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(54) **Title**: DIAGNOSIS OF MELANOMA AND SOLAR LENTIGO BY NUCLEIC ACID ANALYSIS

(57) **Abstract**: The present invention provides methods for diagnosing melanoma and/or solar lentigo in a subject by analyzing nucleic acid molecules obtained from the subject. The present invention also provides methods for distinguishing melanoma from solar lentigo and/or dysplastic nevi and/or normal pigmented skin. The methods include analyzing expression or mutations in epidermal samples, of one or more skin markers. The methods can include the use of a microarray to analyze gene or protein profiles from a sample.

DIAGNOSIS OF MELANOMA AND SOLAR LENTIGO BY NUCLEIC ACID ANALYSIS

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

[0001] The invention relates generally to methods of characterizing pigmented skin lesions suspected of being melanomas using primarily non-invasive skin sampling.

BACKGROUND INFORMATION

[0002] Melanoma is a serious form of skin cancer in humans. It arises from the pigment cells (melanocytes), usually in the skin. The incidence of melanoma is increasing at the fastest rate of all cancers in the United States with a lifetime risk of 1 in 68. Although melanoma accounts for only 4% of all dermatologic cancers, it is responsible for 80% of all deaths from skin cancers. It has long been realized that recognition and diagnosis of melanoma, when it is early stage disease, is key to its cure.

[0003] Given this, it is imperative that research be carried out not only on therapeutics for melanoma, but also on all aspects of melanoma including prevention and detection. Most of these deaths from melanoma could have been prevented if the melanomas, initially located on the skin, could have been detected in their early stages. The ability to cure melanoma in its earliest skin stage, *in situ*, is virtually 100% if the melanoma is adequately surgically excised. If the melanoma is caught in a later stage, where it has invaded to a depth of 4 mm or more, the ten-year survival rate is less than 50%. If the melanoma is not detected until it has spread to distant parts of the body (Stage IV), the prognosis is dismal, with only 7-9% of patients surviving 5 years, with the median survival time being 8-9 months. The long-term "cure" rate for Stage IV melanoma is only 1-2 %.

[0004] To advance early detection of melanoma, several things must be improved. People need to be better educated with regards to the risks of melanoma and how to prevent and detect it on their own skin. Also physicians need to be more alert to the possibility of melanoma and be better trained in detection. But even if these two areas are improved, the diagnosis of melanoma on the skin is still difficult. Studies have shown that even expert clinicians working in pigmented lesion clinics where melanoma is their specialty are only able to determine whether a suspicious pigmented lesion is melanoma or not with 60-80% sensitivity. This leads to the need for surgical biopsy of large numbers of pigmented lesions for every melanoma that is detected, and, doubtless, to the missing of some melanomas in their early stages.

[0005] In current practice melanoma is diagnosed by biopsy and histopathological examination; approximately 20 to 30 biopsies must be performed to find one melanoma and even then some melanomas are missed in the earliest stage. The limitations of visual detection are apparent to dermatologists who are constantly searching for ways to better determine whether suspicious lesions are melanoma or not without having to cut them out first. To this end, epiluminescence microscopy (ELM) has come into use. This is a method whereby lesions are looked at using a device that simultaneously magnifies the lesion while reducing visual interference from refractive index differences at the skin-air interface. While ELM does give a different view, it is of limited improvement. Studies have shown that until one becomes fairly skilled in utilizing the instrument, sensitivity in detection of melanoma actually decreases. Even very skilled users of ELM improve their ability to detect melanomas only by 5-10%. This still leads to an unacceptable sensitivity in detection and the need to biopsy large numbers of benign lesions to detect a few melanomas. And again, some melanomas will be missed completely in their early stages.

[0006] Clearly there is a need for further development of technology that will enable physicians to determine the nature and extent of suspicious lesions of the skin. Such technology would ideally directly assay the physiology of the suspect lesion to enable a sensitive diagnosis.

SUMMARY OF THE INVENTION

[0007] The present invention is based, in part, on the discovery that analysis of nucleic acid molecules or of protein expression products of nucleic acid molecules from specific genes can be used to characterize skin lesions in a subject. The method provides valuable genetic information based on DNA, messenger RNA, or protein expression products obtained therefrom, for example.

[0008] In one embodiment, the method involves use of a non-invasive approach for recovering nucleic acids such as DNA or messenger RNA or proteins from the surface of skin via a tape stripping procedure that permits a direct quantitative and qualitative assessment of biomarkers. Although tape-harvested nucleic acid and protein expression products are shown to be comparable in quality and utility to recovering such molecules by biopsy, the non-invasive method provides information regarding cells of the outermost layers of the skin that may not be obtained using biopsy samples. Finally, the non-invasive method is far less traumatic than a biopsy.

[0009] Thus, the non-invasive method is used to capture cells on pigmented skin lesions that are suspected of being melanomas. Nucleic acid molecules obtained from skin cells captured by the non-invasive method are analyzed in order to diagnose the nature of the lesion (*e.g.*, malignant melanoma). In one embodiment, a nucleic acid molecule is amplified prior to analysis. Secondary outcomes could include tests for diagnosis and prognosis of a variety of pigmented skin lesions and even to predict a therapeutic regimen. In another embodiment, the skin cells are lysed to extract one or more proteins, which are then quantitated to diagnose the nature of the lesion. It should be understood that the methods of the invention are not limited to non-invasive techniques for obtaining skin samples. For example, but not by limitation, one of skill in the art would know other techniques for obtaining a skin sample such as scraping of the skin, biopsy, suction, blowing and other techniques. As described herein, non-invasive tape stripping is an illustrative example for obtaining a skin sample.

[0010] In another embodiment, the methods involve detection of one or more mutations in the nucleic acid sequence of the nucleic acid molecule obtained from the skin. Such mutations may be a substitution, a deletion, and/or an insertion of the nucleic acid sequence that results in a diseased state in the subject from which the skin sample is obtained.

[0011] In one embodiment, the nucleic acid molecule analyzed is listed in Tables 10-12 and 15. In another embodiment, the method further includes analyzing one or more nucleic acid molecules listed Tables 1-8. For example, in one embodiment, the gene analyzed is any one or more of interferon regulatory factor 6, claudin 23, melan-A, osteopetrosis associated transmembrane protein 1, RAS-like family 11 member B, actinin alpha 4, transmembrane protein 68, Glycine-rich protein (GRP3S), Transcription factor 4, hypothetical protein FLJ20489, cytochrome c somatic, transcription factor 4, Forkhead box P1, transducer of ERBB2-2, glutaminyl-peptide cyclotransferase (glutaminyl cyclase), hypothetical protein

FLJ10770, selenophosphate synthetase 2, embryonal Fyn-associated substrate, Kruppel-like factor 8, Discs large homolog 5 (Drosophila), regulator of G-protein signalling 10, ADP-ribosylation factor related protein 2, TIMP metallopeptidase inhibitor 2, 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase, similar to RIKEN cDNA 5730421E18 gene, Regulator of G-protein signalling 10, Nuclear RNA-binding protein putative, tyrosinase-related protein 1, TIMP metallopeptidase inhibitor 2, Claudin 1, transcription factor 4, solute carrier family 16 (monocarboxylic acid transporters) member 6 (similar to solute carrier family 16 member 6; monocarboxylate transporter 6), or any combination thereof. In another embodiment, the nucleic acid molecule is from one or more genes listed in Tables 10-12 and 15.

[0012] Accordingly, provided herein is a method for characterizing and/or diagnosing melanoma in a subject, including obtaining a nucleic acid molecule or protein by biopsy of a skin lesion on the subject, and analyzing the nucleic acid molecule to distinguish melanoma from dysplastic nevi and/or normal pigmented skin in the subject. In this method, at least one nucleic acid molecule whose expression is informative of melanoma is detected in the epidermal sample. In one example, expression of one or more of the genes listed in Tables 1-8, 10-12, 15, or a combination thereof, is detected in the epidermal sample to characterize the melanoma. In one embodiment, the gene is any one or more of interferon regulatory factor 6, claudin 23, melan-A, osteopetrosis associated transmembrane protein 1, RAS-like family 11 member B, actinin alpha 4, transmembrane protein 68, Glycine-rich protein (GRP3S), Transcription factor 4, hypothetical protein FLJ20489, cytochrome c somatic, transcription factor 4, Forkhead box P1, transducer of ERBB2-2, glutaminyl-peptide cyclotransferase (glutaminyl cyclase), hypothetical protein FLJ10770, selenophosphate synthetase 2, embryonal Fyn-associated substrate, Kruppel-like factor 8, Discs large homolog 5 (Drosophila), regulator of G-protein signalling 10, ADP-ribosylation factor related protein 2, TIMP metallopeptidase inhibitor 2, 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase, similar to RIKEN cDNA 5730421E18 gene, Regulator of G-protein signalling 10, Nuclear RNA-binding protein putative, tyrosinase-related protein 1, TIMP metallopeptidase inhibitor 2, Claudin 1, transcription factor 4, solute carrier family 16 (monocarboxylic acid transporters) member 6 (similar to solute carrier family 16 member 6; monocarboxylate transporter 6), or any combination thereof.

[0013] The non-invasive methods of the invention involve applying an adhesive tape to a target area of skin in a manner sufficient to isolate a sample adhering to the adhesive tape, wherein the sample includes nucleic acid molecules or proteins. Typically, at least one nucleic acid molecule or protein whose expression is informative of melanoma is detected in the sample. The method of characterizing skin using tape stripping has a number of applications, such as the following: (i) disease classification/subclassification; (ii) monitoring disease severity and progression; (iii) monitoring treatment efficacy; and (iv) prediction of a particular treatment regimen. All of these applications, which themselves represent embodiments disclosed herein, preferably use non-invasive sampling to recover information that is otherwise difficult or impractical to recover (*e.g.*, through the use of biopsies). The information may be contained in the DNA, protein, or RNA of skin cells close to the surface of the skin. In one embodiment, expression of one or more of the genes listed in Tables 1-8, 10-12, 15, or a combination thereof, is detected in the sample to characterize the sample. This exemplary method is particularly useful for distinguishing melanoma from dysplastic nevi and/or normal pigmented skin. In one embodiment, expression of one or more of the genes listed in Table 12 or 15 is detected in the sample to characterize the sample.

[0014] As such, also provided herein is a method for distinguishing solar lentigines from dysplastic nevi and/or basal cell carcinoma and/or normal pigmented skin in a subject, including applying an adhesive tape to a target area of skin in a manner sufficient to isolate a sample adhering to the adhesive tape, wherein the sample includes nucleic acid molecules. At least one nucleic acid molecule whose expression is informative of solar lentigo is detected in the sample. In one embodiment, expression of one or more of the genes listed in Tables 10-12, 15, or a combination thereof, is detected in the sample to characterize the melanoma. In another embodiment, expression of one or more of the genes listed in Table 12 or 15 is detected in the sample to characterize the solar lentigo.

[0015] Other embodiments are based in part on the discovery that for tape stripping of the skin, non-polar, pliable, adhesive tapes, especially pliable tapes with rubber adhesive, are more effective than other types of adhesive tapes. Using pliable tapes with rubber adhesives, as few as 10 or less tape strippings and in certain examples as few as 4 or even 1 tape stripping can be used to isolate and/or detect nucleic acid molecules from the epidermal layer of the skin.

[0016] In another embodiment, the methods of the invention provide for characterization of a skin lesion *in situ*, including application of a detectably labeled probe directly to a skin lesion for visual analysis. At least one nucleic acid molecule whose expression is informative of melanoma or dysplastic nevi or normal skin is detected on the skin lesion or surrounding margin or tissue using a specific probe. In one example, expression of one or more of the genes listed in Tables 1-8, 10-12, 15, or a combination thereof, is detected on the skin lesion or surrounding margin or tissue to characterize the melanoma. In one embodiment, expression of one or more of the genes listed in Tables 10-12 or 15 is detected in the sample to characterize the melanoma.

[0017] Also provided herein is a method for diagnosing a disease state by establishing a gene expression pattern of a target area suspected of being melanoma on the skin of a subject and comparing the subject's gene expression profile to a reference gene expression profile obtained from a corresponding normal skin sample. In one embodiment, the target area of the skin simultaneously expresses a plurality of genes at the protein level that are markers for melanoma. In another embodiment, the genes are listed in Tables 1-8, 10-12, 15, or any combination thereof. In another embodiment, the genes are listed in Tables 8 or 12.

[0018] In one embodiment, the method of diagnosing a disease state involves detection of one or more mutations in the nucleic acid sequence of the gene. Such mutations may be a substitution, a deletion, and/or an insertion of the nucleic acid sequence that results in a diseased state in the subject from which the skin sample is obtained. In one embodiment, the genes are listed in Tables 1-8, 10-12, 15, or any combination thereof. In another embodiment, the genes are listed in Tables 8 or 12.

[0019] In another aspect, the invention provides kits for characterizing a skin lesion in a subject. In one embodiment, the kit includes a skin sample collection device, such as a biopsy needle or an adhesive tape for non-invasive tape stripping, and one or more probes or primers that selectively bind to one or more nucleic acid molecules in any of Tables 1-8 and 10-12, 15, or to a nucleic acid or protein expression product of a nucleic acid molecule in any of Tables 1-8, 10-12, and 15. For example, in one embodiment, the gene analyzed is any one or more of interferon regulatory factor 6, claudin 23, melan-A, osteopetrosis associated transmembrane protein 1, RAS-like family 11 member B, actinin alpha 4, transmembrane protein 68, Glycine-rich protein (GRP3S), Transcription factor 4, hypothetical protein

FLJ20489, cytochrome c somatic, transcription factor 4, Forkhead box P1, transducer of ERBB2-2, glutaminyl-peptide cyclotransferase (glutaminyl cyclase), hypothetical protein FLJ10770, selenophosphate synthetase 2, embryonal Fyn-associated substrate, Kruppel-like factor 8, Discs large homolog 5 (Drosophila), regulator of G-protein signalling 10, ADP-ribosylation factor related protein 2, TIMP metallopeptidase inhibitor 2, 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase, similar to RIKEN cDNA 5730421E18 gene, Regulator of G-protein signalling 10, Nuclear RNA-binding protein putative, tyrosinase-related protein 1, TIMP metallopeptidase inhibitor 2, Claudin 1, transcription factor 4, solute carrier family 16 (monocarboxylic acid transporters) member 6 (similar to solute carrier family 16 member 6; monocarboxylate transporter 6), or any combination thereof. In another embodiment, the kit includes a microarray containing at least a fragment of a gene or a nucleic acid or protein product of a gene identified in any of Tables 1-8, 10-12, 15, or any combination thereof.

[0020] In another embodiment, the kit for characterizing a skin lesion in a subject includes an applicator and one or more probes or primers that selectively bind to one or more nucleic acid molecules in any of Tables 1-8 and 10-12, 15, or to a nucleic acid or protein expression product of a nucleic acid molecule in any of Tables 1-8, 10-12, and 15. In one embodiment, the probes are detectably labeled for visual identification of expression of RNA.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021] Figures 1A and 1B are graphical diagrams showing data from the EDR, PTP, and PTN as a function of sample size, assuming a threshold for declaring the significance of a probe/gene expression difference between nevi and primary melanoma of $p < 0.05$.

[0022] Figures 2A and 2B are graphical diagrams showing data from a sample size analysis that considered the contrast results for nevi vs. primary melanoma in the context of an analysis of variance (ANOVA) comparing normal skin, nevi, and primary melanoma

[0023] Figures 3A and 3B are graphical diagrams showing data from an analysis focusing exclusively on the posterior true probability (PTP) for different assumed significance levels.

[0024] Figures 4A to 4D are pictorial and graphical diagrams showing the development of a gene classifier for distinguishing melanoma from atypical nevi and normal pigmented skin.

[0025] Figures 5A and 5B are graphical diagrams showing data from prediction analysis of the developed classifiers for distinguishing melanoma from atypical nevi and normal pigmented skin.

[0026] Figures 6A to 6E are graphical diagrams showing data from prediction analysis of the developed classifiers for distinguishing melanoma from atypical nevi and normal pigmented skin.

[0027] Figure 7 is a hierarchial cluster analysis of the identified genes distinguishing melanoma from atypical nevi and normal pigmented skin.

[0028] Figure 8 is a graphical diagram showing results from classification modeling of the identified genes.

[0029] Figure 9 is a graphical diagram showing data of a developed classifier for distinguishing melanoma from atypical nevi and normal pigmented skin.

[0030] Figure 10 is a pictorial diagram showing the development of a classifier to discriminate melanoma from atypical nevi using non-invasive tape strip-based genomic profiling.

[0031] Figure 11 is a pictorial diagram describing the development of a 19-gene classifier that discriminates melanoma from atypical nevi.

[0032] Figure 12 is a pictorial diagram showing a hierarchial cluster analysis of the identified genes from the 19-gene classifier identified in Figure 11.

[0033] Figure 13 is a pictorial diagram showing results from 10 melanoma and 10 nevi samples against the 19-gene classifier identified in Figure 11.

[0034] Figure 14 is a graphical diagram showing data of a developed classifier for distinguishing solar lentigines from normal pigmented skin.

[0035] Figure 15 is a hierarchial cluster analysis of the identified genes from Figure 14 distinguishing solar lentigines from normal pigmented skin.

[0036] Figure 16 is a graphical diagram showing data from prediction analysis of the developed classifiers for distinguishing solar lentigines from normal pigmented skin.

[0037] Figure 17 is a hierarchial cluster analysis of a gene expression profile distinguishing solar lentigines from atypical nevi and basal cell carcinoma.

[0038] Figure 18 is a hierarchial cluster analysis of a gene expression profile distinguishing solar lentigines from lentigo maligna.

[0039] Figure 19 is a hierarchial cluster analysis of a 28-gene classifier distinguishing solar lentigines from lentigo maligna.

DETAILED DESCRIPTION OF THE INVENTION

[0040] The present invention is based, in part, on the discovery that analysis of nucleic acid molecules or of protein expression products of nucleic acid molecules from specific genes can be used to characterize skin lesions in a subject. Accordingly, the present invention provides methods and kits useful for detecting cancer, especially melanoma, by determining the expression profiles of one or more specific genes of interest. In addition, the present invention provides methods and kits useful for distinguishing solar lentigines from cancer by determining the expression profiles of one or more specific genes of interest.

[0041] There are two main motivations for conducting genome wide expression profiling studies in melanoma. First, melanoma is one of the best characterized carcinogenesis models for gradual progression of benign lesions to cancer: normal pigmented cells to nevi to atypical nevi to primary melanoma *in situ* to invasive primary melanoma to aggressive metastatic melanoma. This progression is known to correlate with distinctive chromosomal changes, and is thought to be mediated by stepwise progressive changes in gene expression, suggesting that expression profiling may identify genes responsible for tumorigenesis in melanoma. Indeed, candidate tumor genes have been identified with microarray analyses of melanoma cell lines. The second reason is that molecular characterization of tumors may allow a better staging classification of tumors and prognosis prediction. While histological characteristics such as the thickness and ulceration of tumors have some value as predictors of prognosis, there is lack of informative markers that help determine which patients will do well and which patients will have progressive disease and metastasis. Molecular markers identified in microarray experiments of tumors are already being introduced into clinical practice in the management of breast cancer. Gene expression profiling experiments in melanoma and melanoma cell lines suggest that the classification of melanoma can be improved, but studies are lacking with sufficient power to define molecular criteria for diagnosis or identify prognostic markers; the establishments of such markers would represent a major advance in melanoma care. A major reason for the lack of powerful microarray studies in melanoma is that, unlike most solid tumors, it is necessary to paraffin embed and section the whole lesion for histology, leaving no sample for RNA isolation. Although this situation is now changing, the ability to avoid biopsy until a definitive diagnosis is made would be powerful for subjects that would not normally be eligible for one or more biopsies.

[0042] As used in this specification and the appended claims, the singular forms "a", "an", and "the" include plural references unless the context clearly dictates otherwise. Thus, for example, references to "the method" includes one or more methods, and/or steps of the type described herein which will become apparent to those persons skilled in the art upon reading this disclosure and so forth.

[0043] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods and materials are now described.

[0044] The term "subject" as used herein refers to any individual or patient to which the subject methods are performed. Generally the subject is human, although as will be appreciated by those in the art, the subject may be an animal. Thus other animals, including mammals such as rodents (including mice, rats, hamsters and guinea pigs), cats, dogs, rabbits, farm animals including cows, horses, goats, sheep, pigs, etc., and primates (including monkeys, chimpanzees, orangutans and gorillas) are included within the definition of subject.

[0045] As used herein, the terms "sample" and "biological sample" refer to any sample suitable for the methods provided by the present invention. A sample of cells can be any sample, including, for example, a skin sample obtained by non-invasive tape stripping or biopsy of a subject, or a sample of the subject's bodily fluid. Thus, in one embodiment, the biological sample of the present invention is a tissue sample, *e.g.*, a biopsy specimen such as samples from needle biopsy. In one embodiment, the term "sample" refers to any preparation derived from skin of a subject. For example, a sample of cells obtained using the non-invasive method described herein can be used to isolate nucleic acid molecules or proteins for the methods of the present invention. Samples for the present invention typically are taken from a skin lesion, which is suspected of being the result of a disease or a pathological or physiological state, such as psoriasis or dermatitis, or the surrounding margin or tissue. As used herein, "surrounding margin" or "surrounding tissue" refers to tissue of the subject that is adjacent to the skin lesion, but otherwise appears to be normal or free from lesion.

[0046] As used herein "corresponding normal cells" or "corresponding normal sample" refers to cells or a sample from a subject that is from the same organ and of the same type as the cells being examined. In one aspect, the corresponding normal cells comprise a sample of cells obtained from a healthy individual that does not have a skin lesion or skin cancer. Such corresponding normal cells can, but need not be, from an individual that is age-matched and/or of the same sex as the individual providing the cells being examined. Thus, the term "normal sample" or "control sample" refers to any sample taken from a subject of similar species that is considered healthy or otherwise not suffering from the particular disease, pathological or physiological state, or from the same subject in an area free from skin lesions. As such, a normal/standard level of RNA denotes the level of RNA present in a sample from the normal sample. A normal level of RNA can be established by combining skin samples or cell extracts taken from normal healthy subjects and determining the level of one or more RNAs present. In addition, a normal level of RNA also can be determined as an average value taken from a population of subjects that is considered to be healthy, or is at least free of a particular disease, pathological or physiological state. Accordingly, levels of RNA in subject, control, and disease samples can be compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing or characterizing disease.

[0047] The term "skin" refers to the outer protective covering of the body, consisting of the epidermis (including the stratum corneum) and the underlying dermis, and is understood to include sweat and sebaceous glands, as well as hair follicle structures. Throughout the present application, the adjective "cutaneous" can be used, and should be understood to refer generally to attributes of the skin, as appropriate to the context in which they are used. The epidermis of the human skin comprises several distinct layers of skin tissue. The deepest layer is the stratum basalis layer, which consists of columnar cells. The overlying layer is the stratum spinosum, which is composed of polyhedral cells. Cells pushed up from the stratum spinosum are flattened and synthesize keratohyalin granules to form the stratum granulosum layer. As these cells move outward, they lose their nuclei, and the keratohyalin granules fuse and mingle with tonofibrils. This forms a clear layer called the stratum lucidum. The cells of the stratum lucidum are closely packed. As the cells move up from the stratum lucidum, they become compressed into many layers of opaque squamae. These cells are all flattened remnants of cells that have become completely filled with keratin and have lost all other internal structure, including nuclei. These squamae constitute the outer layer of the epidermis, the stratum corneum. At the bottom of the stratum corneum, the cells are closely compacted and adhere to each other strongly, but higher in the stratum they become loosely packed, and eventually flake away at the surface.

[0048] As used herein, the term "skin lesion" refers to a change in the color or texture in an area of skin. As such, "skin lesions suspected of being melanoma" are skin lesions with characteristics of malignant melanoma, which are well known to those of skill in the art, such as dermatologists and oncologists. Such lesions are sometimes raised and can have a color that is different from the color of normal skin of an individual (*e.g.*, brown, black, red, or blue). Lesions suspected of being melanoma sometimes include a mixture of colors, are often asymmetrical, can change in appearance over time, and may bleed. A skin lesion suspected of being melanoma may be a mole or nevus. Melanoma lesions are usually, but not always, larger than 6 mm in diameter. Melanoma includes superficial spreading melanoma, nodular melanoma, acral lentiginous melanoma, and lentigo maligna melanoma. The term "lentigo maligna" refers to a precancerous lesion on the skin, especially in areas exposed to the sun, that is flat, mottled, and brownish with an irregular outline and grows slowly over a period of years. Melanoma can occur on skin that has been overexposed to the sun. Therefore, in one embodiment the skin sample is taken from an area of skin that has been overexposed to the sun.

[0049] The term "dysplastic nevus" refers to an atypical mole or a mole whose appearance is different from that of common moles. Dysplastic nevi are generally larger than ordinary moles and have irregular and indistinct borders. Their color frequently is not uniform and ranges from pink to dark brown; they usually are flat, but parts may be raised above the skin surface. Dysplastic naevus can be found anywhere, but are most common on the trunk of a subject.

[0050] The term "cancer" as used herein, includes any malignant tumor including, but not limited to, carcinoma and sarcoma. Cancer arises from the uncontrolled and/or abnormal division of cells that then invade and destroy the surrounding tissues. As used herein, "proliferating" and "proliferation" refer to cells undergoing mitosis. As used herein, "metastasis" refers to the distant spread of a malignant tumor from its sight of origin. Cancer cells may metastasize through the bloodstream, through the lymphatic system, across body cavities, or any combination thereof. The term "cancerous cell" as provided herein, includes a cell afflicted by any one of the cancerous conditions provided herein. The term "carcinoma" refers to a malignant new growth made up of epithelial cells tending to infiltrate surrounding tissues, and to give rise to metastases. The term "melanoma" refers to a malignant tumor of melanocytes which are found predominantly in skin but also in bowel and the eye. "Melanocytes" refer to cells located in the bottom layer, the basal lamina, of the skin's epidermis and in the middle layer of the eye. Thus, "melanoma metastasis" refers to the spread of melanoma cells to regional lymph nodes and/or distant organs (*e.g.*, liver, brain, breast, prostate, etc.).

[0051] The term "basal cell carcinoma" or "BCC" refers to a slow-growing neoplasm that is locally invasive but rarely metastasizes. It is derived from basal cells, the deepest layer of epithelial cells of the epidermis or hair follicles. BCC is a common skin cancer that is often associated with overexposure to sunlight.

[0052] The term "solar lentigo" or "solar lentigines," also known as a sun-induced freckle or senile lentigo, is a dark (hyperpigmented) lesion caused by natural or artificial ultraviolet (UV) light. Solar lentigines may be single or multiple. Solar lentigines are benign, but they do indicate excessive sun exposure, a risk factor for the development of skin cancer. The lesions tend to increase in number with age, making them common among the middle age and older population. They can vary in size from about 0.2 to 2.0 cm. These flat lesions usually have discrete borders, are dark in color, and have an irregular shape.

[0053] As used herein, the term "gene" refers to a linear sequence of nucleotides along a segment of DNA that provides the coded instructions for synthesis of RNA, which, when translated into protein, leads to the expression of hereditary character. As such, the term "skin marker" or "biomarker" refers to a gene whose expression level is different between skin surface samples at the site of malignant melanoma and skin surface samples of normal skin or a lesion, which is benign, such as a benign nevus. Therefore, expression of a melanoma skin marker of the invention is related to, or indicative of, melanoma. Many statistical techniques are known in the art, which can be used to determine whether a statistically significant difference in expression is observed at a high (*e.g.*, 90% or 95%) confidence level. As such, an increase or decrease in expression of these genes is related to and can characterize malignant melanoma. In one embodiment, there is at least a two-fold difference in levels between skin sample near the site of malignant melanoma and skin samples from normal skin.

[0054] As used herein, the term "nucleic acid molecule" means DNA, RNA, single-stranded, double-stranded or triple stranded and any chemical modifications thereof. Virtually any modification of the nucleic acid is contemplated. A "nucleic acid molecle" can be of almost any length, from 10, 20, 30, 40, 50, 60, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 6000, 7000, 8000, 9000, 10,000, 15,000, 20,000, 30,000, 40,000, 50,000, 75,000, 100,000, 150,000, 200,000, 500,000, 1,000,000, 1,500,000, 2,000,000, 5,000,000 or even more bases in length, up to a full-length chromosomal DNA molecule. For methods that analyze expression of a gene, the nucleic acid isolated from a sample is typically RNA.

[0055] Micro-RNAs (miRNA) are small single stranded RNA molecules an average of 22 nucleotides long that are involved in regulating mRNA expression in diverse species including humans (reviewed in Bartel 2004). The first report of miRNA was that of the *lin-4* gene, discovered in the worm *C. elegans* (Lee, Feinbaum et al. 1993). Since then hundreds of miRNAs have been discovered in flies, plants and mammals. miRNAs regulate gene expression by binding to the 3'-untranslated regions of mRNA and catalyze either i) cleavage of the mRNA; or 2) repression of translation. The regulation of gene expression by miRNAs is central to many biological processes such as cell development, differentiation, communication, and apoptosis (Reinhart, Slack et al. 2000; Baehrecke 2003; Brennecke, Hipfner et al. 2003; Chen, Li et al. 2004). Recently it has been shown that miRNA are active during embryogenesis of the mouse epithelium and play a significant role in skin morphogenesis (Yi, O'Carroll et al. 2006).

[0056] Given the role of miRNA in gene expression it is clear that miRNAs will influence, if not completely specify the relative amounts of mRNA in particular cell types and thus determine a particular gene expression profile (*i.e.*, a population of specific mRNAs) in different cell types. In addition, it is likely that the particular distribution of specific miRNAs in a cell will also be distinctive in different cell types. Thus, determination of the miRNA profile of a tissue may be used as a tool for expression profiling of the actual mRNA population in that tissue. Accordingly, miRNA levels and/or detection of miRNA mutations are useful for the purposes of disease detection, diagnosis, prognosis, or treatment-related decisions (*i.e.*, indicate response either before or after a treatment regimen has commenced) or characterization of a particular disease in the subject.

[0057] As used herein, the term "protein" refers to at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. A protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration.

[0058] A "probe" or "probe nucleic acid molecule" is a nucleic acid molecule that is at least partially single-stranded, and that is at least partially complementary, or at least partially substantially complementary, to a sequence of interest. A probe can be RNA, DNA, or a combination of both RNA and DNA. It is also within the scope of the present invention to have probe nucleic acid molecules comprising nucleic acids in which the backbone sugar is other that ribose or deoxyribose. Probe nucleic acids can also be peptide nucleic acids. A probe can comprise nucleolytic-activity resistant linkages or detectable labels, and can be operably linked to other moieties, for example a peptide.

[0059] A single-stranded nucleic acid molecule is "complementary" to another single-stranded nucleic acid molecule when it can base-pair (hybridize) with all or a portion of the other nucleic acid molecule to form a double helix (double-stranded nucleic acid molecule), based on the ability of guanine (G) to base pair with cytosine (C) and adenine (A) to base pair with thymine (T) or uridine (U). For example, the nucleotide sequence 5'-TATAC-3' is complementary to the nucleotide sequence 5'-GTATA-3'.

[0060] The term "antibody" as used in this invention is meant to include intact molecules of polyclonal or monoclonal antibodies, as well as fragments thereof, such as Fab and $F(ab')_2$, Fv and SCA fragments which are capable of binding an epitopic determinant. The term "specifically binds" or "specifically interacts," when used in reference to an antibody means that an interaction of the antibody and a particular epitope has a dissociation constant of at least about 1×10^{-6}, generally at least about 1×10^{-7}, usually at least about 1×10^{-8}, and particularly at least about 1×10^{-9} or 1×10^{-10} or less.

[0061] As used herein "hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through base pairing. Hybridization reactions can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. In an *in vitro* situation, suitably stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature, and are well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. For example, hybridization under high stringency conditions could occur in about 50% formamide at about 37°C to 42°C. Hybridization could occur under reduced stringency conditions in about 35% to 25% formamide at about 30°C to 35°C. In particular, hybridization could occur under high stringency conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and 200 mg/ml sheared and denatured salmon sperm DNA. Hybridization could occur under reduced stringency conditions as described above, but in 35% formamide at a reduced temperature of 35°C. The temperature range corresponding to a particular level of stringency can be further narrowed by calculating the purine to pyrimidine ratio of the nucleic acid of interest and adjusting the temperature accordingly. Variations on the above ranges and conditions are well known in the art.

[0062] As used herein, the term "mutation" refers to a change in the genome with respect to the standard wild-type sequence. Mutations can be deletions, insertions, or rearrangements of nucleic acid sequences at a position in the genome, or they can be single base changes at a position in the genome, referred to as "point mutations." Mutations can be inherited, or they can occur in one or more cells during the lifespan of an individual.

[0063] As used herein, the term "kit" or "research kit" refers to a collection of products that are used to perform a biological research reaction, procedure, or synthesis, such as, for example, a detection, assay, separation, purification, etc., which are typically shipped together, usually within a common packaging, to an end user.

[0064] As used herein, the term "ameliorating" or "treating" means that the clinical signs and/or the symptoms associated with the cancer or melanoma are lessened as a result of the actions performed. The signs or symptoms to be monitored will be characteristic of a particular cancer or melanoma and will be well known to the skilled clinician, as will the methods for monitoring the signs and conditions. Thus, a "treatment regimen" refers to any systematic plan or course for treating a disease or cancer in a subject.

[0065] Samples from a tissue can be isolated by any number of means well known in the art. Invasive methods for isolating a sample include, but are not limited to the use of needles or scalpels, for example during biopsies of various tissues. Non-invasive methods for isolating a sample include, but are not limited to tape-stripping and skin scraping.

[0066] Accordingly, in one embodiment, the present invention employs a non-invasive tape stripping technology to obtain samples of suspicious lesions. As such, DNA microarray assays are used to create a non-invasive diagnostic for melanoma and/or distinguishing melanoma from solar lentigo. Tape-stripping removes superficial cells from the surface of the skin as well as adnexal cells. Small amounts of nucleic acid molecules isolated from tape-stripped cells can be amplified and used for microarray analyses and quantitative PCR. In addition, proteins obtained from the lysed cells may be quantitated for diagnosis of disease. Consequently, tape-stripping is a non-invasive diagnostic method, which does not interfere with subsequent histological analyses, thereby bypassing a major limitation to current expression profiling studies on melanoma. While tape stripping will primarily sample superficial cells from the epidermis, this method holds great promise in the diagnoses and prognosis prediction in pigmented lesions for the following reasons: First, in contrast to benign nevi, in many melanomas the pigmented cells migrate into the epidermis and/or adnexa. Consequently, this feature may help differentiate benign pigmented lesions from melanomas based on tape stripping. Second, there are changes in the dermis and epidermis adjacent to melanoma. The epidermal hyperplasia overlying melanoma seems to correlate with both angiogenesis and metastatic potential; these changes are expected to be sampled with the tape stripping method. Finally, some advanced melanomas do reach the surface of the skin and melanoma cancer cells would be sampled directly by the tape stripping. In addition tape stripping is useful in the care of patients with multiple pigmented lesions where it is unpractical to biopsy each and every lesion. Accordingly, the present invention demonstrates that stratum corneum RNA, harvested by tape stripping with Epidermal Genetic Information Retrieval (EGIR) (see U.S. Pat. No. 6,949,338, incorporated herein by reference), can be used to distinguish melanoma from dysplastic nevi in suspicious pigmented lesions.

[0067] As indicated, the tape stripping methods provided herein typically involve applying an adhesive tape to the skin of a subject and removing the adhesive tape from the skin of the subject one or more times. In certain examples, the adhesive tape is applied to the skin and removed from the skin about one to ten times. Alternatively, about ten adhesive tapes can be sequentially applied to the skin and removed from the skin. These adhesive tapes are then combined for further analysis. Accordingly, an adhesive tape can be applied to and removed from a target site 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 time, and/or 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 adhesive tape can be applied to and removed from the target site. In one illustrative example, the adhesive tape is applied to the skin between about one and eight times, in another example, between one and five times, and in another illustrative example the tape is applied and removed from the skin four times.

[0068] The rubber based adhesive can be, for example, a synthetic rubber-based adhesive. The rubber based adhesive in illustrative examples, has high peel, high shear, and high tack. For example, the rubber based adhesive can have a peak force tack that is at least 25%, 50%, or 100% greater than the peak force tack of an acrylic-based tape such as D-SQUAME™. D-SQUAME™ has been found to have a peak force of 2 Newtons, wherein peak force of the rubber based adhesive used for methods provided herein, can be 4 Newtons or greater.

Furthermore, the rubber based adhesive can have adhesion that is greater than 2 times, 5 times, or 10 times that of acrylic based tape. For example, D-SQUAME™ has been found to have adhesion of 0.0006 Newton meters, whereas the rubber based tape provided herein can have an adhesion of about 0.01 Newton meters using a texture analyzer. Furthermore, in certain illustrative examples, the adhesive used in the methods provided herein has higher peel, shear and tack than other rubber adhesives, especially those used for medical application and Duct tape.

[0069] Virtually any size and/or shape of adhesive tape and target skin site size and shape can be used and analyzed, respectively, by the methods of the present invention. For example, adhesive tape can be fabricated into circular discs of diameter between 10 millimeters and 100 millimeters, for example between 15 and 25 millimeters in diameter. The adhesive tape can have a surface area of between about 50 mm^2 and 1000 mm^2, between about 100 mm^2 to 500 mm^2 or about 250 mm^2.

[0070] In antoher embodiment, the sample is obtained by means of an invasive procedure, such as biopsy. Biopsies may be taken instead of or after tape stripping and are subjected to standard histopathologic analysis. Analysis of biopsy samples taken simultaneously with tape stripping samples may then be correlated with the data generated from one or more of analysis of selected lesion RNA samples by DNA microarray, correlation of gene expression data with histopathology, and creation of a candidate expression classifier for diagnosis of melanoma.

[0071] As used herein, "biopsy" refers to the removal of cells or tissues for analysis. There are many different types of biopsy procedures known in the art. The most common types include: (1) incisional biopsy, in which only a sample of tissue is removed; (2) excisional biopsy, in which an entire lump or suspicious area is removed; and (3) needle biopsy, in which a sample of tissue or fluid is removed with a needle. When a wide needle is used, the procedure is called a core biopsy. When a thin needle is used, the procedure is called a fine-needle aspiration biopsy. Other types of biopsy procedures include, but are not limited to, shave biopsy, punch biopsy, curettage biopsy, and *in situ* biopsy. In another embodiment, the skin sample is obtained by scraping the skin with an instrument to remove one or more nucleic acid molecules from the skin.

[0072] The skin sample obtained using the tape stripping method includes, epidermal cells including cells comprising adnexal structures. In certain illustrative examples, the sample includes predominantly epidermal cells, or even exclusively epidermal cells. The epidermis consists predominantly of keratinocytes (> 90%), which differentiate from the basal layer, moving outward through various layers having decreasing levels of cellular organization, to become the cornified cells of the stratum corneum layer. Renewal of the epidermis occurs every 20-30 days in uninvolved skin. Other cell types present in the epidermis include melanocytes, Langerhans cells, and Merkel cells. As illustrated in the Examples herein, the tape stripping method of the present invention is particularly effective at isolating epidermal samples.

[0073] Nucleic acid molecules can also be isolated by lysing the cells and cellular material collected from the skin sample by any number of means well known to those skilled in the art. For example, a number of commercial products available for isolating polynucleotides, including but not limited to, RNeasy™ (Qiagen, Valencia, CA) and TriReagent™ (Molecular Research Center, Inc, Cincinnati, OH) can be used. The isolated polynucleotides can then be tested or assayed for particular nucleic acid sequences, including a polynucleotide encoding a cytokine. Methods of recovering a target nucleic acid molecule within a nucleic acid sample are well known in the art, and can include microarray analysis.

[0074] Nucleic acid molecules may be analyzed in any number of ways known in the art. For example, the presence of nucleic acid molecules can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments of the specific nucleic acid molecule. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the nucleic acid sequences to detect transformants containing the specific DNA or RNA.

[0075] In one embodiment, analysis of the nucleic acid molecules includes genetic analysis is to determine the nucleotide sequence of a gene. Since a difference in length or sequence between DNA fragments isolated from a sample and those of known sequences are due to an insertion, deletion, or substitution of one or more nucleotides, the determination of nucleic acid sequences provides information concerning mutations which have absolute influence on the physiology of the disease state in the subject. These mutations may also include transposition or inversion and are difficult to detect by other techniques than direct sequencing. For example, it has recently been shown that the presence of the c-kit-activating mutation, L576P, is indicative of malignant melanomas (see Table 1). Accordingly, the methods of the present invention may be used to detect genetic mutations in one or more genes listed in Tables 1-8 and 10-12 for diagnosis and/or characterization of a skin lesion in a subject.

[0076] A variety of protocols for detecting and measuring the expression of nucleic acid molecules, using either polyclonal or monoclonal antibodies specific for the protein expression product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; J. Exp. Med. 158:1211-1216).

[0077] In another embodiment, antibodies that specifically bind the expression products of the nucleic acid molecules of the invention may be used to characterize the skin lesion of the subject. The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule.

[0078] A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to the nucleic acid molecules of Tables 1-8, 10-12, and 15 include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the nucleic acid molecules, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits (Pharmacia & Upjohn, (Kalamazoo, Mich.); Promega (Madison Wis.); and U.S. Biochemical Corp., Cleveland, Ohio). Suitable reporter molecules or labels, which may be used for ease of detection, include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

[0079] PCR systems usually use two amplification primers and an additional amplicon-specific, fluorogenic hybridization probe that specifically binds to a site within the amplicon. The probe can include one or more fluorescence label moieties. For example, the probe can be labeled with two fluorescent dyes: 1) a 6-carboxy-fluorescein (FAM), located at the 5'-end, which serves as reporter, and 2) a 6-carboxy-tetramethyl-rhodamine (TAMRA), located at the 3'-end, which serves as a quencher. When amplification occurs, the 5'-3' exonuclease activity of the Taq DNA polymerase cleaves the reporter from the probe during the extension phase, thus releasing it from the quencher. The resulting increase in fluorescence emission of the reporter dye is monitored during the PCR process and represents the number of DNA fragments generated. *In situ* PCR may be utilized for the direct localization and visualization of target nucleic acid molecules and may be further useful in correlating expression with histopathological finding.

[0080] Means for producing specific hybridization probes for nucleic acid molecules of the invention include the cloning of the nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art, commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, radionuclides such as ^{32}P or ^{35}S, or enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

[0081] In order to provide a basis for the diagnosis or characterization of disease associated with expression of the nucleic acid molecules of the invention, a normal or standard profile for expression is established. Standard hybridization may be quantified by comparing the values obtained from subjects of known skin characterization (*e.g.,* from subjects either having melanoma, having dysplastic nevi, and/or having solar lentigines). Standard values obtained from such samples may be compared with values obtained from samples from subjects having skin lesions that are suspected of being melanoma. Deviation between standard and subject values is used to establish the presence of disease.

[0082] Accordingly, in one aspect of the invention, a non-invasive sampling method is provided for the characterization of skin lesion on the skin. In one embodiment, a sample set of pigmented skin lesions is created. Each sample consists of nucleic acid molecules recovered by tape stripping or biopsy sample of the superficial epidermis overlying the lesion. In addition to tape striping, a standard biopsy of the same lesion may also be performed, along with accompanying histology and diagnosis. Nucleic acid molecules recovered by tape stripping the superficial epidermis of normal skin will serve as a negative control.

[0083] In another aspect, the invention provides a method of distinguishing melanoma from solar lentigo and/or dysplastic nevi and/or normal pigmented skin in a subject. In one embodiment, the method includes analyzing a nucleic acid molecule from one or more genes listed in any of Tables 1-8, 10-12, 15, or any combination thereof. A target area of the skin of a subject that suspected of being melanoma is assayed for expression of a large number of genes. Analyzing expression includes any qualitative or quantitative method for detecting expression of a gene, many of which are known in the art. The method can include analyzing expression of specific markers by measuring expression of the markers using a quantitative method, or by using a qualitative method. Non-limiting methods for analyzing polynucleotides and polypeptides are discussed below.

[0084] In another aspect, the invention provides a method of distinguishing solar lentigines from dysplastic nevi and/or basal cell carcinoma and/or normal pigmented skin in a subject. In one embodiment, the method includes analyzing a nucleic acid molecule from one or more genes listed in any of Tables 1-8, 10-12, 15, or any combination thereof. A target area of the skin of a subject that suspected of being melanoma is assayed for expression of a large number of genes. Analyzing expression includes any qualitative or quantitative method for detecting expression of a gene, many of which are known in the art. The method can include analyzing expression of specific markers by measuring expression of the markers using a quantitative method, or by using a qualitative method. Non-limiting methods for analyzing polynucleotides and polypeptides are discussed below

[0085] Methods of analyzing expression of a gene of the present invention can utilize a microarray, or other miniature high-throughput technology, for detecting expression of one or more gene products. Quantitative measurement of expression levels using such microarrays is also known in the art, and typically involves a modified version of a traditional method for measuring expression as described herein. For example, such quantitation can be performed by measuring a phosphor image of a radioactive-labeled probe binding to a spot of a microarray, using a phospohor imager and imaging software.

[0086] In a related aspect, the invention provides a method for diagnosing various disease states in a subject by identifying new diagnostic markers, specifically the classification and diagnosis of melanoma. In addition, the invention provides a method for distinguishing solar lentigines from dysplastic nevi and/or lentigo maligna and/or normal skin. Thus, the invention provides a method for diagnosing various disease states in a subject by identifying new diagnostic markers, specifically the classification and diagnosis of melanoma. By identifying gene sets that are unique to a given state, these differences in the genetic expression can be utilized for diagnostic purposes. In one embodiment, the nucleic acid molecule is RNA, including messenger RNA (mRNA) that is isolated from a sample from the subject. Up-regulated and down-regulated gene sets for a given disease state may be subsequently combined. The combination enables those of skill in the art to identify gene sets or panels that are unique to a given disease state. Such gene sets are of immense diagnostic value as they can be routinely used in assays that are simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets also provide insights into pathogenesis and targets for the design of new drugs.

[0087] A reference database containing a number of reference projected profiles is also created from skin samples of subjects with known states, such as normal (*i.e.*, non-melanoma) and various skin cancer disease states and/or pigmented non-cancer states. The projected profile is then compared with the reference database containing the reference projected profiles. If the projected profile of the subject matches best with the profile of a particular disease state in the database, the subject is diagnosed as having such disease state. Various computer systems and software can be utilized for implementing the analytical methods of this invention and are apparent to one of skill in the art. Exemplary software programs include, but are not limited to, Cluster & TreeView (Stanford, URLs: rana.lbl.gov or microarray.org), GeneCluster (MIT/Whitehead Institute, URL: MPR/GeneCluster/GeneCluster.html), Array Explorer (SpotFire Inc, URL: spotfire.com/products/scicomp.asp#SAE) and GeneSpring (Silicon Genetics Inc, URL: sigenetics.com/Products/GeneSpring/index.html) (for computer systems and software, see also U.S. Pat. No. 6,203,987, incorporated herein by reference).

[0088] In another aspect, the methods of the present invention involve *in situ* analysis of the skin lesion for characterization thereof. For *in situ* methods, nucleic acid molecules do not need to be isolated from the subject prior to analysis. In one embodiment, detectably labeled probes are contacted with a cell or tissue of a subject for visual detection of expressed RNA to characterize the skin lesion.

[0089] In another aspect, the methods of the present invention can also be useful for monitoring the progression of diseases and the effectiveness of treatments. For example, by comparing the projected profile prior to treatment with the profile after treatment. In one embodiment, the method characterizes a cancer as melanoma metastasis based on analysis of one or more nucleic acid molecules from Tables 1-8. In another embodiment, the method characterizes a solar lentigo based on analysis of one or more nucleic acid molecules from Tables 10-12 and 15. It is known that in many cases, by the time a diagnosis of melanoma is established in a subject, metastasis has already occurred since melanomas contain multiple cell populations characterized by diverse growth rates, karyotypes, cell-surface properties, antigenicity, immunogenicity, invasion, metastasis, and sensitivity to cytotoxic drugs or biologic agents. Thus, the present invention may be used to characterize cancer of an organ as having metastasized from melanoma.

[0090] In a related aspect, the methods of the present invention can also be useful for determining an appropriate treatment regimen for a subject having a specific cancer or melanoma. In another related aspect, the methods of the present invention can also be useful for determining an appropriate treatment regimen for a subject having solar lentigo. Thus, the methods of the invention are useful for providing a means for practicing personalized medicine, wherein treatment is tailored to a subject based on the particular characteristics of the cancer or skin lesion in the subject. The method can be practiced, for example, by first determining whether the skin lesion is melanoma or solar lentigo, as described above.

[0091] The sample of cells examined according to the present method can be obtained from the subject to be treated, or can be cells of an established cancer cell line of the same type as that of the subject. In one aspect, the established cell line can be one of a panel of such cell lines, wherein the panel can include different cell lines of the same type of disease and/or different cell lines of different diseases associated with expression of the genes of interest. Such a panel of cell lines can be useful, for example, to practice the present method when only a small number of cells can be obtained from the subject to be treated, thus providing a surrogate sample of the subject's cells, and also can be useful to include as control samples in practicing the present methods.

[0092] Once disease and/or skin lesion characterization is established and a treatment protocol is initiated, the methods of the invention may be repeated on a regular basis to monitor the expression profiles of the genes of interest in the subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months. Accordingly, another aspect of the invention is directed to methods for monitoring a therapeutic regimen for treating a subject having skin cancer. A comparison of the expression profile or mutations in the nucleic acid sequence of the nucleic acid molecule prior to and during therapy will be indicative of the efficacy of the therapy. Therefore, one skilled in the art will be able to recognize and adjust the therapeutic approach as needed.

[0093] The efficacy of a therapeutic regimen for treating a cancer over time can be identified by an absence of symptoms or clinical signs of the particular cancer in a subject at the time of onset of therapy. In subjects diagnosed as having the particular cancer, the efficacy of a method of the invention can be evaluated by measuring a lessening in the severity of the signs or symptoms in the subject or by the occurrence of a surrogate end-point for the disorder.

[0094] In addition, such methods may help identify an individual as having a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

[0095] When performed in a high throughput (or ultra-high throughput) format, the methods of the invention can be performed on a solid support (*e.g.*, a microtiter plate, a silicon wafer, or a glass slide), wherein cell samples and/or genes of interest are positioned such that each is delineated from each other (*e.g.*, in wells). Any number of samples or genes (*e.g.*, 96, 1024, 10,000, 100,000, or more) can be examined in parallel using such a method, depending on the particular support used. Where samples are positioned in an array (*i.e.*, a defined pattern), each sample in the array can be defined by its position (*e.g.*, using an x-y axis), thus providing an "address" for each sample. An advantage of using an addressable array format is that the method can be automated, in whole or in part, such that cell samples, reagents, genes of interest, and the like, can be dispensed to (or removed from) specified positions at desired times, and samples (or aliquots) can be monitored, for example, for expression products and/or mutations in the nucleic acid sequence of the nucleic acid molecules from any one of the genes listed in Tables 1-8, 10-12, and 15.

[0096] Thus, the microarray can be used to monitor the expression level of large numbers of genes simultaneously (to produce a transcript image), and to identify genetic variants, mutations and polymorphisms. Polynucleotides used in the microarray may be oligonucleotides that are specific to a gene or genes of interest in which at least a fragment of the sequence is known or that are specific to one or more unidentified cDNAs which are common to a particular cell type, developmental or disease state. In order to produce oligonucleotides to a known sequence for a microarray, the gene of interest is examined using a computer algorithm which starts at the 5' or more preferably at the 3' end of the nucleotide sequence. The algorithm identifies oligomers of defined length that are unique to the gene, have a GC content within a range suitable for hybridization, and lack predicted secondary structure that may interfere with hybridization. In certain situations it may be appropriate to use pairs of oligonucleotides on a microarray. The "pairs" will be identical, except for one nucleotide which preferably is located in the center of the sequence. The second oligonucleotide in the pair (mismatched by one) serves as a control. The number of oligonucleotide pairs may range from two to one million. The oligomers are synthesized at designated areas on a substrate using a light-directed chemical process. The substrate may be paper, nylon or other type of membrane, filter, chip, glass slide or any other suitable solid support.

[0097] According to another aspect of the present invention, a kit is provided that is useful for detecting cancer in a cell or tissue, *e.g.*, using the methods provided by the present invention for characterizing a skin lesion in a subject. In one embodiment, a kit of the invention includes a skin sample collection device and one or more probes or primers that selectively bind to one or more of the nucleic acid molecules in any of Tables 1-8, 10-12, and 15. In another embodiment, the kit includes one or more applicators in addition to or instead of the skin sample collection device. Such applicators are useful for *in situ* analysis of gene expression on the skin of a subject. For example, an applicator may be used to apply detectably labeled probes for visual detection of expressed RNA to characterize the skin lesion.

[0098] In another embodiment, a kit of the invention includes a probe that binds to a portion of a nucleic acid molecule in any of Tables 1-8, 10-12, and 15. In another embodiment, the kit further includes a microarray that contains at least a fragment of a gene or a nucleic acid molecule or a protein product of any one of the genes listed in Tables 1-8, 10-12, and 15. In some embodiments, many reagents may be provided in a kit of the invention, only some of which should be used together in a particular reaction or procedure. For example, multiple primers may be provided, only two of which are needed for a particular application.

[0099] In another embodiment, the kit of the invention provides a compartmentalized carrier including a first container containing a pair of primers. The primers are typically a forward primer that selectively binds upstream of a gene on one strand, and a reverse primer that selectively binds upstream of a gene on a complementary strand. Optionally the kits of the present invention can further include an instruction insert, *e.g.*, disclosing methods for sample collection using the sample collection device and/or exemplary gene expression profiles for comparison with the expression profile of the sample taken from the subject.

[0100] The following examples are provided to further illustrate the advantages and features of the present invention, but are not intended to limit the scope of the invention. While they are typical of those that might be used, other procedures, methodologies, or techniques known to those skilled in the art may alternatively be used.

EXAMPLE 1

RNA Quantitation and Profiling

[0101] The core hypothesis of this study is that epidermal cells overlying in situ or invasive melanoma, including but not limited to the stratum corneum, stratum lucidum, and stratum granulosum, can be recovered by adhesive means and that the quality and quantity of gene expression in the form of RNA contained within this sample is differently expressed than from a nearby epidermal sample, i.e. that the sampled RNA is diagnostic because of the underlying melanoma. It has been previously shown that changes in gene expression of specific genes are detectable in epidermal hyperplasia overlying cutaneous human melanoma samples obtained from surgical specimens of the epidermis (McCarty et al., 2003).

[0102] The present study is divided into two separate phases, a sample collection and characterization phase (phase 1) and an RNA profiling phase (phase 2). In phase 1 the tape stripped specimens and biopsied sample collections were performed by the principal investigator or trained individuals delegated by the principal investigator to obtain the biopsy sample at various sites. All biopsies are subject to standard histopathologic analysis. The RNA profiling phase (Phase 2), includes, but is not limited to RNA purification and hybridization to DNA microarrays for gene expression profiling.

[0103] **Materials and reagents.** Adhesive tape was purchased from Adhesives Research (Glen Rock, PA) in bulk rolls. These rolls were custom fabricated into small circular discs, 17 millimeters in diameter, by Diagnostic Laminations Engineering (Oceanside, CA). Human spleen total RNA was purchased from Ambion (catalogue # 7970; Austin, TX). RNeasy RNA extraction kit was purchased from Qiagen (Valencia, CA). Reverse transcriptase, PCR primers and probes, and TaqMan Universal Master Mix, which included all buffers and enzymes necessary for the amplification and fluorescent detection of specific cDNAs, were purchased from Applied Biosystems (Foster City, CA). MELT total nucleic acid isolation system was purchased from Ambion (Austin, TX).

[0104] **RNA isolation.** RNA was extracted from tapes using either pressure cycling technology (PCT; Garrett, Tao et al. 2002; Schumacher, Manak et al. 2002) or MELT total nucleic acid system. Tapes were extracted in pairs by insertion into a PULSE™ tube (Pressure Biosciences, Gaithersburg, MD) with 1.2 mls of buffer RLT (supplied in the Qiagen RNeasy kit). PULSE™ tubes were inserted into the PCT-NEP2017 pressure cycler and the sample was extracted using the following parameters: room temperature; 5 pressure cycles of 35 Kpsi with pressure held for 20 seconds at the top and bottom of each cycle. After pressure extraction the buffer was removed and used to process the remaining tapes used to strip that site; the buffer was then processed according to the standard Qiagen RNeasy protocol for the collection of larger RNAs (>200 nucleotides) by application to a purification column to which large RNA molecules (*i.e.* mRNAs) bind, while the column flow-through is saved for microRNA purification. The column flow-through, which contains miRNA separated from mRNA, is processed according to the Qiagen miRNA purification procedure (on the world wide web at qiagen.com/literature/protocols/pdf/RY20.pdf) to purify the microRNA. RNA from the 2 sites stripped on each subject was pooled to create a single sample from each subject.

[0105] RNA isolation using MELT total nucleic acid protocol. Tapes were extracted in a 2 ml eppendorf tube with 192 ml MELT buffer plus 8 ml of MELT cocktail and vortexed for 10 minutes at room temperature. The MELT lysates were transferred to the dispensed binding bead master mix after spinning down for 3 minutes at >10,000 xg and washed with 300 ml of Wash Solution 1 and 2. RNAs were eluted in 100 ml of elution solution.

[0106] Quantitation of mRNA. Experimental data is reported as the number of PCR cycles required to achieve a threshold fluorescence for a specific cDNA and is described as the "C_t" value (Gibson, Heid et al. 1996; Heid, Stevens et al. 1996; AppliedBiosystems 2001). Quantitation of total RNA mass was performed as previously described (Wong, Tran et al. 2004). Briefly, RNA mass recovered from tapes is determined by using quantitative RT-PCR with reference to a standard curve ($C_{t,\ actin}$ vs. log[RNA]; AppliedBiosystems 2001) created from commercially purchased human spleen total RNA. The average of 6 replicate $C_{t,\ actin}$ values was used to calculate the concentration of RNA in a sample with reference to the standard curve.

[0107] RNA amplification and array hybridization. RNA was isolated by the Multi-Enzymatic Liquefaction of Tissue method (Ambion, Austin, TX) and amplified using the WT-Ovation pico amplification system (NuGen, San Carlos, CA). The amplified RNA was hybridized to Affymetrix U133 plus 2.0 microarray and data were processed and analyzed using R from Bioconductor.

[0108] Sample size. Sample size calculations are presented in Example 2. This analysis predicts that in order to find 25 – 40 genes with high predictive value ($p < 0.001$) for discriminating benign nevi from melanoma then approximately 30 melanomas and 30 non-melanoma lesions are needed.

[0109] Preprocessing GeneChip Data. The image files from scanning the Affymetrix GeneChips with the Affymetrix series 3000 scanner will be converted using GCOS software (Affymetrix) to "CEL" format files. Normalization of CEL files will be carried out using software from the Bioconductor suite (on the world wide web at bioconductor.org). In particular, a robust multiarray analysis with adjustments for optical noise and binding affinities of oligonucleotide probes (Wu et al., 2006; and Wu et al., 2004) as implemented by the function "just.gcrma" in the "gcrma" package will be used to normalize the GeneChip Data.

[0110] **Statistical Approach for Microarray Data Analysis.** Two generic statistical problems are addressed in this proposal: (i) identifying genes that are differentially expressed in different classes of lesions (*i.e.* melanoma versus non-melanoma lesions) and (ii) forming (and evaluating) rules for classification of melanoma and non-melanoma lesions into groups based on gene expression data.

[0111] The most important grouping divides melanoma from non-melanoma on the basis of biopsy results. The methods that will be used to address the problems identified above are now standard in the statistical evaluation of microarray data (for reviews see Smyth et al., 2003; and Lee, 2004)). These methods have been applied by others to data from Affymetrix arrays to study gene expression in prostate cancer (Stuart et al., 2004), to characterize changes in gene expression subsequent to HIV infection (Mitchell et al., 2003), and to develop a high throughput genotyping platform (Wolyn et al., 2004; and Borevitz et al., 2003). For identifying differentially expressed genes, permutation based estimates of false discovery rates (reviewed in Efron et al., 2002) are preferred. Scripts for the R quantitative programming environment were developed to implement these methods in our previous work, but will likely use or adapt the "siggenes" package from the Bioconductor suite in this project. The development of classification rules will rely on resampling methods (k-fold cross-validation, the 632 plus bootstrap, and / or bagging (Hastie et al., 2001) applied to the naive Bayes classifier and the nearest shrunken centroid classifier (Tibshirani et al., 2002) and the support vector machine (SVM) which both performed well in classifying prostate tissues as malignant or benign, used in our previous work. The implementation likely to be used is to perform k-fold cross-validation. Within each of the k train/test cycles an initial screen of the training data for differentially expressed genes is performed and genes are ordered according to their posterior probability of differential expression. Naive Bayes and nearest shrunken centroid classifiers based on the r genes with the highest posterior probability of differential expression are formed choosing enough values of r between 1 and

1024 to allow accurate interpolation of the classification error rate. The "one se rule" (Brieman et al., 1984) is applied to the error rates for the test sets to choose the classifier that minimizes the error rate. For SVM, an internal 632+ bootstrap is applied to each training sample to select the number of genes to be used in forming the classifier. The "1 se rule" error rates from the k test sets are used to characterize the classification accuracy.

[0112] In addition to the use of univariate and multivariate statistical analysis tools, sophisticated bioinformatic analysis approaches will help make sense of possible biological links between the genes found to be differentially expressed between, *e.g.*, melanoma and non-melanoma samples. These approaches will focus on the analysis of genetic networks and pathways (Edelman et al., 2006; Kong et al., 2006; and Pang et al., 2006) and have been implemented in software packages such as Ingenuity (on the world wide web at ingenuity.com) and MetaCore (on the world wide web at genego.com). The identification of the biological links between genes that emerge from a gene expression microarray analysis can help put into context the biological meaningfulness of their expression patterns as well as help reduce the set of differentially expressed genes to be represented on a diagnostic panel based on their biology. The end result of this analysis will be to define a candidate expression classifier that will be validated in future, larger clinical trials.

[0113] **QC metrics for RNA, amplified cDNA and microarray data.** Following informed consent, the suspicious pigmented lesion was tape stripped using EGIR and then biopsied as per standard of care. The resulting RNA isolated from the EGIR tape was amplified and profiled on the Affymetrix U133 plus 2.0 GeneChip. Microarray data were normalized by the GCRMA algorithm. To assure high quality of microarray data are generated, QC metrics were established for RNA, amplified cDNA and microarray data. The quality of RNA was assessed by capillary electrophoresis using the Experion system (Biorad, Hercule, CA) and RNA with at least one visible 18S rRNA was further processed for RNA amplification. The amplified cDNA was quantified by the Nanodrop system and quality of the amplified cDNA was also assessed by the Experion system. The yield of the amplified cDNAs greater than 5 mg and the average size distribution of the cDNAs greater than 750 nt were carried forward for microarray hybridization. Quality of the array data was further assessed using simpleaffy program in R and the array data with scaling factor less than 5.0 and % present call greater than 30% were used for further data analysis.

[0114] **Class Modeling – PAM.** After passing the array data QC, 14 melanomas, 40 dysplastic nevi and 12 normal skin specimens were further analyzed. First, gene expression values less than 50 across all samples were filtered out and 16716 probesets were tested. These 16716 probesets were subjected to a statistical analysis for differentially expressed genes among melanomas, dysplastic nevi and normal skin using ANOVA ($p<0.05$), multiple testing correction algorithm (Westafall and Young permutation) and false discover rate (FDR) of 0.05. As indicated above, of the original 117 genes, an 89 gene panel (Table 2) was found to be a potential melanoma classifier. Further testing identified a 5-gene classifier (Table 3), a 30-gene classifier (Table 4) that includes newly identified genes, a 20-gene classifier (Table 5) that includes newly identified genes, and a 19-gene classifier that includes newly identified genes, which may all be used to discriminate melanomas from atypical nevi. The genes and respective classifier panels were analyzed using the Prediction Analysis of Microarrays (PAM) software freely available from Stanford University (Stanford, CA).

[0115] The PAM software uses a modification of the nearest centroid method, which computes a standardized centroid for each class in a training set. This refers to the average gene expression for each gene in each class divided by the within-class standard deviation for that gene. Nearest centroid classification takes the gene expression profile of a new sample, and compares it to each of these class centroids. The class, whose centroid it is closest to, in squared distance, is the predicted class for that new sample.

[0116] These genes were all subjected to a hierarchical clustering analysis and the melanoma specimens grouped together and were clearly distinguished from dysplastic nevi and normal skin. In addition, there are three distinct classes of dysplastic nevi; one is grouped together with normal skin and the second one was in between normal skin and melanomas, while the third one was grouped together with melanomas. These data suggest stratum corneum RNA, harvested by tape stripping with EGIR, can be used to distinguish melanoma from dysplastic nevi in suspiciously pigmented lesions.

[0117] The analysis of the genes as potential melanoma classifiers to discriminate between melanomas and dysplastic nevi was performed using t-test ($p<0.01$), FDR (0.05) and 2-fold difference between melanomas and dysplastic nevi. Of the original 117 genes, an 89 gene panel (Table 2) was found to be a potential melanoma classifier and functions of these 89 genes were subjected to Ingenuity Pathway Analysis (IPA) (Ingenuity, Redwood City, CA).

Among them, 15 genes are involved hair and skin development and function, 18 genes are involved in cellular development, 16 genes are involved in cellular growth and proliferation and 24 genes are related to cancer. Thus, differentially expressed genes are genes related to biological functions in melanocytes including melanin biosynthesis, melanocyte proliferation, differentiation and development. (See Figures 5 and 6).

[0118] **Class Modeling – Random Forests.** Additional work, in which 31 melanomas, 71 atypical nevi, and 15 normal skin controls were analyzed by GeneChip assay, identified 284 differentially expressed genes ($p<0.001$, false discovery rate $q<0.05$). Hierarchical cluster analysis of these genes showed that melanomas can be distinguished from atypical nevi and normal skin, and, suggested the existence of different classes of atypical nevi (Figure 7). Several of the genes were found by Ingenuity Pathways analysis to play a role in melanocyte development and function, as well as, skin development, cellular proliferation, and cancer. These findings further demonstrated that the presence of melanoma, directly or indirectly, alters the gene expression profile of stratum corneum. 229 genes were subject to Random Forests analysis and 61 of those 229 genes were found to discriminate melanoma from atypical nevi (see Figure 8).

[0119] Random Forests analysis is based on Bagging Predictors, which is a method for generating multiple versions of a predictor and using these to get an aggregated predictor. The aggregation averages over the versions when predicting a numerical outcome and does a plurality vote when predicting a class. The multiple versions are formed by making bootstrap replicates of the learning set and using these as new learning sets. Tests on real and simulated data sets using classification and regression trees and subset selection in linear regression show that bagging can give substantial gains in accuracy. If perturbing the learning set can cause significant changes in the predictor constructed, then bagging can improve accuracy.

[0120] **Class Modeling – TREENET®.** 82 additional genes were identified (Table 7). TREENET® software (Salford Systems, San Diego, CA) was used to identify a 20-gene panel (Table 8), which may all be used to discriminate melanomas from atypical nevi (see Figure 9). An additional 19-gene classifier was identified from 7199 differentially expressed genes between melanoma and nevi (Table 6; see also Figures 11 and 12). The 19-gene classifier was tested against independent samples and shown to be 100% sensitive and 88% specific for detection of melanomas. In addition, results from 10 melanomas and 10 nevi indicated that qRT-PCR recapitulated the data obtained using the GeneChip microarray (Figure 12 and see raw data in Tables 13 and 14).

[0121] TREENET® is a data mining tool that is based on boosted decision trees. TREENET® is a model building and function approximation system that also serves as an initial data exploration tool. It can extract relationships in data and calibrate how predictable the outcomes will be, and can handle both classification and regression problems.

EXAMPLE 2

Preliminary Power and Sample Size Studies:

Nevi vs. Primary Melanoma

[0122] The following sample size and power calculations are based exclusively on the large-scale cDNA study data provided in Haqq *et al* (2005). That data focused on normal skin (n=3 samples), nevi (n=9), primary melanomas (n=6) and metastatic melanomas (n=19). For purposes of the sample size calculations, the focus was on the comparison of nevi to primary melanomas. Power and sample size assessments were calculated based on the bootstrap strategy outlined by Page *et al*. Using the raw data available from the Haqq *et al* (2005) study, gene expression differences—based on all 14,772 probes used in their cDNA assay—between nevi and primary melanomas were computed using simple t-tests for each probe/gene. Note that multiple probes can be used interrogate individual genes. In addition, normal skin, nevi, and primary melanoma gene expression differences were also assessed in a three group analysis of variance (ANOVA), with the specific contrast between nevi and primary melanoma computed from this ANOVA. In the figures that follow, three main parameters are used to assess power and sample size. Table 9 (adapted from Page, *et al.*) shows the number of genes truly or not truly differentially expressed, and provides a simple way of describing these parameters, which are defined as follows (with the color of the curves corresponding to each parameter provided in parentheses for Figures 1A and 2A, although Figures 1B and 2B focus exclusively on the EDR as defined below.

[0123] *EDR:* Expected Discovery Rate (from Table 9, D / (B+D)). This reflects the expected proportion of probes/genes that will be declared significantly differentially expressed at the defined threshold (here taken to be, for the most part, $p<0.05$) that are, in fact, differentially expressed between nevi and primary melanomas.

[0124] *PTP*: Expected Proportion of probes/genes that are True Positives (Table 9, D / (C+D)). This proportion reflects the number of probes/genes showing expression differences that are likely to be truly differential expressed out of the total number of genes whose expression values result in test statistics less than the threshold (*e.g.*, 0.05).

[0125] *PTN:* Probability of a True Negative result (Table 9, A / (A+B)). This probability concerns probes/genes that are not significantly different at the assumed threshold (*e.g.*, 0.05) that are, in fact, not differentially expressed between skin and melanoma.

Table 9. Parameters of Relevance for Assessing the Power of Microarray Studies

Result based on array analysis	Not differentially expressed	Truly differentially expressed
Genes not significant	A	B
Genes significant	C	D

These columns represent the number of genes found to satisfy the given constraint; A = genes found not to be differentially expressed in an array experiment and that are truly not differentially expressed; B = genes that are differentially expressed but are not found to be differentially expressed in the array experiment (false negatives); C = genes that are found to be differentially expressed in the array experiment but are not truly differentially expressed (false positives); D = gene found to be differentially expressed in an array experiment and that are truly differentially expressed.

[0126] **Nevi versus Primary data.** The sample size analysis considered the number of samples necessary to "discover" or identify a probe or gene or set of probes/genes that could differentiate nevi from primary melanomas based on the probe/gene expression differences obtained by Haqq et al. (2005). Figure 1a provides a plot of the EDR, PTP, and PTN as a function of sample size, assuming a threshold for declaring the significance of a probe/gene expression difference between nevi and primary melanoma of $p < 0.05$. Thus, from the plot, it appears that in order to "discover," or identify, 80% of all genes that have been interrogated on a chip that exhibit a probe/gene expression difference producing a test statistic p-value < 0.05 that will actually reflect a true probe/gene expression difference, a sample size of roughly 20 per nevi and primary melanoma group will be needed. Note that if all 14,772 probes are considered, one is likely to have 14,772 x 0.05 = 738 exhibit p-values < 0.05 by chance alone, of which 1,727 x 0.80 = 1,381 will likely reflect true gene expression differences at that significance (*i.e.*, p-value) level. If one is interested in identifying a smaller set of genes that have a greater probability of being detected as truly differentially expressed, a more stringent threshold for statistical significance (*e.g.*, 0.001) can be used. This would generate 14,772 x 0.001 = 15 genes with p-values < 0.001 by chance of which ~45% (*i.e.*, 34 x 0.45 = 7 would likely be truly differentially expressed at that level; see Figure 1b; note curves in Figure 1b only correspond to the EDR with different assumed type I error rates).

[0127] A sample size analysis that considered the contrast results for nevi vs. primary melanoma in the context of an analysis of variance (ANOVA) comparing normal skin, nevi, and primary melanoma was also pursued. The rationale for this is that there are more differences between normal skin and either nevi or primary melanoma than there are between nevi and primary melanoma (based on an analysis of the Haqq et al (2005) data), and an analysis that considers normal skin gene expression variation may help reduce the noise in the assessment of nevi vs. primary melanoma gene expression differences. Figures 2a and 2b display the results of these analyses and provide similar sample size guidelines to those reflected in Figures 1a and 1b.

[0128] An analysis focusing exclusively on the posterior true probability (PTP) was also considered since, as discussed, there may be many probes/genes that exhibit differences between nevi and primary melanomas at a certain probability level purely by chance (given the large number of probes/genes interrogated). Thus, the likely fraction of these probes/genes that are truly differentially expressed is important to assess. Figures 3a and 3b reflect the results for different assumed significance levels.

[0129] Thus, an argument can be made that a study with approximately 20 samples per nevi and primary melanoma groups would have sufficient power to detect 80% of all genes that are likely to exhibit differential expression at a p-value level of 0.05 because they are, in fact, differentially expressed at this level. However, the number of genes (or probes) contributing to this set of differentially expressed genes is likely to number in the hundreds, if 10,000-30,000 probes are used or 5,000-10,000 genes are studied. If interest is in identifying a smaller number of probes or genes (~25 – 40) that have a greater probability of being differentially expressed, say, at a p-value of 0.001, then ~30 nevi and 30 primary melanoma samples would be needed (see Figures 1, 2, and 3).

EXAMPLE 3

Tape Stripping to Recover Nucleic Acids from Normal Skin

[0130] The following procedure was used to recover nucleic acids from normal skin (*e.g.*, the mastoid or upper back areas) of a subject.

[0131] Tapes were handled with gloved hands at all times. Locate a particular site that is relatively blemish-free and healthy, unless otherwise specified by the protocol. Preferred normal skin sites are the mastoid process (the bony process behind the ear at the base of the skull) and the upper back, immediately superior to the scapular spine. Shave the site if necessary to remove non-vellus hairs. Cleanse the site with an alcohol wipe (70% isopropyl alcohol). Let the site air dry completely before application of the tape. It is recommended to wait approximately 2 minutes to ensure the site is completely dry before application of the tape.

[0132] Apply the tape to the skin site. If more than one tape is used, apply tapes in sequential order starting from the left side. Use a surgical skin marker and/or a water soluble marker to mark the location of the tape on the skin in order to align subsequent tapes.

[0133] Start the tape harvesting procedure by applying pressure (press on the tape firmly). Ensure that the skin is held taut to ensure that the tape does not move while applying pressure. Then remove the tape slowly in one direction. Place the edge of the tape onto the strip at the top of the packet with the adhesive surface of the tape facing down to protect the sample. Put a second tape on the same site; apply pressure firmly as above. Remove the tape slowly in an opposite direction to that used in the immediately previous application.

[0134] Continue tape stripping by putting additional tapes on the same site, following the steps provided above. The site may stripped with a total of at least four tapes, unless otherwise specified in the protocol. Place the strip into a storage bag and immediately place the samples on dry ice or into storage at -20°C or below until analysis.

EXAMPLE 4

Tape Stripping to Recover Nucleic Acids from Pigmented Lesions

[0135] The following procedure was used to recover nucleic acids from pigmented lesions and/or skin suspected of melanoma of a subject. In contrast to normal skin, lesional skin should have a preoperative biopsy diameter of greater than or equal to about 6 mm, but less than that of the tape disc. Multiple lesions must be at least about 4 mm apart. The area of tape that touches the lesion should be generously demarcated on the tape with an insoluble ink pen so that this area may be cut away from the surrounding tape at the laboratory as part of the RNA extraction procedure.

[0136] As above, tapes were handled with gloved hands at all times. Shave the site if necessary to remove non-vellus hairs. Cleanse the site with an alcohol wipe (70% isopropyl alcohol). Let the site air dry completely before application of the tape. It is recommended to approximately 2 minutes to ensure the site is completely dry before application of the tape.

[0137] Apply the tape to the skin site. If more than one tape is used, apply tapes in sequential order starting from the left side. Use a surgical skin marker and/or a water soluble marker to mark the location of the tape on the skin in order to align subsequent tapes. Apply the tape to the suspect lesion, which should have a diameter that is greater than or equal to about 6 mm.

[0138] Start the tape harvesting procedure by applying pressure directly over the lesion and avoiding surrounding normal skin (press on the tape firmly). Ensure that the skin is held taut to ensure that the tape does not move while applying pressure. Using a marking pen, demarcate a zone around the lesion such that the area of the lesion is encompassed within the inked boundary and the boundary is approximately 1 mm from the lesion border.

[0139] Remove the tape slowly in one direction. Place the edge of the tape onto the adhesive strip with cells facing down to protect the sample. Put a second tape on the same site following directions provided above. Repeat until the lesion has been stripped a total of at least four times, unless otherwise specified in the protocol. Place the strip into a storage bag and immediately place the samples on dry ice or into storage at -20°C or below until analysis.

EXAMPLE 5

Gene Expression Profile to Distinguish Melanoma from Atypical Nevi

[0140] The purpose of this study is to determine whether stratum corneum RNA, harvested by tape stripping with EGIR can be used to distinguish melanoma from atypical nevi in suspicious pigmented lesions. See Figure 4A.

[0141] Suspicious pigmented lesions were tape stripped four times using EGIR and then biopsied as per standard of care. Normal, uninvolved skin was tape stripped to serve as a negative control. All biopsies underwent primary and central review for histopathology. Total RNA was isolated from the tapes using MELT (Ambion, Inc.) and assessed for quality by Experion (Bio-Rad, Inc.) analysis. The yield of RNA was approximately 1 ng, as determined by quantitative RT-PCR of the specimen for β-actin gene expression. Total RNA (200-500 pg) was then amplified using the WT-Ovation Pico RNA Amplification System (NuGen, Inc.) and assayed for gene expression profile using the U133 plus 2.0 GeneChip (Affymetrix, Inc.).

[0142] The resulting RNA isolated from the EGIR tape is then amplified and profiled on the Affymetrix U133 plus 2.0 GeneChip. Microarray data is normalized by the GCRMA algorithm. Further analyses by means of ANOVA analysis ($p<0.05$) with a false discovery rate of 0.05 and multiple correction testing using Westfall and Young permutation identified approximately 117 genes as differentially expressed between melanoma, dysplastic nevi and normal skin (Table 1). Hierarchical clustering of these genes showed that the melanoma specimens grouped together and were clearly distinguished from dysplastic nevi and normal skin (Figure 4B). In addition, 89 of the 117 genes shown in Table 1 were further identified (Table 2) as potential discriminators between melanoma and dysplastic nevi ($p<0.01$, false discovery rate $q<0.05$). When these 89 genes were subjected to Ingenuity Pathways analysis many were found to play roles in melanoma, hair and skin development and function, cellular development, cellular growth and proliferation and cancer. These findings demonstrate that EGIR-harvested RNA from suspicious pigmented skin lesions can be used to differentiate melanoma from dysplastic nevi (Figure 4C). Further, these results suggest that the gene expression profile of stratum corneum is altered, either directly or indirectly, by the presence of melanoma (Figure 4D).

[0143] In subsequent studies that compared normal and inflamed skin, sequential application of four small tapes at the same skin site recovered enough intact RNA to perform quantitative reverse-transcription polymerase chain reaction (qPCR) assay and DNA microarray analysis for investigation of gene expression. The latter assay was performed using the Affymetrix HG-U133A GeneChip following two rounds of amplification of 10 ng of total RNA sample that produced 30-80 μg of anti-sense RNA. Comparison of results from two subjects, each sampled at three separate sites, showed 12% intra- and inter-subject variance in gene measurements, a result that is well within the Affymetrix specified coefficient of variation (CV) for GeneChip assay. Of note is that differential expression of Y-chromosome genes was observed, a result that accurately distinguished the different genders of the 2 subjects. GeneChip assay was then performed on RNA isolated from tape stripping each of 3 subjects from normal, water occluded, and sodium lauryl sulfate-irritated study groups. The majority of 100 genes, whose expression is most significantly altered between untreated and SLS-treated skin showed, were already known to be involved in tissue inflammation and injury functions. Thus, RNA harvested by EGIR technology is more than adequate for microarray-based gene expression profiling and appropriately reflects the pathologic state of skin.

[0144] Recent work by Benson *et al* (2006) demonstrates that RNA can be recovered from psoriatic lesions and that the general RNA expression profile of tape strip recovered RNA is consistent with biopsy RNA derived from lesions on the same patient. Further work (see U.S. Pat. No. 7,183,057, incorporated herein by reference) has shown that psoriatic lesions can be sampled with tape during treatment with Enbrel and that strong correlations could be made between gene expression in week one of treatment and clinical response at weeks 4 and 8. This work further establishes the credentials of tape stripping for the recovery of physiologically relevant RNA from the surface of the skin.

EXAMPLE 6

Gene Expression Profile to Distinguish Solar Lintigenes from Melanoma, Atypical Nevi, and/or Normal Skin

[0145] The purpose of this study is to determine whether stratum corneum RNA, can be used to distinguish solar lentigines from melanoma, atypical nevi, and/or normal skin in suspicious pigmented lesions.

[0146] Suspicious pigmented lesions were tape stripped as above and then biopsied as per standard of care. Normal, uninvolved skin was tape stripped to serve as a negative control. All biopsies underwent primary and central review for histopathology. Total RNA was isolated provided above and then amplified and profiled, as provided above. 1600 genes that were differentially expressed among solar lentigines and normal skin controls were selected. Further testing identified a 103-gene classifier (Table 10), which may be used to discriminate solar lentigines from normal pigmented skin (Figures 14 to 16).

[0147] Additional work, in which 11 solar lentigo samples, 12 atypical nevi samples, and 8 basal cell carcinoma (BCC) samples were analyzed using ANOVA ($p<0.05$), FDR ($p<0.05$) and multiple test correction to identify 82 differentially expressed genes (Table 11). Heirarchical analysis of the 82-gene classifier shows that it may be used to discriminate between solar lentigines and atypical nevi and/or basal cell carcinoma (BCC) (Figure 17). Finally, a 32-gene classifier (Table 12) was identified, which may be used to discriminate between solar lentigines and lentigo maligna (Figure 18). The genes and respective classifier panels were analyzed using the Prediction Analysis of Microarrays (PAM) software freely available from Stanford University (Stanford, CA).

[0148] An additional 28-gene classifier was identified from 2437 differentially expressed genes between lentigo maligna and solar lentigo was identified by TREENET® analysis (Table 15; see also Figure 19). In addition, results from 26 lentigo maligna and 34 solar lentigo samples indicated that qRT-PCR recaptilated data obtained using the GeneChip microarray (see raw data in Tables 16-21).

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Table 1

name	matched term	synonym	description	Entrez Gene ID for Human	Entrez Gene ID for Mouse	Entrez Gene ID for Rat
ACTR1B (includes EG:10120)	202135_s_at	2310066K23Rik, AA960180, ACTR1B, AI851923, ARP1B, CTRN2, MGC36526	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	10120	226977	
ANGEL1	213099_at	1110030H02Rik, KIAA0759, mKIAA0759, RGD1306238	angel homolog 1 (Drosophila)	23357	68737	362765
ANKRD13B	227720_at	AW124583, B930093C12Rik, FLJ20418, FLJ25555, RGD1564005	ankyrin repeat domain 13B	124930	268445	360575
ANKRD44	228471_at	4930444A19Rik, A130096K20, E130014H08Rik, LOC91526, MGC21968, MGC70444, RGD1561893	ankyrin repeat domain 44	91526	329154	301415
ARHGEF19	226857_at	6030432F23, 6430573B13Rik, FLJ33962, RP4-733M16.1, WGEF	Rho guanine nucleotide exchange factor (GEF) 19	128272	213649	362648
ATPBD4	238662_at	5730421E18Rik, MGC14798, RGD1310006	ATP binding domain 4	89978	66632	362191

BARX2	210419_at	2310006E12Rik, Barx2b, MGC133368, MGC133369	BarH-like homeobox 2	8538	12023	
BDNF	206382_s_at	MGC105254, MGC34632	brain-derived neurotrophic factor	627	12064	24225
BLOC1S1	202592_at	AI839753, BLOC-1 subunit 1, BLOS1, GCN5-like protein 1, GCN5L1, MGC87455, RT14	biogenesis of lysosome-related organelles complex-1, subunit 1	2647	14533	288785
BTG2	201236_s_at	AA959598, Agl, An, an-1, APRO1, MGC126063, MGC126064, PC3, TIS21	BTG family, member 2	7832	12227	29619
C16ORF48	223407_at	AI606951, DAKV6410, DKFZP434A1319, E130303B06Rik, RGD1307357	chromosome 16 open reading frame 48	84080	102124	291975
C6ORF218	244829_at	MGC40222	chromosome 6 open reading frame 218	221718		
C8ORF13	233641_s_at	A030013D21, BC065085, D8S265, DKFZp761G151, MGC120649, MGC120650, MGC120651, RGD1561302	chromosome 8 open reading frame 13	83648	219148	498533
CCDC95	227286_at	AI225782, AI854876, Ccdc85, FLJ00079, FLJ90652, MGC31515	coiled-coil domain containing 95	283899	233875	
CCHCR1	37425_g_at	C6orf18, HCR, MGC126371, MGC126372, MGC28303, RGD:1302992, SBP	coiled-coil alpha-helical rod protein 1	54535	240084	406196
CIRBP	230142_s_at	A18 HNRNP, CIRP, R74941	cold inducible RNA binding protein	1153	12696	81825

CLSTN2	219414_at	2900042C18Rik, AI448973, alcagamma, CS2, Cst-2, CSTN2, FLJ39113, FLJ39499, KIAA4134, MGC119560, mKIAA4134	calsyntenin 2	64084	64085	171394
COL7A1	217312_s_at	AW209154, EBD1, EBDCT, EBR1	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive)	1294	12836	301012
DACH1	205471_s_at, 205472_s_at, 228915_at	AI182278, Dac, DACH, E130112M23Rik, FLJ10138	dachshund homolog 1 (Drosophila)	1602	13134	
DCT	205337_at, 205338_s_at	DT, RGD1564975, slaty, slt, TRP-2, TYRP2	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	1638	13190	290484
DOCK10	219279_at	9330153B10RIK, A630054M16Rik, DKFZp781A1532, DRIP2, Jr4, Jr5, mKIAA0694, Nbla10300, R75174, RGD1561963, ZIZ3, Zizimin3	dedicator of cytokinesis 10	55619	210293	301556
DRAP1	1556181_at	2310074H19Rik, MGC156767, NC2-ALPHA, negative cofactor 2 alpha	DR1-associated protein 1 (negative cofactor 2 alpha)	10589	66556	293674
EDNRB	204271_s_at, 206701_x_at	ABCDS, AU022549, Ednra, ET>B<, ET-B, ETB RECEPTOR, ETBR, ETRB, GUSB, HSCR, HSCR2, Sox10m1	endothelin receptor type B	1910	13618	50672
EFNA4	205107_s_at	EFL-4, EPHRIN A4, Epl4, EPLG4, LERK-4, MGC125826	ephrin-A4	1945	13639	310643
EHD2	45297_at	BC027084, C130052H20Rik, MGC25606, MGC38650, MGEPS, PAST2	EH-domain containing 2	30846	259300	361512

ETS1	224833_at	AI196000, AI448617, C-ETS1, D230050P06, Etsoncb, EWSR2, FLJ10768, MGC124638, MGC130355, MGC18571, p42 ETS1, p51 ETS1, Tpl1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2113	23871	24356
FAM33A	225684_at	1110001A07Rik, C78640, EG625534, FLJ12758, MGC109093, MGC110975, MGC151378, RGD1307084	family with sequence similarity 33, member A	348235	66140|625534	287598
FGFR1	210973_s_at, 211535_s_at	AW208770, BFGFR, C-FGR, CD331, CEK, FGF1 RECEPTOR, FGFBR, FGFR1-IIIC, Fgfr1c, FLG, Flk2, FLT2, H5, HBGFR, KAL2, N-SAM	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	2260	14182	79114
FOXO1A	202723_s_at	Afxh, AI876417, FKH1, FKHR, FKHR1, Forkhead, FOXO1	forkhead box O1A (rhabdomyosarcoma)	2308	56458	84482
FOXP1	223936_s_at	12CC4, 3110052D19Rik, 4932443N09Rik, AI461938, AW494214, FLJ23741, hFKH1B, HSPC215, MGC116362, MGC12942, MGC88572, MGC99551, QRF1	forkhead box P1	27086	108655	297480
FRAT2	209864_at	MGC10562, MGC37615	frequently rearranged in advanced T-cell lymphomas 2	23401	212398	

GCLM	203925_at	Gamma gclm, Gamma glutamylcysteine synthase (regulatory), GAMMA GLUTAMYLCYSTEINE SYNTHETASE, Gcs Ls, Gcs, Regulatory, GCS-L, GCS1, Gcslc, GLCLR, glutamat-cystein ligase, regulatory subunit	glutamate-cysteine ligase, modifier subunit	2730	14630	29739
GGA3	209411_s_at	C230037M19Rik, KIAA0154, mKIAA0154	golgi associated, gamma adaptin ear containing, ARF binding protein 3	23163	260302	360658
GLUL	200648_s_at	GLNS, Glutamine Synthase, GLUTAMINE SYNTHETASE, GS, MGC128403, PIG43	glutamate-ammonia ligase (glutamine synthetase)	2752	14645	
GPR161	214104_at	FLJ33952, G-protein coupled receptor af091890, Gm208, Gm208Gpr, RE2, RGD1563245	G protein-coupled receptor 161	23432	240888	289180
HEY2	219743_at	CHF1, GRL, HERP1, HESR2, HRT2, MGC10720	hairy/enhancer-of-split related with YRPW motif 2	23493	15214	155430
HIST2H2AA3	214290_s_at	AI448581, H2A, H2a-615, H2A.2, H2A/O, H2A/q, H2AFO, Hist2, HIST2H2AA, Hist2h2aa1	histone cluster 2, H2aa3	8337	15267	365877
ID1	208937_s_at	AI323524, D2Wsu140e, ID, ID-1H, ID125A, Idb1, MGC156482	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	3397	15901	25261

KALRN	227750_at	2210407G14Rik, AV235988, DUET, Duo, E530005C20Rik, FLJ16443, Gm539, HAPIP, KALIRIN, Kalirin7, Pcip10, TRAD	kalirin, RhoGEF kinase	8997	545156	84009
KDELR1	200922_at	8030486F04Rik, AW215843, ERD2, ERD2.1, HDEL, KDEL RECEPTOR, Kdelr, MGC109169, PM23	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	10945	68137	361577
KIAA0738	210529_s_at	2810407D09Rik, 3321401G04Rik, A230020K05Rik, AI848529, RGD1565474	KIAA0738 gene product	9747	77574	362353
KIT	205051_s_at	Bs, C-KIT, c-Kit Gnnk+, CD117, Fdc, SCFR, Ssm, Tr Kit, white-spotted	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	3815	16590	64030
LGR4	230674_at	9130225G07, A930009A08Rik, GPCR48, GPR48	leucine-rich repeat-containing G protein-coupled receptor 4	55366	107515	286994
LHX2 (includes EG:9355)	211219_s_at	ap, apterous, hLhx2, Lh-2, LH2A, Lhx2, Lim2, MGC138390	LIM homeobox 2	9355	16870	296706
LMO4	209204_at	A730077C12Rik, Crp3, Etohi4, MGC105593	LIM domain only 4	8543	16911	362051
LOC254100	1557131_at		hypothetical protein LOC254100	254100		
LRIG1	236173_s_at, 238339_x_at	D6Bwg0781e, DKFZP586O162 4, Img, LIG-1	leucine-rich repeats and immunoglobulin-like domains 1	26018	16206	312574
MED28	222635_s_at	1500003D12Rik, AI451633, AU045690, DKFZP434N185, EG1, FKSG20, magicin, RGD1305875	mediator of RNA polymerase II transcription, subunit 28 homolog (S. cerevisiae)	80306	66999	305391
MKL1	215292_s_at	AI852829, AMKL, AW743281, AW821984, BSAC, MAL, MRTF-A	megakaryoblastic leukemia (translocation) 1	57591	223701	315151

MLANA	206426_at, 206427_s_at	A930034P04Rik, MART-1, MELAN-A, MGC130556	melan-A	2315	77836	293890
MLLT6	225628_s_at	AF17, AI315037, FLJ23480	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	4302	246198	303504
MLPH	218211_s_at	2210418F23Rik, 5031433I09Rik, AW228792, D1Wsu84e, l(1)-3Rk, l1Rk3, ln, MGC2771, MGC59733, SLAC2-A	melanophilin	79083	171531	316620
MYEF2	222771_s_at, 232676_x_at	9430071B01, FLJ11213, HsT18564, KIAA1341, MEF-2, MGC109392, MGC87325, mKIAA1341, MST156, MSTP156	myelin expression factor 2	50804	17876	362207
MYL6B	204173_at	5730437E04Rik, Atrial Myosin Light Chain 1, BC037527, MGC41229, MLC1SA, RGD1560334	myosin, light chain 6B, alkali, smooth muscle and non-muscle	140465	216459	317454
MYO5A	227761_at	9630007J19Rik, AI413174, AI661011, Br Myosin5a, d-120J, Dbv, Dop, flail, flr, GS1, hcBM-V, MVa, MYH12, MYO5, myosin V, MYOSIN VA, MYOSIN VA EXON CONTAINING, MYOVA, MYOXIN, MYR12, Sev-1	myosin VA (heavy chain 12, myoxin)	4644	17918	25017
NBL1	37005_at	D1S1733E, D4H1S1733E, DAN, Dana, DAND1, MGC123430, MGC8972, NB, NO3	neuroblastoma, suppression of tumorigenicity 1	4681	17965	50594

NFIB	230791_at	6720429L07Rik, CTF/NF1B, E030026I10Rik, NF1-B, NFI-RED, NFIB2, NFIB3, Nuclear factor 1/B	nuclear factor I/B	4781	18028	29227
OSTM1	218196_at	1200002H13Rik, AW123348, GIPN, GL, HSPC019	osteopetrosis associated transmembrane protein 1	28962	14628	445370
PDK3	221957_at	2610001M10Rik, AI035637, MGC6383	pyruvate dehydrogenase kinase, isozyme 3	5165	236900	296849
PKD1	241090_at	FLJ00285, mFLJ00285, MGC118471, PBP, PC-1, POLYCYSTIN1	polycystic kidney disease 1 (autosomal dominant)	5310	18763	24650
PLEKHA5	220952_s_at	2810431N21Rik, AI428202, AK129423, Ayu21-9, FLJ10667, FLJ31492, Gt(pU21)9Imeg, Image:3710928, KIAA1686, MGC38455, PEPP2, TRS1	pleckstrin homology domain containing, family A member 5	54477	109135	246237
PLP1	210198_s_at	DM20, jimpy, jp, MMPL, Msd, PLP, PLP/DM20, PMD, PROTEOLIPID, RSH, SPG2	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)	5354	18823	24943
PLXNC1	213241_at	2510048K12Rik, AW742158, CD232, Plexin C1, VESPR	plexin C1	10154	54712	362873
PPP3CA	202425_x_at	2900074D19Rik, AI841391, AW413465, Calcineurin, Calcineurin A Alpha, CALN, CALNA, CALNA1, CCN1, CN, CnA, CnA-alpha, CNA1, MGC106804, Pp2b Subunit A, PPP2B	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	5530	19055	24674
PRKCSH	200707_at	80K-H, AGE-R2, G19P1, PCLD, PLD, PLD1	protein kinase C substrate 80K-H	5589	19089	300445

PRKD3	222565_s_at	4930557O20Rik, 5730497N19Rik, EPK2, MGC47171, nPKC-NU, PKC-NU, PKD3, PRKCN	protein kinase D3	23683	75292	313834
PRMT1	206445_s_at	6720434D09Rik, ANM1, AW214366, HCP1, heterogeneous ribonucleoproteins methyltransferase-like 2, Hnmt1l2, Hramt, HRMT1L2, IR1B4, Mrmt1	protein arginine methyltransferase 1	3276	15469	60421
PSCD3	225147_at	AI648983, ARNO3, CYTOHESIN-3, GRP1, KIAA4241, MGC124579, mKIAA4241, Sec7, Sec7C	pleckstrin homology, Sec7 and coiled-coil domains 3	9265	19159	116693
PTPRF	200635_s_at, 200637_s_at	AA591035, FLJ43335, FLJ45062, FLJ45567, LAR, Lar ptp2b, LARFN5C, LARS	protein tyrosine phosphatase, receptor type, F	5792	19268	360406
PTPRM	1555579_s_at	HR-PTPU, KIAA4044, MGC90724, mKIAA4044, PTP-MU, PTPRL1, R-PTP-MU, RPTPM, RPTPU	protein tyrosine phosphatase, receptor type, M	5797	19274	29616
PVRL1	225211_at	AI835281, AW549174, CD111, CLPED1, ED4, HIgR, HVEC, MGC142031, MGC16207, NECTIN-1, Nectin1 alpha, Nectin1 delta, OFC7, PRR, PRR1, PVRR, PVRR1, SK-12	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)	5818	58235	192183
RAB40C	227269_s_at	RAB40, RAR3, RARL, RASL8C	RAB40C, member RAS oncogene family	57799	224624	359728

RASSF3	230466_s_at	AW212023, AW322379, MGC119194, MGC119195, MGC119197, RASSF5	Ras association (RalGDS/AF-6) domain family 3	283349	192678	362886
RHOQ	212120_at	ARHQ, RASL7A, Rhot, TC10, TC10 BETA, TC10A	ras homolog gene family, member Q	23433	104215	85428
SAT1	203455_s_at, 210592_s_at, 213988_s_at, 230333_at	AA617398, Ab2-402, DC21, KFSD, MGC72945, SAT, Spermidine/spermine N1-acetyl transferase, SSAT, SSAT-1	spermidine/spermine N1-acetyltransferase 1	6303	20229	302642
SDCBP	200958_s_at	MDA-9, ST1, SYCL, SYNTENIN, Syntenin-1, TACIP18	syndecan binding protein (syntenin)	6386	53378	83841
SEC61A1	217716_s_at, 222385_x_at	AA408394, AA410007, HSEC61, rSEC61alpha p, SEC61, Sec61 alpha, SEC61 ALPHA1, SEC61A	Sec61 alpha 1 subunit (S. cerevisiae)	29927	53421	80843
SEMA3C	236947_at	1110036B02Rik, SEMAE, SEMAPHORIN E, SemE	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	10512	20348	296787
SERGEF	220482_s_at, 232983_s_at	DELGEF, Gef, Gnef, Gnefr, MGC141208, MGC141209, RGD1563497	secretion regulating guanine nucleotide exchange factor	26297	27414	365243
SILV	209848_s_at	D10H12S53E, D12S53E, D12S53Eh, GP100, gp87, ME20, PMEL17, SI, SIL	silver homolog (mouse)	6490	20431	362818
SLC2A4RG	227362_at	GEF, HDBP1, Si-1-2, Si-1-2-19	SLC2A4 regulator	56731		
SLC7A1	212295_s_at	4831426K01Rik, AI447493, ATRC1, CAT-1, EcoR, ER, ERR, HCAT1, mCAT-1, Rec-1, REC1L, REV-1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	6541	11987	25648

SRGAP2	1568957_x_at	9930124L22Rik, AI448945, FBP2, FNBP2, KIAA0456, RGD1566016, srGAP3	SLIT-ROBO Rho GTPase activating protein 2	23380	14270	360840
SSBP3	217991_x_at, 223635_s_at	2610021L12Rik, 2610200M23Rik, 5730488C10Rik, AI854733, AW551939, CSDP, FLJ10355, LAST, MGC124589, SSDP, SSDP1, Ssdp3	single stranded DNA binding protein 3	23648	72475	84354
STAM (includes EG:8027)	203544_s_at	DKFZp686J2352, RGD1564499, Stam, STAM1	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	8027	20844	498798
SYNGR2	201079_at	CELLUGYRIN, Clast2, MGC102914	synaptogyrin 2	9144	20973	89815
TCF7L2 (includes EG:6934)	212759_s_at	mTcf-4B, mTcf-4E, TCF-4, TCF4B, TCF4E, Tcf7l2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	21416	
TIMM17A	215171_s_at	17kDa, Mitochondrial import inner membrane translocase, Mitochondrial protein import protein 2, mTim17a, TIM17, TIM17A, Timm17	translocase of inner mitochondrial membrane 17 homolog A (yeast)	10440	21854	54311
TP53	201746_at	bbl, bfy, bhy, Delta N p53, LFS1, MGC112612, P53, TRP53	tumor protein p53 (Li-Fraumeni syndrome)	7157	22059	24842
TP53INP1	235602_at	2700057G22Rik, DKFZP434M1317, FLJ22139, p53DINP1, SIP, SIP18, SIP27, Stinp, Teap, Thymus Expressed Acidic Protein, TP53DINP1, TP53DINP1alpha, TP53INP1A, TP53INP1B, Trp53inp1	tumor protein p53 inducible nuclear protein 1	94241	60599	297822

TRIB2	202478_at	AW319517, C5fw, GS3955, RGD1564451, TRB-2	tribbles homolog 2 (Drosophila)	28951	217410	313974
TRPM1 (includes EG:4308)	237070_at	4732499L03Rik, AI606771, LTRPC1, melastatin, MLSN, MLSN1, Trpm1	transient receptor potential cation channel, subfamily M, member 1	4308	17364	
TSPAN6	209108_at	6720473L21Rik, AI316786, MGC117923, T245, Tm4sf, TM4SF6	tetraspanin 6	7105	56496	302313
TSTA3	36936_at	AI256181, FX, FX protein, MGC113801, P35B, Tstap35b	tissue specific transplantation antigen P35B	7264	22122	300036
TTC3	208073_x_at, 210645_s_at	2610202A04Rik, AA409221, D16Ium21, D16Ium21e, DCRR1, DKFZp686M0150, KIAA4119, mKIAA4119, Mtprd, RNF105, TPRD, TPRDIII	tetratricopeptide repeat domain 3	7267	22129	360702
TUBB4	212664_at	AI325297, Beta tubulin, BETA TUBULIN 4 ALPHA, Beta tubulin class iv, beta-5, Beta4 Tubulin, M(beta)4, Tubb, TUBB5, TUBULIN BETA (5-BETA), TUBULIN BETA5	tubulin, beta 4	10382	22153	29213
TYR	206630_at	albino, Dopa oxidase, Melanogenesis Related Tyrosinase, OCA1A, OCAIA, skc35, Tyr<c-em>, TYROSINASE	tyrosinase (oculocutaneous albinism IA)	7299	22173	308800

TYRP1	205694_at	b-PROTEIN, brown, CAS2, CATB, GP75, isa, MELANOMA ANTIGEN GP75, TRP, TRP-1, TYRP	tyrosinase-related protein 1	7306	22178	298182
VDR	204255_s_at	NR1I1, VD3R, VITAMIN D RECEPTOR	vitamin D (1,25-dihydroxyvitamin D3) receptor	7421	22337	24873
VGLL4	214004_s_at	BC048841, KIAA0121, MGC109514, MGC54805, VGL-4	vestigial like 4 (Drosophila)	9686	232334	297523
YIPF5	224949_at	2610311I19Rik, AA408236, Ac2-256, DKFZp313L2216, FinGER5, SB140, SMAP-5, YIP1A	Yip1 domain family, member 5	81555	67180	361315
ZFHX1B	1557797_a_at, 203603_s_at	9130203F04Rik, D130016B08Rik, KIAA0569, mKIAA0569, SIP-1, SMADIP1, ZEB2, Zfx1b, Zfxh1b	zinc finger homeobox 1b	9839	24136	311071
	1558019_at	---:Homo sapiens, clone IMAGE:4732650, mRNA				
	233551_at	LOC642776:hypothetical protein LOC642776				
	208646_at	RPS14:ribosomal protein S14 /// similar to ribosomal protein S14				
	208929_x_at	RPL13:ribosomal protein L13				
	214351_x_at	RPL13:ribosomal protein L13 /// similar to ribosomal protein L13				
	200817_x_at	RPS10:ribosomal protein S10				
	213296_at	---:Transcribed locus				
	213692_s_at	---:---				
	227957_at	---:---				
	232462_s_at	FLJ23569:BC040926				

	227722_at	RPS23:ribosomal protein S23				
	217466_x_at	RPS2:ribosomal protein S2 /// similar to ribosomal protein S2				
	235534_at	---:Homo sapiens, clone IMAGE:5723825, mRNA				
	230741_at	---:Full length insert cDNA clone YX74D05				
	229067_at	LOC653464:Similar to SLIT-ROBO Rho GTPase-activating protein 2 (srGAP2) (Formin0binding protein 2)				

Table 2

name	matched term
ANKRD44	228471_at
ARHGEF19	226857_at
ATPBD4	238662_at
BARX2	210419_at
BDNF	206382_s_at
BLOC1S1	202592_at
C16ORF48	223407_at
C6ORF218	244829_at
C8ORF13	233641_s_at
CCHCR1	37425_g_at
CIRBP	230142_s_at
CLSTN2	219414_at
COL7A1	217312_s_at
DACH1	205472_s_at, 228915_at
DCT	205337_at, 205338_s_at
DOCK10	219279_at
DRAP1	1556181_at
EDNRB	204271_s_at, 206701_x_at
EFNA4	205107_s_at
EHD2	45297_at
ETS1	224833_at
FAM33A	225684_at
FGFR1	210973_s_at, 211535_s_at
FOXO1A	202723_s_at
GGA3	209411_s_at
GPR161	214104_at
HIST2H2AA3	214290_s_at
ID1	208937_s_at
KDELR1	200922_at
KIAA0738	210529_s_at
KIT	205051_s_at

LGR4	230674_at
LHX2 (includes EG:9355)	211219_s_at
LMO4	209204_at
LOC254100	1557131_at
LRIG1	238339_x_at
MED28	222635_s_at
MKL1	215292_s_at
MLANA	206426_at, 206427_s_at
MLPH	218211_s_at
MYEF2	222771_s_at, 232676_x_at
MYO5A	227761_at
NBL1	37005_at
OSTM1	218196_at
PDK3	221957_at
PKD1	241090_at
PLEKHA5	220952_s_at
PLP1	210198_s_at
PLXNC1	213241_at
PRKCSH	200707_at
PRKD3	222565_s_at
PRMT1	206445_s_at
PSCD3	225147_at
PTPRF	200637_s_at
PTPRM	1555579_s_at
RAB40C	227269_s_at
RASSF3	230466_s_at
RHOQ	212120_at
RPL13	214351_x_at
RPS23	227722_at
SAT1	203455_s_at, 213988_s_at, 230333_at
SDCBP	200958_s_at
SEC61A1	222385_x_at
SEMA3C	236947_at
SERGEF	232983_s_at
SILV	209848_s_at
SLC2A4RG	227362_at
SLC7A1	212295_s_at
SSBP3	217991_x_at, 223635_s_at
STAM (includes EG:8027)	203544_s_at
SYNGR2	201079_at
TCF7L2 (includes EG:6934)	212759_s_at
TIMM17A	215171_s_at
TRIB2	202478_at
TRPM1 (includes EG:4308)	237070_at
TSPAN6	209108_at
TTC3	208073_x_at, 210645_s_at
TUBB4	212664_at
TYR	206630_at
VDR	204255_s_at
YIPF5	224949_at
ZFHX1B	1557797_a_at, 203603_s_at
	229067_at
	213692_s_at
	227957_at
	213296_at
	235534_at

	233551_at
	1558019_at

Table 3

matched term	description
208073_x_at	TTC3:tetratricopeptide repeat domain 3
210645_s_at	TTC3:tetratricopeptide repeat domain 3
206630_at	TYR:tyrosinase (oculocutaneous albinism IA)
203544_s_at	STAM:signal transducing adaptor molecule (SH3 domain and ITAM motif) 1
230741_at	---:Full length insert cDNA clone YX74D05

Table 4

matched term	description
205694_at	TYRP1:tyrosinase-related protein 1
206427_s_at	MLANA:melan-A
206140_at	LHX2:LIM homeobox 2
206630_at	TYR:tyrosinase (oculocutaneous albinism IA)
203921_at	CHST2:carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
205337_at	DCT:dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
228245_s_at	OVOS2:ovostatin 2 /// similar to cDNA sequence BC048546
205338_s_at	DCT:dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
1557797_a_at	ZFHX1B:Zinc finger homeobox 1b
204271_s_at	EDNRB:endothelin receptor type B
237070_at	TRPM1:transient receptor potential cation channel, subfamily M, member 1
200716_x_at	RPL13A:ribosomal protein L13a
1555579_s_at	PTPRM:protein tyrosine phosphatase, receptor type, M
205051_s_at	KIT:v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
200665_s_at	SPARC:secreted protein, acidic, cysteine-rich (osteonectin) /// secreted protein, acidic, cysteine-rich (osteonectin)
205174_s_at	QPCT:glutaminyl-peptide cyclotransferase (glutaminyl cyclase)
200725_x_at	RPL10:ribosomal protein L10
232602_at	WFDC3:WAP four-disulfide core domain 3
202478_at	TRIB2:tribbles homolog 2 (Drosophila)
209230_s_at	P8:p8 protein (candidate of metastasis 1)
232676_x_at	MYEF2:myelin expression factor 2
222565_s_at	PRKD3:protein kinase D3
212295_s_at	SLC7A1:solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
212594_at	PDCD4:programmed cell death 4 (neoplastic transformation inhibitor)
218211_s_at	MLPH:melanophilin
206426_at	MLANA:melan-A
207065_at	K6HF:cytokeratin type II
202500_at	DNAJB2:DnaJ (Hsp40) homolog, subfamily B, member 2
203706_s_at	FZD7:frizzled homolog 7 (Drosophila)
209969_s_at	STAT1:signal transducer and activator of transcription 1, 91kDa

Table 5

matched term	description
205694_at	tyrosinase-related protein 1
206140_at	LIM homeobox 2
206427_s_at	melan-A
203455_s_at	spermidine/spermine N1-acetyltransferase
206453_s_at	NDRG family member 2
203921_at	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
200958_s_at	syndecan binding protein (syntenin)

209283_at	crystallin, alpha B
204271_s_at	endothelin receptor type B
208073_x_at	tetratricopeptide repeat domain 3
232602_at	WAP four-disulfide core domain 3
202435_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1
209230_s_at	p8 protein (candidate of metastasis 1)
208966_x_at	interferon, gamma-inducible protein 16
205337_at	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
202088_at	solute carrier family 39 (zinc transporter), member 6
211538_s_at	heat shock 70kDa protein 2
201556_s_at	vesicle-associated membrane protein 2 (synaptobrevin 2)
241455_at	Similar to AI661453 protein
237070_at	transient receptor potential cation channel, subfamily M, member 1

Table 6

matched term	description
1555505_a_at	tyrosinase (oculocutaneous albinism IA)
204271_s_at	endothelin receptor type B
208073_x_at	tetratricopeptide repeat domain 3
200958_s_at	syndecan binding protein (syntenin)
205051_s_at	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
201245_s_at	OTU domain, ubiquitin aldehyde binding 1
201603_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A
201605_x_at	calponin 2
201908_at	dishevelled, dsh homolog 3 (Drosophila)
202478_at	tribbles homolog 2 (Drosophila)
1557292_a_at	mucolipin 3
200601_at	actinin, alpha 4
200819_s_at	ribosomal protein S15
209953_s_at	CDC37 cell division cycle 37 homolog (*S. cerevisiae*)
213146_at	jumonji domain containing 3
222670_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
224991_at	c-Maf-inducing protein
226988_s_at	myosin, heavy polypeptide 14
244829_at	Hypothetical protein MGC40222

Table 7

matched term	description
204271_s_at	endothelin receptor type B
244829_at	Hypothetical protein MGC40222
208073_x_at	tetratricopeptide repeat domain 3
213037_x_at	staufen, RNA binding protein (Drosophila)
200601_at	actinin, alpha 4
219387_at	KIAA1212
209168_at	glycoprotein M6B
205051_s_at	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
224991_at	c-Maf-inducing protein
200613_at	adaptor-related protein complex 2, mu 1 subunit
203330_s_at	syntaxin 5A
225009_at	chemokine-like factor superfamily 4
221485_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
218255_s_at	fibrosin 1
227870_at	likely ortholog of mouse neighbor of Punc E11
226988_s_at	myosin, heavy polypeptide 14
204086_at	preferentially expressed antigen in melanoma

213146_at	jumonji domain containing 3
205681_at	BCL2-related protein A1
213940_s_at	formin binding protein 1
202478_at	tribbles homolog 2 (Drosophila)
226702_at	hypothetical protein LOC129607
218402_s_at	Hermansky-Pudlak syndrome 4
227099_s_at	hypothetical LOC387763
218211_s_at	melanophilin
217738_at	pre-B-cell colony enhancing factor 1
228488_at	TBC1 domain family, member 16
215695_s_at	glycogenin 2
241898_at	Transcribed locus, moderately similar to XP_517655.1 PREDICTED: similar to KIAA0825 protein [Pan troglodytes]
202479_s_at	tribbles homolog 2 (Drosophila)
201453_x_at	Ras homolog enriched in brain
228415_at	Adaptor-related protein complex 1, sigma 2 subunit
201908_at	dishevelled, dsh homolog 3 (Drosophila)
225600_at	MRNA; cDNA DKFZp779L1068 (from clone DKFZp779L1068)
221951_at	transmembrane protein 80
203455_s_at	spermidine/spermine N1-acetyltransferase
201603_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A
1558702_at	Testis expressed sequence 10
204527_at	myosin VA (heavy polypeptide 12, myoxin)
235222_x_at	baculoviral IAP repeat-containing 4
1560445_x_at	Rho guanine nucleotide exchange factor (GEF) 1
1556205_at	CDNA FLJ37227 fis, clone BRAMY2000277
226054_at	bromodomain containing 4
210198_s_at	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)
202370_s_at	core-binding factor, beta subunit
209058_at	endothelial differentiation-related factor 1
211755_s_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 ; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1
229713_at	CDNA FLJ13267 fis, clone OVARC1000964
209514_s_at	RAB27A, member RAS oncogene family
201299_s_at	MOB1, Mps One Binder kinase activator-like 1B (yeast)
211909_x_at	prostaglandin E receptor 3 (subtype EP3) ; prostaglandin E receptor 3 (subtype EP3)
209234_at	kinesin family member 1B
207622_s_at	ATP-binding cassette, sub-family F (GCN20), member 2
212421_at	chromosome 22 open reading frame 9
219636_s_at	armadillo repeat containing 9
223407_at	chromosome 16 open reading frame 48
200645_at	GABA(A) receptor-associated protein
242049_s_at	neuroblastoma-amplified protein
230793_at	Leucine rich repeat containing 16
215409_at	PLSC domain containing protein
202984_s_at	BCL2-associated athanogene 5
201864_at	GDP dissociation inhibitor 1
209780_at	putative homeodomain transcription factor 2
218143_s_at	secretory carrier membrane protein 2
228919_at	
228095_at	PHD finger protein 14
213736_at	Cytochrome c oxidase subunit Vb
213655_at	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
218419_s_at	hypothetical protein MGC3123
200755_s_at	calumenin

223220_s_at	poly (ADP-ribose) polymerase family, member 9
237464_at	LAT1-3TM protein 2
229679_at	FLJ40142 protein
	IL-1 RI (Interleukin-1 RI)
	EDN2 (endothelin-2)
	EFNA5 (ephrin-A5)
	IGFBP7 (IGF Binding Protein 7)
	HLA-A0202 heavy chain (Human Leukocyte Antigen-A0202 heavy chain)
	Activin A (βA subunit)
	TNF RII (tumor necrosis factor receptor II)
	SPC4 (Subtilisin-Like Proprotein Convertase, PACE4)
	CNTF Rα (Ciliary neurotrophic factor receptor α)

Table 8

Gene	Description
204271_s_at	endothelin receptor type B
244829_at	Hypothetical protein MGC40222
208073_x_at	tetratricopeptide repeat domain 3
213037_x_at	staufen, RNA binding protein (Drosophila)
200601_at	actinin, alpha 4
219387_at	KIAA1212
209168_at	glycoprotein M6B
205051_s_at	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
224991_at	c-Maf-inducing protein
200613_at	adaptor-related protein complex 2, mu 1 subunit
203330_s_at	syntaxin 5A
225009_at	chemokine-like factor superfamily 4
221485_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
218255_s_at	fibrosin 1
227870_at	likely ortholog of mouse neighbor of Punc E11
226988_s_at	myosin, heavy polypeptide 14
204086_at	preferentially expressed antigen in melanoma
213146_at	jumonji domain containing 3
205681_at	BCL2-related protein A1
213940_s_at	formin binding protein 1

Table 10

Gene	Description
221750_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
225283_at	arrestin domain containing 4
212952_at	Calreticulin
226920_at	Casein kinase 1, alpha 1
201533_at	catenin (cadherin-associated protein), beta 1, 88kDa
225551_at	chromosome 1 open reading frame 71
227736_at	chromosome 10 open reading frame 99
217883_at	chromosome 2 open reading frame 25
226614_s_at	chromosome 8 open reading frame 13
214073_at	cortactin
233929_x_at	CXYorf1-related protein
225035_x_at	CXYorf1-related protein ; CXYorf1-related protein ; CXYorf1-related protein
200953_s_at	cyclin D2
206595_at	cystatin E/M
224831_at	cytoplasmic polyadenylation element binding protein 4

201211_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
200762_at	dihydropyrimidinase-like 2
219648_at	dilute suppressor
202572_s_at	discs, large (Drosophila) homolog-associated protein 4
200664_s_at	DnaJ (Hsp40) homolog, subfamily B, member 1
208811_s_at	DnaJ (Hsp40) homolog, subfamily B, member 6
208370_s_at	Down syndrome critical region gene 1
214445_at	elongation factor, RNA polymerase II, 2
214446_at	elongation factor, RNA polymerase II, 2
201436_at	eukaryotic translation initiation factor 4E
208290_s_at	eukaryotic translation initiation factor 5
200748_s_at	ferritin, heavy polypeptide 1
211628_x_at	ferritin, heavy polypeptide pseudogene 1 ; ferritin, heavy polypeptide pseudogene 1
205409_at	FOS-like antigen 2
200959_at	fusion (involved in t(12;16) in malignant liposarcoma)
201065_s_at	general transcription factor II, i ; general transcription factor II, i, pseudogene 1
218238_at	GTP binding protein 4
201841_s_at	heat shock 27kDa protein 1
225988_at	hect domain and RLD 4
241683_at	HECT domain containing 1
201944_at	hexosaminidase B (beta polypeptide)
219976_at	hook homolog 1 (Drosophila)
213079_at	hypothetical protein DT1P1A10
215434_x_at	hypothetical protein FLJ20719 ; AG1 protein
1569157_s_at	hypothetical protein LOC162993
227052_at	Hypothetical protein LOC201895
225065_x_at	hypothetical protein MGC40157
231733_at	ICEBERG caspase-1 inhibitor
240941_at	Intersectin 2
208881_x_at	isopentenyl-diphosphate delta isomerase 1
204615_x_at	isopentenyl-diphosphate delta isomerase 1
213507_s_at	karyopherin (importin) beta 1
203068_at	kelch-like 21 (Drosophila)
225142_at	KIAA1718 protein
220368_s_at	KIAA2010
1559226_x_at	late cornified envelope 1E
1559224_at	late cornified envelope 1E
200673_at	lysosomal-associated protein transmembrane 4 alpha
223480_s_at	mitochondrial ribosomal protein L47
207121_s_at	mitogen-activated protein kinase 6
214939_x_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4
203315_at	NCK adaptor protein 2
230291_s_at	Nuclear factor I/B
211467_s_at	nuclear factor I/B
213032_at	Nuclear factor I/B
223650_s_at	nuclear receptor binding factor 2
222878_s_at	OTU domain, ubiquitin aldehyde binding 2
217608_at	p18 splicing regulatory protein
200907_s_at	palladin
202290_at	PDGFA associated protein 1
218942_at	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
225147_at	pleckstrin homology, Sec7 and coiled-coil domains 3
216515_x_at	prothymosin, alpha (gene sequence 28) ; hypothetical gene supported by BC013859 ; hypothetical gene supported by BC013859; BC070480

200773_x_at	prothymosin, alpha (gene sequence 28) ; similar to prothymosin alpha ; hypothetical gene supported by BC013859 ; hypothetical gene supported by BC013859; BC070480
212099_at	ras homolog gene family, member B
212124_at	retinoic acid induced 17
200022_at	ribosomal protein L18 ; ribosomal protein L18
201909_at	ribosomal protein S4, Y-linked 1
215127_s_at	RNA binding motif, single stranded interacting protein 1
218143_s_at	secretory carrier membrane protein 2
205185_at	serine peptidase inhibitor, Kazal type 5
1554089_s_at	Shwachman-Bodian-Diamond syndrome ; Shwachman-Bodian-Diamond syndrome pseudogene
208991_at	signal transducer and activator of transcription 3 (acute-phase response factor)
224573_at	similar to DNA segment, Chr 11, Brigham & Womens Genetics 0434 expressed
242687_at	Similar to RIKEN cDNA 9930021J17
206675_s_at	SKI-like
1553602_at	small breast epithelial mucin
213879_at	SMT3 suppressor of mif two 3 homolog 2 (yeast)
208738_x_at	SMT3 suppressor of mif two 3 homolog 2 (yeast) ; similar to SMT3 suppressor of mif two 3 homolog 2
1556839_s_at	Spectrin, beta, non-erythrocytic 5
220983_s_at	sprouty homolog 4 (Drosophila) ; sprouty homolog 4 (Drosophila)
205966_at	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa
217733_s_at	thymosin, beta 10
216438_s_at	thymosin, beta 4, X-linked ; thymosin-like 3
226835_s_at	transaldolase 1 ; similar to RPE-spondin
224680_at	transmembrane emp24 protein transport domain containing 4
210987_x_at	tropomyosin 1 (alpha)
211702_s_at	ubiquitin specific peptidase 32 ; ubiquitin specific peptidase 32
203798_s_at	visinin-like 1
210935_s_at	WD repeat domain 1
224905_at	WD repeat domain 26
215150_at	YOD1 OTU deubiquinating enzyme 1 homolog (yeast)
227309_at	YOD1 OTU deubiquinating enzyme 1 homolog (yeast)
204180_s_at	zinc finger protein 297B
219163_at	zinc finger protein 562
220854_at	
224051_at	
224050_s_at	

Table 11

Gene	Description
225519_at	protein phosphatase 4, regulatory subunit 2
219199_at	AF4/FMR2 family, member 4
203450_at	PKD2 interactor, golgi and endoplasmic reticulum associated 1
213729_at	formin binding protein 3
220748_s_at	zinc finger protein 580
216480_x_at	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
200043_at	enhancer of rudimentary homolog (Drosophila) ; enhancer of rudimentary homolog (Drosophila)
211075_s_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer) ; CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
1555945_s_at	chromosome 9 open reading frame 10
212295_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
212687_at	LIM and senescent cell antigen-like domains 1

224714_at	MKI67 (FHA domain) interacting nucleolar phosphoprotein
218768_at	nucleoporin 107kDa
228196_s_at	La ribonucleoprotein domain family, member 5
217836_s_at	YY1 associated protein 1
212620_at	zinc finger protein 609
226845_s_at	myeloma overexpressed 2
200747_s_at	nuclear mitotic apparatus protein 1
242304_at	within bgcn homolog (Drosophila)
204767_s_at	flap structure-specific endonuclease 1
217869_at	hydroxysteroid (17-beta) dehydrogenase 12
222729_at	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)
201776_s_at	KIAA0494
1552658_a_at	neuron navigator 3
1555972_s_at	F-box protein 28
216242_x_at	DNA directed RNA polymerase II polypeptide J-related gene
231505_s_at	Sideroflexin 4
228738_at	hypothetical protein MGC25181
228942_s_at	DAB2 interacting protein
208959_s_at	thioredoxin domain containing 4 (endoplasmic reticulum)
223407_at	chromosome 16 open reading frame 48
1555278_a_at	cytoskeleton associated protein 5
219375_at	choline/ethanolamine phosphotransferase 1
208728_s_at	cell division cycle 42 (GTP binding protein, 25kDa)
50376_at	zinc finger protein 444
243108_at	RAN binding protein 9
212884_x_at	Apolipoprotein E
65630_at	transmembrane protein 80
214953_s_at	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)
223946_at	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
232926_x_at	ankyrin repeat domain 19
203597_s_at	WW domain binding protein 4 (formin binding protein 21)
223601_at	olfactomedin 2
212365_at	myosin IB
203297_s_at	Jumonji, AT rich interactive domain 2
231019_x_at	Serine/threonine kinase 11 (Peutz-Jeghers syndrome)
201291_s_at	topoisomerase (DNA) II alpha 170kDa
211846_s_at	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
226843_s_at	PAP associated domain containing 5
225243_s_at	sarcolemma associated protein
236651_at	kalirin, RhoGEF kinase
214792_x_at	vesicle-associated membrane protein 2 (synaptobrevin 2)
228922_at	Src homology 2 domain containing F
225537_at	trafficking protein particle complex 6B
46665_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C
209702_at	fatso
203358_s_at	enhancer of zeste homolog 2 (Drosophila)
211310_at	enhancer of zeste homolog 1 (Drosophila)
242767_at	LIM and cysteine-rich domains 1
1555575_a_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1

223151_at	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)
204170_s_at	CDC28 protein kinase regulatory subunit 2
229420_at	Luminal binding protein 1 (BiP-1) (BP1)
202355_s_at	general transcription factor IIF, polypeptide 1, 74kDa
206061_s_at	Dicer1, Dcr-1 homolog (Drosophila)
224597_at	Transcribed locus, strongly similar to XP_523650.1 PREDICTED: similar to keratin 17 [Pan troglodytes]
217739_s_at	pre-B-cell colony enhancing factor 1
218943_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
211087_x_at	mitogen-activated protein kinase 14 ; mitogen-activated protein kinase 14
220193_at	chromosome 1 open reading frame 113
229410_at	progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein)
221844_x_at	CDNA clone IMAGE:6208446
227683_x_at	Nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 2
233621_s_at	Rho guanine nucleotide exchange factor (GEF) 12
214270_s_at	microtubule-associated protein, RP/EB family, member 3
217762_s_at	RAB31, member RAS oncogene family
231271_x_at	HSCARG protein
227330_x_at	similar to hypothetical protein MGC27019
209773_s_at	ribonucleotide reductase M2 polypeptide
225227_at	SKI-like
218428_s_at	REV1-like (yeast)
201556_s_at	vesicle-associated membrane protein 2 (synaptobrevin 2)

Table 12

Gene	Description
1552477_a_at	interferon regulatory factor 6
228707_at	claudin 23
206427_s_at	melan-A
218196_at	osteopetrosis associated transmembrane protein 1
219142_at	RAS-like, family 11, member B
200601_at	actinin, alpha 4
226483_at	transmembrane protein 68
243568_at	Glycine-rich protein (GRP3S)
212382_at	Transcription factor 4
218417_s_at	hypothetical protein FLJ20489
208905_at	cytochrome c, somatic
203753_at	transcription factor 4
244535_at	Forkhead box P1
222243_s_at	transducer of ERBB2, 2
205174_s_at	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)
231851_at	hypothetical protein FLJ10770
200961_at	selenophosphate synthetase 2
210880_s_at	embryonal Fyn-associated substrate
230986_at	Kruppel-like factor 8
229689_s_at	Discs, large homolog 5 (Drosophila)
204319_s_at	regulator of G-protein signalling 10
219842_at	ADP-ribosylation factor related protein 2
224560_at	TIMP metallopeptidase inhibitor 2

208758_at	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
238662_at	similar to RIKEN cDNA 5730421E18 gene
214000_s_at	Regulator of G-protein signalling 10
1559360_at	Nuclear RNA-binding protein, putative
205694_at	tyrosinase-related protein 1
231579_s_at	TIMP metallopeptidase inhibitor 2
238967_at	Claudin 1
222146_s_at	transcription factor 4
230748_at	solute carrier family 16 (monocarboxylic acid transporters), member 6 ; similar to solute carrier family 16, member 6; monocarboxylate transporter 6

Table 13

Sample		Melanoma	Melanoma	Melanoma	Melanoma	Melanoma	Melanoma	Melanoma	Melanoma	Melanoma	Melanoma
gene	description	DT357-M	DT330-M	DT359-M	DT419-M	DT407-M	DT412-M	DT403-M	DT406-M	DT356-M	DT405-M
244829_at	C6orf218	114.5632	19.56224	0.594604	7.412704	53.81737	0.456916	16.44982	10884.59	17.14838	2797.65
204271_s_at	EDNRB	225.972	151.1671	18.89588	16.67945	754.8258	17.26765	81.00842	45073.75	63.11889	11828.67
200601_at	ACTN4	30.90996	23.10287	10.05611	1.484524	60.96883	5.241574	38.85424	4269.94	9.000468	13682.08
226988_s_at	MYH14	0.192109	0.343885	0.032804	0.140632	0.009486	0.554785	0.004613	1	0.164938	1045.516
202478_at	TRIB2	99.73307	75.58353	28.84001	12.72858	464.6498	15.67072	19.42712	1	24.93327	14972.21
1557292_a_at	MCOLN3	28.05138	8.282119	5.464161	4.084049	64.89341	3.555371	3.24901	1067.485	4.756828	1082.386
224991_at	CMIP	0.615572	0.208772	0.214641	0.205898	0.115023	1.741101	1.148698	1	0.122428	1351.176
1555505_a_at	TYR	21.25897	23.26356	9.849155	0.952638	150.1229	5.426417	2.928171	4870.992	2.732081	3468.269
201908_at	DVL3	0.339151	0.088388	0.239816	8.111676	5.502167	4.924578	1.292353	32.89964	4.169863	7281.399
222670_s_at	MAFB	0.070316	0.069348	0.005263	0.00146	0.532185	0.164938	0.145592	1	0.000816	103.9683
201605_x_at	CNN2	150.1229	58.48521	15.13692	13.54793	324.0337	17.5087	28.44297	22226.61	32.67239	46340.95
213146_at	JMJD3	0.005048	0.003879	0.02683	0.00198	0.009486	0.001211	0.018326	37.01402	0.078563	50.91433
201603_at	PPP1R12A	2.188587	4.69134	0.817902	0.281265	7.361501	0.05954	0.926588	481.0356	0.103665	205.0739
209953_s_at	CDC37	12.72858	34.05985	4.756828	0.615572	13.73705	2.732081	21.70567	1226.218	7.310652	9410.137
201245_s_at	OTUB1	9.063071	6.233317	5.464161	1.905276	10.77787	1.580083	11.87619	3691.522	1.840375	4182.066
208073_x_at	TTC3	15.34823	12.72858	8.168097	8.224911	36.50444	6.916298	7.674113	4973.342	1.741101	4299.64
200958_s_at	SDCBP	3.07375	1.197479	0.336808	0.078021	6.916298	0.065154	0.389582	261.3791	0.5	247.2797
205051_s_at	KIT	86.82268	54.1917	2.713209	8.815241	55.71524	4.055838	0.435275	3082.745	12.81712	689.7836
200819_s_at	RPS15	1584.707	1640.591	491.1432	182.2784	3795.305	377.4129	1884.544	389158.9	484.3815	668236.8

Table 14

Sample		Nevus	Nevus	Nevus	Nevus	Nevus	Nevus	Nevus	Nevus	Nevus	Nevus
gene	description	DF543	DF544	DT343	DT342	DT344	DT345	DT427	DT337	DT340	DT338
244829_at	C6orf218	0.094732	0.80107	0.297302	0.00849	0.000905	1	0.550953	0.939523	0.001236	0.479632
204271_s_at	EDNRB	393.44	16	401.7071	0.135842	0.010598	225.972	1136.199	0.20733	0.001236	393.44
200601_at	ACTN4	0.289172	44.3235	5712.87	65.79928	12.21007	14462.21	3350.127	127.1158	64.44516	3236.009
226988_s_at	MYH14	0.094732	1.404445	430.539	48.50293	0.109576	2304.12	867.0672	2.907945	1.265757	410.1478
202478_at	TRIB2	23.26356	6.868523	797.8645	0.00849	0.005601	1	8422.308	4.287094	3.434262	12.46663
1557292_a_at	MCOLN3	0.25	0.882703	0.297302	0.00849	0.000905	1	116.9704	14.12325	0.001236	0.479632
224991_at	CMIP	3.944931	0.664343	132.5139	7.727491	0.61132	1686.714	369.6459	1.021012	1.918528	433.5336
1555505_a_at	TYR	2.297397	9.189587	0.297302	0.00849	0.010167	63.55792	10.33882	1.94531	0.001236	39.67065
201908_at	DVL3	0.094732	2.219139	139.1021	0.993092	0.248273	404.5012	1097.496	6.588728	1.580083	9.38268
222670_s_at	MAFB	0.233258	1.006956	41.93259	1.879045	0.112656	418.7659	12.64066	0.946058	0.002577	51.98415
201605_x_at	CNN2	41.93259	183.5463	21027.65	855.13	50.91433	3615.551	10015.87	181.0193	58.48521	3821.703
213146_at	JMJD3	0.094732	0.496546	4.69134	0.07911	0.000905	1.580083	0.550953	0.628507	0.001236	0.479632
201603_at	PPP1R12A	0.094732	3.680751	85.03589	19.02731	0.543367	16.22335	202.2506	3.160165	0.008373	942.2722
209953_s_at	CDC37	1.918528	8.815241	699.4126	34.5353	0.959264	2957.167	94.35323	60.54769	7.110741	3929.146
201245_s_at	OTUB1	0.094732	11.87619	1663.493	45.25483	11.08088	9026.807	10297.45	47.50475	9.063071	2179.83
208073_x_at	TTC3	0.882703	58.08123	1478.583	12.295	0.132127	6472.018	1937.526	50.56264	0.314253	2836.704
200958_s_at	SDCBP	0.094732	0.188156	3.317278	0.986233	0.016402	7.568461	0.550953	0.346277	0.001236	1.049717
205051_s_at	KIT	0.094732	0.239816	34.5353	2.602684	0.011203	1	37.01402	1.22264	0.001236	0.479632
200819_s_at	RPS15	13124.73	4299.64	205674	11346.82	584.071	736333.6	137588.5	7967.989	600.4915	269513.9

Table 15

Gene	Lentigo Maligna Mean expression	Solar lentigo Mean expression	(Lentigo Maligna) /(Solar Lentigo) fold change	Description
200961_at	455.88	223.03	2.04	selenophosphate synthetase 2
200782_at	379.88	70.68	5.37	annexin A5
206427_s_at	1899.38	165.82	11.45	melan-A
217998_at	416.81	99.94	4.17	pleckstrin homology-like domain, family A, member 1
226602_s_at	117.73	209.24	0.56	breakpoint cluster region; similar to breakpoint cluster region isoform 1
240366_at	70.62	6.65	10.62	Lipoma HMGIC fusion partner-like 3
208325_s_at	760.50	1233.35	0.62	A kinase (PRKA) anchor protein 13
225202_at	196.73	24.59	8.00	Rho-related BTB domain containing 3
225946_at	46.81	5.74	8.16	Ras association (RalGDS/AF-6) domain family 8
1553603_s_at	37.15	61.18	0.61	ADP-ribosylation factor-like 6 interacting protein 2
220625_s_at	125.23	75.62	1.66	E74-like factor 5 (ets domain transcription factor)
229982_at	28.00	20.79	1.35	hypothetical protein FLJ21924
1552283_s_at	17.50	35.56	0.49	zinc finger, DHHC-type containing 11
200723_s_at	203.23	113.68	1.79	membrane component, chromosome 11, surface marker 1
209174_s_at	57.35	106.44	0.54	FLJ20259 protein
233599_at	244.31	403.97	0.60	Chromosome 9 open reading frame 3
201739_at	4791.23	2597.32	1.84	serum/glucocorticoid regulated kinase
209392_at	403.54	12.79	31.54	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
209487_at	185.54	46.44	4.00	RNA binding protein with multiple splicing
221653_x_at	882.08	458.24	1.92	apolipoprotein L, 2
209185_s_at	349.73	118.85	2.94	insulin receptor substrate 2
222809_x_at	227.73	336.12	0.68	chromosome 14 open reading frame 65
223363_at	150.69	280.06	0.54	hypothetical protein MGC10911
208456_s_at	56.19	122.65	0.46	related RAS viral (r-ras) oncogene homolog 2
221449_s_at	69.81	41.09	1.70	T-cell immunomodulatory protein ; T-cell immunomodulatory protein
215268_at	24.12	46.74	0.52	KIAA0754 protein

217188_s_at	146.88	397.50	0.37	chromosome 14 open reading frame 1
236972_at	302.00	27.09	11.15	tripartite motif-containing 63

Table 16

	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo
gene	DF529-S	DF530-S	DF633-S	DF634-S	DF635-S	DF636-S	DF637-S	DF638-S	DF639-S	DF640-S	DF641-S	DF642-S
200961_at	106	217	101	38	161	221	160	336	304	256	63	210
200782_at	122	21	45	8	70	27	104	195	200	63	101	114
206427_s_at	58	28	92	19	132	29	92	72	1708	12	92	190
217998_at	106	67	180	18	86	76	181	95	238	169	7	8
226602_s_at	654	97	144	691	129	265	109	194	137	277	194	130
240366_at	6	6	7	6	5	6	27	6	6	6	6	6
208325_s_at	1523	568	1553	27	1981	1918	1009	868	1369	2444	554	1297
225202_at	5	6	22	9	84	14	13	14	35	8	21	5
225946_at	5	5	5	5	6	5	5	5	13	6	5	5
1553603_s_at	33	70	60	5	67	59	40	26	54	127	21	43
220625_s_at	37	35	6	6	17	173	55	29	42	5	13	5
229982_at	58	17	25	9	15	13	22	17	9	33	16	12
1552283_s_at	14	31	38	14	49	10	14	33	19	23	41	13
200723_s_at	94	159	201	22	263	94	299	157	95	217	75	93
209174_s_at	118	143	64	25	107	89	103	236	46	256	38	110
233599_at	89	322	294	116	433	380	295	370	306	241	252	294
201739_at	1421	958	3724	618	2023	2741	3098	4062	3856	1907	1530	1569
209392_at	7	44	6	19	10	9	9	10	47	6	17	17
209487_at	6	403	9	6	16	6	24	163	94	5	5	23
221653_x_at	88	379	298	349	396	575	322	372	3571	319	1159	1349
209185_s_at	307	365	182	58	86	140	195	127	44	97	165	130
222809_x_at	646	253	322	6	358	262	319	316	490	277	381	654
223363_at	206	112	192	102	324	318	343	323	185	694	706	860
208456_s_at	322	22	30	34	83	22	125	71	129	125	43	122
221449_s_at	35	26	73	7	69	31	51	37	8	52	66	49
215268_at	11	12	43	9	30	8	22	8	44	73	11	51
217188_s_at	1276	36	545	12	519	479	281	801	209	500	99	457
236972_at	6	6	6	11	6	6	6	6	12	6	6	13

Table 17

	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo
gene	DF643-S	DT024-S	DT055-S	DT069-S	DT079-S	DT123-S	DT146-S	DT187-S	DT306-S	DT365-S	DT367-S	DT368-S
200961_at	223	149	159	8	113	202	2155	152	177	56	76	180
200782_at	17	79	6	84	136	8	5	95	65	34	29	11
206427_s_at	9	444	5	13	29	7	11	500	672	5	6	20
217998_at	15	178	8	104	181	64	6	62	31	205	42	16
226602_s_at	286	212	327	97	368	456	57	84	154	301	50	24
240366_at	6	6	6	7	6	6	6	6	6	6	6	6
208325_s_at	1565	923	877	30	973	1508	1981	1326	1289	863	354	3194
225202_at	49	40	8	9	21	101	8	47	22	12	31	8
225946_at	5	6	5	6	6	5	5	5	9	5	5	6
1553603_s_at	54	72	76	21	84	84	44	71	80	71	100	168
220625_s_at	118	5	6	5	5	14	865	17	5	5	6	6
229982_at	8	8	13	8	33	6	16	18	22	13	13	18
1552283_s_at	10	23	9	11	12	9	13	155	122	10	13	67
200723_s_at	32	21	21	7	179	50	220	171	93	92	17	83
209174_s_at	172	38	48	85	256	115	110	147	109	141	27	96
233599_at	594	125	489	243	695	36	931	591	623	1648	346	1044
201739_at	3963	4104	8062	2767	2729	2760	378	2524	1236	3566	2237	785
209392_at	8	8	7	10	10	7	7	35	14	7	9	7
209487_at	39	139	6	7	84	12	201	44	8	19	6	6
221653_x_at	330	198	139	243	341	331	301	382	511	137	564	306
209185_s_at	53	83	133	7	201	137	170	91	84	78	32	86
222809_x_at	323	478	622	65	190	729	938	438	211	284	180	249
223363_at	196	291	109	85	163	290	331	165	279	161	145	234
208456_s_at	43	211	509	472	81	24	298	32	69	19	75	231
221449_s_at	121	78	31	6	39	10	46	74	56	60	6	31
215268_at	36	19	18	8	102	119	104	133	24	14	108	27
217188_s_at	692	225	228	11	480	1467	195	178	306	423	29	189
236972_at	6	34	6	17	5	6	6	6	6	6	7	6

Table 18

	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo	solar lentigo
gene	DT369-S	DT370-S	DT371-S	DT372-S	DT373-S	DT409-S	DT414-S	DT422-S	DT459-S	DT460-S
200961_at	55	39	38	124	262	37	881	60	128	136
200782_at	139	50	248	17	73	48	117	11	53	8
206427_s_at	9	92	20	7	625	9	585	19	7	20
217998_at	496	34	123	58	140	71	22	31	98	182
226602_s_at	123	46	107	349	95	97	184	440	119	117
240366_at	6	6	6	6	6	6	6	6	6	6
208325_s_at	1373	60	557	201	1500	2266	1545	1500	2099	839
225202_at	20	12	9	122	9	8	5	11	40	8
225946_at	6	6	6	6	6	5	5	6	6	5
1553603_s_at	57	101	22	34	47	33	47	39	102	68
220625_s_at	5	6	5	6	6	5	974	6	11	67
229982_at	58	6	13	13	13	8	13	31	117	13
1552283_s_at	65	12	18	9	15	6	87	138	25	81
200723_s_at	95	97	11	41	97	77	253	7	103	329
209174_s_at	177	31	140	123	28	163	134	13	47	84
233599_at	453	300	195	152	58	166	802	300	279	273
201739_at	2723	3494	2757	850	3680	3553	721	897	3544	3472
209392_at	6	9	31	7	7	7	12	10	9	7
209487_at	15	6	7	6	6	6	166	7	23	6
221653_x_at	237	204	353	362	354	249	229	108	171	353
209185_s_at	100	15	10	82	94	6	496	13	101	73
222809_x_at	167	215	248	121	408	209	336	138	226	369
223363_at	121	145	83	121	984	182	227	150	466	229
208456_s_at	168	41	216	39	230	22	77	23	28	134
221449_s_at	34	6	5	10	7	160	18	7	27	61
215268_at	88	9	11	52	55	13	24	9	254	40
217188_s_at	647	119	93	79	122	694	269	111	834	910
236972_at	6	36	619	8	11	6	6	17	5	6

Table 19

	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna
gene	DF569-LM	DF557-LM	DF579-LM	DF580-LM	DF582-LM	DF596-LM	DF623-LM	DF624-LM	DF625-LM	DF626-LM	DF627-LM
200961_at	847	567	158	531	234	359	357	330	347	518	1667
200782_at	154	500	157	193	764	1310	331	27	157	161	16
206427_s_at	1833	2805	95	1327	2219	6320	3253	49	274	193	121
217998_at	185	1245	726	88	907	773	789	182	340	114	10
226602_s_at	49	47	59	51	71	36	50	51	137	91	579
240366_at	139	251	6	43	122	35	15	6	12	25	6
208325_s_at	20	1362	725	408	882	430	568	1583	1867	1460	699
225202_at	25	16	44	312	237	1183	170	33	26	83	8
225946_at	48	57	9	76	12	7	35	5	5	6	28
1553603_s_at	8	21	43	67	45	21	37	38	50	23	10
220625_s_at	5	5	5	288	29	5	132	154	126	206	1427
229982_at	8	8	19	8	28	21	13	44	35	28	93
1552283_s_at	11	14	12	16	5	13	68	10	35	13	13
200723_s_at	159	480	276	85	369	112	349	90	319	242	134
209174_s_at	135	24	48	68	87	130	40	58	85	110	60
233599_at	158	60	524	126	283	385	298	183	228	276	165
201739_at	6073	10285	3008	5935	4757	3159	3792	3462	3128	2916	826
209392_at	772	235	14	1088	210	243	912	9	8	8	7
209487_at	291	148	21	315	280	1146	521	31	16	71	61
221653_x_at	433	203	613	743	1224	5336	983	425	227	141	43
209185_s_at	1935	1458	124	482	85	535	182	98	169	308	154
222809_x_at	33	32	55	45	161	31	36	437	163	170	1483
223363_at	161	136	139	92	156	129	114	241	122	147	105
208456_s_at	20	27	27	21	49	57	8	33	39	210	46
221449_s_at	7	7	28	54	30	50	199	185	57	24	156
215268_at	9	11	157	41	17	11	42	11	27	9	9
217188_s_at	8	8	94	11	148	39	8	1146	455	62	107
236972_at	1318	1977	6	137	77	247	51	8	31	6	13

Table 20

	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna	lentigo maligna
gene	DF629-LM	DF630-LM	DF631-LM	DF632-LM	DT017-LM	DT266-LM	DT268-LM	DT269-LM	DT270-LM	DT331-LM	DT355-LM	DT423-LM
200961_at	350	139	465	196	510	439	435	383	744	306	398	420
200782_at	291	156	265	8	551	52	255	33	825	469	1914	308
206427_s_at	2834	317	1121	5	4173	290	1952	181	3873	3913	9382	990
217998_at	307	241	427	38	521	285	328	48	1470	344	879	184
226602_s_at	114	46	230	74	48	184	81	280	13	46	30	107
240366_at	6	6	6	6	6	43	8	8	115	262	642	47
208325_s_at	529	101	448	1404	956	506	782	632	608	2658	396	642
225202_at	139	152	36	66	143	121	83	46	1987	65	23	31
225946_at	6	6	81	6	28	14	32	9	415	46	202	67
1553603_s_at	34	40	21	32	52	13	37	37	22	56	11	37
220625_s_at	5	6	69	95	11	23	33	90	5	6	6	239
229982_at	36	14	56	47	29	13	21	13	12	13	12	12
1552283_s_at	13	12	10	10	16	10	13	9	38	26	34	13
200723_s_at	321	300	70	118	138	68	21	54	80	97	67	113
209174_s_at	84	52	12	40	38	26	84	70	28	47	63	29
233599_at	296	32	96	80	1338	115	314	86	131	497	62	235
201739_at	2421	3869	4568	3885	2679	4995	4927	4514	12929	5385	9033	5005
209392_at	273	223	464	11	656	26	498	7	1581	287	2683	238
209487_at	101	6	338	6	661	19	36	6	366	33	243	90
221653_x_at	626	873	983	336	1599	265	780	493	516	1548	1540	437
209185_s_at	389	115	164	214	105	201	102	255	1272	161	139	160
222809_x_at	166	105	461	83	125	527	435	453	22	186	56	322
223363_at	314	122	132	90	191	105	206	373	167	113	167	104
208456_s_at	17	26	122	27	44	203	61	36	71	22	27	196
221449_s_at	36	171	107	142	39	74	48	83	11	10	40	162
215268_at	11	7	9	9	43	11	24	16	8	11	11	98
217188_s_at	175	638	24	79	138	166	95	50	8	144	25	84
236972_at	33	34	328	7	365	41	51	9	1766	698	421	200

Table 21

gene	lentigo maligna DT425-LM	lentigo maligna DT461-LM	lentigo maligna DF523-LM
200961_at	798	348	7
200782_at	150	328	502
206427_s_at	177	778	909
217998_at	38	233	135
226602_s_at	492	49	46
240366_at	6	9	6
208325_s_at	20	38	49
225202_at	68	9	9
225946_at	5	6	6
1553603_s_at	168	21	22
220625_s_at	204	6	76
229982_at	58	62	25
1552283_s_at	13	18	10
200723_s_at	863	24	335
209174_s_at	49	12	12
233599_at	93	53	238
201739_at	2997	4238	5786
209392_at	20	9	10
209487_at	6	6	6
221653_x_at	750	1089	728
209185_s_at	273	7	6
222809_x_at	111	35	188
223363_at	107	83	102
208456_s_at	22	10	40
221449_s_at	22	22	51
215268_at	6	6	13
217188_s_at	38	6	63
236972_at	8	7	13

10 Sep 2015 2009246180

[0182] Although the invention has been described with reference to the above examples, it will be understood that modifications and variations are encompassed within the spirit and scope of the invention. Accordingly, the invention is limited only by the following claims.

[0183] Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each claim of this application.

[0184] Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method of detecting melanoma in a human subject comprising:

(a) obtaining a sample of a skin lesion suspected of comprising melanoma from a human subject, wherein the skin lesion sample comprises or is suspected of comprising a nucleic acid molecule expressed from C6orf218;

(b) detecting the presence of a nucleic acid molecule expressed from C6orf218 in the skin lesion sample, whereby the presence of a nucleic acid molecule expressed from C6orf218 in the skin lesion sample in an amount that is greater than the presence of C6orf218 in a non-melanoma sample is indicative of melanoma in the skin lesion sample, wherein detecting the presence of a nucleic acid molecule expressed from C6orf218 is by application of a detectably labeled probe that hybridizes to a nucleic acid molecule expressed from C6orf218; and

(c) characterizing the skin lesion as having melanoma or not having melanoma.

2. The method of claim 1, wherein the nucleic acid molecule is RNA.

3. The method of claim 1 or 2, further comprising amplifying the nucleic acid molecule.

4. The method of any one of claims 1 to 3, wherein the nucleic acid molecule or an amplification product thereof, is quantified using quantitative real-time PCR.

5. The method of claim 1 or 2, further comprising amplifying the nucleic acid molecule and quantifying the amplification product using quantitative real-time PCR.

6. The method of any one of claims 1 to 5, wherein the skin lesion sample is obtained by applying an adhesive tape to a target area of skin in a manner sufficient to isolate the skin lesion sample adhering to the adhesive tape.

7. The method of any one of claims 1 to 5, wherein the skin lesion sample is obtained from a biopsy taken at the site of the skin lesion.

8. The method of claim 6, wherein the tape comprises a rubber adhesive on a polyurethane film

9. The method of claim 6, wherein about one to ten adhesive tapes or one to ten applications of a tape are applied and removed from the skin.

10. The method of claim 6, wherein about one to eight 5 adhesive tapes or one to eight applications of a tape are applied and removed from the skin.

11. The method of claim 6, wherein about one to five adhesive tapes or one to five

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applications of a tape are applied and removed from the skin.

12. The method of claim 6, wherein the method further comprises taking a biopsy of the target area of the skin.

13. The method of claim 1 or 2, wherein the detecting is performed in situ.

14. The method of any one of claims 1 to 13, further comprising determining a treatment regimen.

15. A method for diagnosing melanoma in a subject, comprising:

(a) obtaining a sample of a skin lesion suspected of comprising melanoma from a subject, wherein the skin lesion sample comprises or is suspected of comprising a nucleic acid molecule expressed from C6orf218;

(b) detecting the presence of a nucleic acid molecule expressed from C6orf218 in the skin lesion sample, wherein detecting the presence of a nucleic acid molecule expressed from C6orf218 is by application of a detectably labeled probe that hybridizes to a nucleic acid molecule expressed from C6orf218; and

(c) comparing the presence of a nucleic acid molecule expressed from C6orf218 in the skin lesion sample to the presence of C6orf218 in a non-melanoma sample, whereby the increased presence of a nucleic acid molecule expressed from C6orf218 in the skin lesion sample as compared to the non-melanoma sample is indicative of melanoma, thereby diagnosing the skin lesion as having melanoma.

16. The method of claim 15, further comprising determining a treatment regimen.

17. The method of claim 15 or 16, wherein the presence of a nucleic acid molecule expressed from C6orf218 in the non-melanoma skin sample is contained with a database.

18. The method of claim 15 or 16, wherein the analyzing step is carried out using a computer.

19. The method of any one of claims 1 to 18, substantially as described herein with reference to the Figures and/or Examples.

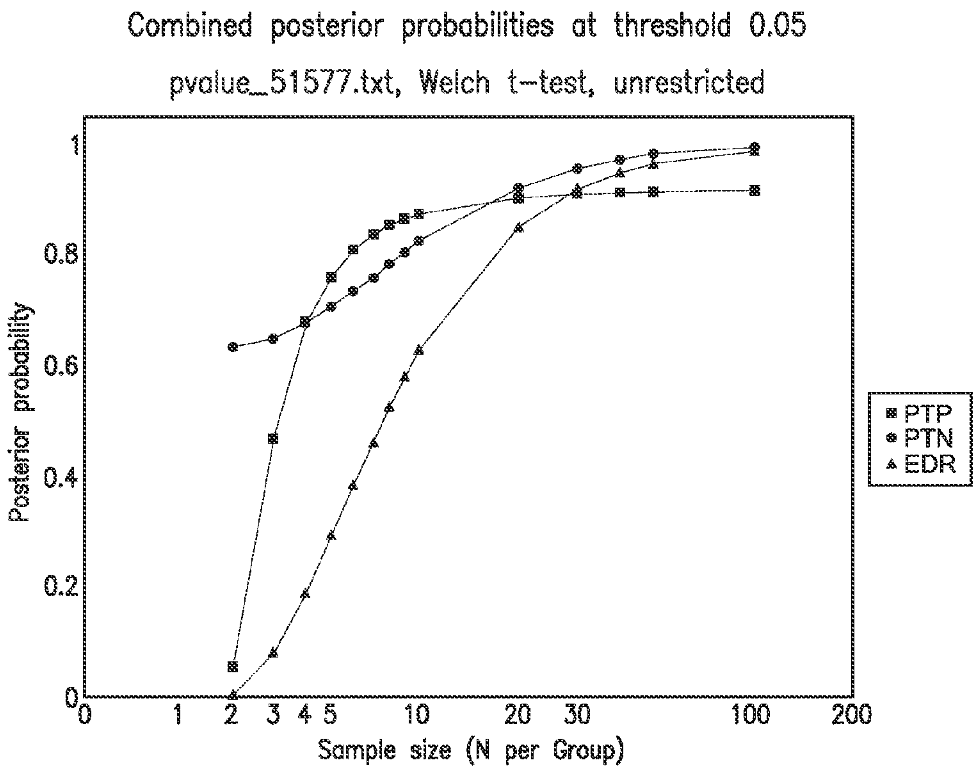

Combined posterior probabilities at threshold 0.05
pvalue_51577.txt, Welch t-test, unrestricted
Posterior probability
0
0.2
0.4
0.6
0.8
1
Sample size (N per Group)
0
1
2
3
4
5
10
20
30
100
200
PTP
PTN
EDR

FIG. 1A

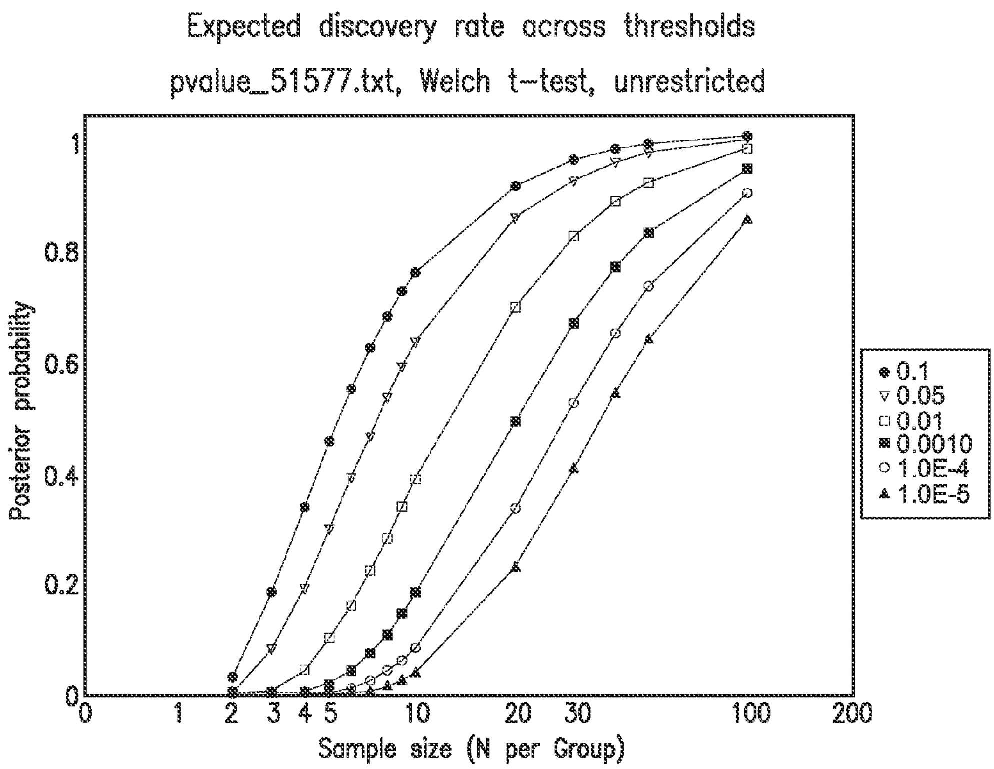

Expected discovery rate across thresholds
pvalue_51577.txt, Welch t-test, unrestricted
Posterior probability
0
0.2
0.4
0.6
0.8
1
Sample size (N per Group)
0
1
2
3
4
5
10
20
30
100
200
0.1
0.05
0.01
0.0010
1.0E-4
1.0E-5

FIG. 1B

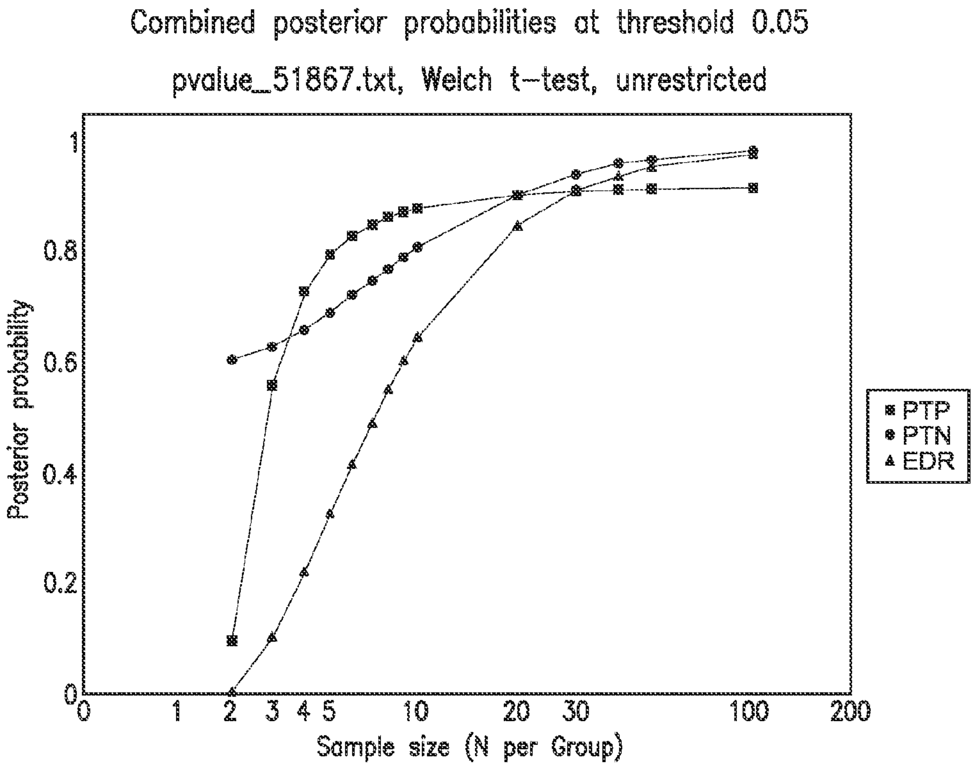

Combined posterior probabilities at threshold 0.05
pvalue_51867.txt, Welch t-test, unrestricted
Posterior probability
Sample size (N per Group)
0
0.2
0.4
0.6
0.8
1
0
1
2
3
4
5
10
20
30
100
200
PTP
PTN
EDR

FIG. 2A

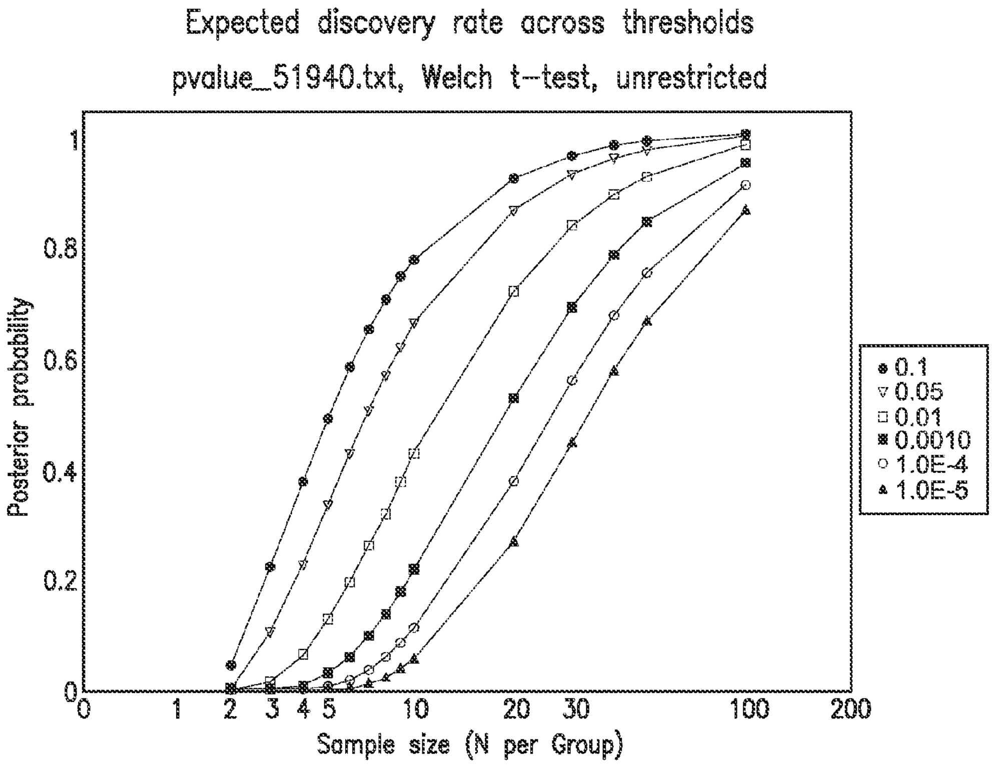

Expected discovery rate across thresholds
pvalue_51940.txt, Welch t-test, unrestricted
Posterior probability
Sample size (N per Group)
0
0.2
0.4
0.6
0.8
1
0
1
2
3
4
5
10
20
30
100
200
0.1
0.05
0.01
0.0010
1.0E-4
1.0E-5

FIG. 2B

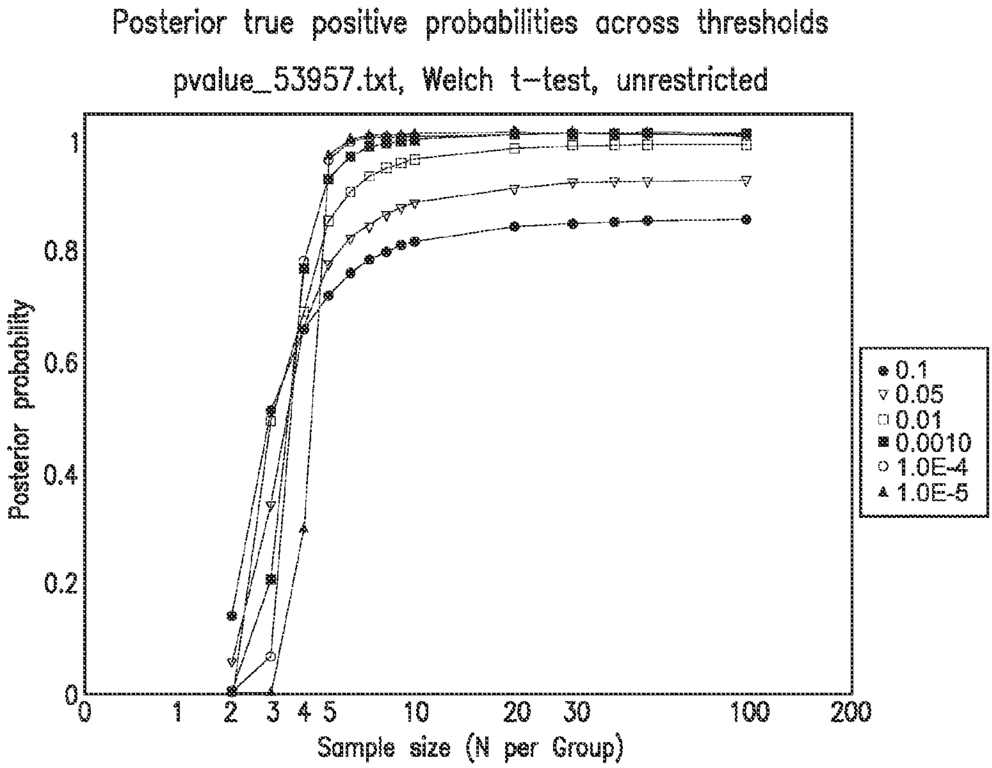

Posterior true positive probabilities across thresholds
pvalue_53957.txt, Welch t-test, unrestricted
Posterior probability
0
0.2
0.4
0.6
0.8
1
0 1 2 3 4 5 10 20 30 100 200
Sample size (N per Group)
0.1
0.05
0.01
0.0010
1.0E-4
1.0E-5

FIG. 3A

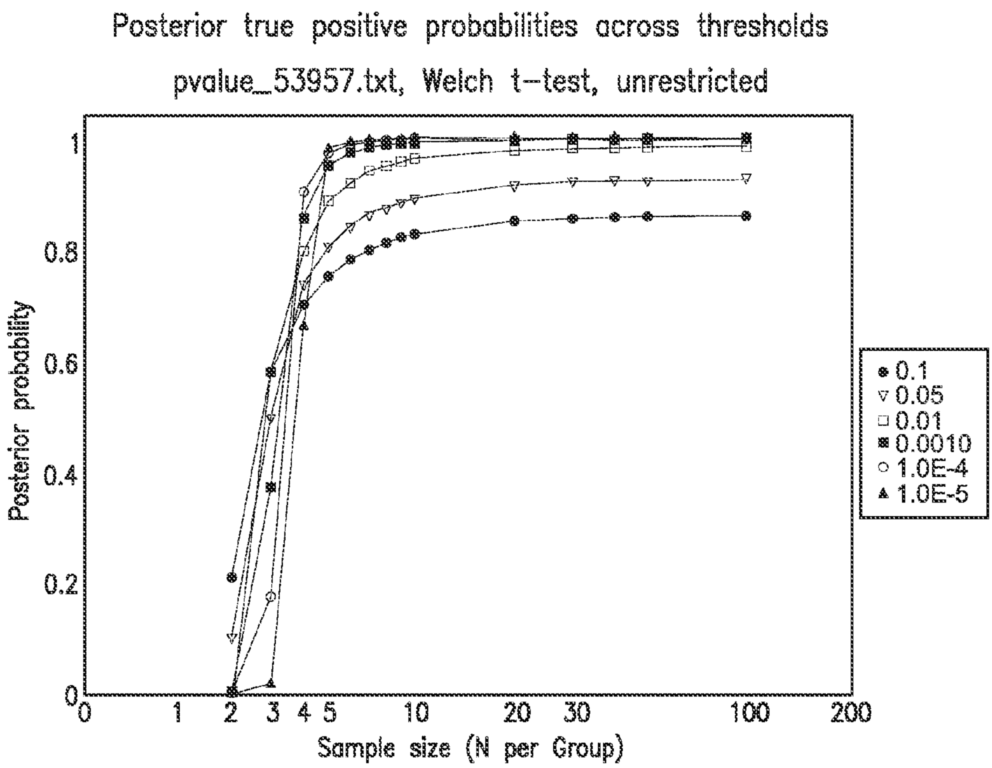

Posterior true positive probabilities across thresholds
pvalue_53957.txt, Welch t-test, unrestricted
Posterior probability
0
0.2
0.4
0.6
0.8
1
0 1 2 3 4 5 10 20 30 100 200
Sample size (N per Group)
0.1
0.05
0.01
0.0010
1.0E-4
1.0E-5

FIG. 3B

Expression Profiling Distinguishes Melanomas from Atypical Nevi and Normal Skin

U133 Plus 2.0 GeneChip assay of specimens

- GCRMA normalization
- Background subtraction: 50
- t-test between melanomas and nevi ($p<0.01$)
- Multiple testing correction
  - Westfall & Young permutation
- False discovery rate ($q<0.05$)
- **317 differentially expressed genes selected**

Hierarchical clustering analysis

- log2-transformed, mean-centered for arrays and genes
- cluster with complete linkage metric
- Melanoma (N=20)
- Atypical nevus (N=62)
- Normal Skin (N=17)

Results:

- Melanomas distinguished from normal skin and atypical nevi

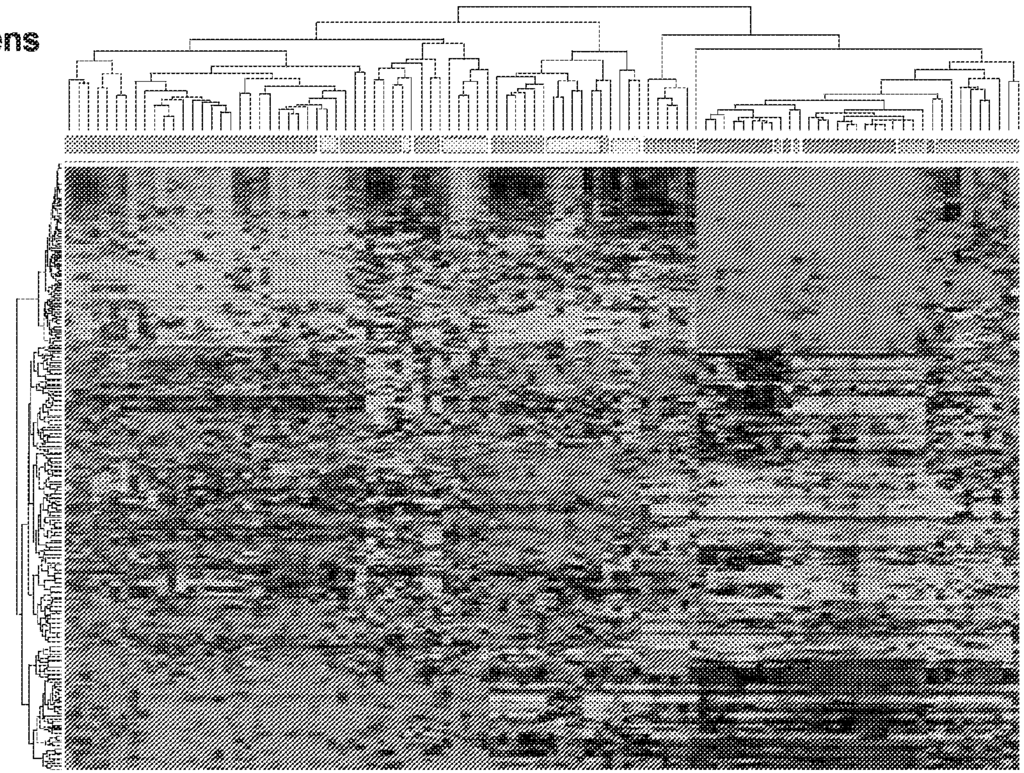


FIG. 4A

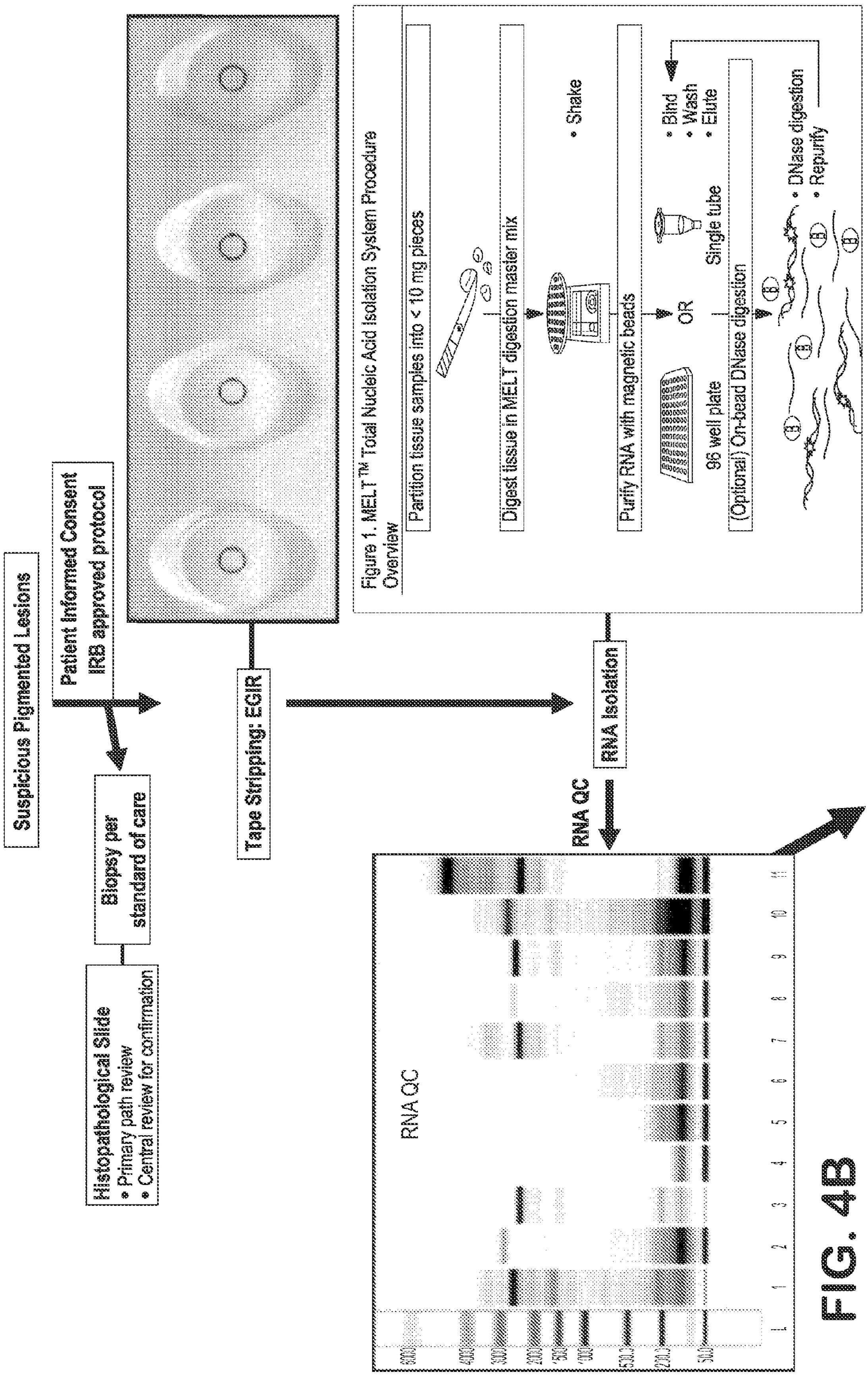

Suspicious Pigmented Lesions
Patient Informed Consent
IRB approved protocol
Biopsy per standard of care
Histopathological Slide
• Primary path review
• Central review for confirmation
Tape Stripping: EGIR
RNA Isolation
RNA QC
Figure 1. MELT™ Total Nucleic Acid Isolation System Procedure Overview
Partition tissue samples into < 10 mg pieces
Digest tissue in MELT digestion master mix
• Shake
Purify RNA with magnetic beads
96 well plate
OR
Single tube
• Bind
• Wash
• Elute
(Optional) On-bead DNase digestion
• DNase digestion
• Repurify
RNA QC

FIG. 4B

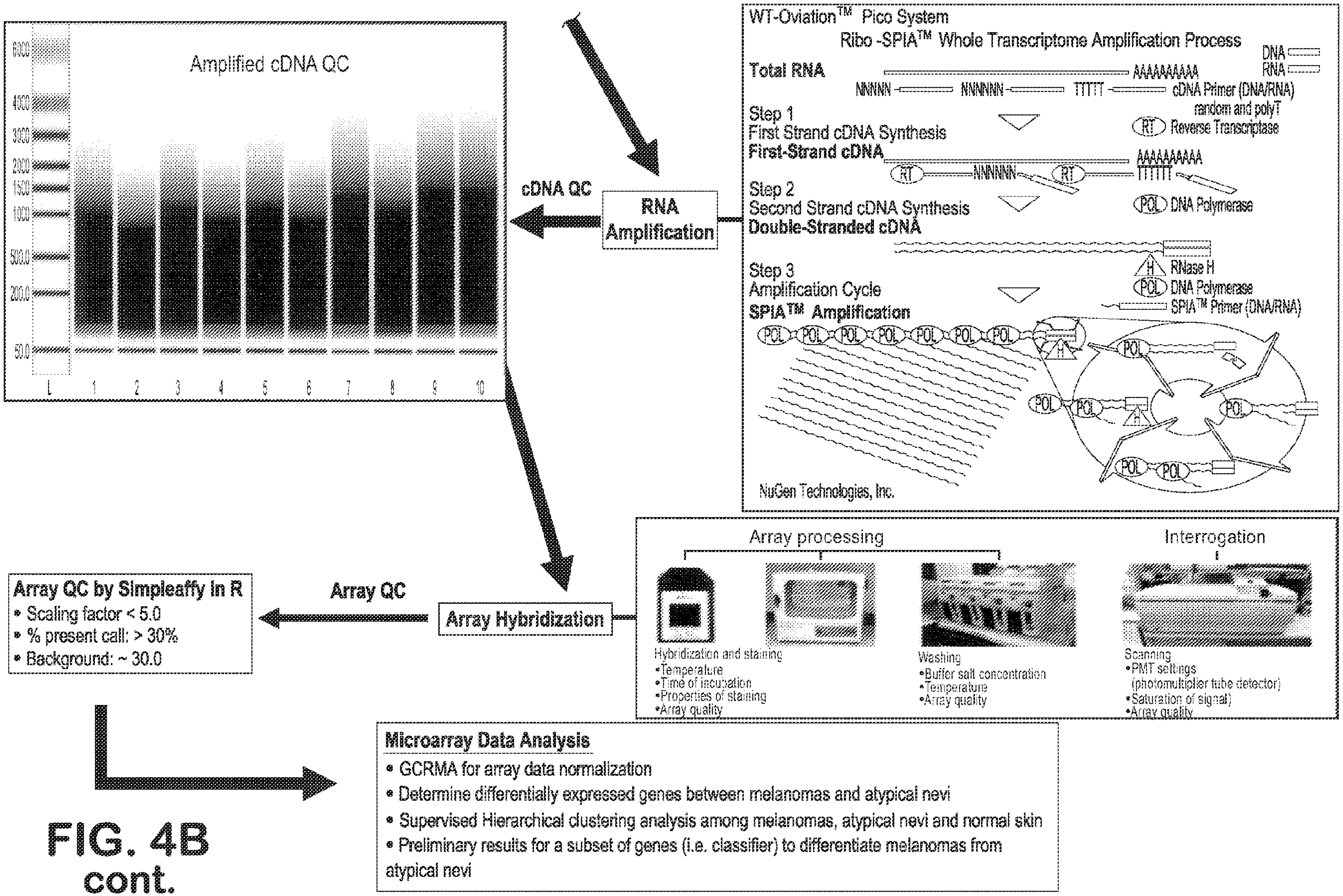
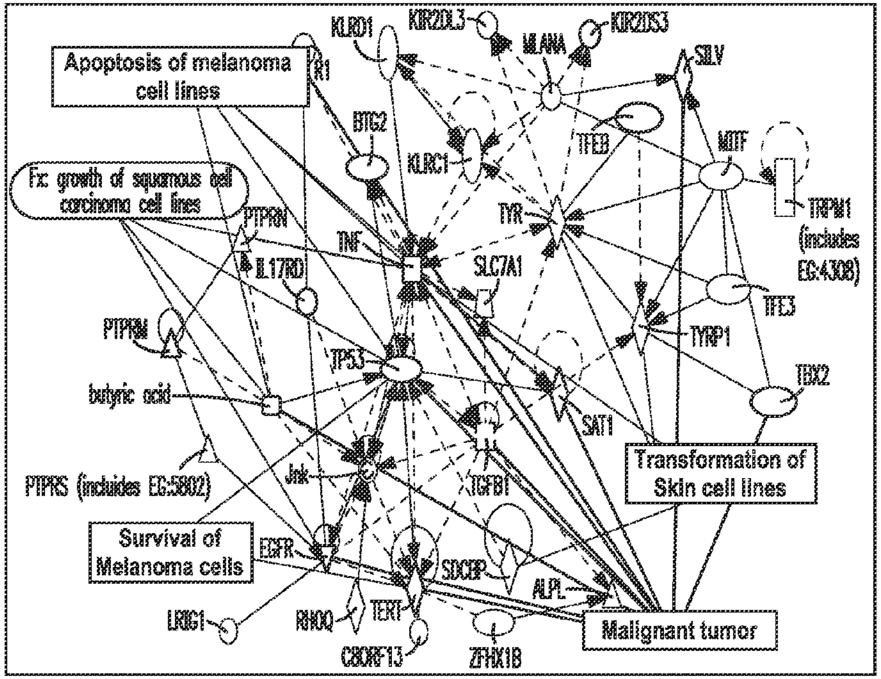

Amplified cDNA QC
6000
4000
3000
2000
1500
1000
500.0
200.0
50.0
L 1 2 3 4 5 6 7 8 9 10
cDNA QC
RNA Amplification
WT-Oviation™ Pico System
Ribo -SPIA™ Whole Transcriptome Amplification Process
DNA
RNA
Total RNA
AAAAAAAAA
NNNNN NNNNNN TTTTT cDNA Primer (DNA/RNA) random and polyT
Step 1
First Strand cDNA Synthesis
First-Strand cDNA
RT Reverse Transcriptase
Step 2
Second Strand cDNA Synthesis
Double-Stranded cDNA
POL DNA Polymerase
Step 3
Amplification Cycle
SPIA™ Amplification
H RNase H
POL DNA Polymerase
SPIA™ Primer (DNA/RNA)
NuGen Technologies, Inc.
Array processing
Interrogation
Hybridization and staining
•Temperature
•Time of incubation
•Properties of staining
•Array quality
Washing
•Buffer salt concentration
•Temperature
•Array quality
Scanning
•PMT settings (photomultiplier tube detector)
•Saturation of signal)
•Array quality
Array Hybridization
Array QC
Array QC by Simpleaffy in R
• Scaling factor < 5.0
• % present call: > 30%
• Background: ~ 30.0
Microarray Data Analysis
• GCRMA for array data normalization
• Determine differentially expressed genes between melanomas and atypical nevi
• Supervised Hierarchical clustering analysis among melanomas, atypical nevi and normal skin
• Preliminary results for a subset of genes (i.e. classifier) to differentiate melanomas from atypical nevi

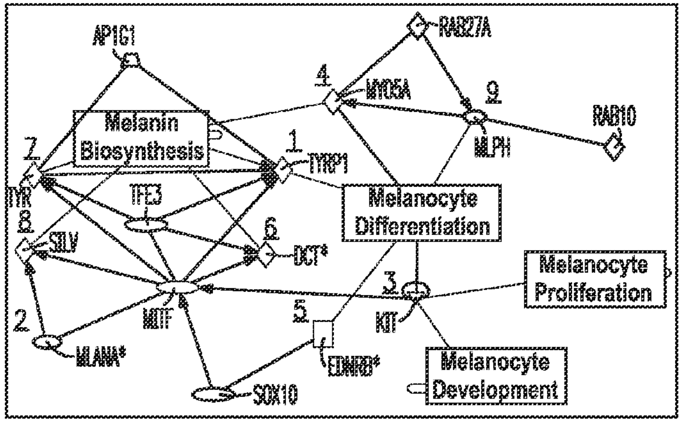
FIG. 4B cont.

Biological Functions of Genes Differentially Expressed Between Melanomas and Nevi

Genes Involved in Cell Death and Cancer



Genes Involved in Melanocyte Function

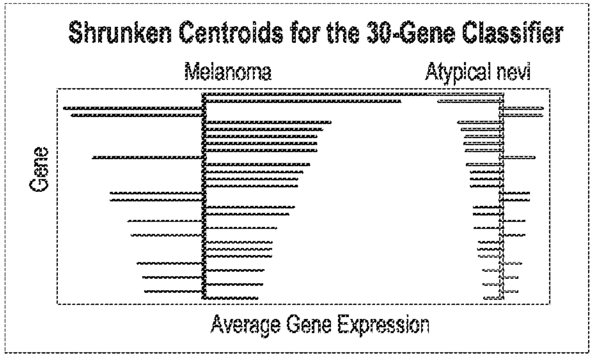


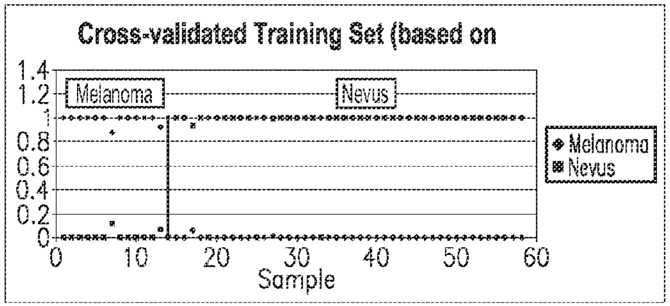
No.	Gene ID	p-value	Description
1	TYRP1	1.22E-09	tyrosinase-related protein 1
2	Melan-A	3.13E-06	melan-A
3	KIT	3.13E-06	KIT
4	MYO5A	4.22E-06	myosin VA
5	ENDRB	5.67E-06	endothelin receptor type B
6	DCT	9.35E-06	dopachrome tautomerase
7	TYR	4.47E-05	tyrosinase
8	SILV	7.86E-05	silver homolog
9	MLPH	0.000233	melanophilin

FIG. 4C

Developing a Classifier to Differentiate Melanomas from Atypical Nevi

- **Prediction Analysis of Microarrays (PAM):class prediction algorithm**
  - Training set: 14 melanomas and 44 atypical nevi
  - Testing set: 6 melanomas and 20 atypical nevi
- **Developing a melanoma classifier**
  - Starting with 317 differentially expressed genes
    - 100% accuracy of prediction on both training and testing sets
  - Select the top 150 ranked genes
    - 100% accuracy of prediction on both training and testing sets
  - Select the top ranked genes until no false negative call on both training and testing sets
    - A 30-gene classifier to discriminate melanomas from atypical nevi
    - Sensitivity: 100%
    - Specificity: greater than 90%





Training Set

	Predicted Class		
	Diagnosis		Percentage Correct
Observed	Melanoma	Atypical nevi	
Melanoma	14	0	100
Atypical nevi	3	41	93.2

Testing Set

	Predicted Class		
	Diagnosis		Percentage Correct
Observed	Melanoma	Atypical nevi	
Melanoma	6	0	100
Atypical nevi	2	18	90

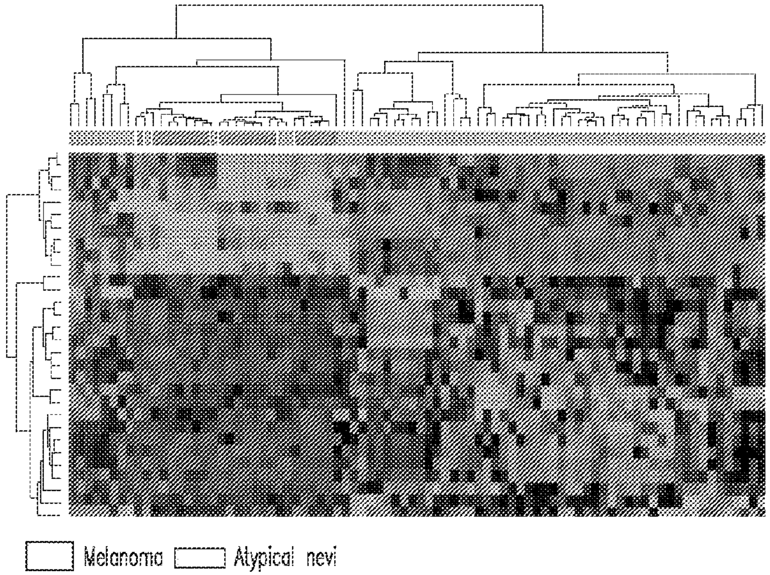


FIG. 4D

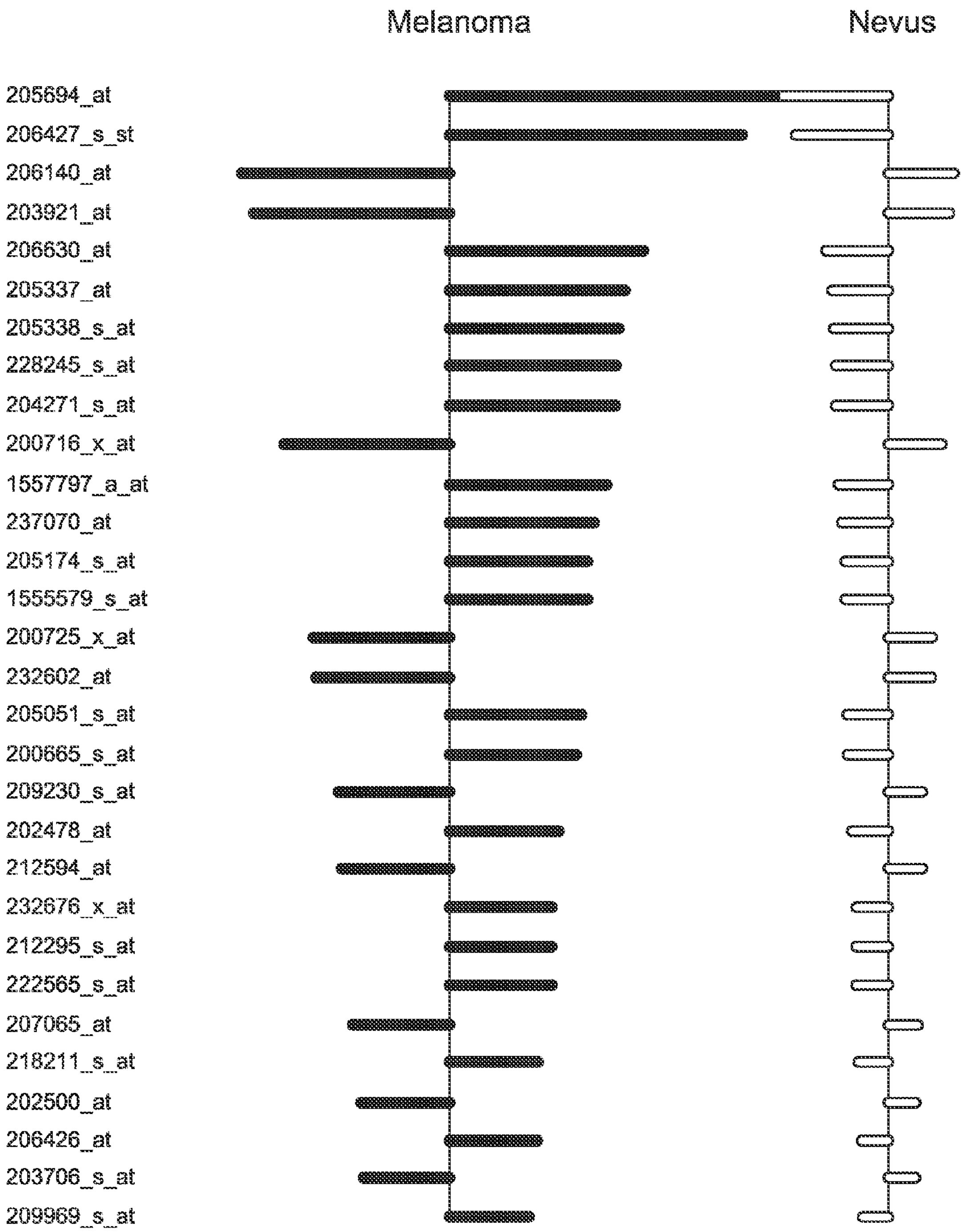

Melanoma
Nevus
205694_at
206427_s_st
206140_at
203921_at
206630_at
205337_at
205338_s_at
228245_s_at
204271_s_at
200716_x_at
1557797_a_at
237070_at
205174_s_at
1555579_s_at
200725_x_at
232602_at
205051_s_at
200665_s_at
209230_s_at
202478_at
212594_at
232676_x_at
212295_s_at
222565_s_at
207065_at
218211_s_at
202500_at
206426_at
203706_s_at
209969_s_at

FIG. 5A

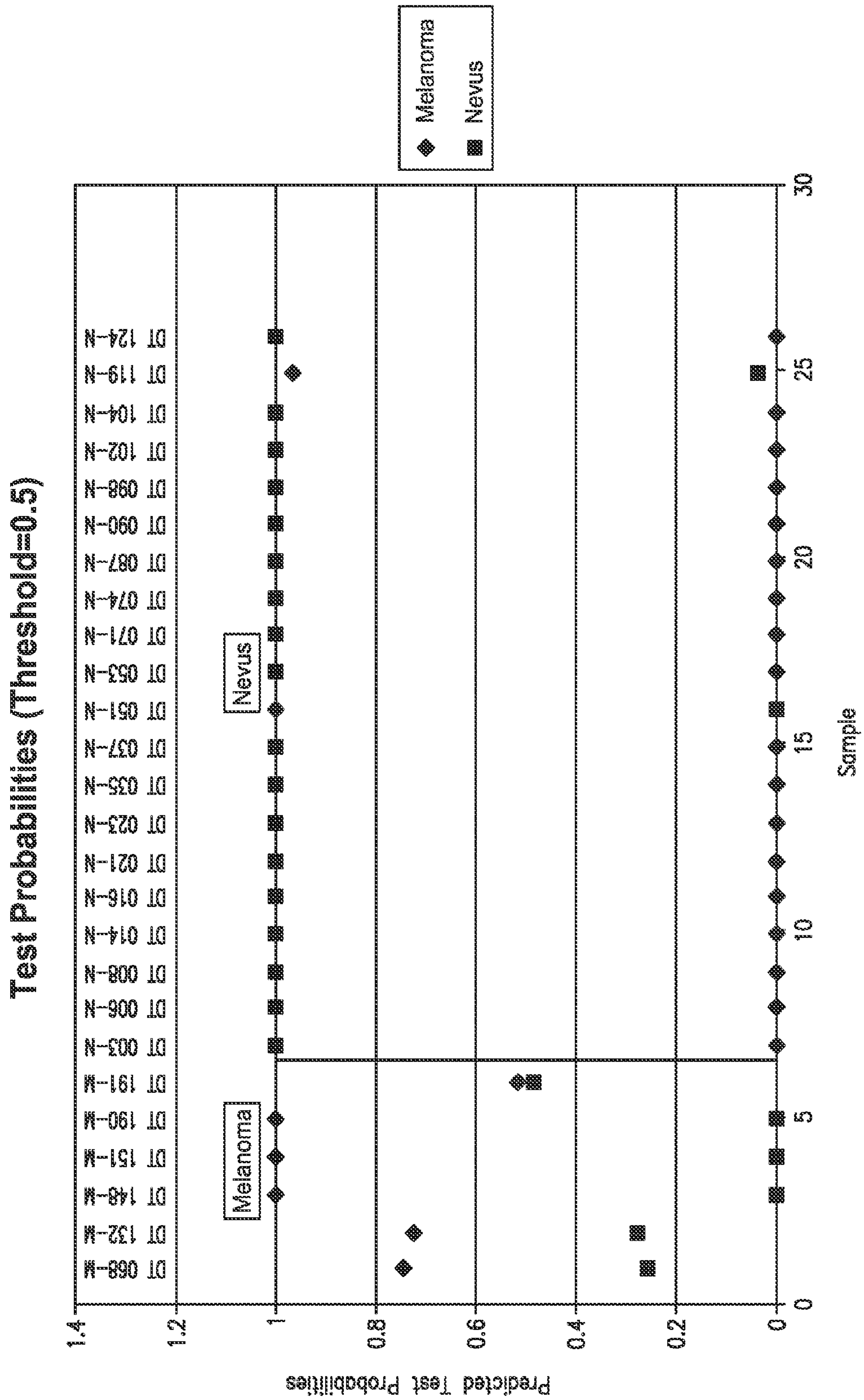

Test Probabilities (Threshold=0.5)
Melanoma
Nevus
Predicted Test Probabilities
Sample
DT 068-M
DT 132-M
DT 148-M
DT 151-M
DT 190-M
DT 191-M
DT 003-N
DT 006-N
DT 008-N
DT 014-N
DT 016-N
DT 021-N
DT 023-N
DT 035-N
DT 037-N
DT 051-N
DT 053-N
DT 071-N
DT 074-N
DT 087-N
DT 090-N
DT 098-N
DT 102-N
DT 104-N
DT 119-N
DT 124-N
0
0.2
0.4
0.6
0.8
1
1.2
1.4
0
5
10
15
20
25
30

FIG. 5B

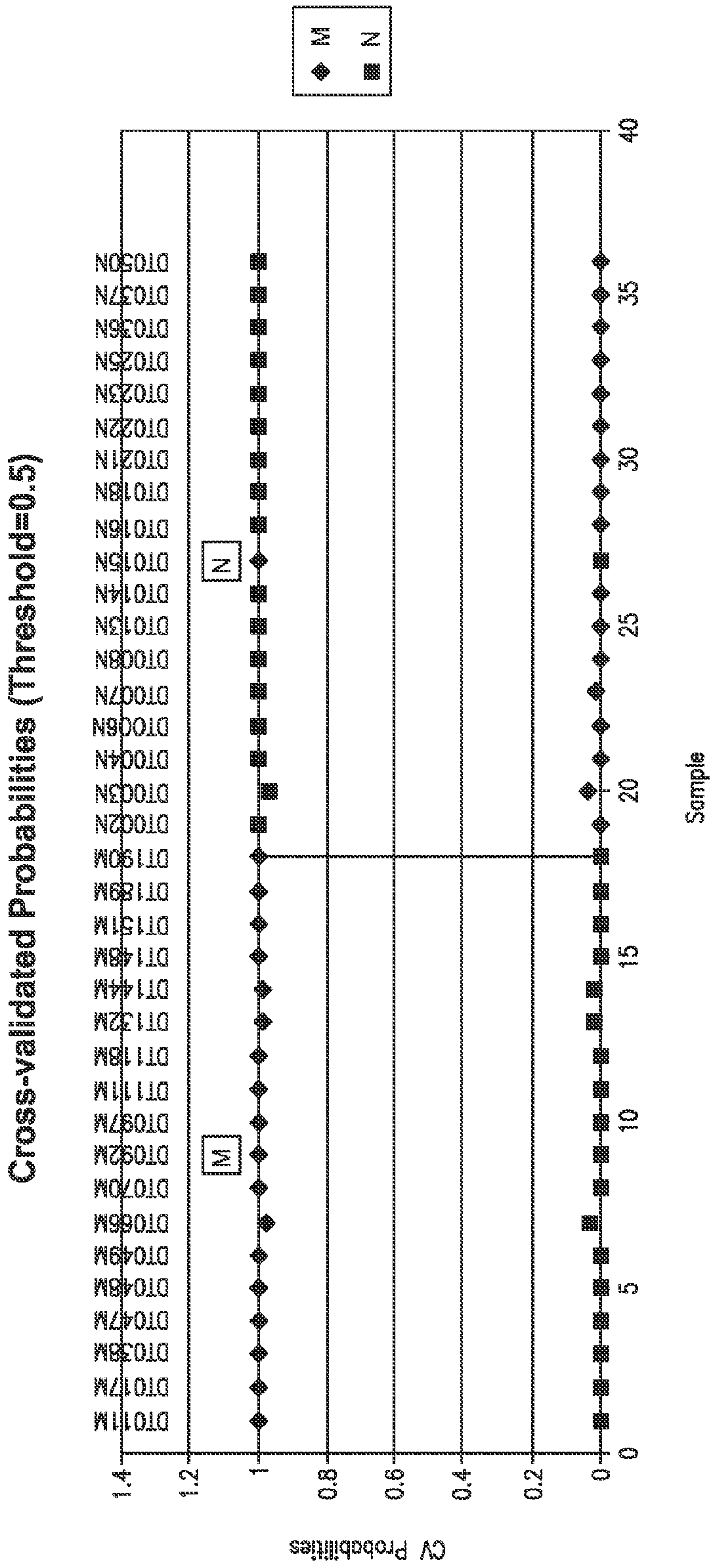

Cross-validated Probabilities (Threshold=0.5)
CV Probabilities
Sample
M
N
0
0.2
0.4
0.6
0.8
1
1.2
1.4
0
5
10
15
20
25
30
35
40
DT011M
DT017M
DT038M
DT047M
DT048M
DT049M
DT066M
DT070M
DT092M
DT097M
DT111M
DT118M
DT132M
DT144M
DT148M
DT151M
DT189M
DT190M
DT002N
DT003N
DT004N
DT006N
DT007N
DT008N
DT013N
DT014N
DT015N
DT016N
DT018N
DT021N
DT022N
DT023N
DT025N
DT036N
DT037N
DT050N

FIG. 6A

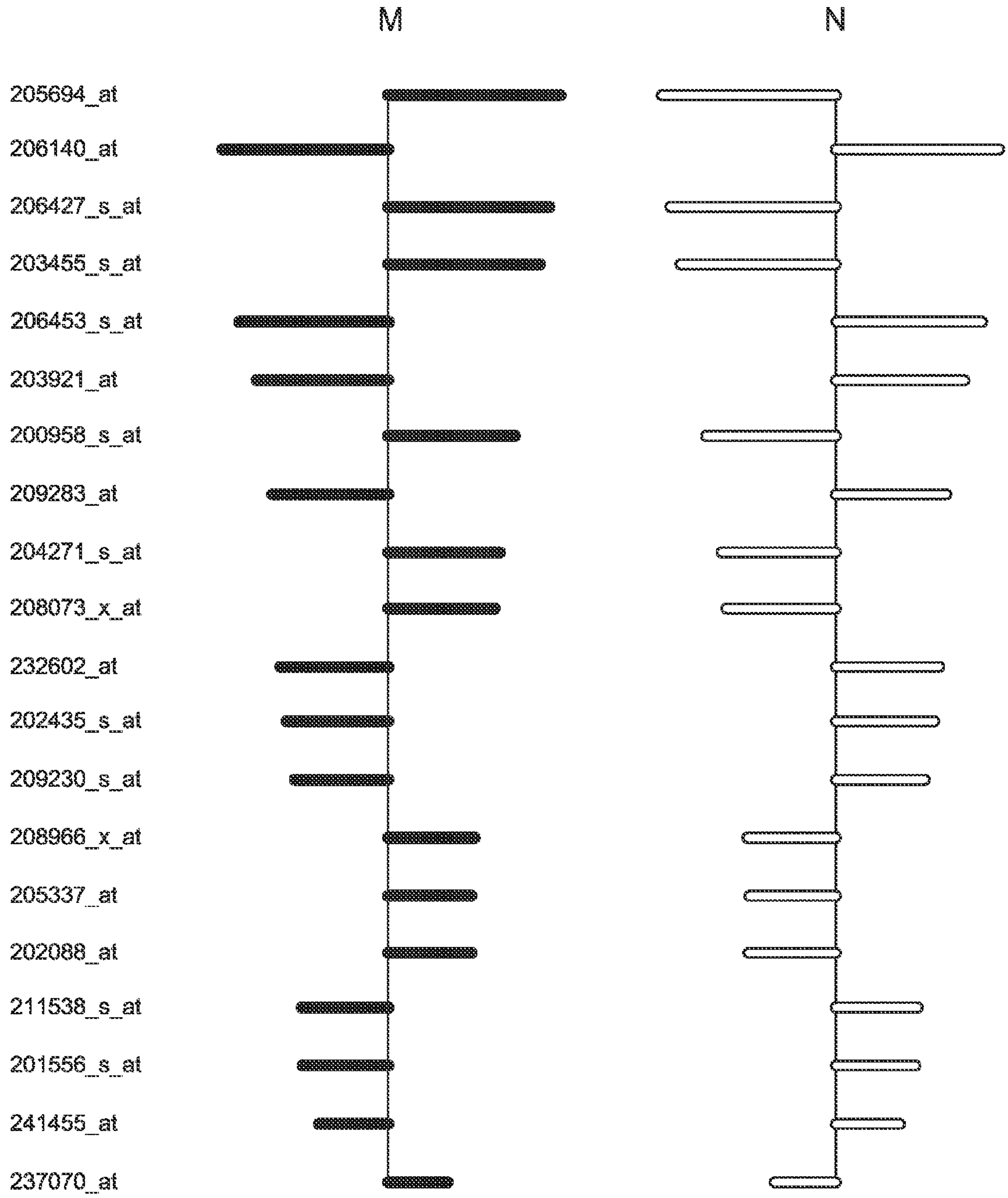

M
N
205694_at
206140_at
206427_s_at
203455_s_at
206453_s_at
203921_at
200958_s_at
209283_at
204271_s_at
208073_x_at
232602_at
202435_s_at
209230_s_at
208966_x_at
205337_at
202088_at
211538_s_at
201556_s_at
241455_at
237070_at

FIG. 6B

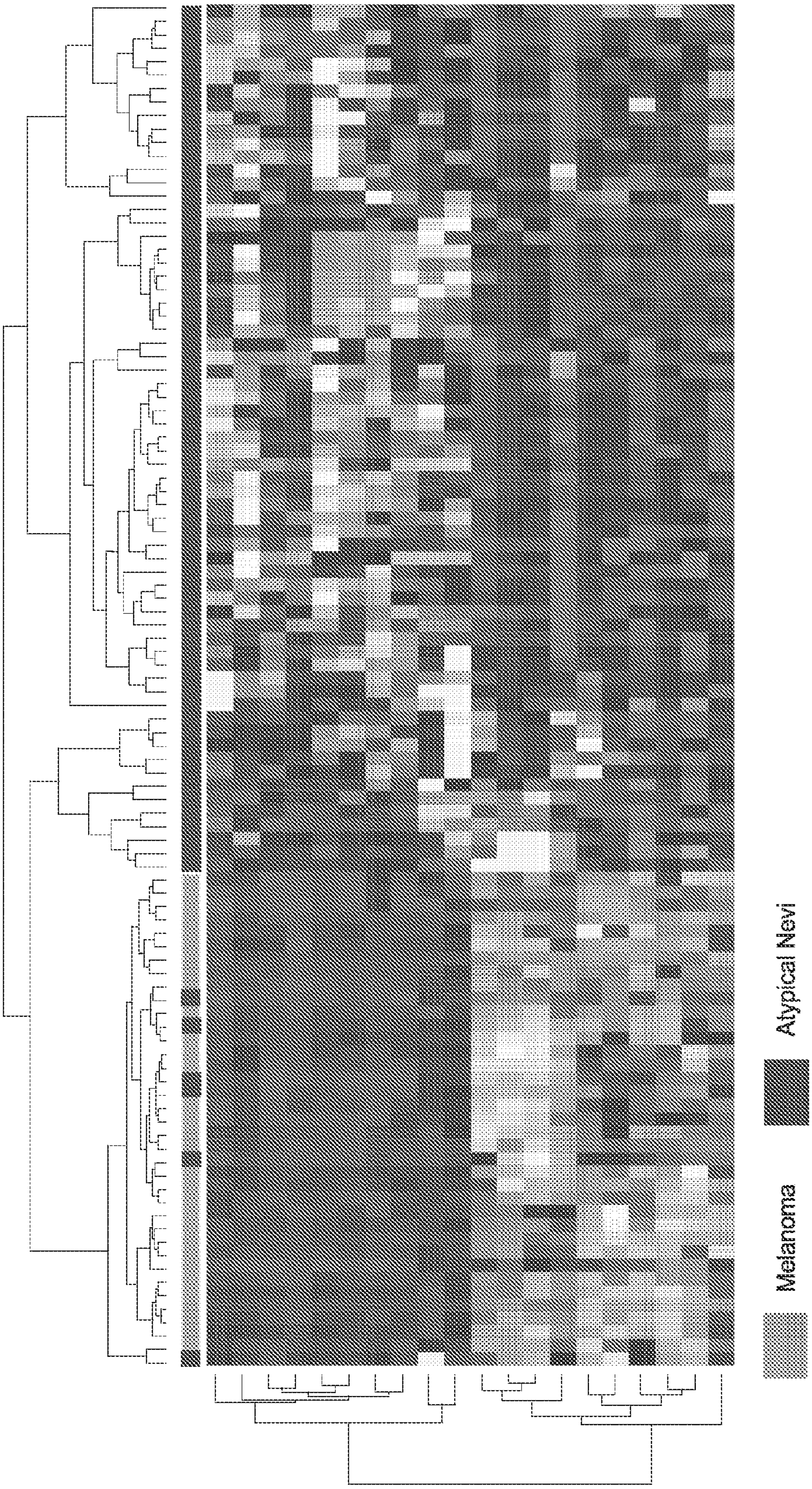


FIG. 6C

- **Prediction Analysis of Microarrays (PAM)**
  - **Training set: 18 Melanomas and 18 atypical nevi**
    - 350 differentially expressed genes selected
      - T-test, P <0.001; FDR <0.05; Multi-testing correction
    - Run PAM with 350 genes
    - Repeat PAM using top 20 ranked genes
  - **Testing set: 13 Melanomas and 53 nevi**

Training Set			Testing Set		
	Predicted Class			Predicted Class	
	Diagnosis			Diagnosis	
Observed	Melanoma	Atypical Nevi	Observed	Melanoma	Atypical Nevi
Melanoma	18	0	Melanoma	13	0
Atypical Nevi	1	17	Atypical Nevi	5	48
Total	19	17	Total	18	48

FIG. 6D

Training Confusion Matrix (Threshold=0.5)			
True\Predicted	M	N	Class Error rate
M	#	0	0
N	1	#	0.055555556
CV Confusion Matrix (Threshold=0.53344)			
True\Predicted	M	N	Class Error rate
M	#	0	0
N	1	#	0.055555556

Settings Name: Settings1							
Offset Quantile	50		Offset Value	758.4297			
	both		RNG Seed	420473			
Prior Distribution (Sample Prior)							
	Class	M	N				
	Prob.	0.5	0.5				
Settings Name: Settings3							
Offset Quantile	50		Offset Value	758.4297			
	both		RNG Seed	420473			
Prior Distribution (Sample Prior)							
	Class	M	N				
	Prob.	0.5	0.5				

FIG. 6E

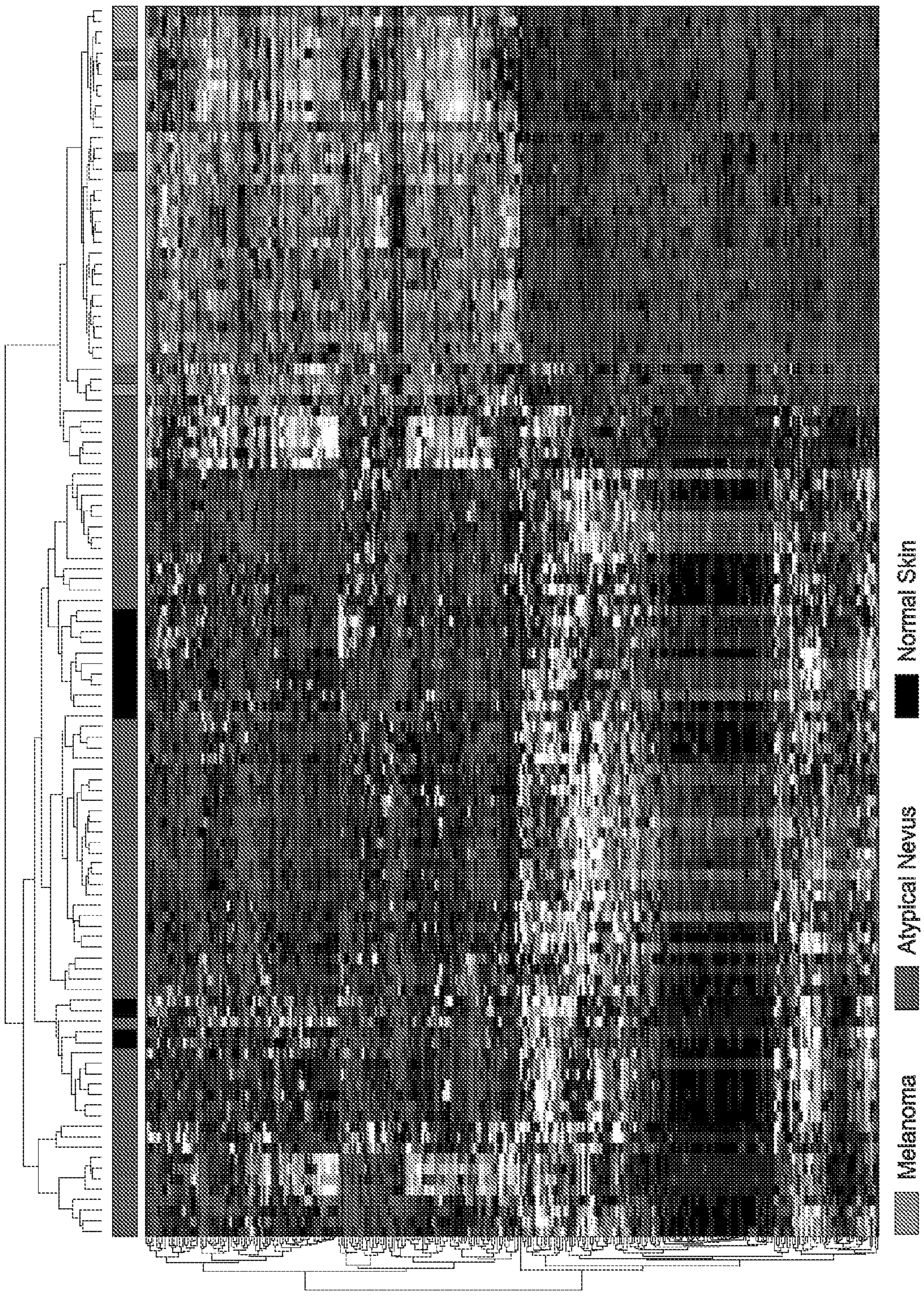


FIG. 7

Classification Modeling Using PAM, Random Forests and TreeNet®

Training set:
Melanoma (37), Atypical nevi (37)

- GCRMA normalization
- background substraction:150
- remove genes ≤ 2x
- t-test with multi-testing correction
  - p < 0.05
  - FDR <0.05

4866 genes

Training Set	PAM		RF		TreeNet	
	Predicted Class		Predicted Class		Predicted Class	
	Diagnosis		Diagnosis		Diagnosis	
Observed	Melanoma	Atypical Nevi	Melanoma	Atypical Nevi	Melanoma	Atypical Nevi
Melanoma	34	3	34	3	37	0
Atypical Nevi	5	32	7	30	2	35
Sensitivity	34/37=92%		34/37=92%		37/37=100%	
Specificity	32/37=87%		30/37=81%		35/37=95%	

11 genes are common between PAM, RF and TreeNet®

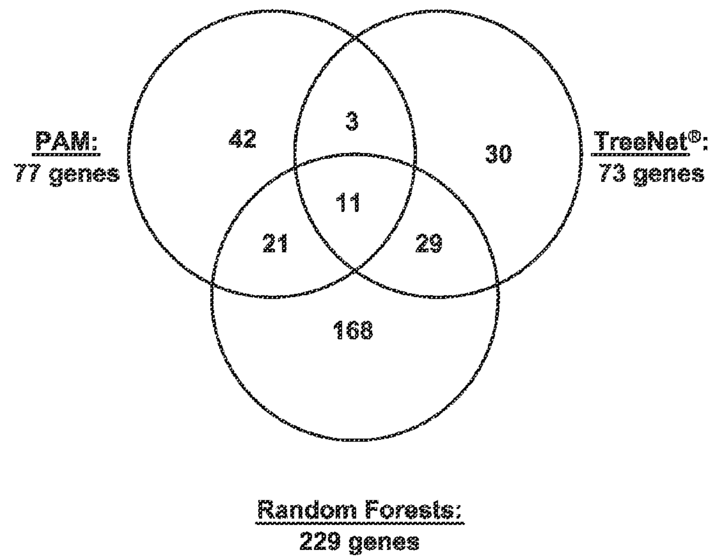


FIG. 8

A 20-Gene Classifier Discriminates Melanoma From Atypical Nevi

- Top 20 of 73 genes selected from TreeNet®
- Perform TreeNet® analysis using only these 20 genes
  - 6 of the 20 genes have known relevance to melanoma

Training Set			Testing Set		
	Predicted Class			Predicted Class	
	Diagnosis			Diagnosis	
Observed	**Melanoma**	**Atypical Nevi**	**Observed**	**Melanoma**	**Atypical Nevi**
Melanoma	37	0	Melanoma	25	0
Atypical Nevi	2	35	Atypical Nevi	9	47
Total	39	35	Total	34	47
Sensitivity	37/37 = 100%		Sensitivity	25/25 = 100%	
Specificity	35/37 = 95%		Specificity	47/56 = 84%	
			PPV	74%	
			NPV	100%	

FIG. 9

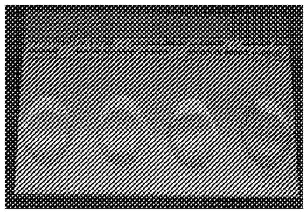
Development of a Classifier to Discriminate Melanoma from Atypical Nevi by a Non-invasive Tape Strip-based Genomic Profiling

Introduction

The incidence of melanoma is increasing at the fastest rate of all cancers in the United States. It is already the seventh most common serious cancer in the United States with a lifetime risk of 1 in 41 in men and 1 in 61 in women. Although melanoma accounts for more than 70% of skin cancer deaths, when detected early it is considered highly curable. In current clinical practice, the detection of melanoma is based upon visual cues, including the "ABCDE" criteria for pigmented nevi and results of optical imaging techniques, such as dermoscopy and confocal microscopy. However, only 1 to 10% of lesions biopsied for suspicion of melanoma are positive for this disease upon histopathologic examination. Thus, there is a need for a test that improves the ease and accuracy of melanoma detection in clinical practice.

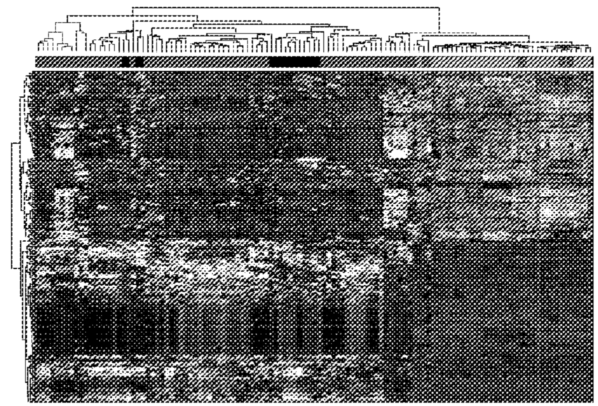
Epidermal Genetic Information Retrieval (EGIR™) (DermTech International, Inc.) uses a custom adhesive film to harvest RNA from stratum corneum. Developed by Morhenn and Rheins (*J Am Acad Dermatol 4*: 687 [1999]), EGIR™ was shown to harvest sufficient cellular RNA for accurate assessment of gene expression by both quantitative RT-PCR and microarray assay (Wong et al. *J Invest Derm 123*: 159 [2004]).

The EGIR™ methodology uses four 20 mm tapes (pictured below) to sample stratum corneum. RNA so harvested has been found to be stable for assay, when kept at ambient temperature for 72 hours. This makes it ideal for use in the office setting.



Preliminary Work

Recent work showed that EGIR™, non-invasive tape stripping of stratum corneum can be used to differentiate melanoma from atypical nevi and normal skin (Wachsman et al. *J Invest Derm 127*: S145 [2007]). Additional work, in which 31 melanomas, 71 atypical nevi, and 15 normal skin controls were analyzed by GeneChip assay, identified 284 differentially expressed genes ($p<0.001$, false discovery rate $q<0.05$). Hierarchical cluster analysis of these genes (see Figure below) showed that melanomas can be distinguished from atypical nevi and normal skin, and, suggested the existence of different classes of atypical nevi. Several of the genes were found by Ingenuity Pathways analysis to play a role in melanocyte development and function, as well as, skin development, cellular proliferation, and cancer. These findings further demonstrated that the presence of melanoma, directly or indirectly, alters the gene expression profile of stratum corneum.



Melanoma Atypical Nevus Normal Skin

FIG. 10

Study Objectives

Within the context of non-invasive EGIR™-based sampling of suspicious pigmented lesions, we sought to:

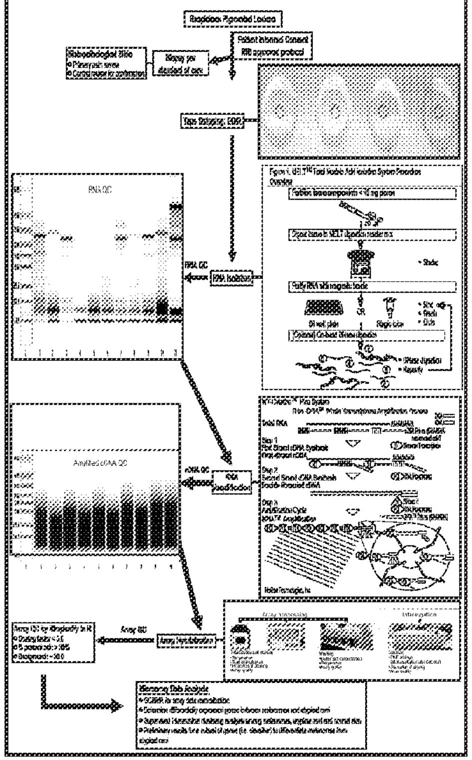
(1)Determine the optimal algorithm for melanoma class prediction by means of classification modeling.

(2) Develop a multi-gene classifier to predict the risk that a lesion contains melanoma.

Study Methods

- Following informed consent, the suspicious pigmented lesion was tape stripped four times using EGIR™ and then biopsied, as per standard of care.
- Normal, uninvolved skin was tape stripped to serve as a negative control. All biopsies underwent primary and central review for histopathology.
- Total RNA was isolated from the tapes using MELT (Ambion, Inc.) and assessed for quality by Experion (Bio-Rad, Inc.) analysis.
- The yield of total RNA was approximately 1 ng, as determined by quantitative RT-PCR of the specimen for β-actin gene expression.
- Total RNA (200-500 pg) was then amplified using the WT-Ovation Pico RNA Amplification System (NuGen, Inc.) and assayed for gene expression using the U133 plus 2.0 GeneChip (Affymetrix, Inc.).

Method and Schema of Workflow



Class Modeling:

- Classification algorithms
  - Prediction of Microarray Aanalysis (PAM)
    - Tibshirani et al. *PNAS 99*: 6567-6572 (2002)
    - Nearest shrunken centroids
  - Random Forests (RF)
    - Brieman. *Machine Learning 24*: 123-140 (1996).
    - Ensembles of trees with random splits.
    - Trees combined via voting (classification).
  - TreeNet® (TN)
    - Friedman. Stochastic gradient boosting. Stanford University (1999).
    - Friedman. Greedy Function Approximation: A Gradient Boosting Machine. Stanford University (1999).
- Training set specimens: 37 melanomas and 37 atypical nevi
  - Melanoma (32)
    - Melanoma in situ (14) and invasive melanoma (18)
  - Lentigo maligna (5)
    - Melanoma in situ (2) and invasive melanoma (3)
  - Atypical nevi (37)
    - Clark (29) and lentiginous (8)
- Test set specimens: 25 melanomas and 56 atypical nevi
  - Melanoma (23)
    - Melanoma in situ (11) and invasive melanoma (12)
  - Lentigo maligna (2)
    - Melanoma in situ (1) and invasive melanoma (1)
  - Atypical nevi (56)
    - Blue nevus (1), Clark (39), congenital (7) and lentiginous (9)

FIG. 10 cont.

Classification Modeling Using PAM, Random Forests and TreeNet®

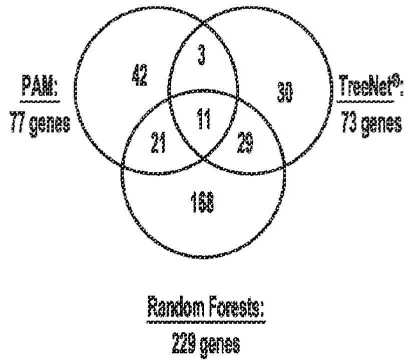
Training set:
Melanoma (37), Atypical nevi (37)

- GCRMA normalization
- background substraction:150
- remove genes ≤ 2x
- t-test with multi-testing correction
  - p < 0.05
  - FDR <0.05

4866 genes

Training Set	PAM		RF		TreeNet	
	Predicted Class		Predicted Class		Predicted Class	
	Diagnosis		Diagnosis		Diagnosis	
Observed	Melanoma	Atypical Nevi	Melanoma	Atypical Nevi	Melanoma	Atypical Nevi
Melanoma	34	3	34	3	37	0
Atypical Nevi	5	32	7	30	2	35
Sensitivity	34/37=92%		34/37=92%		37/37=100%	
Specificity	32/37=87%		30/37=81%		35/37=95%	

11 genes are common between PAM, RF and TreeNet®



Classification Modeling: TreeNet® outperforms PAM and RF

Test set:
Melanoma (25), Atypical nevi (56)

- PAM: 77 genes
- RF: 229 genes
- TreeNet®: 73 genes

Test set	PAM		RF		TreeNet	
	Predicted Class		Predicted Class		Predicted Class	
	Diagnosis		Diagnosis		Diagnosis	
Observed	Melanoma	Atypical Nevi	Melanoma	Atypical Nevi	Melanoma	Atypical Nevi
Melanoma	23	2	24	1	25	0
Atypical Nevi	11	45	12	44	9	45
Sensitivity	23/25= 92%		24/25= 96%		25/25= 100%	
Specificity	45/56= 80%		44/56= 79%		47/56= 84%	

FIG. 10 cont.

A 20-Gene Classifier Discriminates Melanoma From Atypical Nevi

- Top 20 of 73 genes selected from TreeNet®
- Perform TreeNet® analysis using only these 20 genes
  - 6 of the 20 genes have known relevance to melanoma

Training Set			Testing Set		
	Predicted Class			Predicted Class	
	Diagnosis			Diagnosis	
Observed	Melanoma	Atypical Nevi	Observed	Melanoma	Atypical Nevi
Melanoma	37	0	Melanoma	25	0
Atypical Nevi	2	35	Atypical Nevi	9	47
Total	39	35	Total	34	47
Sensitivity	37/37 = 100%		Sensitivity	25/25 = 100%	
Specificity	35/37 = 95%		Specificity	47/56 = 84%	
			PPV	74%	
			NPV	100%	

Summary

- The results demonstrate that EGIR™-harvested stratum corneum RNA can be used for the detection of both in situ and invasive melanoma.
- Class prediction modeling shows that the TreeNet® algorithm outperforms both PAM and Random Forests.
- A 20-gene classifier, developed by TreeNet® analysis, discriminates in situ and invasive superficial spreading melanoma and lentigo maligna from atypical nevi.
- Testing of this 20-gene classifier, using an independent set of sample data, shows it to be 100% sensitive and 84% specific for detection of both melanoma and lentigo maligna.
- In addition, this 20-gene melanoma classifier has a positive predictive value (PPV) of 74% and a negative predictive value (NPV) of 100%.
- The 20-gene classifier provides the basis for the development of a non-invasive genomic assay for the clinical detection of melanoma.

FIG. 10 cont.

Development of a 19-Gene Classifier Accurately Discriminates Melanoma from Atypical Nevi

- **Supervised analysis of GeneChip data**
  - **-Training set: 37 melanomas and 37 atypical nevi**
    - t-test with multi-testing correction identified 7,199 differentially expressed genes ($p < 0.05$; FDR < 0.05)
    - TreeNet analyses of differentially expressed genes identified a 19-gene classifier
    - Sensitivity: 100%, specificity 95%
  - **-Testing set: 39 melanomas and 89 atypical nevi**
    - PPV: 39/50 = 78%, NPV: 78/78 = 100%
    - **Sensitivity 100%, specificity 88%**

Training Set			**Test Set**		
	Predicted Class			**Predicted Class**	
	Diagnosis			Diagnosis	
Observed	**Melanoma**	**Atypical Nevi**	**Observed**	**Melanoma**	**Atypical Nevi**
Melanoma	**37**	**0**	Melanoma	**39**	**0**
Atypical Nevi	**2**	**35**	Atypical Nevi	**11**	**78**
(Total)	**39**	**35**	(Total)	**50**	**78**

FIG. 11

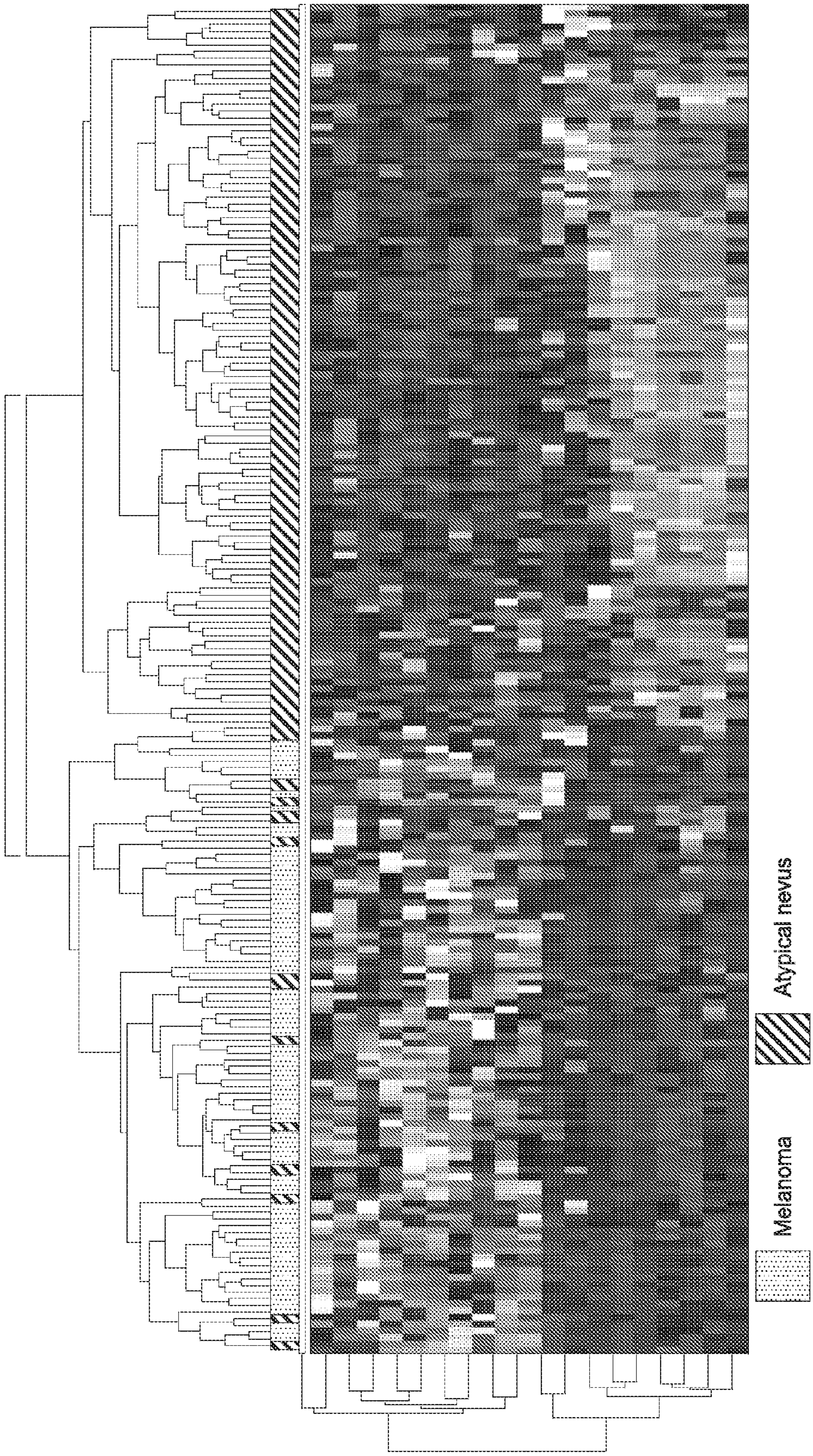


FIG. 12

Translation of the Assay from Microarray to qRT-PCR platform

Goals

- To transition the 19-gene classifier from the microarray discovery platform to a quantitative RT-PCR platform that will improve clinical utility

Method

- Specimens: pre-amplified with WT-Ovation FFPE kit (NuGen, Inc)
- qRT-PCR assay for expression of the 19-gene classifier in triplicate
- Data normalized with a reference control (TRIM65)

Results

- Preliminary results (10 melanomas & 10 atypical nevi) indicate qRT-PCR recapitulates data obtained using the GeneChip microarray

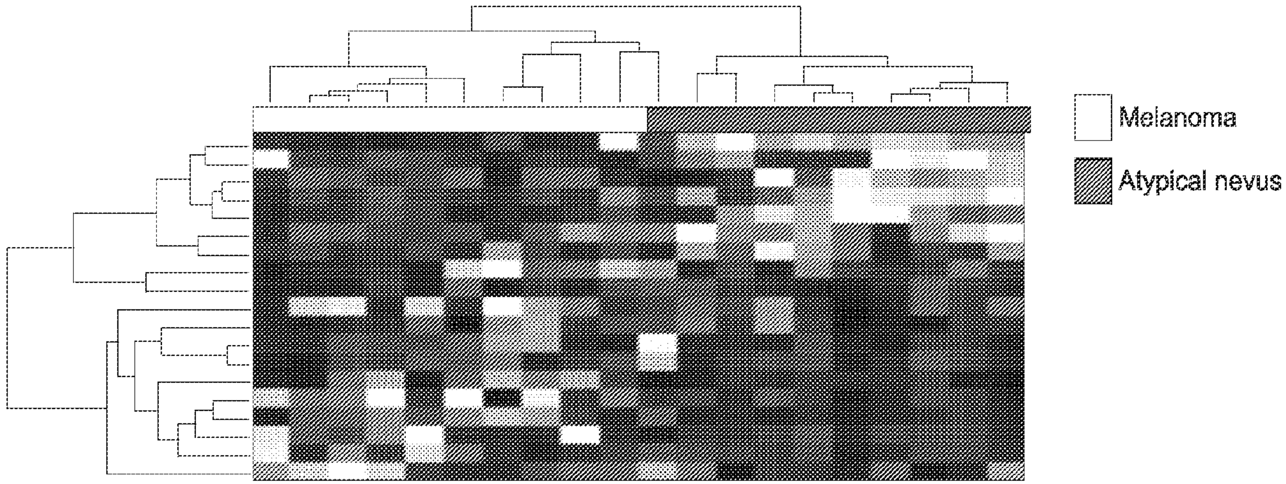


FIG. 13

Discovery of a Multi-Gene Classifier to Differentiate Solar Lentigo from Normal Skin

- **Training set: 8 solar lentigines and 8 normal skin controls**
  - 1600 differentially expressed genes selected
    - T-test, P <0.05
  - **Discover a 100-gene classifier**
- **Testing set: 3 solar lentigines and 3 normal skin controls**
  - **Sensitivity: 100%**
  - **Specificity: 100%**

Training Set			Testing Set		
Observed	Predicted Class		Observed	Predicted Class	
	Diagnosis			Diagnosis	
	Solar Lentigo	Normal Skin		Solar Lentigo	Normal Skin
Solar Lentigo	8	0	Solar Lentigo	3	0
Normal Skin	0	8	Normal Skin	0	3
Total	8	8	Total	3	3

FIG. 14

Cluster Analysis of the 100-Gene Classifier

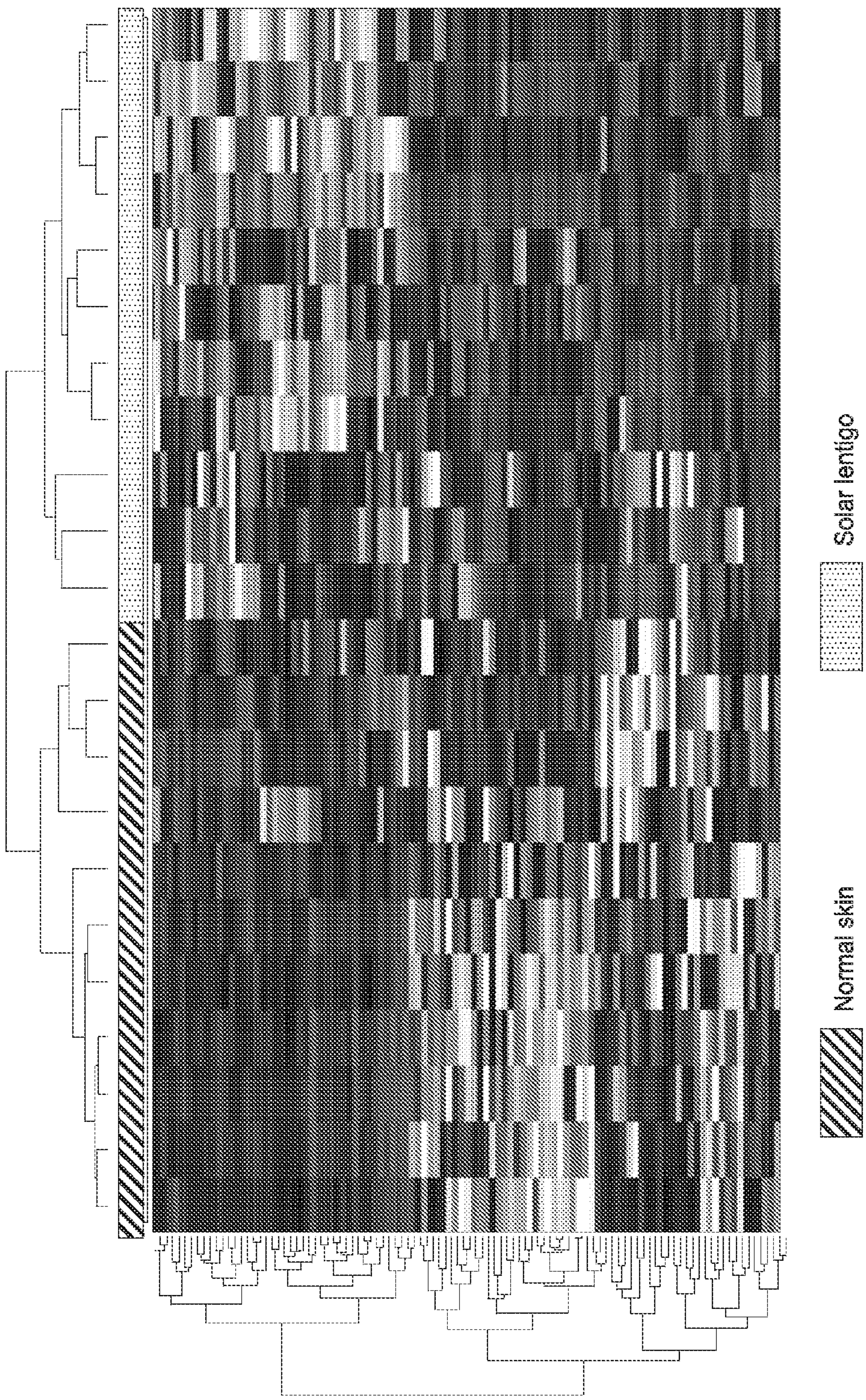


FIG. 15

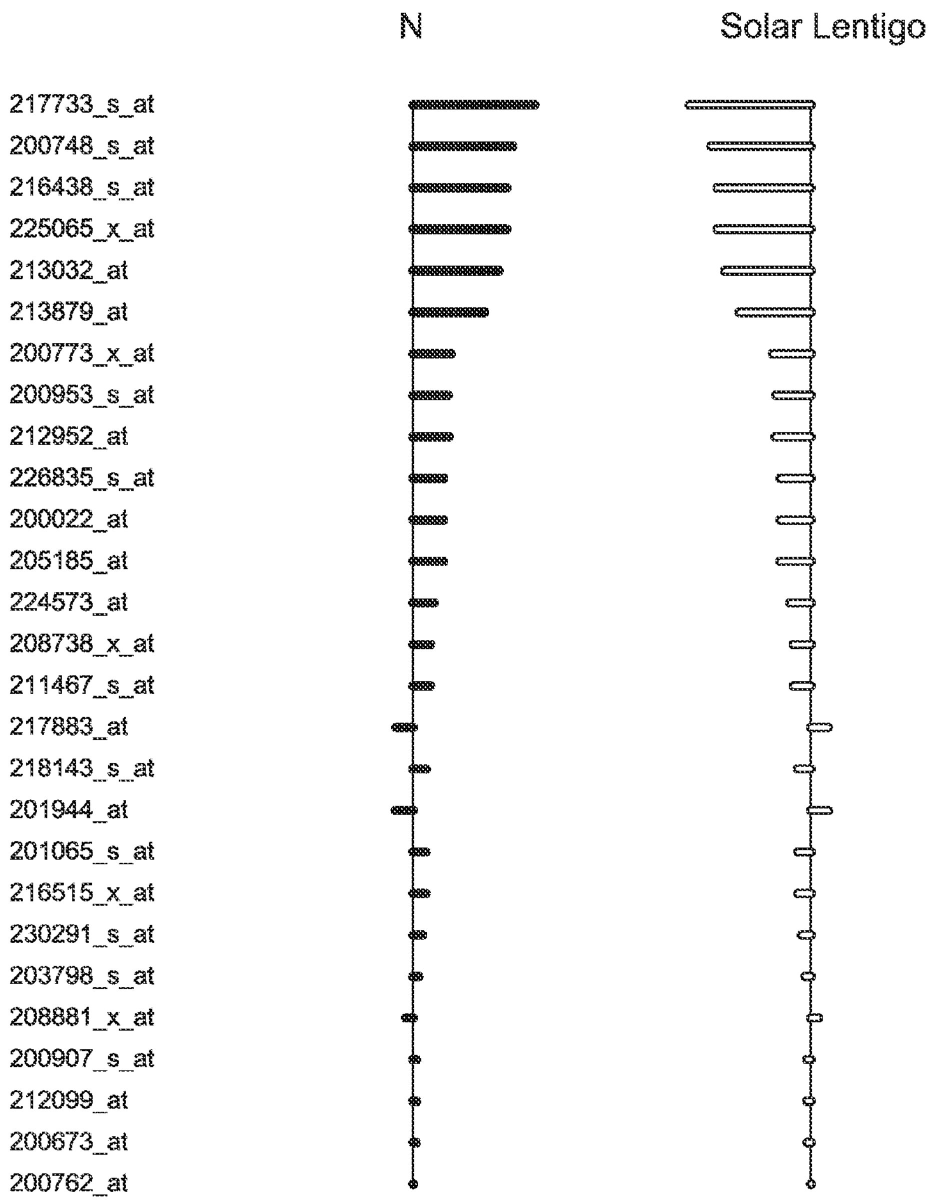

N
Solar Lentigo
217733_s_at
200748_s_at
216438_s_at
225065_x_at
213032_at
213879_at
200773_x_at
200953_s_at
212952_at
226835_s_at
200022_at
205185_at
224573_at
208738_x_at
211467_s_at
217883_at
218143_s_at
201944_at
201065_s_at
216515_x_at
230291_s_at
203798_s_at
208881_x_at
200907_s_at
212099_at
200673_at
200762_at

FIG. 16

Gene Expression Profile: Solar Lentigo Distinguishes from Atypical Nevi and Basal Cell Carcinoma

GeneChip data analysis:

- GCRMA normalization
- Background subtraction: 100
- ANOVA among Solar lentigo, atypical Nevi and basal cell carcinoma (p<0.05)
- Multiple testing correction
    - Benjamini and Hochberg
- False discovery rate (q < 0.05)

- 82 differentially expressed genes selected
    - Hierarchical clustering analysis
        - Solar lentigo (N=11)
        - Atypical nevus (N=12)
        - Basal cell carcinoma (N=8)

Conclusion:

- Solar lentigo distinguishes from atypical nevi and basal cell carcinoma

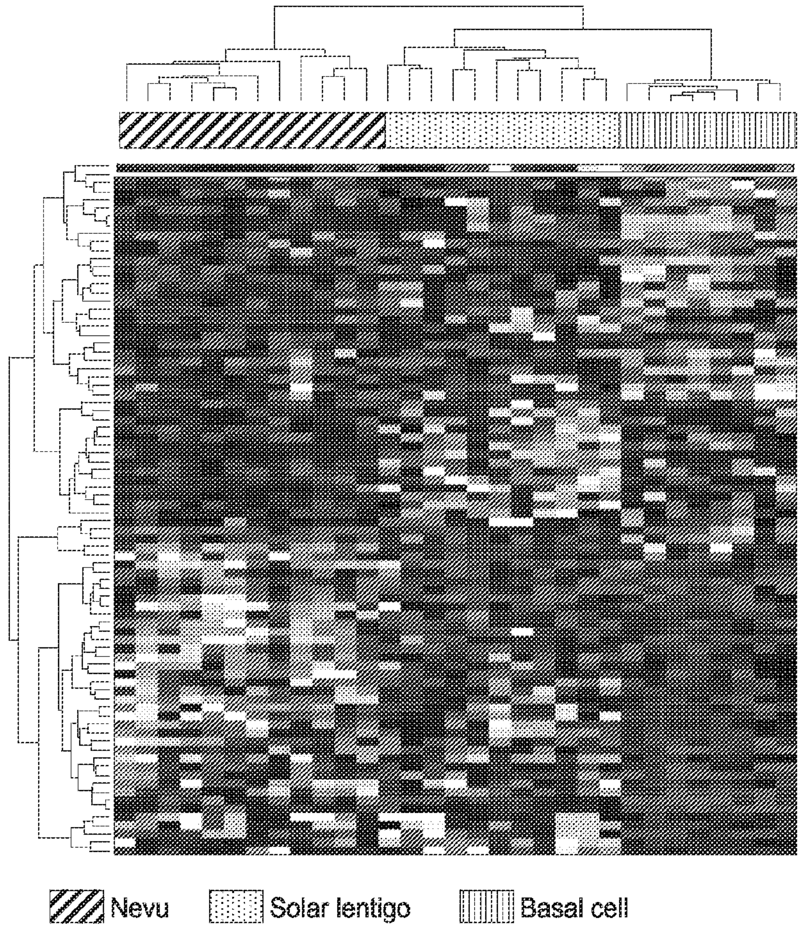


FIG. 17

Gene Expression Profile: Solar Lentigo Distinguishes from Lentigo Maligna

GeneChip data analysis:

- GCRMA normalization
- Background subtraction: 100
- t-test betwen Solar lentigo and Lentigo Maligna ($p<0.01$)
- Multiple testing correction
    - Benjamini and Hochberg
- False discovery rate ($q < 0.05$)

- 32 differentially expressed genes selected
    - Hierarchical clustering analysis
        - Solar lentigo (N=11)
        - Lentigo Maligna (N=7)

Conclusion:

- Solar lentigo distinguishes from lentigo maligna

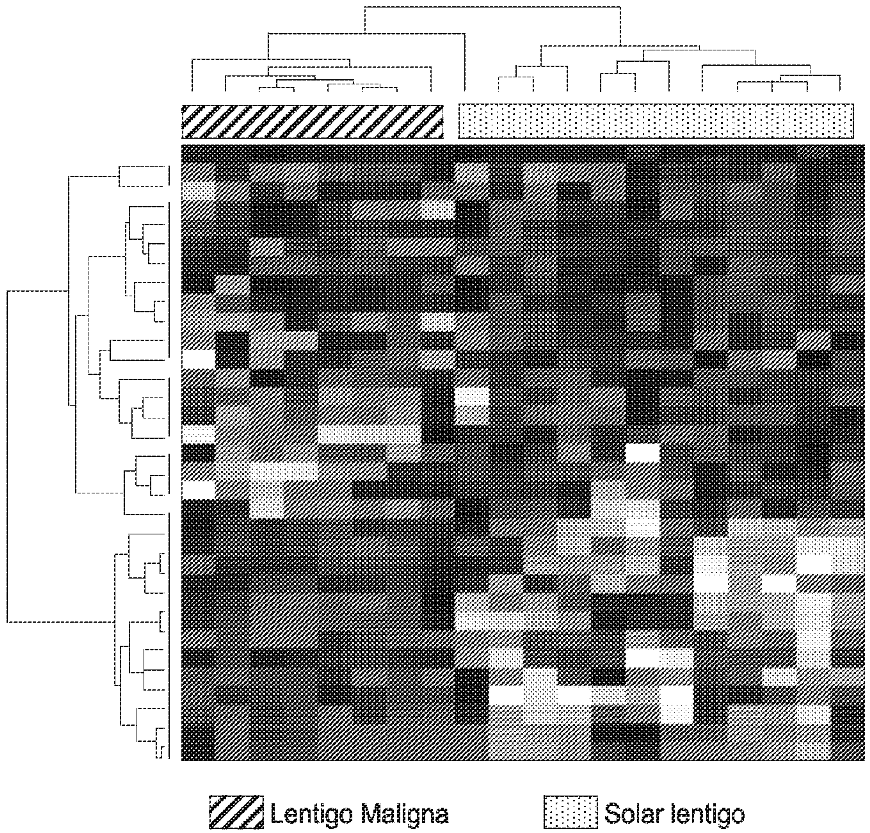


FIG. 18

A 28-Gene Classifier Diffentiates Solar Lentigo from Lentigo Maligna

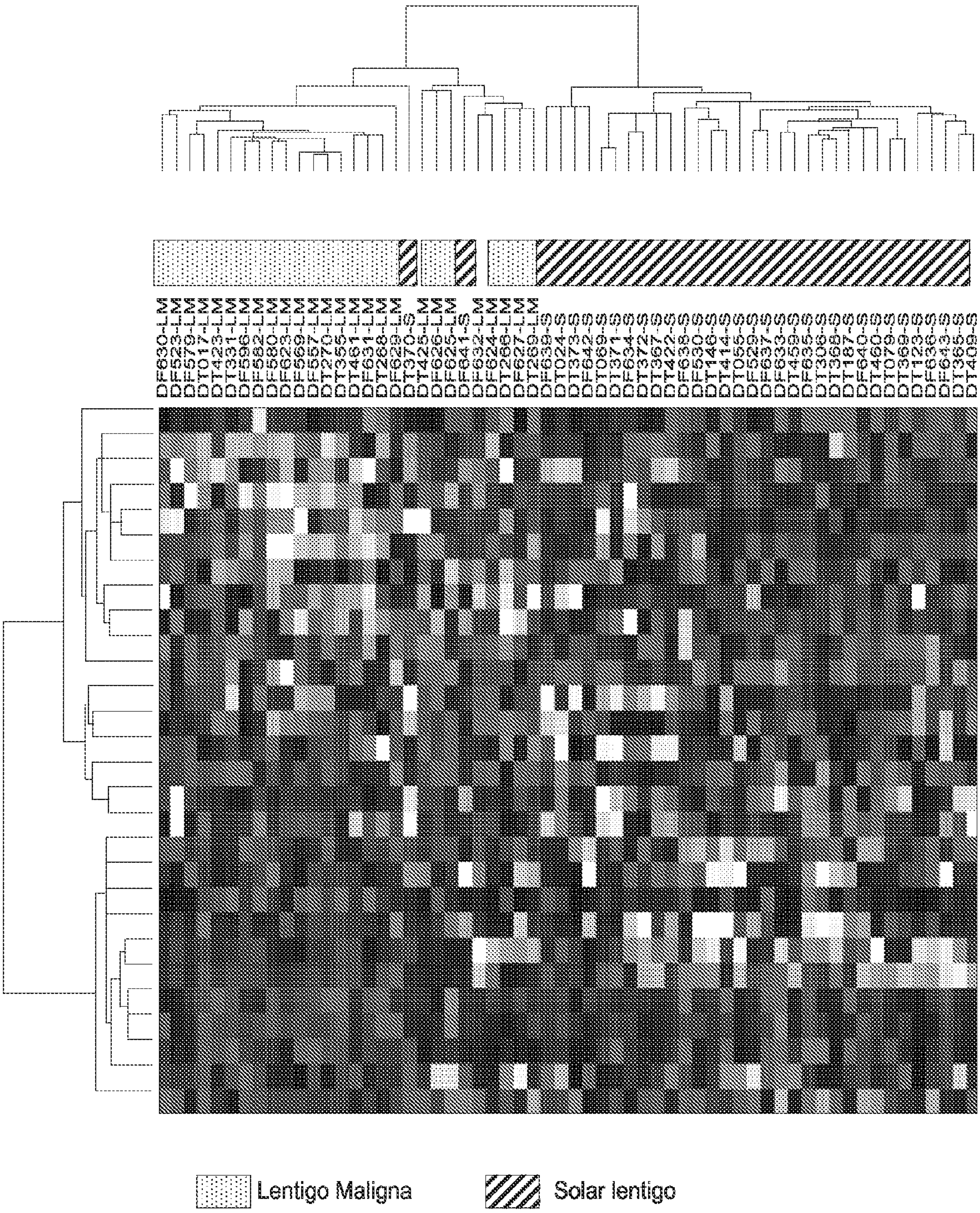


FIG. 19