiological and histological grounds, including primary lung cancers with histological types of small cell lung cancer, squamous cell lung cancer, adenocarinoma of the lung, non-small cell cancer (where histological markers can not distinguish the subtype) and broncho-alveolar carcinoma. Subjects could be of any age and at any stage of treatment after the diagnosis had been confirmed. 239 subjects were recruited, of these 53% were male, the mean FEV1/FVC (1SD) was 61% (14), mean FEV1 as a percentage of predicted was 71 (22). Mean age, cigarettes per day and pack year history was 69 yrs (11), 18 cigarettes/day (11) and 38 pack years (31), respectively. 484 European subjects who had smoked a minimum of twenty pack years and who had never suffered breathlessness and had not been

diagnosed with an obstructive lung disease or lung cancer in the past were also studied. This control group was recruited through clubs for the elderly and consisted of 60% male, the mean FEV1/FVC (1SD) was 76% (8), mean FEV1 as a percentage of predicted was 101 (10). Mean age, cigarettes per day and pack year history was 60 yrs (12), 24 cigarettes/day (12) and 41 pack years (25), respectively. Using a PCR based method (Sandford et al., 1999), all subjects were genotyped for the α1-antitrypsin mutations (S and Z alleles) and those with the ZZ allele were excluded. On regression analysis, the age difference and pack years difference observed between lung cancer sufferers and resistant smokers was found not to determine FEV or lung cancer.

This study shows that polymorphisms found in greater frequency in lung cancer patients compared to resistant smokers may reflect an increased susceptibility to the development of lung cancer. Similarly, polymorphisms found in greater frequency in resistant smokers compared to lung cancer may reflect a protective role.

Summary of characteristics for the lung cancer subjects and resistant smokers.

Parameter: Mean (1 SD)	*Lung Cancer N=239*	*Resistant smokers N=484*	*Differences*
% male	*53%*	*60%*	*ns*
Age (yrs)	*69 (11)*	*60 (12)*	*P<0.05*
Pack years	*38 (31)*	*41 (25)*	*P<0.05*
Cigarettes/day	*18 (11)*	*24(12)*	*ns*
FEV1 (L)	*1.8 (0.6)*	*2.8 (0.7)*	*P<0.05*
FEV1 % predict	*71 (22)*	*101% (10)*	*P<0.05*
FEV1/FVC	*61 (14)*	*76 (8)*	*P<0.05*

Means and 1SD

Polymorphism genotyping using the Sequenom Autoflex Mass Spectrometer

Genomic DNA was extracted from whole blood samples (Maniatis,T., Fritsch, E. F. and Sambrook, J., Molecular Cloning Manual. 1989). Purified genomic DNA was aliquoted (10 ng/ul concentration) into 96 well plates and genotyped on a SequenomTM system (SequenomTM Autoflex Mass Spectrometer and Samsung 24 pin nanodispenser) using the following sequences, amplification conditions and methods.

The following conditions were used for the PCR multiplex reaction: final concentrations were for 10xBuffer 15 mM MgCl2 1.25x, 25mM MgCl2 1.625mM, dNTP mix 25 mM 500uM, primers 4 uM 100nM, Taq polymerase (Quiagen hot start) 0.15U/reaction, Genomic DNA 10 ng/ul. Cycling times were 95°C for 15 min, (5°C for 15 s, 56°C 30s, 72°C 30s for 45 cycles with a prolonged extension time of 3min to finish. We used shrimp alkaline phosphotase (SAP) treatment (2ul to 5ul per PCR reaction) incubated at 35°C for 30 min and extension reaction (add 2ul to 7ul after SAP

treatment) with the following volumes per reaction of: water, 0.76ul; hME 10x termination buffer, 0.2ul; hME primer (10uM), 1ul; MassEXTEND enzyme, 0.04ul.

Table 1. Sequenom conditions for genotyping

SNP_ID	2nd-PCRP	1st-PCRP
rs11571833	ACGTTGGATGCTGAATTCTCCTCAGATGAC [SEQ.ID.NO.1]	ACGTTGGATGAATGCAAGTTCTTCGTCAGC [SEQ.ID.NO.2]
rs7214723	ACGTTGGATGAAAACTCAGACACCAGGAGC [SEQ.ID.NO.3]	ACGTTGGATGAGATCAAGAATGAGCCCGTG [SEQ.ID.NO.4]
rs10115703	ACGTTGGATGCCTCTTATTTCAGCTGCTGG [SEQ.ID.NO.5]	ACGTTGGATGAGAGAACTCTGATTCTGGCG [SEQ.ID.NO.6]
rs2306022	ACGTTGGATGACCTTGCCCGTGTGGTTGAA [SEQ.ID.NO.7]	ACGTTGGATGTGGCAGGGTACACAGTCACA [SEQ.ID.NO.8]
rs1056503	ACGTTGGATGCTGCTGTTTCTCAGAGTTTC [SEQ.ID.NO.9]	ACGTTGGATGGCCTGATTCTTCACTACCTG [SEQ.ID.NO.10]
rs2273953	ACGTTGGATGTGCTCAGGTGTCATTCCTTC [SEQ.ID.NO.26]	ACGTTGGATGGGTGGACTGGGCCATCTTC [SEQ.ID.NO.27]
c74delA	ACGTTGGATGTTCTGTAACCTGGCTTTCTC [SEQ.ID.NO.28]	ACGTTGGATGCCAGGAATTCCCAGCTTCTT [SEQ.ID.NO.29]
rs1799732	ACGTTGGATGCAAAACAAGGGATGGCGGAA [SEQ.ID.NO.30]	ACGTTGGATGAAAGGAGCTGTACCTCCTCG [SEQ.ID.NO.31]
rs2279115	ACGTTGGATGATCAGAAGAGGATTCCTGCC [SEQ.ID.NO.32]	ACGTTGGATGTTCACGCCTCCCCAGGAGA [SEQ.ID.NO.33]
rs2317676	ACGTTGGATGTATGAACTGGGAGATGCTGG [SEQ.ID.NO.34]	ACGTTGGATGTGTTGGGAGTGAGGATGTCT [SEQ.ID.NO.35]
rs5743836	ACGTTGGATGTTGGGATGTGCTGTTCCCTC [SEQ.ID.NO.36]	ACGTTGGATGAGCAGAGACATAATGGAGGC [SEQ.ID.NO.37]
rs6413429	ACGTTGGATGTGTCAGGAGGCCTTCAGGTG [SEQ.ID.NO.38]	ACGTTGGATGGTTTTATGAGGGCACTGGTC [SEQ.ID.NO.39]
rs1139417	ACGTTGGATGAGGCCATAGCTGTCTGGCAT [SEQ.ID.NO.40]	ACGTTGGATGTTCCCTTTGTCCCTGGTCT [SEQ.ID.NO.41]
rs763110	ACGTTGGATGAGGCTGCAAACCAGTGGAAC [SEQ.ID.NO.42]	ACGTTGGATGCTGGGCAAACAATGAAAATG [SEQ.ID.NO.43]

SNP_ID	AMP_LEN	UP_CONF	MP_CONF	Tm(NN)	PcGC	PWARN	UEP_DIR	UEP_MASS
rs11571833	109	96.8	69.1	46.3	44.4		F	5409.5
rs7214723	113	99.3	69.1	61.3	58.3	dH	F	7304.7
rs10115703	101	98.7	69.1	59	50		R	7884.1
rs2306022	111	91.8	90.9	53.8	68.8	D	R	4867.2
rs1056503	104	98.5	90.9	48	42.1		R	5775.8
rs2273953	98	90.6	90.6	49.3	58.8	H	R	5137.3
c74delA	101	94.9	69.7	45.7	25	D	F	7295.8
rs1799732	99	97.3	66.7	59.5	66.7	d	F	6183
rs2279115	99	88.3	78.5	52.3	64.7	d	F	5073.3
rs2317676	97	98.7	66.7	63.3	62.5	DH	R	7298.7
rs5743836	100	98.6	88.1	53	64.7		R	5104.3
rs6413429	93	94.2	66.7	56.5	70.6	D	F	5196.4
rs1139417	99	92.2	99.6	56.2	70.6	d	F	5098.3
rs763110	92	92.8	66.7	56.3	44	d	R	7591.9

SNP_ID	UEP_SEQ	EXT1_ CALL	EXT1_ MASS	EXT1_SEQ
rs11571833	CCTCAGATGACTCCATTT [SEQ.ID.NO.11]	A	5680.7	CCTCAGATGACTCCATTTA [SEQ.ID.NO.12]
rs7214723	TGTTCCCCTGGGTGGACAACTCAC [SEQ.ID.NO.13]	C	7551.9	TGTTCCCCTGGGTGGACAACTCACC [SEQ.ID.NO.14]
rs10115703	TACTCCTGCCTCTAGGAAAGACCACA [SEQ.ID.NO.15]	G	8131.3	TACTCCTGCCTCTAGGAAAGACCACAC [SEQ.ID.NO.16]
rs2306022	CCCTGCCTGGAGGACA [SEQ.ID.NO.17]	G	5114.4	CCCTGCCTGGAGGACAC [SEQ.ID.NO.18]
rs1056503	CTGAGATGTGCTCCTTTTT [SEQ.ID.NO.19]	G	6022.9	CTGAGATGTGCTCCTTTTTC [SEQ.ID.NO.20]
rs2273953	CTTCCTTCCTGCAGAGG [SEQ.ID.NO.44]	T	5408.6	CTTCCTTCCTGCAGAGGA [SEQ.ID.NO.45]
c74delA	GGCTTTCTCTTTTATTTTATAGTT [SEQ.ID.NO.46]	C	7542.9	GGCTTTCTCTTTTATTTTATAGTTC [SEQ.ID.NO.47]
rs1799732	CCCAACCCCTCCTACCCGTTC [SEQ.ID.NO.48]	C	6430.2	CCCAACCCCTCCTACCCGTTCC [SEQ.ID.NO.49]
rs2279115	GGCTCCTTCATCGTCCC [SEQ.ID.NO.50]	C	5320.5	GGCTCCTTCATCGTCCCC [SEQ.ID.NO.51]
rs2317676	GATGCTGGTACATCCCCCAGGCCA [SEQ.ID.NO.52]	G	7545.9	GATGCTGGTACATCCCCCAGGCCAC [SEQ.ID.NO.53]
rs5743836	GCTGTTCCCTCTGCCTG [SEQ.ID.NO.54]	T	5375.5	GCTGTTCCCTCTGCCTGA [SEQ.ID.NO.55]
rs6413429	GGAGGGCTCCACCCTGA [SEQ.ID.NO.56]	G	5483.6	GGAGGGCTCCACCCTGAG [SEQ.ID.NO.57]
rs1139417	CCTGACCTGCTGCTGCC [SEQ.ID.NO.58]	A	5369.5	CCTGACCTGCTGCTGCCA [SEQ.ID.NO.59]
rs763110	AACCCACAGAGCTGCTTTGTATTTC [SEQ.ID.NO.60]	T	7863.2	AACCCACAGAGCTGCTTTGTATTTCA [SEQ.ID.NO.61]

SNP_ID	EXT2 CALL	EXT2 MASS	EXT2_SEQ
rs11571833	T	5736.6	CCTCAGATGACTCCATTTT [SEQ.ID.NO.21]
rs7214723	T	7631.8	TGTTCCCCTGGGTGGACAACTCACT [SEQ.ID.NO.22]
rs10115703	A	8211.2	TACTCCTGCCTCTAGGAAAGACCACAT [SEQ.ID.NO.23]
rs2306022	A	5194.3	CCCTGCCTGGAGGACAT [SEQ.ID.NO.24]
rs1056503	T	6047	CTGAGATGTGCTCCTTTTTA [SEQ.ID.NO.25]
rs2273953	C	5424.6	CTTCCTTCCTGCAGAGGG [SEQ.ID.NO.62]
c74delA	A	7567	GGCTTTCTCTTTTATTTTATAGTTA [SEQ.ID.NO.63]
rs1799732	DEL	6454.2	CCCAACCCCTCCTACCCGTTCA [SEQ.ID.NO.64]
rs2279115	A	5344.5	GGCTCCTTCATCGTCCCA [SEQ.ID.NO.65]
rs2317676	A	7625.8	GATGCTGGTACATCCCCCAGGCCAT [SEQ.ID.NO.66]
rs5743836	C	5391.5	GCTGTTCCCTCTGCCTGG [SEQ.ID.NO.67]
rs6413429	T	5523.5	GGAGGGCTCCACCCTGAT [SEQ.ID.NO.68]
rs1139417	G	5385.5	CCTGACCTGCTGCTGCCG [SEQ.ID.NO.69]
rs763110	C	7879.2	AACCCACAGAGCTGCTTTGTATTTCG [SEQ.ID.NO.70]

SNP_ID	EXT3 CALL	EXT3 MASS	EXT3_SEQ
c74delA	G	7583	GGCTTTCTCTTTTATTTTA TAGTTG [SEQ.ID.NO.71]

SNP_ID	EXT4 CALL	EXT4 MASS	EXT4_SEQ
c74delA	T	7622.8	GGCTTTCTCTTTTATTTTA TAGTTT [SEQ.ID.NO.72]

RESULTS

Univariate analyses:

Table 2. Cerberus 1 (Cer 1) R19W A/G (rs 10115703) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	G	AA	AG	GG
Lung Cancer n=234 (%)	47 (10%)	421 (90%)	2 (1%)	43 (18%)	189 (81%)
Resistant n=472 (%)	66 (7%)	878 (93%)	7 (1%)	52 (11%)	413 (88%)

* number of chromosomes (2n)

Genotype. AA/AG vs GG for lung cancer vs resistant, Odds ratio (OR) =1.7, 95% confidence limits 1.1-2.6, χ^2 (Yates uncorrected)= 5.63, p=0.02,

AA/AG genotype = susceptibility (GG protective)

Allele. A vs G for lung cancer vs resistant, Odds ratio (OR) =1.5, 95% confidence limits 1.0-2.2, χ^2 (Yates uncorrected)= 3.95, p=0.05,

A allele = susceptibility

Table 3. XRCC4 Ser307Ser G/T (rs1056503) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	G	T	GG	GT	TT
Lung Cancer n=221 (%)	68 (15%)	374 (85%)	8 (4%)	52 (24%)	161 (72%)
Resistant n=473 (%)	66 (11%)	838 (89%)	5 (1%)	98 (21%)	370 (78%)

* number of chromosomes (2n)

Genotype. GG/GT vs TT for lung cancer vs resistant, Odds ratio (OR) =1.3, 95% confidence limits 0.9-2.0, χ^2 (Yates uncorrected)= 2.4, p=0.12,

GG/GT genotype = susceptibility (TT protective)

Allele. G vs T for lung cancer vs resistant, Odds ratio (OR) =1.4, 95% confidence limits 1.0-2.0, χ^2 (Yates uncorrected)= 4.28, p=0.04,

G allele = susceptibility

Table 4. BRCA2 K3326X A/T (rs 11571833) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	T	AA	AT	TT
Lung Cancer n=231 (%)	450 (97%)	12 (3%)	220 (95%)	10 (4%)	1 (0.4%)
Resistant n=462 (%)	915 (99%)	9 (1%)	453 (98%)	9 (2%)	0 (0%)

* number of chromosomes (2n)

Genotype. AT/TT vs AA for lung cancer vs resistant, Odds ratio (OR) =2.5, 95% confidence limits 1.0-6.7, χ^2 (Yates uncorrected)= 4.34, p=0.04,

AT/TT genotype = susceptibility (AA protective)

Allele. T vs A for lung cancer vs resistant, Odds ratio (OR) =2.7, 95% confidence limits 1.1-7.0, χ^2 (Yates uncorrected)= 5.44, p=0.02,

T allele = susceptibility

Table 5. Integrin alpha-11 V433M A/G (rs 2306022) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	G	AA	AG	GG
Lung Cancer n=233 (%)	60 (13%)	406 (87%)	12 (5%)	36 (15%)	185 (79%)
Resistant n=476 (%)	89 (9%)	863 (91%)	6 (1%)	77 (16%)	393 (83%)

* number of chromosomes (2n)

Genotype. AA vs AG/GG for lung cancer vs resistant, Odds ratio (OR) =4.3, 95% confidence limits 1.5-12.9, χ^2 (Yates uncorrected)= 9.55, p=0.002,

AA genotype = susceptibility

Allele. A vs G for lung cancer vs resistant, Odds ratio (OR) =1.4, 95% confidence limits 1.0-2.1, χ^2 (Yates uncorrected)= 4.14, p=0.04,

A allele = susceptibility

Table 6. CAMKK1 Calcium/calmodulin-dependent protein kinase kinase 1 E375G T/C (rs7214723) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	T	C	TT	TC	CC
Lung Cancer n=233 (%)	239 (51%)	227 (49%)	62 (26%)	115 (49%)	56 (24%)
Resistant n=463 (%)	514 (56%)	412 (44%)	149 (32%)	216 (47%)	98 (21%)

* number of chromosomes (2n)

Genotype. TT vs TC/CC for lung cancer vs resistant, Odds ratio (OR) =0.76, 95% confidence limits 0.5-1.1, χ^2 (Yates uncorrected)= 2.27, p=0.13,

TT genotype = protective

Allele. T vs C for lung cancer vs resistant, Odds ratio (OR) =0.84, 95% confidence limits 0.7-1.1, χ^2 (Yates uncorrected)= 2.22, p=0.14,

T allele = protective

Table 7. P73 C/T (rs 2273953) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	C	T	CC	CT	TT
Lung Cancer n=229 (%)	316 (69%)	142 (31%)	99 (43%)	118 (52%)	12 (5%)
Resistant n=474 (%)	742 (78%)	206 (22%)	295 (62%)	152 (32%)	27 (6%)

* number of chromosomes (2n)

Genotype. CC vs CT/TT for lung cancer vs resistant, Odds ratio (OR) =0.46, 95% confidence limits 0.33-0.64, $\chi 2$ (Yates uncorrected) = 22.0, $p<0.001$,

CC genotype =protective (CT/TT susceptible)

Allele. C vs T for lung cancer vs resistant, Odds ratio (OR) =0.62, 95% confidence limits0.48-0.80, $\chi 2$ (Yates corrected)= 14.0, $p<0.001$,

C allele = protective

Table 8. CYP 3A43 A/T c74delA polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	T	AA	AT	TT
Lung Cancer n=234 (%)	442 (94%)	26 (6%)	209 (89%)	24 (10%)	1 (0.5%)
Resistant n=483 (%)	935 (97%)	31 (3%)	452 (94%)	31 (6%)	0 (0%)

* number of chromosomes (2n)

Genotype. AT/TT vs AA for lung cancer vs resistant, Odds ratio (OR) =1.74, 95% confidence limits 0.97-3.13, $\chi 2$ = (Yates uncorrected) = 4.0, $p=0.05$,

AT/TT genotype =susceptible

Allele. T vs A for lung cancer vs resistant, Odds ratio (OR) =1.8, 95% confidence limits 1-3.1, $\chi 2$ (Yates uncorrected)= 4.54, $p=0.03$,

T allele = susceptible

Table 9. BCL2 A/C (rs 2279115) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	C	AA	AC	CC
Lung Cancer n=236 (%)	223 (47%)	249 (53%)	55 (23%)	113 (48%)	68 (29%)
Resistant n=479 (%)	513 (54%)	445 (46%)	146 (31%)	221 (46%)	112 (23%)

* number of chromosomes (2n)

Genotype. AA vs AC/CC for lung cancer vs resistant, Odds ratio (OR) =0.69, 95% confidence limits 0.48-1.0, $\chi 2$ (Yates uncorrected) = 4.0, p=0.05,

AA genotype =protective

Allele. A vs C for lung cancer vs resistant, Odds ratio (OR) =0.78, 95% confidence limits 0.62-0.97, $\chi 2$ (Yates corrected)= 5.0, p=0.02,

A allele =protective

Table 10. ITGB3 A/G (rs 2317676) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	G	AA	AG	GG
Lung Cancer n=234 (%)	445 (95%)	23 (5%)	211 (90%)	23 (10%)	0 (0%)
Resistant n=484 (%)	884 (91%)	84 (9%)	406 (84%)	72 (15%)	6 (1%)

* number of chromosomes (2n)

Genotype. AG/GG vs AA for lung cancer vs resistant, Odds ratio (OR) =0.57, 95% confidence limits 0.34-0.95, $\chi 2$ (Yates uncorrected) = 5.2, p=0.02,

AG/GG genotype =protective

Allele. G vs A for lung cancer vs resistant, Odds ratio (OR) =0.54, 95% confidence limits0.33-0.89, $\chi 2$ (Yates uncorrected)= 6.5, p=0.01,

G allele =protective

Integrin beta 3 is also referred to as platelet glycoprotein IIIa or antigen CD61.

Table 11. DAT1 G/T (rs 6413429) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	G	T	GG	GT	TT
Lung Cancer n=232 (%)	427 (92%)	37 (8%)	195 (84%)	37 (16%)	0 (0%)
Resistant n=485 (%)	914 (94%)	56 (6%)	433 (89%)	48 (10%)	4 (1%)

* number of chromosomes (2n)

Genotype. TT/GT vs GG for lung cancer vs resistant, Odds ratio (OR) =1.6, 95% confidence limits 1.0-2.6, $\chi 2$ (Yates uncorrected) = 3.9, p=0.05,

TT/GT genotype = susceptible

Dopamine transporter 1 (DAT1) is also known as solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3).

Table 12. TNFR1 A/G (rs1139417) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	A	G	AA	AG	GG
Lung Cancer n=224 (%)	277 (62%)	171 (38%)	87 (39%)	103 (46%)	34 (15%)
Resistant n=478 (%)	536 (56%)	420 (44%)	143 (30%)	250 (52%)	85 (18%)

* number of chromosomes (2n)

Genotype. AA vs AG/GG for lung cancer vs resistant, Odds ratio (OR) =1.5, 95% confidence limits 1-2.1, $\chi 2$ (Yates uncorrected) = 5.5, p=0.02,

AA genotype = susceptible

Allele. A vs G for lung cancer vs resistant, Odds ratio (OR) =1.3, 95% confidence limits1.0-1.6, $\chi 2$ (Yates uncorrected)= 4.2, p=0.04,

A allele = susceptible

Table 13. DRD2 C/Del (rs 1799732) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	C	Del	CC	CDel	DelDel
Lung Cancer n=231 (%)	426 (92%)	36 (8%)	197 (85%)	32 (14%)	2 (1%)
Resistant n=483 (%)	857 (89%)	109 (11%)	376 (78%)	105 (22%)	2 (0.5%)

* number of chromosomes (2n)

Genotype. CDel/DelDel vs CC for lung cancer vs resistant, Odds ratio (OR) =0.61, 95% confidence limits 0.39-0.94, $\chi 2$ (Yates uncorrected) = 5.4, p=0.02,

CDel/DelDel genotype = protective

Allele. Del vs C for lung cancer vs resistant, Odds ratio (OR) =0.66, 95% confidence limits 0.44-1.0, $\chi 2$ (Yates uncorrected)= 4.2, p=0.04,

Del = protective

Table 14. FasL C/T (rs 763110) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	C	T	CC	CT	TT
Lung Cancer n=229 (%)	302 (66%)	156 (34%)	97 (42%)	108 (47%)	24 (11%)
Resistant n=485 (%)	596 (61%)	374 (39%)	189 (39%)	218 (45%)	78 (16%)

* number of chromosomes (2n)

Genotype. TT vs CC/CT for lung cancer vs resistant, Odds ratio (OR) =0.61, 95% confidence limits 0.36-1.0, $\chi 2$ (Yates uncorrected) = 4.0, p=0.05,

TT genotype =protective

Fas ligand (TNF superfamily, member 6) is also known as FASLG, CD178, CD95L, TNFSF6, and APT1LG1.

Table 15. TLR9 C/T (rs 5743836) polymorphism allele and genotype frequencies in the Lung cancer patients and resistant smokers.

Frequency	Allele*		Genotype		
	T	C	TT	TC	CC
Lung Cancer n=231 (%)	386 (84%)	76 (16%)	164 (71%)	58 (25%)	9 (4%)
Resistant n=465 (%)	791 (85%)	139 (15%)	332 (71%)	127 (27%)	6 (1%)

* number of chromosomes (2n)

Genotype. CC vs TC/TT for lung cancer vs resistant, Odds ratio (OR) =3.1, 95% confidence limits 1.0-9.9, χ^2 (Yates uncorrected) = 5.0, p=0.03,

CC genotype = susceptible

Table 16. Summary table of protective and susceptibility polymorphisms for lung cancer.

Gene and SNP	rs number	Genotype	Phenotype	OR	P value
Cerberus 1 (Cer 1) R19W A/G [1]	rs10115703	AA/AG	susceptiblility	1.7	0.02
XRCC4 Ser307Ser G/T [1]	rs1056503	GG/GT	susceptiblility	1.3	0.04
BRCA2 K3326X A/T [1]	rs11571833	AT/TT	susceptiblility	2.5	0.04
Integrin alpha-11 V433M A/G [1]	rs2306022	AA	susceptiblility	4.3	0.002
CAMKK1 E375G T/C [1]	rs7214723	TT	protective	0.76	0.13
P73	rs2273953	CC	protective	0.46	<0.001
CYP3A43 C74 delA		AT/TT	susceptiblility	1.74	0.05

BCL2	rs2279115	AA	protective	0.69	0.05
ITGB3	rs2317676	AG/GG	protective	0.57	0.02
DAT1	rs6413429	GT/TT	susceptibility	1.6	0.05
TNFR1	rs1139417	AA	susceptibility	1.5	0.02
DRD2	rs1799732	CDel/DelDel	protective	0.61	0.02
FasL	rs763110	TT	protective	0.61	0.05
TLR9	rs5743836	CC	susceptibility	3.1	0.03

1 – included in the 5 SNP panel described below.
Odds ratios and P values derived from univariate analyses described above.

SNP scores for each subject were derived by assigning a score of +1 for the presence of susceptiblility genotypes or -1 for the presence of protective genotypes of the 5 SNPs included in the panel as identified in Table 16 above. The scores are added to derive the total SNP score for each subject. Table 17 below shows the distribution of SNP scores derived from the 5 SNP panel amongst the lung cancer patients and the resistant smoker controls.

Table 17. Distribution of SNP scores (5 SNP panel) in smokers with and without lung cancer.

Cohort	Lung cancer SNP score – 5 SNP panel			
	-1	0	1	2
Lung cancer N=239 (%)	33 (14%)	119 (50%)	75 (31%)	12 (5%)
Control smokers N=484 (%)	104 (21%)	264 (54%)	100 (21%)	16 (3%)
% with lung cancer	33/137 (24%)	119/383 (31%)	75/175 (43%)	12/28 (43%)

The likelihood of having lung cancer according to the lung cancer SNP score generated from the 5 SNP panel is shown graphically in Figure 1. The log odds of having lung cancer according to the SNP score derived from the 5 SNP panel presented in Table 17 is shown in Figure 2.

EXAMPLE 2

This example presents an analysis of distributions of SNP scores derived for lung cancer sufferors and control resistant smokers using the polymorphisms described in Table 18 below. Table 18 presents a summary of selected protective and susceptibility SNPs identified in PCT/NZ2006/000125 (published as WO2006/123955) and related applications (New Zealand Patent Application No.s 540203/541787/543297), and herein that were included in additional panels of SNPs.

SNPs 1-11 identified in Table 18 were included in both the 11 SNP panel A and the 16 SNP panel used to generate SNP scores as discussed below. SNPs 12-16 identified in Table 18 were included in both the 5 SNP panel described in Example 1 above, and in the 16 SNP panel used to generate SNP scores as discussed below. Odd's ratios (OR) and p values are for cancer patients compared to resistant smokers with normal lung function.

Table 18. Summary of selected protective and susceptibility polymorphisms

SNP#	Gene	Polymorphism	Genotype	Phenotype	OR	P value
1	Interleukin -18 (IL-18)	-133 G/C	CG/GG CC	protective susceptibility	1.5	0.09
2	CYP2E1	-1053 C/T (Rsa I)	TT/TC	susceptibility	1.9	0.13
3	N-acetyltransferase 2 (NAT2)	Arg 197 Gln A/G	GG	susceptibility	1.5	0.08
4	Interleukin 1B (IL-1B)	-511 A/G	GG	susceptibility	1.6	0.04
5	Anti-chymotrypsin (ACT)	Ala 15 Thr	GG	susceptibility	1.7	0.06
6	α1-antitrypsin	S allele [1]	AT/TT	susceptibility		
7	Interleukin-8 (IL-8)	-251 A/T	AA	protective	4.1	0.002
8	XPD	Lys -751 Gln G/T	GG	protective	1.7	0.18
9	Superoxide dismutase 3 (SOD3)	Arg 312 Gln (+760 G/C)	CG/GG	protective	3.38	0.03
10	REV1	Phe 257 Ser C/T	CC	protective	0.73	0.20
11	α1-antitrypsin	Z allele [1]	AG	protective		
12	Cerberus 1 (Cer 1)	R19W A/G [2] (rs 10115703)	AA/AG	susceptiblility	1.7	0.02
13	XRCC4	Ser307Ser G/T [2] (rs1056503)	GG/GT	susceptiblility	1.3	0.04
14	BRCA2	K3326X A/T [2] (rs 11571833)	AT/TT	susceptiblility	2.5	0.04
15	Integrin alpha-11	V433M A/G [2] (rs 2306022)	AA	susceptiblility	4.3	0.002
16	CAMKK1	E375G T/C [2] (rs7214723)	TT	protective	0.76	0.13

[1] –discussed in PCT International application PCT/NZ2006/000125.

[2] – included in both the 5 SNP panel (described in Example 1) and the 16 SNP panel.

Table 19 below presents the distribution of SNP scores derived from the 11 SNP panel A consisting of SNPs numbers 1 to 11 from Table 18 in the lung cancer patients and the resistant smoker controls.

Table 19. Distribution of the lung cancer SNP score

Cohort	lung cancer SNP score - 11 SNP panel A										
	0	1	2	3	4	5	6	7	8	9	10+
Lung cancer N=239	2 (1%)	5 (2%)	9 (4%)	12 (5%)	13 (5%)	21 (9%)	47 (20%)	44 (18%)	37 (16%)	24 (10%)	25 (10%)
Smoking controls N=484	23 (5%)	45 (9%)	74 (15%)	69 (14%)	48 (10%)	51 (11%)	68 (14%)	58 (12%)	31 (6%)	14 (3%)	3 (1%)
% with lung cancer	6/80 (8%)	7/68 (10%)	8/73 (11%)	15/72 (21%)	26/79 (33%)	37/107 (37%)	37/82 (45%)	44/79 (56%)	29/44 (66%)	16/22 (73%)	14/17 (82%)

The shaded SNP scores (0, 1, and 2) can be viewed as low to average risk of lung cancer. At this threshold (cut-off), 7% of lung cancer cases were present, while 29% of the control smokers were present. On the graph plotting lung cancer frequency versus SNP score (Figure 3), this equates to an approximately 10% risk of lung cancer. This is the average across all smokers. The likelihood of having lung cancer according to the SNP score derived from the 11 SNP panel A is shown in Figure 3.

The distribution of SNP scores among lung cancer patients and resistant smoker controls were further analysed as follows. Figure 4 depicts a receiver –operator curve analysis with sensitivity and sensitivity for the lung cancer 11 SNP panel A. This was developed according to the model:

(IL18_133_S+CYP2E1_Rsa1_S+NAT2_197_S+IL1B_511_S+ACT_15_S+s_allele_S+ IL8_251_S+z_allele_s)

-

(XPD_751_P+SOD3_213_P+REV1_257_P)

if age > 60 then add 4

if FHx lung Ca then add 3

	Results
Area under the ROC curve	
Area	0.7483
Std. Error	0.01907
95% confidence interval	0.7109 to 0.7856
P value	< 0.0001

Cutoff	Sensitivity	95% CI	Specificity	95% CI	Likelihood ratio
> -0.5000	0.9958	0.9769 to 0.9999	0.004132	0.0005008 to 0.01485	1.00
> 0.5000	0.9916	0.9701 to 0.9990	0.04752	0.03036 to 0.07045	1.04
> 1.500	0.9707	0.9406 to 0.9881	0.1405	0.1108 to 0.1747	1.13
> 2.500	0.9331	0.8936 to 0.9613	0.2934	0.2532 to 0.3362	1.32
> 3.500	0.8828	0.8351 to 0.9207	0.4360	0.3913 to 0.4814	1.57
> 4.500	0.8285	0.7746 to 0.8740	0.5351	0.4896 to 0.5803	1.78
> 5.500	0.7406	0.6801 to 0.7950	0.6405	0.5960 to 0.6833	2.06
> 6.500	0.5439	0.4785 to 0.6083	0.7810	0.7415 to 0.8171	2.48
> 7.500	0.3598	0.2990 to 0.4242	0.9008	0.8707 to 0.9260	3.63
> 8.500	0.2050	0.1557 to 0.2618	0.9649	0.9444 to 0.9794	5.84
> 9.500	0.1046	0.06884 to 0.1505	0.9938	0.9820 to 0.9987	16.88
> 10.50	0.03766	0.01736 to 0.07028	0.9979	0.9885 to 0.9999	18.23
> 11.50	0.004184	0.0001059 to 0.02309	1.000	0.9924 to 1.000	

Figure 5 herein presents a graph showing the distribution of SNP score derived from the 11 SNP panel A among lung cancer sufferers and among resistant smoker controls.

Table 20. Distribution of the lung cancer SNP score derived from the 16 SNP panel

	16 SNP lung cancer SNP score										
	≤1	2	3	4	5	6	7	8	9	10	11+
Lung cancer N=239	6 (2%)	7 (3%)	8 (3%)	15 (6%)	26 (11%)	37 (15%)	37 (15%)	44 (18%)	29 (12%)	16 (7%)	14 (6%)
Smoking controls N=484	74 (15%)	61 (13%)	65 (13%)	57 (12%)	53 (11%)	70 (15%)	45 (9%)	35 (7%)	15 (3%)	6 (1%)	3 (1%)
% with lung cancer	6/80 (8%)	7/68 (10%)	8/73 (11%)	15/72 (21%)	26/79 (33%)	37/107 (37%)	37/82 (45%)	44/79 (56%)	29/44 (66%)	16/22 (73%)	14/17 (82%)

The shaded SNP scores (≤1, 2, and 3) can be viewed as low to average risk of lung cancer. At this cut-off, 8% of lung cancer cases were present, while 41% of control smokers were present. On the graph plotting lung cancer frequency and SNP score (Figure 6), this equates to about a 10% risk of lung cancer, the average across all smokers. The likelihood of having lung cancer according to the SNP score derived from the 16 SNP panel is shown in Figure 6.

The distribution of SNP scores among lung cancer patients and resistant smoker controls were further analysed as follows. Figure 7 depicts a receiver –operator curve analysis with sensitivity and sensitivity for the lung cancer 16 SNP panel. This was developed according to the model:

(IL18_133_S+CYP2E1_Rsa1_S+NAT2_197_S+IL1B_511_S+ACT_15_S+s_allele_S+ IL8_251_S+z_allele_s)

-(XPD_751_P+SOD3_213__P+REV1_257_P)

+

(ITGA11_s+ Cer1_s+BRAC2_s +XRCC4_307_s)

-CAMKK1_p

if age > 60 then add 4

if FHx lung Ca then add 3

	Results
Area under the ROC curve	
Area	0.7621
Std. Error	0.01855
95% confidence interval	0.7257 to 0.7985
P value	< 0.0001

Cutoff	Sensitivity	95% CI	Specificity	95% CI	Likelihood ratio
> -0.5000	0.9958	0.9769 to 0.9999	0.01240	0.004563 to 0.02679	1.01
> 0.5000	0.9874	0.9638 to 0.9974	0.05992	0.04049 to 0.08492	1.05
> 1.500	0.9749	0.9462 to 0.9907	0.1529	0.1220 to 0.1881	1.15
> 2.500	0.9456	0.9088 to 0.9707	0.2789	0.2394 to 0.3212	1.31
> 3.500	0.9121	0.8688 to 0.9448	0.4132	0.3690 to 0.4585	1.55
> 4.500	0.8494	0.7976 to 0.8922	0.5310	0.4854 to 0.5762	1.81
> 5.500	0.7406	0.6801 to 0.7950	0.6405	0.5960 to 0.6833	2.06
> 6.500	0.5858	0.5205 to 0.6489	0.7851	0.7458 to 0.8209	2.73
> 7.500	0.4310	0.3673 to 0.4964	0.8781	0.8456 to 0.9059	3.54
> 8.500	0.2469	0.1935 to 0.3066	0.9504	0.9271 to 0.9680	4.98
> 9.500	0.1255	0.08632 to 0.1743	0.9814	0.9650 to 0.9915	6.75
> 10.50	0.05858	0.03239 to 0.09633	0.9938	0.9820 to 0.9987	9.45
> 11.50	0.02092	0.006827 to 0.04814	1.000	0.9924 to 1.000	

Figure 8 herein presents a graph showing the distribution of SNP score derived from the 16 SNP panel among lung cancer sufferers and among resistant smoker controls.

EXAMPLE 3

This example presents a multivariate analysis using a 9 SNP panel comprising the polymorphisms described in Table 21 below. Table 21 summarises the univariate analysis showing protective and susceptibility SNPs associated with lung cancer as set out in Tables 7-15. Odd's ratios (OR) and p values are for cancer patients compared to resistant smokers with normal lung function.

Table 21. Summary of selected polymorphisms – 9 SNP panel

Gene and SNP	**rs number**	**Genotype**	**Phenotype**	**OR**	**P value**
P73	rs2273953	CC	protective	0.46	<0.001
CYP3A43 C74 delA		AT/TT	susceptiblility	1.74	0.05
BCL2	rs2279115	AA	protective	0.69	0.05
ITGB3	rs2317676	AG/GG	protective	0.57	0.02
DAT1	rs6413429	GT/TT	susceptibility	1.6	0.05
TNFR1	rs1139417	AA	susceptibility	1.5	0.02

DRD2	rs1799732	CDel/DelDel	protective	0.61	0.02
FasL	rs763110	TT	protective	0.61	0.05
TLR9	rs5743836	CC	susceptibility	3.1	0.03

As described above in respect of the 5, 11, and 16 SNP panels, a SNP score was determined for each subject from the univariate data for this 9 SNP panel. The presence of the susceptibility SNP genotype was scored +1, and the presence of the protective SNP genotype was scored -1.

As shown in Figure 9, a linear relationship was observed when the SNP score for lung cancer patients and healthy smoking controls were analysed together and plotted according to the odds of having lung cancer, where those with the highest scores have the greatest risk. In this analysis (floating absolute odds ratio), the lowest SNP score group is referenced as 1. Those with the highest score (5 or more) have an Odds of 13 – they are at 13 fold greater likelihood (or risk) of being diagnosed with lung cancer.

For each subject, a composite score that defines a likelihood of being diagnosed with lung cancer was derived. The SNP score from the 9 SNP panel was combined with scores according to age (+4 for age over 60 yo) and family history (+3 for having a first degree relative with lung cancer) for each subject. This algorithm generated a composite score for each smoker based on genotype, age and family history of lung cancer. Table 22 below shows the results of this multivariate analysis using these 9 SNPs, age and family history.

Table 22. Multivariate analysis

Analysis of Maximum Likelihood Estimates								
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald Chi-Square**	**Pr > ChiSq**	**OR**	**95% Wald Confidence Limits**	
Intercept	1	4.1002	0.8241	24.7553	<.0001			
P73_p	1	0.7646	0.1995	14.6902	0.0001	2.148	1.453	3.176
DRD2_p	1	0.6471	0.2639	6.0107	0.0142	1.910	1.139	3.204
BCL2_p	1	0.3845	0.2310	2.7711	0.0960	1.469	0.934	2.310
FasL_p	1	0.8187	0.2991	7.4906	0.0062	2.267	1.262	4.075
ITGB3_p	1	0.7764	0.2985	6.7636	0.0093	2.174	1.211	3.902
TNFR1_s	1	-0.1094	0.2180	0.2517	0.6159	0.896	0.585	1.374
CYP3A43_s	1	-0.7760	0.3741	4.3036	0.0380	0.460	0.221	0.958
DAT1_s	1	-0.4273	0.2918	2.1431	0.1432	0.652	0.368	1.156
TLR9_s	1	-0.6429	0.6268	1.0520	0.3050	0.526	0.154	1.796

Age	1	-0.0796	0.0104	58.3869	<.0001	0.923	0.905	0.943
FHxLCancer	1	0.3105	0.2582	1.4452	0.2293	1.364	0.822	2.263
		c	0.770					

Figure 10 shows the receiver-operator curve analysis for this composite lung cancer SNP score. The receiver operator curve analysis shows the area under the ROC curve is 0.73 for these 9 SNPs. This indicates an acceptable level of discrimination.

When the frequency distribution for the 9 SNP panel SNP score is compared between lung cancer cases and controls (Figure 11), separation of the lung cancer SNP score between cases and controls is observed. This reflects the ability of the SNP score to discriminate between high and low risk smokers. This data shows that SNPs on their own derive modest levels of risk (small Odds ratios). These SNPs can be analysed in combination to derive a risk score with clinical utility in discriminating smokers at high and low risk of lung cancer based on their genotype, and such analyses can include non-genetic factors such as age and family history.

EXAMPLE 4

This example presents a multivariate analysis using an 11 SNP panel (11 SNP panel B) comprising the polymorphisms described in Table 23 below. Table 23 summarises the univariate analysis showing protective and susceptibility SNPs associated with lung cancer as set out herein. Odd's ratios (OR) and p values are for cancer patients compared to resistant smokers with normal lung function. Stepwise regression analysis was also performed, and chi squared values are presented for each polymorphism.

Table 23. Summary of Selected Polymorphisms –11 SNP Panel B

SNP (rs#)	Genotype	Lung cancer	Smoking controls	Call rate	Univariate OR	P value	Stepwise regression $\chi 2$	P value	Phenotype
Interleukin-18 (-133 G/C)	CC CG/GG	237 (54%) 201 (46%)	208 (45%) 250 (55%)	96%	1.4 (1.1-1.9)	0.009	10.4	0.001	susceptibility
Interleukin-8 (-251 A/T)	TT AT/AA	129 (31%) 284 (69%)	109 (23%) 367 (77%)	96%	1.5 (1.1-2.1)	0.005	6.5	0.01	susceptibility
ITGA11 (rs2306022)	AA GA/GG	14 (3%) 422 (97%)	6 (1%) 470 (99%)	98%	2.6 (0.9-7.6)	0.04			susceptibility
N–acetylcysteine transferase 2 (rs 1799930)	GG AA/AG	239 (56%) 189 (44%)	222 (47%) 253 (53%)	97%	1.4 (1.1-1.9)	0.006	5.8	0.02	susceptibility
α1-antichymotrypsin (-15 A/G)	GG AG/AA	123 (28%) 312 (72%)	96 (20%) 383 (80%)	98%	1.6 (1.2-2.2)	0.004	7.1	0.008	susceptibility
DAT1 (rs6413429)	GT/TT GG	64 (15%) 367 (85%)	50 (10%) 431 (90%)	98%	1.5 (1.0-2.3)	0.04	4.2	0.04	susceptibility
P73 (rs 2273953)	CC TC/TT	219 (52%) 206 (48%)	292 (62%) 178 (38%)	96%	0.65 (0.49-0.85)	0.001	11.8	0.0006	protective
SOD3 (rs1799895)	GG/GC CC	4 (1%) 425 (99%)	15 (3%) 451 (97%)	96%	0.28 (0.10-0.90)	0.02	7.7	0.005	protective
ITGB3 (rs2317676)	GG/GA AA	44 (10%) 391 (90%)	77 (16%) 403 (84%)	98%	0.59 (0.39-0.89)	0.008	6.6	0.01	protective
DRD2 (rs 1799732)	CDel/Del.Del CC	70 (16%) 359 (84%)	107 (22%) 372 (78%)	98%	0.68 (0.48-0.96)	0.02	7.3	0.007	protective
BCL2 (rs 2279115)	AA AC/CC	103 (24%) 328 (76%)	145 (31%) 330 69%)	97%	0.71 (0.53-0.97)	0.03	4.2	0.04	protective

As described above, a SNP score was determined for each subject from the univeriate data for the 11 SNP panel B. The presence of the susceptibility SNP genotype was scored +1, and the presence of the protective SNP genotype was scored -1.

For each subject, a score that defines a likelihood of being diagnosed with lung cancer was derived. Table 23 above shows the results of this multivariate analysis using these 11 SNPS and indicates these SNPs can be analysed in combination to derive a risk score with clinical utility in discriminating smokers at high and low risk of lung cancer based on their genotype.

DISCUSSION

The above results show that several polymorphisms were associated with either increased or decreased risk of developing lung cancer. The associations of individual polymorphisms on their own, while of discriminatory value, are unlikely to offer an acceptable prediction of disease. However, in combination these polymorphisms distinguish susceptible subjects from those who are resistant (for example, between the smokers who develop lung cancer and those with the least risk with comparable smoking exposure). The polymorphisms represent exonic polymorphisms known to alter amino-acid sequence (and likely expression and/or function) in a number of genes involved in processes known to underlie lung remodelling and lung cancer, and in one case a silent mutation having no effect on amino acid composition. The polymorphisms identified here are found in genes encoding proteins central to these processes which include inflammation, matrix remodelling, oxidant stress, DNA repair, cell replication and apoptosis.

In the comparison of smokers with lung cancer and matched smokers with near normal lung function (lowest risk for lung cancer despite smoking), several polymorphisms were identified as being found in significantly greater or lesser frequency than in the comparator groups (sometimes including the blood donor cohort). Due to the small cohort of lung cancer patients, polymorphisms where there are only trends towards differences (P=0.06-0.25) were included in the analyses, although in the combined analyses only those polymorphisms with the most significant differences were utilised.

- In the analysis of the R19W A/G polymorphism of the Cerberus 1 gene, the AA and AG genotypes were found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.7, P=0.02), consistent with each having a susceptibility role (see Table 2). The A allele was found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.5, P=0.05), consistent with a susceptibility role. In contrast, the GG genotype was found to be greater in the resistant smoker control cohort compared to the lung cancer cohort, consistent with a protective role (see Table 2).
- In the analysis of the Ser307Ser G/T polymorphism in the XRCC4 gene, the GG and GT genotypes were found to be greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.3, P=0.12) consistent with each having a susceptibility role. The G allele was found to be significantly greater in the lung cancer cohort compared to the resistant smoker controls (OR=1.4, P=0.04), consistent with a suscepbility role (see Table 3). In contrast, the TT genotype was found to be greater in the resistant smoker control compared to the lung cancer cohort, consistent with a protective role.
- In the analysis of the K3326X A/T polymorphism in the ERCA2 gene, the A/T and TT genotypes were found to be significantly greater in the lung cancer cohort compared to the resistant smoker controls (OR=2.5, P=0.04), consistent with a suscepbility role. The T allele was found to be significantly greater in the lung cancer cohort compared to the resistant smoker controls (OR=2.7, P=0.02), see Table 4. In contrast the AA genotype was found to be greater in the resistant smoker controls compared to the lung cancer cohort, consistant with a protective role.
- In the analysis of the V433M A/G polymorphism, in the Integrin alpha-11 gene, the AA genotype was found to be significantly greater in the lung cancer cohort compared to the resistant smoker controls (OR=4.3, P=0.002) consistent with a susceptibility role (see Table 5). The A allele was found to be significantly greater in the lung cancer cohort compared to the resistant smoker controls (OR=1.4, P=0.04), consistent with a susceptibility role (see Table 5).

- In the analysis of the E375G T/C polymorphism in the Calcium/calmodulin-dependent protein kinase kinase 1 gene, the TT genotype was found to be greater in the resistant smoker controls compared to the lung cancer cohort (OR=0.76, P=0.13), consistent with a protective role (see Table 6). The T allele is found to be greater in resistant smoker controls compared to the lung cancer cohort (OR=0.84, P=0.14), consistent with a protective role (see Table 6).
- In the analysis of the -81 C/T (rs 2273953) polymorphism in the 5' UTR of the gene encoding Tumor protein P73, the CC genotype was found to be significantly greater in the resistant smoker cohort compared to the lung cancer cohort (OR=0.46, P<0.001) consistent with a protective role. The C allele was also found to be significantly greater in the resistant smoker controls compared to the lung cancer cohort (OR=0.62, P<0.001), consistent with a protective role (see Table 7). In contrast, the CT and TT genotypes were found to be greater in the the lung cancer cohort compared to resistant smoker controls, consistent with a susceptibility role.
- In the analysis of the A/T c74delA polymorphism in the gene encoding cytochrome P450 polypeptide CYP3A43, the AT and TT genotypes were found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.74, P=0.05), consistent with each having a susceptibility role (see Table 8). The T allele was found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.8, P=0.03), also consistent with a susceptibility role.
- In the analysis of the A/C (rs2279115) polymorphism in the gene encoding B-cell CLL/lymphoma 2, the AA genotype was found to be significantly greater in the resistant smoker cohort compared to the lung cancer cohort (OR=0.69, P=0.05) consistent with a protective role. The A allele was also found to be significantly greater in the resistant smoker controls compared to the lung cancer cohort (OR=0.78, P=0.02), consistent with a protective role (see Table 9).
- In the analysis of the A/G at +3100 polymorphism in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3, the AG and GG genotypes were found to be significantly greater in the resistant smoker cohort compared to the lung cancer

cohort (OR=0.57, P=0.02) consistent with a protective role. The G allele was also found to be significantly greater in the resistant smoker controls compared to the lung cancer cohort (OR=0.54, P=0.01), consistent with a protective role (see Table 10).

- In the analysis of the -3714 G/T (rs6413429) polymorphism in the gene encoding Dopamine transporter 1, the TT and GT genotypes were found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.6, P=0.05), consistent with each having a susceptibility role (see Table 11).
- In the analysis of the A/G (rs1139417) polymorphism in the gene encoding Tumor necrosis factor receptor 1, the AA genotype was found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.5, P=0.02), consistent with a susceptibility role (see Table 12). The A allele was found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=1.3, P=0.04), also consistent with a susceptibility role.
- In the analysis of the C/Del (rs1799732) polymorphism in the gene encoding Dopamine receptor D2, the CDel and DelDel genotypes were found to be significantly greater in the resistant smoker cohort compared to the lung cancer cohort (OR=0.61, P=0.02) consistent with each having a protective role. The Del allele was also found to be significantly greater in the resistant smoker controls compared to the lung cancer cohort (OR=0.66, P=0.04), consistent with a protective role (see Table 13).
- In the analysis of the C/T (rs763110) polymorphism in the gene encoding Fas ligand, the TT genotype was found to be significantly greater in the resistant smoker cohort compared to the lung cancer cohort (OR=0.61, P=0.05) consistent with a protective role (see Table 14).
- In the analysis of the C/T (rs5743836) polymorphism in the gene encoding Toll-like receptor 9, the CC genotype was found to be significantly greater in the lung cancer cohort compared to the resistant smoker cohort (OR=3.1, P=0.02), consistent with a susceptibility role (see Table 15).

It is accepted that the disposition to lung cancer is the result of the combined effects of the individual's genetic makeup and other factors, including their lifetime exposure to various aero-pollutants including tobacco smoke. Similarly it is accepted that lung cancer encompasses several obstructive lung diseases and characterised by impaired expiratory flow rates (eg FEV1). The data herein suggest that several genes can contribute to the development of lung cancer. A number of genetic mutations working in combination either promoting or protecting the lungs from damage are likely to be involved in elevated resistance or susceptibility to lung cancer.

From the analyses of the individual polymorphisms, 6 protective genotype and 8 susceptibility genotypes were identified and analysed for their frequencies in the smoker cohort consisting of resistant smokers and those with lung cancer. A SNP score was determined for each subject by assigning a score of +1 for the presence of a suscepbility genotype and -1 for the presence of a protective genotype. These scores were added to derive a SNP score for each subject.

When the frequency of resistant smokers and smokers with lung cancer were compared according to the SNP score derived from a 5 SNP panel consisting of the SNPs identified in Table 16 herein, the chances of having lung cancer increased from 24%-31% to 43% in smokers with a SNP score of -1, 0, or 1+, respectively. When the frequencies of resistant smokers and smokers with lung cancer were compared according to a SNP score derived from an 11 SNP panel (11 SNP panel A), it was found that the chances of having lung cancer increased from 8% to 82% in smokers with a SNP score of 0 compared to those with a SNP score of 10+.

A minor increase in the linearity of the relationship between SNP score and frequency of lung cancer was observed when the SNP score was derived from a 16 SNP panel consisting of the SNPs identified in Table 18 herein. Again, the chances of having lung cancer increased from 8%, to 82% in smokers with a SNP score of less than or equal to 1 compared to those with a SNP score of 11+. The slight increase in linearity can be seen in a comparison of Figure 3 (11 SNP panel B) and Figure 4 (16 SNP panel).

When the frequency of resistant smokers and smokers with lung cancer were compared according to the SNP score derived from a 9 SNP panel consisting of the SNPs

identified in Table 21 herein, the chances of having lung cancer was increased 13-fold in smokers with a SNP score of 5+ compared to those with a SNP score of 1.

These findings indicate that the methods of the present invention may be predictive of lung cancer in an individual well before symptoms present.

Importantly, a substantial difference is seen in the distribution of lung cancer patients and control smokers relative to total SNP score when the SNP score is derived from the 16 SNP panel rather than from the 11 SNP panel B (see Figure 8 compared to Figure 5). In this analysis, the addition of the 5 SNPs discussed herein to the 11 SNP panel B results in only a small change to the linear relationship between lung cancer SNP score and frequency of lung cancer for the 11 SNP panel B compared to the 16 SNP panel (see Figures 3 and 6, respectively), and results in only a small difference to the receiver-operator curve analysis with sensitivity and specificity (see Figures 4 and 7, respectively). However, this addition results in a substantial difference to the utility of the SNP score, and identifies a larger subgroup of control smokers who are "low risk" defined by a cut off over the linear scale of SNP score (see Figure 8 compared to Figure 5). A similarly useful discrimination between lung cancer sufferors and resistant controls was observed when a distribution of SNP scores calculated using the 9 SNP panel was derived – see Figure 11. This has important implications in rationing or prioritising medical interventions.

These findings indicate that the methods of the present invention may be used to identify subsets of nominally at risk individuals (and particularly smokers) who are at low to average risk of lung cancer, and are thus not suitable for an intervention.

These findings therefore also present opportunities for therapeutic interventions and/or treatment regimens, as discussed herein. Briefly, such interventions or regimens can include the provision to the subject of motivation to implement a lifestyle change, or therapeutic methods directed at normalising aberrant gene expression or gene product function. In another example, a given susceptibility genotype is associated with increased expression of a gene relative to that observed with the protective genotype. A suitable therapy in subjects known to possess the susceptibility genotype is the administration of an agent capable of reducing expression of the gene, for example using antisense or RNAi methods. An alternative suitable therapy can be the administration to

such a subject of an inhibitor of the gene product. In still another example, a susceptibility genotype present in the promoter of a gene is associated with increased binding of a repressor protein and decreased transcription of the gene. A suitable therapy is the administration of an agent capable of decreasing the level of repressor and/or preventing binding of the repressor, thereby alleviating its downregulatory effect on transcription. An alternative therapy can include gene therapy, for example the introduction of at least one additional copy of the gene having a reduced affinity for repressor binding (for example, a gene copy having a protective genotype).

Suitable methods and agents for use in such therapy are well known in the art, and are discussed herein.

The identification of both susceptibility and protective polymorphisms as described herein also provides the opportunity to screen candidate compounds to assess their efficacy in methods of prophylactic and/or therapeutic treatment. Such screening methods involve identifying which of a range of candidate compounds have the ability to reverse or counteract a genotypic or phenotypic effect of a susceptibility polymorphism, or the ability to mimic or replicate a genotypic or phenotypic effect of a protective polymorphism.

Still further, methods for assessing the likely responsiveness of a subject to an available prophylactic or therapeutic approach are provided. Such methods have particular application where the available treatment approach involves restoring the physiologically active concentration of a product of an expressed gene from either an excess or deficit to be within a range which is normal for the age and sex of the subject. In such cases, the method comprises the detection of the presence or absence of a susceptibility polymorphism which when present either upregulates or downregulates expression of the gene such that a state of such excess or deficit is the outcome, with those subjects in which the polymorphism is present being likely responders to treatment.

EXAMPLE 5

This example describes the analysis of the relationship between SNP score and risk of the four most common types of lung cancer.

The lung cancer cohort described in Example 1 above is typical of that seen in other reported lung cancer studies. In particular, the distribution of the four leading

histological types of primary lung cancer is consistent with larger studies. Here, 45% of subjects had adenocarcinoma, 23% of subjects had squamous cell lung cancer, 16% of subjects had small cell lung cancer, and 13% of subjects had non-small cell lung cancer.

Reporters of epidemiological studies have suggested that smoking plays a greater role in small cell and squamous cell lung cancer and less in adenocarcinoma. The basis of this suggestion is not certain. The role of genetic factors in each histological type of lung cancer is unknown.

When the relationship between SNP score (determined as described above) and risk of lung cancer was examined according to histological type, the risk (Odds ratio) is higher for those with small-cell lung cancer and squamous cell lung cancer while least for those with adenocarcinoma (see Figure 12).

Without wishing to be bound by any theory, this suggests that the genetic effect measured by the SNP score may interact with smoking to confer risk of lung cancer. It also suggests, again without wishing to be bound by any theory, that the SNP score effect, although present, is least for lung cancer of the adenocarcinoma type (typically seen in light smokers or non-smokers). Collectively this example shows that the SNP score has utility in identifying those at risk of all types of lung cancer, and that an analysis of SNP score may be useful in determining not only whether or not an intervention in respect of a subject is warranted or desirable, but also the type of intervention. For example, on the basis of their SNP score, a subject may be considered suitable for more frequent screening (e.g., for rapidly-growing or aggressive lung cancer types).

EXAMPLE 6

This example presents the identification and analysis of a 19 SNP panel (11 susceptibility SNPs) and 8 protective SNPs as shown in Table 24 below useful for the methods of the present invention.

Statistical analysis

Patient characteristics in the lung cancer sufferers and controls were compared by unpaired t-tests for continuous variables and chi-square test or Fisher's exact test for discrete variables. Genotype and allele frequencies were checked for Hardy Weinberg

Equilibrium and population admixture by the Population structure analysis by genotyping 40 unrelated SNPs. Distortions in the genotype frequencies between lung cancer sufferers and controls were identified using 2 by 3 contingency tables. Where the homozygote genotype (recessive model) or combined homozygote and heterozygote genotypes (codominant model) for the minor allele were found in excess in the healthy smokers controls compared to the lung cancer cohort, these SNP genotypes were assigned as protective. Where the homozygote genotype (recessive model) or combined homozygote and heterozygote genotypes (codominant model) for the minor allele were found in excess in the lung cancer cohort compared to healthy smokers controls, these SNP genotypes were assigned as susceptible. The magnitude of the effect from each SNP was analysed using univariate analysis and multivariate analysis. Based on these analyses, SNPs were ranked according to their ability to discriminate between lung cancer sufferers and controls, and combined as described to generate the SNP score. Non-genetic risk factors including age and family history were also analysed, and combined with the SNP score to generate a composite SNP score.

Results

Table 24 below summarises the univariate analysis showing protective and susceptibility SNPs associated with lung cancer as set out herein. Odd's ratios (OR) and p values are for cancer patients compared to resistant smokers with normal lung function. Table 24 also summarises the multivariate analysis, where stepwise regression analysis was performed and chi squared values are presented for each polymorphism.

Table 24. Genotypes and results of regression analysis – 19 SNP panel

SNP (rs#)	Genotype	Lung cancer	Smoking controls	Call rate	Univariate OR	P value	Multivariate Point estimate	P value	Phenotype
CYP 2E1 (Rsa 1 C/T)	TT/TC CC	24 (6%) 379 (94%)	14 (3%) 463 (97%)	95%	2.1 (1.0-4.3)	0.03	0.63 (0.29-1.37)	0.24	susceptibility
Interleukin-18 (-133 G/C)	CC CG/GG	237 (54%) 201 (46%)	208 (45%) 250 (55%)	96%	1.4 (1.1-1.9)	0.009	0.65 (0.48-0.89)	0.007	susceptibility
Interleukin-8 (-251 A/T)	TT AT/AA	129 (31%) 284 (69%)	109 (23%) 367 (77%)	96%	1.5 (1.1-2.1)	0.005	0.72 (0.51-1.02)	0.06	susceptibility
Interleukin 1B (rs 16944)	GG AA/AG	215 (49%) 224 (51%)	212 (44%) 269 (56%)	99%	1.2 (0.9-1.6)	0.14	0.86 (0.63-1.17)	0.33	susceptibility
ITGA11 (rs2306022)	AA GA/GG	14 (3%) 422 (97%)	6 (1%) 470 (99%)	98%	2.6 (0.9-7.6)	0.04	0.28 (0.10-0.84)	0.02	susceptibility
N–acetylcysteine transferase 2 (rs 1799930)	GG AA/AG	239 (56%) 189 (44%)	222 (47%) 253 (53%)	97%	1.4 (1.1-1.9)	0.006	0.76 (0.56-1.03)	0.08	susceptibility
α1-antichymotrypsin (-15 A/G)	GG AG/AA	123 (28%) 312 (72%)	96 (20%) 383 (80%)	98%	1.6 (1.2-2.2)	0.004	0.69 (0.48-0.99)	0.05	susceptibility
Cerberus 1 (rs 10115703)	AA/AG GG	71 (16%) 363 (84%)	59 (12%) 413 (88%)	97%	1.4 (0.9-2.0)	0.10	0.71 0.45-1.10	0.10	susceptibility
DAT1 (rs6413429)	GT/TT GG	64 (15%) 367 (85%)	50 (10%) 431 (90%)	98%	1.5 (1.0-2.3)	0.04	0.68 (0.43-1.10)	0.06	susceptibility
TNFR1 (rs1139417)	AA AG/GG	148 (36%) 258 (64%)	142 (30%) 329 (70%)	96%	1.3 (1.0-1.8)	0.05	0.88 (0.64-1.23)	0.20	susceptibility
TLR9 (rs5743836)	CC CT/TT	12 (3%) 419 (97%)	6 (1%) 455 (99%)	96%	2.2 (0.8-6.6)	0.12	0.57 (0.19-1.75)	0.33	susceptibility
P73 (rs 2273953)	CC TC/TT	219 (52%) 206 (48%)	292 (62%) 178 (38%)	96%	0.65 (0.49-0.85)	0.001	1.50 (1.1-2.04)	0.01	protective
SOD3 (rs1799895)	GG/GC CC	4 (1%) 425 (99%)	15 (3%) 451 (97%)	96%	0.28 (0.10-0.90)	0.02	8.43 (1.65-43.22)	0.01	protective
ITGB3 (rs2317676)	GG/GA AA	44 (10%) 391 (90%)	77 (16%) 403 (84%)	98%	0.59 (0.39-0.89)	0.008	1.4 (1.17-3.00)	0.009	protective
DRD2 (rs 1799732)	CDel/Del.Del CC	70 (16%) 359 (84%)	107 (22%) 372 (78%)	98%	0.68 (0.48-0.96)	0.02	1.80 (1.20-2.70)	0.005	protective
BCL2	AA	103 (24%)	145 (31%)	97%	0.71	0.03	1.4	0.05	protective

(rs 2279115)	AC/CC	328 (76%)	330 69%)		(0.53-0.97)		(1.01-2.04)		
XPD	GG	60 (14%)	81 (18%)	96%	0.74	0.11	1.35	0.18	protective
(rs 13181)	GT/TT	376 (86%)	377 (82%)		(0.51-1.10)		(0.90-2.10)		
REV1	CC	128 (29%)	163 (34%)	98%	0.79	0.10	1.34	0.08	protective
(rs3087386)	TC/TT	310 (71%)	312 (66%)		(0.59-1.10)		(0.97-1.87)		
FasL	TT	53 (12%)	78 (16%)	98%	0.72	0.09	1.46	0.10	protective
(rs763110)	TC/CC	379 (88%)	403 (84%)		(0.49-1.10)		(0.93-2.29)		

Having defined the SNP panel SNP score, the genetic data was then analysed together with non-genetic data (specifically age, family history, history of COPD, and smoking exposure). Using multiple regression analysis, the magnitude of the effect of the 19 SNP panel in relation to age, family history and smoking exposure was determined. A score for age (+4 for those over 60 years old), history of COPD (+4 for those with self reported COPD/emphysema) and family history (+3 to those with a first degree relative with lung cancer) was then assigned. As smoking exposure was a recruitment criteria, only a small contribution from smoking exposure was observed and was thus omitted from the composite SNP score. This SNP score was compared with (a) the frequency of lung cancer, and (b) the floating absolute relative risk among the combined smoking cohort.

A linear relationship was observed across composite lung cancer SNP scores ≤1 to 8+ with lung cancer frequency spanning 15% to 85% (Figure 13a). The magnitude of the effect was examined using the floating absolute risk plotted on a log scale (equivalent to an Odds ratio, OR), which references the lowest frequency group as 1 (referent group, lung cancer score ≤1) and compares each lung cancer score relative to the referent group (Figure 13b). The OR ranged from 1 to 31.5 across the lung cancer scores when subjects are grouped roughly as quintiles. The OR was even higher for those with a SNP score of 9+.

In a receiver operator curve analysis, the area under the curve (AUC, or C statistic) for the 19 SNP panel, age, family history of lung cancer, and history of COPD were 0.68, 0.70, 0.55, and 0.62, respectively. The distribution of the SNP score between cases and controls for the total cohort (n=930) shows a bimodal distribution (Figure 14a). Corresponding sensitivities and specificities on receiver-operator-curve analyses are shown in Table 25 below.

Table 25. Sensitivity and specificity estimates – 19 SNP panel

Lung cancer score	Sensitivity	95% CI	Specificity	95 % CI
≥ 1	95%	94-98%	23%	19-27%
≥ 3	89%	86-92%	44%	39-48%
≥ 7	50%	45-55%	89%	86-91%
≥ 9	28%	23-32%	98%	96-99%

Discussion

The composite SNP score derived from the 19 SNP panel in combination with non-genetic risk factores as described in this example generated a C statistic of 0.78, and a cut off of ≥3 with a sensitivity of 89% and corresponding specificity of 44%.

The C statistic for the SNP score derived from the 19 SNP panel in the absence of non-genetic risk factors was 0.70, indicating its useful predictive and discriminatory utility and suitability for use in the methods described herein, both on its own or in combination with non-genetic risk factors.

EXAMPLE 7

Table 26 below presents representative examples of polymorphisms in linkage disequilibrium with the polymorphisms specified herein. Examples of such polymorphisms can be located using public databases, such as that available at www.hapmap.org. Specified polymorphisms are shown in parentheses. The rs numbers provided are identifiers unique to each polymorphism.

Table 26. Polymorphism reported to be in LD with polymorphisms specified herein.

CAMKK1

rs11078470	rs1029801	rs11650638	rs1029800	**(rs7214723)**
rs6502751	rs7214864	rs9914305	rs2058257	rs8065798
rs9904678	rs7223713	rs4790546	rs7208983	rs9898774
rs7223709	rs7212114	rs11651131	rs7221812	rs12150410
rs7221971	rs9897177			

ITGA11

rs11633421	rs6494734	rs898581	rs1239019	rs964691
rs898580	rs3736495	rs8025985	rs11072008	rs3736494
rs2306025	rs12050550	rs3736493	rs2306024	rs716379
rs8041788	rs2306023	rs1380883	rs8043152	**(rs2306022)**
rs3784342	rs16951774	rs898586	rs1380882	rs1996361
rs12442156	rs3784344	rs5016065	rs7176011	rs3784345
rs2899735	rs7176339	rs11632266	rs2414996	rs898585
rs1124577	rs2414997	rs4776395	rs7177709	rs7171871
rs7182350	rs3784346	rs1516869	rs12908869	rs7180218
rs16951777	rs7161871	rs748891	rs16951778	rs11632400
rs748892	rs3784335	rs898584	rs17266192	rs17318470
rs16951816	rs898579	rs3784336	rs7179347	rs12440936
rs3784337	rs7178537	rs748971	rs16951779	rs7179545
rs8029838	rs898588	rs2125998	rs16951835	rs7163918
rs10162690	rs8031003	rs2271723	rs9302249	rs4776396
rs898587	rs7162991	rs2306021	rs1237911	rs6494735
rs16951841	rs2271722	rs4777040	rs11072006	rs6494736
rs11630928	rs8030178	rs11635643	rs8029230	rs4777037

rs8028967	rs3736491	rs8028971	rs7176267	rs8029113
rs11072007	rs4777041	rs4777038	rs8029452	rs4777039
rs7169899	rs1533469	rs4777042	rs11858293	rs8035990
rs7179228	rs2414998	rs7179598	rs16951819	rs8042664
rs2169214	rs11852504	rs12912832	rs7167822	rs2125997
rs2292745	rs7181259	rs7168069	rs1975874	rs7169698
rs898583	rs6494733	rs16951820	rs970264	rs898582
rs1319223	rs1563894			

CER1

rs10810224	rs17289263	rs3761666	rs13286013	rs7022304
rs7870750	rs10961679	rs7022400	rs10121506	rs10961680
rs11999277	rs10118242	rs10961681	rs1494360	rs10118290
rs951273	rs1494359	rs16932212	rs2131883	rs1494358
rs11794846	rs2131882	rs1494357	rs10122395	rs12338263
rs3747532	rs10125285	rs12338303	**(rs10115703)**	rs1494351
rs12338380	rs10122490	rs1494350	rs2088042	rs7018937
rs10961683	rs12347640	rs12115314	rs10961684	rs10122817
rs7035643	rs11793334	rs12115487	rs10961682	rs7019731
rs11789968	rs7019387	rs10810225	rs3761665	rs3819004
rs10123442	rs7036635	rs10810226		

XRCC4

rs36059813	rs28360323	rs10514256	rs35770549	rs28360322
rs10514255	rs35770061	rs28360321	rs10514254	rs35704249
rs28360320	rs10434637	rs35694031	rs17567561	rs10078343
rs35618200	rs17205881	rs10070866	rs35262280	rs16900371
rs10067830	rs35219614	rs16900367	rs10061326	rs35211331
rs16900363	rs10061086	rs34801422	rs16900362	rs10057194
rs34697956	rs16900361	rs10057054	rs34646294	rs16900359
rs9293337	rs34626079	rs16900357	rs9293336	rs34544738
rs16900353	rs9293335	rs34326210	rs16900343	rs7736592
rs34164901	rs16900342	rs7735781	rs34052855	rs16900341
rs7734849	rs34006354	rs16900340	rs7729473	rs28746479
rs16900339	rs7729020	rs28746478	rs16900330	rs7728486
rs28746477	rs16900328	rs7727606	rs28746476	rs16900325
rs7716696	rs28360351	rs16900322	rs7714809	rs28360350
rs16900317	rs7711016	rs28360349	rs16900315	rs6869679
rs28360348	rs13359237	rs4987240	rs28360347	rs13358544
rs4703951	rs28360346	rs13357939	rs4703950	rs28360345
rs13187520	rs4703568	rs28360344	rs13167490	rs4438854
rs28360343	rs13167223	rs3910950	rs28360342	rs13163691
rs3836874	rs28360341	rs13163534	rs3836873	rs28360340
rs13155538	rs3777020	rs28360339	rs12697728	rs3777019
rs28360338	rs12520831	rs3777018	rs28360337	rs12186876
rs3777015	rs28360336	rs11960030	rs2891980	rs28360335
rs11960003	rs2386275	rs28360334	rs11959198	rs2084099
rs28360333	rs11958342	rs2035990	rs28360332	rs11955413
rs1805377	rs28360331	rs11954157	**(rs1056503)**	rs28360330
rs11953364	rs382069	rs28360329	rs11950724	rs301292
rs28360328	rs11749552	rs301291	rs28360327	rs10805813
rs177712	rs28360326	rs10805812	rs28360325	rs10642662
rs28360324	rs10514257			

BRCA2

rs36116910	rs28897730	rs11571808	rs11571701	rs11571598	rs7337784	rs773032

rs36114000	rs28897729	rs11571807	rs11571700	rs11571597	rs7337574	rs773031
rs36091054	rs28897728	rs11571806	rs11571699	rs11571596	rs7337016	rs773030
rs36073425	rs28897727	rs11571805	rs11571698	rs11571595	rs7336403	rs773029
rs36060526	rs28897726	rs11571804	rs11571697	rs11571594	rs7334543	rs773027
rs36018961	rs28897725	rs11571803	rs11571696	rs11571593	rs7332492	rs766173
rs35979864	rs28897724	rs11571802	rs11571695	rs11571592	rs7331638	rs721185
rs35930474	rs28897723	rs11571801	rs11571694	rs11571591	rs7330025	rs703224
rs35768834	rs28897722	rs11571800	rs11571693	rs11571590	rs7328654	rs703223
rs35697303	rs28897721	rs11571799	rs11571692	rs11571589	rs7328264	rs703213
rs35685866	rs28897720	rs11571798	rs11571691	rs11571588	rs7328101	rs693963
rs35628833	rs28897719	rs11571797	rs11571690	rs11571587	rs7327867	rs664345
rs35596121	rs28897718	rs11571796	rs11571689	rs11571586	rs7327813	rs651906
rs35573139	rs28897717	rs11571794	rs11571688	rs11571585	rs7327677	rs573014
rs35571300	rs28897716	rs11571792	rs11571687	rs11571584	rs7327471	rs559067
rs35563967	rs28897715	rs11571791	rs11571686	rs11571583	rs7324145	rs543304
rs35527903	rs28897714	rs11571790	rs11571685	rs11571582	rs7320990	rs542551
rs35497963	rs28897713	rs11571789	rs11571684	rs11571581	rs7318434	rs517118
rs35486082	rs28897712	rs11571788	rs11571683	rs11571580	rs6561306	rs472817
rs35477961	rs28897711	rs11571787	rs11571682	rs11571579	rs5802644	rs396579
rs35408951	rs28897710	rs11571786	rs11571681	rs11571578	rs4987117	rs206346
rs35382259	rs28897709	rs11571784	rs11571680	rs11571577	rs4987049	rs206344
rs35335654	rs28897708	rs11571782	rs11571679	rs11571576	rs4987048	rs206343
rs35324259	rs28897707	rs11571780	rs11571678	rs11571575	rs4987047	rs206342
rs35315530	rs28897706	rs11571779	rs11571676	rs11571574	rs4987046	rs206341
rs35188168	rs28897705	rs11571778	rs11571675	rs11552891	rs4986860	rs206340
rs35069894	rs28897704	rs11571777	rs11571674	rs11464335	rs4986859	rs206319
rs35029074	rs28897703	rs11571776	rs11571673	rs11460904	rs4986858	rs206318
rs35027705	rs28897702	rs11571775	rs11571672	rs11451886	rs4986856	rs206147
rs35005399	rs28897701	rs11571774	rs11571671	rs11426352	rs4942505	rs206146
rs34959007	rs28897700	rs11571773	rs11571670	rs11371521	rs4942499	rs206145
rs34943677	rs28657708	rs11571772	rs11571669	rs11327981	rs4942486	rs206123
rs34926095	rs28641896	rs11571771	rs11571668	rs11312202	rs4942485	rs206122
rs34925070	rs28569916	rs11571770	rs11571667	rs11306457	rs4942448	rs206121
rs34895626	rs28479757	rs11571769	rs11571666	rs11291838	rs4942443	rs206120
rs34891002	rs28473213	rs11571768	rs11571665	rs11147494	rs4942440	rs206099
rs34842101	rs17692629	rs11571767	rs11571664	rs11147493	rs4942439	rs206098
rs34841049	rs17636116	rs11571766	rs11571663	rs11147492	rs4942423	rs206097
rs34835575	rs17077554	rs11571765	rs11571662	rs11147491	rs4570704	rs206096
rs34816981	rs17077542	rs11571764	rs11571661	rs11147490	rs3837580	rs206095
rs34809891	rs17077541	rs11571763	rs11571660	rs11147489	rs3803282	rs206081
rs34770647	rs17077519	rs11571762	rs11571659	rs11147488	rs3783265	rs206080
rs34704662	rs13378910	rs11571761	rs11571658	rs11147486	rs3764792	rs206079
rs34692639	rs13378905	rs11571760	rs11571657	rs10870659	rs3764791	rs206078
rs34647461	rs13378423	rs11571759	rs11571656	rs10577567	rs3752451	rs206077
rs34578379	rs13378422	rs11571758	rs11571655	rs10492397	rs3752448	rs206076
rs34578349	rs12871316	rs11571757	rs11571654	rs10492396	rs3752447	rs206075
rs34575057	rs12871310	rs11571756	rs11571653	rs10492395	rs3752446	rs206074
rs34469166	rs12869544	rs11571754	rs11571652	rs9943890	rs3210648	rs206073
rs34437679	rs12869093	rs11571753	rs11571651	rs9943888	rs3092990	rs206072
rs34380010	rs12868315	rs11571752	rs11571650	rs9943876	rs3072043	rs206071

rs34370449	rs12862392	rs11571751	rs11571649	rs9634798	rs3072042	rs206070
rs34355306	rs12862064	rs11571750	rs11571648	rs9634797	rs3072040	rs206069
rs34351119	rs12862049	rs11571749	rs11571647	rs9634796	rs2761367	rs206068
rs34345002	rs12859126	rs11571748	rs11571646	rs9634672	rs2761363	rs206067
rs34309943	rs12859094	rs11571747	rs11571644	rs9595469	rs2320236	rs189979
rs34288419	rs12859079	rs11571746	rs11571643	rs9595468	rs2238163	rs176176
rs34273171	rs12858763	rs11571745	rs11571642	rs9595456	rs2238162	rs169548
rs34225677	rs12858735	rs11571744	rs11571641	rs9595402	rs2227944	rs169547
rs34184533	rs12858723	rs11571743	rs11571640	rs9595395	rs2227943	rs169546
rs34178365	rs12858361	rs11571742	rs11571639	rs9590958	rs2219594	rs144848
rs34175773	rs12854843	rs11571741	rs11571638	rs9590951	rs2126042	rs15869
rs34108667	rs12853807	rs11571740	rs11571637	rs9590940	rs2100785	
rs34102917	rs12561064	rs11571739	rs11571636	rs9590939	rs1963505	
rs34080444	rs12429216	rs11571738	rs11571635	rs9590938	rs1853521	
rs34075550	rs12017223	rs11571737	rs11571634	rs9567674	rs1853520	
rs34009686	rs11842816	rs11571736	rs11571633	rs9567670	rs1853519	
rs34001953	rs11841349	rs11571735	rs11571632	rs9567666	rs1801499	
rs28897762	rs11839855	rs11571734	rs11571631	rs9567654	rs1801439	
rs28897761	rs11620336	rs11571733	rs11571630	rs9567639	rs1801426	
rs28897760	rs11616673	rs11571732	rs11571629	rs9567623	rs1801406	
rs28897759	rs11571837	rs11571731	rs11571628	rs9567609	rs1799968	
rs28897758	rs11571836	rs11571730	rs11571627	rs9567605	rs1799956	
rs28897757	rs11571835	rs11571729	rs11571626	rs9567600	rs1799955	
rs28897756	rs11571834	rs11571728	rs11571625	rs9567582	rs1799954	
rs28897755	**(rs11571833)**	rs11571727	rs11571624	rs9567578	rs1799953	
rs28897754	rs11571832	rs11571726	rs11571623	rs9567576	rs1799952	
rs28897753	rs11571831	rs11571725	rs11571622	rs9551726	rs1799951	
rs28897752	rs11571830	rs11571723	rs11571621	rs9534367	rs1799944	
rs28897751	rs11571829	rs11571722	rs11571620	rs9534344	rs1475990	
rs28897750	rs11571828	rs11571721	rs11571619	rs9534342	rs1460817	
rs28897749	rs11571827	rs11571720	rs11571618	rs9534323	rs1460816	
rs28897748	rs11571826	rs11571719	rs11571617	rs9534318	rs1380946	
rs28897747	rs11571825	rs11571718	rs11571616	rs9534286	rs1207954	
rs28897746	rs11571824	rs11571717	rs11571615	rs9534275	rs1207953	
rs28897745	rs11571823	rs11571716	rs11571614	rs9534274	rs1207952	
rs28897744	rs11571822	rs11571715	rs11571613	rs9534270	rs1148321	
rs28897743	rs11571821	rs11571714	rs11571612	rs9534269	rs1148320	
rs28897742	rs11571820	rs11571713	rs11571611	rs9534268	rs1128611	
rs28897741	rs11571819	rs11571712	rs11571610	rs9534262	rs1128610	
rs28897740	rs11571818	rs11571711	rs11571609	rs9534259	rs1062947	
rs28897739	rs11571817	rs11571710	rs11571608	rs9534174	rs1062946	
rs28897738	rs11571816	rs11571709	rs11571607	rs9526165	rs1046984	
rs28897737	rs11571815	rs11571708	rs11571606	rs9526160	rs1045789	
rs28897736	rs11571814	rs11571707	rs11571605	rs9526148	rs1029304	
rs28897735	rs11571813	rs11571706	rs11571604	rs9526131	rs1012130	
rs28897734	rs11571812	rs11571705	rs11571603	rs7992196	rs1012129	
rs28897733	rs11571811	rs11571704	rs11571602	rs7982943	rs811637	
rs28897732	rs11571810	rs11571703	rs11571601	rs7981512	rs798652	
rs28897731	rs11571809	rs11571702	rs11571600	rs7491644	rs773033	

rs3765702	rs1122638	rs3819955	rs5031051	rs3753205	rs3765703
rs12062249	rs3765707	rs5031052	rs3765714	rs10910007	rs2368542
rs12059298	**(rs2273953)**	rs3765715	rs12028205	rs6665164	rs3765708
rs1801173	rs3765716	rs12057230	rs7554226	rs12025725	rs4648547
rs1122723	rs12024891	rs10910009	rs3765709	rs1122724	rs10910008
rs1885874	rs3765710	rs1122725	rs12121199	rs12403618	rs3765711
rs12095743	rs3765705	rs12403927	rs3765712	rs1122639	rs3765706
rs10910010	rs3765713				

CYP3A43

rs2738258	rs1041966	rs2023548	rs688926	rs13236744	rs2687110
rs12721632	rs493380	rs687134	rs13444455	rs17294659	rs12721636
rs1554511	rs4236544	rs10241225	rs12670850	rs12721633	rs667660
rs4646472	rs10225908	rs6970689	rs12721637	rs620020	rs671673
rs2897018	rs11768200	rs1800713	rs17161937	rs660629	rs528144
rs6465753	rs2740574	rs1403195	rs533486	rs6975773	rs4986914
rs473706	rs501275	rs2263430	rs2740573	rs10255255	rs641815
rs6415332	rs11773597	rs585071	rs641761	rs2263431	rs1851426
rs2023165	rs472667	rs2687106	rs12114000	rs1036374	rs579424
rs10270146	rs2740572	rs651430	rs13234698	rs12721619	rs4301384
rs653245	rs549061	rs12721625	rs2740571	rs7807561	rs545400
rs3800957	rs2687103	rs800675	rs4646474	rs7801671	rs7811022
rs558112	rs487813	rs16867648	rs7811025	rs558002	rs1077078
rs2687105	rs2740570	**(C74 delA)**	rs679320	rs2687104	rs4729550
rs13236405	rs678040	rs10264769	rs3958412	rs800674	rs568859
rs2405184	rs1320390	rs800673	rs800667	rs2740575	rs1320389
rs523407	rs6960775	rs2253498	rs2687102	rs642761	rs565079
rs2253493	rs2687101	rs496000	rs675644	rs17161904	rs2740569
rs800672	rs648515	rs4602816	rs2687100	rs4268042	rs800666
rs3991692	rs2737418	rs892753	rs646563	rs6957392	rs760368
rs12671336	rs694939	rs12721634	rs2017121	rs2164226	rs800664

BCL2

rs12458289	rs1473418	rs2551407	rs2849372	rs949037	**(rs2279115)**
rs10460159	rs2615196	rs2849380	rs2551400	rs2849383	rs2849371
rs1462128	rs2551401	rs11663788	rs8098151	rs1462129	rs7243985
rs2849367	rs3786327	rs2051424	rs2551402	rs6810	rs2850757
rs2051423	rs8099294	rs2615201	rs2850756	rs1944422	rs2051422
rs736223	rs2551410	rs2085958	rs1944423	rs898891	rs1893805
rs12455492	rs11659773	rs2850767	rs2032343	rs7239542	rs2551403
rs2850768	rs11152379	rs1541295	rs2551404	rs2551408	rs1541296
rs4987712	rs11660715	rs2236719	rs1809319	rs1893806	rs17687494
rs2849376	rs2003149	rs4987711	rs8094041	rs2849375	rs439670
rs4987710	rs2551405	rs12327344	rs489520	rs1800477	rs2850764
rs2255302	rs3744939	rs1801018	rs10460158	rs12953721	rs428356
rs4987707	rs2551406	rs8083276	rs383770	rs4987706	rs698708
rs7231949					

ITGB3

rs884696	rs8074348	rs951351	rs13380810	rs9303533	rs7219925
rs16941796	rs7218632	rs7223956	rs7214993	rs10514919	rs2015729
rs11651736	rs7220606	rs8075031	rs11870334	rs16941801	rs3785870
rs12162128	rs1051452	rs11870365	rs7217214	rs16941829	rs7224753
rs16941864	rs16941776	rs16941802	rs2292864	rs7221196	**(rs2317676)**
rs16941780	rs7212751	rs12940355	rs12603582	rs3809865	rs11657517
rs11649785	rs12951133	rs12603725	rs9916007	rs11658221	rs1000232

rs12942670	rs10221263	rs8068200	rs8073827	rs2292866	rs12943780
rs12602240	rs9894860	rs12941431	rs2292867	rs12942968	rs11870252
rs12600603	rs11651758	rs16941807	rs12951679	rs11867253	rs9893410
rs12453200	rs11079770	rs12942997	rs11867192	rs7209109	rs11651904
rs8073229	rs12943005	rs3785873	rs7225700	rs11656865	rs11868912
rs13306482	rs9747605	rs4968313	rs7503748	rs1878067	rs1969268
rs9906248	rs2317677	rs11657963	rs988684	rs1533409	rs3760372
rs11658426	rs984370	rs5918	rs15908	rs13306488	rs11650072
rs8080254	rs5920	rs12709459	rs13306489	rs11079772	rs8074094
rs13306485	rs13306483	rs1969267	rs12600865	rs8066295	rs12709458
rs2292863	rs8081202	rs4968314	rs11870620	rs13306486	rs5921
rs16941855	rs7218813	rs11079769	rs5917	rs4642	rs9914944
rs9899121	rs4486970	rs2292699	rs13306487	rs11869835	rs10853089
rs3851806	rs2292700	rs4634	rs12950632	rs6504833	rs16941793
rs8064853	rs7214096	rs3744452	rs7209700	rs9912177	rs7217710
rs3744453	rs4968312	rs13306484	rs7214468	rs11868344	rs8078614
rs12451759	rs11656809	rs11870781	rs3851807	rs5919	rs999323
rs16941861	rs12940207	rs13306476	rs3785872	rs3809863	rs8064871
rs13306477	rs12949936	rs11655943	rs8069732	rs13306478	rs11079771
rs16941863	rs11868894	rs2292865	rs11650022	rs9674670	rs8077753
rs13306480	rs7211018	rs9284377			

DAT1

rs2937639	rs2447848	rs11564751	rs2617592	rs1354139	rs2550961
rs2447847	rs4029364	rs2617591	rs2652505	rs2550962	rs2516289
rs4029363	rs2652508	rs11747778	rs11564757	rs2617601	rs2937637
rs2617590	rs2078247	rs2550963	rs2735855	rs2937636	rs2617589
rs2617584	rs2937638	rs3776485	rs7733388	rs2471921	rs2550939
rs1316830	rs2550967	rs11564750	rs2617588	rs2113330	rs2735859
rs2617600	rs2550956	rs2550949	rs2975224	rs2735858	rs2735854
rs11564749	rs2652506	rs2617583	rs2859604	rs2735935	rs2652510
rs10070282	rs12652860	rs2550965	rs2735934	rs2937635	rs10079467
rs12654851	rs2516291	rs2617599	rs2975225	rs2550947	rs6879432
rs2447850	rs2975227	rs3756450	rs2550946	rs9312868	rs2516290
rs2975226	rs2617595	rs2550945	rs1478435	rs2550966	rs2652513
rs2652509	rs2550944	rs1478434	rs2254255	rs2652512	rs2617594
rs250694	rs10063727	rs2963238	rs456323	rs2550955	rs2550943
rs4639276	rs2617603	rs2617598	rs2550954	rs565988	rs2911493
rs2735853	rs2550953	rs565985	rs2471926	rs2735852	rs2550952
rs250693	rs2447849	rs2617597	rs2550951	rs2550941	rs2617602
rs2652511	rs2550950	rs250692	rs11564752	rs2617596	rs2963236
rs193941	rs2735857	rs2550957	rs2617593	rs565123	rs2735856
(rs6413429)	rs193942	rs2550940			

TNFR1

rs1800693	rs4149636	rs4149581	rs4149625	rs4149618	rs4149642
rs2363888	rs4149580	rs4149571	rs4149617	rs4149641	rs4149635
rs4149579	rs4149624	rs12300705	rs4149587	rs877249	rs4149578
rs4149623	rs11064143	rs4149640	rs4149583	rs4149577	rs4149622
rs7297961	rs12832171	rs4149634	rs4149627	rs4441073	rs11064145
rs11525582	rs2284344	rs4149626	rs767455	rs11608320	rs4149586
rs4149633	rs10774425	**(rs1139417)**	rs11608322	rs4149639	rs4149632
rs11836766	rs2234649	rs2228576	rs12317730	rs4149631	rs4149576
rs4149621	rs1800692	rs4149630	rs4149575	rs4149570	rs4149638
rs887477	rs4149574	rs16932532	rs4149585	rs4149629	rs4149573
rs4149620	rs4149584	rs4149582	rs4149572	rs4149619	rs4149637

rs1860545	rs11615387	rs4149569			

DRD2

rs17529477	rs4337071	rs5013062	rs12099213	rs12361261	rs17601612
rs4630328	rs12364283	rs7934294	rs4466875	rs11214610	rs11214612
rs11214617	rs12574578	rs7131411	rs4245146	rs11214613	rs7110440
rs11301285	rs4429089	rs4245147	rs11214614	rs12808668	rs17602285
rs4245153	rs4936270	rs4350392	rs12785817	rs11214627	rs4245154
rs4936271	rs11601054	rs4483623	rs10891564	rs11214636	rs4936272
rs7930567	rs10891556	rs6589379	rs4938026	rs4274224	rs12225915
rs4424703	rs4938023	rs2002229	rs4245148	rs10891553	rs11214618
rs4503578	rs2002228	rs4460839	rs12421616	rs12800185	rs4254099
rs12280961	rs12576411	rs4245149	rs7121986	rs7111031	rs12291458
rs7109897	rs7102650	rs6589377	rs4938024	rs2514218	rs17115596
rs7939472	rs11214619	rs6589381	rs2511514	rs12805897	rs11214615
rs4482060	rs6589382	rs11214642	rs4581480	rs4938019	rs10891562
rs4245151	rs7122454	rs12417718	rs4421776	rs7949802	rs7948028
rs11214616	rs11214623	rs11214633	rs10891550	rs10891554	rs4611239
rs11214634	rs7131056	rs4533070	rs4245150	rs12275979	rs11214611
rs10789943	rs17602038	rs4938025	rs4936274	rs3935565	rs4938021
rs7928940	rs12291794	rs10789944	rs4936275	rs4479021	rs4648317
rs7116768	rs4936276	rs12418281	rs7109615	rs12281924	rs1986665
rs7479729	rs10891551	**(rs1799732)**	rs12363546	rs7106947	rs4322431
rs1799978	rs12576181	rs4447205	rs7117915	rs5013059	rs10736466
rs1984739	rs10891552	rs5013060	rs4938022	rs4245152	rs7118174
rs5013061	rs12292637	rs4534613			

FasL

rs1894626	rs2859235	rs2639617	rs3021335	rs16844867	rs2639622
rs10912122	rs2859239	rs2933547	rs9787393	rs2639621	rs2639618
rs2639616	rs2859244	rs9787248	rs2859228	rs2859236	rs2131373
rs2859245	rs12080307	rs2859229	rs10798130	rs12130118	rs10753023
rs749154	rs1492899	rs16844856	rs2859240	rs10798133	rs749155
rs12082528	rs2021839	rs2639615	rs2859246	**(rs763110)**	rs4304626
rs2021838	rs2859241	rs2859247	rs2859233	rs2859237	rs2859242
rs2639614	rs2859234	rs2859238	rs2859243	rs2859248	

TLR9

rs353551	rs352168	rs17052020	rs5743847	rs5743838	rs352158
rs352167	rs10212560	rs445676	rs5743837	rs614288	rs352166
rs12629425	rs5743846	**(rs5743836)**	rs6767333	rs13064414	rs9816466
rs5743845	rs187084	rs9828488	rs352165	rs7614535	rs352140
rs352173	rs11712164	rs352162	rs5743844	rs352172	rs17052017
rs5743850	rs5743843	rs3774412	rs9813448	rs6809796	rs5743842
rs709315	rs9813468	rs13080616	rs352139	rs352171	rs352164
rs13060808	rs5743841	rs352170	rs352163	rs5743849	rs5743840
rs352169	rs164640	rs5743848	rs5743839		

INDUSTRIAL APPLICATION

The present invention is directed to methods for assessing a subject's risk of developing lung cancer. The methods comprise the analysis of polymorphisms herein shown to be associated with increased or decreased risk of developing lung cancer, or

the analysis of results obtained from such an analysis. The use of polymorphisms herein shown to be associated with increased or decreased risk of developing lung cancer in the assessment of a subject's risk are also provided, as are nucleotide probes and primers, kits, and microarrays suitable for such assessment. Methods of treating subjects having the polymorphisms herein described are also provided. Methods for screening for compounds able to modulate the expression of genes associated with the polymorphisms herein described are also provided.

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All patents, publications, scientific articles, and other documents and materials referenced or mentioned herein are indicative of the levels of skill of those skilled in the art to which the invention pertains, and each such referenced document and material is hereby incorporated by reference to the same extent as if it had been incorporated by reference in its entirety individually or set forth herein in its entirety. Applicants reserve the right to physically incorporate into this specification any and all materials

and information from any such patents, publications, scientific articles, web sites, electronically available information, and other referenced materials or documents.

The specific methods and compositions described herein are representative of various embodiments or preferred embodiments and are exemplary only and not intended as limitations on the scope of the invention. Other objects, aspects, examples and embodiments will occur to those skilled in the art upon consideration of this specification, and are encompassed within the spirit of the invention as defined by the scope of the claims. It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. The invention illustratively described herein suitably can be practiced in the absence of any element or elements, or limitation or limitations, which is not specifically disclosed herein as essential. Thus, for example, in each instance herein, in embodiments or examples of the present invention, any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms in the specification, thus indicating additional examples, having different scope, of various alternative embodiments of the invention. Also, the terms "comprising", "including", containing", etc. are to be read expansively and without limitation. The methods and processes illustratively described herein suitably may be practiced in differing orders of steps, and that they are not necessarily restricted to the orders of steps indicated herein or in the claims. It is also that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality (for example, a culture or population) of such host cells, and so forth. Under no circumstances may the patent be interpreted to be limited to the specific examples or embodiments or methods specifically disclosed herein. Under no circumstances may the patent be interpreted to be limited by any statement made by any Examiner or any other official or employee of the Patent and Trademark Office unless such statement is specifically and without qualification or reservation expressly adopted in a responsive writing by Applicants.

The terms and expressions that have been employed are used as terms of description and not of limitation, and there is no intent in the use of such terms and expressions to exclude any equivalent of the features shown and described or portions

thereof, but it is recognized that various modifications are possible within the scope of the invention as claimed. Thus, it will be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

CLAIMS:

1. A method of determining a subject's risk of developing lung cancer comprising analysing a sample from said subject for the presence or absence of one or more polymorphisms selected from the group consisting of:
   Ser307Ser G/T (rs1056503) in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene,
   A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43;
   A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2;
   A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3;
   -3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1;
   A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1;
   C/Del (rs1799732) in the gene encoding Dopamine receptor D2;
   C/T (rs763110) in the gene encoding Fas ligand;
   C/T (rs5743836) in the gene encoding Toll-like receptor 9; or
   one or more polymorphisms in linkage disequilibrium with one or more of said polymorphisms, wherein the presence or absence of said polymorphism is indicative of the subject's risk of developing lung cancer.
2. A method according to claim 1 wherein the lung cancer is selected from the group consisting of non–small cell lung cancer including adenocarcinoma and squamous cell carcinoma, small cell lung cancer, carcinoid tumor, lymphoma, or metastatic cancer.
3. A method according to claim 1 wherein the method comprises analysing said sample for the presence or absence of one or more further polymorphisms selected from the group consisting of:
   R19W A/G (rs10115703) in the gene encoding Cerberus 1 (Cer 1);
   K3326X A/T (rs11571833) in the breast cancer 2 early onset gene (BRCA2);
   V433M A/G (rs2306022) in the gene encoding Integrin alpha-11;
   E375G T/C (rs7214723) in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);
   -81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73 (P73);

or one or more polymorphisms which are in linkage disequilibrium with one or more of these polymorphisms.

4. A method according to any one of claims 1 to 3 wherein the presence of one or more of the polymorphisms selected from the group consisting of:
the E375G T/C TT genotype in the gene encoding CAMKK1;
the -81 C/T (rs 2273953) CC genotype the gene encoding P73;
the A/C (rs2279115) AA genotype in the gene encoding BCL2;
the +3100 A/G (rs2317676) AG or GG genotype in the gene encoding ITGB3;
the C/Del (rs1799732) CDel or DelDel genotype in the gene encoding DRD2; or
the C/T (rs763110) TT genotype in the gene encoding Fas ligand;
is indicative of a reduced risk of developing lung cancer.

5. A method according to any one of claims 1 to 4 wherein the presence of one or more of the polymorphisms selected from the group consisting of:
the Ser307Ser G/T GG or GT genotype in the gene encoding XRCC4;
the R19W A/G AA or GG genotype in the gene encoding Cer 1;
the Ser307Ser G/T GG or GT genotype in the XRCC4 gene;
the K3326X A/T AT or TT genotype in the BRCA2 gene;
the V433M A/G AA genotype in the gene encoding Integrin alpha-11;
the A/T c74delA AT or TT genotype in the gene encoding CYP3A43;
the -3714 G/T (rs6413429) GT or TT genotype in the gene encoding DAT1;
the A/G (rs1139417) AA genotype in the gene encoding TNFR1; or
the C/T (rs5743836) CC genotype in the gene encoding TLR9;
is indicative of an increased risk of developing lung cancer.

6. A method according to any one of claims 1 to 3 wherein the method comprises analysing each of the polymorphisms of the group consisting of:
-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;
-251 A/T (rs4073) in the gene encoding Interleukin-8;
Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;
Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;
-3714 G/T (rs6413429) in the gene encoding DAT1;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

7. A method according to any one of claims 1 to 3 wherein the method comprises analysing each of the polymorphisms of the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

8. A method according to any one of claims 1 to 3 wherein the method comprises analysing each of the polymorphisms of the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

V433M A/G (rs2306022) in the gene encoding ITGA11;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

9. A method according to any one of claims 1 to 3 wherein the method comprises analysing each of the polymorphisms of the group consisting of:
Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;
-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;
-251 A/T (rs4073) in the gene encoding Interleukin-8;
-511 A/G (rs 16944) in the gene encoding Interleukin 1B;
V433M A/G (rs2306022) in the gene encoding ITGA11;
Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;
Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;
R19W A/G (rs 10115703) in the gene encoding Cerberus 1;
-3714 G/T (rs6413429) in the gene encoding DAT1;
A/G (rs1139417) in the gene encoding TNFR1;
C/T (rs5743836) in the gene encoding TLR9;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;
Arg 312 Gln (rs1799895) in the gene encoding SOD3;
A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;
C/Del (rs1799732) in the gene encoding DRD2;
A/C (rs2279115) in the gene encoding BCL2;
-751 G/T (rs 13181) in the promoter of the gene encoding XPD;
Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;
C/T (rs763110) in the gene encoding FasL;
or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

10. A method of assessing a subject's risk of developing lung cancer said method comprising the steps:
(i) determining the presence or absence of at least one protective polymorphism associated with a reduced risk of developing lung cancer; and

(ii) in the absence of at least one protective polymorphisms, determining the presence or absence of at least one susceptibility polymorphism associated with an increased risk of developing lung cancer;

wherein the presence of one or more of said protective polymorphisms is indicative of a reduced risk of developing lung cancer, and the absence of at least one protective polymorphism in combination with the presence of at least one susceptibility polymorphism is indicative of an increased risk of developing lung cancer.

11. A method according to claim 10 wherein said at least one protective polymorphism is selected from the group consisting of:
the E375G T/C TT genotype in the gene encoding CAMKK1;
the -81 C/T (rs 2273953) CC genotype the gene encoding P73;
the A/C (rs2279115) AA genotype in the gene encoding BCL2;
the +3100 A/G (rs2317676) AG or GG genotype in the gene encoding ITGB3;
the C/Del (rs1799732) CDel or DelDel genotype in the gene encoding DRD2; or
the C/T (rs763110) TT genotype in the gene encoding Fas ligand.

12. A method according to claim 10 or 11 wherein said at least one susceptibility polymorphism is a genotype selected from the group consisting of:
the Ser307Ser G/T GG or GT genotype in the gene encoding XRCC4;
the R19W A/G AA or GG genotype in the gene encoding Cer 1;
the Ser307Ser G/T GG or GT genotype in the XRCC4 gene;
the K3326X A/T AT or TT genotype in the BRCA2 gene;
the V433M A/G AA genotype in the gene encoding Integrin alpha-11;
the A/T c74delA AT or TT genotype in the gene encoding CYP3A43;
the -3714 G/T (rs6413429) GT or TT genotype in the gene encoding DAT1;
the A/G (rs1139417) AA genotype in the gene encoding TNFR1; or
the C/T (rs5743836) CC genotype in the gene encoding TLR9.

13. A method according to any one of claims 10 to 12 wherein the presence of two or more protective polymorphims irrespective of the presence of one or more susceptibility polymorphisms is indicative of reduced risk of developing lung cancer.

14. A method according to any one of claims 10 to 12 wherein in the absence of a protective polymorphism the presence of one or more susceptibility polymorphisms is indicative of an increased risk of developing lung cancer.
15. A method according to any one of claims 10 to 12 wherein the presence of two or more susceptibility polymorphisms is indicative of an increased risk of developing lung cancer.
16. A method of determining a subject's risk of developing lung cancer, comprising analysing a sample from said subject for the presence of two or more polymorphisms selected from the group consisting of:
the Ser307Ser G/T polymorphism in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4);
R19W A/G in the gene encoding Cerberus 1 (Cer 1);
K3326X A/T in the breast cancer 2 early onset gene (BRCA2);
V433M A/G in the gene encoding Integrin alpha-11;
E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);
A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43;
A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2;
A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3;
-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1;
A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1;
C/Del (rs1799732) in the gene encoding Dopamine receptor D2;
C/T (rs763110) in the gene encoding Fas ligand;
C/T (rs5743836) in the gene encoding Toll-like receptor 9;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73 (P73);
or one or more polymorphisms which are in linkage disequilibrium with any one or more of these polymorphisms.
17. A method according to any one of claims 1 to 16 wherein said method comprises the analysis of one or more epidemiological risk factors.
18. A method of determining a subject's risk of developing lung cancer, said method comprising the steps:

(i) obtaining the result of one or more genetic tests of a sample from said subject; and (ii) analysing the result for the presence or absence of one or more polymorphisms selected from the group consisting of:

Ser307Ser G/T in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4);

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43;

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3;

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1;

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1;

C/Del (rs1799732) in the gene encoding Dopamine receptor D2;

C/T (rs763110) in the gene encoding Fas ligand;

C/T (rs5743836) in the gene encoding Toll-like receptor 9;

or one or more polymorphisms which are in linkage disequilibrium with one or more of these polymorphisms;

wherein a result indicating the presence or absence of one or more of said polymorphisms is indicative of the subject's risk of developing lung cancer.

19. A method according to claim 18 wherein a result indicating the presence of one or more of

the Ser307Ser G/T TT genotype in the gene encoding XRCC4;

the -81 C/T (rs 2273953) CC genotype the gene encoding P73;

the A/C (rs2279115) AA genotype in the gene encoding BCL2;

the +3100 A/G (rs2317676) AG or GG genotype in the gene encoding ITGB3;

the C/Del (rs1799732) CDel or DelDel genotype in the gene encoding DRD2; or

the C/T (rs763110) TT genotype in the gene encoding Fas ligand;

is indicative of a reduced risk of developing lung cancer.

20. A method according to claim 18 wherein a result indicating the presence of one or more of:

the Ser307Ser G/T GG or GT genotype in the gene encoding XRCC4;

the A/T c74delA AT or TT genotype in the gene encoding CYP3A43;

the -3714 G/T (rs6413429) GT or TT genotype in the gene encoding DAT1;

the A/G (rs1139417) AA genotype in the gene encoding TNFR1; or

the C/T (rs5743836) CC genotype in the gene encoding TLR9;

is indicative of an increased risk of developing lung cancer.

21. The method according to any one of claims 18 to 20 additionally comprising analysing the result for the presence or absence of one or more further polymorphisms selected from the group consisting of:

R19W A/G in the gene encoding Cerberus 1 (Cer 1);

K3326X A/T in the breast cancer 2 early onset gene (BRCA2);

V433M A/G in the gene encoding Integrin alpha-11;

E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73 (P73);

or one or more polymorphisms which are in linkage disequilibrium with any or more of these polymorphisms.

22. A method according to any one of claims 18 to 21 comprising analysing the result for the presence or absence of each of the polymorphisms selected from the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

23. A method according to any one of claims 18 to 21 comprising analysing the result for the presence or absence of each of the polymorphisms selected from the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;
Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;
Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;
-3714 G/T (rs6413429) in the gene encoding DAT1;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;
Arg 312 Gln (rs1799895) in the gene encoding SOD3;
A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;
C/Del (rs1799732) in the gene encoding DRD2;
A/C (rs2279115) in the gene encoding BCL2;
or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

24. A method according to any one of claims 18 to 21 comprising analysing the result for the presence or absence of each of the polymorphisms selected from the group consisting of:
-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;
-251 A/T (rs4073) in the gene encoding Interleukin-8;
Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;
Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;
-3714 G/T (rs6413429) in the gene encoding DAT1;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;
Arg 312 Gln (rs1799895) in the gene encoding SOD3;
A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;
C/Del (rs1799732) in the gene encoding DRD2;
A/C (rs2279115) in the gene encoding BCL2;
V433M A/G (rs2306022) in the gene encoding ITGA11;
or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

25. A method according to any one of claims 18 to 21 comprising analysing the result for the presence or absence of each of the polymorphisms selected from the group consisting of:
Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

-511 A/G (rs 16944) in the gene encoding Interleukin 1B;

V433M A/G (rs2306022) in the gene encoding ITGA11;

Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

R19W A/G (rs 10115703) in the gene encoding Cerberus 1;

-3714 G/T (rs6413429) in the gene encoding DAT1;

A/G (rs1139417) in the gene encoding TNFR1;

C/T (rs5743836) in the gene encoding TLR9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

-751 G/T (rs 13181) in the promoter of the gene encoding XPD;

Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;

C/T (rs763110) in the gene encoding FasL;

26. or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.One or more nucleotide probes and/or primers for use in the method of any one of claims 1 to 21 wherein the one or more nucleotide probes and/or primers span, or are able to be used to span, the polymorphic regions of the genes in which the polymorphism to be analysed is present.
27. One or more nucleotide probes and/or primers as claimed in claim 26 comprising the sequence of any one of SEQ.ID.NO.1 to SEQ.ID.NO. 72.
28. A nucleic acid microarray which comprises a substrate presenting nucleic acid sequences capable of hybridizing to nucleic acid sequences which encode one or more of the polymorphisms selected from the group defined in claim 1 or sequences complimentary thereto.
29. The use of one or more polymorphisms selected from the group consisting of:

Ser307Ser G/T polymorphism in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4);

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43;

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3;

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1;

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1;

C/Del (rs1799732) in the gene encoding Dopamine receptor D2;

C/T (rs763110) in the gene encoding Fas ligand;

C/T (rs5743836) in the gene encoding Toll-like receptor 9; or one or more polymorphisms in linkage disequilibrium with one or more of these polymorphisms in the assessment of a subject's risk of developing lung cancer.

30. The use according to claim 29, wherein said use is in conjunction with the use of at least one further polymorphism selected from the group consisting of:

R19W A/G in the gene encoding Cerberus 1 (Cer 1);

K3326X A/T in the breast cancer 2 early onset gene (BRCA2);

V433M A/G in the gene encoding Integrin alpha-11;

E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73 (P73);

or one or more polymorphisms in linkage disequilibrium with any one of said polymorphisms.

31. The use according to claim 29 or 30 wherein said use is of each of the polymorpyisms selected from the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;
C/Del (rs1799732) in the gene encoding DRD2;
or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

32. The use according to claim 29 or 30 wherein said use is of each of the polymorpyisms selected from the group consisting of:
-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;
-251 A/T (rs4073) in the gene encoding Interleukin-8;
Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;
Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;
-3714 G/T (rs6413429) in the gene encoding DAT1;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;
Arg 312 Gln (rs1799895) in the gene encoding SOD3;
A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;
C/Del (rs1799732) in the gene encoding DRD2;
A/C (rs2279115) in the gene encoding BCL2;
or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

33. The use according to claim 29 or 30 wherein said use is of each of the polymorpyisms selected from the group consisting of:
-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;
-251 A/T (rs4073) in the gene encoding Interleukin-8;
Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;
Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;
-3714 G/T (rs6413429) in the gene encoding DAT1;
-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;
Arg 312 Gln (rs1799895) in the gene encoding SOD3;
A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;
C/Del (rs1799732) in the gene encoding DRD2;
A/C (rs2279115) in the gene encoding BCL2;
V433M A/G (rs2306022) in the gene encoding ITGA11;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

34. The use according to claim 29 or 30 wherein said use is of each of the polymorpyisms selected from the group consisting of:

Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

-511 A/G (rs 16944) in the gene encoding Interleukin 1B;

V433M A/G (rs2306022) in the gene encoding ITGA11;

Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

R19W A/G (rs 10115703) in the gene encoding Cerberus 1;

-3714 G/T (rs6413429) in the gene encoding DAT1;

A/G (rs1139417) in the gene encoding TNFR1;

C/T (rs5743836) in the gene encoding TLR9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

-751 G/T (rs 13181) in the promoter of the gene encoding XPD;

Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;

C/T (rs763110) in the gene encoding FasL;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

35. A method of treating a subject having an increased risk of developing lung cancer comprising the step of replicating, genotypically or phenotypically, the presence and/or functional effect of a protective polymorphism selected from the group defined in claim 11 in said subject.

36. A method of treating a subject having an increased risk of developing lung cancer, said subject having a detectable susceptibility polymorphism selected

from the group defined in claim 12 which either upregulates or downregulates expression of a gene such that the physiologically active concentration of the expressed gene product is outside a range which is normal for the age and sex of the subject, said method comprising the step of restoring the physiologically active concentration of said product of gene expression to be within a range which is normal for the age and sex of the subject.

37. A method of determining a subject's risk of developing lung cancer , comprising the analysis of two or more polymorphisms selected from the group consisting of:

Ser307Ser G/T in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4)

R19W A/G in the gene encoding Cerberus 1 (Cer 1);

K3326X A/T in the breast cancer 2 early onset gene (BRCA2);

V433M A/G in the gene encoding Integrin alpha-11; or

E375G T/C in the gene encoding Calcium/calmodulin-dependent protein kinase kinase 1 (CAMKK1);

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43;

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3;

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1;

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1;

C/Del (rs1799732) in the gene encoding Dopamine receptor D2;

C/T (rs763110) in the gene encoding Fas ligand;

C/T (rs5743836) in the gene encoding Toll-like receptor 9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding Tumor protein P73; or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

38. An antibody microarray for use in the methods as claimed in any one of claims 1 to 21 or claim 37, which microarray comprises a substrate presenting antibodies capable of binding to a product of expression of a gene the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism as defined in any one of claims 1 to 5.

39. A method for screening for compounds that modulate the expression and/or activity of a gene, the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism selected from the group defined in any one of claims 1 to 5, said method comprising the steps of:

contacting a candidate compound with a cell comprising a susceptibility or protective polymorphism which has been determined to be associated with the upregulation or downregulation of expression of a gene; and

measuring the expression of said gene following contact with said candidate compound,

wherein a change in the level of expression after the contacting step as compared to before the contacting step is indicative of the ability of the compound to modulate the expression and/or activity of said gene.

40. A method according to claim 39 wherein said cell is a human lung cell which has been pre-screened to confirm the presence of said polymorphism.

41. A method according to claim 39 or 40 wherein said cell comprises a susceptibility polymorphism associated with upregulation of expression of said gene and said screening is for candidate compounds which downregulate expression of said gene.

42. A method according to claim 39 or 40 wherein said cell comprises a susceptibility polymorphism associated with downregulation of expression of said gene and said screening is for candidate compounds which upregulate expression of said gene.

43. A method according to claim 39 or 40 wherein said cell comprises a protective polymorphism associated with upregulation of expression of said gene and said screening is for candidate compounds which further upregulate expression of said gene.

44. A method according to claim 39 or 40 wherein said cell comprises a protective polymorphism associated with downregulation of expression of said gene and said screening is for candidate compounds which further downregulate expression of said gene.

45. A method for screening for compounds that modulate the expression and/or activity of a gene, the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism selected from the group defined in any one of claims 1 to 5, said method comprising the steps of:

contacting a candidate compound with a cell comprising a gene, the expression of which is upregulated or downregulated when associated with a susceptibility or protective polymorphism but which in said cell the expression of which is neither upregulated nor downregulated; and

measuring the expression of said gene following contact with said candidate compound,

wherein a change in the level of expression after the contacting step as compared to before the contacting step is indicative of the ability of the compound to modulate the expression and/or activity of said gene.

46. A method according to claim 45 wherein said cell is a human lung cell which has been pre-screened to confirm the presence, and baseline level of expression, of said gene.

47. A method according to claim 45 or 46 wherein expression of the gene is downregulated when associated with a susceptibility polymorphism and said screening is for candidate compounds which, in said cell, upregulate expression of said gene.

48. A method according to claim 45 or 46 wherein expression of the gene is upregulated when associated with a susceptibility polymorphism and said screening is for candidate compounds which, in said cell, downregulate expression of said gene.

49. A method according to claim 45 or 46 wherein expression of the gene is upregulated when associated with a protective polymorphism and said screening is for compounds which, in said cell, upregulate expression of said gene.

50. A method according to claim 45 or 46 wherein expression of the gene is downregulated when associated with a protective polymorphism and said screening is for compounds which, in said cell, downregulate expression of said gene.

51. A method of assessing the likely responsiveness of a subject predisposed to or diagnosed with lung cancer to a prophylactic or therapeutic treatment, which treatment involves restoring the physiologically active concentration of a product of gene expression to be within a range which is normal for the age and sex of the subject, which method comprises detecting in said subject the presence or absence of a susceptibility polymorphism selected from the group defined in claim 1 which when present either upregulates or downregulates expression of said gene such that the physiological active concentration of the expressed gene product is outside said normal range, wherein the detection of the presence of said polymorphism is indicative of the subject likely responding to said treatment.

52. A method of assessing a subject's suitability for an intervention diagnostic of or therapeutic for lung cancer, the method comprising:

a) providing a net score for said subject, wherein the net score is or has been determined by:

i) providing the result of one or more genetic tests of a sample from the subject, and analysing the result for the presence or absence of protective polymorphisms and for the presence or absence of susceptibility polymorphisms, wherein said protective and susceptibility polymorphisms are associated with lung cancer,

ii) assigning a positive score for each protective polymorphism and a negative score for each susceptibility polymorphism or vice versa;

iii) calculating a net score for said subject by representing the balance between the combined value of the protective polymorphisms and the combined value of the susceptibility polymorphisms present in the subject sample;

and

b) providing a distribution of net scores for lung cancer sufferers and non-sufferers wherein the net scores for lung cancer sufferers and non-sufferers are or have been determined in the same manner as the net score determined for said subject; and

c) determining whether the net score for said subject lies within a threshold on said distribution separating individuals deemed suitable for said intervention from those for whom said intervention is deemed unsuitable;

wherein a net score within said threshold is indicative of the subject's suitability for the intervention, and wherein a net score outside the threshold is indicative of the subject's unsuitability for the intervention.

53. The method according to claim 52 wherein the value assigned to each protective polymorphism is the same.

54. The method according to any one of claims 52 to 53 wherein the value assigned to each susceptibility polymorphism is the same.

55. The method according any one of claims 52 to 54 wherein the intervention is a diagnostic test for lung cancer.

56. The method according to any one of claims 52 to 54 wherein intervention is a therapeutic intervention for lung cancer.

57. The method according to claim 52 wherein the lung cancer is is selected from the group consisting of non–small cell lung cancer including adenocarcinoma and squamous cell carcinoma, small cell lung cancer, carcinoid tumor, lymphoma, or metastatic cancer.

58. The method according to claim 52 wherein the protective and susceptibility polymorphisms are selected from the group consisting of:

the -133 G/C polymorphism in the Interleukin-18 gene;

the -1053 C/T polymorphism in the CYP 2E1 gene;

the Arg197gln polymorphism in the Nat2 gene;

the -511 G/A polymorphism in the Interleukin 1B gene;

the Ala 9 Thr polymorphism in the Anti-chymotrypsin gene;

the S allele polymorphism in the Alpha1-antitrypsin gene;

the -251 A/T polymorphism in the Interleukin-8 gene;

the Lys 751 gln polymorphism in the XPD gene;

the +760 G/C polymorphism in the SOD3 gene;

the Phe257Ser polymorphism in the REV gene;

the Z alelle polymorphism in the Alpha1-antitrypsin gene;

the R19W A/G polymorphism in the Cerberus 1 (Cer 1) gene;

the Ser307Ser G/T polymorphism in the XRCC4 gene;

the K3326X A/T polymorphism in the BRCA2 gene;

the V433M A/G polymorphism in the Integrin alpha-11 gene;

the E375G T/C polymorphism in the CAMKK1 gene;

the A/T c74delA polymorphism in the gene encoding cytochrome P450 polypeptide CYP3A43;

the A/C (rs2279115) polymorphism in the gene encoding B-cell CLL/lymphoma 2;

the A/G at +3100 in the 3'UTR (rs2317676) polymorphism of the gene encoding Integrin beta 3;

the -3714 G/T (rs6413429) polymorphism in the gene encoding Dopamine transporter 1;

the A/G (rs1139417) polymorphism in the gene encoding Tumor necrosis factor receptor 1;

the C/Del (rs1799732) polymorphism in the gene encoding Dopamine receptor D2;

the C/T (rs763110) polymorphism in the gene encoding Fas ligand;

the C/T (rs5743836) polymorphism in the gene encoding Toll-like receptor 9;

the -81 C/T (rs 2273953) polymorphism in the 5' UTR of the gene encoding Tumor protein P73;

or one or more polymorphisms in linkage disequilibrium with one or more of said polymorphisms.

59. The method according to claim 40 wherein the result is analysed for the presence of absence of each of the polymorphisms from the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

60. The method according to claim 40 wherein the result is analysed for the presence of absence of each of the polymorphisms from the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

61. The method according to claim 40 wherein the result is analysed for the presence of absence of each of the polymorphisms from the group consisting of:

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

Arg 197 Gln (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

-3714 G/T (rs6413429) in the gene encoding DAT1;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

V433M A/G (rs2306022) in the gene encoding ITGA11;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

62. The method according to claim 40 wherein the result is analysed for the presence of absence of each of the polymorphisms from the group consisting of:

Rsa 1 C/T (rs2031920) in the gene encoding CYP 2E1;

-133 G/C (rs360721) in the promoter of the gene encoding Interleukin-18;

-251 A/T (rs4073) in the gene encoding Interleukin-8;

-511 A/G (rs 16944) in the gene encoding Interleukin 1B;

V433M A/G (rs2306022) in the gene encoding ITGA11;

Arg 197 Gln A/G (rs 1799930) in the gene encoding N–acetylcysteine transferase 2;

Ala 15 Thr A/G (rs4934) in the gene encoding α1-antichymotrypsin;

R19W A/G (rs 10115703) in the gene encoding Cerberus 1;

-3714 G/T (rs6413429) in the gene encoding DAT1;

A/G (rs1139417) in the gene encoding TNFR1;

C/T (rs5743836) in the gene encoding TLR9;

-81 C/T (rs 2273953) in the 5' UTR of the gene encoding P73;

Arg 312 Gln (rs1799895) in the gene encoding SOD3;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding ITGB3;

C/Del (rs1799732) in the gene encoding DRD2;

A/C (rs2279115) in the gene encoding BCL2;

-751 G/T (rs 13181) in the promoter of the gene encoding XPD;

Phe 257 Ser C/T (rs3087386) in the gene encoding REV1;

C/T (rs763110) in the gene encoding FasL;

or one or more polymorphisms in linkage disequilibrium with any one or more of these polymorphisms.

63. The method according to claim 57 or 58 wherein said intervention is a CT scan for lung cancer.

64. The method according to any one of claims 52 to 58 as described herein with reference to the examples and/or figures.

65. A kit for assessing a subject's risk of developing one or more obstructive lung diseases selected from lung cancer, said kit comprising a means of analysing a sample from said subject for the presence or absence of one or more polymorphisms selected from the group consisting of:

Ser307Ser G/T polymorphism in the X-ray repair complementing defective repair in Chinese hamster cells 4 gene (XRCC4);

A/T c74delA in the gene encoding cytochrome P450 polypeptide CYP3A43;

A/C (rs2279115) in the gene encoding B-cell CLL/lymphoma 2;

A/G at +3100 in the 3'UTR (rs2317676) of the gene encoding Integrin beta 3;

-3714 G/T (rs6413429) in the gene encoding Dopamine transporter 1;

A/G (rs1139417) in the gene encoding Tumor necrosis factor receptor 1;

C/Del (rs1799732) in the gene encoding Dopamine receptor D2;

C/T (rs763110) in the gene encoding Fas ligand;

C/T (rs5743836) in the gene encoding Toll-like receptor 9;

or one or more polymorphisms which are in linkage disequilibrium with one or more of these polymorphisms.

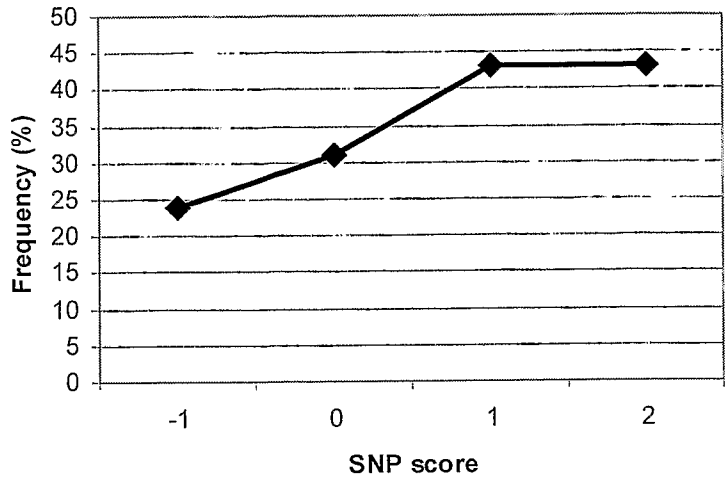


Figure 1

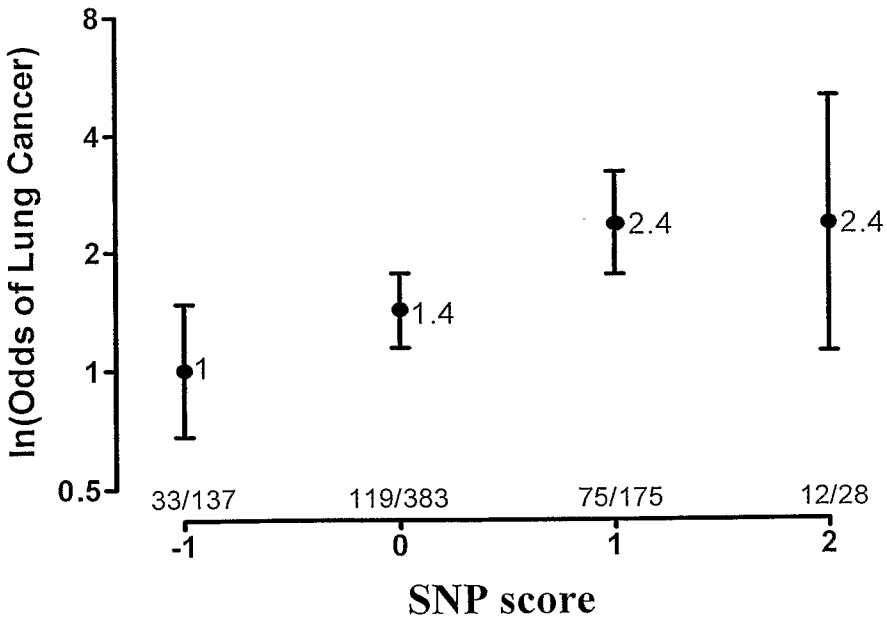


Figure 2

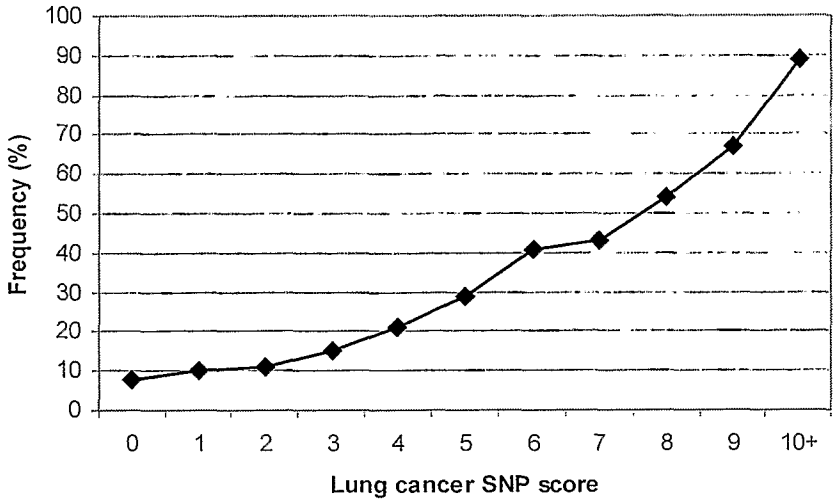


Figure 3

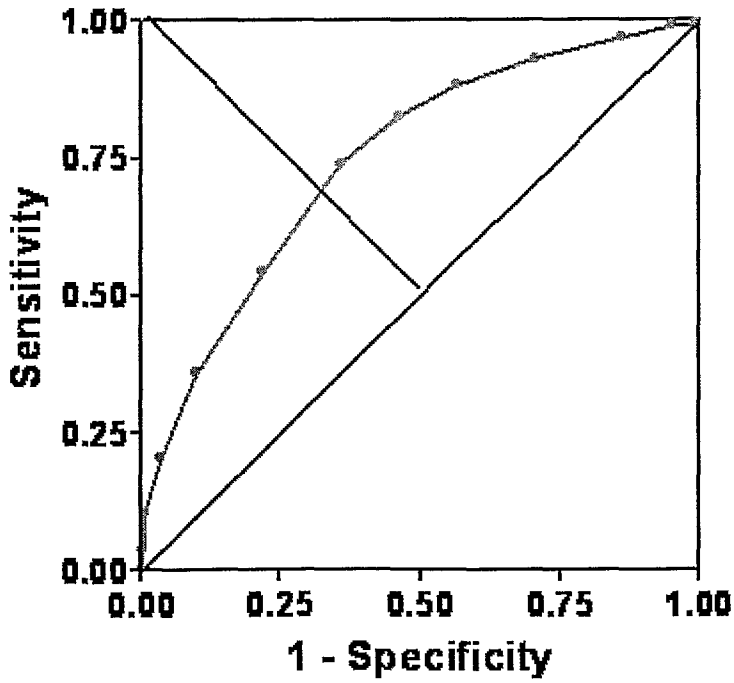


Figure 4

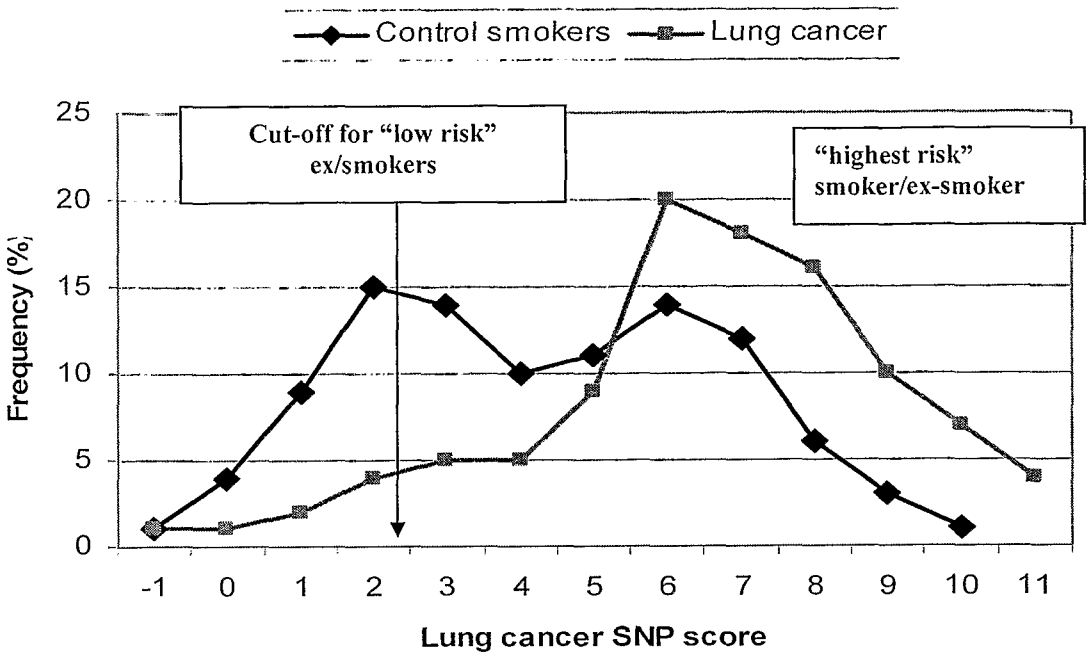


Figure 5

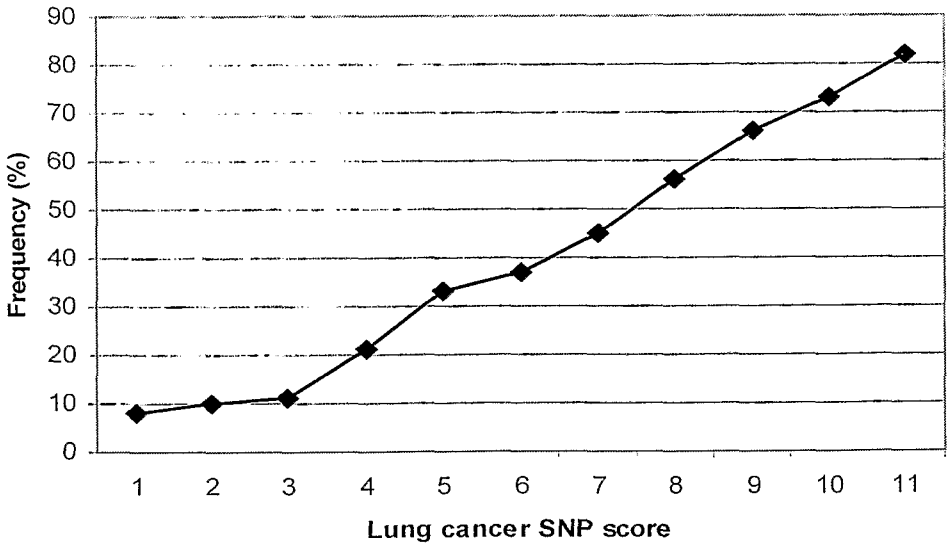


Figure 6

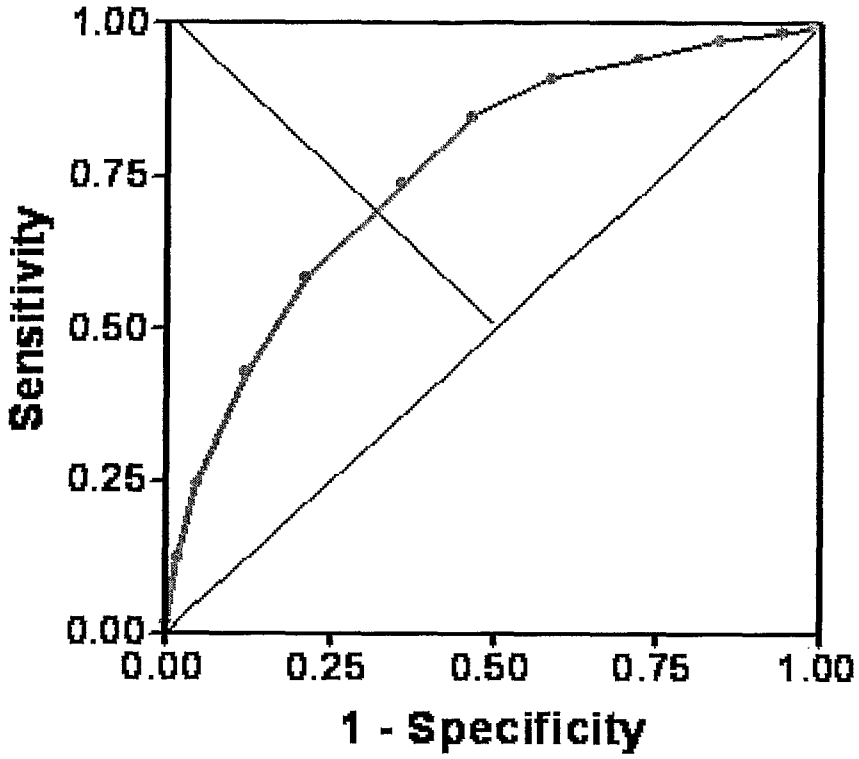


Figure 7

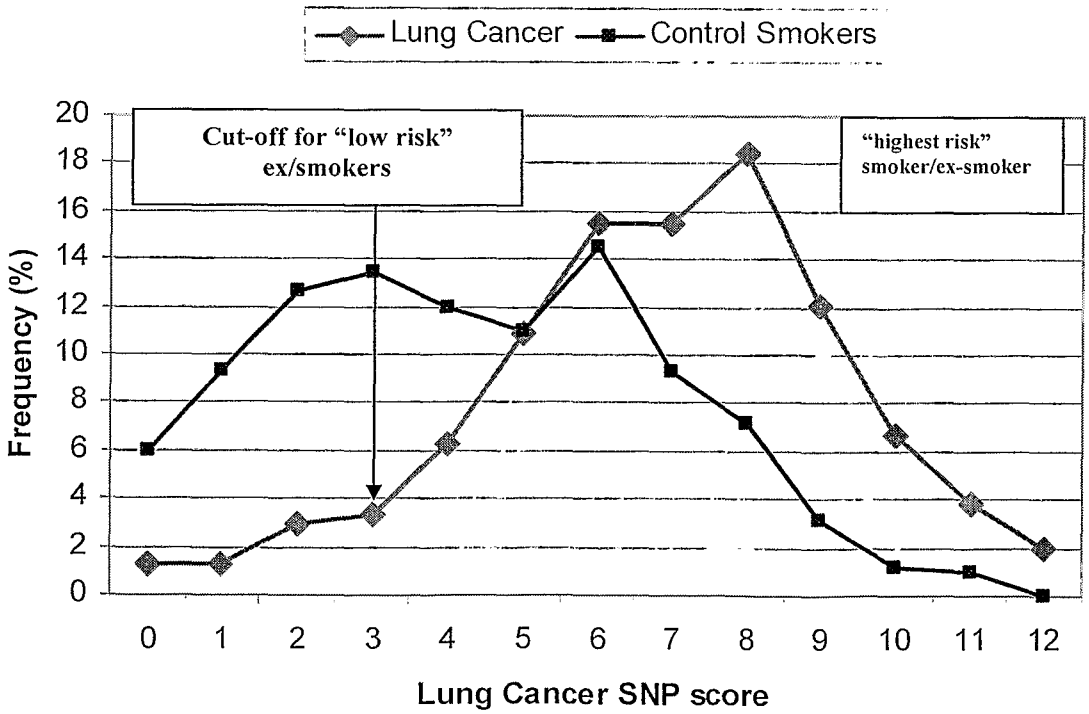


Figure 8

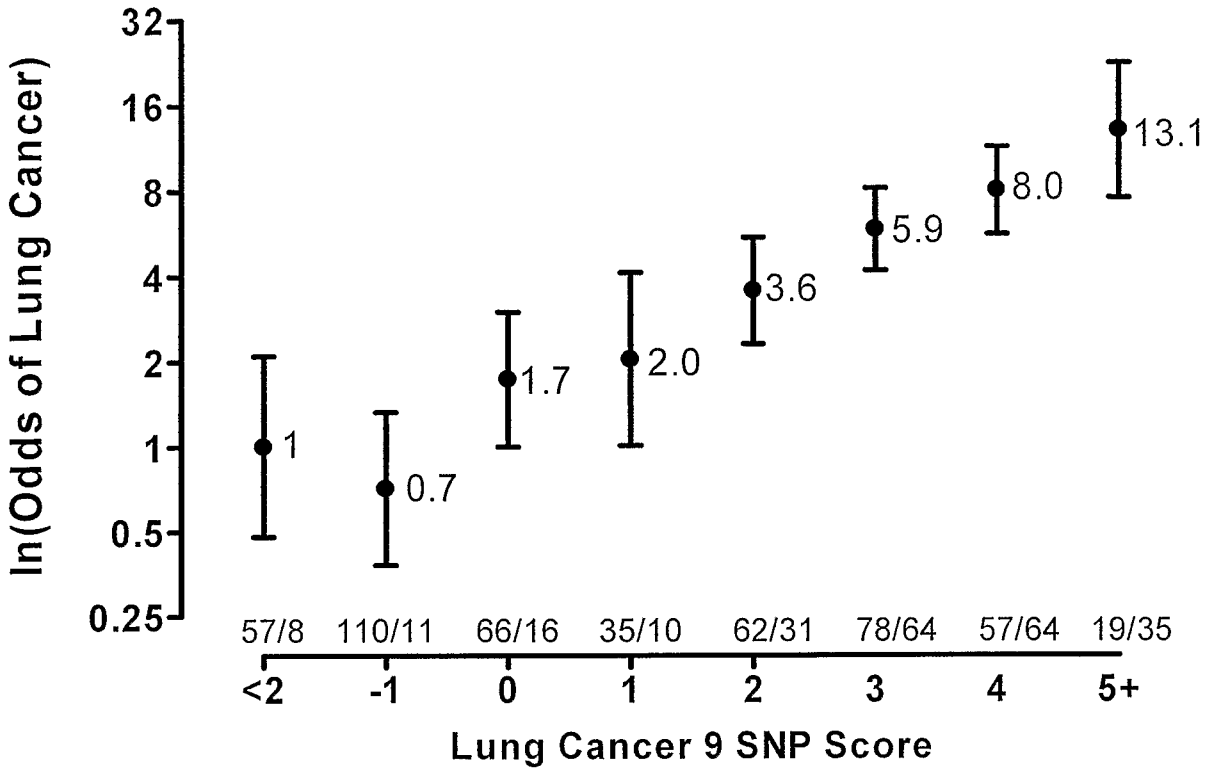
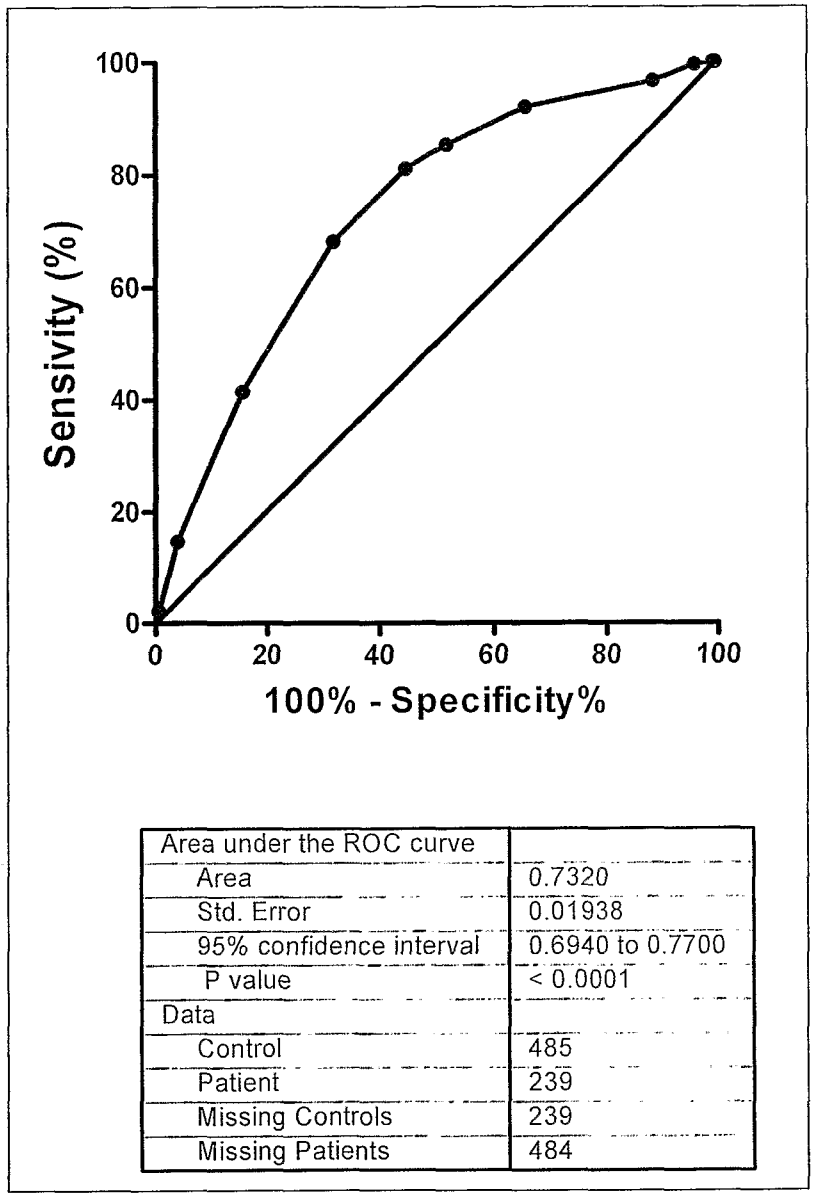

ln(Odds of Lung Cancer)
32
16
8
4
2
1
0.5
0.25
1
0.7
1.7
2.0
3.6
5.9
8.0
13.1
57/8
110/11
66/16
35/10
62/31
78/64
57/64
19/35
<2
-1
0
1
2
3
4
5+
Lung Cancer 9 SNP Score

Figure 9



Area under the ROC curve	
Area	0.7320
Std. Error	0.01938
95% confidence interval	0.6940 to 0.7700
P value	< 0.0001
Data	
Control	485
Patient	239
Missing Controls	239
Missing Patients	484

Figure 10

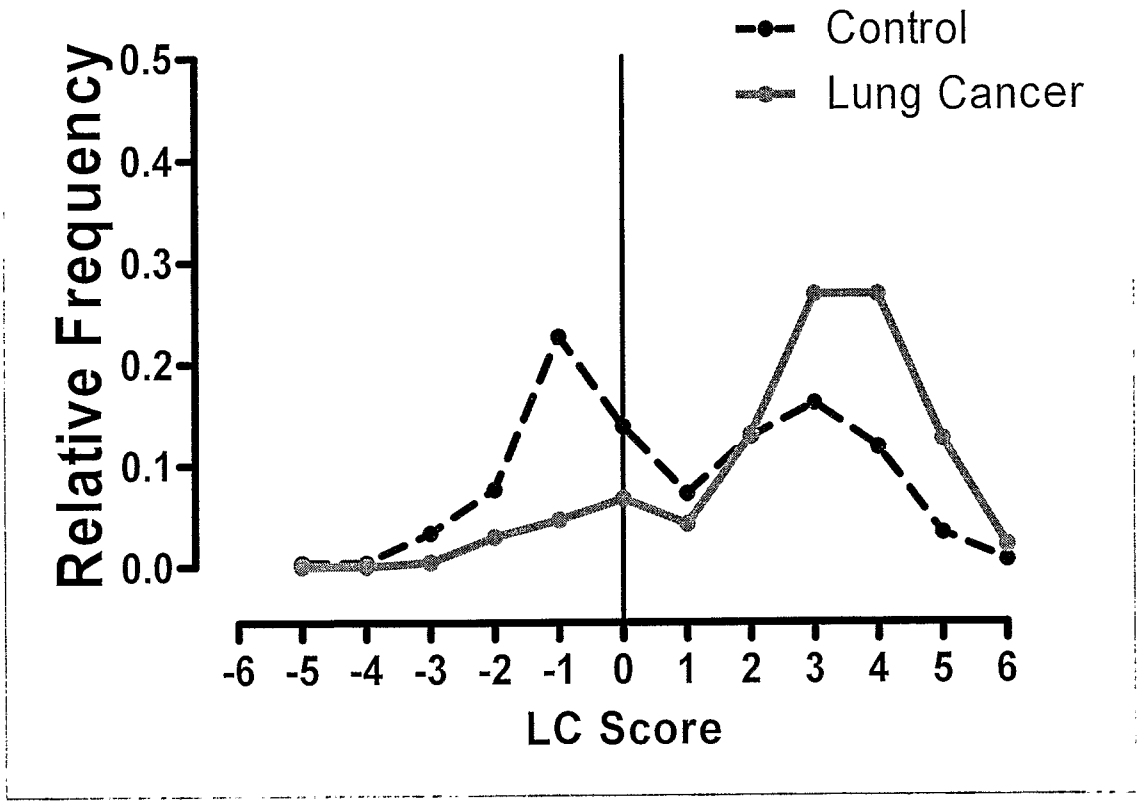

Control
Lung Cancer
Relative Frequency
0.5
0.4
0.3
0.2
0.1
0.0
-6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6
LC Score

Figure 11

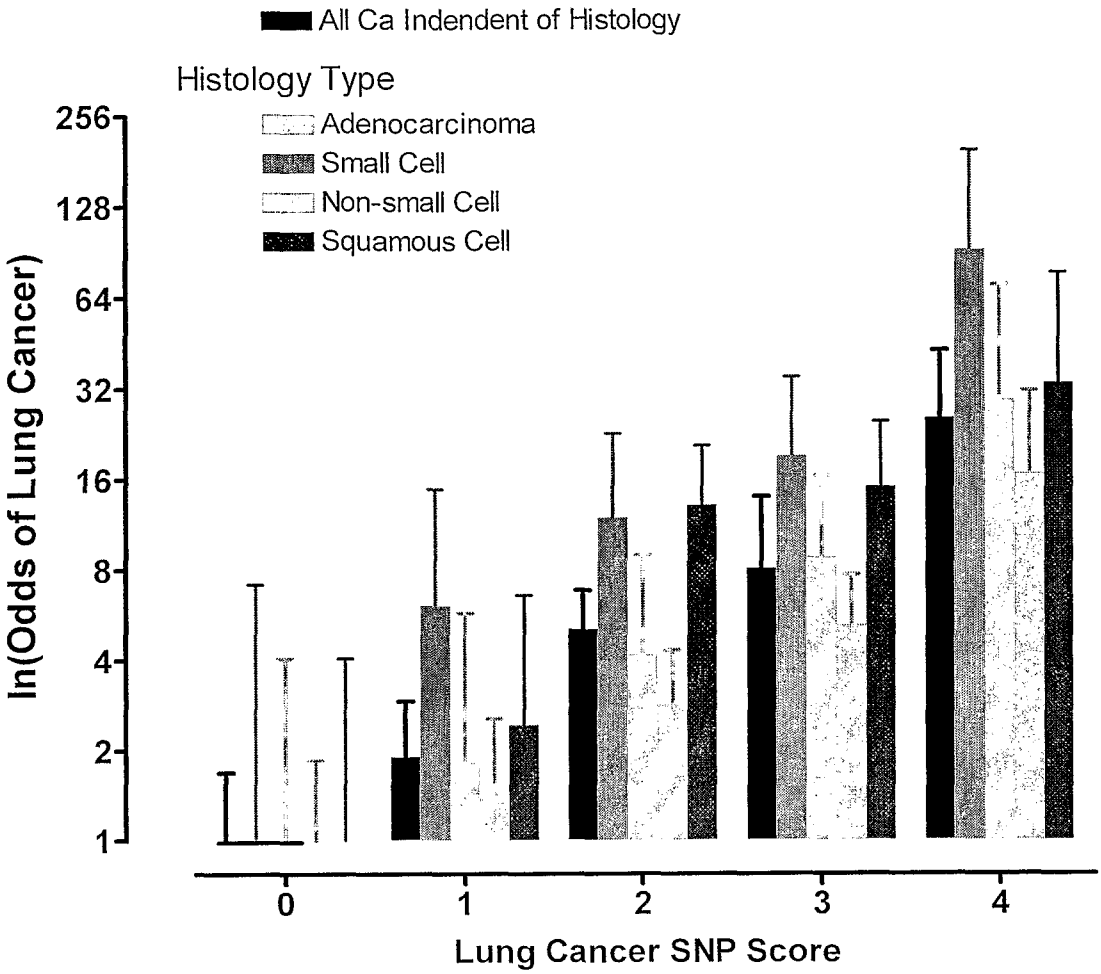

All Ca Indendent of Histology
Histology Type
Adenocarcinoma
Small Cell
Non-small Cell
Squamous Cell
ln(Odds of Lung Cancer)
256
128
64
32
16
8
4
2
1
0
1
2
3
4
Lung Cancer SNP Score

Figure 12

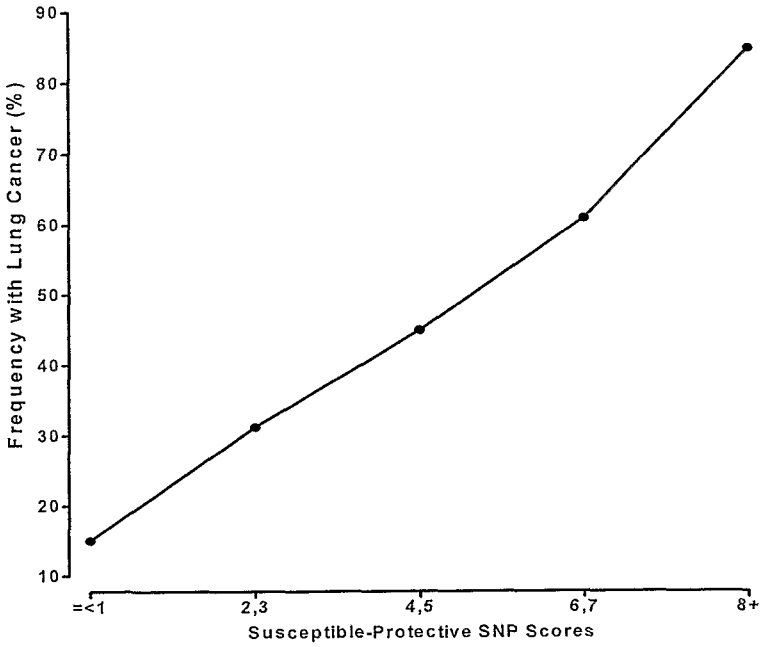


Figure 13a

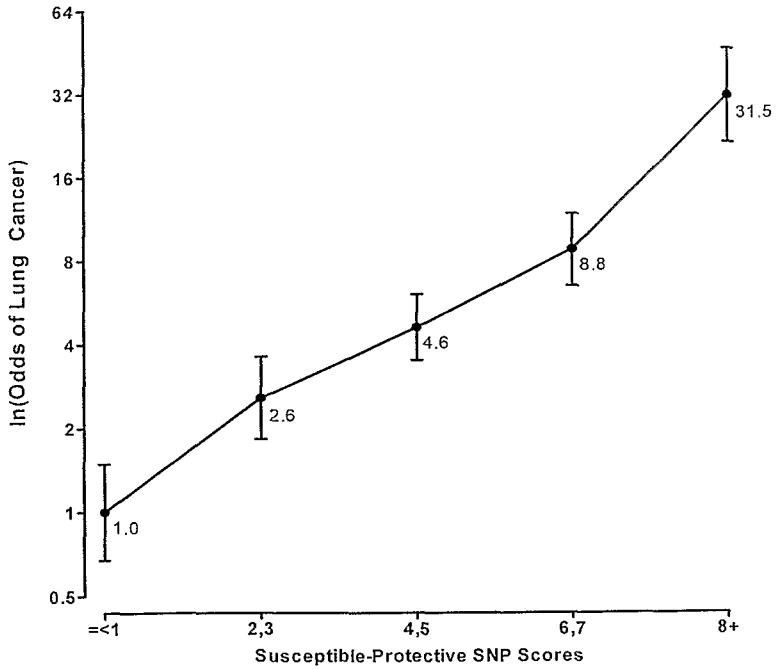


Figure 13b

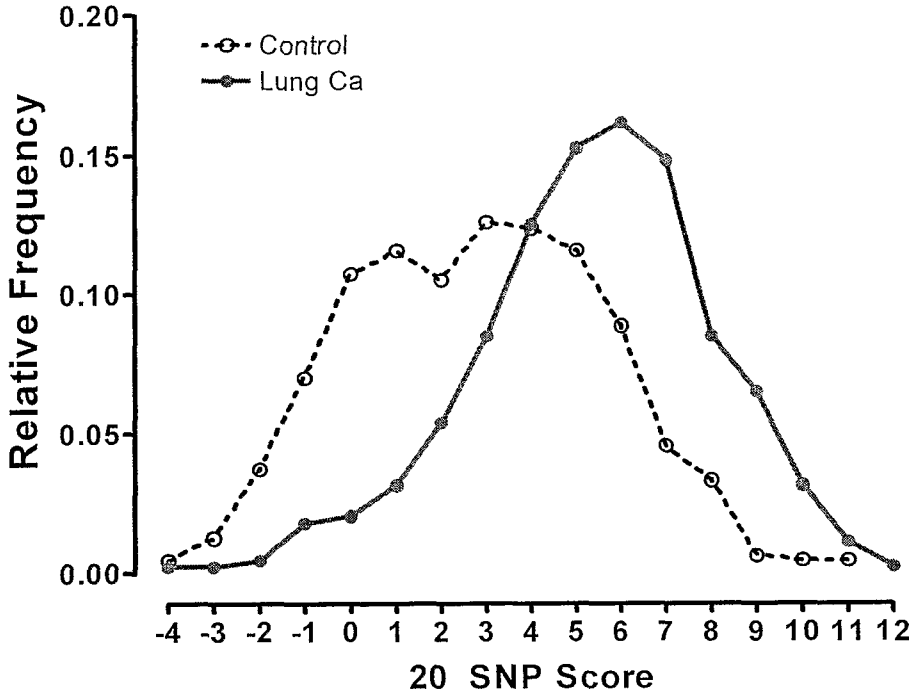

0.20
0.15
0.10
0.05
0.00
Relative Frequency
Control
Lung Ca
-4 -3 -2 -1 0 1 2 3 4 5 6 7 8 9 10 11 12
20 SNP Score

Figure 14