(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
28 May 2015 (28.05.2015)

WIPO | PCT

(10) International Publication Number
WO 2015/077342 A2

(51) International Patent Classification:
A61K 31/7105 (2006.01) *A61K 33/00* (2006.01)

(21) International Application Number:
PCT/US2014/066418

(22) International Filing Date:
19 November 2014 (19.11.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/906,150 19 November 2013 (19.11.2013) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

— *with sequence listing part of description (Rule 5.2(a))*

WO 2015/077342 A2

(54) Title: DETECTION OF ARGININE METHYLATION OF EGFR FOR PREDICTION OF RESISTANCE TO THERAPY

(57) Abstract: This invention provides biomarkers (e.g., methylation of R198 or R200 of EGFR or the presence of an arginine at position 497 of EGFR) for the prediction of resistance to cetuximab therapy. This invention also provides methods for the selection of patients for combination therapy with cetuximab and PRMT inhibitors.

DESCRIPTION

DETECTION OF ARGININE METHYLATION OF EGFR FOR PREDICTION OF RESISTANCE TO THERAPY

[0001] This application claims the benefit of United States Provisional Patent Application No. 61/906,150, filed November 19, 2013, which is incorporated herein by reference in its entirety.

[0002] The sequence listing that is contained in the file names "UTFCP1232WO_ST25.txt", which is 53 KB (as measured in Microsoft Windows) and was created on November 19, 2014, is filed herewith by electronic submission and is incorporated by reference herein.

BACKGROUND OF THE INVENTION

1. Field of the Invention

[0003] The present invention relates generally to the field of oncology. More particularly, it concerns the detection of arginine methylation of EGFR to predict resistance to cetuximab therapy and sensitivity to a combination therapy using a PRMT inhibitor plus cetuximab.

2. Description of Related Art

[0004] Epidermal growth factor receptor (EGFR)-targeted monoclonal antibody, cetuximab, is one of the most effective ways of controlling colorectal cancer progression (Berg and Soreide, 2012). However, resistance to cetuximab has been observed in the clinic (Custodio and Feliu, 2013; Fabian and Berkovcova, 2011; Messner et al., 2013). Currently, the most accepted predictive marker for poor cetuximab response in colorectal cancer is mutant KRAS status due its association with poor patient survival rate (De Roock et al., 2008; Lievre et al., 2008). Nevertheless, studies show increasing evidence that wild-type KRAS is insufficient to confer sensitivity to cetuximab (Fabian and Berkovcova, 2011; Laurent-Puig et al., 2009; Silvestris et al., 2009) and that patients with mutant KRAS are not necessarily refractory to cetuximab (Custodio and Feliu, 2013; Messner et al., 2013; Mao et al., 2013; Tejpar et al., 2013; De Roock et al., 2010). Therefore, other predictors of cetuximab response are needed.

SUMMARY OF THE INVENTION

[0005] In order to address this need, provided herein are biomarkers for the prediction of resistance to cetuximab therapy. Also provided are methods for the selection of patients for combination therapy with cetuximab and PRMT inhibitors. Therefore, in one embodiment, a pharmaceutical composition is provided comprising cetuximab and a protein arginine methyltransferase (PRMT) inhibitor (*e.g.*, sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde) in a pharmaceutically acceptable carrier. In one embodiment, a method is provide for treating cancer comprising administering said pharmaceutical composition to a patient in need thereof.

[0006] In one embodiment, a method is provided for treating a patient having cancer comprising administering an effective amount of cetuximab and a protein arginine methyltransferase (PRMT) inhibitor to a patient in need thereof. In some aspects, the PRMT inhibitor may be sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde. In some aspects, cetuximab and the PRMT inhibitor may be administered essentially simultaneously. In certain aspects, cetuximab may be administered prior to the PRMT inhibitor. In other certain aspects, the PRMT inhibitor may be administered prior to cetuximab.

[0007] In some aspects, the patient may have been determined to have a cancer cell comprising at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of epidermal growth factor receptor (EGFR) protein. In certain aspects, the cancer cell may be from a biopsy sample. In other aspects, the cancer cell may be a circulating tumor cell.

[0008] In certain aspects, the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 of EGFR protein may be detected by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation. In certain aspects, the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 of EGFR protein may be detecting by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200. As a control, the overall level of

EGFR may be determined by a method comprising contacting the sample with an antibody that binds to EGFR regardless of the presence or absence of any post-translational modifications. In some aspects, the presence of (iii) an Arg residue at amino acid position 497 of EGFR protein may be determined by mass spectrometry or by sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

[0009] In one embodiment, a method is provided for treating a patient having cancer comprising administering an effective amount of cetuximab to a patient in need thereof, said patient having been determined to have a cancer cell comprising (i) unmethylated Arg at position 198, (ii) unmethylated Arg at position 200, and (iii) a Lys residue at amino acid position 497 of EGFR protein. In certain aspects, the cancer cell may be from a biopsy sample. In other aspects, the cancer cell may be a circulating tumor cell.

[0010] In certain aspects, the presence of (i) unmethylated Arg at position 198 and/or (ii) unmethylated Arg at position 200 of EGFR protein may be detected by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation. In certain aspects, the presence of (i) unmethylated Arg at position 198 and/or (ii) unmethylated Arg at position 200 of EGFR protein may be detecting by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200. As a control, the overall level of EGFR may be determined by a method comprising contacting the sample with an antibody that binds to EGFR regardless of the presence or absence of any post-translational modifications. In some aspects, the presence of (iii) a Lys residue at amino acid position 497 of EGFR protein may be determined by mass spectrometry or by sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

[0011] In one embodiment, a method is provided for predicting resistance of a cancer patient to cetuximab comprising assaying a cancer cell (*e.g.*, from a biopsy sample or a circulating tumor cell) isolated from the patient to determine the presence of at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of EGFR protein in the cancer cell. In some aspects, if at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of EGFR protein is present, then the cancer may be predicted to be resistant to cetuximab.

[0012] In some aspects, the method may further comprise identifying the patient as having a cancer that is resistant to cetuxmiab if at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of EGFR protein is present. In some aspects, identifying may comprise reporting (*i.e.*, preparing a written or an oral report) whether the patient has a cancer that is resistant to cetuximab. Said reporting may be reporting to the patient, a doctor, a hospital, or an insurance provider.

[0013] In some aspects, identifying the patient as having a cancer that is resistant to cetuxmiab may further comprise identifying the patient having the cancer as a candidate for treatment with a combination of cetuximab and a PRMT inhibitor. In some aspects, the method may further comprise treating the patient with cetuximab in combination with a PRMT inhibitor, such as, for example, sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde. In some aspects, cetuximab and the PRMT inhibitor may be administered essentially simultaneously. In certain aspects, cetuximab may be administered prior to the PRMT inhibitor. In other certain aspects, the PRMT inhibitor may be administered prior to cetuximab.

[0014] In some aspects, the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 may comprise contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200. In some aspects, assaying may comprise performed a Western blot, ELISA, immunoprecipitation, radioimmunoassay, or immunohistochemical assay. In some aspects, assaying may comprise mass spectrometry. In some aspects, the presence of (iii) an Arg residue at amino acid position 497 of EGFR may be determined by mass spectrometry or by sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

[0015] In one embodiment, a method is provided for characterizing a cancer patient comprising selectively testing a cancer cell having been isolated from the patient to determine the methylation status of amino acids Arg198 and/or Arg200 of EGFR protein in the cancer cell. In some aspects, the method may further comprise obtaining a sample of the cancer or a circulating tumor cell from the cancer patient. In some aspects, a positive determination for methylation of amino acid Arg198 and/or Arg200 of EGFR protein may indicate that the cancer patient will be resistant to cetuximab. In some aspects, the method

may further comprise identifying the cancer patient as being eligible for treating with cetuximab in combination with a PRMT inhibitor. In some further aspects, the method may further comprise administering an effective amount of cetuximab in combination with a PRMT inhibitor to the patient.

[0016] In certain aspects, the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 of EGFR protein may be detected by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation. In certain aspects, the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 of EGFR protein may be detecting by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200. As a control, the overall level of EGFR may be determined by a method comprising contacting the sample with an antibody that binds to EGFR regardless of the presence or absence of any post-translational modifications.

[0017] In one embodiment, a method is provided for selecting a drug therapy for a cancer patient comprising assaying a cancer sample isolated from the patient to determine a methylation status of Arg198 and/or Arg200 of EGFR protein in the sample. In some aspects, the method may further comprise selecting a combination of cetuximab and a PRMT inhibitor if Arg198 and/or Arg200 of EGFR protein is determined to be methylated. In some aspects, the methylation status of Arg198 and/or Arg200 of EGFR protein may be determined by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation. In some aspects, the methylation status of Arg198 and/or Arg200 of EGFR protein may be determined by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200. As a control, the overall level of EGFR may be determined by a method comprising contacting the sample with an antibody that binds to EGFR regardless of the presence or absence of any post-translational modifications.

[0018] In one embodiment, a method is provided for sensitizing a cetuximab-resistant cancer to cetuximab comprising administering an effective amount of a PRMT inhibitor to a patient having the cetuximab-resistant cancer. In certain aspects, the method may further comprise administering cetuximab to the patient. In some aspects, the cetuximab may be administered essentially simultaneously with the PRMT inhibitor.

[0019] In some aspects of the various embodiments, the patient may be a human. In certain aspects of the various embodiments, the cancer may be a colorectal, breast, prostate, lung, or pancreatic cancer. In various aspects of the present embodiments, methods of treating may further comprises administering a second (or a third in embodiments comprising coadministration) anticancer therapy, such as, for example, surgical therapy, chemotherapy, radiation therapy, cryotherapy, hormonal therapy, toxin therapy, immunotherapy, or cytokine therapy. In some aspects, the patient may have previously undergone at least one round of anti-cancer therapy.

[0020] In one embodiment, a composition is provided comprising an antibody that specifically binds to Arg198- and/or Arg200-methylated EGFR protein. In some aspects, the antibody may be an IgG1 antibody.

[0021] In one embodiment, a composition is provided comprising a polypeptide comprising at least eight consecutive amino acids of EGFR protein fused to an immunogen, wherein the at least eight consecutive amino acids of EGFR1 protein includes Arg198 and/or Arg200 and wherein Arg198 and/or Arg200 is dimethylated. In certain aspects, the polypeptide may comprise the sequence QCSGRCRGKSPSDC (SEQ ID NO: 1). In some aspects, one or both of the Arg residues may be methylated.

[0022] In one embodiment, a composition is provided comprising cetuximab and a PRMT inhibitor (*e.g.*, sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde) for use in the treatment of a tumor in a subject. In some aspects, the composition may be formulated for intratumoral, intravenous, intradermal, intraarterial, intraperitoneal, intralesional, intracranial, intraarticularly, intraprostatic, intrapleural, intratracheal, intraocular, intranasal, intravitreal, intravaginal, intrarectal, intramuscular, subcutaneous, subconjunctival, intravesicularl, mucosal, intrapericardial, intraumbilical, oral administration. In some aspects, the composition may further comprise at least a third anticancer therapy, such as, for example, chemotherapy, radiation therapy, hormone therapy, immunotherapy or cytokine therapy. In some aspects, the patient may have been determined to have a cancer cell comprising at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of epidermal growth factor receptor (EGFR) protein.

[0023] In one embodiment, the use of cetuximab and a PRMT inhibitor in the manufacture of a medicament for the treatment of a tumor is provided.

[0024] In one embodiment, a method is provided for predicting resistance to cetuximab in a cancer patient comprising (a) obtaining a sample of the patient's cancer; (b) determining the methylation status of R198 or R200 of the epidermal growth factor receptor (EGFR) protein in the sample; and (c) predicting that the patient's cancer is resistant to cetuximab if R198 or R200 of EGFR is determined to be methylated. In one aspect, the method may further comprise treating the patient with cetuximab in combination with a PRMT inhibitor if the patient's cancer is predicted to be resistant to cetuximab.

[0025] In another embodiment, a method is provided of treating a cancer is a patient in need thereof comprising (a) obtaining a sample of the cancer; (b) determining the methylation status of R198 or R200 of the epidermal growth factor receptor (EGFR) protein expressed in the cancer; and (c) treating the patient with cetuximab alone if R198 and R200 of EGFR are determined to be unmethylated or treating the patient with cetuximab and a PRMT inhibitor if R198 or R200 of EGFR is determined to be methylated.

[0026] In some aspects, the methods of the present embodiments may further comprise determining the methylation status of both R198 and R200.

[0027] In one embodiment, a method is provided of treating a cancer in a patient in need thereof comprising (a) obtaining a sample of the cancer: (b) determining the amino acid present at position 497 of the EGFR protein expressed in the cancer; and (c) treating the patient with cetuximab alone if a lysine is present at position 497 of EGFR or treating the patient with cetuximab and a PRMT inhibitor if an arginine is present at position 497 of EGFR. In one aspect, the method may further comprise determining the methylation status of an arginine present at position 497 of EGFR.

[0028] In some aspects, a methylation status may be determined by mass spectrometry, immunohistochemistry, western blotting, or ELISA. Antibody-dependent methods may use either monoclonal or polyclonal antibodies specific for the methylation status of a particular amino acid to be determined. In some aspects, the amino acid present at position 497 of the EGFR protein may be determined by mass spectrometry or sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR gene.

[0029] In some aspects, a cancer may be metastatic, recurrent, or multi-drug resistant. In some aspects, the patient may be treated at least a second time. In some aspects, the patient may be treated over a period of 1 week to 6 months.

[0030] As used herein the specification, "a" or "an" may mean one or more. As used herein in the claim(s), when used in conjunction with the word "comprising," the words "a" or "an" may mean one or more than one.

[0031] The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or." As used herein "another" may mean at least a second or more.

[0032] Throughout this application, the term "about" is used to indicate that a value includes the inherent variation of error for the device, the method being employed to determine the value, or the variation that exists among the study subjects.

[0033] Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0034] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

[0035] **FIGS. 1A-F.** PRMT1-mediated cell proliferation and colony formation are EGFR signaling dependent. **FIG. 1A.** Cell proliferation assay of SKCO1 (left) and GEO (right) cells exogenously expressing PRMT1, PRMT1 shRNA, and control vector. In the top graphs, the top lines represent PRMT1 and the bottom lines represent Vector. In the bottom graphs, the top lines represent Vector and the bottom lines represent PRMT1 shRNA. $P <$

0.05, *t*-test. **FIG. 1B.** Soft agar assay of SKCO1 cells exogenously expressing PRMT1, PRMT1 shRNA and control vector. Representative images from the anchorage-independent growth assay are shown above. *$P < 0.05$, **$P < 0.005$, *t*-test. **FIG. 1C.** Cell proliferation assay of SKCO1 (top) and GEO (bottom) cells expressing PRMT1 or vector control with or without gefitinib treatment. In both graphs, the top solid lines represent PRMT1 and the bottom solid lines represent Vector. In the top graph, the top dashed line represents PRMT1 + gefitinib and the bottom dashed line represents Vector + gefitinib. $P < 0.05$, *t*-test. **FIG. 1D.** Soft agar assay of SKCO1 exogenously expressing PRMT1 and control vector with or without gefitinib treatment. **$P < 0.005$, *t*-test. **FIG. 1E.** Immunoblots comparing pEGFR, pERK, and pAKT levels upon EGF stimulation for the indicated time in SKCO1 (left) and GEO (right) cells expressing PRMT1 or control vector. **FIG. 1F.** Immunoblots evaluating pEGFR, pERK, and pAKT levels upon EGF stimulation for the indicated time in SKCO1 cells expressing two different PRMT1 shRNAs or control vector. All quantitative data were generated from a minimum of three replicates. Data are expressed as mean ± s.d.

[0036] **FIGS. 2A-H.** PRMT1 interacts with EGFR and methylates the EGFR extracellular domain at Arg198 and Arg200. **FIG. 2A.** Top: Reciprocal co-immunoprecipitation of SKCO1 cells using the indicated antibodies. Bottom: Duolink® assay of SKCO1 cells expressing control vector or PRMT1 shRNA. Red spots represent the interaction between PRMT1 and EGFR. **FIG. 2B.** Illustration of EGFR extracellular and intracellular domains that were individually subcloned with GST tags and were purified for *in vitro* methylation assays. **FIG. 2C.** *In vitro* methylation assays showing methylation signals from each GST-tagged EGFR domain after incubation with purified GST-tagged PRMT1. Methylation signals were examined by fluorography. **FIG. 2D.** Sequence alignment of PRMT1 substrates along with EGFR showing a potential GAR motif on EGFR extracellular domain 2. **FIG. 2E.** *In vitro* methylation assay of wild-type EGFR and methylation-site mutant. **FIG. 2F.** Mass spectrum analysis of endogenous EGFR immunopurified from SKCO1 cells. **FIG. 2G.** Dot blot showing specificity of EGFR me-R198/200 Ab. H3R4: Histone H4 arginine 3 asymmetric dimethylated peptide. Asymdi: EGFR asymmetric dimethylated R198/200 peptide. Symdi: EGFR symmetric dimethylated R198/200 peptide. Mono: EGFR monomethylated R198/200 peptide. **FIG. 2H.** Immunoblots comparing the EGFR methylation level of SKCO1 exogenously expressing PRMT1 (left), PRMT1 shRNA (right), and control vector by EGFR methylation antibody. Methylated peptide competition showed antibody specificity for EGFR methylation signal.

[0037] **FIGS. 3A-F.** PRMT1-mediated R198/200 methylation upregulates EGFR dimerization and activation and is correlated with poor patient outcome. **FIG. 3A.** Immunoblot comparing EGFR and downstream ERK activation level of GEO cells expressing control vector, wild-type, and methylation-site mutant (R198/200K) EGFR upon EGF stimulation. **FIG. 3B.** Cell proliferation (left) and anchorage-independent assay (right) of GEO cells expressing control vector, wild-type, and methylation-site mutant EGFR. In the graph of the cell proliferation assay, at the 4-day time point, the top line represents EGFR (wt), the middle line represents Vector, and the bottom line represents EGFR (R198/200K). Representative images of colonies are shown above the quantitative chart. $*P < 0.05$, *t*-test. **FIG. 3C.** Dimerization assay of SKCO1 cells exogenously expressing vector control, PRMT1 (left), PRMT1 shRNA (middle), or GEO cells expressing wild-type and methylation-site mutant EGFR (right). **FIG. 3D.** *In vivo* orthotopic colon tumor growth of GEO cells expressing vector control, wild-type, and methylation sites mutant EGFR (n = 5 per group, $*P < 0.05$, *t*-test.). Top: Representative tumors from each group in the fourth week after inoculation. **FIG. 3E.** Kaplan-Meier plot of overall survival of 215 colorectal cancer cases with low or high methyl-EGFR level detected by me-R198/200 Ab. Low methylation level: methylation level lower than median; High: methylation level higher than median. $P < 0.05$. **FIG. 3F.** Kaplan-Meier plot of recurrence rate of 120 colorectal cancer cases with low or high methyl-EGFR level detected by me-R198/200 Ab. $P < 0.05$. All quantitative data were generated from a minimum of three replicates. Data are expressed as mean ± s.d.

[0038] **FIGS. 4A-H.** PRMT1 enhances EGF binding to EGFR and increases cetuximab resistance in colon cancer cells. **FIG. 4A.** Top: immunoblot showing expression level of PRMT1. Bottom: cell proliferation assay of GEO cells expressing control vector, PRMT1 or PRMT1 shRNA under cetuximab treatment (n = 5). Data are expressed as mean ± s.d. $*P < 0.05$, *t*-test. **FIG. 4B.** Flow cytometric analysis of GEO cells expressing wild-type (top) or methylation-site mutant (middle) EGFR showing binding affinity between APC-conjugated EGF and EGFR in the presence or absence of cetuximab. Bottom: Quantitative results are shown in the bar graph. **FIG. 4C.** Top: immunoblot showing expression level of PRMT1. Bottom: cell proliferation assay of SW48 cells expressing control vector, PRMT1, or PRMT1 shRNA under cetuximab treatment (n = 5). Data are expressed as mean ± s.d. $*P < 0.05$, *t*-test. **FIG. 4D.** Flow cytometry analysis of SW48 cells expressing control vector or PRMT1 showing binding affinity between APC-conjugated EGF and EGFR in the presence or absence of cetuximab. Bottom: Quantitative results are shown in the bar graph. **FIG. 4E.**

Left: Inactive 'tethered' conformation of EGFR. The structure was prepared based on the crystal structure of the inactive human EGFR (PDB accession 1IVO). Domains I-IV are differentially shaded. Arginines 198 and 200 are highlighted. Right: Active dimerized form of EGFR (based on the crystal structure of human EGFR, PDB accession 1NQL). The second EGFR and EGF molecules are shown in gray and black, respectively. **FIGS. 4F-G.** Zoom onto Arg198 (**FIG. 4F**) and Arg200 (**FIG. 4G**), shown as stick figures. Domains I and II are indicated on the surfaces, as is the location of Asp206. **FIG. 4H.** Immunoblot assessing EGFR, ERK, and AKT activation levels of SW48 cells expressing control vector or PRMT1 upon EGF stimulation in the presence or absence of cetuximab.

[0039] **FIGS. 5A-B.** Knock down of PRMT1 reduces the cell proliferation rate of various cancer cell lines and PRMT1-mediated cell growth is correlated with EGFR signaling. MTT assays in the presence or absence of gefitinib of breast cancer cell line, MDA-MB-231 (**FIG. 5A**), and pancreatic cancer cell line, MIA PaCa-2 (**FIG. 5B**). In both graphs, the top solid lines represent Vector and the bottom solid lines represent PRMT1 shRNA. In the bottom graph, the top dashed line represents Vector + gefitinib and the bottom dashed line represents PRMT1 shRNA + gefitinib.

[0040] **FIG. 6.** Mass spectrum analysis showing R497 methylation on immunopurified endogenous EGFR. C_{CAM} stands for S-carbamidomethylcysteine.

[0041] **FIGS. 7A-B.** PRMT1 interacts with and methylates EGFR during protein synthesis. **FIG. 7A.** Immunoblots of the indicated proteins after cell fractionation of SKCO1 cells. **FIG. 7B.** Immunoblots of the indicated proteins after ER isolation of SKCO1 cells expressing control vector or PRMT1 shRNA.

[0042] **FIG. 8.** PRMT1 upregulates EGFR activation. Immunoblot comparing EGFR and downstream ERK activation levels in HT29 cells expressing control vector, WT, and R198/200K mutant EGFR with or without PRMT1 knock down upon EGF stimulation.

[0043] **FIGS. 9A-C.** EGFR methylation regulates EGF binding to EGFR. **FIG. 9A.** Scatchard plot and binding curves (insert) measuring EGFR-EGF binding affinity of HT29 cells expressing WT or R198/200K mutant EGFR with or without cetuximab treatment. **FIG. 9B.** Scatchard plot and binding curves (insert) measuring EGFR-EGF binding affinity of HT29 cells expressing WT or R198/200K mutant EGFR with or without knock down of PRMT1. **FIG. 9C.** Scatchard plot and binding curves (insert) measuring

EGFR-EGF binding affinity of SW48 cells expressing WT or R198/200K mutant EGFR with or without knock down of PRMT1.

[0044] **FIGS. 10A-B.** EGFR methylation does not affect its cell surface expression level. Biotinylated cell surface EGFR from SKCO1 (**FIG. 10A**) and GEO (**FIG. 10B**) cells were captured on streptavidin-agarose beads and detected by immunoblot.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

[0045] This invention provides methods for the identification of subsets of patients who are likely to be either sensitive or resistant to cetuximab therapy. For example, this invention provides biomarkers (*e.g.*, methylation of R198 or R200 of EGFR or the presence of an arginine at position 497 of EGFR) for the prediction of resistance to cetuximab therapy. This invention also provides methods for the selection of patients for combination therapy with cetuximab and PRMT inhibitors. Patients who have arginine methylation on the extracellular domain of EGFR, specifically on residues R198 and R200, or have an arginine at position 497 are likely to be resistant to cetuximab therapy; thus, this invention will help in determining the treatment strategy for this subset of patients. Additionally, for those patients who do have the arginine methylations on EGFR, the present invention provides a combination therapy of cetuximab plus a PRMT inhibitor. The ability to predict patients' response prior to treatment, will allow for a rational treatment strategy either for use of cetuximab alone in the subset of patients without EGFR arginine methylation or use of combination therapy in the patients with EGFR arginine methylation to overcome resistance to cetuximab.

[0046] Without being bound by theory, the inventors provide a mechanism contributing to cetuximab resistance in which protein arginine methyltransferase 1 (PRMT1) methylates the extracellular domain of EGFR at R198 and R200, leading to an increase in the binding affinity between EGF and methylated EGFR, and subsequently receptor dimerization, downstream signaling activation, and cell proliferation *in vitro*. Meanwhile, R/K mutation of the EGFR methylation sites reduces tumor growth in mouse orthotopic xenograft model. Moreover, EGFR methylation level is correlated with poor patient outcomes. Importantly, methylated EGFR retains its signaling activation and cell proliferation in the presence of cetuximab, suggesting that the methylation status of EGFR has the potential to predict resistance to cetuximab treatment in cancer patients.

I. Antibodies

[0047] It will be understood that polyclonal or monoclonal antibodies specific for R198/200 methylated EGFR will have utility in several applications. These include the production of diagnostic kits for use in detecting and diagnosing cancer as well as selecting patients for treatment.

1. Polyclonal Antibodies

[0048] Polyclonal antibodies generally are raised in animals by multiple subcutaneous or intraperitoneal injections of antigen and adjuvant. Animals are immunized against the immunogenic composition or derivatives. Animals are boosted until the titer plateaus. The animals are usually bled through an ear vein or alternatively by cardiac puncture. The removed blood is allowed to coagulate and then centrifuged to separate serum components from whole cells and blood clots. The serum may be used as is for various applications or else the desired antibody fraction may be purified by well-known methods, such as affinity chromatography using another antibody, a peptide bound to a solid matrix, or by using, *e.g.*, protein A or protein G chromatography.

2. Monoclonal antibodies

[0049] The methods for generating monoclonal antibodies (mAbs) generally begin along the same lines as those for preparing polyclonal antibodies. Rodents, such as mice and rats, are preferring animals; however, the use of rabbit, sheep, goat, and monkey cells also is possible. The use of rats may provide certain advantages (Goding, 1986), but mice are preferred, with the BALB/c mouse being most preferred as this is most routinely used and generally gives a higher percentage of stable fusions.

[0050] Monoclonal antibodies are obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies.

[0051] The animals are injected with antigen, generally as described above for polyclonal antibodies. The antigen may be coupled to carrier molecules, such as keyhole limpet hemocyanin, if necessary. The antigen would typically be mixed with adjuvant, such

as Freund's complete or incomplete adjuvant. Booster injections with the same antigen would occur at approximately two-week intervals.

[0052] Following immunization, somatic cells with the potential for producing antibodies, specifically B lymphocytes (B cells), are selected for use in the mAb generating protocol. These cells may be obtained from biopsied spleens or lymph nodes. Spleen cells and lymph node cells are preferred, the former because they are a rich source of antibody producing cells that are in the dividing plasmablast stage.

[0053] Often, a panel of animals will have been immunized and the spleen of an animal with the highest antibody titer will be removed and the spleen lymphocytes obtained by homogenizing the spleen with a syringe. Typically, a spleen from an immunized mouse contains approximately 5×10^7 to 2×10^8 lymphocytes.

[0054] The antibody producing B lymphocytes from the immunized animal are then fused with cells of an immortal myeloma cell, generally one of the same species as the animal that was immunized. Myeloma cell lines suited for use in hybridoma-producing fusion procedures preferably are non-antibody producing, have high fusion efficiency, and have enzyme deficiencies that render them incapable of growing in certain selective media that support the growth of only the desired fused cells (hybridomas).

[0055] Methods for generating hybrids of antibody producing spleen or lymph node cells and myeloma cells usually comprise mixing somatic cells with myeloma cells in a 2:1 proportion, though the proportion may vary from about 20:1 to about 1:1, respectively, in the presence of an agent or agents (chemical or electrical) that promote the fusion of cell membranes. Fusion methods using Sendai virus have been described by Köhler and Milstein (1976), and those using polyethylene glycol (PEG), such as 37% (v/v) PEG. The use of electrically induced fusion methods also is appropriate (Goding, 1986).

[0056] Fusion procedures usually produce viable hybrids at low frequencies, about 1×10^6 to 1×10^8. However, this does not pose a problem, as the viable, fused hybrids are differentiated from the parental, infused cells (particularly the infused myeloma cells that would normally continue to divide indefinitely) by culturing in a selective medium. The selective medium is generally one that contains an agent that blocks the de novo synthesis of nucleotides in the tissue culture media. Exemplary and preferred agents are aminopterin, methotrexate, and azaserine. Aminopterin and methotrexate block de novo synthesis of both

purines and pyrimidines, whereas azaserine blocks only purine synthesis. Where aminopterin or methotrexate is used, the media is supplemented with hypoxanthine and thymidine as a source of nucleotides (HAT medium). Where azaserine is used, the media is supplemented with hypoxanthine.

[0057] The preferred selection medium is HAT. Only cells capable of operating nucleotide salvage pathways are able to survive in HAT medium. The myeloma cells are defective in key enzymes of the salvage pathway, *e.g.*, hypoxanthine phosphoribosyl transferase (HPRT), and they cannot survive. The B cells can operate this pathway, but they have a limited life span in culture and generally die within about two weeks. Therefore, the only cells that can survive in the selective media are those hybrids formed from myeloma and B cells.

[0058] This culturing provides a population of hybridomas from which specific hybridomas are selected. Typically, selection of hybridomas is performed by culturing the cells by single clone dilution in microtiter plates, followed by testing the individual clonal supernatants (after about two to three weeks) for the desired reactivity. The assay should be sensitive, simple, and rapid, such as radioimmunoassays, enzyme immunoassays, cytotoxicity assays, plaque assays, dot immunobinding assays, and the like.

[0059] The selected hybridomas would then be serially diluted and cloned into individual antibody producing cell lines, which clones can then be propagated indefinitely to provide mAbs. The cell lines may be exploited for mAb production in two basic ways.

[0060] A sample of the hybridoma can be injected (often into the peritoneal cavity) into a histocompatible animal of the type that was used to provide the somatic and myeloma cells for the original fusion (*e.g.*, a syngeneic mouse). Optionally, the animals are primed with a hydrocarbon, especially oils, such as pristane (tetramethylpentadecane), prior to injection. The injected animal develops tumors secreting the specific monoclonal antibody produced by the fused cell hybrid. The body fluids of the animal, such as serum or ascites fluid, can then be tapped to provide mAbs in high concentration.

[0061] The individual cell lines could also be cultured in vitro, where the mAbs are naturally secreted into the culture medium from which they can be readily obtained in high concentrations.

[0062] mAbs produced by either means may be further purified, if desired, using filtration, centrifugation and various chromatographic methods such as HPLC or affinity chromatography. Fragments of the monoclonal antibodies of the invention can be obtained from the purified monoclonal antibodies by methods that include digestion with enzymes, such as pepsin or papain, and/or by cleavage of disulfide bonds by chemical reduction. Alternatively, monoclonal antibody fragments encompassed by the present invention can be synthesized using an automated peptide synthesizer.

[0063] It also is contemplated that a molecular cloning approach may be used to generate monoclonals. For this, combinatorial immunoglobulin phagemid libraries are prepared from RNA isolated from the spleen of the immunized animal, and phagemids expressing appropriate antibodies are selected by panning using cells expressing the antigen and control cells, *e.g.*, normal versus tumor cells. The advantages of this approach over conventional hybridoma techniques are that approximately 10^4 times as many antibodies can be produced and screened in a single round, and that new specificities are generated by H and L chain combination, which further increases the chance of finding appropriate antibodies.

II. Biomarker Detection

[0064] In certain embodiments, the method comprises the steps of obtaining a biological sample from a mammal to be tested and detecting the presence of Arg198/200 EGFR methylation or the presence of an arginine at amino acid position 497 of EGFR in the sample. The EGFR gene is alternative spliced resulting in the production of four protein isoforms. All four precursor isoforms (see SEQ ID NOs: 12, 14, 16, and 18) comprise a 24 amino acid signal peptide that is cleaved to produce the mature protein. The numbering system used herein (*i.e.*, regarding positions 198, 200, and 497) refers to the mature protein sequence (see SEQ ID NOs: 13, 15, 17, and 19). Note that the mature isoform C (SEQ ID NO: 17) does not comprise a position 497, but does comprise Arg198 and Arg200.

[0065] In one embodiment, the biological sample is a cell sample from a tumor in the mammal. In another embodiment, the biological sample is a circulating tumor cell isolated from the mammal. As used herein the phrase "selectively measuring" refers to methods wherein only a finite number of protein or nucleic acid (*e.g.*, mRNA) markers are measured rather than assaying essentially all proteins or nucleic acids in a sample. For example, in some aspects "selectively measuring" nucleic acid or protein markers can refer to

measuring no more than 100, 75, 50, 25, 15, 10, 5, or 2 different nucleic acid or protein markers.

[0066] The assays can identify a biomarker for predicting therapy response to a therapeutic regimen, such as anti-EGFR therapy. Assays for response prediction may be run before start of therapy and patients showing levels of a biomarker above or below a threshold level of the biomarker are eligible to receive anti-EGFR therapy.

A. Biological Samples

[0067] The sample obtained from an individual may contain cells affected by the disease, meaning that the cells express the disease-associated protein. Thus, where the protein is expressed in a cell-specific manner, the sample will contain the cell type in which the disease protein is expressed In terms of antigen detection, the sample analyzed may be any body fluid sample that is suspected of containing the antigen, such as, for example, blood serum, cerebrospinal fluid, mucus, saliva, vaginal secretion, and urine, or may be a sample of the diseased tissue itself.

1. Tumor Cell Sample

[0068] The method includes collecting samples from a cancer patient for assessment of biomarker levels. The method can use a patient tissue sample of any type or a derivative thereof, including peripheral blood, serum or plasma fraction from peripheral blood, tumor or suspected tumor tissues (including fresh frozen and fixed or paraffin embedded tissue), cell isolates such as circulating epithelial cells separated or identified in a blood sample, lymph node tissue, bone marrow and fine needle aspirates. The sample suitable for use in the method can comprise any tissue type or cell isolates from any tissue type, including a peripheral blood sample, a tumor tissue or a suspected tumor tissue, a thin layer cytological sample, a fine needle aspirate sample, a bone marrow sample, a lymph node sample, a urine sample, an ascites sample, a lavage sample, an esophageal brushing sample, a bladder or lung wash sample, a spinal fluid sample, a brain fluid sample, a ductal aspirate sample, a nipple discharge sample, a pleural effusion sample, a fresh frozen tissue sample, a paraffin embedded tissue sample or an extract or processed sample produced from any of a peripheral blood sample, a serum or plasma fraction of a peripheral blood sample, a tumor tissue or a suspected tumor tissue, a thin layer cytological sample, a fine needle aspirate sample, a bone marrow sample, a lymph node sample, a urine sample, an ascites sample, a

lavage sample, an esophageal brushing sample, a bladder or lung wash sample, a spinal fluid sample, a brain fluid sample, a ductal aspirate sample, a nipple discharge sample, a pleural effusion sample, a fresh frozen tissue sample or a paraffin embedded tissue sample. For example, a patient peripheral blood sample can be initially processed to extract an epithelial cell population, a plasma fraction or a serum fraction, and this extract, plasma fraction or serum fraction can then be assayed. A microdissection of the tissue sample to obtain a cellular sample enriched with suspected tumor cells can also be used. The tissue sample can be processed by any desirable method for performing protein-based assays.

2. Circulating Tumor Cells

[0069] Circulating tumor cells (CTCs) from any suitable sample type may be used to detect the biomarkers of the present embodiments. As used herein, the term "sample" refers to any sample suitable for the methods provided by the present invention. The sample may be any sample that includes CTCs suitable for detection of a biomarker. Sources of samples include whole blood, serum, bone marrow, pleural fluid, peritoneal fluid, central spinal fluid, urine, saliva and bronchial washes. In one aspect, the sample is a blood sample, including, for example, whole blood or any fraction or component thereof. A blood sample, suitable for use with the present invention may be extracted from any source known that includes blood cells or components thereof, such as venous, arterial, peripheral, tissue, cord, and the like. For example, a sample may be obtained and processed using well known and routine clinical methods (e.g., procedures for drawing and processing whole blood). In one aspect, an exemplary sample may be peripheral blood drawn from a subject with cancer.

[0070] The total number of CTCs in a CTC population is dependent, in part, on the initial sample volume. In various aspects, detection of biomarkers in CTCs from a wide range of initial sample volumes is sufficient to provide clinically significant results. As such, the initial sample volume may be less than about 25 µl, 50 µl, 75 µl, 100 µl, 125 µl, 150 µl, 175 µl, 200 µl, 225 µl, 250 µl, 300 µl, 400 µl, 500 µl, 750 µl, 1 ml, 2 ml, 3 ml, 4 ml, 5 ml, 6 ml, 7 ml, 8 ml, 9 ml or greater than about 10 ml. In an exemplary aspect, the initial sample volume is between about 100 and 200 µl. In another exemplary aspect, a sample processed as described herein includes greater than about 1, 2, 5, 7, 10, 15, 20, 30, 40, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, or even 1000 CTCs.

[0071] As used herein, biomarker detection analysis includes any method that allows direct or indirect isolation of CTCs and may be in vivo or ex vivo. For example,

analysis may include, but not limited to, ex vivo microscopic or cytometric detection and visualization of cells bound to a solid substrate, flow cytometry, fluorescent imaging, and the like. In an exemplary aspect, CTCs are isolated using antibodies directed to CTC-specific cell surface markers.

[0072] In another embodiment, the CTCs are captured by techniques commonly used to enrich a sample for CTCs, for example those involving immunospecific interactions, such as immunomagnetic capture. Immunomagnetic capture, also known as immunomagnetic cell separation, typically involves attaching antibodies directed to proteins found on a particular cell type to small paramagnetic beads. When the antibody-coated beads are mixed with a sample, such as blood, they attach to and surround the particular cell. The sample is then placed in a strong magnetic field, causing the beads to pellet to one side. After removing the blood, captured cells are retained with the beads. Many variations of this general method are well known in the art and suitable for use to isolate CTCs.

[0073] Isolation of CTCs and characterization of biomarkers therein, using the methods of the invention, is useful in assessing cancer prognosis and in monitoring therapeutic efficacy for early detection of treatment failure that may lead to disease relapse. This is because the presence of CTCs has been associated and/or correlated with tumor progression and spread, poor response to therapy, relapse of disease, and/or decreased survival over a period of time. Thus, enumeration of CTCs and characterization of biomarkers therein provide methods to stratify patients for baseline characteristics that predict initial risk and subsequent risk based upon response to therapy.

[0074] Accordingly, in another embodiment, the invention provides a method for diagnosing or prognosing cancer in a subject. CTCs isolated according to the methods disclosed herein may be analyzed to diagnose or prognose cancer in the subject. As such, the methods of the present invention may be used, for example, to evaluate cancer patients and those at risk for cancer. In any of the methods of diagnosis or prognosis described herein, either the presence or the absence of one or more indicators of cancer, such as a R198/200 EGFR methylation event, may be used to generate a diagnosis or prognosis.

[0075] In one aspect, a blood sample is drawn from the patient and CTCs are analyzed as described herein. Using the method of the invention, the number of CTCs in the blood sample may be determined and the CTCs subsequently analyzed. For example, the

cells may be labeled with one or more antibodies that bind to a CTC-specific cell surface marker, such as, for example, cytokeratin or EpCAM, and the antibodies may have a covalently bound fluorescent label. Analysis may then be performed to characterize the CTCs in the sample, and from this measurement.

B. Detection Methods

[0076] In one embodiment, the methods described herein provide for detecting the presence a posttranslational modification of a protein (e.g., R198, R200, and/or R497 methylation of EGFR) or a sequence alteration of a gene (e.g., the presence of an arginine at amino acid position 497 of EGFR) in a biological sample obtained from an individual.

[0077] In some embodiment of the methods described herein, detecting the presence a biomarker in a biological sample obtained from an individual comprises determining the presence of a modified polypeptide in the sample. A polypeptide can be detected by any of a number of means known to those of skill in the art, including analytical biochemical methods, such as electrophoresis, capillary electrophoresis, high performance liquid chromatography ("HPLC"), thin layer chromatography ("TLC"), hyperdiffusion chromatography, and the like, or various immunological methods, such as fluid or gel precipitation reactions, immunodiffusion (single or double), immunoelectrophoresis, radioimmunoassay ("RIA"), enzyme-linked immunosorbent assay ("ELISA"), immunofluorescent assays, flow cytometry, FACS, western blotting, and the like.

[0078] Techniques for detecting arginine 497 in EGFR in a sample include reverse transcription of mRNA, followed by PCR amplification with primers specific for EGFR mRNA (e.g., RT-PCR or quantitative RT-PCR), and finally sequencing of the amplification product. Alternatively, the mRNA may be sequenced directly without the need for amplification.

1. Immunological Methods

[0079] The presence of a modified polypeptide can be determined by contacting the sample with an antibody that specifically binds to the modified polypeptide product (*e.g.*, R198/200 methylated EGFR) and detecting or measuring the formation of the complex between the antibody and the modified polypeptide. An antibody can be labeled (*e.g.*, radioactive, fluorescently, biotinylated or HRP-conjugated) to facilitate detection of the

complex. Appropriate assay systems for detecting polypeptides include, but are not limited to, flow cytometry, enzyme-linked immunosorbent assay (ELISA), competition ELISA assays, radioimmuno-assays (RIA), immunofluorescence, gel electrophoresis, western blot, chemiluminescent assays, bioluminescent assays, and immunohistochemical assays using antibodies having specificity for the modified polypeptide. Numerous methods and devices are well known to the skilled artisan for the detection and analysis of the instant invention. With regard to polypeptides or proteins in test samples, immunoassay devices and methods are often used. These devices and methods can utilize labeled molecules in various sandwich, competitive, or non-competitive assay formats, to generate a signal that is related to the presence or amount of a biomarker of interest. Additionally, certain methods and devices, such as but not limited to, biosensors and optical immunoassays, may be employed to determine the presence or amount of biomarkers without the need for a labeled molecule.

[0080] In general, immunological methods include obtaining a sample suspected of containing an antigen, contacting the sample with a first monoclonal antibody that binds the antigen, and contacting the sample with a composition capable of selectively binding or detecting the complex, e.g., a labeled second antibody, under conditions effective to allow immune complex (antigen/antibody) formation. Examples of compositions capable of selectively binding or detecting the antigen include, but are not limited to, antibodies, aptamers, or other ligands that can be labeled using a variety of markers, *e.g.*, biotin/avidin ligand binding arrangement, as is known in the art. One skilled in the art may also use a labeled third antibody.

[0081] "Under conditions effective to allow immune complex (antigen/antibody) formation" means that the conditions preferably include diluting the antigens and/or antibodies with solutions such as BSA, bovine gamma globulin (BGG), or phosphate buffered saline (PBS)/Tween. These agents tend to assist in the reduction of nonspecific background. The "suitable" conditions also means that the incubation is at a temperature or for a period of time sufficient to allow effective binding. Incubation steps are typically from about 1 to 2 to 4 hours or so, at temperatures preferably on the order of 25 °C to 27 °C, or may be overnight at about 4 °C or so.

[0082] Contacting the patient sample with the first antibody under effective conditions and for a period of time sufficient to allow the formation of immune complexes (primary immune complexes) is generally a matter of simply adding the antibody

composition to the sample and incubating the mixture for a period of time long enough for the antibodies to form immune complexes with, i.e., to bind to, any antigens present, i.e., methylated EGFR. After this time, the sample-antibody composition, such as an ELISA plate, dot blot, or western blot, will generally be washed to remove any non-specifically bound antibody species, allowing only those antibodies specifically bound with the antigen to be detected.

[0083] The antigen, antibody, or antigen:antibody complex employed in the detection may itself be linked to a detectable label, wherein one would then simply detect this label, thereby allowing the amount of the antigen in the sample to be determined. Alternatively, the first antibody that becomes bound within the antigen may be detected by means of a second binding ligand that has binding affinity for the antibody. In these cases, the second binding ligand may be linked to a detectable label. The second binding ligand is itself often an antibody, which may thus be termed a "secondary" antibody. The primary immune complexes are contacted with the labeled, secondary binding ligand, or antibody, under effective conditions and for a period of time sufficient to allow the formation of secondary immune complexes. The secondary immune complexes are then generally washed to remove any non-specifically bound labeled secondary antibodies or ligands, and the remaining label in the secondary immune complexes is then detected.

[0084] Further methods include the detection of a primary immune complex by a two step approach. A second binding ligand, such as an antibody, that has binding affinity for the antibody is used to form secondary immune complexes, as described above. After washing, the secondary immune complexes are contacted with a third binding ligand or antibody that has binding affinity for the second antibody, again under effective conditions and for a period of time sufficient to allow the formation of immune complexes (tertiary immune complexes). The third ligand or antibody is linked to a detectable label, allowing detection of the tertiary immune complexes thus formed. This system may provide for signal amplification if this is desired.

[0085] Immunohistochemical staining may be used to detect the presence of a biomarker. This method enables the localization of a protein in the cells of a tissue section by interaction of the protein with a specific antibody. For this, the tissue may be fixed in formaldehyde or another suitable fixative, embedded in wax or plastic, and cut into thin sections (from about 0.1 mm to several mm thick) using a microtome. Alternatively, the

tissue may be frozen and cut into thin sections using a cryostat. The sections of tissue may be arrayed onto and affixed to a solid surface (*i.e.*, a tissue microarray). The sections of tissue are incubated with a primary antibody against the antigen of interest, followed by washes to remove the unbound antibodies. The primary antibody may be coupled to a detection system, or the primary antibody may be detected with a secondary antibody that is coupled to a detection system. The detection system may be a fluorophore or it may be an enzyme, such as horseradish peroxidase or alkaline phosphatase, which can convert a substrate into a colorimetric, fluorescent, or chemiluminescent product. The stained tissue sections are generally scanned under a microscope. Because a sample of tissue from a subject with cancer may be heterogeneous, i.e., some cells may be normal and other cells may be cancerous, the percentage of positively stained cells in the tissue may be determined. This measurement, along with a quantification of the intensity of staining, may be used to generate an expression value for the biomarker.

[0086] An enzyme-linked immunosorbent assay, or ELISA, may be used to measure the expression of a plurality of biomarkers. There are many variations of an ELISA assay. All are based on the immobilization of an antigen or antibody on a solid surface, generally a microtiter plate. The original ELISA method comprises preparing a sample containing the biomarker proteins of interest, coating the wells of a microtiter plate with the sample, incubating each well with a primary antibody that recognizes a specific antigen, washing away the unbound antibody, and then detecting the antibody-antigen complexes. The antibody-antibody complexes may be detected directly. For this, the primary antibodies are conjugated to a detection system, such as an enzyme that produces a detectable product. The antibody-antibody complexes may be detected indirectly. For this, the primary antibody is detected by a secondary antibody that is conjugated to a detection system, as described above. The microtiter plate is then scanned and the raw intensity data may be converted into expression values using means known in the art.

[0087] The western blot is a method of assaying for the presence of a particular protein within a biological sample. The general methodology of the western blot is comprised of applying the sample to a polyacrylamide gel and separating the proteins through the technique of gel electrophoresis. The proteins, which have been separated into discrete bands, are subsequently transferred to a sheet (*e.g.*, nitrocellulose or PVDF) by way of a blotting chamber. Once the protein bands have been transferred, the blot is treated with

antibody specific to the particular antigen of interest; if the antigen is present, the antibody will bind to the antigen. Free antibody is washed away, the blot is treated with a second antibody which is capable of binding to a site on the first antibody, and the blot is rinsed again to remove excess antibody. In order to detect binding, the second antibody may carry a radiolabel or fluorescent label or may be linked to an enzyme as in the ELISA technique. The enzyme linked to the antibody may then in turn react with a substrate applied to the blot which, for example, generates a colored product. In the case of a radiolabel, the bands may be visualized through the technique of autoradiography, where the radioactive blot is exposed to photographic film for a time sufficient to visualize the protein band or bands of interest. In the case of a fluorescent label, the bands may be visualized using an Odyssey imaging system (LI-COR). The presence of very small quantities of antigen may be detected due to the highly sensitive nature of the western blotting technique.

[0088] An antibody microarray may also be used to measure the differential expression of a plurality of biomarkers. For this, a plurality of antibodies is arrayed and covalently attached to the surface of the microarray or biochip. A protein extract containing the biomarker proteins of interest is generally labeled with a fluorescent dye. The labeled biomarker proteins are incubated with the antibody microarray. After washes to remove the unbound proteins, the microarray is scanned. The raw fluorescent intensity data may be converted into expression values using means known in the art.

[0089] As detailed above, immunoassays, in their most simple and/or direct sense, are binding assays. Certain preferred immunoassays are the various types of enzyme-linked immunosorbent assays (ELISAs) and/or radioimmunoassays (RIA) known in the art. Immunohistochemical detection using tissue sections is also particularly useful. However, it will be readily appreciated that detection is not limited to such techniques, and western blotting, dot blotting, FACS analyses, and/or the like may also be used.

2. Analytical Biochemical Methods

[0090] Alternatively, the presence of methylated EGFR polypeptide may be detected using analytical biochemical methods, such as, for example, techniques including gel electrophoresis, isoelectric focusing (IEF), cation exchange HPLC, or mass spectrometry. Mass spectrometric analysis has been used for the detection of proteins in serum samples. Mass spectroscopy methods include Surface Enhanced Laser Desorption Ionization (SELDI)

mass spectrometry (MS), SELDI time-of-flight mass spectrometry (TOF-MS), Maldi Qq TOF, MS/MS, TOF-TOF, ESI-Q-TOF and ION-TRAP.

[0091] In one embodiment of the method, mass spectrometry methods are used to identify proteolytic disease peptides derived from mutant or modified disease proteins. Such methods are efficient, accurate methods to isolate and identify biomolecules and are well suited to separation and identification of proteolytic disease peptides having a disease mutation that may differ by a single amino acid or that may differ with respect to post-translational modifications as compared to a proteolytic non-disease peptide which may be contained in the same sample of a heterozygous individual.

[0092] Thus, techniques such as MALDI-TOF mass spectrometry, LC/MS/MS (MRM) or high resolution LC/MS may be used. Preparation of the sample fraction containing the proteolytic peptides may be done in accordance with routine methods. For example, the fraction of the sample containing the proteolytic peptides may be mixed with a UV-absorbing matrix prior to laser irradiation in a mass spectrometer or injected for LC/MS.

[0093] Techniques such as tandem mass spectroscopy (MS/MS) and liquid chromatography/mass spectroscopy (LC/MS and LC/MS/MS) can be used to obtain the sequence of individual peptides in the sample. Briefly, in LC/MS, different peptides are separated by a reverse phase column according to their hydrophobicity and sprayed into a mass spectrometer for mass measurement. In LC/MS/MS, the peptide is further fragmented in the mass spectrometer to generate fragments, and one, a few, or all of the fragments can be measured in the mass spectrometer to increase specificity.

[0094] Thus, for example, the use of selected reaction monitoring (SRM) mode and multiple reaction monitoring mode (MRM) can be performed using tandem MS methods in order to identify the sequences of the particular peptides contained within the sample.

[0095] As indicated above, mass spectroscopy methods can also be used to identify differences in post-translational modification between proteolytic peptides containing a disease mutation and non-disease peptides.

[0096] If desired, the results obtained with the sample from the individual to be diagnosed may be compared with samples containing known non-disease proteolytic peptides without any mutation/modification and/or with samples containing known disease proteolytic peptides containing known disease mutations/modifications.

III. Treatment of Neoplastic Conditions

[0097] "Treatment" and "treating" refer to administration or application of a therapeutic agent to a subject or performance of a procedure or modality on a subject for the purpose of obtaining a therapeutic benefit of a disease or health-related condition. For example, a treatment may include administration of a pharmaceutically effective amount of an EGFR-targeted therapeutic (*e.g.*, EGFR-targeted monoclonal antibody) either alone or in combination with a PRMT inhibitor.

[0098] The term "therapeutic benefit" or "therapeutically effective" as used throughout this application refers to anything that promotes or enhances the well-being of the subject with respect to the medical treatment of the condition. This includes, but is not limited to, a reduction in the frequency or severity of the signs or symptoms of a disease. For example, treatment of cancer may involve, for example, a reduction in the invasiveness of a tumor, reduction in the growth rate of the cancer, or prevention of metastasis. Treatment of cancer may also refer to prolonging survival of a subject with cancer.

[0099] The term "subject," as used herein, refers to any individual or patient to which the subject methods are performed. Generally the subject is human, although as will be appreciated by those skilled in the art, the subject may be an animal. Thus other animals, including mammals such as rodents (including mice, rats, hamsters and guinea pigs), cats, dogs, rabbits, farm animals including cows, horses, goats, sheep, pigs, etc., and primates (including monkeys, chimpanzees, orangutans and gorillas) are included within the definition of subject.

[00100] The term "cancer," as used herein, includes a variety of cancer types that are well known in the art, including but not limited to, dysplasias, hyperplasias, solid tumors and hematopoietic cancers. Many types of cancers are known to metastasize and shed circulating tumor cells or be metastatic, for example, a secondary cancer resulting from a primary cancer that has metastasized. Tumors for which the present treatment methods are useful include any malignant cell type, such as those found in a solid tumor or a

hematological tumor. Exemplary solid tumors can include, but are not limited to, a tumor of an organ or organ system selected from the group consisting of cardiac, genitourinary tract, reproductive, liver, bone, nervous system, skin, pancreas, colon, cecum, stomach, adrenal gland, brain, head, neck, ovary, kidney, larynx, sarcoma, lung, bladder, melanoma, prostate, and breast. Exemplary hematological tumors include tumors of the bone marrow, T or B cell malignancies, leukemias, lymphomas, blastomas, myelomas, and the like. Further examples of cancers that may be treated using the methods provided herein include, but are not limited to, lung cancer (including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the peritoneum, gastric or stomach cancer (including gastrointestinal cancer and gastrointestinal stromal cancer), pancreatic cancer, cervical cancer, ovarian cancer, liver cancer, bladder cancer, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, various types of head and neck cancer, vascular cancer, and melanoma.

[00101] The cancer may specifically be of the following histological type, though it is not limited to these: neoplasm, malignant; carcinoma; carcinoma, undifferentiated; giant and spindle cell carcinoma; small cell carcinoma; papillary carcinoma; squamous cell carcinoma; lymphoepithelial carcinoma; basal cell carcinoma; moles dysplastic nevi; pilomatrix carcinoma; transitional cell carcinoma; papillary transitional cell carcinoma; adenocarcinoma; gastrinoma, malignant; cholangiocarcinoma; hepatocellular carcinoma; combined hepatocellular carcinoma and cholangiocarcinoma; trabecular adenocarcinoma; adenoid cystic carcinoma; adenocarcinoma in adenomatous polyp; adenocarcinoma, familial polyposis coli; solid carcinoma; carcinoid tumor, malignant; branchiolo-alveolar adenocarcinoma; papillary adenocarcinoma; chromophobe carcinoma; acidophil carcinoma; oxyphilic adenocarcinoma; basophil carcinoma; clear cell adenocarcinoma; granular cell carcinoma; follicular adenocarcinoma; papillary and follicular adenocarcinoma; nonencapsulating sclerosing carcinoma; adrenal cortical carcinoma; endometroid carcinoma; skin appendage carcinoma; apocrine adenocarcinoma; sebaceous adenocarcinoma; ceruminous adenocarcinoma; mucoepidermoid carcinoma; cystadenocarcinoma; papillary cystadenocarcinoma; papillary serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous adenocarcinoma; signet ring cell carcinoma; infiltrating duct carcinoma; medullary carcinoma; lobular carcinoma; inflammatory carcinoma; lipoma; angioma; dermatofibroma; keloids; mammary cancer; paget's disease,

mammary; acinar cell carcinoma; adenosquamous carcinoma; adenocarcinoma w/squamous metaplasia; thymoma, malignant; ovarian stromal tumor, malignant; thecoma, malignant; granulosa cell tumor, malignant; androblastoma, malignant; sertoli cell carcinoma; leydig cell tumor, malignant; lipid cell tumor, malignant; paraganglioma, malignant; extra-mammary paraganglioma, malignant; pheochromocytoma; glomangiosarcoma; malignant melanoma; amelanotic melanoma; superficial spreading melanoma; lentigo malignant melanoma; acral lentiginous melanomas; nodular melanomas; malignant melanoma in giant pigmented nevus; epithelioid cell melanoma; blue nevus, malignant; sarcoma; fibrosarcoma; fibrous histiocytoma, malignant; myxosarcoma; liposarcoma; leiomyosarcoma; rhabdomyosarcoma; embryonal rhabdomyosarcoma; alveolar rhabdomyosarcoma; stromal sarcoma; mixed tumor, malignant; mullerian mixed tumor; nephroblastoma; hepatoblastoma; carcinosarcoma; mesenchymoma, malignant; brenner tumor, malignant; phyllodes tumor, malignant; synovial sarcoma; mesothelioma, malignant; dysgerminoma; embryonal carcinoma; teratoma, malignant; struma ovarii, malignant; choriocarcinoma; mesonephroma, malignant; hemangiosarcoma; hemangioendothelioma, malignant; Kaposi's sarcoma; hemangiopericytoma, malignant; lymphangiosarcoma; osteosarcoma; juxtacortical osteosarcoma; osteoblastic osteocarcinoma; chondrosarcoma; chondroblastoma, malignant; mesenchymal chondrosarcoma; giant cell tumor of bone; ewing's sarcoma; odontogenic tumor, malignant; ameloblastic odontosarcoma; ameloblastoma, malignant; ameloblastic fibrosarcoma; uterine leiomyomas; pinealoma, malignant; chordoma; choroid plexus carcinoma; glioma, malignant; Schwannoma; medulloblastoma; ependymoma; astrocytoma; protoplasmic astrocytoma; fibrillary astrocytoma; astroblastoma; glioblastoma; oligodendroglioma; oligodendroblastoma; primitive neuroectodermal; cerebellar sarcoma; ganglioneuroblastoma; neuroblastoma; retinoblastoma; olfactory neurogenic tumor; meningioma, malignant; neurofibrosarcoma; neurilemmoma, malignant; granular cell tumor, malignant; malignant lymphoma; hodgkin's disease; hodgkin's; paragranuloma; malignant lymphoma, small lymphocytic; malignant lymphoma, large cell, diffuse; malignant lymphoma, follicular; mycosis fungoides; other specified non-hodgkin's lymphomas; B-cell lymphoma; low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; Waldenstrom's macroglobulinemia; malignant histiocytosis; multiple myeloma; mast cell sarcoma; immunoproliferative small intestinal disease; leukemia; lymphoid leukemia; plasma cell

leukemia; erythroleukemia; lymphosarcoma cell leukemia; myeloid leukemia; basophilic leukemia; eosinophilic leukemia; monocytic leukemia; mast cell leukemia; megakaryoblastic leukemia; myeloid sarcoma; hairy cell leukemia; chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); acute myeloid leukemia (AML); and chronic myeloblastic leukemia.

[00102] An effective response of a patient or a patient's "responsiveness" to treatment refers to the clinical or therapeutic benefit imparted to a patient at risk for, or suffering from, a disease or disorder. Such benefit may include cellular or biological responses, a complete response, a partial response, a stable disease (without progression or relapse), or a response with a later relapse. For example, an effective response can be reduced tumor size or progression-free survival in a patient diagnosed with cancer.

[00103] Treatment outcomes can be predicted and monitored and/or patients benefiting from such treatments can be identified or selected via the methods described herein.

[00104] Regarding neoplastic condition treatment, depending on the stage of the neoplastic condition, neoplastic condition treatment involves one or a combination of the following therapies: surgery to remove the neoplastic tissue, radiation therapy, and chemotherapy. Other therapeutic regimens may be combined with the administration of the anticancer agents, e.g., therapeutic compositions and chemotherapeutic agents. For example, the patient to be treated with such anti-cancer agents may also receive radiation therapy and/or may undergo surgery.

[00105] For the treatment of disease, the appropriate dosage of a therapeutic composition will depend on the type of disease to be treated, as defined above, the severity and course of the disease, the patient's clinical history and response to the agent, and the discretion of the attending physician. The agent is suitably administered to the patient at one time or over a series of treatments.

IV. Pharmaceutical Preparations

[00106] It is contemplated that pharmaceutical preparations can be administered systemically or locally to inhibit tumor cell growth and, most preferably, to kill cancer cells in cancer patients with locally advanced or metastatic cancers. They can be

administered intravenously, intrathecally, and/or intraperitoneally. They can be administered alone or in combination with other anti-proliferative drugs. In one embodiment, they are administered to reduce the cancer load in the patient prior to surgery or other procedures. Alternatively, they can be administered after surgery to ensure that any remaining cancer (*e.g.*, cancer that the surgery failed to eliminate) does not survive.

[00107] It is not intended that the present invention be limited by the particular nature of the therapeutic preparation. For example, such compositions can be provided in formulations together with physiologically tolerable liquid, gel, solid carriers, diluents, or excipients. These therapeutic preparations can be administered to mammals for veterinary use, such as with domestic animals, and clinical use in humans in a manner similar to other therapeutic agents. In general, the dosage required for therapeutic efficacy will vary according to the type of use and mode of administration, as well as the particular requirements of individual subjects.

[00108] Where clinical applications are contemplated, it may be necessary to prepare pharmaceutical compositions comprising proteins, antibodies, and drugs in a form appropriate for the intended application. Generally, pharmaceutical compositions may comprise an effective amount of one or more EGFR-targeting antibody or additional agents dissolved or dispersed in a pharmaceutically acceptable carrier. The phrases "pharmaceutical or pharmacologically acceptable" refers to molecular entities and compositions that do not produce an adverse, allergic, or other untoward reaction when administered to an animal, such as, for example, a human, as appropriate. The preparation of a pharmaceutical composition comprising an EGFR-targeting antibody and/or optionally a PRMT inhibitor as disclosed herein, or additional active ingredient will be known to those of skill in the art in light of the present disclosure, as exemplified by Remington's Pharmaceutical Sciences, 18th Ed., 1990, incorporated herein by reference. Moreover, for animal (*e.g.*, human) administration, it will be understood that preparations should meet sterility, pyrogenicity, general safety, and purity standards as required by the FDA Office of Biological Standards.

[00109] Further in accordance with certain aspects of the present invention, the composition suitable for administration may be provided in a pharmaceutically acceptable carrier with or without an inert diluent. As used herein, "pharmaceutically acceptable carrier" includes any and all aqueous solvents (*e.g.*, water, alcoholic/aqueous solutions, ethanol, saline solutions, parenteral vehicles, such as sodium chloride, Ringer's dextrose,

etc.), non-aqueous solvents (*e.g.*, fats, oils, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), vegetable oil, and injectable organic esters, such as ethyloleate), lipids, liposomes, dispersion media, coatings (*e.g.*, lecithin), surfactants, antioxidants, preservatives (*e.g.*, antibacterial or antifungal agents, anti-oxidants, chelating agents, inert gases, parabens (*e.g.*, methylparabens, propylparabens), chlorobutanol, phenol, sorbic acid, thimerosal or combinations thereof), isotonic agents (*e.g.*, sugars and sodium chloride), absorption delaying agents (*e.g.*, aluminum monostearate and gelatin), salts, drugs, drug stabilizers, gels, resins, fillers, binders, excipients, disintegration agents, lubricants, sweetening agents, flavoring agents, dyes, fluid and nutrient replenishers, such like materials and combinations thereof, as would be known to one of ordinary skill in the art. The carrier should be assimilable and includes liquid, semi-solid, *i.e.*, pastes, or solid carriers. In addition, if desired, the compositions may contain minor amounts of auxiliary substances, such as wetting or emulsifying agents, stabilizing agents, or pH buffering agents. The pH and exact concentration of the various components in a pharmaceutical composition are adjusted according to well-known parameters. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion, and by the use of surfactants.

[00110] A pharmaceutically acceptable carrier is particularly formulated for administration to a human, although in certain embodiments it may be desirable to use a pharmaceutically acceptable carrier that is formulated for administration to a non-human animal but that would not be acceptable (*e.g.*, due to governmental regulations) for administration to a human. Except insofar as any conventional carrier is incompatible with the active ingredient (*e.g.*, detrimental to the recipient or to the therapeutic effectiveness of a composition contained therein), its use in the therapeutic or pharmaceutical compositions is contemplated. In accordance with certain aspects of the present invention, the composition is combined with the carrier in any convenient and practical manner, *i.e.*, by solution, suspension, emulsification, admixture, encapsulation, absorption, and the like. Such procedures are routine for those skilled in the art.

[00111] Certain embodiments of the present invention may comprise different types of carriers depending on whether it is to be administered in solid, liquid, or aerosol form, and whether it needs to be sterile for the route of administration, such as injection. The compositions can be administered intravenously, intradermally, transdermally, intrathecally,

intraarterially, intraperitoneally, intranasally, intravaginally, intrarectally, intramuscularly, subcutaneously, mucosally, orally, topically, locally, by inhalation (*e.g.*, aerosol inhalation), by injection, by infusion, by continuous infusion, by localized perfusion bathing target cells directly, via a catheter, via a lavage, in lipid compositions (*e.g.*, liposomes), or by other methods or any combination of the forgoing as would be known to one of ordinary skill in the art (see, for example, Remington's Pharmaceutical Sciences, 18th Ed., 1990, incorporated herein by reference).

[00112] The active compounds can be formulated for parenteral administration, *e.g.*, formulated for injection via the intravenous, intramuscular, sub-cutaneous, or even intraperitoneal routes. Typically, such compositions can be prepared as either liquid solutions or suspensions; solid forms suitable for use to prepare solutions or suspensions upon the addition of a liquid prior to injection can also be prepared; and the preparations can also be emulsified.

[00113] The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions; formulations including sesame oil, peanut oil, or aqueous propylene glycol; and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that it may be easily injected. It also should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi.

[00114] The therapeutics may be formulated into a composition in a free base, neutral, or salt form. Pharmaceutically acceptable salts include the acid addition salts, *e.g.*, those formed with the free amino groups of a proteinaceous composition, or which are formed with inorganic acids, such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, or mandelic acid and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases, such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides; or such organic bases as isopropylamine, trimethylamine, histidine, or procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms, such as formulated for parenteral administrations, such as injectable

solutions, or aerosols for delivery to the lungs, or formulated for alimentary administrations, such as drug release capsules and the like.

[00115] In a specific embodiment of the present invention, the composition is combined or mixed thoroughly with a semi-solid or solid carrier. The mixing can be carried out in any convenient manner, such as grinding. Stabilizing agents can be also added in the mixing process in order to protect the composition from loss of therapeutic activity, *i.e.*, denaturation in the stomach. Examples of stabilizers for use in a composition include buffers, amino acids, such as glycine and lysine, carbohydrates, such as dextrose, mannose, galactose, fructose, lactose, sucrose, maltose, sorbitol, mannitol, *etc.*

[00116] In further embodiments, the present invention may concern the use of a pharmaceutical lipid vehicle composition comprising one or more lipids and an aqueous solvent. As used herein, the term "lipid" will be defined to include any of a broad range of substances that is characteristically insoluble in water and extractable with an organic solvent. This broad class of compounds is well known to those of skill in the art, and as the term "lipid" is used herein, it is not limited to any particular structure. Examples include compounds that contain long-chain aliphatic hydrocarbons and their derivatives. A lipid may be naturally occurring or synthetic (*i.e.*, designed or produced by man). However, a lipid is usually a biological substance. Biological lipids are well known in the art, and include for example, neutral fats, phospholipids, phosphoglycerides, steroids, terpenes, lysolipids, glycosphingolipids, glycolipids, sulphatides, lipids with ether- and ester-linked fatty acids, polymerizable lipids, and combinations thereof. Of course, compounds other than those specifically described herein that are understood by one of skill in the art as lipids are also encompassed by the compositions and methods.

[00117] One of ordinary skill in the art would be familiar with the range of techniques that can be employed for dispersing a composition in a lipid vehicle. For example, the therapeutic agent may be dispersed in a solution containing a lipid, dissolved with a lipid, emulsified with a lipid, mixed with a lipid, combined with a lipid, covalently bonded to a lipid, contained as a suspension in a lipid, contained or complexed with a micelle or liposome, or otherwise associated with a lipid or lipid structure by any means known to those of ordinary skill in the art. The dispersion may or may not result in the formation of liposomes.

[00118] The term "unit dose" or "dosage" refers to physically discrete units suitable for use in a subject, each unit containing a predetermined quantity of the therapeutic composition calculated to produce the desired responses discussed above in association with its administration, *i.e.*, the appropriate route and treatment regimen. The quantity to be administered, both according to number of treatments and unit dose, depends on the effect desired. The actual dosage amount of a composition of the present invention administered to a patient or subject can be determined by physical and physiological factors, such as body weight, the age, health, and sex of the subject, the type of disease being treated, the extent of disease penetration, previous or concurrent therapeutic interventions, idiopathy of the patient, the route of administration, and the potency, stability, and toxicity of the particular therapeutic substance. For example, a dose may also comprise from about 1 μg/kg/body weight to about 1000 mg/kg/body weight (this such range includes intervening doses) or more per administration, and any range derivable therein. In non-limiting examples of a derivable range from the numbers listed herein, a range of about 5 μg/kg/body weight to about 100 mg/kg/body weight, about 5 μg/kg/body weight to about 500 mg/kg/body weight, *etc.*, can be administered. The practitioner responsible for administration will, in any event, determine the concentration of active ingredient(s) in a composition and appropriate dose(s) for the individual subject.

[00119] The actual dosage amount of a composition administered to an animal patient can be determined by physical and physiological factors, such as body weight, severity of condition, the type of disease being treated, previous or concurrent therapeutic interventions, idiopathy of the patient, and on the route of administration. Depending upon the dosage and the route of administration, the number of administrations of a preferred dosage and/or an effective amount may vary according to the response of the subject. The practitioner responsible for administration will, in any event, determine the concentration of active ingredient(s) in a composition and appropriate dose(s) for the individual subject.

[00120] In certain embodiments, pharmaceutical compositions may comprise, for example, at least about 0.1% of an active compound. In other embodiments, an active compound may comprise between about 2% to about 75% of the weight of the unit, or between about 25% to about 60%, for example, and any range derivable therein. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the

compound. Factors, such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations, will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

[00121] In other non-limiting examples, a dose may also comprise from about 1 microgram/kg/body weight, about 5 microgram/kg/body weight, about 10 microgram/kg/body weight, about 50 microgram/kg/body weight, about 100 microgram/kg/body weight, about 200 microgram/kg/body weight, about 350 microgram/kg/body weight, about 500 microgram/kg/body weight, about 1 milligram/kg/body weight, about 5 milligram/kg/body weight, about 10 milligram/kg/body weight, about 50 milligram/kg/body weight, about 100 milligram/kg/body weight, about 200 milligram/kg/body weight, about 350 milligram/kg/body weight, about 500 milligram/kg/body weight, to about 1000 milligram/kg/body weight or more per administration, and any range derivable therein. In non-limiting examples of a derivable range from the numbers listed herein, a range of about 5 milligram/kg/body weight to about 100 milligram/kg/body weight, about 5 microgram/kg/body weight to about 500 milligram/kg/body weight, *etc.*, can be administered, based on the numbers described above.

V. Combination Treatments

[00122] Administration in combination can include simultaneous administration of two or more agents in the same dosage form, simultaneous administration in separate dosage forms, and separate administration. That is, the subject therapeutic composition and another therapeutic agent can be formulated together in the same dosage form and administered simultaneously. Alternatively, subject therapeutic composition and another therapeutic agent can be simultaneously administered, wherein both the agents are present in separate formulations. In another alternative, the therapeutic agent can be administered just followed by the other therapeutic agent or vice versa. In the separate administration protocol, the subject therapeutic composition and another therapeutic agent may be administered a few minutes apart, or a few hours apart, or a few days apart.

[00123] The methods and compositions, including combination therapies, enhance the therapeutic or protective effect, and/or increase the therapeutic effect of another anti-cancer or anti-hyperproliferative therapy. Therapeutic and prophylactic methods and

compositions can be provided in a combined amount effective to achieve the desired effect, such as the killing of a cancer cell and/or the inhibition of cellular hyperproliferation. A tissue, tumor, or cell can be contacted with one or more compositions or pharmacological formulation(s) comprising one or more of the agents or by contacting the tissue, tumor, and/or cell with two or more distinct compositions or formulations. Also, it is contemplated that such a combination therapy can be used in conjunction with radiotherapy, surgical therapy, or immunotherapy.

[00124] An anti-EGFR therapeutic may be administered before, during, after, or in various combinations relative to an anti-cancer treatment, such as a PRMT inhibitor. The administrations may be in intervals ranging from concurrently to minutes to days to weeks. In embodiments where an anti-EGFR therapeutic is provided to a patient separately from an anti-cancer agent, one would generally ensure that a significant period of time did not expire between the time of each delivery, such that the two compounds would still be able to exert an advantageously combined effect on the patient. In such instances, it is contemplated that one may provide a patient with an anti-EGFR therapeutic and the anti-cancer therapy within about 12 to 24 or 72 h of each other and, more particularly, within about 6-12 h of each other. In some situations it may be desirable to extend the time period for treatment significantly where several days (2, 3, 4, 5, 6, or 7) to several weeks (1, 2, 3, 4, 5, 6, 7, or 8) lapse between respective administrations.

[00125] In certain embodiments, a course of treatment will last 1-90 days or more (this such range includes intervening days). It is contemplated that one agent may be given on any day of day 1 to day 90 (this such range includes intervening days) or any combination thereof, and another agent is given on any day of day 1 to day 90 (this such range includes intervening days) or any combination thereof. Within a single day (24-hour period), the patient may be given one or multiple administrations of the agent(s). Moreover, after a course of treatment, it is contemplated that there is a period of time at which no anti-cancer treatment is administered. This time period may last 1-7 days, and/or 1-5 weeks, and/or 1-12 months or more (this such range includes intervening days), depending on the condition of the patient, such as their prognosis, strength, health, *etc.* It is expected that the treatment cycles would be repeated as necessary.

[00126] Various combinations may be employed. For the example below an anti-EGFR therapeutic either alone or in combination with a PRMT inhibitor is "A" and an anti-cancer therapy is "B":

A/B/A B/A/B B/B/A A/A/B A/B/B B/A/A A/B/B/B B/A/B/B
B/B/B/A B/B/A/B A/A/B/B A/B/A/B A/B/B/A B/B/A/A
B/A/B/A B/A/A/B A/A/A/B B/A/A/A A/B/A/A A/A/B/A

[00127] Administration of any compound or therapy of the present invention to a patient will follow general protocols for the administration of such compounds, taking into account the toxicity, if any, of the agents. Therefore, in some embodiments there is a step of monitoring toxicity that is attributable to combination therapy.

A. Chemotherapy

[00128] A wide variety of chemotherapeutic agents may be used in accordance with the present invention. The term "chemotherapy" refers to the use of drugs to treat cancer. A "chemotherapeutic agent" is used to connote a compound or composition that is administered in the treatment of cancer. These agents or drugs are categorized by their mode of activity within a cell, for example, whether and at what stage they affect the cell cycle. Alternatively, an agent may be characterized based on its ability to directly cross-link DNA, to intercalate into DNA, or to induce chromosomal and mitotic aberrations by affecting nucleic acid synthesis.

[00129] Examples of chemotherapeutic agents include alkylating agents, such as thiotepa and cyclosphosphamide; alkyl sulfonates, such as busulfan, improsulfan, and piposulfan; aziridines, such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines, including altretamine, triethylenemelamine, trietylenephosphoramide, triethiylenethiophosphoramide, and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards, such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin,

phenesterine, prednimustine, trofosfamide, and uracil mustard; nitrosureas, such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimnustine; antibiotics, such as the enediyne antibiotics (*e.g.,* calicheamicin, especially calicheamicin gammaII and calicheamicin omegaI1); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antiobiotic chromophores, aclacinomysins, actinomycin, authrarnycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, such as mitomycin C, mycophenolic acid, nogalarnycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, and zorubicin; anti-metabolites, such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues, such as denopterin, pteropterin, and trimetrexate; purine analogs, such as fludarabine, 6-mercaptopurine, thiamiprine, and thioguanine; pyrimidine analogs, such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, and floxuridine; androgens, such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, and testolactone; anti-adrenals, such as mitotane and trilostane; folic acid replenisher, such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids, such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSKpolysaccharide complex; razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; taxoids, *e.g.*, paclitaxel and docetaxel gemcitabine; 6-thioguanine; mercaptopurine; platinum coordination complexes, such as cisplatin, oxaliplatin, and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; vinorelbine; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; irinotecan (*e.g.*, CPT-11); topoisomerase inhibitor RFS 2000; difluorometlhylornithine (DMFO); retinoids, such as retinoic acid; capecitabine;

carboplatin, procarbazine,plicomycin, gemcitabien, navelbine, farnesyl-protein tansferase inhibitors, transplatinum, and pharmaceutically acceptable salts, acids, or derivatives of any of the above.

B. Radiotherapy

[00130] Other factors that cause DNA damage and have been used extensively include what are commonly known as γ-rays, X-rays, and/or the directed delivery of radioisotopes to tumor cells. Other forms of DNA damaging factors are also contemplated, such as microwaves, proton beam irradiation (U.S. Patents 5,760,395 and 4,870,287), and UV-irradiation. It is most likely that all of these factors affect a broad range of damage on DNA, on the precursors of DNA, on the replication and repair of DNA, and on the assembly and maintenance of chromosomes. Dosage ranges for X-rays range from daily doses of 50 to 200 roentgens for prolonged periods of time (3 to 4 wk), to single doses of 2000 to 6000 roentgens. Dosage ranges for radioisotopes vary widely, and depend on the half-life of the isotope, the strength and type of radiation emitted, and the uptake by the neoplastic cells.

C. Immunotherapy

[00131] The skilled artisan will understand that additional immunotherapies may be used in combination or in conjunction with methods of the invention. In the context of cancer treatment, immunotherapeutics, generally, rely on the use of immune effector cells and molecules to target and destroy cancer cells. Rituximab (Rituxan®) is such an example. The immune effector may be, for example, an antibody specific for some marker on the surface of a tumor cell. The antibody alone may serve as an effector of therapy or it may recruit other cells to actually affect cell killing. The antibody also may be conjugated to a drug or toxin (chemotherapeutic, radionuclide, ricin A chain, cholera toxin, pertussis toxin, *etc.*) and serve merely as a targeting agent. Alternatively, the effector may be a lymphocyte carrying a surface molecule that interacts, either directly or indirectly, with a tumor cell target. Various effector cells include cytotoxic T cells and NK cells.

[00132] In one aspect of immunotherapy, the tumor cell must bear some marker that is amenable to targeting, *i.e.*, is not present on the majority of other cells. Many tumor markers exist and any of these may be suitable for targeting in the context of the present invention. Common tumor markers include CD20, carcinoembryonic antigen, tyrosinase (p97), gp68, TAG-72, HMFG, Sialyl Lewis Antigen, MucA, MucB, PLAP, laminin receptor,

erb B, and p155. An alternative aspect of immunotherapy is to combine anticancer effects with immune stimulatory effects. Immune stimulating molecules also exist including: cytokines, such as IL-2, IL-4, IL-12, GM-CSF, gamma-IFN, chemokines, such as MIP-1, MCP-1, IL-8, and growth factors, such as FLT3 ligand.

[00133] Examples of immunotherapies currently under investigation or in use are immune adjuvants, *e.g.*, Mycobacterium bovis, Plasmodium falciparum, dinitrochlorobenzene, and aromatic compounds (U.S. Patents 5,801,005 and 5,739,169; Hui and Hashimoto, 1998; Christodoulides *et al.*, 1998); cytokine therapy, *e.g.*, interferons α, β, and γ, IL-1, GM-CSF, and TNF (Bukowski *et al.*, 1998; Davidson *et al.*, 1998; Hellstrand *et al.*, 1998); gene therapy, *e.g.*, TNF, IL-1, IL-2, and p53 (Qin *et al.*, 1998; U.S. Patents 5,830,880 and 5,846,945); and monoclonal antibodies, *e.g.*, anti-CD20, anti-ganglioside GM2, and anti-p185 (Hollander, 2012; Hanibuchi *et al.*, 1998; U.S. Patent 5,824,311). It is contemplated that one or more anti-cancer therapies may be employed with the antibody therapies described herein.

D. Surgery

[00134] Approximately 60% of persons with cancer will undergo surgery of some type, which includes preventative, diagnostic or staging, curative, and palliative surgery. Curative surgery includes resection in which all or part of cancerous tissue is physically removed, excised, and/or destroyed and may be used in conjunction with other therapies, such as the treatment of the present invention, chemotherapy, radiotherapy, hormonal therapy, gene therapy, immunotherapy, and/or alternative therapies. Tumor resection refers to physical removal of at least part of a tumor. In addition to tumor resection, treatment by surgery includes laser surgery, cryosurgery, electrosurgery, and microscopically-controlled surgery (Mohs' surgery).

[00135] Upon excision of part or all of cancerous cells, tissue, or tumor, a cavity may be formed in the body. Treatment may be accomplished by perfusion, direct injection, or local application of the area with an additional anti-cancer therapy. Such treatment may be repeated, for example, every 1, 2, 3, 4, 5, 6, or 7 days, or every 1, 2, 3, 4, and 5 weeks or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 months. These treatments may be of varying dosages as well.

E. Other Agents

[00136] It is contemplated that other agents may be used in combination with certain aspects of the present invention to improve the therapeutic efficacy of treatment. These additional agents include agents that affect the upregulation of cell surface receptors and GAP junctions, cytostatic and differentiation agents, inhibitors of cell adhesion, agents that increase the sensitivity of the hyperproliferative cells to apoptotic inducers, or other biological agents. Increases in intercellular signaling by elevating the number of GAP junctions would increase the anti-hyperproliferative effects on the neighboring hyperproliferative cell population. In other embodiments, cytostatic or differentiation agents can be used in combination with certain aspects of the present invention to improve the anti-hyperproliferative efficacy of the treatments. Inhibitors of cell adhesion are contemplated to improve the efficacy of the present invention. Examples of cell adhesion inhibitors are focal adhesion kinase (FAKs) inhibitors and Lovastatin. It is further contemplated that other agents that increase the sensitivity of a hyperproliferative cell to apoptosis, such as the antibody c225, could be used in combination with certain aspects of the present invention to improve the treatment efficacy.

VI. Kits

[00137] Certain aspects of the present invention may provide kits, such as diagnostic or therapeutic kits. For example, a kit may comprise one or more pharmaceutical compositions as described herein and optionally instructions for their use. Kits may also comprise one or more devices for accomplishing administration of such compositions. For example, a subject kit may comprise a pharmaceutical composition and catheter for accomplishing direct intravenous injection of the composition into a cancerous tumor. In other embodiments, a subject kit may comprise pre-filled ampoules of an anti-EGFR therapeutic and a PRMT inhibitor, optionally formulated as a pharmaceutical, or lyophilized, for use with a delivery device.

[00138] It also is contemplated that the above reagents maybe packaged in a kit that may be produced commercially for detecting a biomarker, *e.g.*, a methylated EGFR polypeptide, described herein. Such a kit can be prepared from readily available materials and reagents and housed in a sealed container. For example, such a kit can comprise any one or more of the following materials: reaction tubes, buffers, detergent, antibodies, and labeled probes (*e.g.*, labeled antibodies). In a preferred embodiment, a kit of the present invention

would allow a practitioner to detect the presence of methylated EGFR in a patient sample. Instructions for performing the assays can also be included in the kit.

[00139] Kits may comprise a container with a label. Suitable containers include, for example, bottles, vials, and test tubes. The containers may be formed from a variety of materials, such as glass or plastic. The container may hold a composition that includes an anti-EGFR therapeutic and/or a PRMT inhibitor that is effective for therapeutic or non-therapeutic applications, such as described above. The label on the container may indicate that the composition is used for a specific therapy or non-therapeutic application, and may also indicate directions for either *in vivo* or *in vitro* use, such as those described above. The kit of the invention will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

VII. Examples

[00140] The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Materials and Methods

[00141] *Constructs, reagents, peptides and antibodies.* EGFR and PRMT1 constructs were prepared as described previously (Hsu et al., 2011). Four extracellular domains, juxtamembrane domain, kinase domain and C-terminal tail of EGFR were further subcloned into pGEX vector for the preparation of truncated EGFR recombinant proteins. EGFR (R198/200K) mutagenesis was generated using the QuickChange® Site-Directed Mutagenesis Kit according to the manufacturer's protocol (Stratagene). Epidermal growth factor (EGF; Sigma) was prepared according to the manufacturers' instructions. Unmodified (Ac-QCSGRCRGKSPSD-C; SEQ ID NO: 1), asymmetric dimethylated (Ac-

QCSG(asymmetric dimethyl-R)C(asymmetric dimethyl-R)GKSPSD-C), symmetric dimethylated (Ac-QCSG(symmetric dimethyl-R)C(symmetric dimethyl-R)GKSPSD-C), and monomethylated (Ac-QCSG(monomethyl-R)C(monomethyl-R)GKSPSD-C) EGFR peptides were chemically synthesized by Lifetein for antibody production in mice and dot blot and peptide competition assays. Anti-EGFR antibody (06-847, 1:2,000; Millipore) was used to detect full-length EGFR. Antibodies against phospho-Tyr 1086 and -Tyr 1148 (Abcam) were used for detection of EGFR activation. Antibodies to ERK (1:5,000; Millipore) and phospho-ERK (1:5,000; Cell Signaling) were used to detect the EGFR downstream signaling activation. Anti-PRMT1 (Cell Signaling) was used to detect PRMT1 level after overexpression or knockdown. Anti-tubulin antibody was purchased from Sigma.

[00142] *Cell culture.* SKCO1 and SW48 were purchased form ATCC. GEO cell was a kindly gift from Dr. Zhen Fan (MD Anderson cancer center). GEO and SW48 cells were cultured in DMEM/F-12 with 10% fetal calf serum. SKCO1 cell were cultured in MEM with 10% fetal calf serum. All cell lines were characterized as mycoplasma negative. Before EGF stimulation, 80% confluent cells were serum-starved for 20 h, and then stimulated with 50 ng/ml EGF for indicated time.

[00143] *shRNA construct and transfection.* Lentiviral-based pLKO.1 PRMT1 shRNA vector was obtained from Academia Sinica (Taipei, Taiwan). The pLKO.1 scrambled shRNA vector was purchased from Addgene. (Cambridge, MA). The PRMT1-targeting shRNA#1 sequence used in lentivirus construct was: 5'-CCGGCCGGCAGTACAAAGACTACAACTCGAGTTGTAGTCTTTGTACTGCCGGTTTTTG-3' (SEQ ID NO: 2). The PRMT1-targeting shRNA#2 was: 5'-CCGGGCAAGTGAAGCGGAATGACTACTCGAGTAGTCATTCCGCTTCACTTGCTTTTTG-3' (SEQ ID NO: 3). For lentiviral production, PLKO.1 PRMT1 shRNA vector, packaging (pCMV-dr8.Z dvpr) and envelope (pCMV-VSV-G) plasmids were co-transfected into 293T cells using Lipofectamine® Reagent (Invitrogen, Carlsbad, California). After 48-hr transfection, colon cancer cell lines were infected with viral particles. Stable knockdown clones were selected by culturing cells in medium with 4 μg/ml puromycin for 1 month.

[00144] *Cell proliferation assay.* Cells were seeded in 6-well plates (triplicate), and fresh medium (with or without gefitinib or cetuximab) were added every day. Cells were then trypsinized and cell numbers counted on a daily basis.

[00145] *Anchorage-independent growth assay for colony formation.* The base layer of cell growth matrix containing DMEM/F12 medium, 10% FBS, and 0.5% agar was paved in 6-well plates (1.5 ml per well). After solidification of the base layer, the top layer (1.5 ml per well) containing DMEM/F12 medium, 10% FBS, and 0.35% agarose and 1,000 cells was plated. Culture medium (1 ml) was added to each well and changed every 3 days. After 4-week culture, colonies were stained by 0.005% crystal violet. Colonies with a diameter larger than 0.5 mm were counted.

[00146] *In vitro methylation assay.* GST-tagged PRMT1 and GST-tagged EGFR fragments were expressed in *E. coli* individually and purified using *Glutathione Sepharose* 4B. They were then incubated together in the presence of 2.2 Ci S-adenosyl-L-[methyl-^{3}H] methionine (85 Ci/mmol from a 0.55 mCi/ml stock solution; MP Biomedicals) for 1 h at 30°C in a final volume of 50 µl of phosphate-buffered saline. After reaction, samples were separated by SDS-PAGE and transferred to PVDF membrane. Methylation levels were examined by fluorography.

[00147] *Mass spectrometry.* EGFR was isolated by immunoprecipitation with anti-EGFR antibody and then was analyzed by SDS-PAGE. The protein band corresponding to EGFR was excised and subjected to in-gel digestion with trypsin. After isolation by immobilized metal affinity chromatography, the enriched methyl-peptides were analyzed by micro-liquid chromatography/tandem MS.

[00148] *In vivo protein interaction by Duolink® assay.* Cells were seeded in 8-well chamber slides. When harvesting cells, cells were washed with cold PBS twice and fixed with 4% paraformadehyde at 4°C for 2 h. After two more PBS washes, cells were permeabilized by cold 0.2% Triton® X-100 for 30 min at room temperature and subjected to Doulink assay (Olink Bioscience) according to the manufacturers' instructions.

[00149] *Dimerization assay.* Cells were starved in serum free medium for 24 h. After starvation, cold PBS containing 50 ng/ml EGF was added onto plates for 30 min at 4°C. Then, cells were washed with cold PBS (137 mM NaCl, 0.67 mM KCl, 8 mM Na_2HPO_4, 1.4 mM KH_2PO_4) three times and incubated for 2 h at 4°C with 5 mM cross linker BS^3 (bis[sulfosuccinimidyl] suberate; Thermo scientific) in PBS. After washing three times with cold PBS, cross linking reactions were stopped by incubating cells in 50 mM Tris buffer (pH

7.5) for 15 min at ambient temperature. Cells were subsequently lysed and cell lysates analyzed by Western blotting.

[00150] *Clonogenic assay.* Cells (500 cells per well, 12 wells per cell type) were seeded in 6-well plates. Culture medium was changed every three days. After 2 weeks of cell culture, cells were washed by cold PBS twice and fixed by 4% paraformadehyde for 1 h. Cells then were stained by 0.005% crystal violet at 4°C overnight. After washed by ddH_2O, colonies with a diameter larger than 0.5 mm were counted.

[00151] *Orthotopic colon cancer mouse model.* All animal experiments were carried out in accordance with approved protocol from Institutional Animal Care and Use Committee (IACUC) at MD Anderson Cancer Center. Nude female mice at 4-5 weeks of age were maintained at the MD Anderson Animal Facility for 1 week prior to injection of cancer cells. The cecum was exteriorized through a small midline laparotomy and 10^7 GEO cells expressing wild-type EGFR, EGFR methylation-site mutant, or vector control were injected into the cecal wall. After injection, the abdominal wall was closed by wound clips. One month after surgery, tumors were harvested and tumor weight measured.

[00152] *Immunohistochemical staining (IHC).* IHC of methylated EGFR was performed using homemade me-R198/200 antibody. Colorectal cancer tissue microarrays were purchased from National Cancer Institute Cancer Diagnosis Program. Samples were deparaffinized and rehydrated. Antigen retrieval was done by using 0.01 M sodium-citrate buffer (pH 6.0) in a microwave oven. The sections were treated with 1% hydrogen peroxide in methanol for 30 min to block endogenous peroxidase activity. After 1 h preincubation in 10% normal serum to prevent nonspecific staining, the samples were incubated with primary antibodies at 4°C overnight. The sections were then treated with biotinylated secondary antibody, followed by incubations with avidinbiotin peroxidase complex solution for 1 h at room temperature. Color was developed with the 3-amino-9-ethylcarbazole solution. Counterstaining was carried out using Mayer's hematoxylin. All immunostained slides were scanned on the Automated Cellular Image System III (ACIS® III) (Dako, Denmark) for quantification by digital image analysis. A total score of protein expression was calculated automatically from the percentage of immunopositive cells and immunostaining intensity.

Example 1 – PRMT1 Regulates EGFR Signaling and Cetuximab Response in Colorectal Cancer

[00153] Epidermal growth factor receptor (EGFR)-targeted monoclonal antibody, cetuximab, has been shown to be effective in many cancer types including colon cancer. However, resistance to cetuximab has been observed in clinical setting for colon cancer. Even-more, the outcomes from clinical trials in breast and pancreatic cancer were not satisfactory, suggesting that resistance mechanisms exist. As a result, cetuximab has not been approved for treatment of breast and pancreatic cancer. The inventors have identified arginine methylations of the extracellular domain of EGFR that induce resistance to the cetuximab. Specifically, the inventors found that protein arginine methyltransferase 1 (PRMT 1) methylates the extracellular domain of EGFR at R198 and R200 leading to an increase in the binding affinity between EGF and methylated EGFR, and subsequently receptor dimerization, downstream signaling activation, and cell proliferation *in vitro*. Meanwhile, R/K mutation of the EGFR methylation sites reduces tumor growth in a mouse orthotopic xenograft model. Moreover, EGFR methylation level is correlated with poor patient outcomes. Importantly, the increased EGFR methylation retains its signaling activation and cell proliferation in the presence of cetuximab, suggesting that the methylation status of EGFR has the potential to predict resistance to cetuximab treatment. Thus, the arginine methylation of EGFR R198 and R200 may serve as biomarkers to predict resistance to cetuximab therapy. In addition, the combination of cetuximab plus a PRMT inhibitor may be a therapeutic strategy able to overcome resistance to cetuximab therapy. Another EGFR arginine site (R497) was also shown to have arginine/lysine polymorphism, in which the presence of the arginine amino acid leads to resistance to cetuximab, while with the lysine amino acid it is more sensitive to cetuximab. Thus, EGFR R497 methylation is also likely to cause resistance to cetuximab and combination with a PRMT inhibitor may be a potential strategy for overcoming this resistance.

[00154] Protein arginine methylation is involved in many biological processes, including cancer development. Among the ten mammalian protein arginine methyltransferases (PRMTs), PRMT1 is the best characterized (Bedford and Richard, 2005; Le Romancer et al., 2008). In particular, aberrant high expression of PRMT1 has been observed in colorectal, breast, prostate, and lung cancers and suggested as a predictive marker for poor clinical outcomes (Yang and Bedford, 2013; Papdokostopoulou et al., 2009).

Although PRMT1 appears to play a crucial role during colorectal cancer tumorigenesis, how it is involved in colorectal cancer pathophysiology remains obscure. Given that high PRMT1 expression has been observed to correlate with colorectal cancer patient progression (Mathioudaki et al., 2008), whether this contributes to cancer cell proliferation was examined. Indeed, stable transfectants that ectopically expressed PRMT1 had higher cell proliferation rates (FIG. 1A) and anchorage-independent colony formation ability (FIG. 1B) than control cells in both SKCO1 and GEO colorectal cancer cell lines, while knockdown of PRMT1 attenuated these effects. Interestingly, addition of gefitinib, an EGFR tyrosine kinase inhibitor, significantly inhibited cell proliferation (FIG. 1C) and colony formation (FIG. 1D) in both PRMT1-overexpressing and vector control (expressing endogenous PRMT1) cells. These phenomena were also observed in other non-colorectal cancer cell lines (FIG. 5), raising an interesting possibility that PRMT1-mediated cell growth is dependent on EGFR signaling. Interestingly, the activation status of EGFR and two main downstream signaling, ERK and AKT were stronger in PRMT1-overexpressing than vector control cells (FIG. 1E) upon EGF stimulation, and knockdown of PRMT1 severely blocked EGF-induced EGFR, ERK and AKT activation (FIG. 1F). Collectively, these results suggest that PRMT1 enhances EGFR signaling in response to EGF stimulation.

[00155] Next, whether PRMT1 affects EGFR signaling through protein arginine methylation of EGFR was determined. Results from reciprocal coimmunoprecipitation (FIG. 2A, top) and Duolink® assay (FIG. 2A, bottom) demonstrated a physiological association between endogenous PRMT1 and EGFR. Among various functional domains of EGFR (FIG. 2B), PRMT1 specifically methylated the extracellular domain 2 (D2) of EGFR (FIG. 2C). PRMT1 frequently methylates arginine residues found within glycine-arginine rich (GAR) domains (Boisvert et al., 2005; Yu et al., 2012) and generates asymmetric dimethylated arginine. Sequence alignment between the GAR domains of known PRMT1 substrates and D2 of EGFR revealed a putative GAR domain with two arginine residues, R198 and R200 (FIG. 2D). PRMT1 methylated wild-type but not R198/200K D2 mutant EGFR (FIG. 2E), indicating that these two arginine residues are the major targets of PRMT1-mediated EGFR methylation. In addition, mass spectrum analysis of immuno-purified endogenous EGFR proteins indicated R198 and R200 of EGFR were dimethylated (FIG. 2F). A specific anti-me-R198/200 antibody was generated by using a synthesized asymmetric dimethylated EGFR peptide. Dot blot assays showed that this me-R198/200 antibody recognized asymmetric dimethylated EGFR peptide but not unmodified

peptide or other methylation forms (FIG. 2G). The antibody was then used to analyze the methylation status of endogenous EGFR in SKCO1 cells. Indeed, the level of EGFR methylation was proportional to PRMT1 expression and could be competed off by methylated but not by unmodified peptide (FIG. 2H), indicating a positive regulatory role of PRMT1 on EGFR R198/200 methylation. Immunochemistry staining of colon cancer tissue using the EGFR methylation antibody, me-R198/200, showed that the antibody competed with synthesized methylated EGFR peptide, but not unmodified EGFR peptide or histone H4R3 methylated peptide, showing the capability of the EGFR methylation antibody to detect methylation signals in tumor tissue. The me-R198/200 antibody was also used in immunohistochemistry studies of GEO cells expressing either wild-type EGFR or R198/200K D2 mutant EGFR. Positive staining was seen with wild-type EGFR expression but not R198/200K D2 mutant EGFR. Furthermore, the staining seen with wild-type EGFR expression was eliminated by the presence of an asymmetric dimethylated R198/200 EGFR peptide competitor, but not by an unmodified R198/200 EGFR peptide competitor or asymmetric dimethylated histone H4R3 peptide competitor. Taken together, these results indicate that PRMT1 interacts with and methylates R198 and R200 of EGFR.

[00156] To determine the role of EGFR R198/200 methylation in EGFR signaling, a full-length EGFR R198/200K mutant that cannot be methylated by PRMT1 was constructed for comparison with wild-type EGFR. Since both pEGFR and pERK were significantly changed by overexpression or knockdown of PRMT1 (FIGS. 1E and 1F), they used as markers to monitor EGFR signaling. Notably, the phosphorylation of EGFR and ERK (FIGS. 3A and 8), cell proliferation rate (FIG. 3B, left), as well as anchorage-independent colony formation ability (FIG. 3B, right) were significantly reduced in cells expressing the R198/200K mutant compared with those expressing the wild-type EGFR. The effect of EGFR R198/200 methylation by PRMT1 on EGFR signaling and subsequent cell growth prompted an investigation into how this modification leads to these changes. Interestingly, upon EGF stimulation, endogenous EGFR of PRMT1-expressing SKCO1 cells showed higher receptor dimerization ability, which is partially regulated by the D2 of EGFR (Chung et al., 2010), than cells expressing control vector (FIG. 3C, top). In contrast, EGFR in PRMT1 shRNA-expressing cells had lower dimer formation than cells expressing control vector (FIG. 3C, middle). Consistently, loss of methylation of EGFR R198/200K mutant significantly reduced its dimerization ability compared with wild-type EGFR in GEO cells (FIG. 3C, bottom). These results support a model that methylation at R198/200 of EGFR by

PRMT1 enhances its dimerization ability, and provide an explanation for PRMT1-upregulated EGFR signaling and cell proliferation.

[00157] Whether PRMT1-mediated EGFR methylation contributes to tumorigenesis in an orthotopic colon cancer mouse model was further examined. One month after injection, cells expressing wild-type EGFR generated significantly larger tumors than those expressing R198/200K EGFR or vector control (FIG. 3D). A retrospective study of clinical colorectal cancer specimens further indicated that EGFR R198/200 methylation level as detected by me-R198/200 Ab correlated significantly with poor patient survival (FIG. 3E) and higher recurrence rate (FIG. 3F). Collectively, these results suggest that the methylation status of EGFR has the potential to serve as a predictive marker for patient prognosis.

[00158] Clinically, cetuximab is used to treat metastatic colorectal cancer by disabling the interaction between EGF ligand and EGFR and attenuating EGFR signaling (Gill et al., 1984; Li et al., 2005). Given that the extracellular domain of EGFR is the target of cetuximab, whether R198/200 methylations affect the efficacy of cetuximab was examined. In GEO cells expressing exogenous PRMT1, cell growth rate in the presence of cetuximab was higher than vector control cells while knockdown of PRMT1 sensitized cells to cetuximab (FIG. 4A). To further determine how R198/200 methylation affects cetuximab response, the binding affinity between EGFR and EGF was evaluated in the presence or absence of cetuximab by flow cytometry. As shown in FIG. 4B, GEO cells expressing wild-type EGFR (left) had higher binding affinity (18.91%) to APC-conjugated EGF than those expressing the R198/200K mutant (9.93%; middle). Moreover, cetuximab was more effective in reducing the number of EGF-bound cells in cells expressing R198/200K mutant than in those expressing wild-type EGFR (84% versus 49%; FIG. 4B, bottom), suggesting that methylated EGFR responds better to EGF binding and is more resistant to cetuximab treatment (FIG. 10A). Because only patients with wild-type KRAS are recommended to receive cetuximab therapy for current colorectal cancer treatment (Morton and Hammond, 2009), the cell growth of SW48 cells, a wild-type KRAS cell line, expressing exogenous PRMT1, PRMT1 shRNA, or control vector under cetuximab treatment was investigated. Similar to KRAS G12A mutant GEO cells, SW48 cells expressing exogenous PRMT1 had higher growth rate than vector control cells in the presence of cetuximab while cells expressing PRMT1 shRNA had lower growth rate (FIG. 4C). Consistently, cells expressing PRMT1 (FIG. 4D, top; FIGS. 10B-C) had higher EGF binding affinity (51.6% versus 31.5%)

and lower cetuximab response than vector control cells (50% versus 70% reduction; FIG. 4D, middle and bottom; FIGS. 10B-C). These observations are further supported by structural analysis of the extracellular portion of EGFR dynamically transitioning between a monomeric inactive, 'tethered' conformation and an active, dimeric conformation (FIG. 4E). Arginines 198 and 200 are situated in the hinge region between domains I and II (Ogiso et al., 2002; Ferguson et al., 2003). In the inactive conformation, EGFR domain I only provides a narrow pocket for Arg 198 (FIG. 4F, left). Asymmetric dimethylation by PRMT1 would increase the volume of the Arg198 side chain sufficiently to cause unfavorable steric clashes with domain I, and hence disfavor the inactive conformation. In the active form, the same binding pocket is substantially enlarged (FIG. 4F, right) and would provide sufficient space and some hydrophobic surface patches to accommodate asymmetric dimethylation. Meanwhile, in the inactive form, Arg200 compensates for the charge of Asp206 (FIG. 4G, left), and the backbone carbonyl of Asp206 binds to the backbone nitrogen of Arg200. In the active form, the side chain of Asp206 is rotated away and exposed to the solvent, and the Asp206 carbonyl forms a hydrogen bond with Arg200. Due to these rearrangements, Arg200 is positioned close to the hydrophobic surface provided by Pro219 (FIG. 4G, right). Asymmetric dimethylation of Arg200 appears more favorable in the active conformation, because it provides a more hydrophobic environment for Arg200. Cetuximab binds exclusively to the domain III of the extracellular portion of EFGR in its inactive ('tethered') conformation (FIG. 4E). In doing so, cetuximab partially hides the ligand-binding site and sterically prevents EGFR from adopting the active ('open') conformation required for ligand binding and dimerization (Li et al., 2005). By favoring the active dimeric conformation and ligand binding, methylation of arginines 198 and 200 would oppose the interactions of EGFR with cetuximab. In line with the higher EGF binding affinity and higher EGFR methylation level, PRMT1-expressing SW48 cells demonstrated higher EGFR and ERK activation after EGF stimulation, and the upregulated pEGFR and pERK remained relatively strong even in the presence of cetuximab in comparison to vector control cells (FIG. 4H). Together, the results suggest that PRMT1-mediated R198/200 methylation of EGFR favors EGF ligand binding and results in resistance to cetuximab.

[00159] Interestingly, although some studies have shown that mutant KRAS leads to constitutive activation of ERK and bypasses EGFR signaling (van Houdt et al., 2010), ERK activation was still regulated by EGF stimulation in two KRAS mutant cell lines, GEO (KRAS G12A) and SKCO1 (KRAS G12V). Moreover, knockdown of PRMT1

sensitized cells to cetuximab treatment regardless of KRAS mutation status (FIGs. 4A and 4C), implying that EGFR R198/200 methylation has the potential to serve as a predictive marker for cetuximab resistance in clinical colorectal cancer therapy. It is noteworthy to mention that colorectal cancer patients carrying R497 polymorphism on EGFR extracellular domain 4 exhibit more unfavorable responses to cetuximab than those carrying K497 (Hsieh et al., 2012). Although endogenous EGFR R497 methylation was also observed from mass spectrum analysis (FIG. 6), indicating that this arginine methylation event may be another factor that contributes to cetuximab resistance, PRMT1 is not the methyltransferase for R497 methylation, at least from the present *in vitro* methylation assay (FIG. 2C). Further work will be performed to identify the PRMT that methylates R497.

[00160] EGFR methylation is relatively new (Hsu et al., 2011) and not well characterized. The extracellular domain of tyrosine kinase receptor can also be methylated in addition to glycosylation. EGFR extracellular domain methylation, similar to glycosylation, occurs during protein synthesis (FIGS. 7A-B) and therefore cannot be regulated by EGF stimulation. Indeed, the PRMT1-EGFR interaction was found to occur on the endoplasmic reticulum surface, where protein syntheses occurs. Duolink® assays of SKCO1 cells found that PRMT1, EGFR, and the endoplasmic reticulum marker calnexin all co-localize. Furthermore, PRMT1 interacts with and methylates EGFR during protein synthesis (FIGS. 7A-B) without affecting the level of EGFR cell surface expression (FIGS. 10A-B). However, the signal that triggers PRMT1-mediated EGFR methylation is still unknown and needs further investigation. Overall, the role of PRMT1-mediated EGFR methylation in colorectal cancer tumorigenesis and its correlation with poor patient outcomes and cetuximab response by affecting the EGF-EGFR binding affinity (FIGS. 9A-C) provide an insight into the response to EGFR-targeted therapy and also open an avenue toward the understanding of how arginine methylation regulates the function of receptor tyrosine kinases.

Example 2 – Combination Therapy with a PRMT Inhibitor and Cetuximab

[00161] The arginine methylation status of EGFR in patient samples treated with cetuximab will be determined in order to compare the status in those that respond to cetuximab with those that do not respond. PRMT inhibitors for use in combination with cetuximab will be identified, the effectiveness of the combination will be tested *in vitro* and *in vivo*. Additionally, studies will be performed to show that EGFR Rl98 and R200 methylation occurs in and induces resistance in other cancer types besides colorectal cancer.

* * *

[00162] All of the methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

REFERENCES

The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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U.S. Patent No. 5,739,169

U.S. Patent No. 5,760,395

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CLAIMS

1. A method of treating a patient having cancer comprising administering an effective amount of cetuximab and a protein arginine methyltransferase (PRMT) inhibitor to a patient in need thereof.

2. The method of claim 1, wherein the PRMT inhibitor is sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde.

3. The method of claim 1, wherein cetuximab and the PRMT inhibitor are administered essentially simultaneously.

4. The method of claim 1, wherein the patient is a human.

5. The method of claim 1, wherein the cancer is colorectal, breast, prostate, lung, or pancreatic cancer.

6. The method of claim 1, further comprising administering a second anticancer therapy.

7. The method of claim 6, wherein the second anticancer therapy is a surgical therapy, chemotherapy, radiation therapy, cryotherapy, hormonal therapy, toxin therapy, immunotherapy, or cytokine therapy.

8. The method of claim 1, wherein the patient has been determined to have a cancer cell comprising at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of epidermal growth factor receptor (EGFR) protein.

9. The method of claim 8, wherein the cancer cell is from a biopsy sample.

10. The method of claim 8, wherein the cancer cell is a circulating tumor cell.

11. The method of claim 8, wherein the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 of EGFR protein is detected by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation.

12. The method of claim 8, wherein the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 of EGFR protein is detecting by a method

comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200.

13. The method of claim 8, wherein the presence of (iii) an Arg residue at amino acid position 497 of EGFR protein is determined by mass spectrometry or by sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

14. A method of treating a patient having cancer comprising administering an effective amount of cetuximab to a patient in need thereof, said patient having been determined to have a cancer cell comprising (i) unmethylated Arg at position 198, (ii) unmethylated Arg at position 200, and (iii) a Lys residue at amino acid position 497 of EGFR protein.

15. The method of claim 14, further comprising administering a second anticancer therapy.

16. The method of claim 16, wherein the second anticancer therapy is a surgical therapy, chemotherapy, radiation therapy, cryotherapy, hormonal therapy, toxin therapy, immunotherapy, or cytokine therapy.

17. The method of claim 14, wherein the cancer is colorectal, breast, prostate, lung, or pancreatic cancer.

18. The method of claim 14, wherein the cancer cell is from a biopsy sample.

19. The method of claim 14, wherein the cancer cell is a circulating tumor cell.

20. The method of claim 14, wherein the presence of (i) unmethylate Arg at position 198 and (ii) unmethylate Arg at position 200 of EGFR protein is detected by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation.

21. The method of claim 14, wherein the presence of (i) unmethylate Arg at position 198 and (ii) unmethylate Arg at position 200 of EGFR protein is detecting by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and Arg200.

22. The method of claim 14, wherein the presence of (iii) a Lys residue at amino acid position 497 of EGFR protein is determined by mass spectrometry or by sequencing a

nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

23. A method of predicting resistance of a cancer patient to cetuximab comprising assaying a cancer cell isolated from the patient to determine the presence of at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of EGFR protein in the cancer cell.

24. The method of claim 23, wherein if at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of EGFR protein is present, then the cancer is predicted to be resistant to cetuximab.

25. The method of claim 24, further comprising identifying the patient as having a cancer that is resistant to cetuxmiab if at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of EGFR protein is present.

26. The method of claim 25, wherein identifying comprises reporting whether the patient has a cancer that is resistant to cetuximab.

27. The method of claim 26, wherein reporting comprises preparing a written or an oral report.

28. The method of claim 26, further comprising reporting to the patient, a doctor, a hospital, or an insurance provider.

29. The method of claim 25, wherein identifying the patient as having a cancer that is resistant to cetuxmiab further comprises identifying the patient having the cancer as a candidate for treatment with a combination of cetuximab and a PRMT inhibitor.

30. The method of claim 29, further comprising treating the patient with cetuximab in combination with a PRMT inhibitor.

31. The method of claim 30, wherein the PRMT inhibitor is sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde.

32. The method of claim 30, wherein the cetuximab and the PRMT inhibitor are administered essentially simultaneously.

33. The method of claim 30, further comprising administering a second anticancer therapy.

34. The method of claim 33, wherein the second anticancer therapy is a surgical therapy, chemotherapy, radiation therapy, cryotherapy, hormonal therapy, toxin therapy, immunotherapy, or cytokine therapy.

35. The method of claim 23, wherein the cancer cell is from a biopsy sample.

36. The method of claim 23, wherein the cancer cell is a circulating tumor cell.

37. The method of claim 23, wherein the presence of (i) methylated Arg at position 198 and/or (ii) methylated Arg at position 200 comprises contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200.

38. The method of claim 37, wherein assaying comprises performed a Western blot, ELISA, immunoprecipitation, radioimmunoassay, or immunohistochemical assay.

39. The method of claim 23, wherein assaying comprises mass spectrometry.

40. The method of claim 23, wherein the presence of (iii) an Arg residue at amino acid position 497 of EGFR is determined by mass spectrometry or by sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

41. The method of claim 23, wherein the cancer is colorectal, breast, prostate, lung, or pancreatic cancer.

42. The method of claim 23, wherein the patient has previously undergone at least one round of anti-cancer therapy.

43. The method of claim 23, wherein the patient is a human.

44. A method of characterizing a cancer patient comprising selectively testing a cancer cell having been isolated from the patient to determine the methylation status of amino acids Arg198 and/or Arg200 of EGFR protein in the cancer cell.

45. The method of claim 44, further comprising obtaining a sample of the cancer or a circulating tumor cell from the cancer patient.

46. The method of claim 44, wherein a positive determination for methylation of amino acid Arg198 and/or Arg200 of EGFR protein indicates that the cancer patient will be resistant to cetuximab.

47. The method of claim 46, further comprising identifying the cancer patient as being eligible for treating with cetuximab in combination with a PRMT inhibitor.

48. The method of claim 47, further comprising administering an effective amount of cetuximab in combination with a PRMT inhibitor to the patient.

49. The method of claim 44, wherein the methylation status of amino acids Arg198 and/or Arg200 of EGFR protein is detected by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation.

50. The method of claim 44, wherein the methylation status of amino acids Arg198 and/or Arg200 of EGFR protein is detecting by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200.

51. A method of selecting a drug therapy for a cancer patient comprising assaying a cancer sample isolated from the patient to determine a methylation status of Arg198 and/or Arg200 of EGFR protein in the sample.

52. The method of claim 51, further comprising selecting a combination of cetuximab and a PRMT inhibitor if Arg198 and/or Arg200 of EGFR protein is determined to be methylated.

53. The method of claim 51, wherein the methylation status of Arg198 and/or Arg200 of EGFR protein is determined by mass spectrometry, ELISA, flow cytometry, immunohistochemistry, western blot, radioimmunoassay, or immunoprecipitation.

54. The method of claim 51, wherein the methylation status of Arg198 and/or Arg200 of EGFR protein is determined by a method comprising contacting the sample with an antibody that binds specifically to EGFR methylated at Arg198 and/or Arg200.

55. A method of sensitizing a cetuximab-resistant cancer to cetuximab comprising administering an effective amount of a PRMT inhibitor to a patient having the cetuximab-resistant cancer.

56. The method of claim 55, further comprising administering cetuximab to the patient.

57. The method of claim 56, wherein the cetuximab is administered essentially simultaneously with the PRMT inhibitor.

58. A pharmaceutical composition comprising cetuximab and a PRMT inhibitor in a pharmaceutically acceptable carrier.

59. The composition of claim 58, wherein the PRMT inhibitor is sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde.

60. A composition comprising an antibody that specifically binds to Arg198- and/or Arg200-methylated EGFR protein.

61. The composition of claim 60, wherein the antibody is an IgG1 antibody.

62. A composition comprising a polypeptide comprising at least eight consecutive amino acids of EGFR protein fused to an immunogen, wherein the at least eight consecutive amino acids of EGFR1 protein includes Arg198 and/or Arg200 and wherein Arg198 and/or Arg200 is dimethylated.

63. The polypeptide of claim 62, wherein the polypeptide comprises the sequence QCSGRCRGKSPSDC (SEQ ID NO: 1).

64. A composition comprising cetuximab and a PRMT inhibitor for use in the treatment of a tumor in a subject.

65. The composition of claim 64, wherein the composition is formulated for intratumoral, intravenous, intradermal, intraarterial, intraperitoneal, intralesional, intracranial, intraarticularly, intraprostatic, intrapleural, intratracheal, intraocular, intranasal, intravitreal, intravaginal, intrarectal, intramuscular, subcutaneous, subconjunctival, intravesicularl, mucosal, intrapericardial, intraumbilical, oral administration.

66. The composition of claim 64, further comprising at least a third anticancer therapy.

67. The composition of claim 66, wherein the third anticancer therapy is chemotherapy, radiation therapy, hormone therapy, immunotherapy or cytokine therapy.

68. The composition of claim 64, wherein the patient has been determined to have a cancer cell comprising at least one of (i) methylated Arg at position 198, (ii) methylated Arg at position 200, and/or (iii) an Arg residue at amino acid position 497 of epidermal growth factor receptor (EGFR) protein.

69. The composition of claim 64, wherein the PRMT inhibitor is sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde.

70. Use of cetuximab and a PRMT inhibitor in the manufacture of a medicament for the treatment of a tumor.

71. A method of treating cancer comprising administering a composition of claim 58 to a patient in need thereof.

72. A method of predicting resistance to cetuximab in a cancer patient comprising:

(a) obtaining a sample of the patient's cancer;

(b) determining the methylation status of R198 or R200 of the epidermal growth factor receptor (EGFR) protein in the sample; and

(c) predicting that the patient's cancer is resistant to cetuximab if R198 or R200 of EGFR is determined to be methylated.

73. The method of claim 72, further comprising treating the patient with cetuximab in combination with a protein arginine methyltransferase (PRMT) inhibitor.

74. A method of treating a cancer in a patient in need thereof comprising:

(a) obtaining a sample of the cancer;

(b) determining the methylation status of R198 or R200 of the epidermal growth factor receptor (EGFR) protein expressed in the cancer; and

(c) treating the patient with cetuximab alone if R198 and R200 of EGFR are determined to be unmethylated or treating the patient with cetuximab and a PRMT inhibitor if R198 or R200 of EGFR is determined to be methylated.

75. The method of claim 72 or 74, further comprising determining the methylation status of both R198 and R200.

76. A method of treating a cancer in a patient in need thereof comprising:

(a) obtaining a sample of the cancer:

(b) determining the amino acid present at position 497 of the EGFR protein expressed in the cancer; and

(c) treating the patient with cetuximab alone if a lysine is present at position 497 of EGFR or treating the patient with cetuximab and a PRMT inhibitor if an arginine is present at position 497 of EGFR.

77. The method of claim 76, further comprising determining the methylation status of an arginine present at position 497 of EGFR.

78. The method of claim 72, 74, or 76, further comprising preparing a report of the determining.

79. The method of claim 72, 74, or 77, wherein the methylation status is determined by mass spectrometry, immunohistochemistry, western blotting, or ELISA.

80. The method of claim 76, wherein the amino acid present at position 497 of the EGFR protein is determined by mass spectrometry or sequencing a nucleic acid comprising at least a portion of the protein coding sequence of the EGFR protein.

81. The method of any one of claims 72-80, wherein the patient is a human patient.

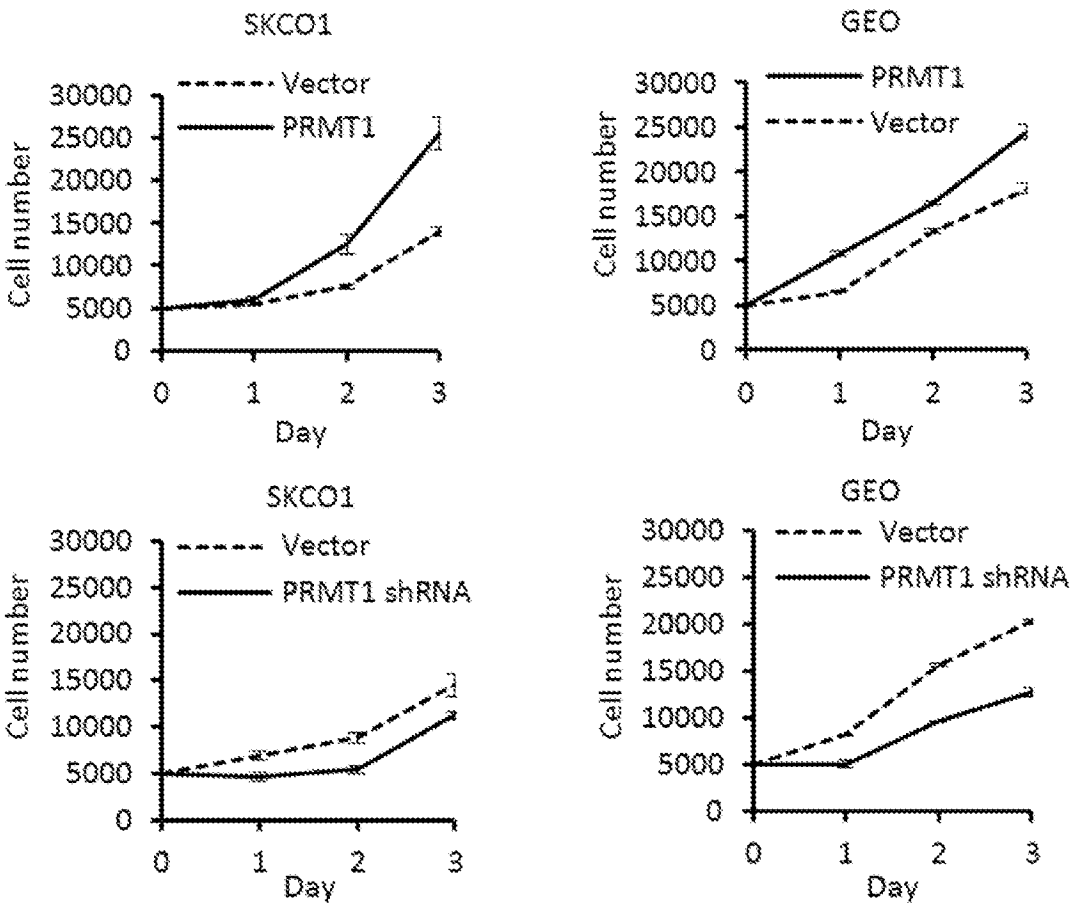
82. The method of claim 73, 74, or 76, wherein the PRMT inhibitor is sinefungin, S-adenosylhomocysteine, AMI-1, AMI-408, MDL 28,842, methylthioadenosine, C21, Eosin Y, disodium trihydrate, Cpd4, or adenosine dialdehyde.

83. The method of any one of claims 72-82, wherein the cancer is a colorectal, breast, prostate, lung, or pancreatic cancer.

84. The method of any one of claims 72-82, wherein the cancer is metastatic, recurrent, or multi-drug resistant.

85. The method of any one of claims 74-82, wherein the patient is treated at least a second time.

86. The method of any one of claims 74-82, wherein the patient is treated over a period of 1 week to 6 months.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15000
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3
Day
GEO
PRMT1
Vector
Cell number
30000
25000
20000
15000
10000
5000
0
0
1
2
3
Day
SKCO1
Vector
PRMT1 shRNA
Cell number
30000
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Day
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3
Day

FIG. 1A

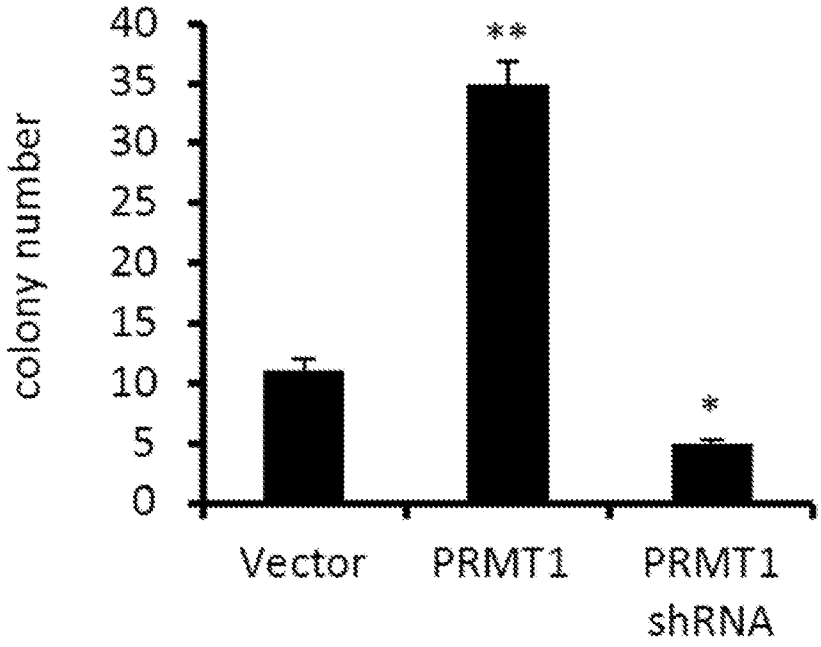


FIG. 1B

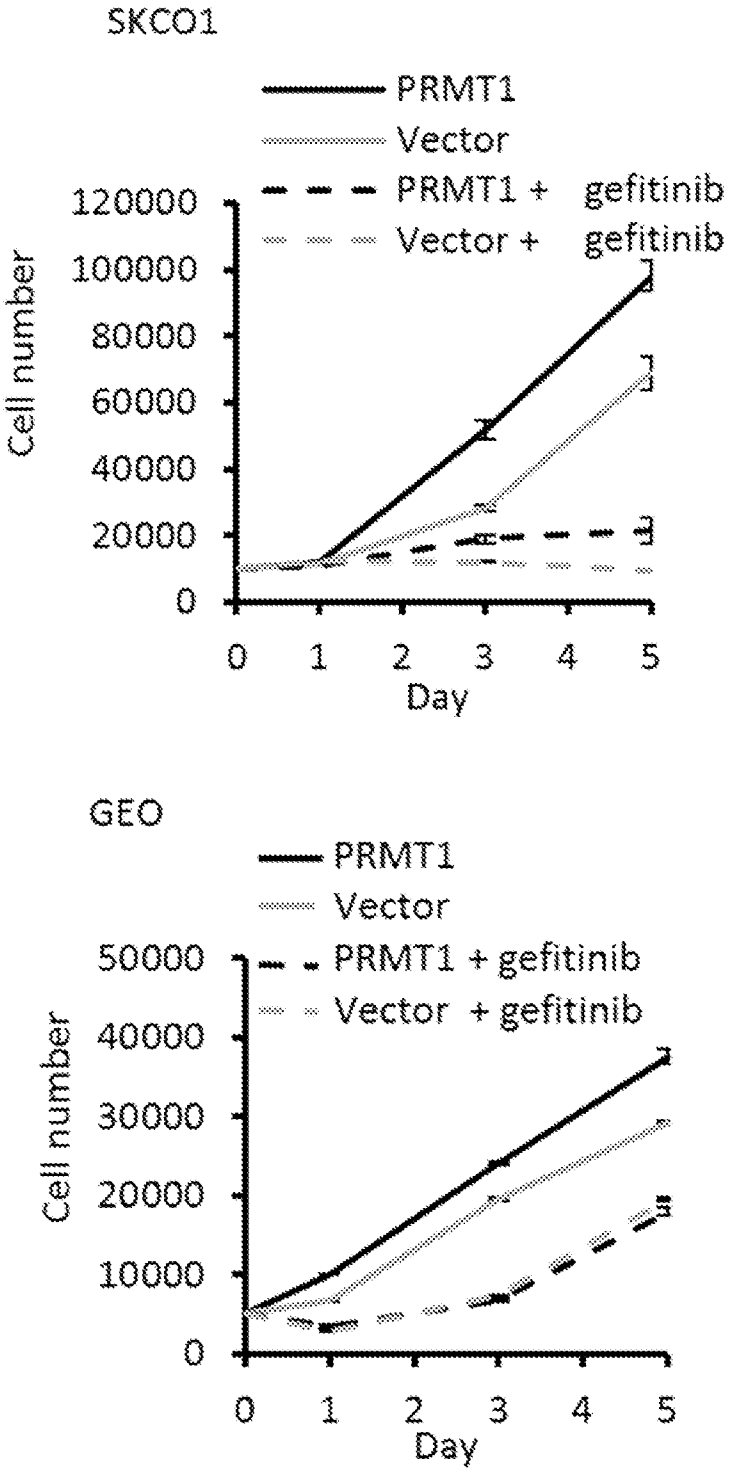

SKCO1
PRMT1
Vector
PRMT1 + gefitinib
Vector + gefitinib
Cell number
120000
100000
80000
60000
40000
20000
0
0 1 2 3 4 5
Day
GEO
PRMT1
Vector
PRMT1 + gefitinib
Vector + gefitinib
Cell number
50000
40000
30000
20000
10000
0
0 1 2 3 4 5
Day

FIG. 1C

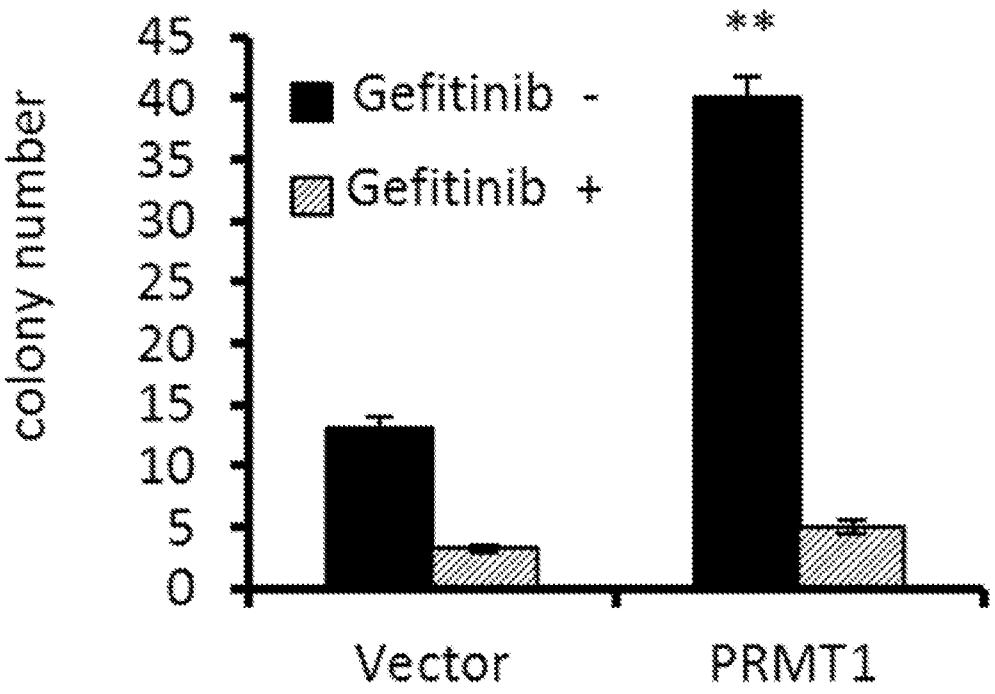

colony number
45
40
35
30
25
20
15
10
5
0
Gefitinib -
Gefitinib +
**
Vector
PRMT1

FIG. 1D

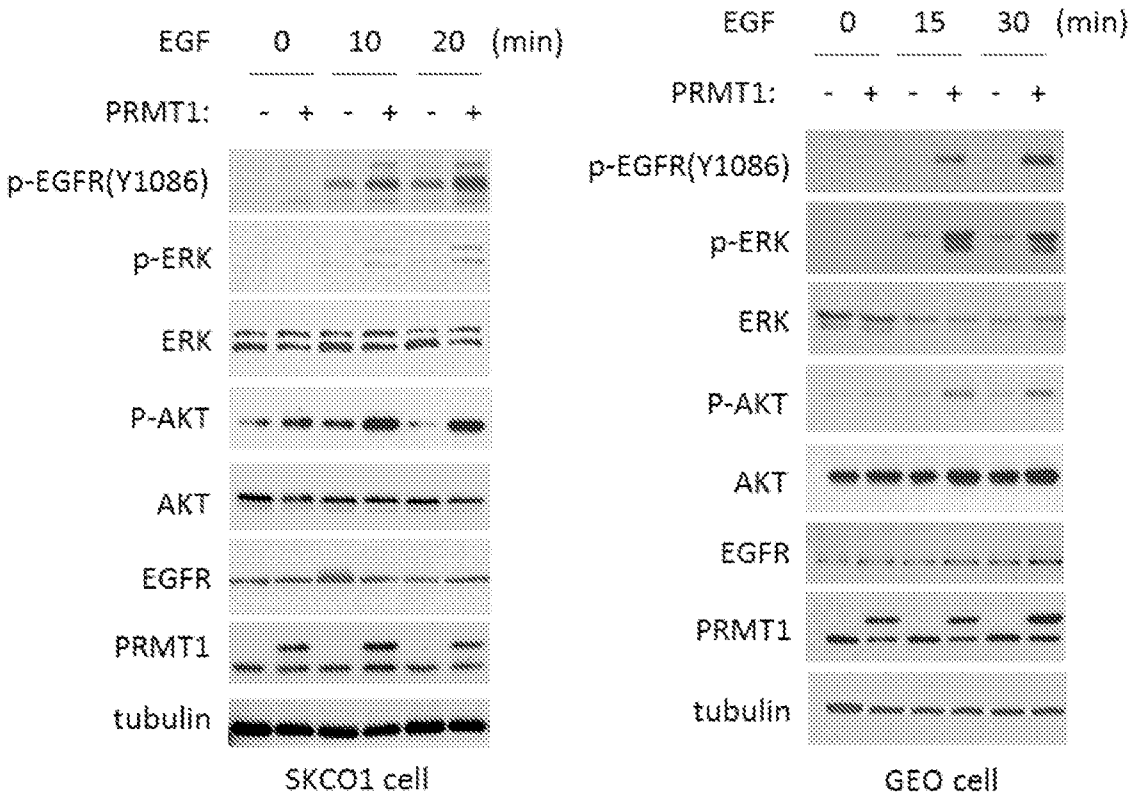

EGF 0 10 20 (min)
PRMT1: - + - + - +
p-EGFR(Y1086)
p-ERK
ERK
P-AKT
AKT
EGFR
PRMT1
tubulin
SKCO1 cell
EGF 0 15 30 (min)
PRMT1: - + - + - +
p-EGFR(Y1086)
p-ERK
ERK
P-AKT
AKT
EGFR
PRMT1
tubulin
GEO cell

FIG. 1E

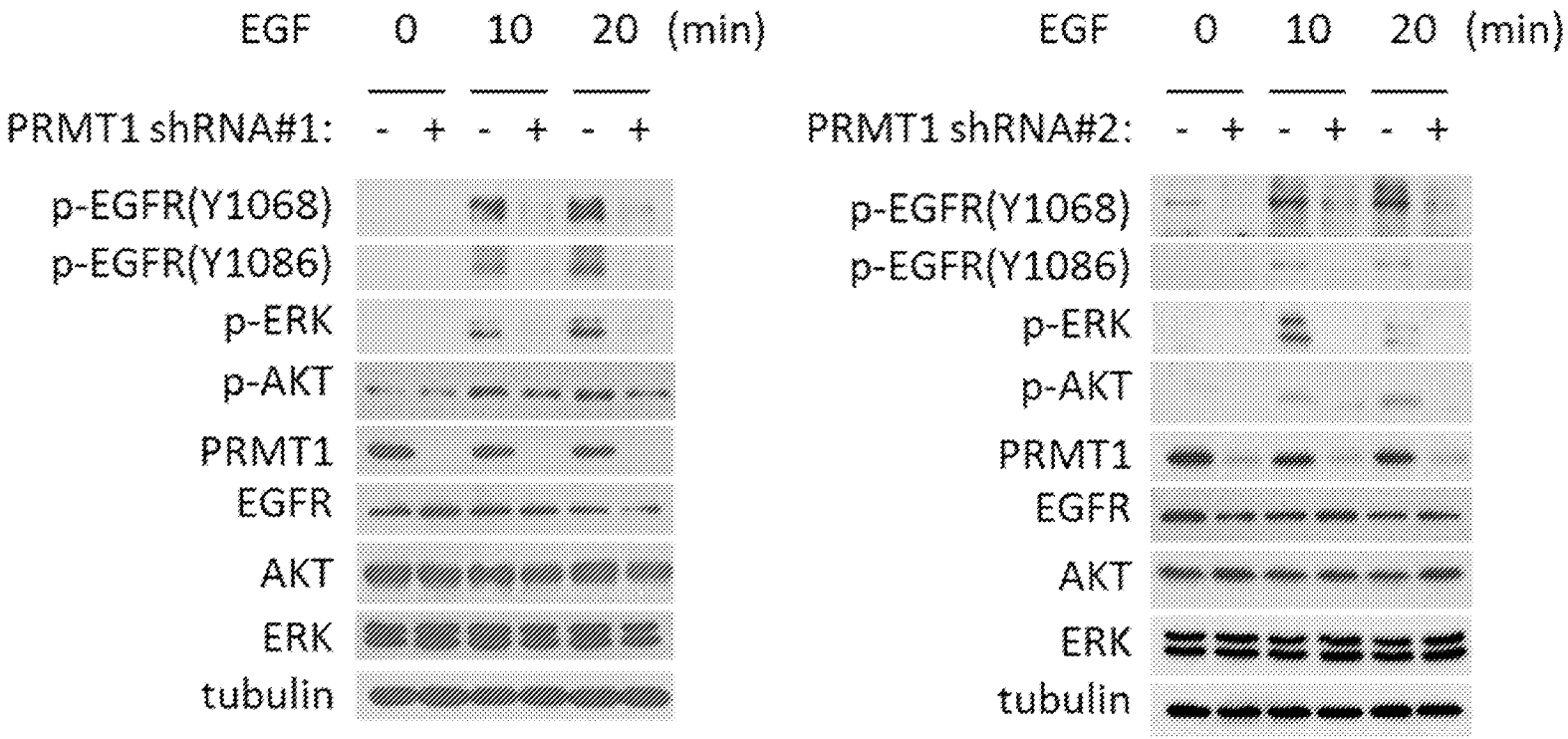
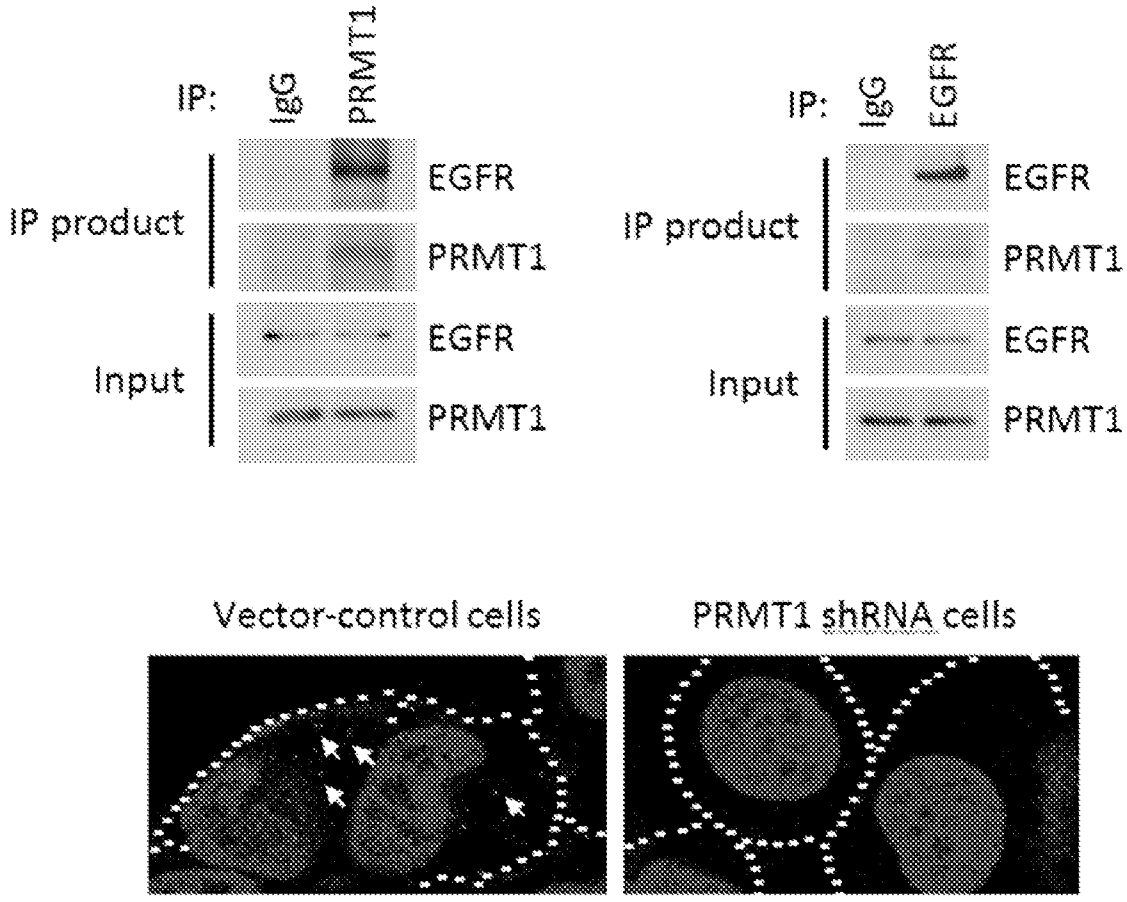

EGF 0 10 20 (min)
PRMT1 shRNA#1: - + - + - +
p-EGFR(Y1068)
p-EGFR(Y1086)
p-ERK
p-AKT
PRMT1
EGFR
AKT
ERK
tubulin
EGF 0 10 20 (min)
PRMT1 shRNA#2: - + - + - +
p-EGFR(Y1068)
p-EGFR(Y1086)
p-ERK
p-AKT
PRMT1
EGFR
AKT
ERK
tubulin

FIG. 1F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IgG
PRMT1
IP product
EGFR
PRMT1
Input
EGFR
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IgG
EGFR
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EGFR
PRMT1
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EGFR
PRMT1
Vector-control cells
PRMT1 shRNA cells

FIG. 2A

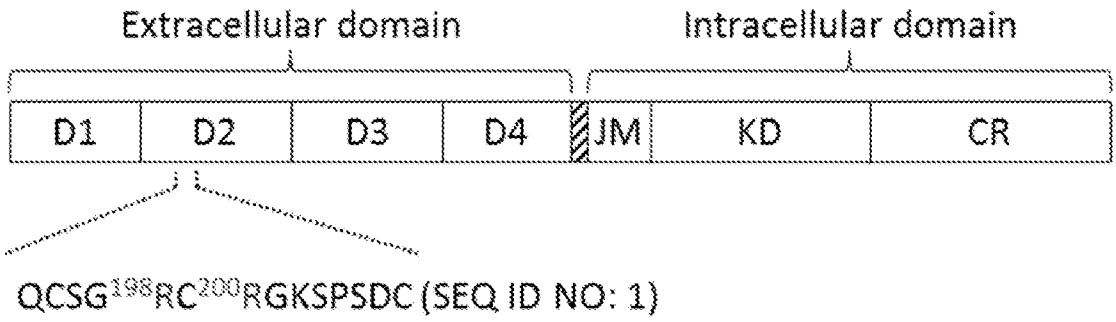

Extracellular domain
Intracellular domain
D1
D2
D3
D4
JM
KD
CR
QCSG198RC200RGKSPSDC (SEQ ID NO: 1)

FIG. 2B

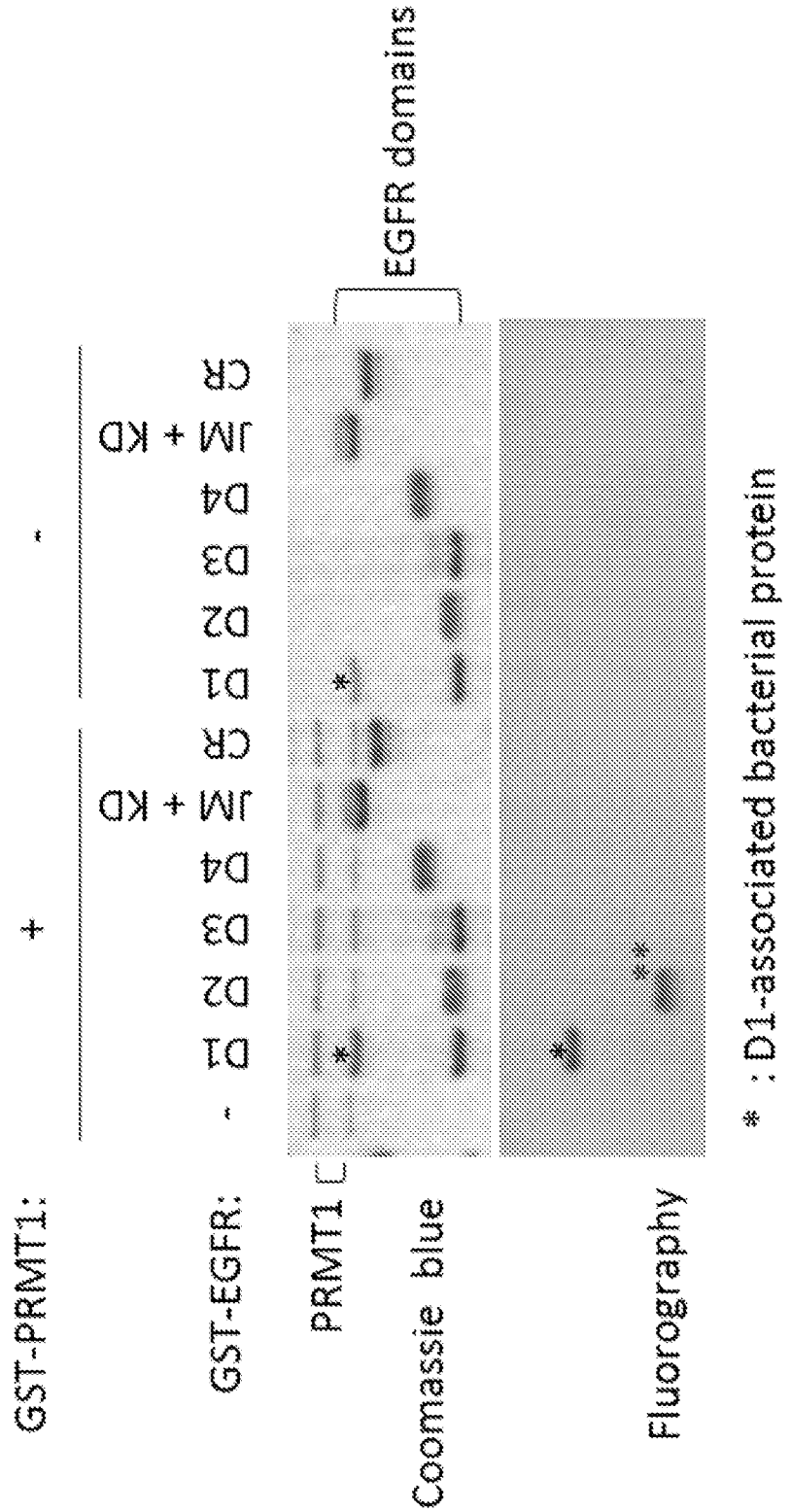

GST-PRMT1:
+
-
GST-EGFR:
-
D1
D2
D3
D4
JM + KD
CR
D1
D2
D3
D4
JM + KD
CR
EGFR domains
PRMT1
Coomassie blue
Fluorography
* : D1-associated bacterial protein
** : Methylated D2

FIG. 2C

PRMT1 substrate	GAR motif	SEQ ID NO:
EGFR	196-SGRCRGKSP-204	4
p53	331-QIRGRERFE-339	5
p80 coilon	411-GMRGRGRGR-419	6
Sm D1	98-RGRGRGRGR-106	7
Sm D3	110-RGRGRGMGR-118	8
Histone H4	1-MSGRG KGG-8	9
Histone H3	7-TARKSTGGK-15	10

FIG. 2D

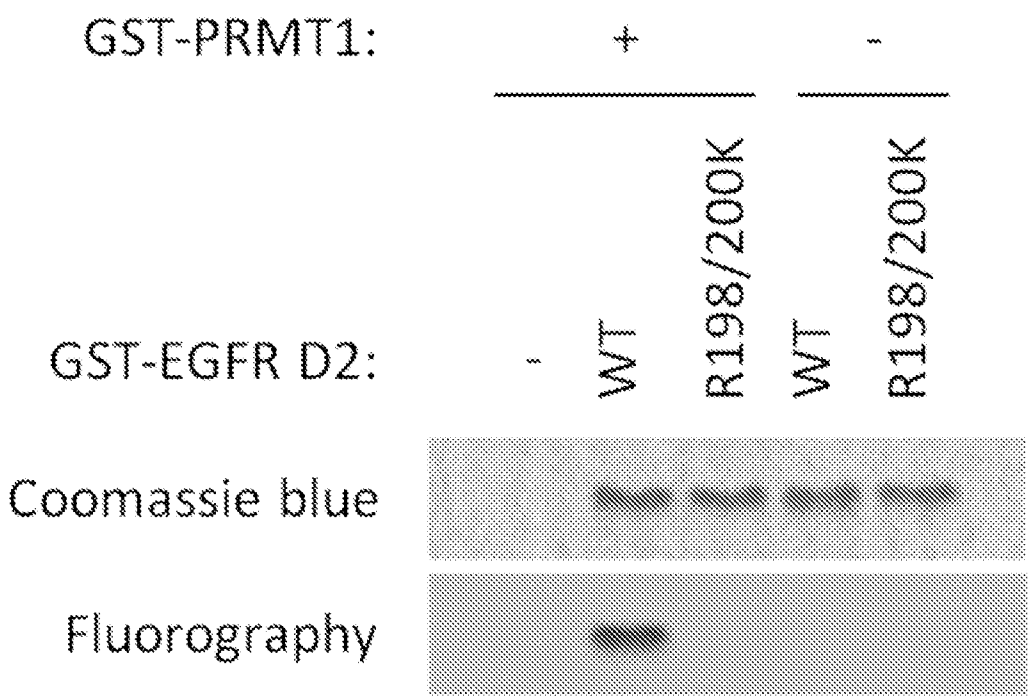
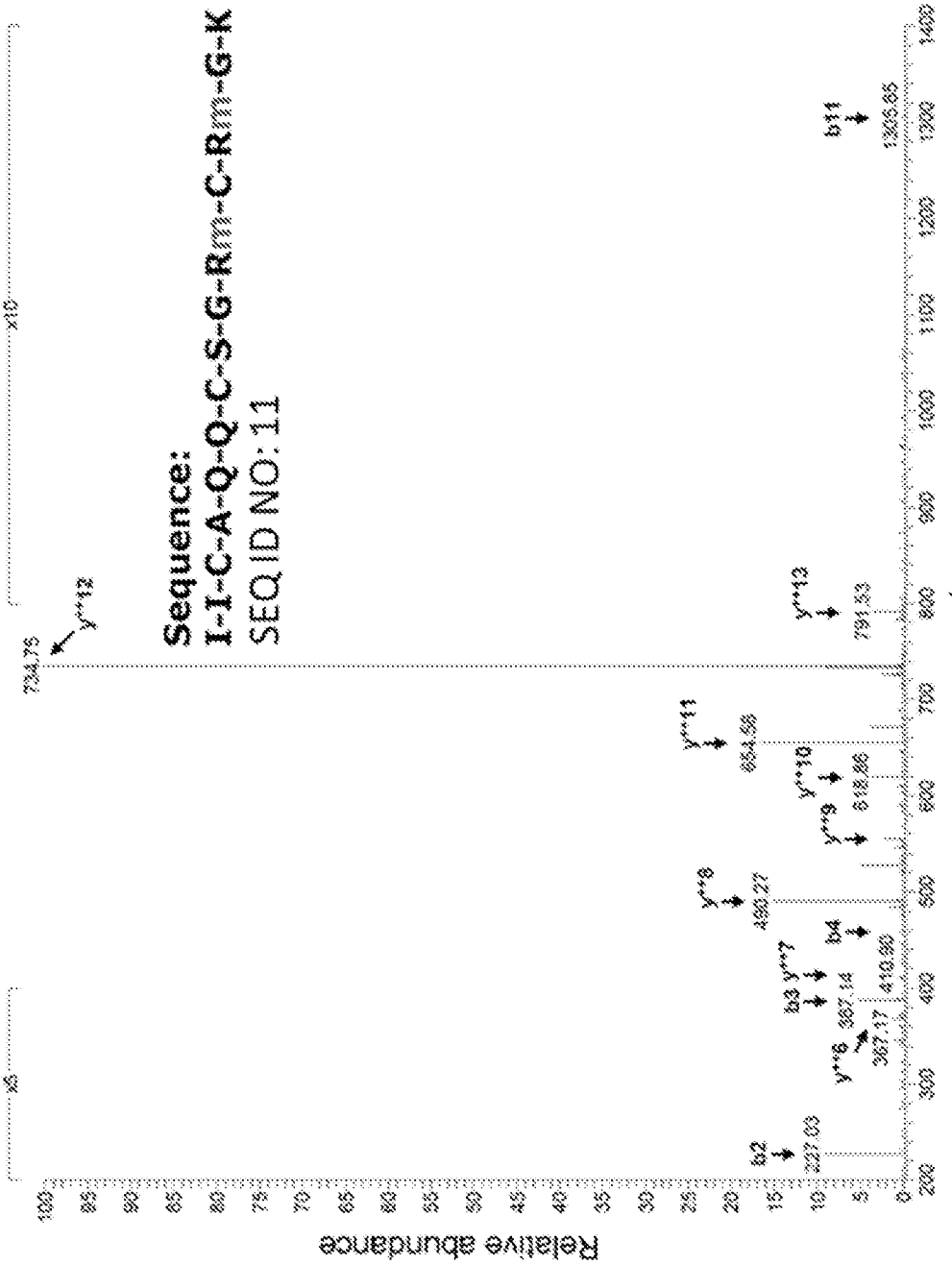

GST-PRMT1:
+
-
GST-EGFR D2:
-
WT
R198/200K
WT
R198/200K
Coomassie blue
Fluorography

FIG. 2E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SEQ ID NO: 11
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x10
y''12
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y''13
791.53
b11
1305.65
y''11
654.56
y''10
618.86
y''9
y''8
490.27
b4
b3 y''7
410.80
367.14
y''6
367.17
b2
227.03

FIG. 2F

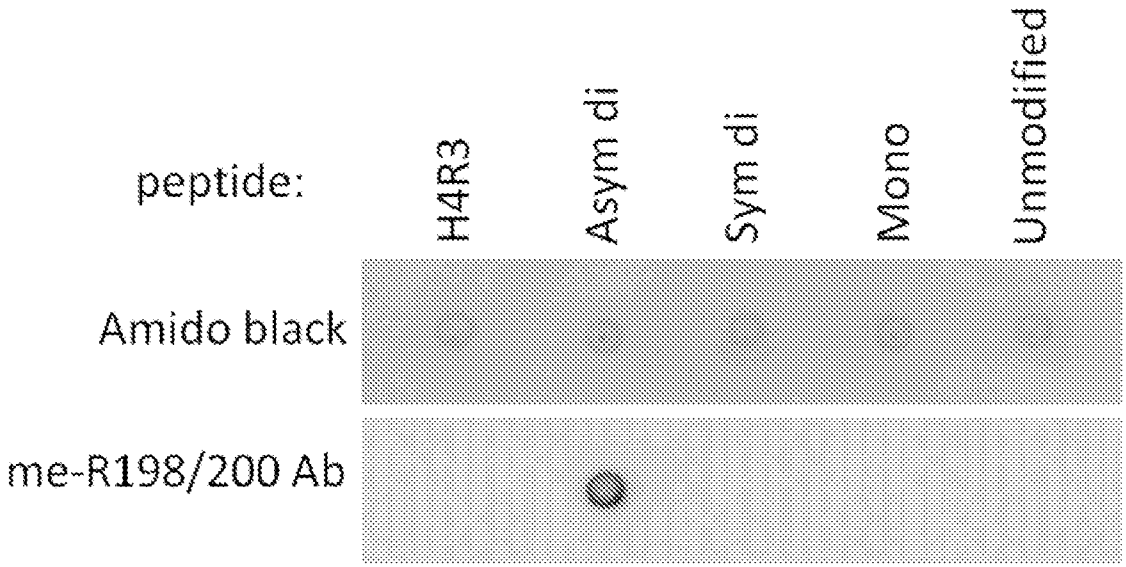

peptide:
H4R3
Asym di
Sym di
Mono
Unmodified
Amido black
me-R198/200 Ab

FIG. 2G

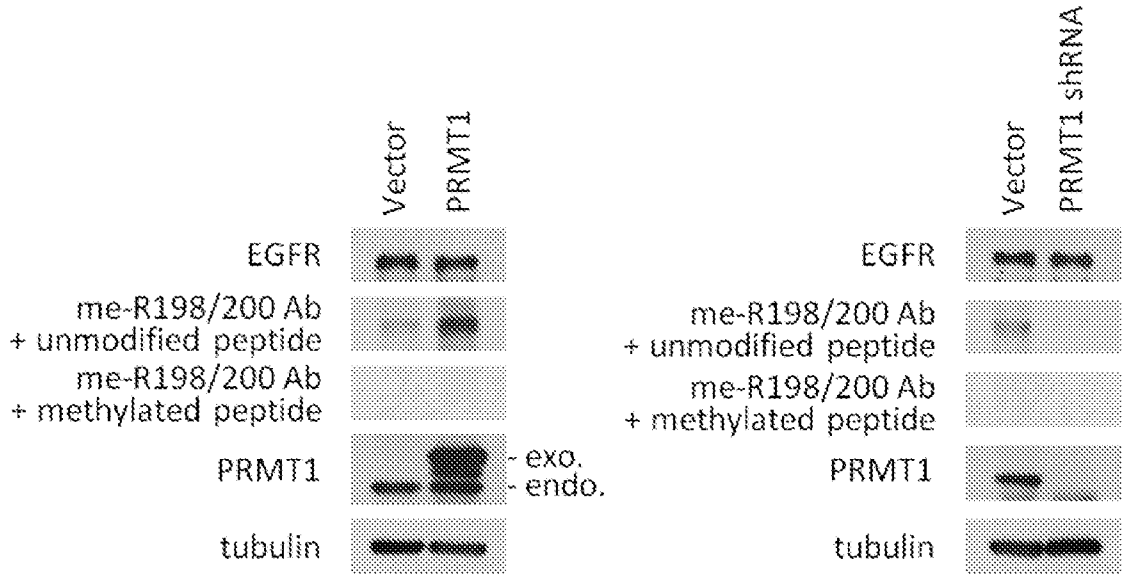

Vector
PRMT1
EGFR
me-R198/200 Ab
+ unmodified peptide
me-R198/200 Ab
+ methylated peptide
PRMT1
- exo.
- endo.
tubulin
Vector
PRMT1 shRNA
EGFR
me-R198/200 Ab
+ unmodified peptide
me-R198/200 Ab
+ methylated peptide
PRMT1
tubulin

FIG. 2H

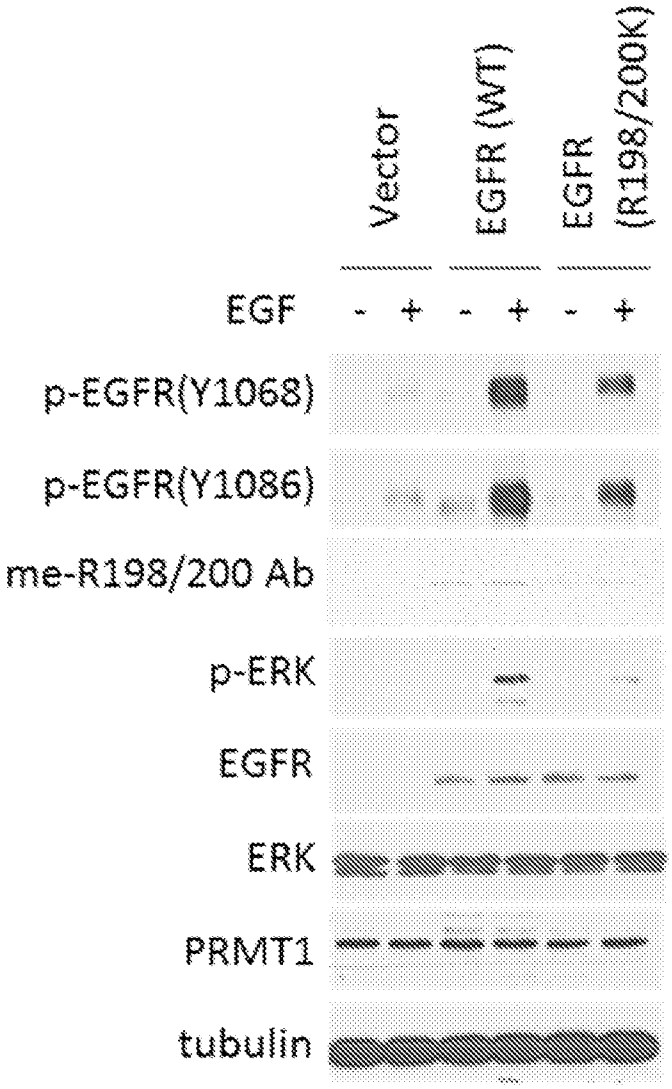

Vector
EGFR (WT)
EGFR (R198/200K)
EGF - + - + - +
p-EGFR(Y1068)
p-EGFR(Y1086)
me-R198/200 Ab
p-ERK
EGFR
ERK
PRMT1
tubulin

FIG. 3A

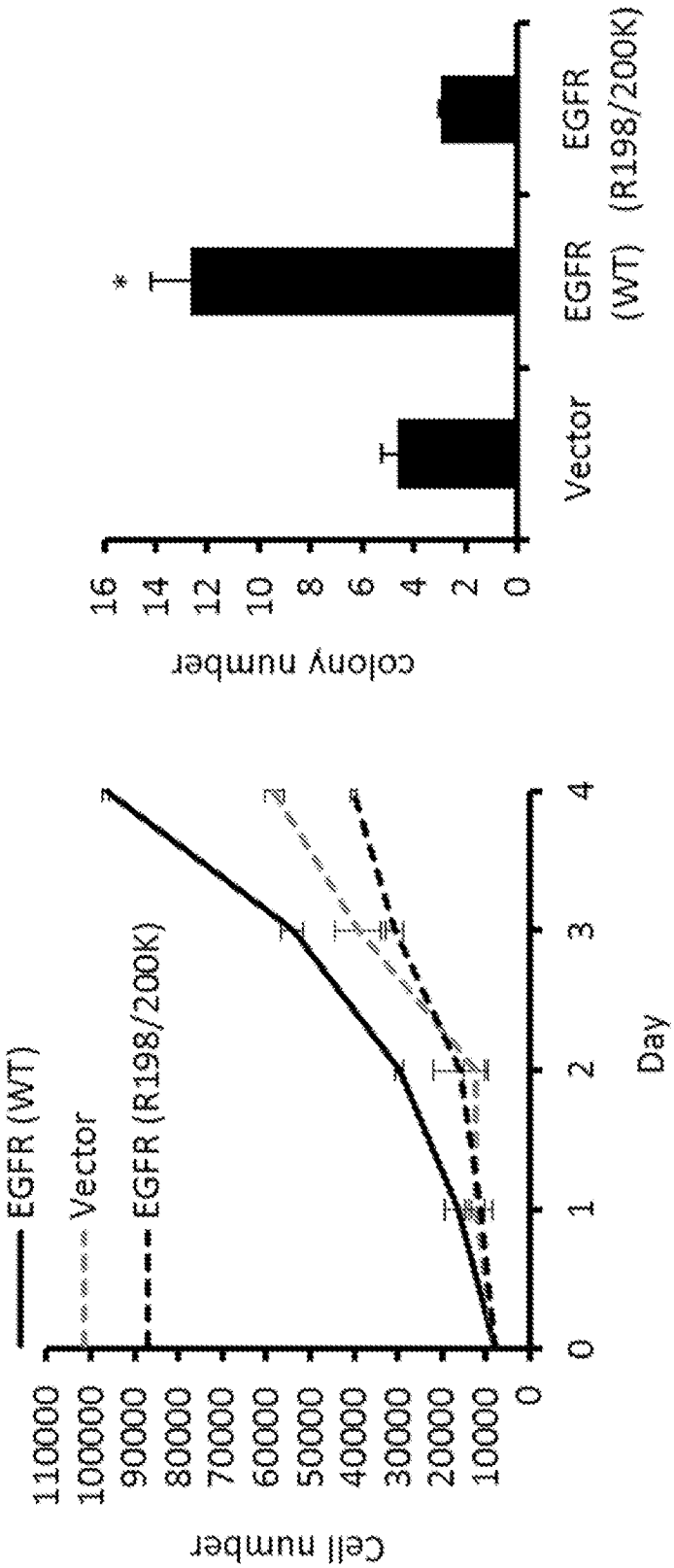
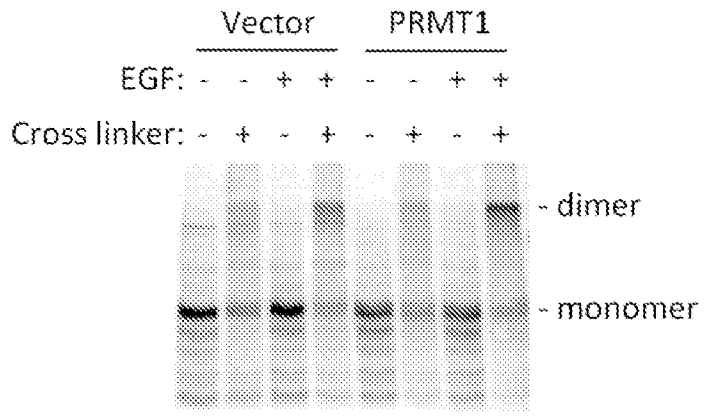
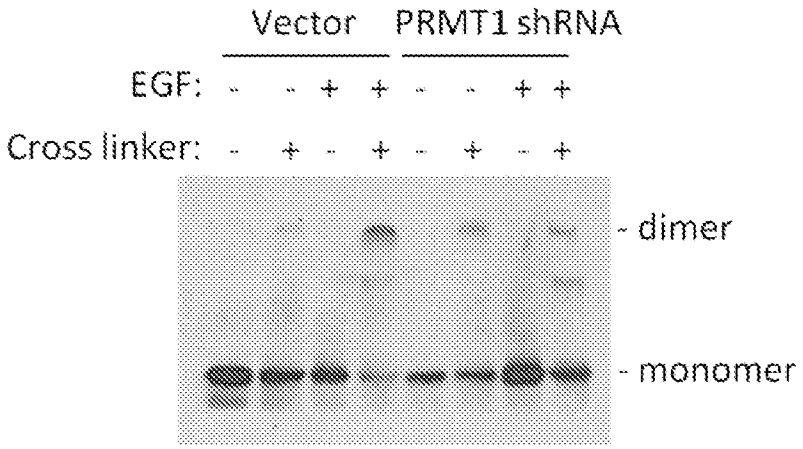

colony number
16
14
12
10
8
6
4
2
0
*
Vector
EGFR (WT)
EGFR (R198/200K)
Cell number
110000
100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
0
1
2
3
4
Day
EGFR (WT)
Vector
EGFR (R198/200K)

FIG. 3B


Vector
PRMT1
EGF: - - + + - - + +
Cross linker: - + - + - + - +
dimer
monomer


Vector
PRMT1 shRNA
EGF: - - + + - - + +
Cross linker: - + - + - + - +
dimer
monomer

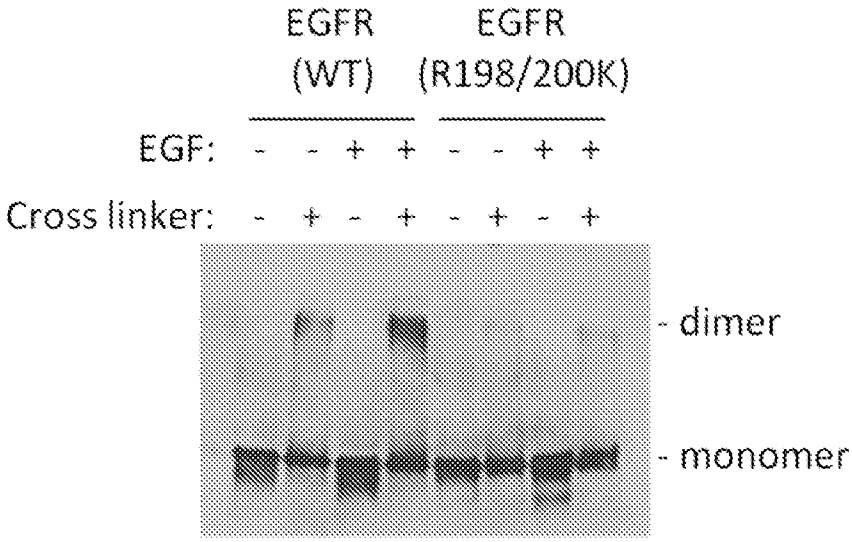

EGFR (WT)
EGFR (R198/200K)
EGF: - - + + - - + +
Cross linker: - + - + - + - +
dimer
monomer

FIG. 3C

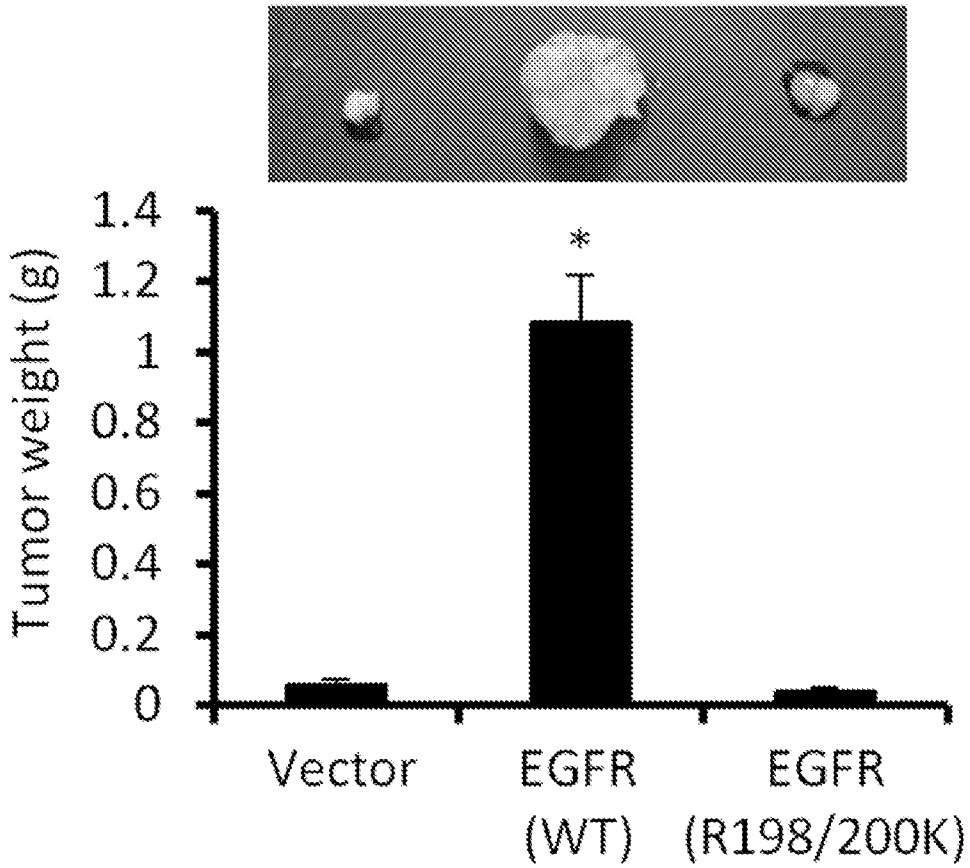

Tumor weight (g)
1.4
1.2
1
0.8
0.6
0.4
0.2
0
*
Vector
EGFR (WT)
EGFR (R198/200K)

FIG. 3D

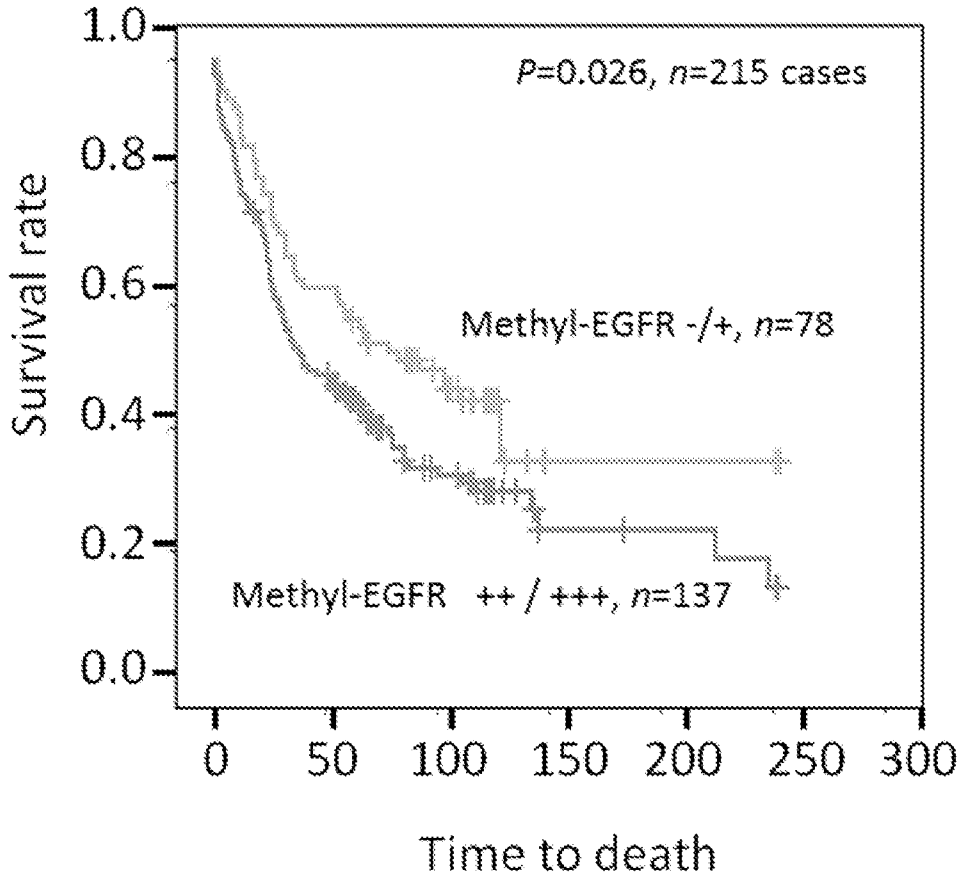

1.0
0.8
0.6
0.4
0.2
0.0
Survival rate
P=0.026, n=215 cases
Methyl-EGFR -/+, n=78
Methyl-EGFR ++ / +++, n=137
0
50
100
150
200
250
300
Time to death

FIG. 3E

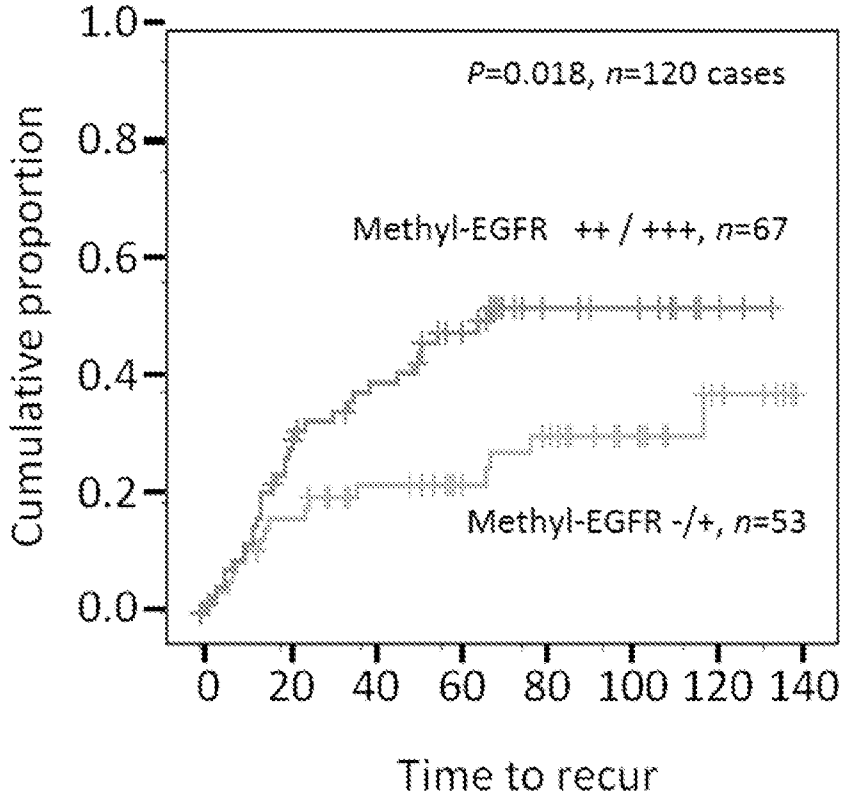

1.0
0.8
0.6
0.4
0.2
0.0
Cumulative proportion
P=0.018, n=120 cases
Methyl-EGFR ++ / +++, n=67
Methyl-EGFR -/+, n=53
0
20
40
60
80
100
120
140
Time to recur

FIG. 3F

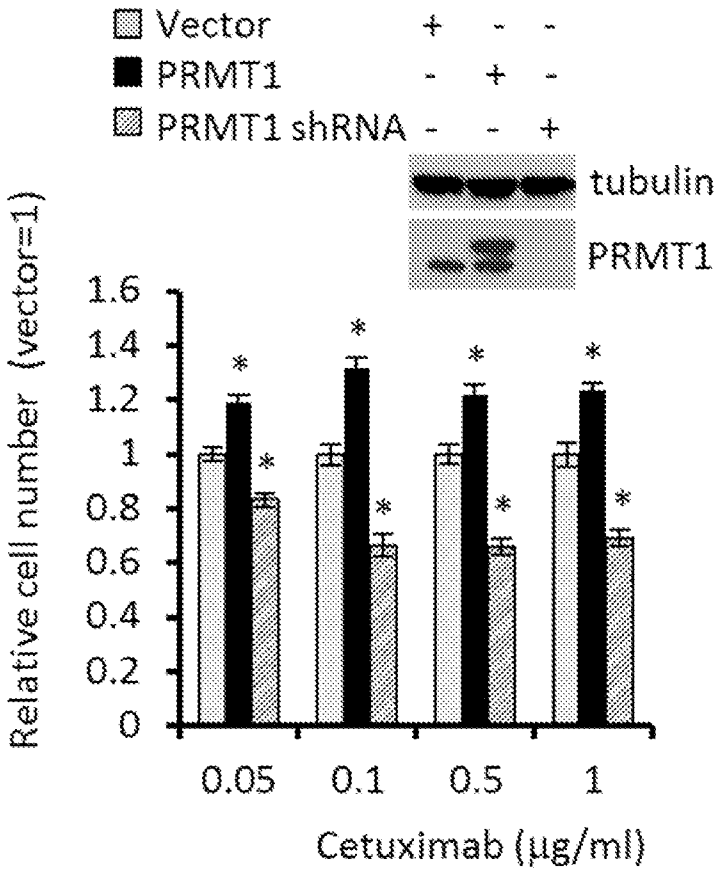

Vector + - -
PRMT1 - + -
PRMT1 shRNA - - +
tubulin
PRMT1
Relative cell number (vector=1)
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.05
0.1
0.5
1
Cetuximab (μg/ml)

FIG. 4A

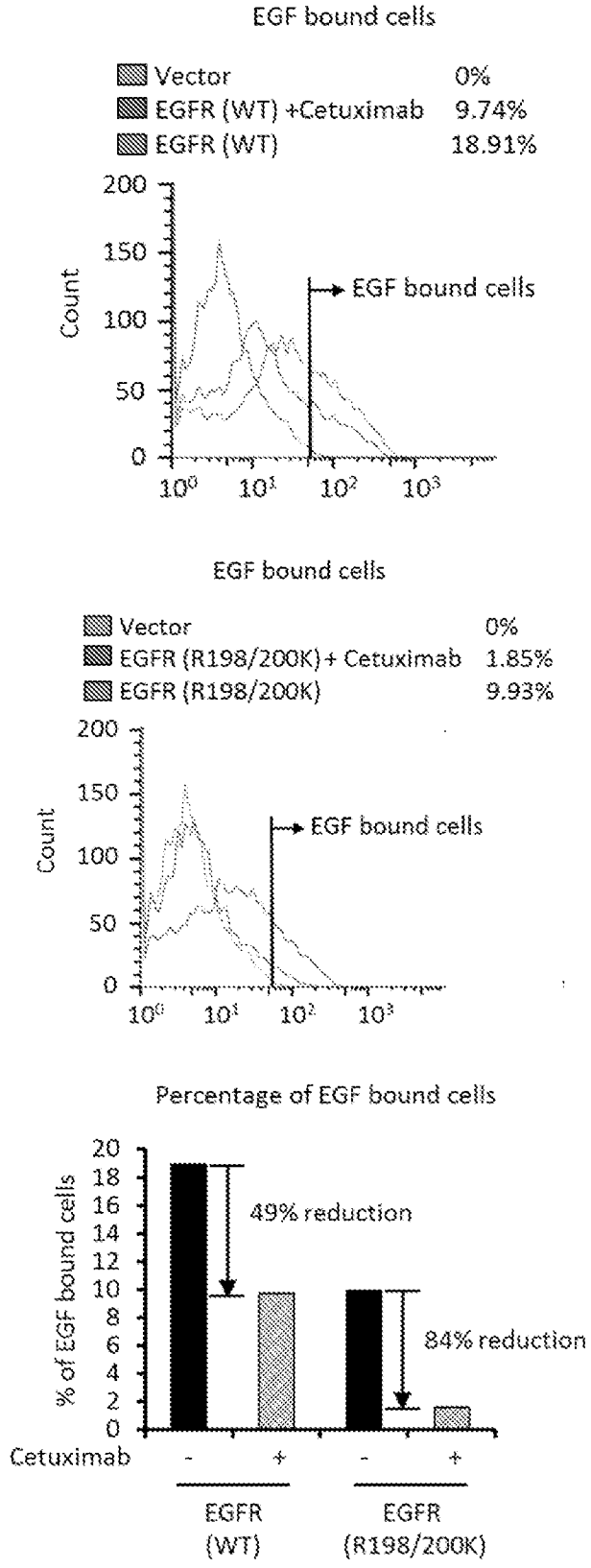

EGF bound cells
Vector 0%
EGFR (WT) +Cetuximab 9.74%
EGFR (WT) 18.91%
Count
EGF bound cells
EGF bound cells
Vector 0%
EGFR (R198/200K) + Cetuximab 1.85%
EGFR (R198/200K) 9.93%
Count
EGF bound cells
Percentage of EGF bound cells
% of EGF bound cells
49% reduction
84% reduction
Cetuximab
EGFR (WT)
EGFR (R198/200K)

FIG. 4B

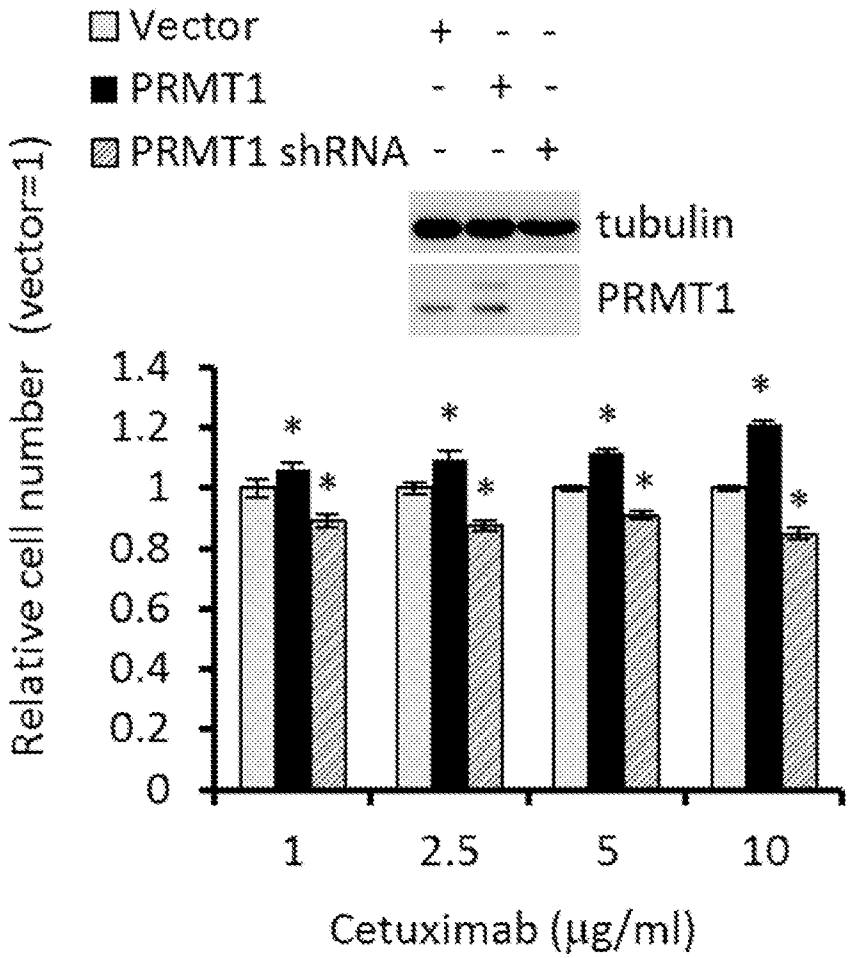

Vector + - -
PRMT1 - + -
PRMT1 shRNA - - +
tubulin
PRMT1
Relative cell number (vector=1)
1.4
1.2
1
0.8
0.6
0.4
0.2
0
1
2.5
5
10
Cetuximab (μg/ml)

FIG. 4C

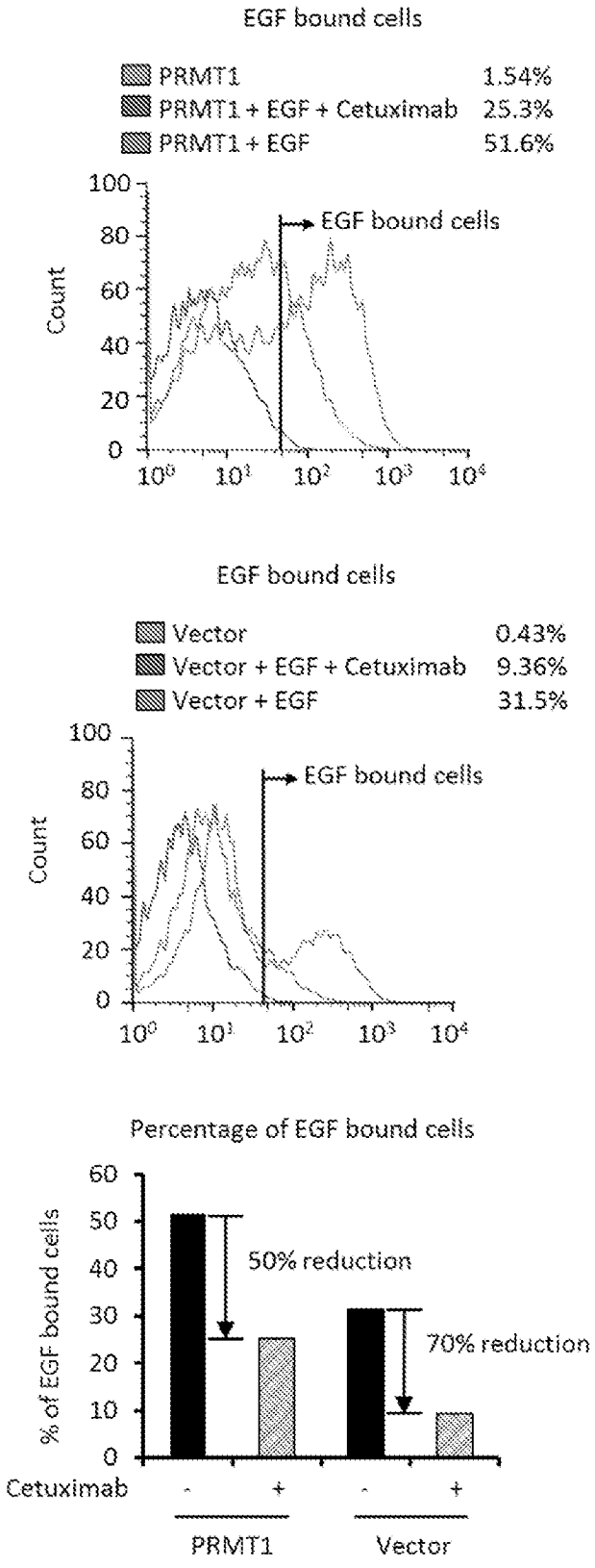

EGF bound cells
PRMT1 1.54%
PRMT1 + EGF + Cetuximab 25.3%
PRMT1 + EGF 51.6%
Count
EGF bound cells
EGF bound cells
Vector 0.43%
Vector + EGF + Cetuximab 9.36%
Vector + EGF 31.5%
Count
EGF bound cells
Percentage of EGF bound cells
% of EGF bound cells
50% reduction
70% reduction
Cetuximab
PRMT1
Vector

FIG. 4D

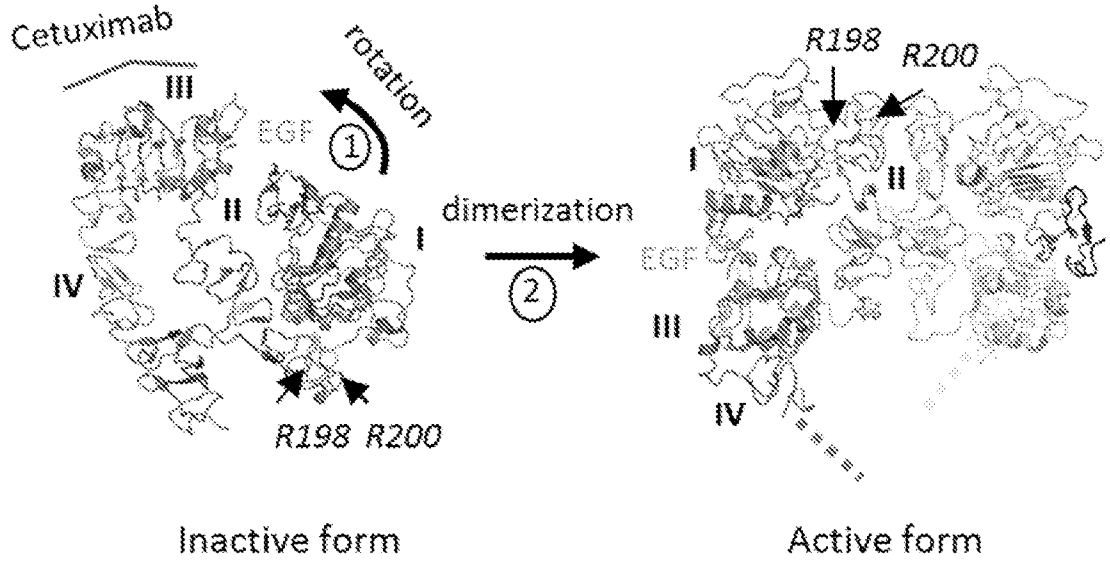

Cetuximab
III
EGF
rotation
1
II
I
IV
R198 R200
dimerization
2
R198
R200
I
II
EGF
III
IV
Inactive form
Active form

FIG. 4E

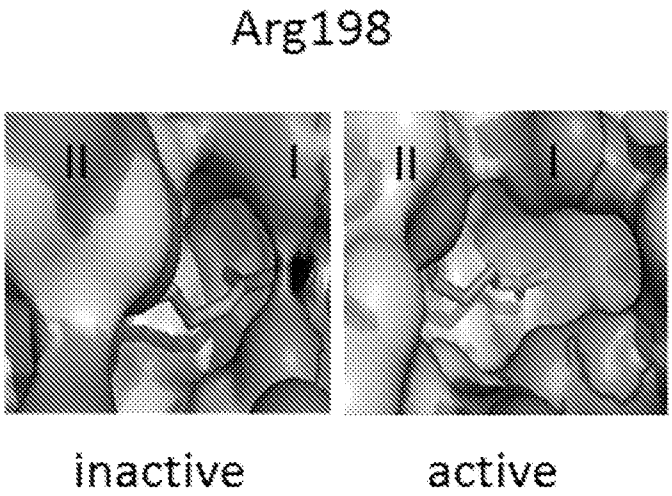


FIG. 4F

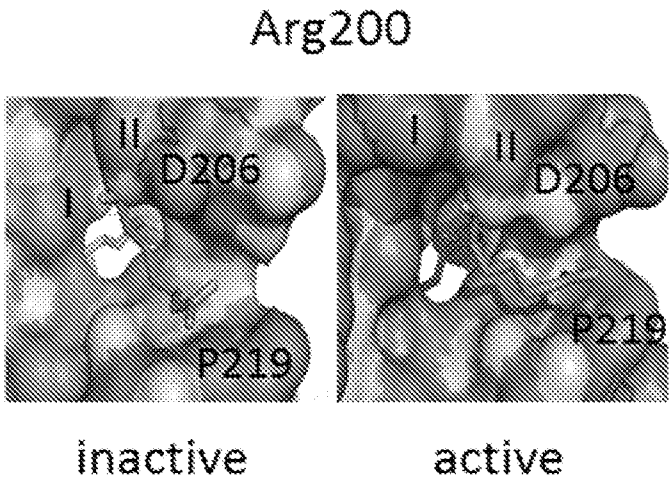


FIG. 4G

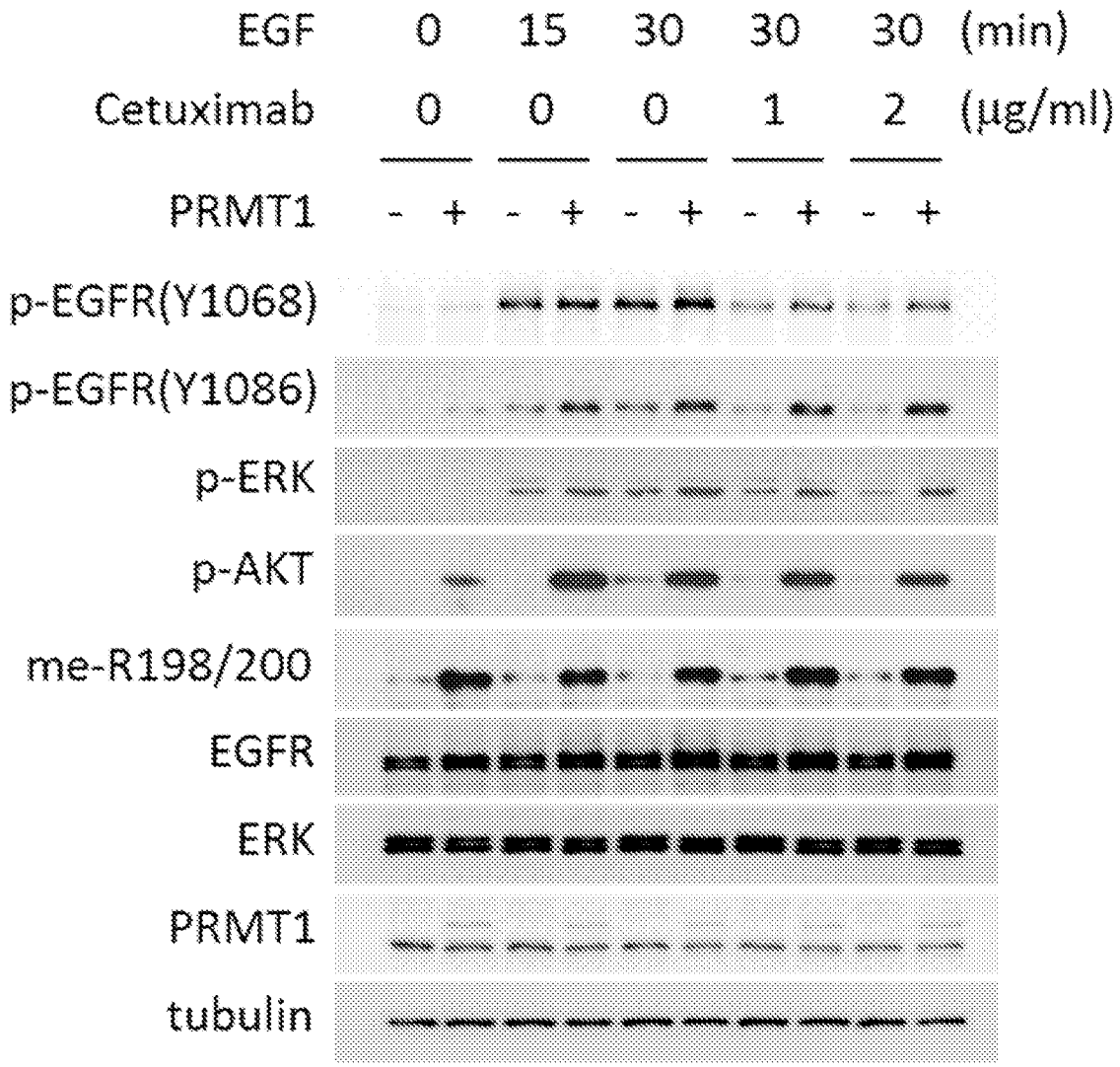
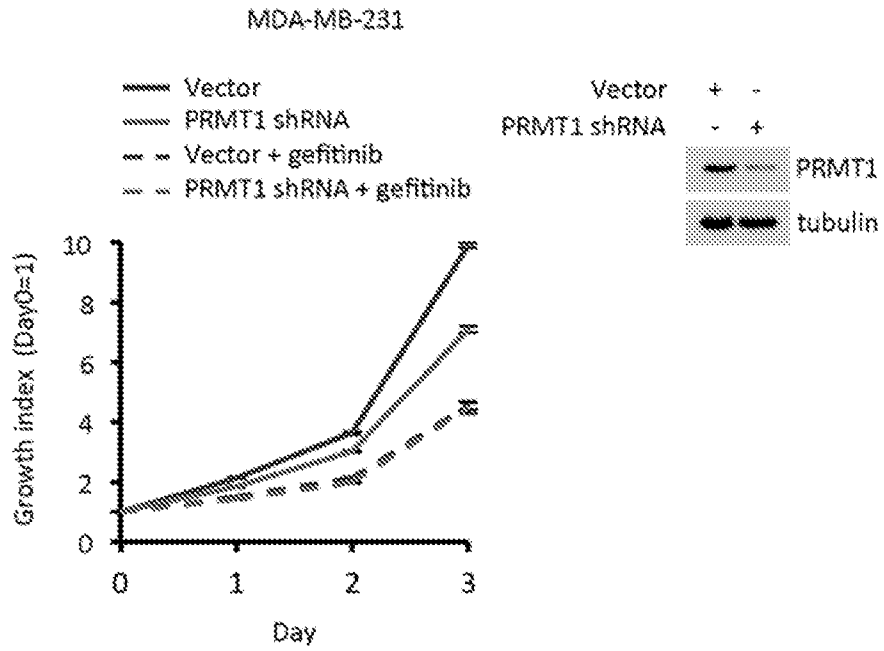
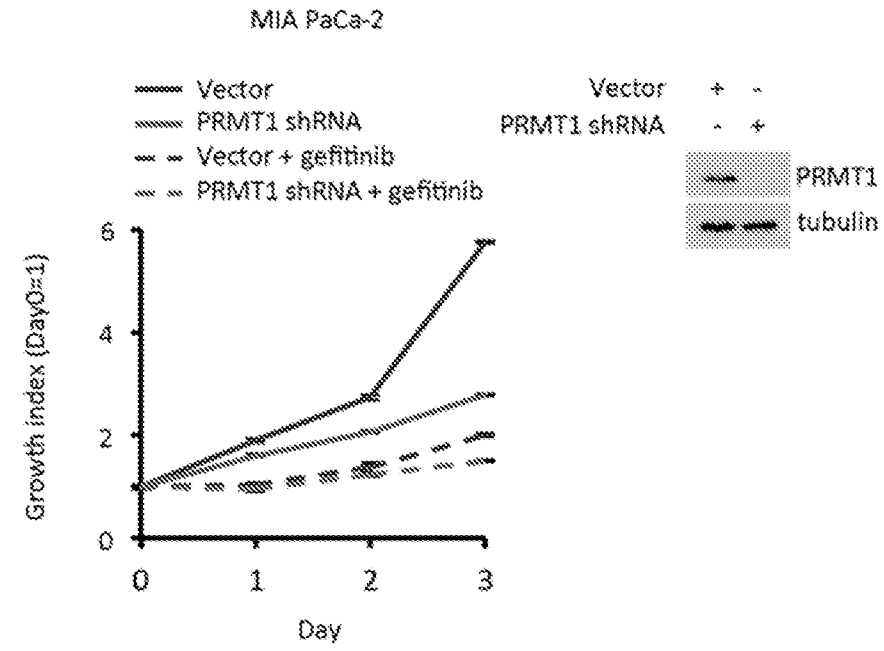

EGF 0 15 30 30 30 (min)
Cetuximab 0 0 0 1 2 (μg/ml)
PRMT1 - + - + - + - + - +
p-EGFR(Y1068)
p-EGFR(Y1086)
p-ERK
p-AKT
me-R198/200
EGFR
ERK
PRMT1
tubulin

FIG. 4H

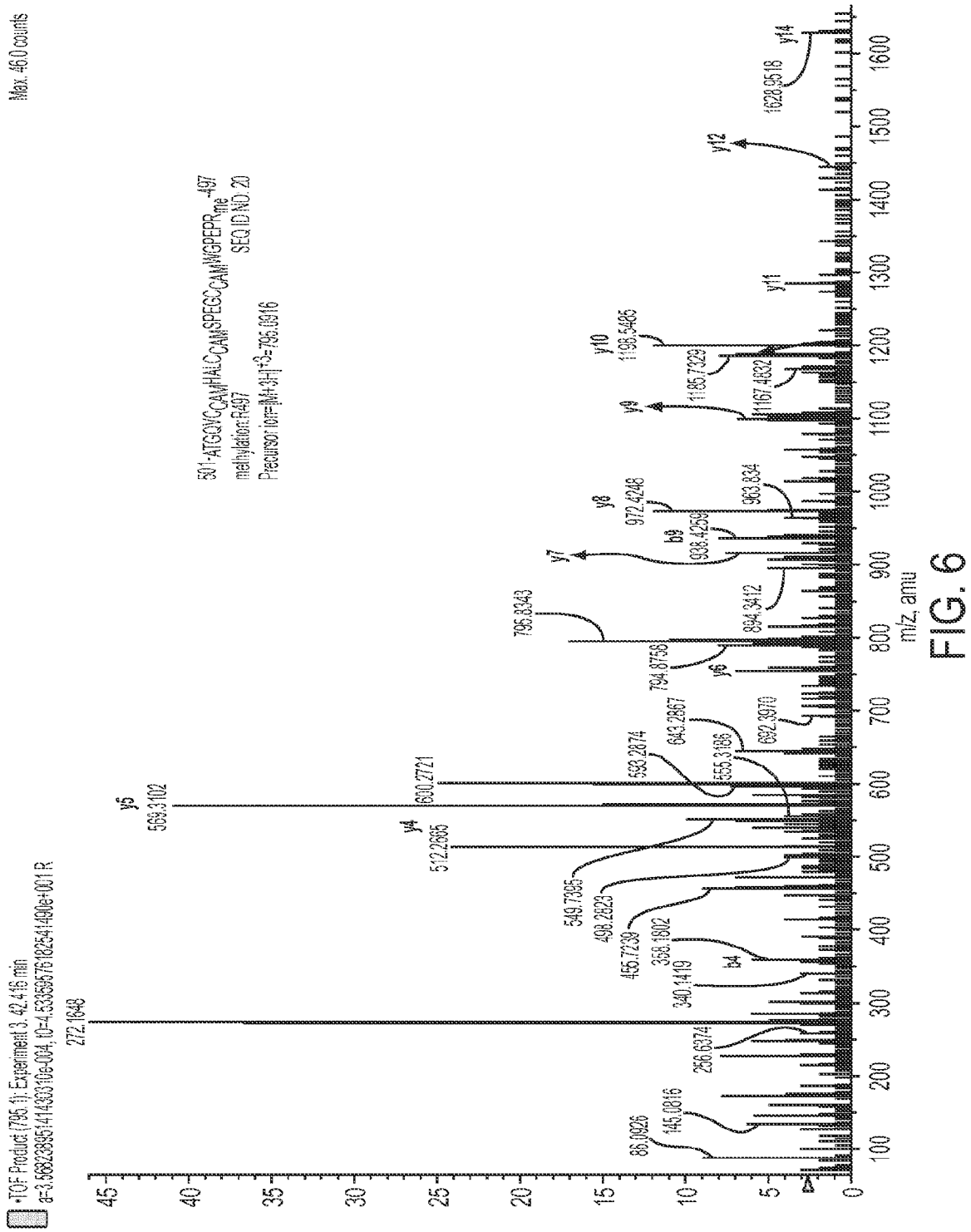
a


MDA-MB-231
Vector
PRMT1 shRNA
Vector + gefitinib
PRMT1 shRNA + gefitinib
Growth index (Day0=1)
Day
Vector + -
PRMT1 shRNA - +
PRMT1
tubulin

b


MIA PaCa-2
Vector
PRMT1 shRNA
Vector + gefitinib
PRMT1 shRNA + gefitinib
Growth index (Day0=1)
Day
Vector + -
PRMT1 shRNA - +
PRMT1
tubulin

FIGS. 5A-B


Max. 46.0 counts
TOF Product (795.1): Experiment 3, 42.416 min
501-ATGGNVCCAMHALCCAMSPEGCCAMWGPEPRme-497
methylation:R497
SEQ ID NO: 20
Precursor ion=[M+3H]3+=795.0916
y5
569.3102
y4
512.2685
610.2721
y7
795.8343
y8
972.4248
y10
1198.5485
y9
1185.7329
y12
1628.9518
y11
1167.4832
y14
b9
938.4256
y6
794.8758
894.9412
963.834
643.2867
593.2874
555.3186
692.3979
549.7995
498.2823
456.7239
358.1802
340.1419
b4
272.1648
256.6374
145.0816
86.0926
m/z, amu
FIG. 6

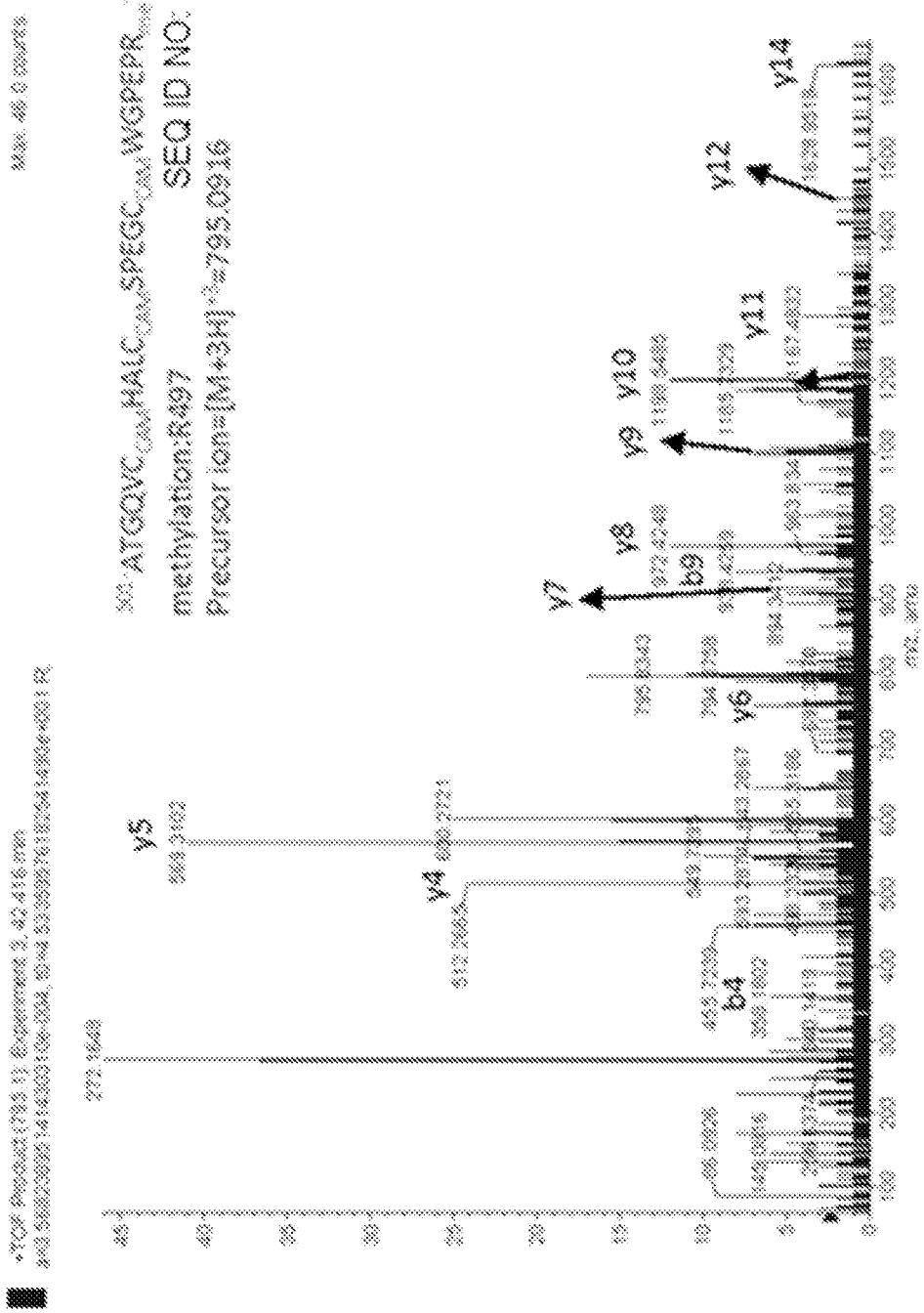
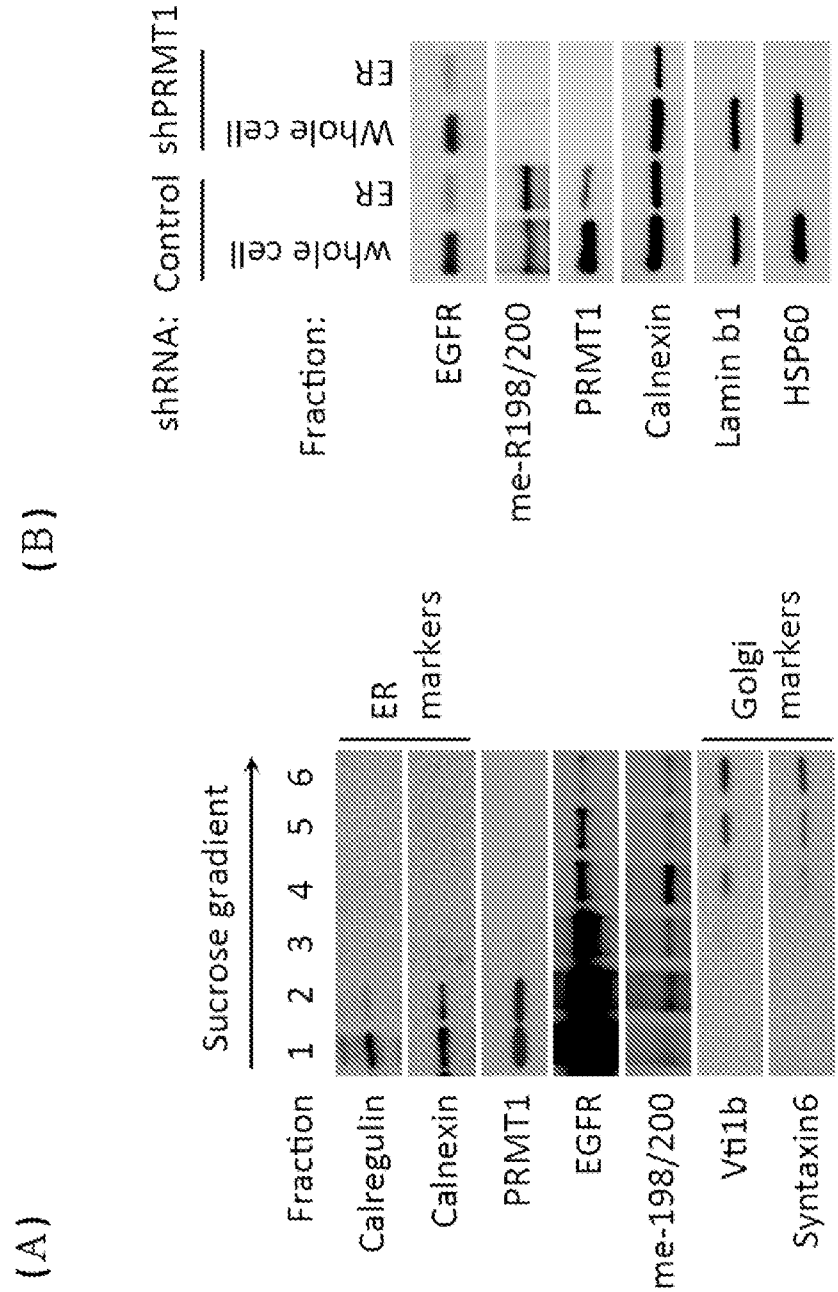

SEQ ID NO: 20
methylation:R497
Precursor Ion=[M+3H]3+=795.0916
y5
y4
y7
y8
y9
y10
y11
y12
y14
b4
b9

FIG. 6


(A)
Sucrose gradient
Fraction 1 2 3 4 5 6
Calregulin
Calnexin
PRMT1
EGFR
me-198/200
Vti1b
Syntaxin6
ER markers
Golgi markers
(B)
shRNA: Control shPRMT1
Fraction: Whole cell ER Whole cell ER
EGFR
me-R198/200
PRMT1
Calnexin
Lamin b1
HSP60

FIGS. 7A-B

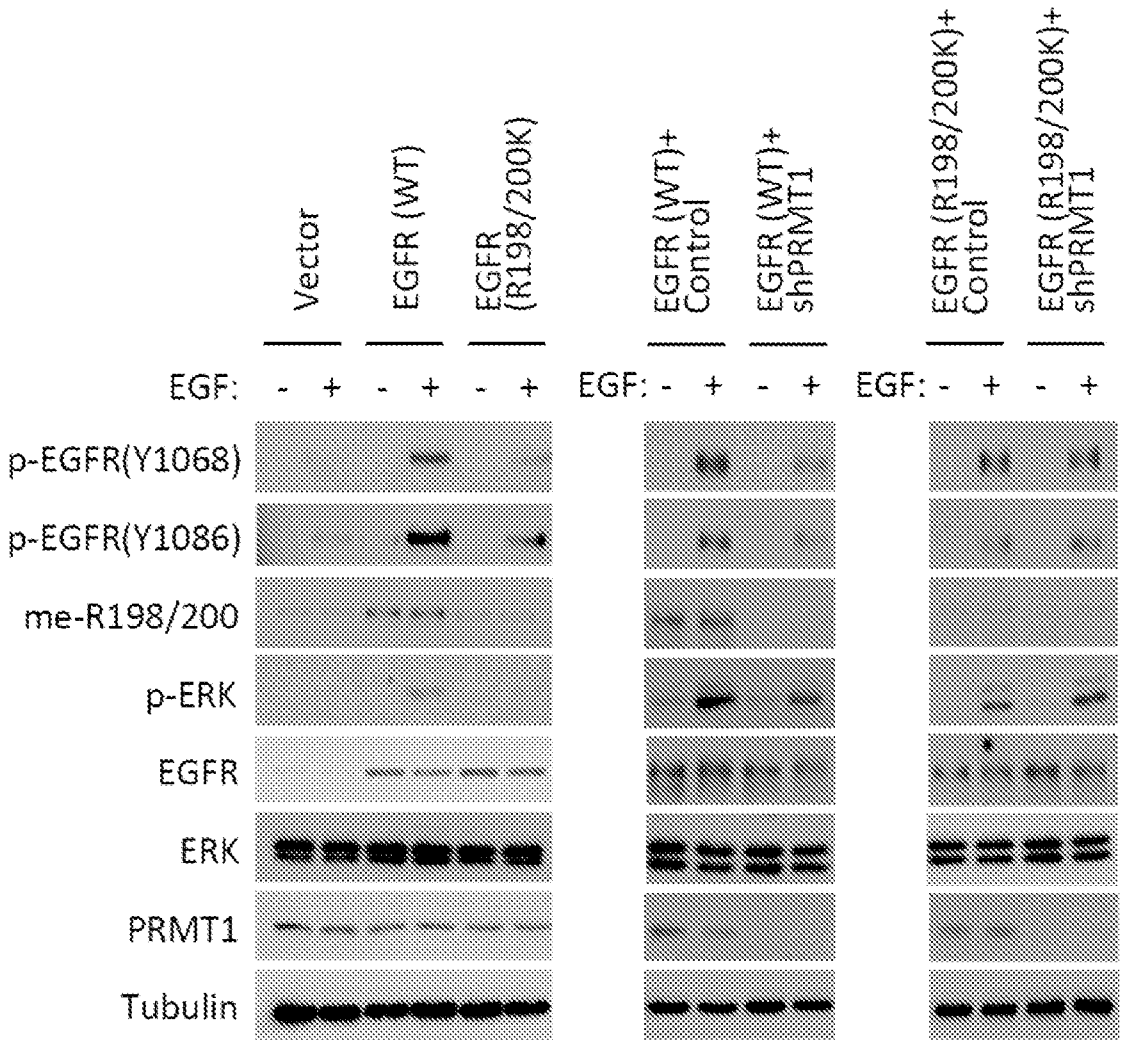

Vector
EGFR (WT)
EGFR (R198/200K)
EGFR (WT)+ Control
EGFR (WT)+ shPRMT1
EGFR (R198/200K)+ Control
EGFR (R198/200K)+ shPRMT1
EGF: - + - + - + EGF: - + - + EGF: - + - +
p-EGFR(Y1068)
p-EGFR(Y1086)
me-R198/200
p-ERK
EGFR
ERK
PRMT1
Tubulin

FIG. 8

(A)

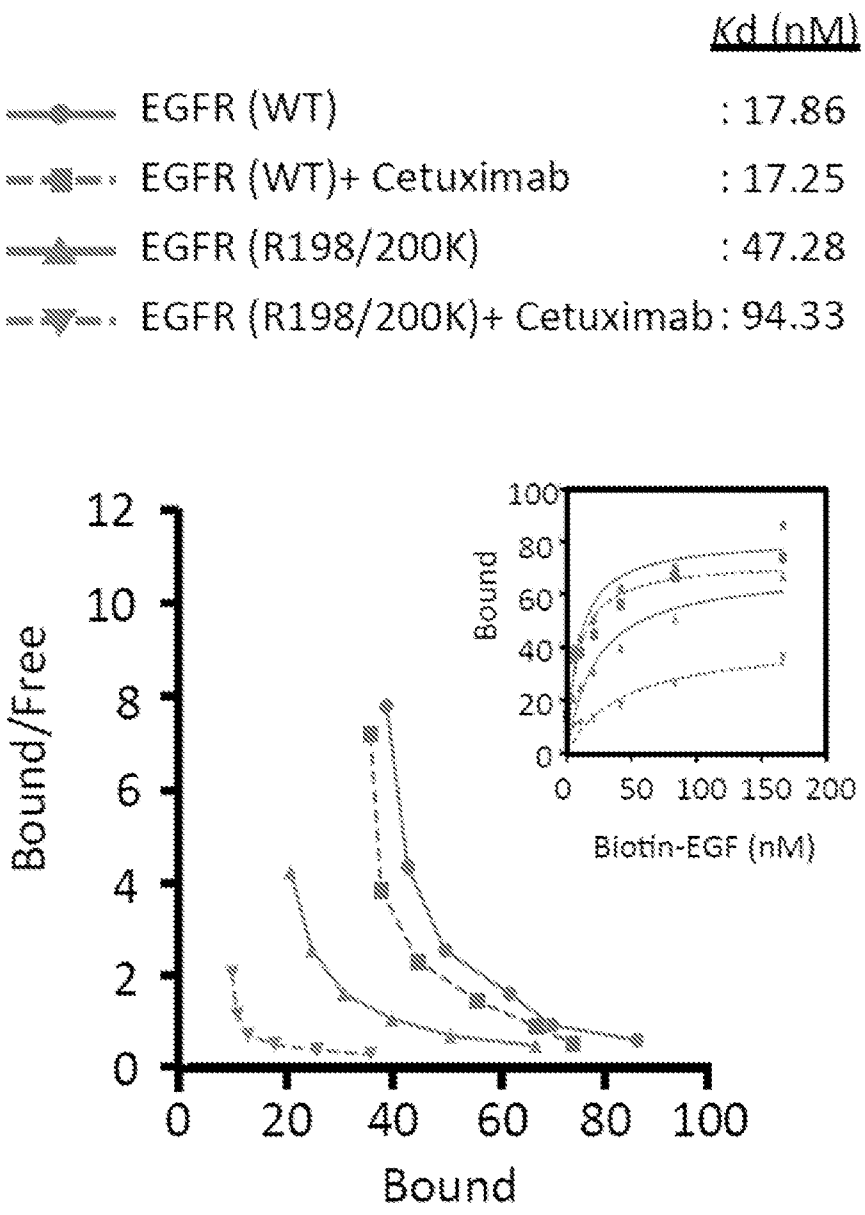

Kd (nM)
EGFR (WT) : 17.86
EGFR (WT)+ Cetuximab : 17.25
EGFR (R198/200K) : 47.28
EGFR (R198/200K)+ Cetuximab : 94.33
Bound/Free
Bound
0
2
4
6
8
10
12
0
20
40
60
80
100
Bound
Biotin-EGF (nM)
0
50
100
150
200
0
20
40
60
80
100

FIG. 9A

(B)

	Kd (nM)
EGFR (WT)+ control	: 16.03
EGFR (WT)+ shPRMT1	: 44.32
EGFR (R198/200K)+ control	: 52.16
EGFR (R198/200K)+ shPRMT1	: 55.09

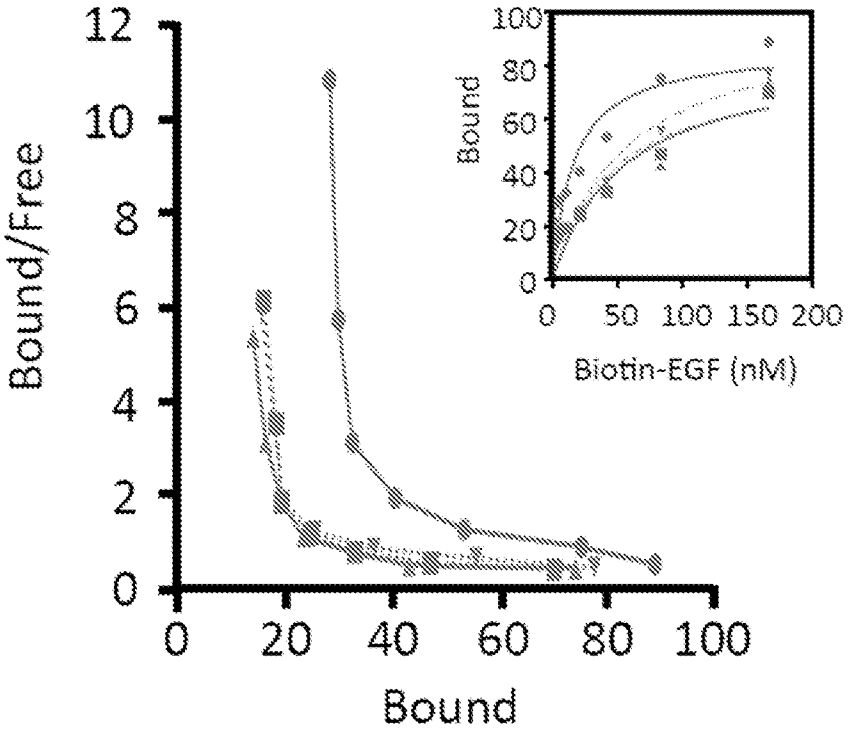


FIG. 9B

(C)

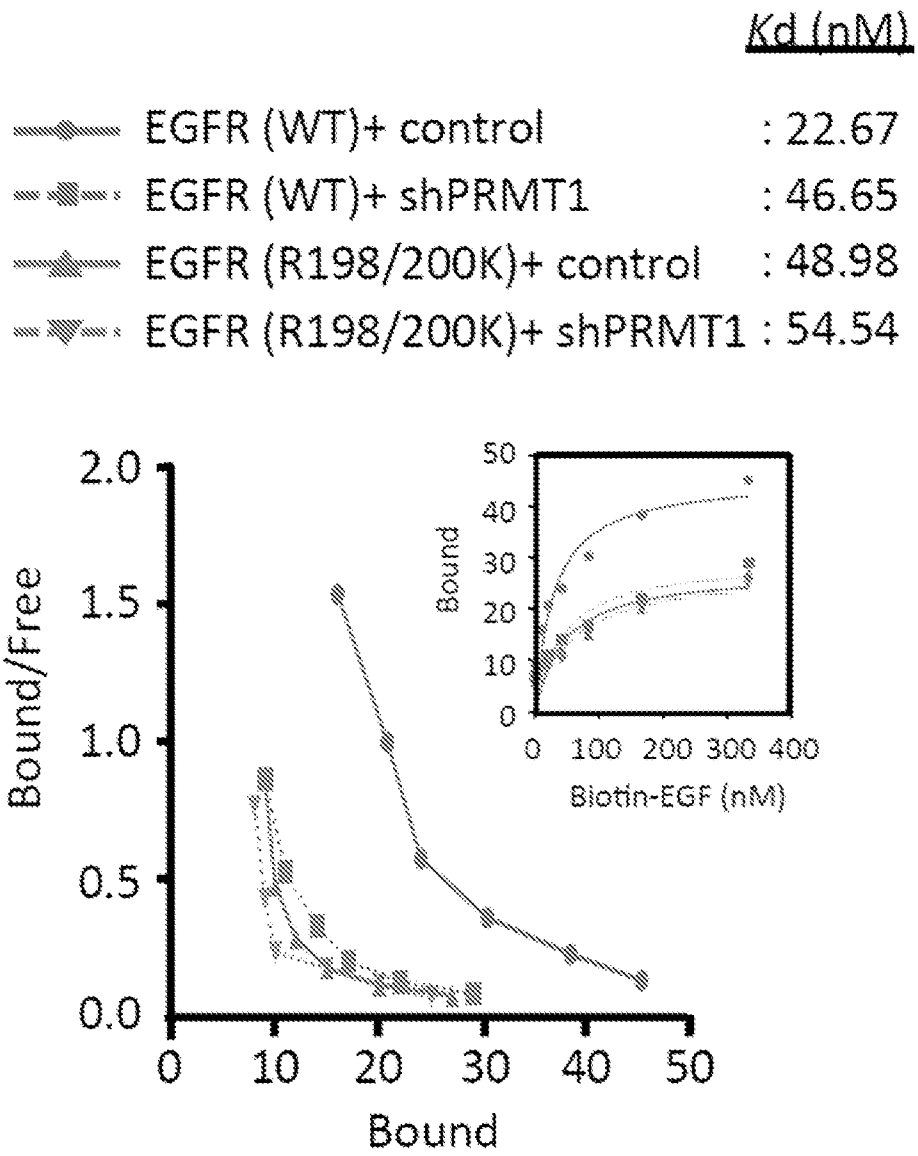
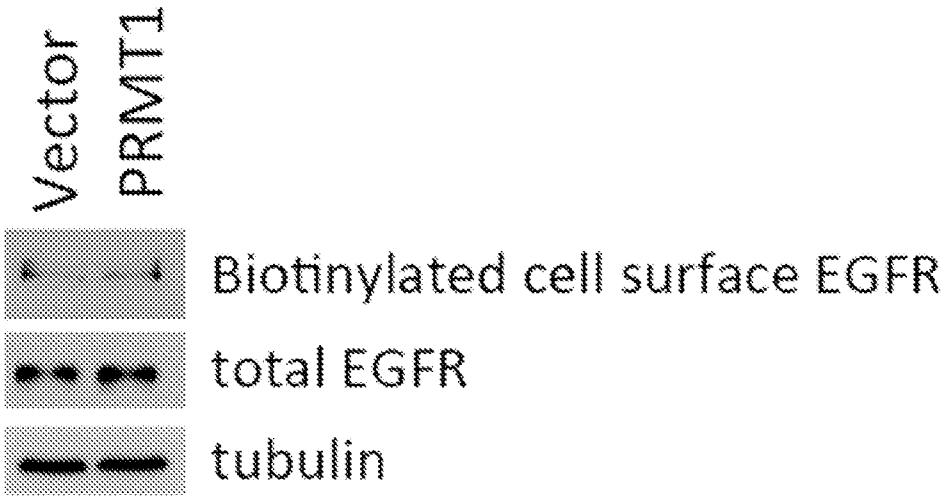
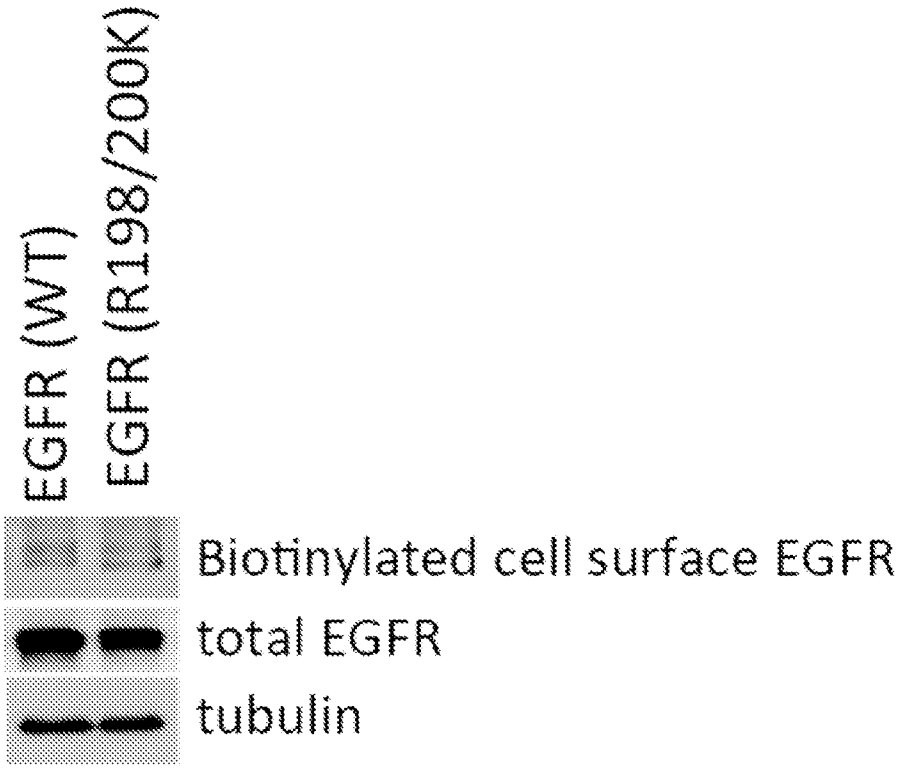

Kd (nM)
EGFR (WT)+ control : 22.67
EGFR (WT)+ shPRMT1 : 46.65
EGFR (R198/200K)+ control : 48.98
EGFR (R198/200K)+ shPRMT1 : 54.54
Bound/Free
Bound
2.0
1.5
1.0
0.5
0.0
0
10
20
30
40
50
Bound
Biotin-EGF (nM)
0
100
200
300
400

FIG. 9C

A


Vector
PRMT1
Biotinylated cell surface EGFR
total EGFR
tubulin

B


EGFR (WT)
EGFR (R198/200K)
Biotinylated cell surface EGFR
total EGFR
tubulin

FIGS. 10A-B