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(54) **BIOMARKERS OF RESPONSE TO NAE INHIBITORS**

BIOMARKER FÜR DIE REAKTION AUF NAE-INHIBITOREN

BIOMARQUEURS DE RÉPONSE AUX INHIBITEURS DE NAE

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Description

Related Applications

[0001] This application claims priority to U.S. Provisional Application number 61/552,686 filed on October 28, 2011.

Sequence Listing

[0002] This application contains a Sequence Listing which is submitted herewith in electronically readable format. The Sequence Listing file was created on October 26, 2012, is named "sequencelisting.txt," and its size is 149 kb (153,088 bytes).

Background

[0003] Cells become cancerous when their genotype or phenotype alters in a way that there is uncontrolled growth that is not subject to the confines of the normal tissue environment. One or more genes is mutated, amplified, deleted, overexpressed or underexpressed. Chromosome portions can be lost or moved from one location to another. Some cancers have characteristic patterns by which genotypes or phenotypes are altered.

[0004] Many genes have mutations which are associated with cancer. Some genes have multiple sites where mutations can occur. Many cancers have mutations in and/or mis-expression of more than one gene. Gene mutations can facilitate tumor progression, tumor growth rate or whether a tumor will metastasize. Some mutations can affect whether a tumor cell will respond to therapy.

[0005] A variety of agents treat cancers. Cancers of the blood and bone marrow often are treated with steroids/glucocorticoids, imids, proteasome inhibitors and alkylating agents. Cancers of other tissues often are treated with alkylating agents, topoisomerase inhibitors, kinase inhibitors, microtubule inhibitors, angiogenesis inhibitors or other agents. Some patients respond to one therapy better than another, presenting the potential for a patient to follow multiple therapeutic routes to effective therapy. Valuable time early in a patient's treatment program can be lost pursuing a therapy which eventually is proven ineffective for that patient. Many patients cannot afford the time for trial-and-error choices of therapeutic regimens. Expedient and accurate treatment decisions lead to effective management of the disease.

[0006] DATABASE GeO [Online] ("Affymetrix GeneChip Human Genome U133 Array Set HGU133A", GeO, NCBI, (20020311), Database accession no. gl96, Pages 61, 243, 418) describes array with probes for marker genes NF2, SMAD4 and FBXW7.

[0007] Bignell, G. R. et al. (2010) (Signatures of mutation and selection in the cancer genome. Nature, 463(7283), 893) describes genes involved in cancer and describes the use of primers to screen for mutations in such genes.

[0008] International (PCT) Application published as WO 2011/068863 (A1) describes a combination of therapeutic agents for use in treating a patient suffering from cancer, the combination comprising at least one polyploidy inducing agent and at least one Bel-2 family protein inhibitor. Described also are diagnostic assays useful in classification of patients for treatment with one or more therapeutic agents.

Summary

[0009] The subject matter for which protection is sought is as defined in the claims. The present disclosure relates to prognosis and planning for treatment of tumors by measurement of the amount, presence or changes of markers provided herein. The markers are predictive of whether there will be a favorable outcome (*e.g.*, good response, long time-to-progression, and/or long term survival) after treatment with a NEDD8-activating enzyme (NAE) inhibitor, such as a 1-substituted methyl sulfamate. Testing samples comprising tumor cells, e.g., *in vitro,* to determine the presence, amounts or changes of genetic markers, e.g., the mutational status of at least one marker gene, identifies particular patients who are expected to have a favorable outcome with treatment, *e.g.*, with an NAE inhibitor, such as a 1-substituted methyl sulfamate, and whose disease may be managed by standard or less aggressive treatment, as well as those patients who are expected have an unfavorable outcome with the treatment and may require an alternative treatment to, a combination of treatments and/or more aggressive treatment with an NAE inhibitor to ensure a favorable outcome and/or successful management of the disease.

[0010] In one aspect, the invention provides kits useful in determination of characteristics, e.g., amounts, presence or changes, of the markers. In another aspect, the invention provides methods for determining prognosis and treatment or disease management strategies. In these aspects, the characteristic, e.g., size, sequence, composition or amount of marker in a sample comprising tumor cells is measured. In one embodiment, the tumor is a liquid, e.g., hematological tumor, e.g., acute myelogenous leukemia, myelodysplastic syndrome or multiple myeloma. In another embodiment, the tumor is a solid tumor, *e.g.*, melanoma, non-small cell lung cancer, esophageal cancer, bladder cancer, neuroblastoma

cancer, mesothelioma, pancreatic cancer.

[0011] In various embodiments, the characteristic, e.g., size, sequence, composition or amount of DNA, the size, sequence, composition or amount of RNA and/or the size, sequence, composition or amount of protein corresponding to a marker gene with one or more mutation, e.g., somatic mutation, described herein is measured. Useful information leading to the prognosis or treatment or disease management strategies is obtained when assays reveal information about a marker gene, e.g., whether the gene is mutated, or not, the identity of the mutation, and/or whether the RNA or protein amount of a mutated gene or genes indicates overexpression or underexpression. In one embodiment, the strategy is determined for E1 enzyme inhibition, *e.g.*, NAE inhibition, e.g., MLN4924, therapy.

[0012] A marker gene useful to test for determination of prognosis or treatment or disease management strategy according to methods of the disclosure is selected from the group consisting of neurofibromin 2 (NF2), mothers against decapentaplegic homolog 4 (SMAD4), lysine-specific demethylase 6A (KDM6A), tumor protein p53 (TP53), cyclin-dependent kinase inhibitor 2A (CDKN2A), cyclin-dependent kinase inhibitor 2A p14 variant (CDKN2A_p14), in some cases, F-box and WD repeat domain containing 7 (FBXW7) and, in some cases adenomatous polyposis coli (APC). Each marker gene includes mutations or alterations whose presence in DNA or whose effects, *e.g.,* on marker RNA and/or protein characteristics, e.g., amounts, size, sequence or composition, can provide information for determination of prognosis or treatment or disease management. In some description, a gene or a mutant or modified form thereof useful as a marker, has a DNA, an RNA and/or protein characteristic, e.g., size, sequence, composition or amount, *e.g.*, in a sample comprising tumor cells, which is different than a normal DNA, RNA and/or protein. Described herein are examples of modifications of these genes, referred to as "marker genes" whose mutation or amounts can provide such information.

[0013] The mutation of the markers of the present invention, provide information about outcome after treatment, *e.g.*, with an NAE inhibitor, such as a 1-substituted methyl sulfamate. By examining the characteristic, e.g., size, sequence, composition or amount of one or more of the identified markers in a tumor, it is possible to determine which therapeutic agent, combination of agents, dosing and/or administration regimen is expected to provide a favorable outcome upon treatment. By examining the characteristic, e.g., size, sequence, composition or amount of one or more of the identified markers or marker sets in a cancer, it is also possible to determine which therapeutic agent, combination of agents, dosing and/or administration regimen is less likely to provide a favorable outcome upon treatment. By examining the characteristic, e.g., size, sequence, composition or amount of one or more of the identified markers, it is therefore possible to eliminate ineffective or inappropriate therapeutic agents or regimens. Importantly, these determinations can be made on a patient-by-patient basis. Thus, one can determine whether or not a particular therapeutic regimen is likely to benefit a particular patient or type of patient, and/or whether a particular regimen should be started or avoided, continued, discontinued or altered.

[0014] The present invention is directed to methods of identifying and/or selecting a cancer patient who is expected to demonstrate a favorable outcome upon administration of a therapeutic regimen, *e.g.*, a therapeutic regimen comprising an NAE inhibitor, such as a 1-substituted methyl sulfamate treatment. Additionally provided are methods of identifying a patient who is expected to have an unfavorable outcome upon administration of such a therapeutic regimen. These methods typically include measuring, determining, receiving, storing or transmitting information about the characteristic, e.g., size, sequence, composition or amount of one or more markers or mutation of marker gene(s) in a patient's tumor (*e.g.,* a patient's cancer cells, *e.g.*, hematological cancer cells or solid tumor cells), optionally comparing that to the characteristic, *e.g.*, size, sequence, composition or amount of a reference marker, and in a further embodiment, identifying or advising whether result from the sample corresponds to a favorable outcome of a treatment regimen, *e.g.*, an NAE inhibitor, such as a 1-substituted methyl sulfamate treatment regimen.

[0015] Additionally provided methods include therapeutic methods which further include the step of beginning, continuing, or commencing a therapy accordingly where the presence of a mutation in a marker gene or the characteristic, e.g., size, sequence, composition or amount of a patient's marker or markers indicates that the patient is expected to demonstrate a favorable outcome with the therapy, *e.g.,* the NAE inhibitor, such as a 1-substituted methyl sulfamate therapeutic regimen. In addition, the methods include therapeutic methods which further include the step of stopping, discontinuing, altering or halting a therapy accordingly where the presence of a mutation in a marker gene or the characteristic, e.g., size, sequence, composition or amount of a patient's marker indicates that the patient is expected to demonstrate an unfavorable outcome with the treatment, *e.g.*, with the NAE inhibitor, such as a 1-substituted methyl sulfamate regimen, *e.g.*, as compared to a patient identified as having a favorable outcome receiving the same therapeutic regimen. In another aspect, methods are provided for analysis of a patient not yet being treated with a therapy, *e.g.,* an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy and identification and prediction of treatment outcome based upon the presence of a mutation in a marker gene or characteristic, e.g., size, sequence, composition or amount of one or more of a patient's marker described herein. Such methods can include not being treated with the therapy, *e.g.*, NAE inhibitor, such as a 1-substituted methyl sulfamate therapy, being treated with therapy, *e.g.*, NAE inhibitor, or being treated with a 1-substituted methyl sulfamate therapy in combination with one more additional therapies, being treated with an alternative therapy to an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy, or being treated with a more aggressive dosing and/or administration regimen of a therapy, *e.g.,* E1 enzyme inhibitor, such as an NAE

inhibitor, *e.g.*, as compared to the dosing and/or administration regimen of a patient identified as having a favorable outcome to standard NAE inhibitor, such as a 1-substituted methyl sulfamate therapy. Thus, the provided methods of the invention can eliminate ineffective or inappropriate use of therapy, *e.g.*, NAE inhibitor, such as 1-substituted methyl sulfamate therapy regimens.

[0016] Additional methods of the disclosure include methods to determine the activity of an agent, the efficacy of an agent, or identify new therapeutic agents or combinations. Such methods include methods to identify an agent as useful, *e.g.,* as an NAE inhibitor, such as a 1-substituted methyl sulfamate, for treating a cancer, *e.g.,* a hematological cancer (*e.g.,* multiple myeloma, leukemias, lymphoma, etc) or solid tumor cancer (e.g., melanoma, esophageal cancer or bladder cancer), based on its ability to affect the presence of a mutation in a marker gene or characteristic, e.g., size, sequence, composition or amount of a marker or markers of the invention. For example, an inhibitor which decreases or increases the presence of a mutation in a marker gene or characteristic, e.g., size, sequence, composition or amount of a marker or markers provided in a manner that indicates favorable outcome of a patient having cancer would be a candidate agent for the cancer. Alternatively, an agent which is able to decrease the viability of a tumor cell comprising a marker indicative of an unfavorable outcome would be a candidate agent for the cancer.

[0017] The present invention is also directed to an NAE inhibitor for use in methods of treating a cancer patient, with a therapeutic regimen, *e.g.*, an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy regimen (*e.g.*, alone, or in combination with an additional agent such as a chemotherapeutic agent, *e.g.,* a glucocorticoid agent, a proteasome inhibitor, an alkylating agent, a kinase inhibitor or a topoisomerase inhibitor), which includes the step of selecting for treatment a patient whose marker characteristic, e.g., size, sequence, composition or amount indicates that the patient is expected to have a favorable outcome with the therapeutic regimen, and treating the patient with the therapy, *e.g.*, NAE inhibition, such as a 1-substituted methyl sulfamate therapy. In some embodiments, the method can include the step of selecting a patient whose marker characteristic, e.g., size, sequence, composition or amount or amounts indicates that the patient is expected have a favorable outcome and administering a therapy other than an NAE inhibitor therapy that demonstrates similar expected survival times as the NAE inhibitor, such as a 1-substituted methyl sulfamate therapy.

[0018] Additional methods of treating a cancer patient include selecting patients that are unlikely to experience a favorable outcome upon treatment with a cancer therapy (*e.g.*, NAE inhibitor, such as a 1-substituted methyl sulfamate therapy). Such methods can further include one or more of: administering a higher dose or increased dosing schedule of a therapy, *e.g.*, NAE inhibitor, such as a 1-substituted methyl sulfamate as compared to the dose or dosing schedule of a patient identified as having a favorable outcome with standard therapy; administering a cancer therapy other than an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy; administering an NAE inhibitor, such as a 1-substituted methyl sulfamate agent in combination with an additional agent. Further provided are methods for selection of a patient having aggressive disease which is expected to demonstrate more rapid time to progression and death.

[0019] Additional methods of the disclosure include a method to evaluate whether to treat or pay for the treatment of cancer, *e.g.,* hematological cancer (*e.g.,* multiple myeloma, leukemias, lymphoma, *etc.*) or solid tumor cancer (*e.g.,* melanoma, esophageal cancer or bladder cancer) by reviewing the amount of a patient's marker or markers for indication of outcome to a cancer therapy, *e.g.,* an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy regimen, and making a decision or advising on whether payment should be made.

[0020] The entire contents of all publications, patent applications, patents and other references mentioned herein are referred to.

[0021] Other features and advantages of the invention will be apparent from the following detailed description, drawings and from the claims.

Drawings

[0022]

Figure 1. General structure of 1-substituted methyl sulfamate. G^1 is -O- or -CH_2-; G^2 is -H or -OH; G^3 is -H or -OH; G^4 is -NH-, -O- or a covalent bond; and G^5 is substituted heteroaryl.

Figure 2. General pathways for cullin-ring ligase (CRL) ubiquitination of protein substrates and for neddylation. In CRLs, the cullin subunit must be modified on a conserved lysine by the ubiquitin-like protein NEDD8 to activate holoenzyme activity. NEDD8 activation and conjugation to cullin proteins is catalyzed via an enzymatic cascade that is homologous to ubiquitination involving NEDD8's E1 (NAE) and E2 (Ubc12). Removal of NEDD8 from cullin is catalyzed by the COP9 signalosome. Deneddylation facilitates dissociation of CRL components. The cullin-RING core is sequestered in an inactive state by binding to CAND1 until it is recruited to form a new CRL.

Figure 3. Response of a cell line panel 2 to MLN4924. Each point represents one cell line.

Figures 4A-B. Comparison of responses of cell line panels to MLN4924. A. Ordering of cell line panel 2 by EC50. Darkened lines represent cell lines that are present in panel 1. There are 114 cell lines with identical names in both panels. B. Comparison of Percent of Control (POC) viability for the cell lines which are present in both panels. The

results of the overlapping cell lines have a Spearman Rank Order Correlation of 0.72, p-value < 2.2e-16.

Figure 5. Tissue association of resistance with TP53 mutations. TP53 mutant colon cancer cell lines are more resistant (higher percent of control viability) to MLN4924 treatment than TP53 wt cell lines.

Figures 6A-D. Effect of TP53 Loss on Viability of Cancer Cell Lines Following Treatment with Different Doses of MLN4924 at Multiple Time Points. The effect of TP53 knock-out on the sensitivity of paired HCT-116 colon cancer cell lines to MLN4924 was measured by ATPlite, across a range of MLN4924 concentrations and time points. Data are represented as mean ± SEM, N = 3. Dotted line, p53 knock-out; solid line, p53 wild type.

Detailed Description

[0023] One of the continued problems with therapy in cancer patients is individual differences in response to therapies. While advances in development of successful cancer therapies progress, only a subset of patients respond to any particular therapy. With the narrow therapeutic index and the toxic potential of many available cancer therapies, such differential responses potentially contribute to patients undergoing unnecessary, ineffective and even potentially harmful therapy regimens. If a designed therapy could be optimized to treat individual patients, such situations could be reduced or even eliminated. Furthermore, targeted designed therapy may provide more focused, successful patient therapy overall. Accordingly, there is a need to identify particular cancer patients who are expected to have a favorable outcome when administered particular cancer therapies as well as particular cancer patients who may have a favorable outcome using more aggressive and/or alternative cancer therapies, *e.g.*, alternative to previous cancer therapies administered to the patient. It would therefore be beneficial to provide for the diagnosis, staging, prognosis, and monitoring of cancer patients, including, *e.g.,* hematological cancer patients (*e.g.,* multiple myeloma, leukemias, lymphoma, *etc.*) or solid tumor cancer (*e.g.,* melanoma, esophageal cancer or bladder cancer) who would benefit from particular cancer inhibition therapies as well as those who would benefit from a more aggressive and/or alternative cancer inhibition therapy, *e.g.,* alternative to a cancer therapy or therapies the patient has received, thus resulting in appropriate preventative measures.

[0024] The present invention is based, in part, on the recognition that mutation of a marker gene can be associated with sensitivity of a cell comprising the mutated gene to an NAE inhibitor, such as a 1-substituted methyl sulfamate. In some embodiments, the marker gene is involved in the cullin ring ligase (CRL) pathway, e.g., a gene whose encoded protein interacts with a CRL or a CRL- associated protein, or is a CRL substrate. A protein encoded by a marker gene can have a wild type function as a tumor suppressor. Examples of marker genes include NF2, SMAD4 and/or KDM6A. Other examples of marker genes include TP53, APC, CDKN2A and/or CDKN2A_p14. Marker genes can exhibit mutations, e.g., somatic mutations, whose presence can affect expression or activity of the encoded gene product. In some embodiments, there can be more than one mutation in a marker gene or more than one marker gene with a mutation in a tumor cell or tumor. In additional embodiments, there can be marker gene mutations in cells which have mutations in additional genes, including mutations that can lead to tumorigenesis, but the additional mutated genes may not be marker genes as considered herein. In some embodiments, the mutation is an inactivating mutation. In other embodiments, the mutation affects the expression of the marker gene. In other embodiments, a mutation can result in an altered interaction of the encoded gene product with a cellular binding partner. The identification and/or measurement of the mutation in the marker gene can be used to determine whether a favorable outcome can be expected by treatment of a tumor, *e.g.*, with an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy or whether an alternative therapy to and/or a more aggressive therapy with, *e.g.,* an NAE inhibitor, such as a 1-substituted methyl sulfamate inhibitor may enhance expected survival time. For example, the compositions and methods provided herein can be used to determine whether a patient is expected to have a favorable outcome to an NAE inhibitor, such as a 1-substituted methyl sulfamate therapeutic agent or an NAE inhibitor, such as a 1-substituted methyl sulfamate dosing or administration regimen. In general, mutation in the tumor suppressor marker genes described herein is associated with sensitivity to or favorable outcome of treatment with a NAE inhibitor. Examples of marker genes which can function as a tumor suppressor in pathways related to cullin ring ligase and whose mutation is associated with sensitivity to NAE inhibition include NF2, SMAD4, KDM6A, FBXW7, CDKN2A and/or CDKN2A_p14. However, TP53 and APC also are tumor suppressor marker genes. In particular, TP53 pathway genes are associated with NAE inhibitor effects. As described herein, in some embodiments for many tumor types, mutation in TP53, and in some cases, APC, leads to resistance to NAE inhibition. Accordingly, a wild type marker gene from the group consisting TP53 and APC can be associated with NAE sensitivity. In some embodiments, mutation of a marker gene selected from the group consisting of TP53 and APC is associated with resistance to an NAE inhibitor.

[0025] Based on these identifications, the present disclosure provides, without limitation: 1) methods and compositions for determining whether an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy regimen will or will not be effective to achieve a favorable outcome and/or manage the cancer; 2) methods and compositions for monitoring the effectiveness of an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy (alone or in a combination of agents) and dosing and administrations used for the treatment of tumors; 3) methods and compositions for treatments of tumors comprising, *e.g.*, NAE inhibitor, such as a 1-substituted methyl sulfamate inhibition therapy regimen; 4) methods and

compositions for identifying specific therapeutic agents and combinations of therapeutic agents as well as dosing and administration regimens that are effective for the treatment of tumors in specific patients; and 5) methods and compositions for identifying disease management strategies.

[0026] Ubiquitin and other ubiquitin-like molecules (ubls) are activated by a specific enzyme (an E1 enzyme) which catalyzes the formation of an acyl-adenylate intermediate with the C-terminal glycine of the ubl. The activated ubl is then transferred to a catalytic cysteine residue within the E1 enzyme through formation of a thioester bond intermediate. The E1-ubl intermediate and an E2 associate, resulting in a thioester exchange wherein the ubl is transferred to the active site cysteine of the E2. The ubl is then conjugated to the target protein, either directly or in conjunction with an E3 ligase, through isopeptide bond formation with the amino group of a lysine side chain in the target protein. The ubl named Neural precursor cell-Expressed Developmentally Downregulated 8 (NEDD8) is activated by the heterodimer NEDD8-activating enzyme (NAE, also known as APPBP1-UBA3, UBE1C (ubiquitin-activating enzyme E1C)) and is transferred to one of two E2 conjugating enzymes (ubiquitin carrier protein 12 (UBC12) and UBC17), ultimately resulting in ligation of NEDD8 to cullin proteins by the cullin-RING subtype of ubiquitin ligases (see Figure 2). A function of neddylation is the activation of cullin-based ubiquitin ligases involved in the turnover of many cell cycle and cell signaling proteins, including p27 and I-κB. See Pan et al., Oncogene 23:1985-97 (2004). Inhibition of NAE can disrupt cullin-RING ligase-mediated protein turnover and can lead to apoptotic death in cells, e.g., tumor cells or cells of a pathogenic organism, e.g. a parasite. See Soucy et al. (2010) Genes & Cancer 1:708-716.

[0027] As used herein, the term "E1," "E1 enzyme," or "E1 activating enzyme" refers to any one of a family of related ATP-dependent activating enzymes involved in activating or promoting ubiquitin or ubiquitin-like (collectively "ubl") conjugation to target molecules. E1 activating enzymes function through an adenylation/thioester intermediate formation to transfer the appropriate ubl to the respective E2 conjugating enzyme through a transthiolation reaction. The resulting activated ubl-E2 promotes ultimate conjugation of the ubl to a target protein. A variety of cellular proteins that play a role in cell signaling, cell cycle, and protein turnover are substrates for ubl conjugation which is regulated through E1 activating enzymes (*e.g.,* NAE, UAE, SAE). Unless otherwise indicated by context, the term "E1 enzyme" is meant to refer to any E1 activating enzyme protein, including, without limitation, NEDD8 activating enzyme (NAE (APPBP1/Uba3)), ubiquitin activating enzyme (UAE (Uba1)), sumo activating enzyme (SAE (Aos1/Uba2)), UBA4, UBA5, UBA6, ATG7 or ISG15 activating enzyme (Ube1L).

[0028] The term "E1 enzyme inhibitor" or "inhibitor of E1 enzyme" is used to signify a compound having a structure as defined herein, which is capable of interacting with an E1 enzyme and inhibiting its enzymatic activity. Inhibiting E1 enzymatic activity means reducing the ability of an E1 enzyme to activate ubiquitin like (ubl) conjugation to a substrate peptide or protein (*e.g.*, ubiquitination, neddylation, sumoylation). In some embodiments, an E1 enzyme inhibitor can inhibit more than one E1 enzyme. In other embodiments, an E1 enzyme inhibitor is specific for a particular E1 enzyme. In various embodiments, such reduction of E1 enzyme activity is at least about 50%, at least about 75%, at least about 90%, at least about 95%, or at least about 99%. In various embodiments, the concentration of E1 enzyme inhibitor required to reduce an E1 enzymatic activity is less than about 1 μM, less than about 500 nM, less than about 100 nM, less than about 50 nM, or less than about 10 nM.

[0029] As used herein, the term "NAE inhibitor" refers to an inhibitor of the NAE heterodimer. Examples of NAE inhibitors include 1-substituted methyl sulfamates (see Figure 1), including MLN4924. Langston S. et al. U.S. patent application serial no. 11/700,614, whose PCT application was published as WO07/092213, WO06084281 and WO2008/019124, disclose compounds which are effective inhibitors of E1 activating enzymes, e.g., NAE. In some embodiments, NAE inhibitors do not inhibit, or are very poor at inhibiting, other (non-NAE) E1 enzymes. The compounds are useful for inhibiting E1 activity *in vitro* and *in vivo* and are useful for the treatment of disorders of cell proliferation, e.g., cancer, and other disorders associated with E1 activity, such as pathogenic infections and neurodegenerative disorders. One class of compounds described in Langston *et al.* are 4-substituted ((IS, 2S, 4*R*)-2-hydroxy-4-{7H-pyrrolo[2,3-d]pyrimidin-7-yl}cyclopentyl)methyl sulfamates.

[0030] MLN4924 (((1S,2S,4R)-4-{4-[(1S)-2,3-dihydro-1H-inden-1-ylamino]-7H-pyrrolo[2,3-d]pyrimidin-7-yl}-2-hydroxycyclopentyl)methyl sulphamate) is an NAE-specific E1 inhibitor which disrupts cullin-RING ligase-mediated protein turnover leading to apoptotic death in human tumor cells by perturbation of cellular protein homeostasis (Soucy et al. (2009) Nature 458:732-736). The evaluation of MLN4924 in cellular and tumor xenograft studies has revealed two distinct mechanisms of action. The first is the induction of DNA re-replication, DNA damage and cell death through MLN4924-mediated dysregulation of the $CRL1^{SKP2}$ and $CRL4^{DDB1}$ substrate Cdt-1 (Milhollen et al. (2011) Cancer Res. 71:3042-3051). It has been shown that p53 status does not impact the induction of DNA re-replication but may make cells more prone to undergo apoptosis or senescence depending on the appropriate genetic background (Milhollen et al. (2011) *supra,* Lin et al. (2010) Nature 464:374-379 and Lin et al. (2010) Cancer Res.70:10310-20). The second mechanism is the inhibition of NF-κB pathway activity in NF-κB dependent Diffuse Large B-Cell Lymphomas primarily through dysregulation of $CRL1^{\beta TRCP}$ mediated turnover of phosphorylated IκBα (Milhollen et al. (2010) Blood 116:1515-1523). In addition, pre-clinical models of Acute Myelogenous Leukemia (AML) are sensitive to MLN4924 inhibition in both cell lines and primary patient blasts through mechanisms related to Cdt-1 dysregulation, NF-κB inhibition

and induction of reactive oxygen species (Swords et al. (2010) Blood 115:3796-3800).

[0031] Genes such as NF2 (reviewed by Ahronowitz et al. (2007) Human Mutation 28:1-2), KDM6A (reviewed by van Haaften et al. (2009) Nat. Genet. 41:521-523), FBXW7, TP53, CDKN2A and CDKN2A_p14 are mutated in many cancer types. SMAD4 is mutated in a number of cancers, but many of SMAD4 mutations are found in cancers of the intestine, pancreas (reviewed by Miyaki and Kuroki (2003) Biochem. Biophys. Res. Commun. 306:799-804) or thyroid gland.

[0032] As used herein, "NF2" refers to the longer isoform of the gene associated with GenBank Accession No. NM_000268, SEQ ID NO:1 (open reading frame is SEQ ID NO:2, nucleotides 444 to 2231 of SEQ ID NO:1), encoding GenPept Accession No. NP_000259, SEQ ID NO:3). Other names for NF2 include ACN, BANF, SCH and merlin (moesin-ezrin-radixin-like protein). NF2 functions as a tumor suppressor gene and can be found on chromosome 22. NF2 interacts with the cytoskeleton, cell surface proteins and may be involved in cytoskeletal dynamics and regulating ion transport. Functions of NF2 that can relate it to sensitivity to NAE inhibition, e.g., MLN4924 include its ability to inhibit the E3 ubiquitin ligase $CRL4^{DCAF1}$ (Li et al. (2010) Cell 140:477-490). Mutations in NF2 can disrupt its inhibitory activity and lead to uncontrolled ubiquitination of substrates of $CRL4^{DCAF1}$ and proliferation of cells harboring the mutated gene.

[0033] As used herein, "SMAD4" refers to the gene associated with GenBank Accession No. NM_005359, SEQ ID NO:4 (open reading frame is SEQ ID NO:5, nucleotides 539 to 2197 of SEQ ID NO:4), encoding GenPept Accession No. NP_005350, SEQ ID NO:6. Other names for SMAD4 include deleted in pancreatic carcinoma locus 4 (DPC4), JIP, or mothers against decapentaplegic, Drosophila, homolog of, 4 (MAD4). SMAD4 is a signal transduction protein involved in transforming growth factor (TGF)-beta signaling. SMAD4 can act as a tumor suppressor and can be targeted for degradation by ubiquitination by the Skp-Cullin-F-box protein (SCF) complex.

[0034] As used herein, "KDM6A" refers to the gene associated with GenBank Accession No. NM_021140, SEQ ID NO:7 (open reading frame is SEQ ID NO:8, nucleotides 376 to 4581 of SEQ ID NO:7, or SEQ ID NO:9), encoding GenPept Accession No. NP_066963, SEQ ID NO:10 or SEQ ID NO:11 (SEQ ID NO:10 with a V instead of an L at position 173 and an R instead of L at 584, an N instead of S at position 601 and/or K instead of E at position 629). Other names for KDM6A include ubiquitously-transcribed tetratricopeptide repeat protein X-linked or ubiquitously-transcribed TPR gene on the X chromosome (UTX), or bA286N14.2. KDM6A is a histone demethylase and can function as a tumor suppressor.

[0035] As used herein, "FBXW7" refers to the gene associated with GenBank Accession No. NM_033632, SEQ ID NO:12 (open reading frame is SEQ ID NO:13, nucleotides 150 to 2273 of SEQ ID NO:12), encoding GenPept Accession No. NP_361014, SEQ ID NO:14. Other names for FBXW7 include homolog of C elegans sel-10 (SEL10), archipelago homolog (AGO), F-box protein FBX30 (FBXO30), or cell division control protein 4 (CDC4). FBXW7 can associate into a ubiquitin protein ligase complex to participate in phosphorylation-dependent ubiquitination of proteins, including proteins involved in cell cycle and survival. FBXW7 can act as a tumor suppressor. Use of FBXW7 as marker gene may be organ-specific, i.e., it can be a marker of sensitivity in tumors arising in some tissues but not others. For example, FBXW7 can be a marker of sensitivity in tumors of the uterus, cervix or liver, but not a marker of sensitivity in tumors of the digestive tract, where mutations in other genes may dominate to result in the insensitivity or resistance of cells from those tumors to MLN4924.

[0036] As used herein, "TP53" refers to the gene associated with GenBank Accession No. NM_000546, SEQ ID NO:15 (open reading frame is SEQ ID NO:16, nucleotides 203 to 1384 of SEQ ID NO:15, or a variant wherein the nucleotide at position 417 is a guanine instead of a cytosine), encoding GenPept Accession No. NP_000537, SEQ ID NO:17 or a variant wherein the amino acid residue at position 72 is an arginine, R instead of a proline, P). Other names for TP53 include BCC7, LFS1 and p53. TP53 binds DNA and activates transcription factors and can function as a tumor suppressor.

[0037] As used herein, "CDKN2A" refers to the gene associated with GenBank Accession No. NM_000077, SEQ ID NO:18 (open reading frame is SEQ ID NO:19, nucleotides 307 to 777 of SEQ ID NO:18), encoding GenPept Accession No. NP_000068, SEQ ID NO:20. Other names for CDKN2A include alternate open reading frame (ARF), p16, p16ARF, inhibitor of cyclin-dependent kinase 4 (INK4) and multiple tumor suppressor gene-1 (MTS1). Variants of CDKN2A differ in the first exon. One variant is "CDKN2A_p14" or "CDKN2A.p14," also known as p14ARF, is associated with GenBank accession number NM_058195, SEQ ID NO:21 (open reading frame is SEQ ID NO:22, nucleotides 38 to 559 of SEQ ID NO:21); GenPept NP_478102, SEQ ID NO:23 or a variant which begins at amino acid residue 42 of SEQ ID NO:23. CDKN2A_p14 results from translation in a different reading frame than p16ARF (p16INK4a, CDKN2A). CDKN2A and CDKN2A_p14 inhibit cyclin dependent kinase 4, can stabilize p53 and can regulate cell cycle G1 progression. CDKN2A and CDKN2A_p14 can act as a tumor suppressor.

[0038] As used herein, "APC" refers to adenomatous polyposis coli, the gene associated with GenBank Accession No. NM_000038, SEQ ID NO:24 (open reading frame SEQ ID NO:25, or a variant with a thymine instead of a cytosine at nucleotide 1458), encoding GenPept Accession No. NP_000029, SEQ ID NO:26. Other names for APC include BTSP2, and DP2. APC binds microtubules and inhibits the Wnt-signalling pathway and can function as a tumor suppressor.

[0039] There has been interest in public cataloging mutations associated with cancers. Examples of public databases which include information about mutations associated with cancers are the Database of Genotypes and Phenotypes

(dbGaP) maintained by the National Center for Biotechnology Information (Bethesda, MD) and Catalogue of Somatic Mutations in Cancer (COSMIC) database maintained by the Wellcome Trust Sanger Institute (Cambridge, UK).

[0040] Compositions and methods are provided to determine the mutational status, e.g., to identify mutations in marker genes in hematological (*e.g.,* multiple myeloma, leukemias, lymphoma, *etc.*) or solid (*e.g.,* melanoma, esophageal cancer, lung cancer or bladder cancer) tumors to predict response to treatment, time-to-progression and survival upon treatment. Compositions and methods provided herein also can identify mutations in marker genes in solid tumors such as from colon cancer, breast cancer, head and neck cancer, or central nervous system cancer.

[0041] Markers were identified based on genetic profiles of tumor cells which exhibit sensitivity to treatment to MLN4924. TP53 marker also was identified based on the behavior of isogenic cell lines which differ in the deletion of the TP53 gene. Observed sensitivity can be consistent among tumor cells tested by more than one method.

[0042] Unless otherwise defined, all technical and scientific terms used herein have the meanings which are commonly understood by one of ordinary skill in the art to which this invention belongs. Generally, nomenclature utilized in connection with, and techniques of cell and tissue culture, molecular biology and protein and oligo- or polynucleotide chemistry and hybridization described herein are those known in the art. GenBank or GenPept accession numbers and useful nucleic acid and peptide sequences can be found at the website maintained by the National Center for Biotechnology Information, Bethesda, MD. The content of all database accession records (*e.g.*, from Affymetrix HG133 annotation files, Entrez, GenBank, RefSeq, COSMIC) cited throughout this application (including the Tables) are referred to. Standard techniques are used for recombinant DNA, oligonucleotide synthesis, protein purification, tissue culture and transformation and transfection (e.g., electroporation, lipofection, etc). Enzymatic reactions are performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein. The foregoing techniques and procedures generally are performed according to methods known in the art, e.g., as described in various general and more specific references that are cited and discussed throughout the present specification. See e.g., Sambrook et al. (2000) Molecular Cloning: A Laboratory Manual (3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or Harlow, E. and Lane, D. (1988) Antibodies: A Laboratory Manual (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are known in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation and delivery, and treatment of patients. Furthermore, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. In the case of conflict, the present specification, including definitions, will control.

[0043] The articles "a," "an" and "at least one" are used herein to refer to one or to more than one of the grammatical object of the article. By way of example, "an element" means one or more than one element, at least one element. In the case of conflict, the present specification, including definitions, will control.

[0044] As used herein, a "favorable" outcome or prognosis refers to long term survival, long time-to-progression (TTP), and/or good response. Conversely, an "unfavorable" prognosis refers to short term survival, short time-to-progression (TTP) and/or poor response.

[0045] A "marker" as used herein, includes a material associated with a marker gene which has been identified as having a mutation in tumor cells of a patient and furthermore that mutation is characteristic of a patient whose outcome is favorable or unfavorable with treatment e.g., by an NAE inhibitor, such as a 1-substituted methyl sulfamate. Examples of a marker include a material, e.g., a chromosome locus, DNA for a gene, RNA for a gene or protein for a gene. For example, a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein which demonstrates a characteristic, e.g., size, sequence, composition or amount indicative of a short term survival patient; alternatively a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein which demonstrates a mutation or characteristic, e.g., size, sequence, composition or amount indicative of a long term survival patient. In another example, a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein whose mutation or characteristic, e.g., size, sequence, composition or amount is indicative of a patient with a poor response to treatment; alternatively a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein whose mutation or characteristic, e.g., size, sequence, composition or amount is indicative of a patient with a good response. In a further example, a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein whose mutation or characteristic, e.g., size, sequence, composition or amount is indicative of a patient whose disease has a short time-to-progression (TTP) upon treatment; alternatively a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein whose mutation or characteristic, e.g., size, sequence, composition or amount is indicative of a patient whose disease has a long TTP. In a yet a further example, a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein whose mutation or characteristic, e.g., size, sequence, composition or amount is indicative of a patient whose disease has a short term survival upon treatment; alternatively a marker includes a marker gene material, e.g., a chromosome locus, DNA, RNA or protein whose mutation or characteristic, e.g., size, sequence, composition or amount is indicative of a patient whose disease has a long term survival. Thus, as used herein, marker is intended to include each and every one of these possibilities, and further can include each single marker individually as a marker; or alternatively can include one or more, or all of the characteristics collectively when reference

is made to "markers" or "marker sets."

[0046] A chromosome locus marker useful to measure for determination of prognosis or treatment or disease management strategy is selected from the group consisting of chromosome 22q12.2 (NF2), e.g., from base pair 29999545 to 30094589, chromosome 18q21.1-21.2 (SMAD4), e.g., from base pair 48556583 to 48611412, chromosome Xp11.2 (KDM6A), e.g., from base pair 44732423 to 44971847, chromosome 4q31.3 (FBXW7), e.g., from base pair 153242410-153456172, chromosome 17p13.1 (TP53), e.g., from base pair 7571720 to 7590868, and 9p21 (CDKN2A and CDKN2A_p14), e.g., from base pair 21967751 to 21994490. Chromosome locus numbers are based on the reference human genome Build 37.3 (current as of October 5, 2011) in the NCBI Gene database. A marker DNA, marker RNA or marker protein can correspond to base pairs on a chromosome locus marker. For example, a marker DNA can include genomic DNA from a chromosome locus marker, marker RNA can include a polynucleotide transcribed from a locus marker, and a marker protein can include a polypeptide resulting from expression at a chromosome locus marker in a sample, e.g., comprising tumor cells.

[0047] A "marker nucleic acid" is a nucleic acid (*e.g.*, genomic DNA, mRNA, cDNA) encoded by or corresponding to a marker gene of the invention. Such marker nucleic acids include DNA, e.g., sense and anti-sense strands of genomic DNA (*e.g.*, including any introns occurring therein), comprising the entire or a partial sequence, e.g., one or more of the exons of the genomic DNA, up to and including the open reading frame of any of the marker genes or the complement of such a sequence. The marker nucleic acids also include RNA comprising the entire or a partial sequence of any marker or the complement of such a sequence, wherein all thymidine residues are replaced with uridine residues, RNA generated by transcription of genomic DNA (*i.e.* prior to splicing), RNA generated by splicing of RNA transcribed from genomic DNA, and proteins generated by translation of spliced RNA (*i.e.* including proteins both before and after cleavage of normally cleaved regions such as transmembrane signal sequences). As used herein, a "marker nucleic acid" may also include a cDNA made by reverse transcription of an RNA generated by transcription of genomic DNA (including spliced RNA). A marker nucleic acid also includes sequences which differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a protein which corresponds to a marker, e.g., a mutated marker, of the invention, and thus encode the same protein, e.g., mutated protein. As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence. Such naturally occuring allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals, e.g., in cells, e.g., germline cells, of individuals without cancer. This can be readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Detection of any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of naturally occurring allelic variation and that do not alter the functional activity of a wild type marker gene is intended to be within the scope of the wild type version of a marker described herein. A "marker protein" is a protein encoded by or corresponding to a marker, e.g., a mutant nucleic acid, of the invention. The terms "protein" and "polypeptide' are used interchangeably. A protein of a marker specifically can be referred to by its name or amino acid sequence, but it is understood by those skilled in the art, that mutations, deletions and/or post-translational modifications can affect protein structure, appearance, cellular location and/or behavior. Unless indicated otherwise, such differences are not distinguished herein, and a marker described herein is intended to include any or all such varieties.

[0048] As used herein, a "marker gene" refers to a gene which can have a mutation such that its DNA, RNA and/or protein has a characteristic, e.g., size, sequence, composition or amount(s) which provide information about prognosis (*i.e.*, are "informative") upon treatment. Marker genes described herein as linked to outcome after NAE inhibitor, such as 1-substituted methyl sulfamate (*e.g.*, MLN4924) treatment are examples of genes within the chromosome locus markers described above and are provided in Table 1. Sequences of mRNA, open reading frames and proteins corresponding to marker genes also are listed in Table 1. A marker gene listed in Table 1 can have isoforms which are either ubiquitous or have restricted expression. Except for the separate listing of the CDKN2A_p14 isoform, the DNA SEQ ID NOs in Table 1 refer to the mRNA encoding the major or longest isoform and the protein SEQ ID NOs represent at least a precursor of such isoform and not necessarily the mature protein. These sequences are not intended to limit the marker gene identity to that isoform or precursor. The additional isoforms and mature proteins are readily retrievable and understandable to one of skill in the art by reviewing the information provided under the Entrez Gene (database maintained by the National Center for Biotechnology Information, Bethesda, MD) identified by the ID number listed in Table 1.

Table 1 Marker Gene Description for NAE Inhibitor Treatment

Marker Gene ID	Marker Gene Name	Entrez Gene ID	Chromosome location	Start base pair	End base pair	SEQ ID NOs:
NF2	neurofibromin 2	4771	22q	29999545	30094589	1, 2, 3

(continued)

Marker Gene ID	Marker Gene Name	Entrez Gene ID	Chromosome location	Start base pair	End base pair	SEQ ID NOs:
SMAD4	mothers against decapentaplegic homolog 4	4089	18q	48556583	48611412	4, 5, 6
KDM6A	lysine-specific demethylase 6A	7403	Xp	44732423	44971847	7,8,9, 10, 11
FBXW7	F-box and WD repeat domain containing 7	55294	4q	153242410	153456172	12, 13, 14
TP53	tumor protein p53	7157	17p	7571720	7590868	15, 16, 17
CDKN2A	cyclin-dependent kinase inhibitor 2A	1029	9p	21967751	21994490	18, 19, 20
CDKN2A_ p14	cyclin-dependent kinase inhibitor 2A p14 variant	1029	9p	21967751	21994490	21, 22, 23
APC	adenomatous polyposis coli	324	5q	112043202	112181936	24, 25, 26

[0049] As used herein, an "informative" characteristic, e.g., size, sequence, composition or amount of a marker refers to a characteristic, e.g., size, sequence, composition or amount whose value or difference is correlated to prognosis or outcome. The informative characteristic, e.g., size, sequence, composition or amount of a marker can be obtained by analyzing either nucleic acid, *e.g.,* DNA or RNA, or protein corresponding to the marker gene. The characteristic, e.g., size (*e.g.,* length or molecular weight), sequence (e.g., nucleic acid sequence or protein sequence), composition (*e.g.*, base or amino acid composition or peptide digest or gene fragment pattern) or amount (*e.g.*, copy number and/or expression level) of a marker, *e.g.,* a chromosome locus marker or a marker in a sample from a patient can be "informative" if it is different than the wild type or allelic variant of the substance being analyzed. In some embodiments, a characteristic of a marker is informative if it indicates that the marker gene is wild type. In an embodiment where the amount of a marker is being measured, an amount is "informative" if it is greater than or less than a reference amount by a degree greater than the standard error of the assay employed to assess expression. The informative expression level of a marker can be determined upon statistical correlation of the measured expression level and the outcome, *e.g.*, good response, poor response, long time-to-progression, short time-to-progression, short term survival or long term survival. The result of the statistical analysis can establish a threshold for selecting markers to use in the methods described herein. Alternatively, a marker, *e.g.,* a chromosome locus marker, or a marker gene that has differential characteristic, e.g., size, sequence, composition or amounts will have typical ranges of amounts that are predictive of outcome. An informative characteristic, e.g., size, sequence, composition or amount is a characteristic, e.g., size, sequence, composition or amount that falls within the range of characteristic, e.g., size, sequence, composition or amounts determined for the outcome. Still further, a set of markers may together be "informative" if the combination of their characteristics, e.g., sizes, sequences, compositions or amounts either meets or is above or below a pre-determined score for a marker, *e.g.,* a chromosome locus marker, or a marker gene, set as determined by methods provided herein. Gene translocation, transcript splice variation, deletion and truncation are examples of events which can change marker size, sequence or composition, in addition to point mutations which can change marker sequence or composition. Measurement of only one characteristic, e.g., marker, of a marker gene (i.e., DNA, RNA or protein) can provide a prognosis, i.e., indicate outcome. Measurement of more than one characteristic, e.g., marker, of a marker gene can provide a prognosis when the informative amounts of the two characteristics are consistent with each other, *i.e.,* the biologies of the results are not contradictory. Examples of consistent results from measurement of multiple characteristics of a marker gene can be identification of a nonsense mutation or deletion in a DNA or RNA and a low amount or low molecular weight of encoded protein, or a mutation in a region which encodes a binding pocket or active site of a protein and low activity of the encoded protein. A different example can occur when a protein is in a pathway with a feedback loop controlling its synthesis based on its activity level. In this example, a low amount or activity of protein can be associated with a high amount of its mutated mRNA as a tissue, due to the marker gene mutation, thus is starved for the protein activity and repeatedly signals the production of the protein.

[0050] As used herein, "gene deletion" refers to an amount of DNA copy number less than 2 and "amplification" refers

to an amount of DNA copy number greater than 2. A "diploid" amount refers to a copy number equal to 2. The term "diploid or amplification" can be interpreted as "not deletion" of a gene copy. In a marker whose alternative informative amount is gene deletion, amplification generally would not be seen. Conversely, the term "diploid or deletion" can be interpreted as "not amplification" of copy number. In a marker whose alternative informative amount is amplification, gene deletion generally would not be seen. For the sake of clarity, sequence deletion can occur within a gene as a result of marker gene mutation and can result in absence of transcribed protein or a shortened mRNA or protein. Such a deletion may not affect copy number.

[0051] The terms "long term survival" and "short term survival" refer to the length of time after receiving a first dose of treatment that a cancer patient is predicted to live. A "long term survivor" refers to a patient expected have a slower rate of progression or later death from the tumor than those patients identified as short term survivors. "Enhanced survival" or "a slower rate of death" are estimated life span determinations based upon characteristic, e.g., size, sequence, composition or amount of one or more of markers described herein, e.g., as compared to a reference standard such that 70%, 80%, 90% or more of the population will be alive a sufficient time period after receiving a first dose of treatment. A "faster rate of death" or "shorter survival time" refer to estimated life span determinations based upon characteristic, e.g., size, sequence, composition or amount of one or more of markers described herein, e.g., as compared to a reference standard such that 50%, 40%, 30%, 20%, 10% or less of the population will not live a sufficient time period after receiving a first dose of treatment. In some embodiments, the sufficient time period is at least 6, 12, 18, 24 or 30 months measured from the first day of receiving a cancer therapy.

[0052] A cancer is "responsive" to a therapeutic agent or there is a "good response" to a treatment if its rate of growth is inhibited as a result of contact with the therapeutic agent, compared to its growth in the absence of contact with the therapeutic agent. Growth of a cancer can be measured in a variety of ways, for instance, the characteristic, e.g., size of a tumor or the expression of tumor markers appropriate for that tumor type may be measured. For example, the response definitions used to support the identification of markers associated with myeloma and its response to an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy, the Southwestern Oncology Group (SWOG) criteria as described in Blade et al. (1998) Br J Haematol. 102:1115-23 can be used. These criteria define the type of response measured in myeloma and also the characterization of time to disease progression which is another important measure of a tumor's sensitivity to a therapeutic agent. For solid tumors, the Response Evaluation Criteria in Solid Tumors (RECIST) guidelines (Eisenhauer et al. (2009) E. J. Canc. 45:228-247) can be used to support the identification of markers associated with solid tumors and response of solid tumors to an NAE inhibitor. International Working Groups convene periodically to set, update and publish response criteria for various types of cancers. Such published reports can be followed to support the identification of markers of the subject tumors and their response to NAE inhibitors. Examples are criteria for Acute Myelogenous Leukemia (AML, Cheson et al. (2003) J.Clin. Oncol. 21:4642-4649), lymphomas, e.g., non-Hodgkin's and Hodgkin's lymphoma (Cheson et al. (2007) J.Clin. Oncol. 25:579-596). Criteria take into account analysis methods such as Positron Emission Tomography (PET), e.g., for identifying sites with measurable altered metabolic activity (e.g., at tumor sites) or to trace specific markers into tumors *in vivo,* immunohistochemistry, e.g., to identify tumor cells by detecting binding of antibodies to specific tumor markers, and flow cytometry, e.g., to characterize cell types by differential markers and fluorescent stains, in addition to traditional methods such as histology to identify cell composition (e.g., blast counts in a blood smear or a bone marrow biopsy, presence and number of mitotic figures) or tissue structure (e.g., disordered tissue architecture or cell infiltration of basement membrane). The quality of being responsive to an NAE inhibitor, such as a 1-substituted methyl sulfamate therapy can be a variable one, with different cancers exhibiting different levels of "responsiveness" to a given therapeutic agent, under different conditions. Still further, measures of responsiveness can be assessed using additional criteria beyond growth size of a tumor, including patient quality of life, degree of metastases, etc. In addition, clinical prognostic markers and variables can be assessed (e.g., M protein in myeloma, PSA levels in prostate cancer) in applicable situations.

[0053] A cancer is "non-responsive" or has a "poor response" to a therapeutic agent or there is a poor response to a treatment if its rate of growth is not inhibited, or inhibited to a very low degree, as a result of contact with the therapeutic agent when compared to its growth in the absence of contact with the therapeutic agent. As stated above, growth of a cancer can be measured in a variety of ways, for instance, the size of a tumor or the expression of tumor markers appropriate for that tumor type may be measured. For example, the response definitions used to support the identification of markers associated with non-response of tumors to therapeutic agents, guidelines such as those described above can be used. The quality of being non-responsive to a therapeutic agent can be a highly variable one, with different cancers exhibiting different levels of "non-responsiveness" to a given therapeutic agent, under different conditions. Still further, measures of non-responsiveness can be assessed using additional criteria beyond growth size of a tumor, including patient quality of life, degree of metastases, etc. In addition, clinical prognostic markers and variables can be assessed (e.g., M protein in myeloma, PSA levels in prostate cancer) in applicable situations.

[0054] As used herein, "long time-to-progression, "long TTP" and "short time-to-progression," "short TTP" refer to the amount of time until when the stable disease brought by treatment converts into an active disease. On occasion, a treatment results in stable disease which is neither a good nor a poor response, *e.g.,* MR, the disease merely does not

get worse, *e.g.,* become a progressive disease, for a period of time. This period of time can be at least 4-8 weeks, at least 3-6 months or more than 6 months.

[0055] "Treatment" shall mean the use of a therapy to prevent or inhibit further tumor growth, as well as to cause shrinkage of a tumor, and to provide longer survival times. Treatment is also intended to include prevention of metastasis of tumor. A tumor is "inhibited" or "treated" if at least one symptom (as determined by responsiveness/non-responsiveness, time to progression, or indicators known in the art and described herein) of the cancer or tumor is alleviated, terminated, slowed, minimized, or prevented. Any amelioration of any symptom, physical or otherwise, of a tumor pursuant to treatment using a therapeutic regimen (*e.g.*, NAE inhibitor, such as a 1-substituted methyl sulfamate regimen) as further described herein, is within the scope of the invention.

[0056] As used herein, the term "agent" is defined broadly as anything that cancer cells, including tumor cells, may be exposed to in a therapeutic protocol. In the context of the present invention, such agents include, but are not limited to, an NAE inhibitor, such as a 1-substituted methyl sulfamate agents, as well as chemotherapeutic agents as known in the art and described in further detail herein.

[0057] The term "probe" refers to any molecule, e.g., an isolated molecule, which is capable of selectively binding to a specifically intended target molecule, for example a marker of the invention. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic monomers.

[0058] A "normal" characteristic, e.g., size, sequence, composition or amount of a marker may refer to the characteristic, e.g., size, sequence, composition or amount in a "reference sample." A reference sample can be a matched normal, e.g., germline, sample from the same patient from whom the tumor, e.g., with a somatic mutation, is derived. A reference sample can be a sample from a healthy subject not having the marker-associated disease or a reference characteristic e.g., the average characteristic, e.g., size, sequence, composition or amount of the wild type marker in several healthy subjects. A reference sample characteristic, e.g., size, sequence, composition or amount may be comprised of a characteristic, e.g., size, sequence, composition or amount of one or more markers from a reference database. Alternatively, a "normal" characteristic, e.g., size, sequence, composition or level of expression of a marker is the characteristic, e.g., size, sequence, composition or amount of the marker, e.g., marker gene in non-tumor cells in a similar environment or response situation from the same patient from whom the tumor is derived. The normal amount of DNA copy number is 2 or diploid, with the exception of X-linked genes in males, where the normal DNA copy number is 1.

[0059] "Over-expression" and "under-expression" of a marker gene, refer to expression of the marker gene of a patient at a greater or lesser level (*e.g.* more than three-halves-fold, at least two-fold, at least three-fold, greater or lesser level etc.), respectively, than normal level of expression of the marker gene, e.g., as measured by mRNA or protein, in a test sample that is greater than the standard error of the assay employed to assess expression. A "significant" expression level may refer to a level which either meets or is above or below a pre-determined score for a marker gene set as determined by methods provided herein.

[0060] "Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. In an embodiment, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, at least about 75%, at least about 90%, or at least about 95% or all of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

[0061] "Homologous" as used herein, refers to nucleotide sequence similarity between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue (i.e., by percent identity). By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share homology with 50% identity. In one embodiment, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. In an embodiment of 100% identity, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

[0062] Unless otherwise specified herewithin, the terms "antibody" and "antibodies" broadly encompass naturally-occurring forms of antibodies, e.g., polyclonal antibodies (*e.g.*, IgG, IgA, IgM, IgE) and monoclonal and recombinant antibodies such as single-chain antibodies, two-chain and multi-chain proteins, chimeric, CDR-grafted, human and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments (e.g., dAbs, scFv, Fab, $F(ab)'_2$, Fab') and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody. The term "antibody" also includes synthetic and genetically engineered variants.

[0063] A "kit" is any article of manufacture (*e.g.*, a package or container) comprising at least one reagent, *e.g.* a probe, for specifically detecting a marker or marker set of the invention. The article of manufacture may be promoted, distributed, sold or offered for sale as a unit for performing, e.g., *in vitro,* the methods of the present invention, e.g., on a sample having been obtained from a patient. The reagents included in such a kit can comprise at least one nucleic acid probe and, optionally, one or more primers and/or antibodies for use in detecting marker characteristics, e.g., size, sequence composition or amount, e.g., expression. In addition, a kit of the present invention can contain instructions which describe a suitable detection assay. Such a kit can be conveniently used, *e.g.,* in a clinical or a contract testing setting, to generate information, e.g., on expression levels, characteristic, e.g., size, sequence or composition of one or more marker, to be recorded, stored, transmitted or received to allow for diagnosis, evaluation or treatment of patients exhibiting symptoms of cancer, in particular patients exhibiting the possible presence of a cancer capable of treatment with NAE inhibition therapy, including, *e.g.,* hematological cancers *e.g.,* myelomas (*e.g.,* multiple myeloma), lymphomas (*e.g.,* non-hodgkins lymphoma), leukemias (*e.g.,* acute myelogenous leukemia), and solid tumors (*e.g.,* tumors of skin, lung, breast, ovary, *etc*.).

[0064] The present methods and compositions are designed for use in diagnostics and therapeutics for a patient suffering from cancer. A cancer or tumor is treated or diagnosed according to the present methods. "Cancer" or "tumor" is intended to include any neoplastic growth in a patient, including an initial tumor and any metastases. The cancer can be of the hematological or solid tumor type. Hematological tumors include tumors of hematological origin, including, *e.g.,* myelomas (*i.,* multiple myeloma), leukemias (*e.g.,* Waldenstrom's syndrome, chronic lymphocytic leukemia, acute myelogenous leukemia, chronic myelogenous leukemia, other leukemias), lymphomas (*e.g.*, B-cell lymphomas, non-Hodgkin's lymphoma) and myelodysplastic syndrome. Solid tumors can originate in organs, and include cancers such as in skin, lung, brain, breast, prostate, ovary, colon, kidney, pancreas, liver, esophagus, stomach, intestine, bladder, uterus, cervix, head and neck, central nervous system, bone, testis, adrenal gland, etc. The cancer can comprise a cell in which a marker gene has a mutation. As used herein, cancer cells, including tumor cells, refer to cells that divide at an abnormal (increased) rate or whose control of growth or survival is different than for cells in the same tissue where the cancer cell arises or lives. Cancer cells include, but are not limited to, cells in carcinomas, such as squamous cell carcinoma, basal cell carcinoma, sweat gland carcinoma, sebaceous gland carcinoma, adenocarcinoma, papillary carcinoma, papillary adenocarcinoma, cystadenocarcinoma, medullary carcinoma, undifferentiated carcinoma, bronchogenic carcinoma, melanoma, renal cell carcinoma, hepatoma-liver cell carcinoma, bile duct carcinoma, cholangiocarcinoma, papillary carcinoma, transitional cell carcinoma, choriocarcinoma, semonoma, embryonal carcinoma, mammary carcinomas, gastrointestinal carcinoma, colonic carcinomas, bladder carcinoma, prostate carcinoma, and squamous cell carcinoma of the neck and head region; sarcomas, such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordosarcoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, synoviosarcoma and mesotheliosarcoma; hematologic cancers, such as myelomas, leukemias (*e.g.*, acute myelogenous leukemia, chronic lymphocytic leukemia, granulocytic leukemia, monocytic leukemia, lymphocytic leukemia), and lymphomas (*e.g.*, follicular lymphoma, mantle cell lymphoma, diffuse large Bcell lymphoma, malignant lymphoma, plasmocytoma, reticulum cell sarcoma, or Hodgkins disease); and tumors of the nervous system including glioma, meningoma, medulloblastoma, schwannoma or epidymoma.

[0065] As used herein, the term "noninvasive" refers to a procedure which inflicts minimal harm to a subject. In the case of clinical applications, a noninvasive sampling procedure can be performed quickly, e.g., in a walk-in setting, typically without anaesthesia and/or without surgical implements or suturing. Examples of noninvasive samples include blood, serum, saliva, urine, buccal swabs, throat cultures, stool samples and cervical smears. Noninvasive diagnostic analyses include x-rays, magnetic resonance imaging, positron emission tomography, etc.

[0066] Described herein is the assessment of outcome for treatment of a tumor through measurement of the amount of pharmacogenomic markers. Also described are assessing the outcome by noninvasive, convenient or low-cost means, for example, from blood samples. Typical methods to determine extent of cancer or outcome of a hematological tumor, *e.g.*, lymphoma, leukemia, *e.g.,* acute myelogenous leukemia, myeloma (*e.g.,* multiple myeloma) can employ bone marrow biopsy to collect tissue for genotype or phenotype, *e.g.*, histological analysis. The invention provides methods for determining, assessing, advising or providing an appropriate therapy regimen for treating a tumor or managing disease in a patient. Monitoring a treatment using the kits and methods disclosed herein can identify the potential for unfavorable outcome and allow their prevention, and thus a savings in morbidity, mortality and treatment costs through adjustment in the therapeutic regimen, cessation of therapy or use of alternative therapy.

[0067] The term "biological sample" is intended to include a patient sample, e.g, tissue, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject and can be obtained from a patient or a normal subject. In hematological tumors of the bone marrow, *e.g.*, myeloma tumors, primary analysis of the tumor can be performed on bone marrow samples. However, some tumor cells, (*e.g.,* clonotypic tumor cells, circulating endothelial cells), are a percentage of the cell population in whole blood. These cells also can be mobilized into the blood during treatment of the patient with granulocyte-colony stimulating factor (G-CSF) in preparation for a bone marrow transplant, a standard treatment for hematological tumors, *e.g.*, leukemias, lymphomas and myelomas. Examples of circulating tumor cells in multiple myeloma have been studied e.g., by Pilarski et al. (2000) Blood 95:1056-65 and Rigolin et al. (2006) Blood 107:2531-5. Thus, noninvasive samples, *e.g.,* for *in vitro* measurement of markers to determine outcome of treatment, can include peripheral blood samples. Accordingly, cells within peripheral blood can be tested for marker amount. For patients with hematological tumors, a control, reference sample for normal characteristic, e.g., size, sequence, composition or amount can be obtained from skin or a buccal swab of the patient. For solid tumors, a typical tumor sample is a biopsy of the tumor and thus comprises solid tumor cells. Alternatively, a sample of tumor cells shed or scraped from the tumor site can be collected noninvasively, such as in blood, sputum, a nipple aspirate, urine, stool, cervical smear, etc. For solid tumors, a control reference sample for normal characteristic, e.g., size, sequence, composition or amount can be obtained from blood of the patient.

[0068] Blood collection containers can comprise an anti-coagulant, *e.g.*, heparin or ethylene-diaminetetraacetic acid (EDTA), sodium citrate or citrate solutions with additives to preserve blood integrity, such as dextrose or albumin or buffers, *e.g.*, phosphate. If the amount of marker is being measured by measuring the level of its DNA in the sample, a DNA stabilizer, *e.g.*, an agent that inhibits DNAse, can be added to the sample. If the amount of marker is being measured by measuring the level of its RNA in the sample, an RNA stabilizer, *e.g.*, an agent that inhibits RNAse, can be added to the sample. If the amount of marker is being measured by measuring the level of its protein in the sample, a protein stabilizer, *e.g.*, an agent that inhibits proteases, can be added to the sample. An example of a blood collection container is PAXGENE® tubes (PREANALYTIX, Valencia, CA), useful for RNA stabilization upon blood collection. Peripheral blood samples can be modified, *e.g.*, fractionated, sorted or concentrated (*e.g.*, to result in samples enriched with tumor or depleted of tumor (e.g., for a reference sample)). Examples of modified samples include clonotypic myeloma cells, which can be collected by *e.g.,* negative selection, *e.g.,* separation of white blood cells from red blood cells (*e.g.*, differential centrifugation through a dense sugar or polymer solution (*e.g.*, FICOLL® solution (Amersham Biosciences division of GE healthcare, Piscataway, NJ) or HISTOPAQUE®-1077 solution, Sigma-Aldrich Biotechnology LP and Sigma-Aldrich Co., St. Louis, MO)) and/or positive selection by binding B cells to a selection agent *(e.g.,* a reagent which binds to a tumor cell or myeloid progenitor marker, such as CD34, CD38, CD138, or CD133, for direct isolation (*e.g.*, the application of a magnetic field to solutions of cells comprising magnetic beads (*e.g.*, from Miltenyi Biotec, Auburn, CA) which bind to the B cell markers) or fluorescent-activated cell sorting).

[0069] Alternatively, a tumor cell line, *e.g.,* OCI-Ly3, OCI-Ly10 cell (Alizadeh et al. (2000) Nature 403:503-511), a RPMI 6666 cell, a SUP-B15 cell, a KG-1 cell, a CCRF-SB cell, an 8ES cell, a Kasumi-1 cell, a Kasumi-3 cell, a BDCM cell, an HL-60 cell, a Mo-B cell, a JM1 cell, a GA-10 cell or a B-cell lymphoma (*e.g.*, BC-3) or a cell line or a collection of tumor cell lines (see e.g., McDermott et al. (2007) PNAS 104:19936-19941 or ONCOPANEL™ anti-cancer tumor cell profiling screen (Ricerca Biosciences, Bothell, WA)) can be assayed. A skilled artisan readily can select and obtain the appropriate cells (*e.g.,* from American Type Culture Collection (ATCC®), Manassas, VA) that are used in the present method. If the compositions or methods are being used to predict outcome of treatment in a patient or monitor the effectiveness of a therapeutic protocol, then a tissue or blood sample having been obtained from the patient being treated is a useful source of cells or marker gene or gene products for an assay.

[0070] The sample, *e.g.*, tumor, *e.g.*, biopsy or bone marrow, blood or modified blood, (*e.g.*, comprising tumor cells) and/or the reference, *e.g.*, matched control (*e.g.*, germline), sample can be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.*, nucleic acid and/or protein extraction, fixation, storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, *etc.*) prior to assessing the amount of the marker in the sample.

[0071] In an embodiment, mutational status of a marker gene, e.g., a mutation in a marker can be identified by sequencing a nucleic acid, e.g., a DNA, RNA, cDNA or a protein correlated with the marker gene. There are several sequencing methods known in the art to sequence nucleic acids. A nucleic acid primer can be designed to bind to a region comprising a potential mutation site or can be designed to complement the mutated sequence rather than the wild type sequence. Primer pairs can be designed to bracket a region comprising a potential mutation in a marker gene. A primer or primer pair can be used for sequencing one or both strands of DNA corresponding to the marker gene. A primer can be used in conjunction with a probe, e.g., a nucleic acid probe, e.g., a hybridization probe, to amplify a region of interest prior to sequencing to boost sequence amounts for detection of a mutation in a marker gene. Examples of regions which can be sequenced include an entire gene, transcripts of the gene and a fragment of the gene or the transcript, e.g., one or more of exons or untranslated regions. Examples of mutations to target for primer selection and sequence or composition analysis can be found in public databases which collect mutation information, such as COSMIC and dbGaP. Some mutations of marker genes such as NF2, SMAD, KDM6A or FBXW7 are listed in Tables 8-11 in the

Examples as examples of mutations that can be associated with sensitivity to NAE inhibition, e.g., inhibition by 1-methyl sulfamates, e.g., MLN4924.

[0072] Sequencing methods are known to one skilled in the art. Examples of methods include the Sanger method, the SEQUENOM™ method and Next Generation Sequencing (NGS) methods. The Sanger method, comprising using electrophoresis, e.g., capillary electrophoresis to separate primer-elongated labeled DNA fragments, can be automated for high-throughput applications. The primer extension sequencing can be performed after PCR amplification of regions of interest. Software can assist with sequence base calling and with mutation identification. SEQUENOM™ MASSARRAY® sequencing analysis (San Diego, CA) is a mass-spectrometry method which compares actual mass to expected mass of particular fragments of interest to identify mutations. NGS technology (also called "massively parallel sequencing" and "second generation sequencing") in general provides for much higher throughput than previous methods and uses a variety of approaches (reviewed in Zhang et al. (2011) J. Genet. Genomics 38:95-109 and Shendure and Hanlee (2008) Nature Biotech. 26:1135-1145). NGS methods can identify low frequency mutations in a marker in a sample. Some NGS methods (see, e.g., GS-FLX Genome Sequencer (Roche Applied Science, Branford, CT), Genome analyzer (Illumina, Inc. San Diego, CA) SOLID™ analyzer (Applied Biosystems, Carlsbad, CA), Polonator G.007 (Dover Systems, Salem, NH), HELISCOPE™ (Helicos Biosciences Corp., Cambridge, MA)) use cyclic array sequencing, with or without clonal amplification of PCR products spatially separated in a flow cell and various schemes to detect the labeled modified nucleotide that is incorporated by the sequencing enzyme (e.g., polymerase or ligase). In one NGS method, primer pairs can be used in PCR reactions to amplify regions of interest. Amplified regions can be ligated into a concatenated product. Clonal libraries are generated in the flow cell from the PCR or ligated products and further amplified ("bridge" or "cluster" PCR) for single-end sequencing as the polymerase adds a labeled, reversibly terminated base that is imaged in one of four channels, depending on the identity of the labeled base and then removed for the next cycle. Software can aid in the comparison to genomic sequences to identify mutations.

[0073] Composition of proteins and nucleic acids can be determined by many ways known in the art, such as by treating them in ways that cleave, degrade or digest them and then analyzing the components. Mass spectrometry, electrophoresis and chromatography can separate and define components for comparison. Mutations which cause deletions or insertions can be identified by size or charge differences in these methods. Protein digestion or restriction enzyme nucleic acid digestion can reveal different fragment patterns after some mutations. Antibodies that recognize particular mutant amino acids in their structural contexts can identify and detect these mutations in samples (see below).

[0074] In an embodiment, DNA, e.g., genomic DNA corresponding to the wild type or mutated marker can be analyzed both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. DNA can be directly isolated from the sample or isolated after isolating another cellular component, e.g., RNA or protein. Kits are available for DNA isolation, e.g., QIAAMP® DNA Micro Kit (Qiagen, Valencia, CA). DNA also can be amplified using such kits.

[0075] In another embodiment, mRNA corresponding to the marker can be analyzed both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. An example of a method for measuring expression level is included in the Examples. For example a nucleic acid probe can be used to hybridize to a marker and the amount of probe hybridized can be measured. Many expression detection methods use isolated RNA. For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from tumor cells (see, *e.g.,* Ausubel et al., ed., Current Protocols in Molecular Biology, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155). RNA can be isolated using standard procedures (see *e.g.,* Chomczynski and Sacchi (1987) Anal. Biochem. 162:156-159), solutions (*e.g.,* trizol, TRI REAGENT® (Molecular Research Center, Inc., Cincinnati, OH; see U.S. Patent No. 5,346,994) or kits (*e.g.,* a QIAGEN® Group RNEASY® isolation kit (Valencia, CA) or LEUKOLOCK™ Total RNA Isolation System, Ambion division of Applied Biosystems, Austin, TX).

[0076] Additional steps may be employed to remove DNA from RNA samples. Cell lysis can be accomplished with a nonionic detergent, followed by microcentrifugation to remove the nuclei and hence the bulk of the cellular DNA. DNA subsequently can be isolated from the nuclei for DNA analysis. In one embodiment, RNA is extracted from cells of the various types of interest using guanidinium thiocyanate lysis followed by CsCl centrifugation to separate the RNA from DNA (Chirgwin et al. (1979) Biochemistry 18:5294-99). Poly(A)+RNA is selected by selection with oligo-dT cellulose (see Sambrook et al. (1989) Molecular Cloning-A Laboratory Manual (2nd ed.), Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.). Alternatively, separation of RNA from DNA can be accomplished by organic extraction, for example, with hot phenol or phenol/chloroform/isoamyl alcohol. If desired, RNAse inhibitors may be added to the lysis buffer. Likewise, for certain cell types, it may be desirable to add a protein denaturation/digestion step to the protocol. For many applications, it is desirable to enrich mRNA with respect to other cellular RNAs, such as transfer RNA (tRNA) and ribosomal RNA (rRNA). Most mRNAs contain a poly(A) tail at their 3' end. This allows them to be enriched by affinity chromatography, for example, using oligo(dT) or poly(U) coupled to a solid support, such as cellulose or SEPHADEX.R™. medium (see Ausubel et al. (1994) Current Protocols In Molecular Biology, vol. 2, Current Protocols Publishing, New York). Once bound, poly(A)+mRNA is eluted from the affinity column using 2 mM EDTA/0.1% SDS.

[0077] The characteristic of a marker of the invention in a biological sample, e.g., after obtaining a biological sample (*e.g.,* a bone marrow sample, a tumor biopsy or a reference sample) from a test subject, may be assessed by any of a wide variety of well known methods for detecting or measuring the characteristic, e.g., of a nucleic acid (*e.g.,* RNA, mRNA, genomic DNA, or cDNA) and/or translated protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods. These methods include gene array/chip technology, RT-PCR, TAQMAN® gene expression assays (Applied Biosystems, Foster City, CA), e.g., under GLP approved laboratory conditions, *in situ* hybridization, immunohistochemistry, immunoblotting, FISH (flourescence *in situ* hybridization), FACS analyses, northern blot, southern blot, INFINIUM® DNA analysis Bead Chips (Illumina, Inc., San Diego, CA), quantitative PCR, bacterial artificial chromosome arrays, single nucleotide polymorphism (SNP) arrays (Affymetrix, Santa Clara, CA) or cytogenetic analyses. The detection methods of the invention can thus be used to detect RNA, mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample *in vitro* as well as *in vivo.* Furthermore, *in vivo* techniques for detection of a polypeptide or nucleic acid corresponding to a marker of the invention include introducing into a subject a labeled probe to detect the biomarker, *e.g*., a nucleic acid complementary to the transcript of a biomarker or a labeled antibody, Fc receptor or antigen directed against the polypeptide, *e.g*., wild type or mutant marker. For example, the antibody can be labeled with a radioactive isotope whose presence and location in a subject can be detected by standard imaging techniques. These assays can be conducted in a variety of ways. A skilled artisan can select from these or other appropriate and available methods based on the nature of the marker(s), tissue sample and mutation in question. Some methods are described in more detail in later sections. Different methods or combinations of methods could be appropriate in different cases or, for instance in different types of tumors or patient populations.

[0078] *In vitro* techniques for detection of a polypeptide corresponding to a marker of the invention include enzyme linked immunosorbent assays (ELISAs), Western blots, protein array, immunoprecipitations and immunofluorescence. In such examples, expression of a marker is assessed using an antibody (*e.g*., a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g*., an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair (*e.g*., biotin-streptavidin)), or an antibody fragment (*e.g*., a single-chain antibody, an isolated antibody hypervariable domain, *etc.*) which binds specifically with a marker protein or fragment thereof, e.g., a protein or fragment comprising a region which can be mutated or a portion comprising a mutated sequence, or a mutated residue in its structural context, including a marker protein which has undergone all or a portion of its normal post-translational modification. An antibody can detect a protein with an amino acid sequence selected from the group consisting of SEQ ID NO:3, 6, 10, 11, 14, 17, 20 and 23. Alternatively, an antibody can detect a mutated protein with a variant amino acid sequence selected from the group consisting of a mutant of SEQ ID NO:3, 6, 10, 11, 14, 17, 20 and 23. Residues listed as mutated in public databases such as COSMIC of dbGaP can be prepared in immunogenic compositions for generation of antibodies that will specifically recognize and bind to the mutant residues. Another method can employ pairs of antibodies, wherein one of the pair would bind a marker protein upstream, i.e. N-terminal to the region of expected mutation, e.g., nonsense or deletion and the other of the pair would bind the protein downstream. Wild type protein would bind both antibodies of the pair, but a protein with a nonsense or deletion mutation would bind only the N-terminal antibody of the pair. An assay such as a sandwich ELISA assay could detect a loss of quantity of the wild type protein in the tumor sample, e.g., in comparison to the reference sample, or a standard ELISA would comparison of the levels of binding of the antibodies to infer that a mutation is present in a tumor sample.

[0079] Indirect methods for determining the amount or functionality of a protein marker also include measurement of the activity of the protein. For example, a sample, or a protein isolated from the sample or expressed from nucleic acid isolated, cloned or amplified from the sample can be assessed for marker protein activity. NF2 activity can be measured by its ability to associate with binding partners, e.g., in a cell-free assay or in a cell-based assay. In an example, the ability of NF2 to bind to red blood cell membranes or p55/MPPI can be measured (Seo et al. (2009) Exp. Biol. Med. 234:255-262). In another example, SMAD4 activity can be measured by its activity in signal transduction, e.g., in a cell-free assay or in a cell-based assay. In an example, the phosphorylation state of SMAD4 can be measured, the binding of SMAD4 to DNA at a Smad-binding element, e.g., in a gel shift assay or in a reporter assay (see, e.g., Kuang and Chen (2004) Oncogene 23:1021-1029), can be measured or the translocation of SMAD4 between the nucleus and cytoplasm can be visualized and quantified on cell images. In another example KDM6A activity can be measured by its ability to demethylate proteins, e.g., histones. For example, an assay can measure the level of demethylation of lysine 27 of histone 3 (Hong et al. (2007) PNAS 104:18439-18444). In another example, FBXW7 activity can be measured by its ability to bind cyclin E or to associate into the Skp-cullin-F-box ubiquitin ligase complex. In another example, TP53 activity can be measured by the ability to bind to DNA or to form tetramers.

[0080] In one embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.,* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide, e.g., an isolated nucleic acid probe, e.g., a hybridization probe, which is a complement of a marker nucleic acid, or a fragment thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods prior to hybrid-

ization with the reference polynucleotide. Expression of one or more markers likewise can be detected using quantitative PCR to assess the level of expression of the marker(s). An example of the use of measuring mRNA levels is that an inactivating mutation in a marker gene can result in an altered level of mRNA in a cell. The level can be upregulated due to feedback signaling protein production in view of nonfunctional or absent protein or downregulated due to instability of an altered mRNA sequence. Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc., discussed above) of a marker of the invention may be used to detect occurrence of a mutation in a marker gene in a patient.

[0081] An example of direct measurement is quantification of transcripts. As used herein, the level or amount of expression refers to the absolute amount of expression of an mRNA encoded by the marker or the absolute amount of expression of the protein encoded by the marker. As an alternative to making determinations based on the absolute expression amount of selected markers, determinations may be based on normalized expression amounts. Expression amount can be normalized by correcting the absolute expression level of a marker upon comparing its expression to the expression of a control marker that is not a marker, *e.g.*, in a housekeeping role that is constitutively expressed. Suitable markers for normalization also include housekeeping genes, such as the actin gene or beta-2 microglobulin. Reference markers for data normalization purposes include markers which are ubiquitously expressed and/or whose expression is not regulated by oncogenes. Constitutively expressed genes are known in the art and can be identified and selected according to the relevant tissue and/or situation of the patient and the analysis methods. Such normalization allows one to compare the expression level in one sample, to another sample, *e.g.*, between samples from different times or different subjects. Further, the expression level can be provided as a relative expression level. The baseline of a genomic DNA sample, *e.g.*, diploid copy number, can be determined by measuring amounts in cells from subjects without a tumor or in non-tumor cells from the patient. To determine a relative amount of a marker or marker set, the amount of the marker or marker set is determined for at least 1, or 2, 3, 4, 5, or more samples, *e.g.*, 7, 10, 15, 20 or 50 or more samples in order to establish a baseline, prior to the determination of the expression level for the sample in question. To establish a baseline measurement, the mean amount or level of each of the markers or marker sets assayed in the larger number of samples is determined and this is used as a baseline expression level for the biomarkers or biomarker sets in question. The amount of the marker or marker set determined for the test sample (*e.g.*, absolute level of expression) is then divided by the baseline value obtained for that marker or marker set. This provides a relative amount and aids in identifying abnormal levels of marker protein activity.

[0082] Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe can comprise a label group attached thereto, *e.g.,* a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

[0083] In addition to the nucleotide sequences described in the database records described herein, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to naturally occuring allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (*e.g.,* by affecting regulation or degradation).

[0084] Primers or nucleic acid probes comprise a nucleotide sequence complementary to a specific a marker or a mutated region thereof and are of sufficient length to selectively hybridize with a marker gene or nucleic acid associated with a marker gene, e.g., they can bind to the nucleic acid with base sequence specificity and remain bound, after washing. Primers and probes can be used to aid in the isolation and sequencing of marker nucleic acids. In one embodiment, the primer or nucleic acid probe, *e.g.,* a substantially purified oligonucleotide, an isolated nucleic acid, comprises a region having a nucleotide sequence which hybridizes, e.g., under stringent conditions, to about 6, 8, 10, 12, 15, 20, 25, 30, 40, 50, 60, 75, 100, 200, 350, 500 or more consecutive nucleotides of a marker gene or a region comprising a mutation in a marker gene or transcript therefrom or a complement. In another embodiment, the primer or nucleic acid probe is capable of hybridizing to a marker nucleic acid comprising a nucleotide sequence of any sequence set forth in any of SEQ ID NOs: 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 or a sequence on chromosome 22q from base pair 29999545 to 30094589, chromosome 18q from base pair 48556583 to 48611412, chromosome Xp from base pair 44732423 to 44971847, chromosome 4q from base pair 153242410 to 153456172, chromosome 17p from base pair 7571720 to 7590868, chromosome 9p from base pair 21967751 to 21994490, or a complement of any of the foregoing. For example, a primer or nucleic acid probe comprising a nucleotide sequence of at least about 10 consecutive nucleotides, at least about 15 consecutive nucleotides, at least about 25 consecutive nucleotides, at least about 35 consecutive nucleotides, at least about 50 consecutive nucleotides, or having from about 15 to about 20 nucleotides set forth in any of SEQ ID NOs: 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 or a sequence on chromosome 22q from base pair 29999545 to 30094589, chromosome 18q from base pair 48556583 to 48611412, chromosome Xp from

base pair 44732423 to 44971847, chromosome 4q from base pair 153242410 to 153456172, chromosome 17p from base pair 7571720 to 7590868, chromosome 9p from base pair 21967751 to 21994490, or a complement of any of the foregoing are provided by the invention. Primers or nucleic acid probes having a sequence of more than about 25, 40 or 50 nucleotides are also within the scope of the invention. In another embodiment, a primer or nucleic acid probe can have a sequence at least 70%, at least 75%, 80% or 85%, or at least, 90%, 95% or 97% identical to the nucleotide sequence of any sequence set forth in any of SEQ ID NOs: 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 or a sequence on chromosome 22q from base pair 29999545 to 30094589, chromosome 18q from base pair 48556583 to 48611412, chromosome Xp from base pair 44732423 to 44971847, chromosome 4q from base pair 153242410 to 153456172, chromosome 17p from base pair 7571720 to 7590868, chromosome 9p from base pair 21967751 to 21994490, or a complement of any of the foregoing. Nucleic acid analogs can be used as binding sites for hybridization. An example of a suitable nucleic acid analogue is peptide nucleic acid (see, *e.g.,* Egholm et al., Nature 363:566 568 (1993); U.S. Pat. No. 5,539,083).

[0085] In some embodiments, nucleic acid probe can be designed to bind to the wild type sequence, so the presence of a mutation in that region can cause a decrease, e.g., measurable decrease, in binding or hybridization by that probe. In another embodiment, a nucleic acid probe can be designed to bind to a mutant sequence, so the presence of a mutation in that region can cause an increase in binding or hybridization by that probe. In other embodiments, a probe and primer set or a primer pair can be designed to bracket a region in a marker that can have a mutation so amplification based on that set or pair can result in nucleic acids which can be sequenced to identify the mutation.

[0086] Primers or nucleic acid probes can be selected using an algorithm that takes into account binding energies, base composition, sequence complexity, cross-hybridization binding energies, and secondary structure (see Friend *et al.,* International Patent Publication WO 01/05935, published Jan. 25, 2001; Hughes et al., Nat. Biotech. 19:342-7 (2001). Useful primers or nucleic acid probes of the invention bind sequences which are unique for each transcript, e.g., target mutated regions and can be used in PCR for amplifying, detecting and sequencing only that particular nucleic acid, e.g., transcript or mutated transcript. Examples of some mutations of marker genes, e.g., NF2, SMAD4, KDM6A and FBXW7 are found in Tables in the Examples (Tables 8-11). Other mutations are described in reference articles cited herein and in public databases described herein. One of skill in the art can design primers and nucleic acid probes for the markers disclosed herein or related markers with similar characteristics, *e.g.*, markers on the chromosome loci, or mutations in different regions of the same marker gene described herein, using the skill in the art, *e.g.*, adjusting the potential for primer or nucleic acid probe binding to standard sequences, mutants or allelic variants by manipulating degeneracy or GC content in the primer or nucleic acid probe. Computer programs that are well known in the art are useful in the design of primers with the required specificity and optimal amplification properties, such as Oligo version 5.0 (National Biosciences, Plymouth, MN). While perfectly complementary nucleic acid probes and primers can be used for detecting the markers described herein and mutants, polymorphisms or alleles thereof, departures from complete complementarity are contemplated where such departures do not prevent the molecule from specifically hybridizing to the target region. For example, an oligonucleotide primer may have a non-complementary fragment at its 5' end, with the remainder of the primer being complementary to the target region. Alternatively, non-complementary nucleotides may be interspersed into the nucleic acid probe or primer as long as the resulting probe or primer is still capable of specifically hybridizing to the target region.

[0087] An indication of treatment outcome can be assessed by studying the amount of 1 marker, 2 markers, 3 markers or 4 markers, or more, *e.g.,* 5, 6, 7, 8, 9, 10, 15, 20, or 25 markers, or mutated portions thereof e.g., marker genes which participate in or interact with the cullin ring ligase pathway e.g., tumor suppressors, e.g., which can be inactivated by somatic mutation in cancer. Markers can be studied in combination with another measure of treatment outcome, *e.g.,* biochemical markers (*e.g.,* M protein in myeloma, kidney health marker such as proteinuria, serum levels of C-reactive protein or cytokeratin 19, cytokeratin fragment 21-1 (CYFRA21-1) for NSCLC, urine levels of fibrinogen/fibrinogen degradation products for bladder cancer, urine or blood levels of catecholamines for neuroblastoma, serum levels of carbohydrate antigen 19-9 (CA 19-9) or metabolic profiling for pancreatic cancer or blood levels of soluble mesothelin-related peptides (SMRP) in mesothelioma) or histology assessment (e.g., blast count, number of mitotic figures per unit area, depth measurement of invasion of melanoma tumors, esophageal tumors or bladder tumors).

[0088] Statistical methods can assist in the determination of treatment outcome upon measurement of the amount of markers, *e.g.*, measurement of DNA, RNA or protein. The amount of one marker can be measured at multiple timepoints, *e.g.*, before treatment, during treatment, after treatment with an agent, *e.g.,* an NAE inhibitor. To determine the progression of change in expression of a marker from a baseline, *e.g.*, over time, the expression results can be analyzed by a repeated measures linear regression model (Littell, Miliken, Stroup, Wolfinger, Schabenberger (2006) SAS for Mixed Models, 2nd edition. SAS Institute, Inc., Cary, NC)):

Equation 1

$$Y_{ijk} - Y_{ij0} = Y_{ij0} + treatment_i + day_k + (treatment * day)_{ik} + \varepsilon_{ijk}$$

where Y_{ijk} is the $\log_2$ transformed expression (normalized to the housekeeping genes) on the k^{th} day of the j^{th} animal in the i^{th} treatment, Y_{ij0} is the defined baseline $\log_2$ transformed expression (normalized to the housekeeping genes) of the j^{th} animal in the i^{th} treatment, day_k is treated as a categorical variable, and ε_{ijk} is the residual error term. A covariance matrix (*e.g.*, first-order autoregressive, compound symmetry, spatial power law) can be specified to model the repeated measurements on each animal over time. Furthermore, each treatment time point can be compared back to the same time point in the vehicle group to test whether the treatment value was significantly different from vehicle.

[0089] A number of other methods can be used to analyze the data. For instance, the relative expression values could be analyzed instead of the cycle number. These values could be examined as either a fold change or as an absolute difference from baseline. Additionally, a repeated-measures analysis of variance (ANOVA) could be used if the variances are equal across all groups and time points. The observed change from baseline at the last (or other) time point could be analyzed using a paired t-test, a Fisher exact test (p-value = $\sum$ P(X=x) from x=1 to the number of situations, e.g., mutations, tested that show sensitivity to NAE inhibition) for testing significance of data of small sample sizes, or a Wilcoxon signed rank test if the data is not normally distributed, to compare whether a tumor patient was significantly different from a normal subject.

[0090] A difference in amount from one timepoint to the next or from the tumor sample to the normal sample can indicate prognosis of treatment outcome. A baseline level can be determined by measuring expression at 1, 2, 3, 4, or more times prior to treatment, e.g., at time zero, one day, three days, one week and/or two weeks or more before treatment. Alternatively, a baseline level can be determined from a number of subjects, *e.g.*, normal subjects or patients with the same health status or disorder, who do not undergo or have not yet undergone the treatment, as discussed above. Alternatively, one can use expression values deposited with the Gene Expression Omnibus (GEO) program at the National Center for Biotechnology Information (NCBI, Bethesda, MD). For example, datasets of myeloma mRNA expression amounts sampled prior to proteasome inhibition therapy include GEO Accession number GSE9782, also analyzed in Mulligan, et al. (2006) Blood 109:3177-88 and GSE6477, also analyzed by Chng et al. (2007) Cancer Res. 67:292-9. To test the effect of the treatment on the tumor, the expression of the marker can be measured at any time or multiple times after some treatment, *e.g.*, after 1 day, 2 days, 3 days, 5 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 1 month, 2 months, 3 months and/or 6 or more months of treatment. For example, the amount of a marker can be measured once after some treatment, or at multiple intervals, *e.g.*, 1-week, 2-week, 4-week or 2-month, 3-month or longer intervals during treatment. In some embodiments, the measurement of a marker during treatment can be compared to the same marker measurement at baseline. In other embodiments, the measurement of a marker during treatment can be compared to the same marker measurement at an earlier timepoint. Conversely, to determine onset of progressive disease after stopping the administration of a therapeutic regimen, the amount of the marker can be measured at any time or multiple times after, *e.g.,* 1 day, 2 days, 3 days, 5 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 1 month, 2 months, 3 months and/or 6 or more months after the last treatment. The measurement of a marker after treatment can be compared to the same marker measurement at the end of treatment. One of skill in the art would determine the timepoint or timepoints to assess the amount of the marker depending on various factors, *e.g.,* the pharmacokinetics of the treatment, the treatment duration, pharmacodynamics of the treatment, age of the patient, the nature of the disorder or mechanism of action of the treatment. A trend in the negative direction or a decrease in the amount relative to baseline or a pre-determined standard of expression of a marker of sensitivity to NAE inhibition therapy, e.g., a decrease in a sensitivity marker identified in Table 3, can indicate a decrease in response of the tumor to the therapy, *e.g.*, increase in resistance. A trend toward a favorable outcome relative to the baseline or a pre-determined standard of expression of a marker of treatment outcome indicates usefulness of the therapeutic regimen or continued benefit of the therapy. A trend toward an increase in a resistance marker e.g., an increase in a resistance marker identified in Table 3, can indicate an unfavorable outcome.

[0091] Any marker, *e.g.,* marker gene or combination of marker, *e.g.,* marker genes of the invention, or mutations thereof as well as any known markers in combination with the markers, *e.g.*, marker genes of the invention, may be used in the compositions, kits, and methods of the present invention. In general, markers are selected for as great as possible ability to judge mutational status of a marker gene to predict outcome of treatment with NAE inhibitor. For example, the choice of markers are selected for as great as possible difference between the characteristic, e.g., size, sequence, composition or amount of the marker in samples comprising tumor cells and the characteristic, e.g., size, sequence, composition or amount of the same marker in control cells. Although this difference can be as small as the limit of detection of the method for assessing the amount of the marker, in another embodiment, the difference can be at least greater than the standard error of the assessment method. In the case of RNA or protein amount, a difference can be at least 1.5-, 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater. "Low" RNA or protein amount can be that expression relative to the overall mean across tumor samples (*e.g.*, hematological tumor, *e.g.*, myeloma) is low. In the case of amount of DNA, e.g., copy number, the amount is 0, 1, 2, 3, 4, 5, 6, or more copies. A deletion causes the copy number to be 0 or 1; an amplification causes the copy number to be greater than 2. The difference can be qualified by a confidence level, e.g., $p < 0.05$, $p < 0.02$, $p < 0.01$ or lower p-value.

[0092] Measurement of more than one marker, *e.g.,* a set of 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, or 25 or more markers

can provide an expression profile or a trend indicative of treatment outcome. In some embodiments, the marker set comprises no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, or 25 markers. In some embodiments, the marker set includes a plurality of chromosome loci, a plurality of marker genes, or a plurality of markers of one or more marker genes (e.g., nucleic acid and protein, genomic DNA and mRNA, or various combinations of markers described herein). Analysis of treatment outcome through assessing the amount of markers in a set can be accompanied by a statistical method, *e.g.,* a weighted voting analysis which accounts for variables which can affect the contribution of the amount of a marker in the set to the class or trend of treatment outcome, *e.g.*, the signal-to-noise ratio of the measurement or hybridization efficiency for each marker. A marker set, *e.g.,* a set of 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, or 25 or more markers, can comprise a primer, probe or primers to analyze at least one marker DNA or RNA described herein, *e.g.,* a marker on chromosome 22q from base pair 29999545 to 30094589, chromosome 18q from base pair 48556583 to 48611412, chromosome Xp from base pair 44732423 to 44971847, chromosome 4q from base pair 153242410 to 153456172, chromosome 17p from base pair 7571720 to 7590868, chromosome 9p from base pair 21967751 to 21994490, NF2, SMAD4, KDM6A, FBXW7, TP53, CDKN2A, CDKN2A_p14, or a complement of any of the foregoing. A marker set, e.g., a set of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, or 25 or more markers, can comprise a primer, probe or primers to detect at least one or at least two or more markers, or at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, or 25 or more mutations on the markers *e.g.*, of NF2, SMAD4, KDM6A, TP53, CDKN2A, CDKN2A_p14 and/or FBXW7. In another embodiment, a marker set can comprise markers for assessing characteristics of NF2, SMAD4 and/or KDM6A. In an embodiment, a marker set for cancer of the uterus or cervix comprises at least one marker for assessing at least one characteristic of FBXW7. In an embodiment, a marker set for cancer of the intestine, breast, lung, head and neck, cervix or skin comprises at least one marker for assessing at least one characteristic of TP53. In an embodiment, a marker set for cancer of the intestine comprises markers for assessing at least one characteristic of each of TP53 and APC. In an embodiment, a marker set for cancer of the skin or central nervous system comprises at least one marker for assessing at least one characteristic of CDKN2A_p14. In an embodiment, a marker set for cancer of the head and neck or skin comprises at least one marker for assessing at least one characteristic of CDKN2A. In an embodiment, a marker set for cancer of the head and neck comprises at least one marker for assessing at least one characteristic of SMAD4. Selected marker sets can be assembled from the markers provided herein or selected from among markers using methods provided herein and analogous methods known in the art. A way to qualify a new marker for use in an assay of the invention is to correlate DNA copy number in a sample comprising tumor cells with differences in expression (e.g., fold-change from baseline) of a marker, *e.g.,* a marker gene. A useful way to judge the relationship is to calculate the coefficient of determination r2, after solving for r, the Pearson product moment correlation coefficient and/or preparing a least squares plot, using standard statistical methods. A correlation can analyze DNA copy number versus the level of expression of marker, *e.g.,* a marker gene. A gene product can be selected as a marker if the result of the correlation (r2, e.g., the linear slope of the data in this analysis), is at least 0.1- 0.2, at least 0.3-0.5, or at least 0.6-0.8 or more. Markers can vary with a positive correlation to response, TTP or survival (i.e., change expression levels in the same manner as copy number, e.g., decrease when copy number is decreased). Markers which vary with a negative correlation to copy number (i.e., change expression levels in the opposite manner as copy number levels, e.g., increase when copy number is decreased) provide inconsistent determination of outcome.

[0093] Another way to qualify a new marker for use in the assay would be to assay the expression of large numbers of markers in a number of subjects before and after treatment with a test agent. The expression results allow identification of the markers which show large changes in a given direction after treatment relative to the pre-treatment samples. One can build a repeated-measures linear regression model to identify the genes that show statistically significant changes or differences. To then rank these significant genes, one can calculate the area under the change from *e.g.*, baseline vs time curve. This can result in a list of genes that would show the largest statistically significant changes. Then several markers can be combined together in a set by using such methods as principle component analysis, clustering methods (*e.g.*, k-means, hierarchical), multivariate analysis of variance (MANOVA), or linear regression techniques. To use such a gene (or group of genes) as a marker, genes which show 2-, 2.5-, 3-, 3.5-, 4-, 4.5-, 5-, 7-, 10- fold, or more differences of expression from baseline would be included in the marker set. An expression profile, *e.g.,* a composite of the expression level differences from baseline or reference of the aggregate marker set would indicate at trend, *e.g.,* if a majority of markers show a particular result, *e.g.,* a significant difference from baseline or reference, e.g., 60%, 70%, 80%, 90%, 95% or more markers; or more markers, *e.g.*, 10% more, 20% more, 30% more, 40% more, show a significant result in one direction than the other direction.

[0094] In embodiments when the compositions, kits, and methods of the invention are used for characterizing treatment outcome in a patient, the marker or set of markers of the invention is selected such that a significant result is obtained in at least about 20%, at least about 40%, 60%, or 80%, or in substantially all patients treated with the test agent. The marker or set of markers of the invention can be selected such that a positive predictive value (PPV) of greater than about 10% is obtained for the general population and additional confidence in a marker can be inferred when the PPV is coupled with an assay specificity greater than 80%.

Therapeutic Agents

[0095] The markers and marker sets of the present invention assess the likelihood of favorable outcome of therapy (e.g., sensitivity to a therapeutic agent) in patients, e.g., cancer patients, *e.g.,* patients having a hematological cancer (*e.g.,* multiple myeloma, leukemias, lymphoma, etc) or solid tumor cancer (e.g., skin cancer such as melanoma, head and neck cancer, such as esophageal cancer, bladder cancer, lung cancer, such as non-small cell lung cancer (NSCLC), adenocarcinoma of the lung, central nervous system cancer such as lung metastases in the brain or neuroblastoma, pancreatic cancer, breast cancer, mesothelioma, cervical cancer or intestinal cancer such as colon or rectum adenocarcinoma), based on its ability to affect the characteristic, e.g., composition or amount of a marker or markers of the invention. Using this prediction, cancer therapies can be evaluated to design a therapy regimen best suitable for patients in either category.

[0096] In particular, the methods can be used to predict patient sensitivity to NAE inhibitors as described in earlier sections. The agents tested in the present methods can be a single agent or a combination of agents. The methods of the invention include combination of NAE inhibition therapy with proteasome inhibition therapy and/or other or additional agents, e.g., selected from the group consisting of chemotherapeutic agents. For example, the present methods can be used to determine whether a single chemotherapeutic agent, such as an NAE inhibitor (*e.g*., MLN4924) can be used to treat a cancer or whether a one or more agents should be used in combination with the NAE inhibitor (*e.g*., MLN4924). Useful combinations can include agents that have different mechanisms of action, *e.g.,* the use of an anti-mitotic agent in combination with an alkylating agent and an NAE inhibitor.

[0097] As used herein, the term "proteasome inhibitor" refers to any substance which directly inhibits enzymatic activity of the 20S or 26S proteasome *in vitro* or *in vivo.* In some embodiments, the proteasome inhibitor is a peptidyl boronic acid. Examples of peptidyl boronic acid proteasome inhibitors suitable for use in the methods of the invention are disclosed in Adams et al., U.S. Patent Nos. 5,780,454 (1998), 6,066,730 (2000), 6,083,903 (2000); 6,297,217 (2001), 6,465,433 (2002), 6,548,668 (2003), 6,617,317 (2003), and 6,747,150 (2004). In some embodiments, the peptidyl boronic acid proteasome inhibitor is selected from the group consisting of: N (4 morpholine)carbonyl-β-(1-naphthyl)-L-alanine-L-leucine boronic acid; N (8 quinoline)sulfonyl-β-(1-naphthyl)-L-alanine-L-alanine-L-leucine boronic acid; N (pyrazine)carbonyl-L-phenylalanine-L-leucine boronic acid, and N (4 morpholine)¬carbonyl-[O-(2-pyridylmethyl)]-L-tyrosine-L-leucine boronic acid. In a particular embodiment, the proteasome inhibitor is N (pyrazine)carbonyl-L-phenylalanine-L-leucine boronic acid (bortezomib; VELCADE®; formerly known as MLN341 or PS-341). Publications describe the use of the disclosed boronic ester and boronic acid compounds to reduce the rate of muscle protein degradation, to reduce the activity of NF-kB in a cell, to reduce the rate of degradation of p53 protein in a cell, to inhibit cyclin degradation in a cell, to inhibit the growth of a cancer cell, and to inhibit NF-kB dependent cell adhesion. Bortezomib specifically and selectively inhibits the proteasome by binding tightly (Ki=0.6 nM) to one of the enzyme's active sites. Bortezomib is selectively cytotoxic, and has a novel pattern of cytotoxicity in National Cancer Institute (NCI) in vitro and in vivo assays. Adams J, et al. Cancer Res 59:2615-22.(1999).

[0098] Additionally, proteasome inhibitors include peptide aldehyde proteasome inhibitors (Stein et al., U.S. Patent No. 5,693,617 (1997); Siman et al., international patent publication WO 91/13904; Iqbal et al., J. Med. Chem. 38:2276-2277 (1995); and Iinuma *et al.,* international patent publication WO 05/105826, peptidyl epoxy ketone proteasome inhibitors (Crews et al., U.S. Patent No. 6,831,099; Smyth et al., international patent publication WO 05/111008; Bennett et al., international patent publication WO 06/045066; Spaltenstein et al. Tetrahedron Lett. 37:1343 (1996); Meng, Proc. Natl. Acad. Sci. 96: 10403 (1999); and Meng, Cancer Res. 59: 2798 (1999)), alpha-ketoamide proteasome inhibitors (Chatterjee and Mallamo, U.S. Patent Nos. 6,310,057 (2001) and 6,096,778 (2000); and Wang et al., U.S. Patent Nos. 6,075,150 (2000) and 6,781,000 (2004)), peptidyl vinyl ester proteasome inhibitors (Marastoni et al., J. Med. Chem. 48:5038 (2005), and peptidyl vinyl sulfone and 2-keto-1,3,4-oxadiazole proteasome inhibitors, such as those disclosed in Rydzewski et al., J. Med. Chem. 49:2953 (2006); and Bogyo et al., Proc. Natl. Acad. Sci. 94:6629 (1997)), azapeptoids and (Bouget et al., Bioorg. Med. Chem. 11:4881 (2003); Baudy-Floc'h *et al.,* international patent publication WO 05/030707; and Bonnemains *et al.,* international patent publication WO 03/018557), efrapeptin oligopeptides (Papathanassiu, international patent publication WO 05/115431), lactacystin and salinosporamide and analogs thereof (Fenteany *et al.,* U.S. Patent Nos. 5,756,764 (1998), 6,147,223 (2000), 6,335,358 (2002), and 6,645,999 (2003); Fenteany et al., Proc. Natl. Acad. Sci. USA (1994) 91:3358; Fenical *et al.,* international patent publication WO 05/003137; Palladino *et al.,* international patent publication WO 05/002572; Stadler et al., international patent publication WO 04/071382; Xiao and Patel, U.S. patent publication 2005/023162; and Corey, international patent publication WO 05/099687).

[0099] Additional therapeutic agents for use in combination with an NAE inhibitor (*e.g*., MLN4924) in the methods of the invention can comprise a known class of therapeutic agents comprising glucocorticoid steroids. Glucocorticoid therapy generally comprises at least one glucocorticoid agent (*e.g*., dexamethasone). In certain applications of the invention, the agent used in methods of the invention is a glucocorticoid agent. One example of a glucocorticoid utilized in the treatment of multiple myeloma patients as well as other cancer therapies is dexamethasone. Additional glucocorticoids utilized in treatment of hematological and combination therapy in solid tumors include hydrocortisone, predisolone,

prednisone, and triamcinolone.

[0100] Other therapeutic agents for use in combination with NAE inhibition therapy include chemotherapeutic agents. A "chemotherapeutic agent" is intended to include chemical reagents which inhibit the growth of proliferating cells or tissues wherein the growth of such cells or tissues is undesirable. Chemotherapeutic agents such as antimetabolic agents, *e.g.,* Ara AC, 5-FU and methotrexate, antimitotic agents, *e.g.,* taxane, vinblastine and vincristine, alkylating agents, *e.g.*, melphanlan, Carmustine (BCNU) and nitrogen mustard, Topoisomerase II inhibitors, *e.g.*, VW-26, topotecan and Bleomycin, strand-breaking agents, *e.g.*, doxorubicin and Mitoxantrone (DHAD), cross-linking agents, *e.g.*, cisplatin and carboplatin (CBDCA), radiation and ultraviolet light and are well known in the art (see *e.g.*, Gilman A.G., et al., The Pharmacological Basis of Therapeutics, 8th Ed., Sec 12:1202-1263 (1990)), and are typically used to treat neoplastic diseases. Examples of chemotherapeutic agents generally employed in chemotherapy treatments are listed below in Table 2.

TABLE 2: Chemotherapeutic Agents

CLASS	TYPE OF AGENT	NONPROPRIETARY NAMES (OTHER NAMES)
Alkylating	Nitrogen Mustards	Mechlorethamine (HN_2) Cyclophosphamide Ifosfamide Melphalan (L-sarcolysin) Chlorambucil
	Ethylenimines And Methylmelamines	Hexamethylmelamine Thiotepa
	Alkyl Sulfonates	Busulfan
Alkylating	Nitrosoureas	Carmustine (BCNU) Lomustine (CCNU) Semustine (methyl-CCNU) Streptozocin (streptozotocin)
Alkylating	Triazenes	Decarbazine (DTIC; dimethyltriazenoimidazolecarboxamide)
	Alkylator	cis-diamminedichloroplatinum II (CDDP)
Antimetabolites	Folic Acid Analogs	Methotrexate (amethopterin)
	Pyrimidine Analogs	Fluorouracil (’5-fluorouracil; 5-FU) Floxuridine (fluorode-oxyuridine; FUdR) Cytarabine (cytosine arabinoside)
	Purine Analogs and Related Inhibitors	Mercaptopuine (6-mercaptopurine; 6-MP) Thioguanine (6-thioguanine; TG) Pentostatin (2’ - deoxycoformycin)
Natural Products	Vinca Alkaloids	Vinblastin (VLB) Vincristine
	Topoisomerase Inhibitors	Etoposide Teniposide Camptothecin Topotecan 9-amino-campotothecin CPT-11
	Antibiotics	Dactinomycin (actinomycin D) Adriamycin Daunorubicin (daunomycin; rubindomycin) Doxorubicin Bleomycin Plicamycin (mithramycin)

(continued)

CLASS	TYPE OF AGENT	NONPROPRIETARY NAMES (OTHER NAMES)
Natural Products		Mitomycin (mitomycin C) TAXOL Taxotere
	Enzymes	L-Asparaginase
	Biological Response Modifiers	Interfon alfa Interleukin 2
	Platinum Coordination Complexes	cis-diamminedichloroplatinum II (CDDP) Carboplatin
	Anthracendione	Mitoxantrone
	Substituted Urea	Hydroxyurea
Miscellaneous Agents	Methyl Hydraxzine Derivative Adrenocortical Suppressant	Procarbazine (N-methylhydrazine,(MIH) Mitotane (o,p'-DDD) Aminoglutethimide
Hormones and Antagonists	Progestins	Hydroxyprogesterone caproate Medroxyprogesterone acetate Megestrol acetate
	Estrogens	Diethylstilbestrol Ethinyl estradiol
	Antiestrogen	Tamoxifen
	Androgens	Testosterone propionate Fluoxymesterone
	Antiandrogen	Flutamide
	Gonadotropin-releasing Hormone analog	Leuprolide

[0101] The agents tested in the present methods can be a single agent or a combination of agents. For example, the present methods can be used to determine whether a single chemotherapeutic agent, such as methotrexate, can be used to treat a cancer or whether a combination of two or more agents can be used in combination with an NAE inhibitor (*e.g.*, MLN4924). Useful combinations can include agents that have different mechanisms of action, *e.g.*, the use of an anti-mitotic agent in combination with an alkylating agent and an NAE inhibitor.

[0102] The agents disclosed herein may be administered by any route, including intradermally, subcutaneously, orally, intraarterially or intravenously. In one embodiment, administration will be by the intravenous route. Parenteral administration can be provided in a bolus or by infusion.

[0103] The concentration of a disclosed compound in a pharmaceutically acceptable mixture will vary depending on several factors, including the dosage of the compound to be administered, the pharmacokinetic characteristics of the compound(s) employed, and the route of administration. The agent may be administered in a single dose or in repeat doses. Treatments may be administered daily or more frequently depending upon a number of factors, including the overall health of a patient, and the formulation and route of administration of the selected compound(s).

Screens for NAE inhibitors

[0104] The disclosure provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.,* candidate or test compounds or agents (*e.g.,* proteins, peptides, peptidomimetics, peptoids, small molecules or other drugs) which bind to NAE, or other E1 enzyme variant proteins, have a stimulatory or inhibitory effect on, for example, NAE, or other E1 enzyme expression or enzyme activity, or have a stimulatory or inhibitory effect on, for example, the expression or activity of a NAE, or other E1 enzyme substrate or proteins in the E1 enzyme pathway, e.g.,

in the NAE pathway, e.g. with a relationship to the activity of a cullin ring ligase. Compounds thus identified can be used to modulate the activity of target gene products (*e.g.*, NAE, or other E1 enzyme genes) in a therapeutic protocol, to elaborate the biological function of the target gene product, or to identify compounds that disrupt NAE, or other E1 enzyme pathway interactions.

[0105] In one description the disclosure provides a method of identifying a compound as an NAE inhibitor, e.g., as an agent that modulates the drug resistance of a cell, by first contacting a cell comprising at least one mutation in at least one marker gene with a test compound and then measuring the viability of the cell or the inhibition of the growth of the cell. In some descriptions, the cell comprises a resistance gene identified in Table 3. In other descriptions, the cell comprises a sensitivity gene identified in Table 3. The effect of the NAE inhibitor can be compared to a control cell not exposed to the compound. In some descriptions, the effect of an agent on a cell comprising a sensitivity marker gene can be compared with the effect of an agent on a cell comprising a resistance marker gene (see, e.g., Table 3). The compound is identified as modulator of drug resistance or an NAE inhibitor agent when the cell viability or cell growth is decreased. The compounds identified as an NAE inhibitor, e.g., as modulating resistance, that are identified in the foregoing methods are also included within the invention.

Detection Methods

[0106] A general principle of prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

[0107] For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay. One example of such an embodiment includes use of an array or chip which contains a predictive marker or marker set anchored for expression analysis of the sample.

[0108] There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (*N*-hydroxy-succinimide) using techniques known in the art (*e.g.,* biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

[0109] Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

[0110] In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

[0111] In an embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art. The term "labeled", with regard to the probe (*e.g.*, nucleic acid or antibody), is intended to encompass direct labeling of the probe by coupling (*i.e.,* physically linking) a detectable substance to the probe, as well as indirect labeling of the probe by reactivity with another reagent that is directly labeled. An example of indirect labeling includes detection of a primary antibody using a fluorescently labeled secondary antibody. It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (FET, see, for example, Lakowicz et al., U.S. Patent No. 5,631,169; Stavrianopoulos, et al., U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon excitation with incident light of appropriate wavelength, its emitted fluorescent

energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

[0112] In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis (BIA) (see, *e.g.,* Sjolander, S. and Urbaniczky, C. (1991) Anal. Chem. 63:2338-2345 and Szabo et al. (1995) Curr. Opin. Struct. Biol. 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIACORE™). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

[0113] Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P. (1993) Trends Biochem Sci. 18:284-7). Standard chromatographic techniques also can be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.,* Heegaard, N.H. (1998) J. Mol. Recognit. 11:141-8; Hage, D.S., and Tweed, S.A. (1997) J. Chromatogr. B. Biomed. Sci. Appl. 699:499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, *e.g.,* Ausubel et al., ed., Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In some embodiments, non-denaturing gel matrix materials and conditions in the absence of reducing agent are used in order to maintain the binding interaction during the electrophoretic process. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

[0114] The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction and TAQMAN® gene expression assays (Applied Biosystems, Foster City, CA) and probe arrays. One diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe, e.g., a hybridization probe) that can hybridize to the mRNA encoded by the gene or mutant being detected. In some embodiments, nucleic acids comprising mutations of marker genes can be used as probes or primers. The nucleic acid probes or primers of the invention can be single stranded DNA (*e.g.,* an oligonucleotide), double stranded DNA (*e.g.*, double stranded oligonucleotide) or RNA. Primers of the invention refer to nucleic acids which hybridize to a nucleic acid sequence which is adjacent to the region of interest and can be extended over a region of interest, e.g., in a primer extension or amplification reaction, or which covers the region of interest, e.g., a nucleic acid region comprising a marker gene or mutation thereof. A nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 20, 25, 30, 50, 75, 100, 125, 150, 175, 200, 250 or 500 or more consecutive nucleotides of the marker nucleic acid sequence or complement thereof and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention or a complement thereof. The exact length of the nucleic acid probe will depend on many factors that are routinely considered and practiced by the skilled artisan. Nucleic acid probes of the invention may be prepared by chemical synthesis using any suitable methodology known in the art, may be produced by recombinant technology, or may be derived from a biological sample, for example, by restriction digestion. Other suitable probes for use in the diagnostic assays of the invention are described herein. The probe can comprise a label group attached thereto, *e.g.,* a radioisotope, a fluorescent compound, an enzyme, an enzyme co-factor, a hapten, a sequence tag, a protein or an antibody. The nucleic acids can be modified at the base moiety, at the sugar moiety, or at the phosphate backbone. An example of a nucleic acid label is incorporated using SUPER™ Modified Base Technology (Nanogen, Bothell, WA, see U.S. Patent No. 7,045,610). The level of expression can be measured as general nucleic acid levels, *e.g.,* after measuring

the amplified DNA levels (e.g. using a DNA intercalating dye, *e.g.,* the SYBR green dye (Qiagen Inc., Valencia, CA) or as specific nucleic acids, *e.g.*, using a probe based design, with the probes labeled. TAQMAN® assay formats can use the probe-based design to increase specificity and signal-to-noise ratio.

[0115] Such primers or probes can be used as part of a diagnostic test kit for identifying cells or tissues which express the protein, such as by measuring amounts of a nucleic acid molecule transcribed in a sample of cells from a subject, *e.g.*, detecting transcript, mRNA levels or determining whether a gene encoding the protein has been mutated or deleted. Hybridization of an RNA or a cDNA with the nucleic acid probe can indicate that the marker in question is being expressed. The invention further encompasses detecting nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a marker protein (*e.g.*, protein having the sequence of the SEQ ID NOs:3, 6, 10, 11, 14, 17, 20, 23 or 26), and thus encode the same protein. It will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals, e.g., normal samples from individuals. This can be readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Detecting any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (*e.g.,* by affecting regulation or degradation).

[0116] As used herein, the term "hybridizes" is intended to describe conditions for hybridization and washing under which nucleotide sequences that are significantly identical or homologous to each other remain hybridized to each other. In some embodiments, the conditions are such that sequences at least about 70%, at least about 80%, at least about 85%, 90% or 95% identical to each other remain hybridized to each other for subsequent amplification and/or detection. Stringent conditions vary according to the length of the involved nucleotide sequence but are known to those skilled in the art and can be found or determined based on teachings in Current Protocols in Molecular Biology, Ausubel et al., eds., John Wiley & Sons, Inc. (1995), sections 2, 4 and 6. Additional stringent conditions and formulas for determining such conditions can be found in Molecular Cloning: A Laboratory Manual, Sambrook et al., Cold Spring Harbor Press, Cold Spring Harbor, NY (1989), chapters 7, 9 and 11. A non-limiting example of stringent hybridization conditions for hybrids that are at least 10 basepairs in length includes hybridization in 4X sodium chloride/sodium citrate (SSC), at about 65-70°C (or hybridization in 4X SSC plus 50% formamide at about 42-50°C) followed by one or more washes in IX SSC, at about 65-70°C. A non-limiting example of highly stringent hybridization conditions for such hybrids includes hybridization in IX SSC, at about 65-70°C (or hybridization in IX SSC plus 50% formamide at about 42-50°C) followed by one or more washes in 0.3X SSC, at about 65-70°C. A non-limiting example of reduced stringency hybridization conditions for such hybrids includes hybridization in 4X SSC, at about 50-60°C (or alternatively hybridization in 6X SSC plus 50% formamide at about 40-45°C) followed by one or more washes in 2X SSC, at about 50-60°C. Ranges intermediate to the above-recited values, e.g., at 65-70°C or at 42-50°C are also intended to be encompassed by the present invention. Another example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C. A further example of stringent hybridization buffer is hybridization in 1 M NaCl, 50 mM 2-(N-morpholino)ethanesulfonic acid (MES) buffer (pH 6.5), 0.5% sodium sarcosine and 30% formamide. SSPE (1xSSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes each after hybridization is complete The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6($\log_{10}$[Na^+]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1xSSC = 0.165 M). It will also be recognized by the skilled practitioner that additional reagents may be added to hybridization and/or wash buffers to decrease non-specific hybridization of nucleic acid molecules to membranes, for example, nitrocellulose or nylon membranes, including but not limited to blocking agents (*e.g.*, BSA or salmon or herring sperm carrier DNA), detergents (*e.g.,* SDS), chelating agents (*e.g.,* EDTA), Ficoll, polyvinylpyrrolidone (PVP) and the like. When using nylon membranes, in particular, an additional non-limiting example of stringent hybridization conditions is hybridization in 0.25-0.5M NaH_2PO_4, 7% SDS at about 65°C, followed by one or more washes at 0.02M NaH_2PO_4, 1% SDS at 65°C, see *e.g.,* Church and Gilbert (1984) Proc. Natl. Acad. Sci. USA 81:1991-1995, (or alternatively 0.2X SSC, 1% SDS). A primer or nucleic acid probe can be used alone in a detection method, or a primer can be used together with at least one other primer or nucleic acid probe in a detection method. Primers can also be used to amplify at least a portion of a nucleic acid. Nucleic acid probes of the invention refer to nucleic acids which hybridize to the region of interest and which are not further extended. For example, a nucleic

acid probe is a nucleic acid which specifically hybridizes to a mutant region of a biomarker, and which by hybridization or absence of hybridization to the DNA of a patient or the type of hybrid formed can be indicative of the presence or identity of the mutation of the biomarker or the amount of marker activity.

[0117] In one format, the RNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated RNA on an agarose gel and transferring the RNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the nucleic acid probe(s) are immobilized on a solid surface and the RNA is contacted with the probe(s), for example, in an AFFYMETRIX® gene chip array or a SNP chip (Santa Clara, CA) or customized array using a marker set comprising at least one marker indicative of treatment outcome. A skilled artisan can readily adapt known RNA and DNA detection methods for use in detecting the amount of the markers of the present invention. For example, the high density microarray or branched DNA assay can benefit from a higher concentration of tumor cell in the sample, such as a sample which had been modified to isolate tumor cells as described in earlier sections. In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (*e.g.,* at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker nucleic acid. If polynucleotides complementary to or homologous with the marker are differentially detectable on the substrate (*e.g.,* detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (*e.g.,* a "gene chip" microarray of polynucleotides fixed at selected positions). In an embodiment when a method of assessing marker expression is used which involves hybridization of one nucleic acid with another, the hybridization can be performed under stringent hybridization conditions.

[0118] An alternative method for determining the amount of RNA corresponding to a marker of the present invention in a sample involves the process of nucleic acid amplification, *e.g.,* by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, Proc. Natl. Acad. Sci. USA, 88:189-193), self sustained sequence replication (Guatelli et al., 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh et al., 1989, Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi et al., 1988, Bio/Technology 6:1197), rolling circle replication (Lizardi et al., U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to about 30 nucleotides in length and flank a region from about 50 to about 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

[0119] For *in situ* methods, RNA does not need to be isolated from the cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to RNA that encodes the marker.

[0120] In another embodiment of the present invention, a polypeptide corresponding to a marker is detected. In some embodiments, an agent for detecting a polypeptide of the invention is an antibody capable of binding to a polypeptide corresponding to a marker of the invention. In related embodiments, the antibody has a detectable label. Antibodies can be polyclonal, or monoclonal. An intact antibody, or a fragment thereof (*e.g.,* Fab or $F(ab')_2$) can be used.

[0121] A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can readily adapt known protein/antibody detection methods for use in determining whether B cells express a marker of the present invention.

[0122] Another method for determining the level of a polypeptide corresponding to a marker is mass spectrometry. For example, intact proteins or peptides, *e.g.,* tryptic peptides can be analyzed from a sample, *e.g.,* a blood sample, a lymph sample or other sample, containing one or more polypeptide markers. The method can further include treating the sample to lower the amounts of abundant proteins, *e.g.,* serum albumin, to increase the sensitivity of the method. For example, liquid chromatography can be used to fractionate the sample so portions of the sample can be analyzed separately by mass spectrometry. The steps can be performed in separate systems or in a combined liquid chromatography/mass spectrometry system (LC/MS, see for example, Liao, et al. (2004) Arthritis Rheum. 50:3792-3803). The mass spectrometry system also can be in tandem (MS/MS) mode. The charge state distribution of the protein or peptide mixture can be acquired over one or multiple scans and analyzed by statistical methods, e.g. using the retention time and mass-to-charge ratio (m/z) in the LC/MS system, to identify proteins expressed at statistically significant levels differentially in samples from patients responsive or non-responsive to NAE inhibition therapy. Examples of mass spectrometers which can be used are an ion trap system (ThermoFinnigan, San Jose, CA) or a quadrupole time-of-flight mass spectrometer (Applied Biosystems, Foster City, CA). The method can further include the step of peptide mass

fingerprinting, e.g. in a matrix-assisted laser desorption ionization with time-of-flight (MALDI-TOF) mass spectrometry method. The method can further include the step of sequencing one or more of the tryptic peptides. Results of this method can be used to identify proteins from primary sequence databases, *e.g.,* maintained by the National Center for Biotechnology Information, Bethesda, MD, or the Swiss Institute for Bioinformatics, Geneva, Switzerland, and based on mass spectrometry tryptic peptide m/z base peaks.

Electronic Apparatus Readable Arrays

[0123] Electronic apparatus, including readable arrays comprising at least one predictive marker of the present invention is also contemplated for use in conjunction with the methods of the invention. As used herein, "electronic apparatus readable media" refers to any suitable medium for storing, holding or containing data or information that can be read and accessed directly by an electronic apparatus. As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention and monitoring of the recorded information include stand-alone computing apparatus; networks, including a local area network (LAN), a wide area network (WAN) Internet, Intranet, and Extranet; electronic appliances such as personal digital assistants (PDAs), cellular phone, pager and the like; and local and distributed processing systems. As used herein, "recorded" refers to a process for storing or encoding information on the electronic apparatus readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on known media to generate manufactures comprising the markers of the present invention.

[0124] For example, microarray systems are well known and used in the art for assessment of samples, whether by assessment gene expression (*e.g.,* DNA detection, RNA detection, protein detection), or metabolite production, for example. Microarrays for use according to the invention include one or more probes of predictive marker(s) of the invention characteristic of response and/or non-response to a therapeutic regimen as described herein. In one embodiment, the microarray comprises one or more probes corresponding to one or more of markers selected from the group consisting of markers which demonstrate increased expression in short term survivors, and genes which demonstrate increased expression in long term survivors in patients. A number of different microarray configurations and methods for their production are known to those of skill in the art and are disclosed, for example, in U.S. Pat. Nos: 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,556,752; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,561,071; 5,571,639; 5,593,839; 5,624,711; 5,700,637; 5,744,305; 5,770,456; 5,770,722; 5,837,832; 5,856,101; 5,874,219; 5,885,837; 5,919,523; 5981185; 6,022,963; 6,077,674; 6,156,501; 6261776; 6346413; 6440677; 6451536; 6576424; 6610482; 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; 5,848,659; and 5,874,219; Shena, et al. (1998), Tibtech 16:301; Duggan et al. (1999) Nat. Genet. 21:10; Bowtell et al. (1999) Nat. Genet. 21:25; Lipshutz et al. (1999) Nature Genet. 21:20-24, 1999; Blanchard, et al. (1996) Biosensors and Bioelectronics, 11:687-90; Maskos, et al., (1993) Nucleic Acids Res. 21:4663-69; Hughes, et al. (2001) Nat. Biotechol. 19:342, 2001. A tissue microarray can be used for protein identification (see Hans et al. (2004) Blood 103:275-282). A phage-epitope microarray can be used to identify one or more proteins in a sample based on whether the protein or proteins induce auto-antibodies in the patient (Bradford et al. (2006) Urol. Oncol. 24:237-242).

[0125] A microarray thus comprises one or more probes corresponding to one or more markers identified herein, *e.g.,* those indicative of treatment outcome, e.g., to identify wild type marker genes, normal allelic variants and mutations of marker genes. The microarray can comprise probes corresponding to, for example, at least 2, at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 75, or at least 100, biomarkers and/or mutations thereof indicative of treatment outcome. The microarray can comprise probes corresponding to one or more biomarkers as set forth herein. Still further, the microarray may comprise complete marker sets as set forth herein and which may be selected and compiled according to the methods set forth herein. The microarray can be used to assay expression of one or more predictive markers or predictive marker sets in the array. In one example, the array can be used to assay more than one predictive marker or marker set expression in a sample to ascertain an expression profile of markers in the array. In this manner, up to about 44,000 markers can be simultaneously assayed for expression. This allows an expression profile to be developed showing a battery of markers specifically expressed in one or more samples. Still further, this allows an expression profile to be developed to assess treatment outcome.

[0126] The array is also useful for ascertaining differential expression patterns of one or more markers in normal and abnormal (*e.g.,* sample, *e.g.,* tumor) cells. This provides a battery of markers that could serve as a tool for ease of identification of treatment outcome of patients. Further, the array is useful for ascertaining expression of reference markers for reference expression levels. In another example, the array can be used to monitor the time course of expression of one or more markers in the array.

[0127] In addition to such qualitative determination, the invention allows the quantification of marker expression. Thus,

predictive markers can be grouped on the basis of marker sets or outcome indications by the amount of the marker in the sample. This is useful, for example, in ascertaining the outcome of the sample by virtue of scoring the amounts according to the methods provided herein.

[0128] The array is also useful for ascertaining the effect of the expression of a marker on the expression of other predictive markers in the same cell or in different cells. This provides, for example, a selection of alternate molecular targets for therapeutic intervention if patient is predicted to have an unfavorable outcome.

Reagents and Kits

[0129] The invention also encompasses kits for detecting the presence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample (*e.g.* a bone marrow sample, tumor biopsy or a reference sample). Such kits can be used to determine mutational status of at least one marker gene to assess treatment outcome, *e.g.,* determine if a subject can have a favorable outcome, *e.g.,* after NAE inhibitor treatment. For example, the kit can comprise a labeled compound or agent capable of detecting a genomic DNA segment, a polypeptide or a transcribed RNA corresponding to a marker of the invention or a mutation of a marker gene in a biological sample and means for determining the amount of the genomic DNA segment, the polypeptide or RNA in the sample. Suitable reagents for binding with a marker protein include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a marker nucleic acid (*e.g.,* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. The label can be directly attached to the marker binding agent, e.g., probe, e.g., nucleic acid reagent such as a probe or primer or protein reagent, such as a specific binding agent or antibody, or a secondary reagent can comprise a label for indirect labeling. The kit can also contain a control or reference sample or a series of control or reference samples which can be assayed and compared to the test sample. For example, the kit may have a positive control sample, e.g., including one or more markers or mutations described herein, or reference markers, *e.g.* housekeeping markers to standardize the assay among samples or timepoints or reference genomes, *e.g.,* form subjects without tumor *e.g.,* to establish diploid copy number baseline or reference expression level of a marker. By way of example, the kit may comprise fluids (*e.g.,* buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds and one or more sample compartments. The kit of the invention may optionally comprise additional components useful for performing the methods of the invention, *e.g.,* a sample collection vessel, *e.g.,* a tube, and optionally, means for optimizing the amount of marker detected, for example if there may be time or adverse storage and handling conditions between the time of sampling and the time of analysis. For example, the kit can contain means for increasing the number of tumor cells in the sample, as described above, a buffering agent, a preservative, a stabilizing agent or additional reagents for preparation of cellular material or probes for use in the methods provided; and detectable label, alone or conjugated to or incorporated within the provided probe(s). In one exemplary embodiment, a kit comprising a sample collection vessel can comprise *e.g.,* a tube comprising anti-coagulant and/or stabilizer, e.g., an RNA stabilizer, as described above, or known to those skilled in the art. The kit can further comprise components necessary for detecting the detectable label (*e.g.,* an enzyme or a substrate). For marker sets, the kit can comprise a marker set array or chip for use in detecting the biomarkers. Kits also can include instructions for interpreting the results obtained using the kit. The kit can contain reagents for detecting one or more biomarkers, *e.g.,* 2, 3, 4, 5, or more biomarkers described herein.

[0130] In one embodiment, the kit comprises a probe to detect at least one biomarker, e.g., a marker indicative of treatment outcome (*e.g.,* upon NAE inhibitor treatment). In an exemplary embodiment, the kit comprises a nucleic acid probe to detect a marker gene selected from the group consisting of SEQ ID NO: 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 or a sequence on chromosome 22q from base pair 29999545 to 30094589, chromosome 18q from base pair 48556583 to 48611412, chromosome Xp from base pair 44732423 to 44971847, chromosome 4q from base pair 153242410 to 153456172, chromosome 17p from base pair 7571720 to 7590868, chromosome 9p from base pair 21967751 to 21994490, or a complement of any of the foregoing or SEQ ID NO: 3, 6, 10, 11, 14, 17, 20, 23 and/or 26. In some embodiments, the kit comprises a probe to detect a marker selected from the group consisting of NF2, SMAD4, KDM6A, FBXW7, TP53, CDKN2A, CDKN2A_p14 and APC. In other embodiments, the kit comprises a probe to detect a mutation in a marker gene selected from the group consisting of NF2, SMAD4, KDM6A, FBXW7, TP53, CDKN2A, CDKN2A_p14 and APC. In an embodiment, a kit comprises probes to detect a marker set comprising two or more markers from the group consisting of NF2, SMAD4, KDM6A, FBXW7, TP53, CDKN2A, CDKN2A_p14 and APC. In another embodiment, a kit comprises a probe to detect FBXW7 in cancer of the uterus or cervix. In an embodiment, a kit comprises a probe to detect TP53 in cancer of the intestine, breast, lung, head and neck, cervix or skin. In an embodiment, a kit comprises a probe to detect TPC and APC in cancer of the intestine. In an embodiment, a kit comprises a probe to detect CDKN2A_p14 in cancer of the skin or central nervous system. In an embodiment, a kit comprises a probe to detect CDKN2A in cancer of the head and neck or skin. In an embodiment, a kit comprises a probe to detect SMAD4 in cancer of the head and neck. In related embodiments, the kit comprises a nucleic acid probe comprising or derived from (*e.g.,* a fragment, mutant or variant (*e.g.,* homologous or complementary) thereof) a nucleic acid sequence

selected from the group consisting of SEQ ID NOs: 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, and 25. For kits comprising nucleic acid probes, *e.g.,* oligonucleotide-based kits, the kit can comprise, for example: one or more nucleic acid reagents such as an oligonucleotide (labeled or non-labeled) which hybridizes to a nucleic acid sequence corresponding to a marker of the invention, optionally fixed to a substrate; and can optionally further comprise labeled oligonucleotides not bound with a substrate, a primer, a pair of PCR primers, e.g., useful for amplifying a nucleic acid molecule corresponding to a marker of the invention, molecular beacon probes, a marker set comprising oligonucleotides which hybridize to at least two nucleic acid sequences corresponding to markers of the invention, and the like. The kit can contain an RNA-stabilizing agent.

[0131] For kits comprising protein probes, *e.g.,* ligand or antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.,* attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable label. The kit can contain a protein stabilizing agent. The kit can contain reagents to reduce the amount of non-specific binding of non-biomarker material from the sample to the probe. Examples of reagents to reduce non-specific binding include nonioinic detergents, non-specific protein containing solutions, such as those containing albumin or casein, or other substances known to those skilled in the art.

[0132] An isolated polypeptide corresponding to a predictive marker of the invention, or a fragment or mutant thereof, can be used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. For example, an immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.,* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. In still a further aspect, the invention provides monoclonal antibodies or antigen binding fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 8, 10, 12, 15, 20 or 25 consecutive amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent.

[0133] Methods for making human antibodies are known in the art. One method for making human antibodies employs the use of transgenic animals, such as a transgenic mouse. These transgenic animals contain a substantial portion of the human antibody producing genome inserted into their own genome and the animal's own endogenous antibody production is rendered deficient in the production of antibodies. Methods for making such transgenic animals are known in the art. Such transgenic animals can be made using XENOMOUSE™ technology or by using a "minilocus" approach. Methods for making XENOMICE™ are described in U.S. Pat. Nos. 6,162,963, 6,150,584, 6,114,598 and 6,075,181. Methods for making transgenic animals using the "minilocus" approach are described in U.S. Pat. Nos. 5,545,807, 5,545,806 and 5,625,825; also see International Publication No. WO93/12227.

[0134] Antibodies include immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.,* molecules that contain an antigen binding site which specifically binds an antigen, such as a polypeptide of the invention, *e.g.,* an epitope of a polypeptide of the invention. A molecule which specifically binds to a given polypeptide of the invention is a molecule which binds the polypeptide, but does not substantially bind other molecules in a sample, *e.g.,* a biological sample, which naturally contains the polypeptide. For example, antigen-binding fragments, as well as full-length monomeric, dimeric or trimeric polypeptides derived from the above-described antibodies are themselves useful. Useful antibody homologs of this type include (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., Nature 341:544-546 (1989)), which consists of a VH domain; (vii) a single domain functional heavy chain antibody, which consists of a VHH domain (known as a nanobody) see *e.g.,* Cortez-Retamozo, et al., Cancer Res. 64: 2853-2857(2004), and references cited therein; and (vii) an isolated complementarity determining region (CDR), e.g., one or more isolated CDRs together with sufficient framework to provide an antigen binding fragment. Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see *e.g.,* Bird et al. Science 242:423-426 (1988); and Huston et al. Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988). Such single chain antibodies are also intended to be encompassed within the term

"antigen-binding fragment" of an antibody. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies. Antibody fragments, such as Fv, $F(ab')_2$ and Fab may be prepared by cleavage of the intact protein, e.g. by protease or chemical cleavage. The invention provides polyclonal and monoclonal antibodies. Synthetic and genetically engineered variants (See U.S. Pat. No. 6,331,415) of any of the foregoing are also contemplated by the present invention. Polyclonal and monoclonal antibodies can be produced by a variety of techniques, including conventional murine monoclonal antibody methodology e.g., the standard somatic cell hybridization technique of Kohler and Milstein, Nature 256: 495 (1975) the human B cell hybridoma technique (see Kozbor et al., 1983, Immunol. Today 4:72), the EBV-hybridoma technique (see Cole et al., pp. 77-96 In Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., 1985) or trioma techniques. See generally, Harlow, E. and Lane, D. (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; and Current Protocols in Immunology, Coligan et al. ed., John Wiley & Sons, New York, 1994. For diagnostic applications, the antibodies can be monoclonal antibodies, e.g., generated in mouse, rat, or rabbit. Additionally, for use in *in vivo* applications the antibodies of the present invention can be human or humanized antibodies. Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, *e.g.,* using a standard ELISA assay.

[0135] If desired, the antibody molecules can be harvested or isolated from the subject (*e.g.,* from the blood or serum of the subject) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected or (*e.g.,* partially purified) or purified by, *e.g.,* affinity chromatography to obtain substantially purified and purified antibody. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein or polypeptide of the invention, and at most 20%, at most 10%, or at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

[0136] An antibody directed against a polypeptide corresponding to a marker of the invention (*e.g.,* a monoclonal antibody) can be used to detect the marker (*e.g.,* in a cellular sample) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in a blood sample or urine) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

[0137] Accordingly, in one aspect, the invention provides substantially purified antibodies or fragments thereof, and non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence encoded by a marker identified herein. The substantially purified antibodies of the invention, or fragments thereof, can be human, non-human, chimeric and/or humanized antibodies.

[0138] In another aspect, the invention provides non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence which is encoded by a nucleic acid molecule of a predictive marker of the invention. Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies.

[0139] The substantially purified antibodies or fragments thereof may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic loop of a polypeptide of the invention. The substantially purified antibodies or fragments thereof, the non-human antibodies or fragments thereof, and/or the monoclonal antibodies or fragments thereof, of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of the present invention.

[0140] The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the invention is a diagnostic composition comprising a probe of the invention and a pharmaceutically acceptable carrier. In one embodiment, the diagnostic composition contains an antibody of the invention, a detectable moiety, and a pharmaceutically acceptable carrier.

Sensitivity Assays

[0141] A sample of cancerous cells is obtained from a patient. An expression level is measured in the sample for a

marker corresponding to at least one of the markers described herein. A marker set can be utilized comprising markers identified described herein, and put together in a marker set using the methods described herein. Such analysis is used to obtain an expression profile of the tumor in the patient. Evaluation of the expression profile is then used to determine whether the patient is expected to have a favorable outcome and would benefit from treatment, *e.g.*, NAE inhibition therapy (e.g., treatment with a NAE inhibitor (e.g., MLN4924) alone, or in combination with additional agents)), or an alternative agent expected to have a similar effect on survival. Evaluation of the expression profile can also be used to determine whether a patient is expected to have an unfavorable outcome and would benefit from a cancer therapy other than NAE inhibition therapy or would benefit from an altered NAE inhibition therapy regimen. Evaluation can include use of one marker set prepared using any of the methods provided or other similar scoring methods known in the art (e.g., weighted voting, combination of threshold features (CTF), Cox proportional hazards analysis, principal components scoring, linear predictive score, K-nearest neighbor, etc), e.g., using expression values deposited with the Gene Expresion Omnibus (GEO) program at the National Center for Biotechnology Information (NCBI, Bethesda, MD). Still further, evaluation can comprise use of more than one prepared marker set. A NAE inhibition therapy will be identified as appropriate to treat the cancer when the outcome of the evaluation demonstrates a favorable outcome or a more aggressive therapy regimen will be identified for a patient with an expected unfavorable outcome.

[0142] In one aspect, the invention features a method of evaluating a patient, e.g., a patient with cancer, e.g. a hematological cancer (e.g., multiple myeloma, leukemias, lymphoma, etc) or solid tumor cancer (e.g., melanoma, esophageal cancer or bladder cancer) for treatment outcome. The method includes providing an evaluation of the expression of the markers in a marker set of markers in the patient, wherein the marker set has the following properties: it includes a plurality of genes, each of which is differentially expressed as between patients with identified outcome and non-afflicted subjects and it contains a sufficient number of differentially expressed markers such that differential amount (e.g., as compared to a level in a non-afflicted reference sample) of each of the markers in the marker set in a subject is predictive of treatment outcome with no more than about 15%, about 10%, about 5%, about 2.5%, or about 1% false positives (wherein false positive means predicting that a patient as responsive or non-responsive when the subject is not); and providing a comparison of the amount of each of the markers in the set from the patient with a reference value, thereby evaluating the patient.

[0143] Examining the amount of one or more of the identified markers or marker sets in a tumor sample taken from a patient during the course of NAE inhibition therapy, it is also possible to determine whether the therapeutic agent is continuing to work or whether the cancer has become non-responsive (refractory) to the treatment protocol. For example, a patient receiving a treatment of MLN4924 would have tumor cells removed and monitored for the expression of a marker or marker set. If the profile of the amount of one or more markers identified herein more typifies favorable outcome in the presence of the agent, e.g., the NAE inhibitor, the treatment would continue. However, if the profile of the amount of one or more markers identified herein more typifies unfavorable outcome in the presence of the agent, then the cancer may have become resistant to therapy, e.g., NAE inhibition therapy, and another treatment protocol should be initiated to treat the patient. For example, the cancer may comprise a mutation in a marker gene associated with resistance to NAE inhibition.

[0144] Importantly, these determinations can be made on a patient-by-patient basis or on an agent-by-agent (or combinations of agents). Thus, one can determine whether or not a particular NAE inhibition therapy is likely to benefit a particular patient or group/class of patients, or whether a particular treatment should be continued.

Use of Information

[0145] In one method of the disclosure, information, e.g., about the mutational status of a patient's tumor, e.g., the patient's marker(s) characteristic, e.g., size, sequence, composition or amount (e.g., the result of evaluating a marker or marker set described herein), or about whether a patient is expected to have a favorable outcome, is provided (e.g., communicated, e.g., electronically communicated) to a third party, e.g., a hospital, clinic, a government entity, reimbursing party or insurance company (e.g., a life insurance company). For example, choice of medical procedure, whether to pay for a medical procedure, payment by a reimbursing party, or cost for a service or insurance can be function of the information. E.g., the third party receives the information, makes a determination based at least in part on the information, and optionally communicates the information or makes a choice of procedure, payment, level of payment, coverage, etc. based on the information. In the method, informative expression level of a marker or a marker set selected from or derived from Table 1 and/or described herein is determined.

[0146] In one description of the disclosure, a premium for insurance (e.g., life or medical) is evaluated as a function of information about one or more marker expression levels, e.g., a marker or marker set, e.g., a level of expression associated with treatment outcome (e.g., the informative amount). For example, premiums can be increased (e.g., by a certain percentage) if the marker genes of a patient or a patient's marker set described herein have different characteristic, e.g., size, sequence, composition or amount between an insured candidate (or a candidate seeking insurance coverage) and a reference value (e.g., a non-afflicted person) or a reference sample, e.g., matched control. Premiums

can also be scaled depending on the result of evaluating a marker or marker set described herein. For example, premiums can be assessed to distribute risk, e.g., as a function of marker, e.g., the result of evaluating a marker or marker set described herein. In another example, premiums are assessed as a function of actuarial data that is obtained from patients that have known treatment outcomes.

[0147] Information about marker characteristic, e.g., size, sequence, composition or amount, e.g., the result of evaluating a marker or marker set described herein (e.g., the informative amount), can be used, e.g., in an underwriting process for life insurance. The information can be incorporated into a profile about a subject. Other information in the profile can include, for example, date of birth, gender, marital status, banking information, credit information, children, and so forth. An insurance policy can be recommended as a function of the information on marker characteristic, e.g., size, sequence, composition or amount, e.g., the result of evaluating a marker or marker set described herein, along with one or more other items of information in the profile. An insurance premium or risk assessment can also be evaluated as function of the marker or marker set information. In one implementation, points are assigned on the basis of expected treatment outcome.

[0148] In one description of the disclosure, information about marker characteristic, e.g., size, sequence, composition or amount, e.g., the result of evaluating a marker or marker set described herein, is analyzed by a function that determines whether to authorize the transfer of funds to pay for a service or treatment provided to a subject (or make another decision referred to herein). For example, the results of analyzing a characteristic, e.g., size, sequence, composition or amount of a marker or marker set described herein may indicate that a subject is expected to have a favorable outcome, suggesting that a treatment course is needed, thereby triggering an result that indicates or causes authorization to pay for a service or treatment provided to a subject. In one example, informative characteristic, e.g., size, sequence, composition or amount of a marker or a marker set selected from or derived from Table 1 and/or described herein is determined and payment is authorized if the informative amount identifies a favorable outcome. For example, an entity, e.g., a hospital, care giver, government entity, or an insurance company or other entity which pays for, or reimburses medical expenses, can use the result of a method described herein to determine whether a party, e.g., a party other than the subject patient, will pay for services (e.g., a particular therapy) or treatment provided to the patient. For example, a first entity, e.g., an insurance company, can use the outcome of a method described herein to determine whether to provide financial payment to, or on behalf of, a patient, e.g., whether to reimburse a third party, e.g., a vendor of goods or services, a hospital, physician, or other care-giver, for a service or treatment provided to a patient. For example, a first entity, e.g., an insurance company, can use the outcome of a method described herein to determine whether to continue, discontinue, enroll an individual in an insurance plan or program, e.g., a health insurance or life insurance plan or program.

[0149] In one description, the disclosure features a method of providing data. The method includes providing data described herein, e.g., generated by a method described herein, to provide a record, e.g., a record described herein, for determining if a payment will be provided. In some descriptions, the data is provided by computer, compact disc, telephone, facsimile, email, or letter. In some descriptions, the data is provided by a first party to a second party. In some descriptions, the first party is selected from the subject, a healthcare provider, a treating physician, a health maintenance organization (HMO), a hospital, a governmental entity, or an entity which sells or supplies the drug. In some descriptions, the second party is a third party payor, an insurance company, employer, employer sponsored health plan, HMO, or governmental entity. In some descriptions, the first party is selected from the subject, a healthcare provider, a treating physician, an HMO, a hospital, an insurance company, or an entity which sells or supplies the drug and the second party is a governmental entity. In some descriptions, the first party is selected from the subject, a healthcare provider, a treating physician, an HMO, a hospital, an insurance company, or an entity which sells or supplies the drug and the second party is an insurance company.

[0150] In another description, the disclosure features a record (e.g., computer readable record) which includes a list and value of characteristic, e.g., size, sequence, composition or amount for the marker or marker set for a patient. In some descriptions, the record includes more than one value for each marker.

[0151] The present invention will now be illustrated by the following Examples, which are not intended to be limiting in any way.

EXAMPLES

Example 1. Cell line panel screens

[0152] To support clinical development and identify potential biomarkers of tumor sensitivity or resistance, two large cancer cell line panels (Panel 1, N=653 (McDermott et al. (2007) PNAS 104:19936-19941); Panel 2, N=240 (O'Day et al. (2010) Fourth AACR International Conference on Molecular Diagnostics in Cancer Therapeutic Development)) were treated with MLN4924 and cell viability data (IC50, EC50, and POC - Percentage of Control) were generated.

Panel 1 (McDermott et al., *supra*). The cell lines were exposed to three MLN4924 concentrations (20 nM, 200 nM,

and 2 μM) for 72 hours. Viability, i.e., cell number, was quantified by measuring fluorescence of a cell-permeant nucleic acid stain. Mean of triplicate values for each sample were taken and compared to DMSO control to calculate percentage of control. In the results, control or no activity value is given a value of about 1, sensitivity is indicated by a value less than 1, with 0 as death of the entire cell population and resistance indicated by a value greater than 1. A continuum of viability values was obtained for each concentration, so some values were selected as cut-offs for final determination of sensitivity or resistance. For example, median POC values of less than the median value of all POC's recorded in the panel (<0.34) indicated sensitivity, values of 0.34 to 0.75 indicated borderline sensitivity, values greater than the 3rd quartile of all POC's in the panel (>0.75) insensitivity or resistance. In general, a dose response relationship was observed with sensitive cell lines. Final judgment of cell line as sensitive, insensitive or resistant was determined by its viability at 2 μM.

Panel 2 (Ricerca Biosciences, Inc., Bothell, WA). MLN4924 was added in half-log dilutions for 10 concentrations and treated for 72 hours. High-content cell screening by fluorescence microscopy included image analysis to generate several types of data. Results included EC50 values (after measurement of cell numbers, the EC50 concentration was calculated from the inflection point of a curve of percent of control (POC) against log of MLN4924 concentration), IC50 values (from the POC-log MLN4924 plot, IC50 is the concentration at 50% maximal possible response), apoptosis (measurement of activation of caspase 3 plotted against log of MLN4924 concentration, determined as the concentration for >5 fold induction), and mitotic activity (determined by measuring the fold increase of phospho-histone 3). A comparison of EC50 to IC50 (Figure 3) allowed assignment of cell lines to sensitive, insensitive or resistant. Final identification of a cell line as sensitive or resistant was based on the EC50 values. The cutoff for sensitivity is a median EC50 of less than the median value of all POC's recorded in the panel (<0.36), borderline sensitivity was associated with median EC50 of 0.36 to 1.67 and insensitive or resistant cell lines were identified by EC50 greater than the 3rd quartile of all POC's in the panel (>1.67).

[0153] Overlapping cell lines between the panels 1 and 2 (114 overlaps) showed consistent growth inhibition effects (Spearman Correlation coefficient = 0.72). In addition, histology and mutation analysis on each cell line panel as a whole (not just overlapping cell lines), also generated consistent observations between the two panels (Figures 4A and B).

[0154] Fisher's Exact Test using median percentage of control values was used to evaluate associations of individual mutations in the cell lines to MLN4924 sensitivity or resistance. See Table 3 for a summary of p values for selected genes. Genes whose mutations were linked to sensitivity in the Fisher Exact test include NF2, SMAD4, KDM6A, CDKN2A and CDKN2A_p14. RB1 and TP53 were linked to insensitivity.

Table 3. Confidence of mutated marker association with response to MLN4924

Mutated Gene	Total N panel 1	Number sensitive panel 1	Panel 1 p-value	Total N panel 2	Number sensitive panel 2	Panel 2 p-value	Phenotype
NF2	10	8	0.067	5	4	0.187	Sensitive
SMAD4	24	15	0.197	11	6	0.509	Sensitive
KDM6A	6	6	0.019	4	4	0.062	Sensitive
RB1	32	12	0.062	14	17	1.00	Resistant*
TP53	235	112	0.013	98	45	0.107	Resistant
CDKN2A	153	94	0.001	68	38	0.146	Sensitive
CDKN2A_ p14	114	70	0.01	59	33	0.178	Sensitive
* denotes phenotype for RB1 association not conclusive across all cell types. Some tumor types were more associated with resistance than others: tumors from brain, bladder, bone and lung (NSCLC) have p-values of 0.102, 0.205, 0.226, and 0.281, respectively. The result that RB1 is not a sensitivity marker agrees with the result of Jia et al. ((2011) Neoplasia 13:561-569) which excluded the involvement of RB1 in MLN4924 mechanism.							

Example 2. Analysis of Mutation Associations

[0155] One difficulty with correlating mutations of genes in cell lines with sensitivity to a therapeutic agent is that many cell lines have more than one mutated gene. For example, cell line named 8505C from thyroid carcinoma has mutations in BRAF, TP53, NF2 and CDKN2A. In particular, TP53 and CDKN2A mutations co-occurred with other mutations in the cell lines. To learn which mutant is associated with sensitivity or resistance in the cell line panels, sub-analyses were

performed.

[0156] APC vs TP53. In cell line panel 1, 23 cell lines have a mutation in APC. Of these, 18 cell lines also have a mutation in TP53. It was difficult to determine whether APC is a driver of resistance to MLN4924, or just a passenger mutation found frequently in TP53 mutants. Further analysis of the cell lines was undertaken by subtraction of cell lines with double mutants which included TP53 (Table 4).

Table 4. Comparison of TP53 mutant cell lines with APC and other mutant cell lines in panel 1

A.	**Subtract TP53 mutants**		
Gene	**sens(78)**	**res(51)**	**p-value**
RB1	0	2	0.154433
NRAS	7	7	0.285024
APC	2	3	0.30657
SMAD4	2	3	0.30657
BRCA2	0	1	0.395349
FAM123B	0	1	0.395349
MAP2K4	0	1	0.395349
B.	**Subtract APC mutants**		
Gene	**sens(184)**	**res(158)**	**p-value**
TP53	108	110	0.0234828
RB1	12	19	0.0573067
MAP2K4	2	5	0.1665217
C.	**Double Mutants**		
Gene	**sens(190)**	**res(175)**	**p-value**
APC+TP53	4	14	0.00842

[0157] As can be seen in Table 4A, subtracting TP53 mutants from the cell line panel leaves an N too small to allow conclusion of association of remaining mutations with resistance of the TP53 wt cell lines to treatment with MLN4924. After removing all 23 APC mutants, TP53 still appears to be associated with resistance (Table 4B). Nevertheless, cell lines with both APC and TP53 mutations show strong association to resistance (Table 4C). Additionally, a majority of the cell lines in the APC+TP53 mutant subgroup are from intestinal cancer tumor samples (Table 5, which also includes cell lines and data from panel 2 and six panel 1 cell lines which were not included in the original subtractive analysis).

Table 5. Subset of cell lines with mutations in APC and TP53

Cell line	Tumor Tissue Source	Tumor Histology	Viability at 2 μM Panel 1	EC50 Panel 2	Co-occurring mutations
HT55	intestine	colon carcinoma	0.5143		APC:APC:TP53
SW 1116	intestine	colon adenocarcinoma	1.1599	10	APC:APC:KRAS:SMAD4: TP53
COCM1	intestine	colon carcinoma	1.1438		APC:APC:PIK3CA:SMAD4: TP53
LS1034	intestine	adenocarcinoma		3.76	APC:KRAS:TP53
SW 1463	intestine	rectum adenocarcinoma	0.8963		TP53:FBXW7:KRAS:APC

(continued)

Cell line	Tumor Tissue Source	Tumor Histology	Viability at 2 μM Panel 1	EC50 Panel 2	Co-occurring mutations
NCI-H630	intestine	colorectal adenocarcinoma	0.75		APC:TP53
SW1417	intestine	colon adenocarcinoma	0.6374	9.03	APC:TP53:BRAF:PIK3R1
SW837	intestine	rectum adenocarcinoma	0.702	0.694	APC: APC: FAM123B:TP53: FBXW7:KRAS
SW620	intestine	colon adenocarcinoma	0.4928	0.387	APC:TP53:TP53:KRAS: MAP2K4:SM AD4
NCI-H1581	lung NSCLC	squamous cell carcinoma	0.7365		APC:TP53
HCT-15	intestine	colon adenocarcinoma	0.6654	0.836	APC:BRCA2:FAM123B: KRAS:MSH6: PIK3CA: TP53
C2BBe1	intestine	colorectal adenocarcinoma	0.7159		APC:TP53
T84	intestine	colon carcinoma	0.5777	0.556	KRAS:PIK3CA:TP53:APC
SW626	ovary	adenocarcinoma	0.5541		TP53:KRAS:APC
HT29	intestine	colorectal adenocarcinoma	0.4376	0.25	APC: PIK3CA:TP53: BRAF: SMAD4:AP C
LK-2	lung	lung NSCLC	0.2893		TP53:APC:CDKN2A
MKN28	stomach	metastasis	0.2847		APC:TP53:NF1
COLO-205	intestine	colon adenocarcinoma	0.144	0.0923	TP53:BRAF:APC:SMAD4
HGC-27	stomach	gastric carcinoma	0.1291		TP53:APC:PTEN:PIK3CA
NCIH747	intestine	cecum adenocarcinoma		2.07	APC:APC:KRAS:TP53
SKUT1	smooth muscle	leiomyosarcoma		0.0856	APC:APC:PIK3CA:PTEN: PTEN:RB1:T P53:TP53
SK-MEL-30	skin	malignant melanoma	0.7728		APC:NRAS:TP53
COLO320 HSR	intestine	colon adenocarcinoma		1.78	APC:TP53
NCI-H520	lung NSCLC	squamous cell carcinoma	0.5577	0.261	CDKN2A:APC:TP53
NCI-H1703	lung NSCLC	adenosquamous carcinoma	0.1101		TP53:APC:CDKN2A
NCI-H1975	lung	adenocarcinoma	0.3049		TP53:APC:CDKN2A:PIK3CA: EGFR
RCM-1	intestine	rectum adenocarcinoma	0.7666		TP53:KRAS:APC
SK-OV-3	ovary	adenocarcinoma	0.397	10	TP53:PIK3CA:CDKN2A:APC

[0158] Association with histology. It is possible that some TP53 mutations associate with resistance in some types of tumor more than others. TP53 mutant cell lines were analyzed within tissue types by a Mann-Whitney (nonparametric)

test. As can be seen in Figure 5, TP53 mutations are significantly correlated with resistance to MLN4924 in colon cancer cell lines (p-value = 0.04022).

[0159] Similar analysis of associations in other tissues indicates that TP53 mutation is associated with MLN4924 resistance in breast cancer and lung cancer (NSCLC) cell lines.

[0160] Additional mutations were analyzed for possible association of tumor histology with resistance or sensitivity to MLN4924 treatment. Table 6 provides results from analysis of panel 1 and Table 7 provides results from analysis of panel 2, whose smaller size proved a challenge for this type of analysis. The cutoff of association with the tissues was chosen at p-values of < 0.05.

Table 6. Association of mutation with histology in Panel 1

Tumor Tissue Source	Mutation	N mutants this cancer	N wild type this cancer	N mutants all cancers	N wild type all cancers	Association	p-value
Head_Neck	TP53	15	1	111	79	sensitive	0.0001
Head_Neck	CDKN2A	12	4	94	96	sensitive	0.0072
Head_Neck	SMAD4	3	13	15	175	sensitive	0.0262
Cervix	TP53	1	6	124	51	resistant	0.0027
Lung	RB1	2	4	19	156	resistant	0.0178
Bone	RB1	1	5	12	178	sensitive	0.0477

Table 7. Association of mutation with histology in Panel 2

Tumor Tissue Source	Mutation	N mutants this cancer	N wild type this cancer	N mutants all cancers	N wild type all cancers	Association	p-value
skin	CDKN2A	8	1	30	43	resistant	0.0022
skin	CDKN2A.p14	6	3	26	47	resistant	0.0004
skin	TP53	2	7	53	20	resistant	0.0036
CNS	CDKN2A.p14	5	4	26	47	resistant	0.0466*
* p-value for CNS derived from percent of control viability. For skin, p-value derived from EC50.							

[0161] In contrast to the general association of TP53 with resistance to MLN4924, in head and neck cancer, TP53 mutation is associated with sensitivity. A similar contrast was found for CDKN2A mutations in skin and central nervous system (CNS). CDKN2A or CDKN2A.p14 mutations were associated with resistance to MLN4924 treatment in skin and CNS tumor cell lines, despite the general association with CDKN2A mutation and sensitivity to MLN4924 treatment. Tables 6 and 7 also show that TP53 mutations are significantly associated with resistance in cervical cancer and skin cancer; CDKN2A mutations are significantly associated with sensitivity in head and neck cancer; SMAD4 mutations are significantly associated with sensitivity in head and neck cancer; RB1 mutations are significantly associated with resistance in lung cancer; and RB1 mutations are significantly associated with sensitivity in bone cancer.

Example 3. Individual cell line screening results

[0162] The following tables include results of the individual cell line screens which led to conclusions about markers whose mutations confer sensitivity to MLN4924.
Notation of the mutations and explanation of mutation syntax can be found in the COSMIC database.

Table 8. Results of screens of cell lines with mutations in NF2.

Cell line	ORF mutation (SEQ ID NO:2)	Protein mutation (SEQ ID NO:3)	Tumor Tissue Source	Tumor type	Viability at 2 μM Panel 1	EC50 Panel 2	Phenotype	Co-occurring mutations
647-V	c.115-1G>C	p.?	urinary_tract	primary	**0.038**	**0.283**	sensitive	MAP2K4:NF2:RB1:TP53:TP53
ACHN	c.169C>T	p.R57*	kidney	primary	**0.0621**	**0.652**	sensitive	CDKN2A:CDKN2a(p14):N F2
CAL-62	c.643G>T	p.E215*	thyroid	primary	**0.0676**	**0.0837**	sensitive	CDKN2A:CDKN2a(pl4):KRAS: NF2:TP53
NUGC-3	c.683de1A	p.K228fs*23	stomach	primary	**0.098**		sensitive	NF2:TP53
SW1573	c.1_363del363	p.?	lung	primary	**0.1114**		sensitive	CDKN2A:CDKN2a(p14): CTNNB1: KRAS:N F2: PIK 3CA: SMAD4
8505C	c.385G>T	p.E129*	thyroid	primary	**0.1405**		sensitive	BRAF:CDKN2A:NF2:TP53
CaR-1	c. 115_1737del1623	p.?	large_ intestine	primary	**0.3244**		sensitive	CDKN2A:CDKN2a(p14):NF2: STK11:TP53
SN12C	c.115-1G>C	p.?	kidney	primary	**0.3357**		sensitive	NF2:TP53
MDA-MB-231	c.691G>T	p.E231*	breast	primary	**0.5284**	**0.871**	insensitive	BRAF:CDKN2A:CDKN2a(p14): KRAS:NF2:TP53
S-117	c.221G>A	p.W74*	soft_tissue	primary	**0.6412**		resistant	CDKN2A:CDKN2a(p14):NF2: TP53
RL95-2	c.514delA c. 1084C>T	p.R172fs*2 p.Q362*	endometrium	primary		**0.094**	sensitive	BRCA2:BRCA2:HRAS:NF2: NF2:PTEN:PTEN:TP5 3:TP53

Table 9. Results of screens of cell lines with mutations in SMAD4.

Cell line	ORF mutation (SEQ ID NO:5)	Protein mutation (SEQ ID NO:6)	Tumor Tissue Source	Tumor type	Viability at 2 μM Panel 1	EC50 Panel 2	Phenotype	Co-occurring mutations
CAL-27	c.733C>T	p.Q245*	upper_ aerodig estive_tract	primary	0.0271	0.139	sensitive	CDKN2A:SMAD4:TP53
KP-4	c.1_1659del1659	p.0?	pancreas	metastasis	0.0518		sensitive	CDKN2A:CDKN2a(p14):KRAS: SMAD4
GAMG	c.1_249del249	p.?	central_ nervou s_ system	primary	0.0721		sensitive	CDKN2A:CDKN2a(p14): SMAD4:TP53
PANC-03-27	c.905_1659del755	p.?	pancreas	primary	0.0724		sensitive	CDKN2A:CDKN2a(p14):KRAS: SMAD4:TP53
FADU	c.1_1659del1659	p.0?	upper_ aerodig estive_tract	primary	0.073	0.261	sensitive	CDKN2A:SMAD4:TP53:TP53
SW1573	c.1_1659del1659	p.0?	lung	primary	0.1114		sensitive	CDKN2A:CDKN2a(p14): CTNNB1:KRAS:NF2:PIK3 CA: SMAD4
KYSE-150	c.788-1G>A	p.?	oesophagus	primary	0.1279		sensitive	SMAD4:TP53
COLO-205	c.1_667del667	p.?	large_ intestine	primary	0.144	0.0923	sensitive	APC:BRAF:SMAD4:TP53
CAL-33	c.766C>T	p.Q256*	upper_ aerodig estive_tract	primary	0.1445		sensitive	CDKN2A:PIK3CA:SMAD4: TP53
NCI-N87	c.1_955del955	p.?	stomach	metastasis	0.1461		sensitive	SMAD4:TP53
CAPAN-1	c.1028C>G	p.S343*	pancreas	metastasis	0.1473	0.365	sensitive?	BRCA2:CDKN2A:CDKN2a (p14):KRAS:SMAD4:TP 53
YAPC	c.1543de1A	p.R515fs*22	pancreas	primary	0.1871	0.234	sensitive	CDKN2A:CDKN2a(p14):KRAS: SMAD4:TP53
NCI-H2405	c.1_1659del1659	p.0?	lung	metastasis	0.2554		sensitive	BRAF:CDKN2A:CDKN2a(p14): MAP2K4:SMAD4:T P53

(continued)

Cell line	ORF mutation (SEQ ID NO:5)	Protein mutation (SEQ ID NO:6)	Tumor Tissue Source	Tumor type	Viability at 2 μM Panel 1	EC50 Panel 2	Phenotype	Co-occurring mutations
CFPAC-1	c.1_1659del1659	p.0?	pancreas	metastasis	0.2822	6.37	sensitive?	KRAS:SMAD4:TP53
MDA-MB-468	c.1_1659del1659	p.0?	breast	metastasis	0.2965	0.0267	sensitive	PTEN:RB1:SMAD4:TP53
MKN45	c.1_1659del1659	p.0?	stomach	metastasis	0.3614		insensitive	CDKN2A:CDKN2a(p14):SMAD4
BxPC-3	c.1_1659del1659	p.0?	pancreas	primary	0.4186	0.251	insensitive	CDKN2A:CDKN2a(p14):MAP2K4:SMAD4:TP53
HT-29	c.931C>T	p.Q311*	large_intestine	primary	0.4376	0.25	insensitive	APC:APC:BRAF:PIK3CA:SMAD4:TP53
UMC-11	c.1606_1612delCTAGACG	p.L536fs*14	lung	primary	0.4472		insensitive	CDKN2A:CDKN2a(p14):SMAD4:STK11:TP53
SW620	c.955+5G>C	p.?	large_intestine	primary	0.4928	0.387	insensitive	APC:KRAS:MAP2K4:SMAD4:TP53:TP53
PANC-08-13	c.366_367insA	p.C123fs*2	pancreas	primary	0.7767		resistant	CDKN2A:CDKN2a(p14):KRAS:SMAD4
COLO-678	c.1_1659del1659	p.0?	large_intestine	metastasis	0.814		resistant	APC:CDKN2A:CDKN2a(p14):FAM123B:KRAS:SM AD4
CoCM-1	c.956_1659del704	p.?	large_intestine	primary	1.1438		resistant	APC:APC:PIK3CA:SMAD4:TP53
SW954	c.378_379delC T	p.V128fs*14	vulva	primary		0.324	sensitive	SMAD4:TP53

Table 10. Results of screens of cell lines with mutations in KDM6A.

Cell line	ORF mutation (SEQ ID NO:8 or 9)	Protein mutation (SEQ ID NO:10 or 11)	Tumor Tissue Source	Tumor type	Viability at 2 μM Panel 1	EC50 Panel 2	Phenotype	Co-occurring mutations
HCC1806	c.444_564del121	p.0	breast	primary	**0.0116**		sensitive	CDKN2A:CDKN2a(p14): KDM6A:STK11:TP53
KU-19-19	c.2587C>T	p.Q863*	urinary_tract	primary	**0.058**		sensitive	CDKN2A:CDKN2a(p14): KDM6A:NRAS
MIA-PaCa-2	c.1_4206del42 06	p.0?	pancreas	primary	**0.1145**	**0.239**	sensitive	CDKN2A:CDKN2a(p14): KDM6A:KRAS:TP53
KYSE-450	c.385_654del270	p.0	oesophagus	primary	**0.1426**		sensitive	CDKN2A:CDKN2a(p14): EGFR:KDM6A:NOTCH1: TP53:TP53
KYSE-180	c.997C>T	p.Q333*	oesophagus	primary	**0.2154**		sensitive	CDKN2A:CDKN2a(p14): KDM6A:TP53
LS-174T	c.3945_3946ins A	p.E1316fs*17	large_intestine	primary	**0.3262**	**0.137**	sensitive	CTNNB1:KDM6A:KRAS: PIK3CA
BV-173	c.226_384del159	p.0	haematopoietic, lymphoid_tissue	primary		**0.131**	sensitive	CDKN2A:CDKN2a(p14): KDM6A
THP-1	c.1_1923del1923	p.0	haematopoietic, lymphoid_tissue	primary		**0.148**	sensitive	CDKN2A:CDKN2a(p14): KDM6A:NRAS:TP53

Table 11. Sampling of results of screens of cell lines with mutations in FBXW7.

Cell line	ORF mutation (SEQ ID NO:13)	Protein mutation (SEQ ID NO:14)	Tumor Tissue Source	Tumor type	Viability at 2 μM Panel 1	EC50 Panel 2	Phenotype	Co-occurring mutations
AN3CA	c. 1321C>T	p.R441W	Uterus	metastasis	0.1944		sensitive	PTEN: TP53: PIK3R1
ESS-1	c. 1393C>T	p.R465C	Uterus	primary	0.0529		sensitive	FBXW7 : TP53 : PIK3CA : RB1
C-33a	c. 1394G>A	p.R465H	Cervix	primary	0.0822		sensitive	RB1 : TP53: MSH2: PIK3CA : PTEN
HuCCT1	c.881C>G	p.S294*	Liver	primary	0.1262		sensitive	TP53: KRAS
MKN1	c. 1393C>T	p.R465C	Stomach	metastasis	0.4631		insensitive	TP53: PIK3CA
AsPC-1	c. 1393C>T	p.R465C	Pancreas	metastasis	0.9889		resistant	CDKN2A: MAP2K4: KRAS: TP53
RCM-1	c. 1513C>T	p.R505C	Intestine	primary	0.7666		resistant	TP53: KRAS
SW1463	c. 1436G>A	p.R479Q	Intestine	primary	0.8963		resistant	TP53 : KRAS : APC

Example 4. Association of TP53 deletion with Resistance

[0163] Another approach to determine the role of TP53 in responsiveness to MLN4924 was a study in which the TP53 gene was deleted. In earlier studies, the importance of p53 in the rereplication response to MLN4924 seemed to be dependent on the specific genetic manipulation and was expected to closely mirror that of CDT1 overexpression (Cdtl is a substrate of two alternative CRL complexes and is stabilized by MLN4924 in many cell lines). In knockdown studies, p53 appeared to behave similarly to CDT1 knockdown at early timepoints, but not later timepoints, unless higher concentrations of MLN4924 were used. Western blotting suggested efficient p53 protein knockdown by the siRNA SMART-pool, although RNAi generally does not result in the complete loss of protein. Therefore, the residual protein may still affect the response to MLN4924, particularly since MLN4924 results in the stabilization of p53 (Liao et al. (2011) Mol. Cell Proteomics 10: 10. 1074/mcp.MI 11.009183). The viability effect of MLN4924 was assessed on HCT-116 cells that were genetically deleted for p53 together with their parental control.

[0164] Paired isogenic HCT-116 cell lines that were either wild-type (+/+) or null (-/-) for p53 expression (HD PAR-018 and HD 104-001, respectively, Horizon Discovery Ltd) were seeded in separate 384-well plates and then treated the following day with a titration of MLN4924 in triplicate, and incubated for 24, 36, 48 or 72 h, with seeding densities of 1600, 1200, 800, and 400 cells/well, respectively. Following compound incubation, viability of HCT-116 cells was assessed by ATPlite assay (Perkin Elmer) according to the manufacturer's instructions using the LEADseeker imaging system (GE Healthcare).

[0165] HCT-116 *TP53* +/+ cells (MLN4924 LC_{50} = 21 ± 1 nM) demonstrated greater MLN4924 sensitivity at 72 h than HCT-116 *TP53* -/- cells (MLN4924 LC_{50} = 74 ± 5 nM; Figures 6A-D). These results suggest that p53 deficiency makes HCT-116 less sensitive to MLN4924, suggesting that the overarching role of p53 at 72 h is proapoptotic. Earlier time

points reinforce this interpretation, as *TP53* -/- cells have less cell death at the highest drug concentrations at 24, 36, and 48 h. Western blots showed that p21 was still up-regulated by MLN4924 in *TP53* -/-HCT-116 cells. In HCT-116 cells, the stabilization of p21 may be a direct effect of inhibition of CRL4-Cdt2 (Nishitani et al., 2008; Abbas et al., 2008; Kim et al., 2008).

[0166] This result is contrary to the conclusion in Lin et al. (2010) Cancer Res. 70:10310-10320) using the HCT116-/-p53 knockout cells. In that study, it was concluded that the TP53 knockout cells were more susceptible to overall cell death or growth inhibition by MLN4924. The reason the present study comes to a different conclusion than in Lin et al. is the amount of time the cells were treated with MLN4924. In Lin et al, the cells were treated for 8 hours before a washout. In the present studies and in the cell line panels of the earlier examples, the cells were treated with MLN4924 continuously over 72 hours. In the washout, the p53 levels are allowed to stabilize and take advantage of activating alternative pathways than the earlier pathways which were initially inhibited and led to the earlier susceptibility.

Example 5. Isolation of nucleic acid and nucleic acid sequencing methods

[0167] Genomic isolations and DNA sequencing. DNA isolation from cells and tumors is conducted using DNAEASY® isolation kit (Qiagen, Valencia, CA). RNA isolation is conducted using MegaMax (Ambion division of Applied Biosystems, Austin, TX). Genomic isolations are conducted following manufacturer recommend protocols.

[0168] SANGER Sequencing methodology. PCR amplifications are conducted using optimized cycling conditions per gene-exon. Primer extension sequencing is performed using Applied Biosystems BigDye version 3.1. The reactions are then run on Applied Biosystem's 3730x1 DNA Analyzer. Sequencing base calls are done using KBTM Basecaller (Applied Biosystems). Somatic Mutation calls are determined by Mutation Surveyor (SoftGenetics) and confirmed manually by aligning sequencing data with the corresponding reference sequence using Seqman (DNASTAR).

[0169] SEQUENOM sequencing methodology. Sequenom (San Diego, CA) assays are designed using TypePLEX® chemistry with single-base extension. This process consists of three steps: 1) A text file containing the SNPs or mutations of interest and flanking sequence is uploaded at mysequenom.com where it is run through a web based program ProxSNP, 2) The output of ProxSNP is run through PreXTEND and 3) the output of PreXTEND is run through Assay Design which determines the expected mass weight of the extend products to ensure separation between all potential peaks found within a multiplexed reaction.

[0170] PCR primers are then designed to bracket the region identified in the assay design steps. The region of interest is amplied in PCR reactions using the primers. 15 nl of amplified and extended product is spotted on a 384 SpectroCHIP II using a Nanodispenser RS1000. A 3-point calibrant is added to every chip to ensure proper performance of the Sequenom Maldi-tof compact mass spectrometer.

[0171] The SpectroCHIP II is placed in the Sequenom MALDI-TOF compact mass spectrometer. The mass spectrometer is set to fire a maximum of 9 acquisitions for each spot on the 384 well spectroCHIP. TypePLEX Gold kit SpectroCHIP II from Sequenom (10142-2) is used following manufacturers recommended protocols. Analysis is performed using Sequenom analysis software, MassARRAY® Typer Analyzer v4.

[0172] NEXT GENERATION SEQUENCING (NGS) methodology. Targeted NGS using the Illumina platform (Illumina, Inc. San Diego, CA) is used to confirm and identify low frequency mutations in a marker. Primer pairs are designed to amplify coding exons. PCR products are quantified using a PicoGreen assay and combined in equal molar ratios for each sample. The purified products are end-repaired and concatenated by ligation. The concatenated products are used for Hi-Seq 2000 library preparation. The concatenated PCR products are sheared and used to make barcoded Hi-Seq 2000 libraries consisting of 12 barcoded samples per multiplexed pool. The pooled Hi-Seq 2000 libraries undergo clonal amplification by cluster generation on eight lanes of a Hi-Seq 2000 flow cell and are sequenced using 1x100 single-end sequencing on a Hi-Seq 2000. Matching of primary sequencing reads to the human genome build Hg18, as well as SNP analysis are performed using Illumina's CASAVA software version 1.7.1.

General Procedures

Quantitative RT-PCR

[0173] cDNA synthesis and quantitative RT-PCR is performed using ABI Gene Expression Assays, reagents, and ABI PRISM® 7900HT Sequence Detection Systems (Applied Biosystems, Foster City, CA) using the following cycle conditions: hold at 50°C for 2 minutes for AmpErase UNG activation, then 95.0°C for 10 minutes to activate DNA polymerase then run 40 two-part cycles of 95.0°C for 15 seconds and 60.0°C for 1 minute. The dCt is calculated by using the average Ct of control genes B2M (Hs99999907_ml) and RPLPO (Hs99999902_ml). Relative mRNA expression quantification is derived using the Comparative Ct Method (Applied Biosystems). mRNA expression fold change values are generated from a normal sample and corresponding tumor sample.

Sample Handling for myeloma samples

[0174] Upon collection of patient bone marrow aspirate, the myeloma cells are enriched via rapid negative selection. The enrichment procedure employs a cocktail of cell-type specific antibodies coupled with an antibody that binds red blood cells RosetteSep (Stem Cell Technologies). The antibody cocktail has antibodies with the following specificity: CD14 (monocytes), CD2 (T and NK cells), CD33 (myeloid progenitors and monocytes), CD41 (platelets and megakaryocytes), CD45RA (naive B and T cells) and CD66b (granulocytes). The antibodies cross-link the non-myeloma cell types to the red blood cells in the samples. The bound cell types are removed using a modified ficoll density gradient. Myeloma cells are then collected and frozen.

[0175] Total RNA is isolated using a QIAGFN® Group RNEASY® isolation kit (Valencia, CA) and quantified by spectrophotometry.

[0176] DNA is isolated from the flow through fraction of the column used in the RNA isolation method.

Analysis of Myeloma Gene Expression on an Array

[0177] RNA is converted to biotinylated cRNA by a standard T7 based amplification protocol (AFFYMETRIX® Inc., Santa Clara, CA). A small number of samples with ≥0.5 - 2.0 μg are also labeled and subsequently hybridized if 6 μg of cRNA is produced. For the automated T7 amplification procedure, the cDNA and the biotin labeled cRNA are purified using AMPURF® PCR Purification System, following the manufacturer's protocol (AGENCOURT® Bioscience Corporation, Beverly, MA). The cRNA yield is assessed by spectrophotometry and 10 μg of cRNA is fragmented and further processed for triplicate hybridization on the AFFYMETRIX® Human Genome HG-U133A and HG-U133B GFNFCHIP® arrays. In cases where cRNA yield ranged between 6 μg to 10 μg, the entire cRNA sample is fragmented.

[0178] cRNA for each sample is hybridized to the U133A/B arrays in triplicate; operators, chip lots, clinical sites and scanners (GENECHIP® Scanner 3000) are controlled throughout. Background subtraction, smoothing adjustment, noise corrections, and signal calculations are performed with AFFYMETRIX® MAS5.0. Quality control metrics include: percent present call (>25) scale factor (< 11), β-actin 3':5' ratio (<15) and background (<120). Samples that fall outside these metrics are excluded from subsequent analysis.

[0179] The myeloma purity score examines expression of genes known in the literature to be expressed highly in myeloma cells (and their normal plasma precursor cells), to expression of genes known to be expressed highly in erythroid cells, neutrophils and T cells - see list of 14 markers below). The myeloma score= expression of myeloma markers (#1-4 below) / erythroid (#5-7) + neutrophil (#8-11) + T cell (#12-14):

1. 205692_s_at CD38 CD38 antigen (p45) myeloma/plasma cell
2. 201286_at SDC1 syndecan-1 myeloma/plasma cell
3. 201891_s_at B2M beta-2 microglobulin myeloma/plasma cell
4. 211528_x_at B2M beta-2 microglobulin myeloma/plasma cell
5. 37986_at EpoR erythropoetin receptor erythroid cell
6. 209962_at EpoR erythropoetin receptor erythroid cell
7. 205838_at GYPA glycophorinA erythroid cell
8. 203948_s_at MPO myeloperoxidase neutrophil
9. 203591_s_at CSFR3colony stimulating factor 3receptor (granulocyte) neutrophil
10. 204039_at CEBPACCAAT/enhancer bindingprotein (C/EBP), alpha neutrophil
11. 214523_at CEBPECCAAT/enhancer bindingprotein (C/EBP), epsilon neutrophil
12. 209603_at GATA3 GATA binding protein 3 T lymphocyte
13. 209604_s_at GATA4 GATA binding protein 4 T lymphocyte
14. 205456_at CD3ECD3E antigen, epsilon polypeptide T lymphocyte

Samples with a myeloma purity score less than 10 are excluded from further analysis.

Equivalents

[0180] Although embodiments of the invention have been described using specific terms, such description are for illustrative purposes only, and it is to be understood that changes and variations may be made without departing from the invention. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

SEQUENCE LISTING

[0181]

<110> Smith, Peter G Blakemore, Stephen J. Li, Bin Mulligan, George J. Schu, Matthew C. Millennium Pharmaceuticals, Inc.

<120> BIOMARKERS OF RESPONSE TO NAE INHIBITORS

<130> MPI11-009P1RNWO2M

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<151> 2011-10-28

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Cys Gln Leu Gly His Phe Asn Leu Leu Leu Glu Asp Tyr Pro Lys Ala
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Tyr Lys Leu Ala Val Glu Arg Tyr Glu Trp Asn Lys Leu Gln Ser Val
    1250                1255                1260
Lys Ser Ile Val Pro Met Val His Leu Ser Trp Asn Met Ala Arg Asn
1265                1270                1275                1280
Ile Lys Val Ser Asp Pro Lys Leu Phe Glu Met Ile Lys Tyr Cys Leu
```

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                1285                1290                1295
Leu Arg Thr Leu Lys Gln Cys Gln Thr Leu Arg Glu Ala Leu Ile Ala
            1300                1305                1310
Ala Gly Lys Glu Ile Ile Trp His Gly Arg Thr Lys Glu Glu Pro Ala
        1315                1320                1325
His Tyr Cys Ser Ile Cys Glu Val Glu Val Phe Asp Leu Leu Phe Val
    1330                1335                1340
Thr Asn Glu Ser Asn Ser Arg Lys Thr Tyr Ile Val His Cys Gln Asp
1345                1350                1355                1360
Cys Ala Arg Lys Thr Ser Gly Asn Leu Glu Asn Phe Val Val Leu Glu
                1365                1370                1375
Gln Tyr Lys Met Glu Asp Leu Met Gln Val Tyr Asp Gln Phe Thr Leu
            1380                1385                1390
Ala Pro Pro Leu Pro Ser Ala Ser Ser
        1395                1400
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<210> 11
<211> 1401
<212> PRT
<213> Homo sapiens

<400> 11

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Ala Phe Gly Asp Glu Glu Lys Lys Met Ala Ala Gly Lys Ala Ser Gly
            20                  25                  30
Glu Ser Glu Glu Ala Ser Pro Ser Leu Thr Ala Glu Glu Arg Glu Ala
        35                  40                  45
Leu Gly Gly Leu Asp Ser Arg Leu Phe Gly Phe Val Arg Phe His Glu
    50                  55                  60
Asp Gly Ala Arg Thr Lys Ala Leu Leu Gly Lys Ala Val Arg Cys Tyr
65                  70                  75                  80
Glu Ser Leu Ile Leu Lys Ala Glu Gly Lys Val Glu Ser Asp Phe Phe
                85                  90                  95
Cys Gln Leu Gly His Phe Asn Leu Leu Leu Glu Asp Tyr Pro Lys Ala
            100                 105                 110
Leu Ser Ala Tyr Gln Arg Tyr Tyr Ser Leu Gln Ser Asp Tyr Trp Lys
        115                 120                 125
Asn Ala Ala Phe Leu Tyr Gly Leu Gly Leu Val Tyr Phe His Tyr Asn
    130                 135                 140
Ala Phe Gln Trp Ala Ile Lys Ala Phe Gln Glu Val Leu Tyr Val Asp
145                 150                 155                 160
Pro Ser Phe Cys Arg Ala Lys Glu Ile His Leu Arg Val Gly Leu Met
                165                 170                 175
Phe Lys Val Asn Thr Asp Tyr Glu Ser Ser Leu Lys His Phe Gln Leu
            180                 185                 190
Ala Leu Val Asp Cys Asn Pro Cys Thr Leu Ser Asn Ala Glu Ile Gln
        195                 200                 205
Phe His Ile Ala His Leu Tyr Glu Thr Gln Arg Lys Tyr His Ser Ala
    210                 215                 220
Lys Glu Ala Tyr Glu Gln Leu Leu Gln Thr Glu Asn Leu Ser Ala Gln
225                 230                 235                 240
Val Lys Ala Thr Val Leu Gln Gln Leu Gly Trp Met His His Thr Val
                245                 250                 255
Asp Leu Leu Gly Asp Lys Ala Thr Lys Glu Ser Tyr Ala Ile Gln Tyr
            260                 265                 270
Leu Gln Lys Ser Leu Glu Ala Asp Pro Asn Ser Gly Gln Ser Trp Tyr
        275                 280                 285
Phe Leu Gly Arg Cys Tyr Ser Ser Ile Gly Lys Val Gln Asp Ala Phe
    290                 295                 300
Ile Ser Tyr Arg Gln Ser Ile Asp Lys Ser Glu Ala Ser Ala Asp Thr
305                 310                 315                 320
```

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Trp Cys Ser Ile Gly Val Leu Tyr Gln Gln Asn Gln Pro Met Asp
                325                 330                 335
Ala Leu Gln Ala Tyr Ile Cys Ala Val Gln Leu Asp His Gly His Ala
            340                 345                 350
Ala Ala Trp Met Asp Leu Gly Thr Leu Tyr Glu Ser Cys Asn Gln Pro
        355                 360                 365
Gln Asp Ala Ile Lys Cys Tyr Leu Asn Ala Thr Arg Ser Lys Ser Cys
    370                 375                 380
Ser Asn Thr Ser Ala Leu Ala Ala Arg Ile Lys Tyr Leu Gln Ala Gln
385                 390                 395                 400
Leu Cys Asn Leu Pro Gln Gly Ser Leu Gln Asn Lys Thr Lys Leu Leu
                405                 410                 415
Pro Ser Ile Glu Glu Ala Trp Ser Leu Pro Ile Pro Ala Glu Leu Thr
            420                 425                 430
Ser Arg Gln Gly Ala Met Asn Thr Ala Gln Gln Asn Thr Ser Asp Asn
        435                 440                 445
Trp Ser Gly Gly His Ala Val Ser His Pro Pro Val Gln Gln Gln Ala
    450                 455                 460
His Ser Trp Cys Leu Thr Pro Gln Lys Leu Gln His Leu Glu Gln Leu
465                 470                 475                 480
Arg Ala Asn Arg Asn Asn Leu Asn Pro Ala Gln Lys Leu Met Leu Glu
                485                 490                 495
Gln Leu Glu Ser Gln Phe Val Leu Met Gln Gln His Gln Met Arg Pro
            500                 505                 510
Thr Gly Val Ala Gln Val Arg Ser Thr Gly Ile Pro Asn Gly Pro Thr
        515                 520                 525
Ala Asp Ser Ser Leu Pro Thr Asn Ser Val Ser Gly Gln Gln Pro Gln
    530                 535                 540
Leu Ala Leu Thr Arg Val Pro Ser Val Ser Gln Pro Gly Val Arg Pro
545                 550                 555                 560
Ala Cys Pro Gly Gln Pro Leu Ala Asn Gly Pro Phe Ser Ala Gly His
                565                 570                 575
Val Pro Cys Ser Thr Ser Arg Thr Arg Gly Ser Thr Asp Thr Ile Leu
            580                 585                 590
Ile Gly Asn Asn His Ile Thr Gly Asn Gly Ser Asn Gly Asn Val Pro
        595                 600                 605
Tyr Leu Gln Arg Asn Ala Leu Thr Leu Pro His Asn Arg Thr Asn Leu
    610                 615                 620
Thr Ser Ser Ala Lys Glu Pro Trp Lys Asn Gln Leu Ser Asn Ser Thr
625                 630                 635                 640
Gln Gly Leu His Lys Gly Gln Ser Ser His Ser Ala Gly Pro Asn Gly
                645                 650                 655
Glu Arg Pro Leu Ser Ser Thr Gly Pro Ser Gln His Leu Gln Ala Ala
            660                 665                 670
Gly Ser Gly Ile Gln Asn Gln Asn Gly His Pro Thr Leu Pro Ser Asn
        675                 680                 685
Ser Val Thr Gln Gly Ala Ala Leu Asn His Leu Ser Ser His Thr Ala
    690                 695                 700
Thr Ser Gly Gly Gln Gln Gly Ile Thr Leu Thr Lys Glu Ser Lys Pro
705                 710                 715                 720
Ser Gly Asn Ile Leu Thr Val Pro Glu Thr Ser Arg His Thr Gly Glu
                725                 730                 735
Thr Pro Asn Ser Thr Ala Ser Val Glu Gly Leu Pro Asn His Val His
            740                 745                 750
Gln Met Thr Ala Asp Ala Val Cys Ser Pro Ser His Gly Asp Ser Lys
        755                 760                 765
Ser Pro Gly Leu Leu Ser Ser Asp Asn Pro Gln Leu Ser Ala Leu Leu
    770                 775                 780
Met Gly Lys Ala Asn Asn Asn Val Gly Thr Gly Thr Cys Asp Lys Val
785                 790                 795                 800
Asn Asn Ile His Pro Ala Val His Thr Lys Thr Asp Asn Ser Val Ala
                805                 810                 815
Ser Ser Pro Ser Ser Ala Ile Ser Thr Ala Thr Pro Ser Pro Lys Ser
```

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            820                 825                 830
Thr Glu Gln Thr Thr Thr Asn Ser Val Thr Ser Leu Asn Ser Pro His
        835                 840                 845
Ser Gly Leu His Thr Ile Asn Gly Glu Gly Met Glu Glu Ser Gln Ser
    850                 855                 860
Pro Met Lys Thr Asp Leu Leu Leu Val Asn His Lys Pro Ser Pro Gln
865                 870                 875                 880
Ile Ile Pro Ser Met Ser Val Ser Ile Tyr Pro Ser Ser Ala Glu Val
                885                 890                 895
Leu Lys Ala Cys Arg Asn Leu Gly Lys Asn Gly Leu Ser Asn Ser Ser
            900                 905                 910
Ile Leu Leu Asp Lys Cys Pro Pro Pro Arg Pro Pro Ser Ser Pro Tyr
        915                 920                 925
Pro Pro Leu Pro Lys Asp Lys Leu Asn Pro Pro Thr Pro Ser Ile Tyr
    930                 935                 940
Leu Glu Asn Lys Arg Asp Ala Phe Phe Pro Pro Leu His Gln Phe Cys
945                 950                 955                 960
Thr Asn Pro Asn Asn Pro Val Thr Val Ile Arg Gly Leu Ala Gly Ala
                965                 970                 975
Leu Lys Leu Asp Leu Gly Leu Phe Ser Thr Lys Thr Leu Val Glu Ala
            980                 985                 990
Asn Asn Glu His Met Val Glu Val Arg Thr Gln Leu Leu Gln Pro Ala
        995                 1000                1005
Asp Glu Asn Trp Asp Pro Thr Gly Thr Lys Lys Ile Trp His Cys Glu
    1010                1015                1020
Ser Asn Arg Ser His Thr Thr Ile Ala Lys Tyr Ala Gln Tyr Gln Ala
1025                1030                1035                1040
Ser Ser Phe Gln Glu Ser Leu Arg Glu Glu Asn Glu Lys Arg Ser His
                1045                1050                1055
His Lys Asp His Ser Asp Ser Glu Ser Thr Ser Ser Asp Asn Ser Gly
            1060                1065                1070
Arg Arg Arg Lys Gly Pro Phe Lys Thr Ile Lys Phe Gly Thr Asn Ile
        1075                1080                1085
Asp Leu Ser Asp Asp Lys Lys Trp Lys Leu Gln Leu His Glu Leu Thr
    1090                1095                1100
Lys Leu Pro Ala Phe Val Arg Val Val Ser Ala Gly Asn Leu Leu Ser
1105                1110                1115                1120
His Val Gly His Thr Ile Leu Gly Met Asn Thr Val Gln Leu Tyr Met
                1125                1130                1135
Lys Val Pro Gly Ser Arg Thr Pro Gly His Gln Glu Asn Asn Asn Phe
            1140                1145                1150
Cys Ser Val Asn Ile Asn Ile Gly Pro Gly Asp Cys Glu Trp Phe Val
        1155                1160                1165
Val Pro Glu Gly Tyr Trp Gly Val Leu Asn Asp Phe Cys Glu Lys Asn
    1170                1175                1180
Asn Leu Asn Phe Leu Met Gly Ser Trp Trp Pro Asn Leu Glu Asp Leu
1185                1190                1195                1200
Tyr Glu Ala Asn Val Pro Val Tyr Arg Phe Ile Gln Arg Pro Gly Asp
                1205                1210                1215
Leu Val Trp Ile Asn Ala Gly Thr Val His Trp Val Gln Ala Ile Gly
            1220                1225                1230
Trp Cys Asn Asn Ile Ala Trp Asn Val Gly Pro Leu Thr Ala Cys Gln
        1235                1240                1245
Tyr Lys Leu Ala Val Glu Arg Tyr Glu Trp Asn Lys Leu Gln Ser Val
    1250                1255                1260
Lys Ser Ile Val Pro Met Val His Leu Ser Trp Asn Met Ala Arg Asn
1265                1270                1275                1280
Ile Lys Val Ser Asp Pro Lys Leu Phe Glu Met Ile Lys Tyr Cys Leu
                1285                1290                1295
Leu Arg Thr Leu Lys Gln Cys Gln Thr Leu Arg Glu Ala Leu Ile Ala
            1300                1305                1310
Ala Gly Lys Glu Ile Ile Trp His Gly Arg Thr Lys Glu Glu Pro Ala
        1315                1320                1325
```

```
His Tyr Cys Ser Ile Cys Glu Val Glu Val Phe Asp Leu Leu Phe Val
    1330                1335                1340
Thr Asn Glu Ser Asn Ser Arg Lys Thr Tyr Ile Val His Cys Gln Asp
1345                1350                1355                1360
Cys Ala Arg Lys Thr Ser Gly Asn Leu Glu Asn Phe Val Val Leu Glu
                1365                1370                1375
Gln Tyr Lys Met Glu Asp Leu Met Gln Val Tyr Asp Gln Phe Thr Leu
            1380                1385                1390
Ala Pro Pro Leu Pro Ser Ala Ser Ser
        1395                1400
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<210> 12
<211> 3896
<212> DNA
<213> Homo sapiens

<400> 12

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tccaagaagt agcaagctgg cttttggaaa tgaatcagga actgctctct gtgggcagca 180
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agcacactgc aaggaatggt gaagttgttg gagtagaacc tagacctgga ggccaaaatg 360
attcccagca aggacagttg gaagaaaaca ataatagatt tatttcggta gatgaggact 420
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gtagcagaga agatgaacat acacatacta acagtgtcac gaactccagt agtattgtgg 600
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<210> 13
<211> 2124
<212> DNA
<213> Homo sapiens

<400> 13

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<210> 14
<211> 707
<212> PRT
<213> Homo sapiens

<400> 14

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Gly Ser Leu Arg Gly Asn Pro Ser Ser Ser Gln Val Asp Glu Glu Gln
            20                  25                  30
Met Asn Arg Val Val Glu Glu Glu Gln Gln Gln Gln Leu Arg Gln Gln
        35                  40                  45
Glu Glu Glu His Thr Ala Arg Asn Gly Glu Val Val Gly Val Glu Pro
    50                  55                  60
Arg Pro Gly Gly Gln Asn Asp Ser Gln Gln Gly Gln Leu Glu Glu Asn
65                  70                  75                  80
Asn Asn Arg Phe Ile Ser Val Asp Glu Asp Ser Ser Gly Asn Gln Glu
                85                  90                  95
Glu Gln Glu Glu Asp Glu Glu His Ala Gly Glu Gln Asp Glu Glu Asp
            100                 105                 110
Glu Glu Glu Glu Glu Met Asp Gln Glu Ser Asp Asp Phe Asp Gln Ser
        115                 120                 125
Asp Asp Ser Ser Arg Glu Asp Glu His Thr His Thr Asn Ser Val Thr
    130                 135                 140
Asn Ser Ser Ser Ile Val Asp Leu Pro Val His Gln Leu Ser Ser Pro
145                 150                 155                 160
Phe Tyr Thr Lys Thr Thr Lys Met Lys Arg Lys Leu Asp His Gly Ser
                165                 170                 175
Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
            180                 185                 190
Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
        195                 200                 205
Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
    210                 215                 220
Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
225                 230                 235                 240
Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
                245                 250                 255
Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
            260                 265                 270
Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
        275                 280                 285
Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
    290                 295                 300
Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
305                 310                 315                 320
Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
                325                 330                 335
Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
            340                 345                 350
Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
        355                 360                 365
Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
    370                 375                 380
Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
385                 390                 395                 400
Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
                405                 410                 415
Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
            420                 425                 430
Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
        435                 440                 445
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Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
    450                 455                 460
Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
465                 470                 475                 480
Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
                485                 490                 495
Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
            500                 505                 510
Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
        515                 520                 525
Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
    530                 535                 540
Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
545                 550                 555                 560
Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
                565                 570                 575
Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
            580                 585                 590
Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
        595                 600                 605
Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
    610                 615                 620
Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
625                 630                 635                 640
Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
                645                 650                 655
Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
            660                 665                 670
Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
        675                 680                 685
Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
    690                 695                 700
Asp Met Lys
705
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<210> 15
<211> 2591
<212> DNA
<213> Homo sapiens

<400> 15

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gcgttcgggc tgggagcgtg ctttccacga cggtgacacg cttccctgga ttggcagcca 180
gactgccttc cgggtcactg ccatggagga gccgcagtca gatcctagcg tcgagccccc 240
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ccccttgccg tcccaagcaa tggatgattt gatgctgtcc ccggacgata ttgaacaatg 360
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tctgaggggt g 2591

<210> 16
<211> 1182
<212> DNA
<213> Homo sapiens

<400> 16

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gatgatttga tgctgtcccc ggacgatatt gaacaatggt tcactgaaga cccaggtcca 180
gatgaagctc ccagaatgcc agaggctgct ccccgcgtgg cccctgcacc agcagctcct 240
acaccggcgg cccctgcacc agccccctcc tggccctgt catcttctgt cccttcccag 300
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tgccctgtgc agctgtgggt tgattccaca ccccgcccg gcacccgcgt ccgcgccatg 480
gccatctaca agcagtcaca gcacatgacg gaggttgtga ggcgctgccc ccaccatgag 540
cgctgctcag atagcgatgg tctggccct cctcagcatc ttatccgagt ggaaggaaat 600
ttgcgtgtgg agtatttgga tgacagaaac acttttcgac atagtgtggt ggtgccctat 660
gagccgcctg aggttggctc tgactgtacc accatccact acaactacat gtgtaacagt 720
tcctgcatgg gcggcatgaa ccggaggccc atcctcacca tcatcacact ggaagactcc 780
agtggtaatc tactgggacg gaacagcttt gaggtgcgtg tttgtgcctg tcctgggaga 840
gaccggcgca cagaggaaga gaatctccgc aagaaagggg agcctcacca cgagctgccc 900
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aaaccactgg atggagaata tttcaccctt cagatccgtg ggcgtgagcg cttcgagatg 1020
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gggagcaggg ctcactccag ccacctgaag tccaaaaagg gtcagtctac ctcccgccat 1140
aaaaaactca tgttcaagac agaagggcct gactcagact ga                    1182
```

<210> 17
<211> 393
<212> PRT
<213> Homo sapiens

<400> 17

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Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
 1               5                  10                  15
Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
            20                  25                  30
Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
        35                  40                  45
```

```
Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
    50                  55                  60
Arg Met Pro Glu Ala Ala Pro Arg Val Ala Pro Ala Pro Ala Ala Pro
65                  70                  75                  80
Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
                85                  90                  95
Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
            100                 105                 110
Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
        115                 120                 125
Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
    130                 135                 140
Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145                 150                 155                 160
Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
                165                 170                 175
Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
            180                 185                 190
His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
        195                 200                 205
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
    210                 215                 220
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225                 230                 235                 240
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
                245                 250                 255
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
            260                 265                 270
Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
        275                 280                 285
Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
    290                 295                 300
Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305                 310                 315                 320
Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
                325                 330                 335
Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
            340                 345                 350
Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
        355                 360                 365
Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
    370                 375                 380
Phe Lys Thr Glu Gly Pro Asp Ser Asp
385                 390
```

<210> 18
<211> 1267
<212> DNA
<213> Homo sapiens

<400> 18

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ccccttgcct ggaaagatac cgcggtccct ccagaggatt tgagggacag ggtcggaggg 180
ggctcttccg ccagcaccgg aggaagaaag aggaggggct ggctggtcac cagagggtgg 240
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agcagcatgg agccggcggc ggggagcagc atggagcctt cggctgactg gctggccacg 360
gccgcggccc ggggtcgggt agaggaggtg cgggcgctgc tggaggcggg ggcgctgccc 420
aacgcaccga atagttacgg tcggaggccg atccaggtca tgatgatggg cagcgcccga 480
gtggcggagc tgctgctgct ccacggcgcg gagcccaact gcgccgaccc cgccactctc 540
acccgacccg tgcacgacgc tgcccgggag ggcttcctgg acacgctggt ggtgctgcac 600
cgggccgggg cgcggctgga cgtgcgcgat gcctggggcc gtctgcccgt ggacctggct 660

gaggagctgg gccatcgcga tgtcgcacgg tacctgcgcg cggctgcggg gggcaccaga 720
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catgtgggca tttcttgcga gcctcgcagc ctccggaagc tgtcgacttc atgacaagca 1140
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aatggcagaa ccaaagctca aataaaaata aaataatttt cattcattca ctcaaaaaaa 1260
aaaaaaa 1267

<210> 19
<211> 471
<212> DNA
<213> Homo sapiens

<400> 19

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gcccggggtc gggtagagga ggtgcgggcg ctgctggagg cgggggcgct gcccaacgca 120
ccgaatagtt acggtcggag gccgatccag gtcatgatga tgggcagcgc ccgagtggcg 180
gagctgctgc tgctccacgg cgcggagccc aactgcgccg accccgccac tctcacccga 240
cccgtgcacg acgctgcccg ggagggcttc ctggacacgc tggtggtgct gcaccgggcc 300
ggggcgcggc tggacgtgcg cgatgcctgg ggccgtctgc ccgtggacct ggctgaggag 360
ctgggccatc gcgatgtcgc acggtacctg cgcgcggctg cgggggggcac cagaggcagt 420
aaccatgccc gcatagatgc cgcggaaggt ccctcagaca tccccgattg a 471

<210> 20
<211> 156
<212> PRT
<213> Homo sapiens

<400> 20

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Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1               5                  10                  15
Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
            20                  25                  30
Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
        35                  40                  45
Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
    50                  55                  60
Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65                  70                  75                  80
Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
                85                  90                  95
Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
            100                 105                 110
Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
        115                 120                 125
Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
    130                 135                 140
Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145                 150                 155
```

<210> 21
<211> 1164
<212> DNA
<213> Homo Sapiens

<400> 21

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tcccagtctg cagttaaggg ggcaggagtg gcgctgctca cctctggtgc caaagggcgg 120

cgcagcggct gccgagctcg gccctggagg cggcgagaac atggtgcgca ggttcttggt 180
gaccctccgg attcggcgcg cgtgcggccc gccgcgagtg agggttttcg tggttcacat 240
cccgcggctc acgggggagt gggcagcgcc aggggcgccc gccgctgtgg ccctcgtgct 300
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ccgaccccgc cactctcacc cgacccgtgc acgacgctgc ccgggagggc ttcctggaca 480
cgctggtggt gctgcaccgg gccggggcgc ggctggacgt gcgcgatgcc tggggccgtc 540
tgcccgtgga cctggctgag gagctgggcc atcgcgatgt cgcacggtac ctgcgcgcgg 600
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acatccccga ttgaaagaac cagagaggct ctgagaaacc tcgggaaact tagatcatca 720
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cgacttcatg acaagcattt tgtgaactag ggaagctcag gggggttact ggcttctctt 1080
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```

<210> 22
<211> 522
<212> DNA
<213> Homo sapiens

<400> 22

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aacatggtgc gcaggttctt ggtgaccctc cggattcggc gcgcgtgcgg cccgccgcga 180
gtgagggttt tcgtggttca catcccgcgg ctcacggggg agtgggcagc gccaggggcg 240
cccgccgctg tggccctcgt gctgatgcta ctgaggagcc agcgtctagg gcagcagccg 300
cttcctagaa gaccaggtca tgatgatggg cagcgcccga gtggcggagc tgctgctgct 360
ccacggcgcg gagcccaact gcgccgaccc cgccactctc acccgacccg tgcacgacgc 420
tgcccgggag ggcttcctgg acacgctggt ggtgctgcac cgggccgggg cgcggctgga 480
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```

<210> 23
<211> 173
<212> PRT
<213> Homo sapiens

<400> 23

```
Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln
 1               5                  10                  15
Glu Trp Arg Cys Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala
            20                  25                  30
Glu Leu Gly Pro Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
        35                  40                  45
Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
    50                  55                  60
Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
65                  70                  75                  80
Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
                85                  90                  95
Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
            100                 105                 110
Pro Ser Gly Gly Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
        115                 120                 125
Arg Pro Arg His Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly
    130                 135                 140
Leu Pro Gly His Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly
145                 150                 155                 160
Arg Ala Arg Cys Leu Gly Pro Ser Ala Arg Gly Pro Gly
                165                 170
```

<210> 24
<211> 10740
<212> DNA
<213> Homo sapiens

<400> 24

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tcatcttaca aaactggaaa ctgaggcatc taatatgaag gaagtactta aacaactaca 240
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taaagagctt aacttagata gcagtaattt ccctggagta aaactgcggt caaaaatgtc 360
cctccgttct tatggaagcc gggaaggatc tgtatcaagc cgttctggag agtgcagtcc 420
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<400> 26

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            20                  25                  30
His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
        35                  40                  45
Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
    50                  55                  60
Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
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Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
                85                  90                  95
Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
            100                 105                 110
Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
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Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
145                 150                 155                 160
Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu
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Asn Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu
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Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
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Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr
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Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly
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Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala
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Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser
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        675                 680                 685
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Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys
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Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu
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Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr
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Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro
            820                 825                 830
Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
        835                 840                 845
Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His
    850                 855                 860
Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
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Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
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    2530                2535                2540
Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
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Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
                2565                2570                2575
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            2580                2585                2590
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        2595                2600                2605
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Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
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Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
        2835                2840
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Claims

1. A method for identifying a cancer patient for treatment with a NEDD8-activating enzyme (NAE) inhibitor comprising:

   a) determining a mutational status of at least one marker gene in a sample comprising tumor cells obtained from the cancer patient, wherein the at least one marker gene is a tumor suppressor in a cullin ring ligase pathway;
   b) determining whether the mutational status is indicative of a favorable outcome of treatment with the NAE inhibitor, wherein the NAE inhibitor is ((1S,2S,4R)-4-{4-[(1S)-2,3-dihydro-1H-inden-1-ylamino]-7H-pyrrolo[2,3-d]pyrimidin-7-yl}-2-hydroxycyclopentyl)methyl sulphamate; and
   c) identifying the patient for treatment with the NAE inhibitor if the mutational status indicates a favorable outcome of treatment with the NAE inhibitor;

   wherein the at least one marker gene is selected from the group consisting of *TP53, CDKN2A, CDKN2A_p14* and *APC.*

2. The method of claim 1, wherein the mutational status of the at least one marker gene is mutant.

3. The method of claim 1, wherein the mutational status of the at least one marker gene is wild type.

4. The method of claim 2, wherein the mutant is an inactivating mutant.

5. The method of any one of the preceding claims, wherein the sample comprises hematological tumor cells or solid tumor cells.

6. The method of claim 5, wherein the sample comprising hematological tumor cells is blood.

7. The method of any one of claims 1-6, wherein the at least one marker gene is at least two marker genes.

8. The method of claim 2, wherein the at least one marker gene is CDKN2A or CDKN2A_p14.

9. The method of claim 3, wherein the at least one marker gene is TP53.

10. The method of claim 7, wherein the at least two marker genes are at least TP53 and APC.

11. The method of any one of the preceding claims, wherein the mutational status is determined by measuring at least one characteristic of at least one marker associated with the at least one marker gene.

12. The method of claim 11, wherein the at least one characteristic is selected from the group consisting of size, sequence, composition, and amount.

13. The method of claim 11 or 12, wherein the at least one marker is selected from the group consisting of a chromosome locus, a nucleic acid, and a protein associated with the at least one marker gene.

14. The method of claim 13, wherein the nucleic acid is genomic DNA, mRNA, or cDNA.

15. The method of any one of claims 11-14, wherein the at least one characteristic is a sequence and the at least one marker is a nucleic acid.

16. The method of any one of claims 1 to 4, wherein the cancer patient has a hematological cancer or a solid tumor cancer.

17. The method of claim 16, wherein the hematological cancer is acute or chronic myelogenous leukemia.

18. The method of claim 16, wherein the hematological cancer is myelodysplastic syndrome.

19. The method of claim 16, wherein the solid tumor cancer is head and neck cancer.

20. The method of any one of the preceding claims, further comprising:

a) identifying a mutational status of the at least one marker gene in a second sample from the patient, wherein the patient has been treated with the NAE inhibitor prior to the second sample being obtained;
b) determining whether the mutational status is indicative of a favorable outcome of treatment with the NAE inhibitor; and
c) determining to continue treatment with the NAE inhibitor if the mutational status of the second sample indicates a favorable outcome of treatment with the NAE inhibitor.

21. Use of a kit in identifying a cancer patient for treatment with a NEDD8-activating enzyme (NAE) inhibitor, the kit comprising a reagent to determine a mutational status of at least one marker gene in a sample comprising tumor cells obtained from the cancer patient, wherein the NAE inhibitor is a 1- substituted methyl sulfamate, wherein the at least one marker gene is a tumor suppressor in a cullin ring ligase pathway, and wherein the at least one marker gene is selected from the group consisting of *TP53, CDKN2A, CDKN2A_p14* and *APC.*

22. The use of the kit of claim 21, wherein the mutational status is determined by measurement of at least one characteristic of at least one marker of the at least one marker gene, wherein the at least one marker is selected from the group consisting of nucleic acid and protein associated with the at least one marker gene.

23. The use of the kit of any one of claims 21-22, the kit further comprising a stabilizer to add to the sample.

24. The use of the kit of claim 22, wherein the at least one marker is nucleic acid and the reagent is at least one primer.

25. The use of the kit of claim 24, wherein the at least one primer hybridizes to a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 or a sequence on chromosome 22q from base pair 29999545 to 30094589, chromosome 18q from base pair 48556583 to 48611412, chromosome Xp from base pair 44732423 to 44971847, chromosome 4q from base pair 153242410 to 153456172, chromosome 17p from base pair 7571720 to 7590868, chromosome 9p from base pair 21967751 to 21994490, and a complement of any of the foregoing.

26. An NAE inhibitor for use in a method of treating a cancer patient, the method comprising:

a) using the mutational status of at least one marker gene in a patient's tumor, wherein the at least one marker gene is selected from the group consisting of *TP53, CDKN2A, CDKN2A_p14* and *APC,* to select a cancer patient who is expected to have a favorable outcome of treatment with the NAE inhibitor, and
b) treating the cancer patient with the NAE inhibitor, wherein the NAE inhibitor is a 1-substituted methyl sulfamate.

27. The NAE inhibitor for use according to claim 26, wherein the NAE inhibitor is ((1S,2S,4R)-4-{4-[(1S)-2,3-dihydro-1H-inden-1-ylamino]-7H-pyrrolo[2,3-d]pyrimidin-7-yl}-2-hydroxycyclopentyl)methyl sulphamate.

28. The NAE inhibitor for use of claim 26 or 27, wherein the cancer patient has a hematological cancer or a solid tumor cancer.

29. The NAE inhibitor for use of claim 28, wherein the hematological cancer is acute or chronic myelogenous leukemia.

30. The NAE inhibitor for use of claim 28, wherein the hematological cancer is myelodysplastic syndrome.

31. The NAE inhibitor for use of claim 28, wherein the solid tumor cancer is head and neck cancer.

Patentansprüche

1. Verfahren zum Identifizieren eines Krebspatienten für eine Behandlung mit einem NEDD8-aktivierendes-Enzym(NAE)-Inhibitor, umfassend:

a) Bestimmen eines Mutationsstatus mindestens eines Markergens in einer Tumorzellen umfassenden Probe, die von dem Krebspatienten erhalten wurde, wobei das mindestens eine Markergen ein Tumorsuppressor in einem Cullin-Ring-Ligase-Weg ist;
b) Bestimmen, ob der Mutationsstatus für ein günstiges Ergebnis einer Behandlung mit dem NAE-Inhibitor indikativ ist, wobei der NAE-Inhibitor ((1S,2S,4R)-4-{4-[(1S)-2,3-Dihydro-1H-inden-1-ylamino]-7H-pyrrolo[2,3-

d]pyrimidin-7-yl}-2-hydroxycyclopentyl)methylsulfamat ist; und
c) Identifizieren des Patienten für eine Behandlung mit dem NAE-Inhibitor, wenn der Mutationsstatus auf ein günstiges Ergebnis einer Behandlung mit dem NAE-Inhibitor hindeutet;

wobei das mindestens eine Markergen aus der Gruppe ausgewählt ist bestehend aus *TP53, CDKN2A, CDKN2A_p14* und *APC.*

2. Verfahren nach Anspruch 1, wobei der Mutationsstatus des mindestens einen Markergens mutiert ist.

3. Verfahren nach Anspruch 1, wobei der Mutationsstatus des mindestens einen Markergens Wildtyp ist.

4. Verfahren nach Anspruch 2, wobei die Mutante eine inaktivierende Mutante ist.

5. Verfahren nach einem der vorhergehenden Ansprüche, wobei die Probe hämatologische Tumorzellen oder solide Tumorzellen umfasst.

6. Verfahren nach Anspruch 5, wobei die Probe, die hämatologische Tumorzellen umfasst, Blut ist.

7. Verfahren nach einem der Ansprüche 1-6, wobei das mindestens eine Markergen mindestens zwei Markergene ist.

8. Verfahren nach Anspruch 2, wobei das mindestens eine Markergen CDKN2A oder CDKN2A_p14 ist.

9. Verfahren nach Anspruch 3, wobei das mindestens eine Markergen TP53 ist.

10. Verfahren nach Anspruch 7, wobei die mindestens zwei Markergene mindestens TP53 und APC sind.

11. Verfahren nach einem der vorhergehenden Ansprüche, wobei der Mutationsstatus durch Messen mindestens eines Merkmals mindestens eines mit dem mindestens einen Markergen assoziierten Markers bestimmt wird.

12. Verfahren nach Anspruch 11, wobei das mindestens eine Merkmal aus der Gruppe ausgewählt ist bestehend aus Größe, Sequenz, Zusammensetzung und Menge.

13. Verfahren nach Anspruch 11 oder 12, wobei der mindestens eine Marker aus der Gruppe ausgewählt ist bestehend aus einem Chromosomenlocus, einer Nukleinsäure und einem Protein, die mit dem mindestens einen Markergen assoziiert sind.

14. Verfahren nach Anspruch 13, wobei die Nukleinsäure genomische DNA, mRNA oder cDNA ist.

15. Verfahren nach einem der Ansprüche 11-14, wobei das mindestens eine Merkmal eine Sequenz ist und der mindestens eine Marker eine Nukleinsäure ist.

16. Verfahren nach einem der Ansprüche 1 bis 4, wobei der Krebspatient einen hämatologischen Krebs oder einen Krebs in Form eines soliden Tumors hat.

17. Verfahren nach Anspruch 16, wobei der hämatologische Krebs akute oder chronische myeloische Leukämie ist.

18. Verfahren nach Anspruch 16, wobei der hämatologische Krebs myelodysplastisches Syndrom ist.

19. Verfahren nach Anspruch 16, wobei der Krebs in Form eines soliden Tumors Kopf- und Halskrebs ist.

20. Verfahren nach einem der vorhergehenden Ansprüche, ferner umfassend:

a) Identifizieren eines Mutationsstatus des mindestens eines Markergens in einer zweiten Probe von dem Patienten, wobei der Patient vor der Entnahme der zweiten Probe mit dem NAE-Inhibitor behandelt wurde;
b) Bestimmen, ob der Mutationsstatus für ein günstiges Ergebnis einer Behandlung mit dem NAE-Inhibitor indikativ ist, und
c) Ermitteln der Fortsetzung der Behandlung mit dem NAE-Inhibitor, wenn der Mutationsstatus der zweiten Probe auf ein günstiges Ergebnis der Behandlung mit dem NAE-Inhibitor hindeutet.

21. Verwendung eines Kits beim Identifizieren eines Krebspatienten für eine Behandlung mit einem NEDD8-aktivierendes-Enzym(NAE)-Inhibitor, wobei das Kit ein Reagenz zum Bestimmen eines Mutationsstatus mindestens eines Markergens in einer Tumorzellen umfassenden Probe, die von dem Krebspatienten erhalten wurde, umfasst, wobei der NAE-Inhibitor ein 1-substituiertes Methylsulfamat ist, wobei das mindestens eine Markergen ein Tumorsuppressor in einem Cullin-Ring-Ligase-Weg ist und wobei das mindestens eine Markergen aus der Gruppe ausgewählt ist bestehend aus *TP53, CDKN2A, CDKN2A_p14* und *APC.*

22. Verwendung des Kits nach Anspruch 21, wobei der Mutationsstatus durch Messen mindestens eines Merkmals mindestens eines Markers des mindestens einen Markergens bestimmt wird, wobei der mindestens eine Marker aus der Gruppe ausgewählt ist bestehend aus Nukleinsäure und Protein, die mit dem mindestens einen Markergen assoziiert sind.

23. Verwendung des Kits nach einem der Ansprüche 21-22, wobei das Kit ferner einen Stabilisator für die Zugabe zur Probe umfasst.

24. Verwendung des Kits nach Anspruch 22, wobei der mindestens eine Marker Nukleinsäure ist und das Reagenz mindestens ein Primer ist.

25. Verwendung des Kits nach Anspruch 24, wobei der mindestens eine Primer an eine Nukleinsäuresequenz hybridisiert, ausgewählt aus der Gruppe bestehend aus SEQ ID NO: 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 oder einer Sequenz auf Chromosom 22q von Basenpaar 29999545 bis 30094589, Chromosom 18q von Basenpaar 48556583 bis 48611412, Chromosom Xp von Basenpaar 44732423 bis 44971847, Chromosom 4q von Basenpaar 153242410 bis 153456172, Chromosom 17p von Basenpaar 7571720 bis 7590868, Chromosom 9p von Basenpaar 21967751 bis 21994490 und einem Komplement eines der Vorstehenden.

26. NAE-Inhibitor zur Verwendung bei einem Verfahren zur Behandlung eines Krebspatienten, wobei das Verfahren Folgendes umfasst:

    a) Verwenden eines Mutationsstatus mindestens eines Markergens in einem Tumor des Patienten, wobei das mindestens eine Markergen aus der Gruppe ausgewählt ist bestehend aus *TP53, CDKN2A, CDKN2A_p14* und *APC*, um einen Krebspatienten auszuwählen, bei dem ein günstiges Ergebnis einer Behandlung mit dem NAE-Inhibitor zu erwarten ist, und
    b) Behandeln des Krebspatienten mit dem NAE-Inhibitor, wobei der NAE-Inhibitor ein 1-substituiertes Methylsulfamat ist.

27. NAE-Inhibitor zur Verwendung nach Anspruch 26, wobei der NAE-Inhibitor ((1S,2S,4R)-4-{4-[(1S)-2,3-Dihydro-1H-inden-1-ylamino]-7H-pyrrolo[2,3-d]pyrimidin-7-yl}-2-hydroxycyclopentyl)methylsulfamat ist.

28. NAE-Inhibitor zur Verwendung nach Anspruch 26 oder 27, wobei der Krebspatient einen hämatologischen Krebs oder einen Krebs in Form eines soliden Tumors hat.

29. NAE-Inhibitor zur Verwendung nach Anspruch 28, wobei der hämatologische Krebs akute oder chronische myeloische Leukämie ist.

30. NAE-Inhibitor zur Verwendung nach Anspruch 28, wobei der hämatologische Krebs myelodysplastisches Syndrom ist.

31. NAE-Inhibitor zur Verwendung nach Anspruch 28, wobei der Krebs in Form eines soliden Tumors Kopf- und Halskrebs ist.

Revendications

1. Méthode d'identification d'un patient cancéreux pour un traitement par un inhibiteur de l'enzyme d'activation de NEDD8 (NAE), comprenant :

    a) la détermination d'un état mutationnel d'au moins un gène marqueur dans un échantillon comprenant des cellules tumorales obtenues auprès du patient cancéreux, où le au moins un gène marqueur est un suppresseur

tumoral dans une voie de la ligase culline-RING ;
b) la détermination du fait que l'état mutationnel constitue ou non une indication d'une issue favorable de traitement par l'inhibiteur de NAE, où l'inhibiteur de NAE est le sulfamate de ((1S,2S,4R)-4-{4-[(1S)-2,3-dihydro-1H-indén-1-ylamino]-7H-pyrrolo[2,3-d]pyrimidin-7-yl}-2-hydroxycyclopentyl)méthyle ; et
c) l'identification du patient pour un traitement par l'inhibiteur de NAE si l'état mutationnel indique une issue favorable d'un traitement par l'inhibiteur de NAE ;

dans laquelle le au moins un gène marqueur est choisi dans le groupe constitué par *TP53, CDKN2A, CDKN2A_p14* et *APC.*

2. Méthode selon la revendication 1, dans laquelle l'état mutationnel du au moins un gène marqueur est mutant.

3. Méthode selon la revendication 1, dans laquelle l'état mutationnel du au moins un gène marqueur est de type sauvage.

4. Méthode selon la revendication 2, dans laquelle le mutant est un mutant inactivant.

5. Méthode selon l'une quelconque des revendications précédentes, dans laquelle l'échantillon comprend des cellules de tumeurs hématologiques ou des cellules de tumeurs solides.

6. Méthode selon la revendication 5, dans laquelle l'échantillon comprenant des cellules de tumeurs hématologiques est constitué de sang.

7. Méthode selon l'une quelconque des revendications 1-6, dans laquelle le au moins un gène marqueur est constitué d'au moins deux gènes marqueurs.

8. Méthode selon la revendication 2, dans laquelle le au moins un gène marqueur est *CDKN2A* ou *CDKN2A_p14.*

9. Méthode selon la revendication 3, dans laquelle le au moins un gène marqueur est *TP53.*

10. Méthode selon la revendication 7, dans laquelle les au moins deux gènes marqueurs sont au moins *TP53* et *APC.*

11. Méthode selon l'une quelconque des revendications précédentes, dans laquelle l'état mutationnel est déterminé par la mesure d'au moins une caractéristique d'au moins un marqueur associé au au moins un gène marqueur.

12. Méthode selon la revendication 11, dans laquelle la au moins une caractéristique est choisie dans le groupe constitué par la taille, la séquence, la composition, et la quantité.

13. Méthode selon la revendication 11 ou 12, dans laquelle le au moins un marqueur est choisi dans le groupe constitué par un locus de chromosome, un acide nucléique, et une protéine associée au au moins un gène marqueur.

14. Méthode selon la revendication 13, dans laquelle l'acide nucléique est un ADN génomique, un ARNm, ou un ADNc.

15. Méthode selon l'une quelconque des revendications 11-14, dans laquelle la au moins une caractéristique est une séquence et le au moins un marqueur est un acide nucléique.

16. Méthode selon l'une quelconque des revendications 1 à 4, dans laquelle le patient cancéreux souffre d'un cancer hématologique ou d'un cancer à tumeur solide.

17. Méthode selon la revendication 16, dans laquelle le cancer hématologique est une leucémie myéloïde chronique ou aiguë.

18. Méthode selon la revendication 16, dans laquelle le cancer hématologique est un syndrome myélodysplasique.

19. Méthode selon la revendication 16, dans laquelle le cancer à tumeur solide est un cancer de la tête et du cou.

20. Méthode selon l'une quelconque des revendications précédentes, comprenant en outre :

a) l'identification d'un état mutationnel du au moins un gène marqueur dans un deuxième échantillon issu du

patient, où le patient a été traité par l'inhibiteur de NAE préalablement à l'obtention du deuxième échantillon ;
b) la détermination du fait que l'état mutationnel constitue ou non une indication d'une issue favorable de traitement par l'inhibiteur de NAE ; et
c) la détermination de la poursuite du traitement par l'inhibiteur de NAE, si l'état mutationnel du deuxième échantillon indique une issue favorable de traitement par l'inhibiteur de NAE.

21. Utilisation d'un kit dans l'identification d'un patient cancéreux pour un traitement par un inhibiteur de l'enzyme d'activation de NEDD8 (NAE), le kit comprenant un réactif destiné à déterminer un état mutationnel d'au moins un gène marqueur dans un échantillon comprenant des cellules tumorales obtenues auprès du patient cancéreux, où l'inhibiteur de NAE est un sulfamate de méthyle 1-substitué, où le au moins un gène marqueur est un suppresseur tumoral dans une voie de la ligase culline-RING, et où le au moins un gène marqueur est choisi dans le groupe constitué par *TP53, CDKN2A, CDKN2A_p14* et *APC.*

22. Utilisation du kit selon la revendication 21, dans laquelle l'état mutationnel est déterminé par la mesure d'au moins une caractéristique d'au moins un marqueur du au moins un gène marqueur, où le au moins un marqueur est choisi dans le groupe constitué par un acide nucléique et une protéine associée au au moins un gène marqueur.

23. Utilisation du kit selon l'une quelconque des revendications 21-22, le kit comprenant en outre un stabilisant à ajouter à l'échantillon.

24. Utilisation du kit selon la revendication 22, dans laquelle le au moins un marqueur est un acide nucléique et le réactif est au moins une amorce.

25. Utilisation du kit selon la revendication 24, dans laquelle la au moins une amorce s'hybride avec une séquence d'aide nucléique choisie dans le groupe constitué par SEQ ID n° 1, 2, 4, 5, 7, 8, 9, 12, 13, 15, 16, 18, 19, 21, 22, 24, 25 ou une séquence sur le chromosome 22q des paires de base 29999545 à 30094589, le chromosome 18q des paires de base 48556583 à 48611412, le chromosome Xp des paires de base 44732423 à 44971847, le chromosome 4q des paires de base 153242410 à 153456172, le chromosome 17p des paires de base 7571720 à 7590868, le chromosome 9p des paires de base 21967751 à 21994490, et un complément de l'un quelconque parmi ce qui précède.

26. Inhibiteur de NAE pour une utilisation dans une méthode de traitement d'un patient cancéreux, la méthode comprenant :

a) l'utilisation de l'état mutationnel d'au moins un gène marqueur dans une tumeur du patient, où le au moins un gène marqueur est choisi dans le groupe constitué par *TP53, CDKN2A, CDKN2A_p14* et *APC*, afin de sélectionner un patient cancéreux qui est prévu comme présentant une issue favorable vis-à-vis d'un traitement par l'inhibiteur de NAE ; et
b) le traitement du patient cancéreux par l'inhibiteur de NAE, où l'inhibiteur de NAE est un sulfamate de méthyle 1-substitué.

27. Inhibiteur de NAE pour une utilisation selon la revendication 26, l'inhibiteur de NAE étant le sulfamate de ((1S,2S,4R)-4-{4-[(1S)-2,3-dihydro-1H-indén-1-yl-amino]-7H-pyrrolo[2,3-d]pyrimidin-7-yl}-2-hydroxycyclopentyl)méthyle.

28. Inhibiteur de NAE pour une utilisation selon la revendication 26 ou 27, où le patient cancéreux souffre d'un cancer hématologique ou d'un cancer à tumeur solide.

29. Inhibiteur de NAE pour une utilisation selon la revendication 28, où le cancer hématologique est une leucémie myéloïde chronique ou aiguë.

30. Inhibiteur de NAE pour une utilisation selon la revendication 28, où le cancer hématologique est un syndrome myélodysplasique.

31. Inhibiteur de NAE pour une utilisation selon la revendication 28, où le cancer à tumeur solide est un cancer de la tête et du cou.

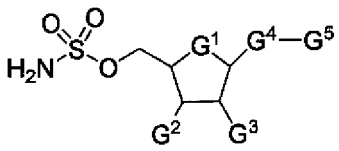


Figure 1

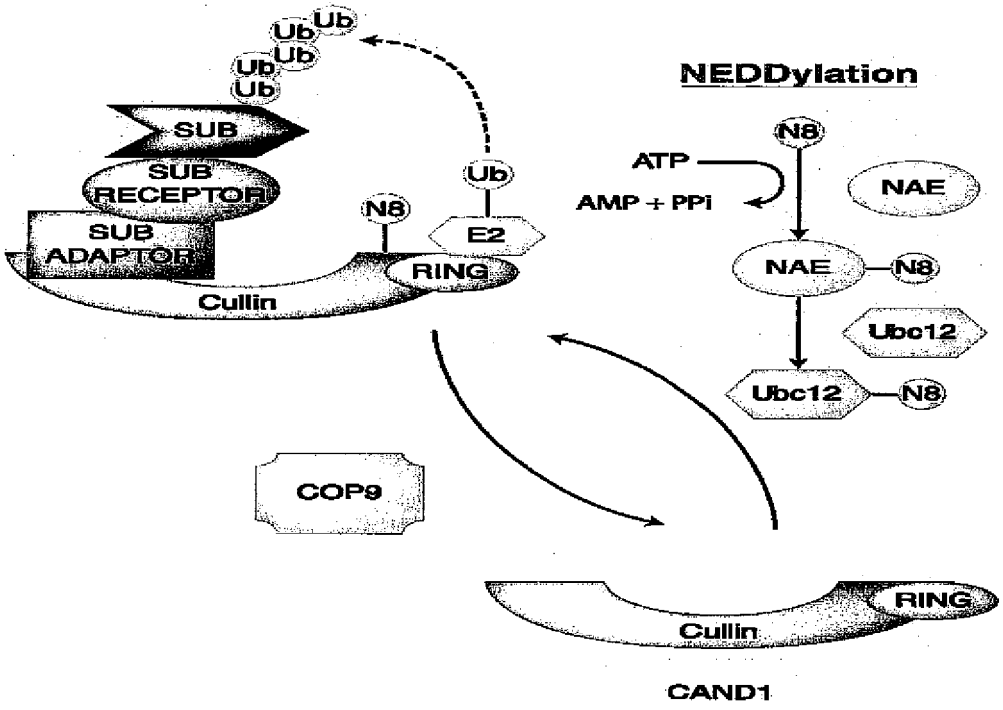

Ub
Ub
Ub
Ub
Ub
SUB
SUB RECEPTOR
SUB ADAPTOR
Cullin
RING
N8
E2
Ub
NEDDylation
ATP
AMP + PPi
N8
NAE
NAE
N8
Ubc12
Ubc12
N8
COP9
RING
Cullin
CAND1

FIG. 2

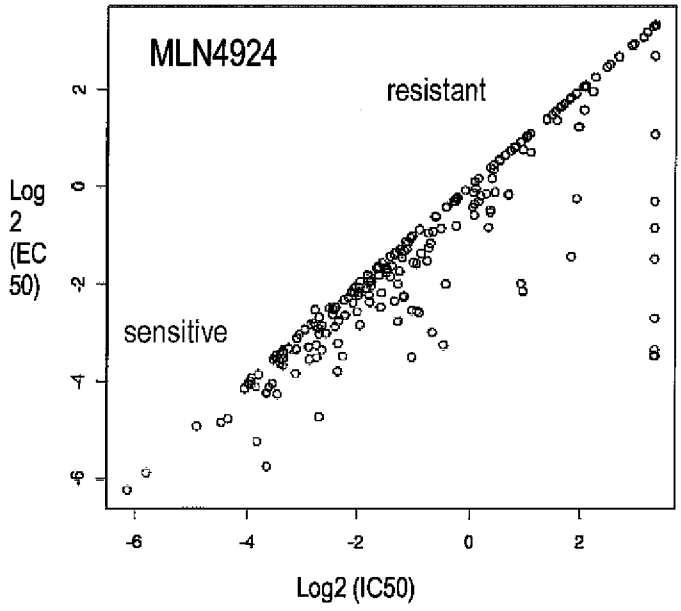


FIG. 3

FIG4A.

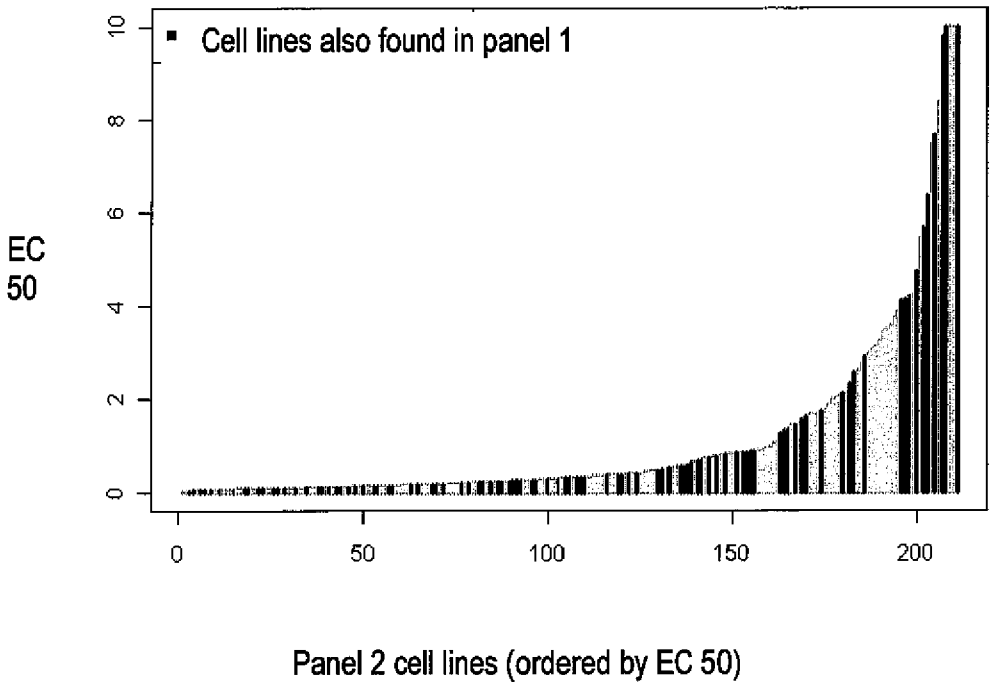


FIG4B.

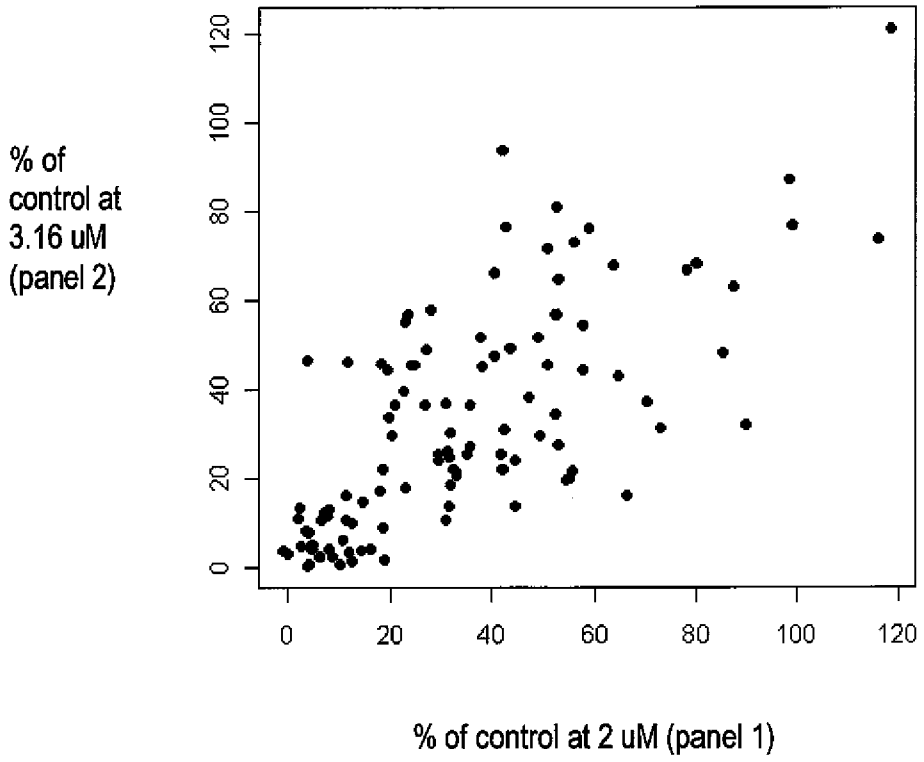


FIG. 4

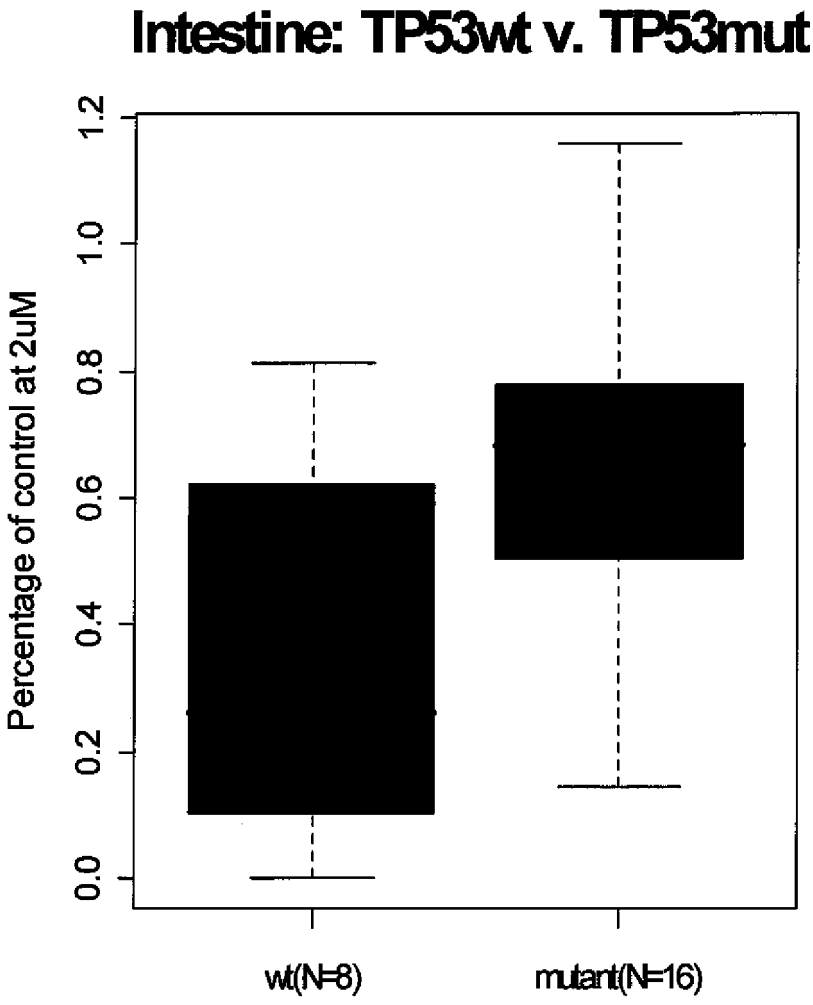

Intestine: TP53wt v. TP53mut
Percentage of control at 2uM
0.0
0.2
0.4
0.6
0.8
1.0
1.2
wt(N=8)
mutant(N=16)

FIG. 5

FIG. 6A

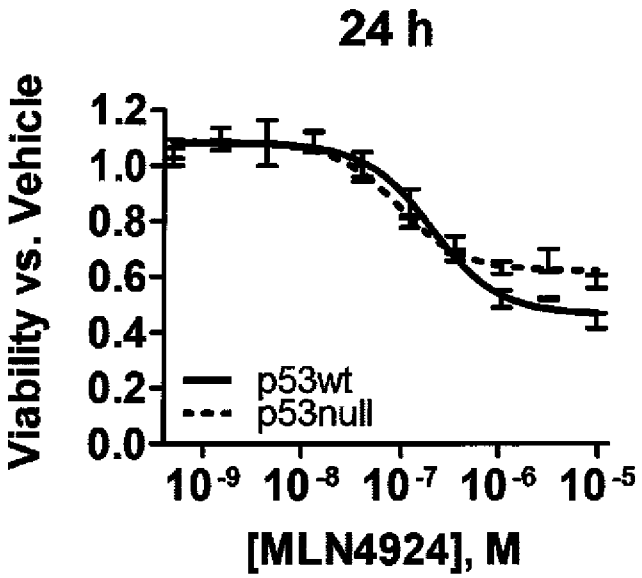

24 h
Viability vs. Vehicle
1.2
1.0
0.8
0.6
0.4
0.2
0.0
p53wt
p53null
10-9 10-8 10-7 10-6 10-5
[MLN4924], M

FIG. 6B

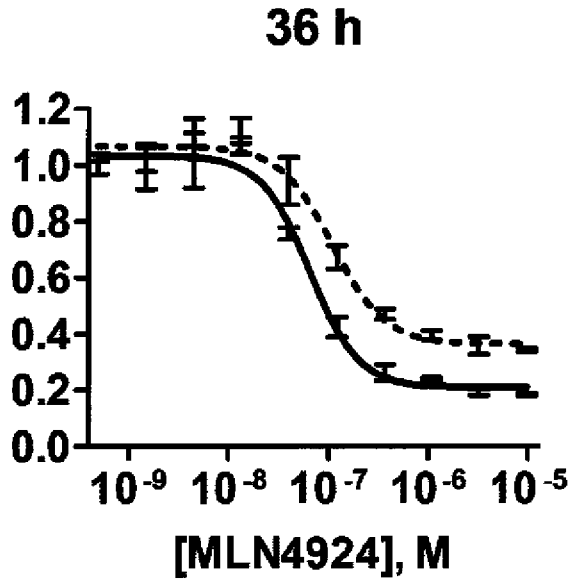

36 h
1.2
1.0
0.8
0.6
0.4
0.2
0.0
10-9 10-8 10-7 10-6 10-5
[MLN4924], M

FIG. 6C

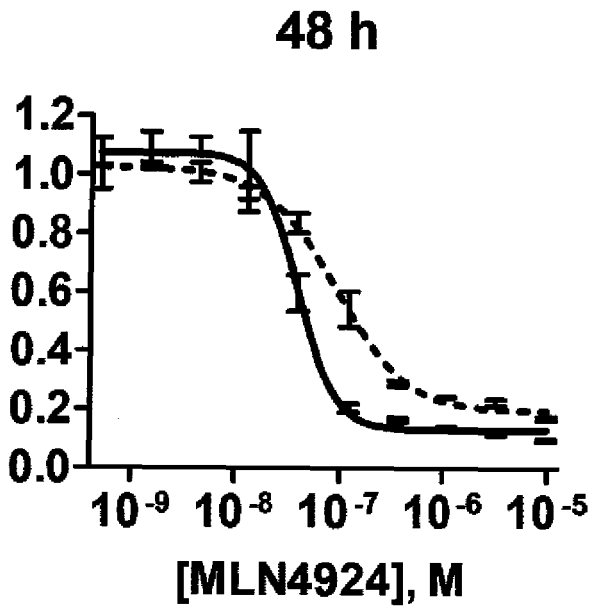
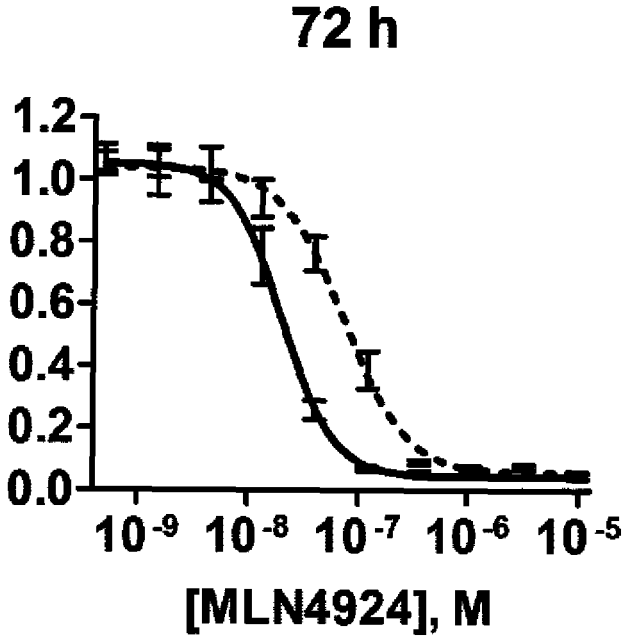

48 h
1.2
1.0
0.8
0.6
0.4
0.2
0.0
10-9 10-8 10-7 10-6 10-5
[MLN4924], M

FIG. 6D


72 h
1.2
1.0
0.8
0.6
0.4
0.2
0.0
10-9 10-8 10-7 10-6 10-5
[MLN4924], M

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当前申请(专利权)人(译)	千年制药，INC. 马萨诸塞州总医院		
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摘要(译)

本文公开了其突变状态与NAE抑制剂治疗敏感性相关的标志物。 通过测量与标志物基因相关的标志物的特征来确定突变状态。 提供了用于评估标记基因的标记以预测对NAE抑制治疗的反应的组合物和方法。