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(54) **Title**: BIOMARKERS FOR RESPONSE TO RAPAMYCIN ANALOGS

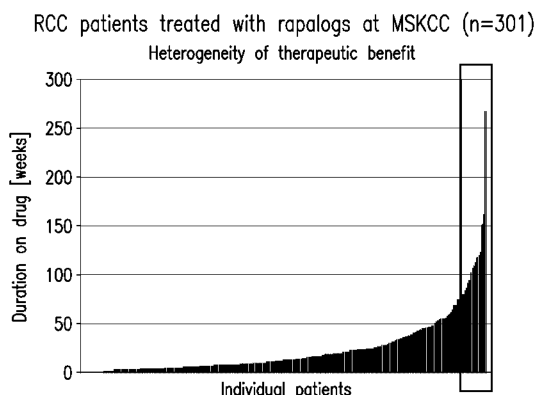

FIG. 1

(57) **Abstract**: The present invention relates to the use of one or more biomarkers to evaluate the likelihood that a rapamycin analog would produce an anti-cancer effect in a subject. It is based, at least in part, on the results of experiments employing an integrated next-generation sequencing approach to interrogate spatially separated tumor specimens from the same individuals to decipher intratumor and intertumor heterogeneity and determine the oncogenomic basis of exceptional therapeutic benefit to rapalogs in kidney cancer patients. These experiments implicated loss of function mutations in TSC1 and/or TSC2 and/or gain-of- function of mTOR in therapeutic responsiveness to rapamycin analogs. Accordingly, in non-limiting embodiments, the present invention provides for assay methods and kits for determining the presence of loss of function mutations in TSC1 and/or TSC2 and/or gain-of- function of mTOR, and methods of using such determinations in selecting a therapeutic regimen for a cancer patient and in methods of treating cancer patients. In particular non-limiting embodiments, a plurality of tumor sites are evaluated and the composite effect of the genetic background on mTOR function is assessed.

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BIOMARKERS FOR RESPONSE TO RAPAMYCIN ANALOGS

PRIORITY CLAIM

This application claims priority to United States Provisional
5 Applications Nos. 61/798,020 and 61/852,109, both filed March 15, 2013, the contents of which are incorporated by reference in their entireties herein.

GRANT INFORMATION

Not applicable.

10

1. INTRODUCTION

The present invention relates to biomarkers which may be used to evaluate the likelihood that a rapamycin analog would produce an anti-cancer effect in a subject. As such, these biomarkers may be used in methods of treating cancer
15 patients.

2. BACKGROUND OF THE INVENTION

Targeted therapies, including vascular endothelial growth factor receptor (VEGFR) inhibitors such as sunitinib (first line therapy), and mTOR
20 inhibitors such as temsirolimus and everolimus (second line therapy), are standard of care in treating advanced renal cell carcinoma (RCC; 1-4) . Temsirolimus and everolimus are rapamycin analogs (rapalogs) that inhibit the mammalian target of rapamycin complex 1 (mTORC1)5-7. International phase III trials led to their approval for treating kidney cancer, yet only demonstrated modest clinical benefit
25 with median progression free survival (PFS) of 4.9-5.5 months (8-11).

However, extended periods of freedom from disease progression with rapalogs have been reported in isolated patients among whom some were refractory to first line antiangiogenic agents (10,12,13). These clinical data raise a testable hypothesis that genomic alterations may dictate clinical response.

30 Hyperactive PI3K/AKT/mTOR signaling, through its effects on protein synthesis, cell survival, and metabolism, has long been implicated in promoting tumor growth. The serine-threonine kinase mTOR exerts its actions as the enzymatic component of two structurally and functionally distinct multi-protein complexes, mTORC1 and mTORC2 (6,7). Therapeutic inhibition of mTORC1 is the mechanism

of action for rapalogs. Components of the PI3K/mTOR pathway can either act as activators (PI3K, AKT, and Rheb) or repressors (PTEN, TSC1, and TSC2) of the mTORC1 signaling (14). Functional loss of TSC1 and TSC2 was shown in preclinical models to sensitize tumors to rapalogs (15), and everolimus has been approved for treating subependymal giant-cell astrocytomas and angiomyolipoma in patients with Tuberous Sclerosis Complex (16,17). Recent reports have also implicated TSC1 as a tumor suppressor in RCC and bladder cancer patients (18,19). However, the recent elucidation of intra-tumor heterogeneity of kidney cancer challenges the predictability of genomic biomarkers derived from single biopsies (20).

3. SUMMARY OF THE INVENTION

The present invention relates to the use of one or more biomarkers to evaluate the likelihood that a rapamycin analog would produce an anti-cancer effect in a subject. It is based, at least in part, on the results of experiments employing an integrated next-generation sequencing approach to interrogate spatially separated tumor specimens from the same individuals to decipher intra-tumor and intertumor heterogeneity and determine the oncogenomic basis of exceptional therapeutic benefit to rapalogs in kidney cancer patients. These experiments implicated loss of function mutations in TSC1 and/or TSC2 and/or gain-of-function of mTOR in therapeutic responsiveness to rapamycin analogs.

Accordingly, in non-limiting embodiments, the present invention provides for assay methods and kits for determining the presence of loss of function mutations in TSC1 and/or TSC2 and/or gain-of-function of mTOR, and methods of using such determinations in selecting a therapeutic regimen for a cancer patient and in methods of treating cancer patients.

In particular non-limiting embodiments, a plurality of tumor sites are evaluated and the composite effect of the genetic background on mTOR function is assessed.

4. BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1. Heterogeneity of therapeutic benefit of renal carcinoma patients treated with rapalog (n=301). Duration of rapalog treatment (in weeks) for individual patients are shown. Box marks patients deemed to have received substantial therapeutic benefit.

FIGURE 2A-B. Characteristics of clinical "outlier" patients (A) from among the group receiving substantial therapeutic benefit ("Long-term Responders") or (B) from among those who did not substantially benefit from treatment ("Poor Responders").

5 FIGURE 3A-B. (A) Integrated Mutation Profiling of Actionable Cancer Targets ("IMPACT") analysis. Image adapted from Wagle, Berger et al., 2012, Cancer Discovery 2:82-93, reference 36. (B) Genes included in IMPACT panel. Genes of interest to mTOR pathway are enlarged and in bold.

FIGURE 4. Summary of results for responders.

10 FIGURE 5A-C. Results for patient 1, diagnosed with clear cell RCC and showing long-term response to temsirolimus. (A) Normalized coverage (tumor/normal) across the genome. (B) Schematic showing tumor sampling sites. (C) Genetic results.

FIGURE 6A-C. Results for patient 2, diagnosed with unclassified

15 RCC and showing long-term response to temsirolimus. (A) Normalized coverage (tumor/normal) across the genome (B) Schematic showing tumor sampling sites. (C) Genetic results.

FIGURE 7A-B. Results for patient 3, diagnosed with clear cell RCC and showing long-term response to everolimus. (A) Schematic showing tumor

20 sampling sites. (B) Genetic results.

FIGURE 8A-D. Results for patient 3 (see above). (A) Normalized coverage (tumor/normal) across the genome for tumor site 1. (B) Immunoblots of S6K (T389) showing phosphorylation of S6K, downstream of mTOR. (C) Genetic results. (D) Map of mTOR gene showing exons and functional domains.

25 FIGURE 9A-D. Results for patient 4, diagnosed with unclassified RCC and showing long-term response to everolimus. (A) Schematic showing tumor sites in kidneys. (B) Normalized coverage (tumor/normal) across the genome for tumor site 1 - no mutations found, but homozygous loss of TSC2. (C) Normalized coverage (tumor/normal) across the genome for tumor site 2. (D) Genetic results.

30 FIGURE 10. Summary of results of long-term responders.

FIGURE 11. Summary of results of poor responders.

FIGURE 12A-F. Genomic alterations along the core mTORC1 pathway are identified in patients with exceptional rapalog response using the IMPACT assays. (A, B) Integrated Genomics Viewer (IGV) snapshots of region 1

(R1) of the primary tumors and matched adjacent normal tissues illustrate the P311fs*4 and the I580fs*7 frameshift mutations of TSC1 in patients #1 (a) and #2 (b), respectively. Number of reads carrying the mutation is noted. (C) A magnified copy number plot of tumor 1 (T1) in patient #4 illustrates the homozygous loss of chromosome 16p where TSC2 resides. (D) IGV snapshots of R1 and adjacent normal in patient #3 illustrate the mTOR Q2223K missense kinase domain mutation. (E) Copy number plots of patients #1 to #6 with notations on pertinent chromosomal alterations. TSC1, TSC2, and mTOR reside on chromosome bands 9q34, 16p13, and 1p36, respectively. (F) A diagram of the central mTORC1 signaling pathway illustrates mutations identified in the core components from rapalog (everolimus and temsirolimus) responders.

FIGURE 13A-F. The Q2223K mutation of mTOR causes hyperactivation of mTORC1. (A) The mTOR Q2223K mutant induces more phosphorylation of endogenous S6K at threonine 389 (T389) than wild-type mTOR. HEK293T cells, transfected with the indicated FlagmTOR constructs for 24 hours, were serum-deprived overnight and then exposed to 1% serum-containing medium for 1 hour. Cellular lysates were subjected to immunoblot analysis using the indicated antibodies. Levels of Flag-mTOR and β-actin indicate equivalent transfection and protein loading, respectively. n.s. denotes non-specific bands. (B) Immunoblots of S6K (T389) and S6 (Serine 235/236; S235/236) phosphorylation demonstrate the hyperactivity of Q2223K mTORC1 over a range of serum concentrations. HEK293T cells, transfected with the indicated Flag-mTOR constructs for 24 hours, were washed with serum free medium, exposed to medium containing the indicated serum concentrations for 1 hour, and analyzed by immunoblots using the indicated antibodies. (C) The hyperactivity of Q2223K mTORC1 can be inhibited by rapamycin. The Q2223K mutant is as sensitive as wild-type mTORC1 to rapamycin as determined by the phosphorylation of S6K (T389). Experiments were performed as in (B), except with addition of the indicated concentrations (nM) of rapamycin in medium containing 10% serum in the final hour prior to harvest. (D,E) Cells in (D) and (E) were treated similarly to (b) and (c), respectively, except with the co-transfection of Myc-tagged S6K. (F) Structural simulation of the mTOR kinase active site, based on the solved PI3K kinase domain, illustrates the position of glutamine 2,223. Q2223 shown in yellow sticks is localized on a loop in close proximity to the ATP binding site (shown as colored lines - gray: carbon; red: oxygen; blue: nitrogen;

orange: phosphorus). The kinase activation and catalytic loops are colored red and green, respectively.

FIGURE 14A-C. Clustered mTOR activating mutations in kidney cancer in MSKCC, COSMIC, and KIRC TCGA datasets. (A) Schematics depict the highly similar localizations between human mTOR mutations identified in kidney cancer and yeast Tor2 gain-of-function mutations identified in a genetic screen. (B) 293T cells were co-transfected with Myc-S6K and the indicated Flag-mTOR constructs, and 24 hours later, washed with serum free medium, and then exposed to serum (10%) containing medium for 1 hour prior to harvest. Cellular lysates were analyzed with the indicated antibodies. The T389 phosphorylation of S6K was quantified. Corresponding regions of the mTOR protein are shown above the respective blots. (C) Cells were transfected and treated as described in (B), in the absence (-) or presence (+) of 50nM of rapamycin during the last hour prior to harvest for immunoblot analyses.

FIGURE 15A-D. Pertinent genetic findings discovered on patients #1 to #4 (A-D) are illustrated as braided cancer rivers to model both genetic divergence and pathway convergence during cancer evolutions in given patients. T, R, and M denote primary tumor, region, and metastasis, respectively.

FIGURE 16. Bar graph depicts the relative activity of mTORC1, comparing individual mTOR mutants to Wild-type mTOR, based on S6K (T389) phosphorylation.

FIGURE 17. Flow chart depicts the IMPACT assay mutation identification and filtering algorithm.

FIGURE 18. Flow chart depicts the WEC assay mutation identification and filtering algorithm.

FIGURE 19. Sanger validations of mutations in mTORC1 pathway indentified by IMPACT.

FIGURE 20. Copy number plots for patient #4 showing inherited one copy loss of TSC2 in the germline DNA and the current somatic loss (homozygous deletion) in the tumor.

FIGURE 21. Sanger validations of additional mutations in the mTORC1 pathway identified by IMPACT assays in patients #1, #3, and #4. Nucleotide changes are circled in red.

FIGURE 22. Copy number plots for multiple tumor regions in patient #3 showing the loss of chromosome 9 only in tumor regions (R3, R4) carrying the TSC1 nonsense mutation.

FIGURE 23. Gene maps of mTOR mutations across published TCGA cancer studies.

FIGURE 24. mTOR mutants associated with therapeutic response to rapalogs are more resistant to serum than wild-type mTOR. Hela cells, transfected with the indicated Flag-mTOR constructs, were cultured either without serum (-) or in the presence of 10% serum (+) for 1 hour. Cellular lysates were then subjected to immunoblot analysis using the indicated antibodies.

FIGURE 25. mTOR mutants associated with therapeutic response to rapalogs are more resistant to AKT inhibitor than wild-type mTOR. Hela cells, transfected with the indicated FlagmTOR constructs, were cultured in medium with (+) or without (-) 1 μM MK2206, an AKT inhibitor for 2 hours. Cellular lysates were then subjected to immunoblot analysis using the indicated antibodies.

FIGURE 26. mTOR mutants associated with therapeutic response to rapalogs are senstive to rapamycin or to INK128, an ATP-competitive inhibitor of mTORC1 and mTORC2. Hela cells, transfected with the indicated Flag-mTOR constructs, were cultured in medium with (+) or without (-) 25 nM rapamycin or 100 nM INK128 for 2 hours. Cellular lysates were then subjected to immunoblot analysis using the indicated antibodies.

FIGURE 27A-D. F188lL/L2230 double mutation has a synergistic effect at increasing mTOR activity. (A) Phosphorylation of S6K in the presence of single F1881L and L2230V mutations. (B) Phosphorylation of S6K where both mutations are present (other single mutants shown for comparison). (C) Phosphorylation of S6K in cells bearing the double mutant, relative to wild-type control, when serum starved for 1, 3, 6 or 20 hours. (D) Phosphorylation of S6K in cells bearing the double mutant in serum-free medium relative to wild-type and single mutants, compared with cells grown in PBS.

5. DETAILED DESCRIPTION OF THE INVENTION

The detailed description of the invention is divided into the following subsections for clarity and not by way of limitation:

5 (i) biomarkers and methods of measurement;

(ii) TSC biomarkers;

(iii) mTOR biomarkers;

(iv) cancer targets;

(v) rapamycin analogs;

10 (vi) methods of use; and

(vii) kits.

5.1 BIOMARKERS AND METHODS OF MEASUREMENT

Biomarkers, as that term is used herein, includes nucleic acid, protein, 15 and/or chromosomal markers (i) disclosed below and/or (ii) that are related to the activity level of mTOR, of which rapamycin analogs are inhibitors, in a subject. In certain non-limiting embodiments, a biomarker is an allelic variant or mutation of the version of the gene or protein present in a given population.

A subject may be a human or a non-human subject. Non-limiting 20 examples of non-human subjects include non-human primates, dogs, cats, mice, rats, guinea pigs, rabbits, fowl, pigs, horses, cows, goats, sheep, etc.

A biomarker may be a nucleic acid. Methods of detecting a biomarker which is a nucleic acid include but are not limited to polymerase chain reaction, in situ hybridization (for example but not limited to Fluorescent In Situ Hybridization 25 (“FISH”)), gel electrophoresis, sequencing and sequence analysis, and microarray analysis.

A biomarker may be a protein. Methods of detecting a biomarker which is a protein include but are not limited to mass spectrometry techniques, 1-D or 2-D gel-based analysis systems, chromatography, enzyme linked immunosorbent 30 assays (ELISAs), radioimmunoassays (RIA), enzyme immunoassays (EIA), Western Blotting, immunoprecipitation, and immunohistochemistry. Antibody arrays or protein chips may also be employed.

A biomarker may be a chromosome or a chromosome fragment. Methods of detecting a biomarker which is a chromosome or a chromosome fragment

include but are not limited to karyotyping and fluorescent in situ hybridization (FISH).

In certain non-limiting embodiments of the invention, a biomarker may be assessed for its effect on mTOR function. For example, the activity of mTOR may be evaluated in a cell, which may or may not be a cancer cell, containing the biomarker. As one non-limiting example, as illustrated in the working examples below, mTOR activity is reflected by phosphorylation of S6K at T389. The level of mTOR function in a cell or cells containing the biomarker may be compared to the level of mTOR function in the absence of the biomarker.

In certain non-limiting embodiments of the invention, a biomarker may be assessed for its effect on TSC1 and/or TSC2 function. For example, the activity of TSC1 and/or TSC2 may be evaluated in a cell containing the TSC1 or TSC2 biomarker. In a certain non-limiting embodiment, the activity of TSC1 and/or TSC2 may be evaluated by evaluating mTOR function, where the activity of TSC1 and/or TSC2 is/are inversely proportional to the activity of mTOR. The level of TSC1 and/or TSC2 function in a cell or cells containing the TSC1 or TCS2 biomarker may be compared to the level of TSC1 and/or TSC2 function in a cell or cells having a different type of TSC1 or TSC2.

A healthy control level of mTOR function (healthy control activity)may be established using a non-cancer cell or cells from a healthy control subject.

A healthy control level of TSC1 and/or TSC2 function (healthy control activity) may be established using a non-cancer cell or cells from a healthy control subject.

5.2 TSC BIOMARKERS

Tuberous sclerosis 1 protein is denoted TSC1 herein.

Tuberous sclerosis 2 protein is denoted TSC2 herein.

In a specific non-limiting embodiment, a reference TSC1 molecule is a human TSC1 nucleic acid molecule which has the nucleic acid sequence as set forth in NCBI database accession no. NM_000368 or a TSC1 protein molecule which has the amino acid sequence as set forth in NCBI database accession no. NP_000359. The functional activity of a TSC1 protein having the foregoing amino acid sequence is referred to as a human TSC1 reference control activity.

In a specific non-limiting embodiment, a reference TSC2 molecule is a human TSC2 nucleic acid molecule which has the nucleic acid sequence as set forth in NCBI database accession no. NM_000548 or a TSC2 protein molecule which has the amino acid sequence as set forth in NCBI database accession no. NP_000539 .The functional activity of a TSC2 protein having the foregoing amino acid sequence is referred to as a human TSC2 reference control activity.

Reference TSC1 and/or TSC2 nucleic acids and proteins for non-human species are known or can be determined according to methods known in the art, for example where the reference sequence is the allele represented in the majority of a population.

Where comparisons to a reference control activity are referred to herein, the biomarker is assessed relative to the reference control activity within the same species. For example, a human TSC1 biomarker activity is compared with a human TSC1 reference control activity.

A TSC1 biomarker is a biomarker which manifests as reduced TSC1 function relative to a TSC1 reference control activity or a TSC1 healthy control activity and/or increased mTOR function relative to a mTOR reference control activity or a mTOR healthy control activity.

A TSC2 biomarker is a biomarker which manifests as reduced TSC2 function relative to a TSC2 reference control activity and/or increased mTOR function relative to a mTOR reference control activity.

In certain non-limiting embodiments a TSC1 or TSC2 biomarker is a nucleic acid bearing an insertion, deletion, or substitution relative to a reference TSC1 or TSC2 gene, or a protein encoded by said nucleic acid. Said insertion, deletion, or substitution may result in a nonsense mutation, a frameshift mutation, a missense mutation, or a termination relative to protein expression.

In certain non-limiting embodiments a TSC1 or TSC2 biomarker is a protein bearing an insertion, deletion, or substitution relative to a reference TSC1 or TSC2 protein.

In certain non-limiting embodiments a TSC1 or TSC2 biomarker is a chromosome bearing a deletion, substitution, duplication or inversion which includes the TSC1 or TSC2 locus.

In one specific non-limiting embodiment, a TSC1 biomarker for a human subject is the P311fs*4 frameshift mutation.

In one specific non-limiting embodiment, a TSC1 biomarker for a human subject is the I580fs*7 frameshift mutation.

In one specific non-limiting embodiment, a TSC1 biomarker for a human subject is the Q527* nonsense mutation.

5 In one specific non-limiting embodiment, a TSC1 biomarker for a human subject is the Q781* nonsense mutation.

In one specific non-limiting embodiment, a TSC1 biomarker for a human subject is the S334* nonsense mutation.

In one specific non-limiting embodiment, a TSC2 biomarker for a

10 human subject is the Q794* nonsense mutation.

In one specific non-limiting embodiment, a TSC2 biomarker for a human subject is the R611W missense mutation.

In one specific non-limiting embodiment, a TSC2 biomarker for a human subject is the S1498N missense mutation.

15 In one specific non-limiting embodiment, a TSC1 biomarker for a human subject is a chromosomal abnormality involving chromosome position 9q34.

For example, the chromosomal abnormality may be an insertion, deletion, duplication, inversion, etc. of one or both chromosome(s) including or in immediate proximity to position 9q34.

20 In one specific non-limiting embodiment, a TSC2 biomarker for a human subject is a chromosomal abnormality involving chromosome position 16p13. For example, the chromosomal abnormality may be an insertion, deletion, duplication, inversion, etc. of one or both chromosome(s) including or in immediate proximity to position 16p13.

25

5.3 mTOR MUTATIONS

Mammalian target of rapamycin is denoted mTOR herein and is also known as FRAP (FKBP12-rapamcyin-associated protein), RAFT1 (rapamycin and FKBP12 target), RAPT 1 (rapamycin target 1), or SEP (sirolimus effector protein).

5 In a specific non-limiting embodiment, a reference mTOR molecule is a human mTOR nucleic acid molecule which has the nucleic acid sequence as set forth in NCBI database accession no. NM_004958 or a mTOR protein molecule which has the amino acid sequence as set forth in NCBI database accession no. NP_004949. The functional activity of a mTOR protein having the foregoing amino

10 acid sequence is referred to as a human mTOR reference control activity

Reference mTOR nucleic acids and proteins for non-human species are known or can be determined according to methods known in the art, for example where the reference sequence is the allele represented in the majority of a population.

A mTOR biomarker is a biomarker which manifests as increased

15 mTOR function and/or activity relative to a mTOR reference control activity or a mTOR healthy control activity. In certain non-limiting embodiments, an increase in mTOR function and/or activity is manifested as (i.e., indicated by) an increase in phosphporylation of S6K, for example at residue T389, relative to reference (e.g., wild type) mTOR. In certain non-limiting embodiments, an increase in mTOR

20 function and/or activity is manifested as increased growth in serum-depleted medium (for example, medium containing less than or equal to 2 percent serum, medium containing less than or equal to 1 percent serum or serum-free medium) relative to reference (e.g. wild type) mTOR. In certain non-limiting embodiments, an increase in mTOR function and/or activity is manifested as increased resistance to AKT

25 inhibition relative to reference (e.g., wild type) mTOR. In certain non-limiting embodiments, an increase in mTOR function and/or activity is manifested as the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

In certain non-limiting embodiments, a mTOR biomarker may be associated with one or more, or two or more, or three or more, or four or more, of the

30 following indicators of increased activity: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR: and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

A mTOR protein comprising one or more of the biomarkers disclosed herein may further comprise additional variations from the wild-type sequence.

In certain non-limiting embodiments a mTOR biomarker is a nucleic acid bearing one or more mutation, which may be an insertion, deletion, or substitution relative to the reference mTOR gene, or a protein encoded by said nucleic acid. Said insertion, deletion, or substitution may result in a nonsense mutation, a frameshift mutation, a missense mutation, or a termination relative to protein expression.

In certain non-limiting embodiments a mTOR biomarker is a protein bearing one or more mutation, which may be an insertion, deletion, or substitution relative to the mTOR reference protein.

In certain non-limiting embodiments a mTOR biomarker is a chromosome bearing one or more mutation, which may be an insertion, deletion, substitution, duplication or inversion which includes the mTOR gene.

In the following description of mTOR biomarkers, amino acid numbering is based on the amino acid sequence set forth as NCBI Accession No. NP_004949.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a Q2223 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a R2505 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a L2431 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a S2215 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a V2406 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a M2327 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a L2230 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a I2228 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a L2220 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a V2006 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a T1977 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a I1973 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a F1888 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a F1888 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a F1888 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a F1888 mutation in combination with a L2230 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a C1483 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a L1460 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a A1459 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a L1433 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a A1105 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a E919 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a K860 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a I2500 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a K1452 mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a Y1463 mutation.]

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the Q2223K frameshift mutation.

5 In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the R2505P mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the L2431P mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a 10 human subject is the S2215F mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the V2406A mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the M2327I mutation.

15 In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the L2230V mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the I2228T mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a 20 human subject is the L2220F mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the V2006L mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the T1977K mutation.

25 In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the I1973F mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the F1888V mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a 30 human subject is the F1888I mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the F1888L mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the F1888L mutation in combination with the L2230V mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the C1483F or the C1483Y mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the L1460P mutation.

5 In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the A1459P mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the L1433S mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a

10 human subject is the A1105P mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the E919V mutation.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is the K860N mutation. A mTOR biomarker of the

15 invention may comprise more than one of the above-listed mutations.

In certain non-limiting embodiments, a mTOR biomarker involves a mutation in a FAT or KINASE domain of mTOR.

In certain non-limiting embodiments, a mTOR biomarker is one or more mutation in the FAT domain of mTOR, for example, which increases mTOR

20 activity. In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of one or more residue of amino acid residues 1382-1982 of the amino acid sequence set forth in NCBI Accession No. NP_004949. In certain non-limiting embodiments, the mutated sequence is at least 95 or at least 98 or at least 99 or at least 99.5 percent homologous to the wild-type sequence (as determined, for example,

25 by standard software such as BLAST or FASTA). In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of one or more residue of amino acid residues of the following amino acid sequence which represents residues 1382-1982:

LLGERAAKC RAYAKALHYK ELEFQKGPTP AILESLISIN

30 NKLQQPEAAA GVLEYAMKHF GELEIQATWY EKLHEWEDAL

VAYDKKMDTN KDDPELMLGR MRCLEALGEW GQLHQQCCEK

WTLVNDETQA KMARMAAAAA WGLGQWDSME EYTCMIPRDT

HDGAFYRAVL ALHQDLFSLA QQCIDKARDL LDAELTAMAG

ESYSRAYGAM VSCHMLSELE EVIQYKLVPE RREIIRQIWW

ERLQGCQRIV EDWQKILMVR SLVVSPHEDM RTWLKYASLC
GKSGRLALAH KTLVLLLGVD PSRQLDHPLP TVHPQVTYAY
MKNMWKSARK IDAFQHMQHF VQTMQQQAQH AIATEDQQHK
QELHKLMARC FLKLGEWQLN LQGINESTIP KVLQYYSAAT
5 EHDRSWYKAW HAWAVMNFEA VLHYKHQNQA RDEKKKLRHA
SGANITNATT AATTAATATT TASTEGSNSE SEAESTENSP
TPSPLQKKVT EDLSKTLLMY TVPAVQGFFR SISLSRGNNL
QDTLRVLTLW FDYGHWPDVN EALVEGVKAI QIDTWLQVIP
QLIARIDTPR PLVGRLIHQL LTDIGRYHPQ ALIYPLTVAS KS (SEQ ID
10 NO:1).

In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of one or more residue of amino acid residues 1400-1500 of the amino acid sequence set forth in NCBI Accession No. NP_004949. In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of one or more residue of amino acid
15 residues of the following amino acid sequence which represents residues 1400-1500 :

K ELEFQKGPTP AILESLISIN NKLQQPEAAA GVLEYAMKHF
GELEIQATWY EKLHEWEDAL VAYDKKMDTN KDDPELMLGR
MRCLEALGEW GQLHQQCCEK (SEQ ID NO:2).

In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of
20 one or more residue of amino acid residues 1850-1982 of the amino acid sequence set forth in NCBI Accession No. NP_004949. In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of one or more residue of amino acid residues of the following amino acid sequence which represents residues 1850-1982 :

E SEAESTENSP TPSPLQKKVT EDLSKTLLMY TVPAVQGFFR
25 SISLSRGNNL QDTLRVLTLW FDYGHWPDVN EALVEGVKAI
QIDTWLQVIP QLIARIDTPR PLVGRLIHQL LTDIGRYHPQ
ALIYPLTVAS KS (SEQ ID NO:3).

In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of L1433, a mutation of A1459, a mutation of L1460, a mutation of C1483, a mutation
30 of F1888, a mutation of I1973, a mutation of T1977, or a combination thereof. In certain non-limiting embodiments, the mutation is one or more of L1433S, A1459P, L1460P, C1483F, C1483Y, F1888 L, I or V, I1973F, or T1977K.

In certain non-limiting embodiments, a mTOR biomarker is one or more mutation in the PI3 kinase domain of mTOR, for example, which increases

mTOR activity. In certain non-limiting embodiments, the mutation in the PI3 kinase domain is a mutation of one or more residue of amino acid residues 2182-2516 of the amino acid sequence set forth in NCBI Accession No. NP_004949. In certain non-limiting embodiments, the mutated sequence is at least 95 or at least 98 or at least 99 or at least 99.5 percent homologous to the wild-type sequence (as determined, for example, by standard software such as BLAST or FASTA). In certain non-limiting embodiments, the mutation in the PI3 kinase domain is a mutation of one or more residue of amino acid residues of the following amino acid sequence which represents residues 2182-2516:

FVFLLKGHE DLRQDERVMQ LFGLVNTLLA NDPTSLRKNL
SIQRYAVIPL STNSGLIGWV PHCDTLHALI RDYREKKKIL
LNIEHRIMLR MAPDYDHLTL MQKVEVFEHA VNNTAGDDLA
KLLWLKSPSS EVWFDRRTNY TRSLAVMSMV GYILGLGDRH
PSNLMLDRLS GKILHIDFGD CFEVAMTREK FPEKIPFRLT
RMLTNAMEVT GLDGNYRITC HTVMEVLREH KDSVMAVLEA
FVYDPLLNWR LMDTNTKGNK RSRTRTDSYS AGQSVEILDG
VELGEPAHKK TGTTVPESIH SFIGDGLVKP EALNKKAIQI
INRVRDKLTG RDFSHD (SEQ ID NO:4).

In certain non-limiting embodiments, the mutation in the PI3 kinase domain is a mutation of one or more residue of amino acid residues 2200-2250 of the amino acid sequence set forth in NCBI Accession No. NP_004949. In certain non-limiting embodiments, the mutation in the FAT domain is a mutation of one or more residue of amino acid residues of the following amino acid sequence which represents residues 2200-2250:

Q LFGLVNTLLA NDPTSLRKNL SIQRYAVIPL STNSGLIGWV
PHCDTLHALI (SEQ ID NO:5).

In certain non-limiting embodiments, the mutation in the PI3 kinase domain is a mutation of L2230, L2220, Q2223, M2327, V2406, S2215, L2431, R2505, or a combination thereof. In certain non-limiting embodiments, the mutation in the PI3 kinase domain is a mutation of L2230, L2220, Q2223, S2215, or a combination thereof. In certain non-limiting embodiments, the mutation is one or more of L2230V, L2220F, Q2223K, M2327I, V2406A, S2215F, L2431P, or R2505P.

Specific non-limiting examples of biomarkers are set forth in FIGURE 14B and FIGURE 16 herein.

In one specific non-limiting embodiment, a mTOR biomarker for a human subject is a chromosomal abnormality involving chromosome position 1p36. For example, the chromosomal abnormality may be one or more insertion, deletion, duplication, inversion, etc. of one or both chromosome(s) including or in immediate
5 proximity to position 1p36.

In further non-limiting embodiments, a mTOR biomarker is a molecule other than the mTOR gene or protein which increases the activity of mTOR. Non-limiting examples of such mTOR biomarkers include Rheb, Raptor, Deptor, PRAS40, AMPK, REDD1/2, LKB1 and variants or mutations thereof relative to reference
10 sequences. In specific non-limiting embodiments, Deptor, AMPK, LKB1, PRAS40, RED1/2 nucleic acid or protein comprising one or more insertion, deletion, or substitution, which may result in a frameshift, nonsense or missense mutation which decrease the functionality of the subject protein and increase function of mTOR may serve as a mTOR biomarker.

15

5.4 CANCER TARGETS

Non-limiting examples of cancers that may be subject to the present invention include renal cell carcinoma (RCC), supependymal giant cell astrocytoma, supependymal giant cell astrocytoma associated with tuberous sclerosis, hormone
5 receptor positive HER-2 negative breast cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, melanoma, and progressive neuroendocrine tumors of pancreatic origin.

5.5 RAPAMYCIN ANALOGS

Non-limiting examples of rapamycin analogs include sirolimus and its
10 analogs/derivatives including everolimus, temsirolimus, deforolimus, and zotarolimus.

5.6 NON-RAPAMYCIN MTOR INHIBITORS

In certain non-limiting embodiments, cancers that are found to express
15 mTOR biomarkers, where the activity of mTOR is increased relative to wild-type, may be treated with non-rapamycin mTOR inhibitors. Non-limiting examples of such mTOR inhibitors include INK128, AZD8055, AZD2014 and analogs having a morpholino pyrazolopyrimidine scaffold; and mTOR/PI3 kinase dual inhibitors such as, but not limited to, NVP-BEZ235, BGT226, SF1126, PKI-587. The present
20 invention, in non-limiting embodiments, provides for producing an anti-cancer effect in a cancer cell expressing a mTOR biomarker that increases mTOR activity by exposing said cell to an effective amount of a non-rapamycin mTOR activity, and provides for methods of treatment of a subject having a cancer in which said cancer cells are present.

25

5.7 METHODS OF USE

In certain non-limiting embodiments, the present invention provides for a method of determining whether an anti-cancer effect is likely to be produced in a cancer by a rapamycin analog, comprising determining whether cells of the cancer
30 contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where if the TSC1, TSC2, and/or mTOR

biomarker is present, it is more likely that a rapamycin analog would have an anti-cancer effect on the cancer.

TSC1 biomarkers, TCS2 biomarkers, and mTOR biomarkers are described in the sections above. Cancers suitable for treatment are described above.
5 Rapamycin analogs are described above.

In certain non-limiting embodiments, the present invention provides for a method of producing an anti-cancer effect in a cancer, comprising determining whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, and, where a TSC1
10 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is present, administering a therapeutically effective amount of a rapamycin analog to produce an anti-cancer effect.

An anti-cancer effect means one or more of a reduction in aggregate cancer cell mass, a reduction in cancer cell growth rate, a reduction in cancer cell
15 proliferation, a reduction in tumor mass, a reduction in tumor volume, a reduction in tumor cell proliferation, a reduction in tumor growth rate, and/or a reduction in tumor metastasis.

In certain non-limiting embodiments, the present invention provides for a method of treating a subject suffering from a cancer, comprising determining
20 whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, and, where a TSC1 biomarker, a TCS2 biomarker, and/or a mTOR biomarker is present, treating the subject with a therapeutically effective amount of a rapamycin analog. In certain non-limiting embodiments, where cells of the cancer do not contain a TSC1, TSC2 or
25 mTOR biomarker, the subject is not treated with a rapamycin analog but treatment with another modality, for example an alternative chemotherapeutic agent, biologic anticancer agent, or radiation therapy, is administered.

A therapeutically effective amount is an amount that is able to achieve one or more of an anticancer effect, prolongation of survival, and/or prolongation of
30 period until relapse.

In certain non-limiting embodiments, the present invention provides for a method of determining whether an anti-cancer effect is likely to be produced in a cancer by a rapamycin analog, comprising obtaining a sample of the cancer, and determining, in the sample, whether cells of the cancer contain a biomarker selected

from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where if the TSC1, TSC2, and/or mTOR biomarker is present, it is more likely that a rapamycin analog would have an anti-cancer effect on the cancer. Methods for determining the presence of a biomarker are set forth in section 5.1
5 above.

In certain non-limiting embodiments, the present invention provides for a method of treating a subject suffering from a cancer, comprising obtaining a plurality of samples from different locations of cancer in the subject, determining, in each sample, whether cells of the cancer contain a biomarker selected from a TSC1
10 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, and, where a TSC1 biomarker, a TCS2 biomarker, and/or a mTOR biomarker is present in a sample or a plurality of the samples or in all of the samples, treating the subject with a therapeutically effective amount of a rapamycin analog. In certain non-limiting embodiments, a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is
15 present in all the samples. As exemplified below, the TSC1, TCS2, and/or mTOR biomarkers in multiple samples need not be the same. In certain non-limiting embodiments, the different locations of cancer giving rise to the samples are part of the same tumor mass. In certain non-limiting embodiments, the different locations of cancer giving rise to the samples are not all part of the same tumor mass (for example,
20 one or more may arise from a tumor at a separate body location, such as a metastasis). In a certain, non-limiting embodiment, where one or more of the samples does not contain a TSC1, TSC2 or mTOR biomarker, the subject is not treated with a rapamycin analog but treatment with another modality, for example an alternative chemotherapeutic agent, biologic anticancer agent, or radiation therapy, is
25 administered.

5.7 KITS

In non-limiting embodiments, the present invention provides for a kit for determining whether an anti-cancer effect is likely to be produced in a cancer by a
30 rapamycin analog, comprising a means for detecting a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof. TSC1 biomarkers, TSC2 biomarkers, and mTOR biomarkers are set forth in the preceding sections.

Types of kits include, but are not limited to, packaged probe and primer sets (e.g. TaqMan probe/primer sets), arrays/microarrays, biomarker-specific antibodies and beads, which further contain one or more probes, primers, or other detection reagents for detecting one or more biomarkers of the present invention.

5 In a specific, non-limiting embodiment, a kit may comprise a pair of oligonucleotide primers, suitable for polymerase chain reaction (PCR) or nucleic acid sequencing, for detecting the biomarker(s) to be identified. A pair of primers may comprise nucleotide sequences complementary to a biomarker set forth above, and be of sufficient length to selectively hybridize with said biomarker. Alternatively, the 10 complementary nucleotides may selectively hybridize to a specific region in close enough proximity 5' and/or 3' to the biomarker position to perform PCR and/or sequencing. Multiple biomarker-specific primers may be included in the kit to simultaneously assay large number of biomarkers. The kit may also comprise one or more polymerases, reverse transcriptase, and nucleotide bases, wherein the nucleotide 15 bases can be further detectably labeled.

In non-limiting embodiments, a primer may be at least about 10 nucleotides or at least about 15 nucleotides or at least about 20 nucleotides in length and/or up to about 200 nucleotides or up to about 150 nucleotides or up to about 100 nucleotides or up to about 75 nucleotides or up to about 50 nucleotides in length.

20 In a further non-limiting embodiment, the oligonucleotide primers may be immobilized on a solid surface or support, for example, on a nucleic acid microarray, wherein the position of each oligonucleotide primer bound to the solid surface or support is known and identifiable.

In a specific, non-limiting embodiment, a kit may comprise at least one 25 nucleic acid probe, suitable for in situ hybridization or fluorescent in situ hybridization, for detecting the biomarker(s) to be identified. Such kits will generally comprise one or more oligonucleotide probes that have specificity for various biomarkers. Means for testing multiple biomarkers may optionally be comprised in a single kit.

30 In other non-limiting embodiments, a kit may comprise at least one antibody for immunodetection of the biomarker(s) to be identified. Antibodies, both polyclonal and monoclonal, specific for a biomarker, may be prepared using conventional immunization techniques, as will be generally known to those of skill in the art. The immunodetection reagents of the kit may include detectable labels that

are associated with, or linked to, the given antibody or antigen itself. Such detectable labels include, for example, chemiluminescent or fluorescent molecules (rhodamine, fluorescein, green fluorescent protein, luciferase, Cy3, Cy5, or ROX), radiolabels (3H, 35S, 32P, 14C, 131I) or enzymes (alkaline phosphatase, horseradish peroxidase).

5 In a further non-limiting embodiment, the biomarker-specific antibody may be provided bound to a solid support, such as a column matrix, an array, or well of a microtiter plate. Alternatively, the support may be provided as a separate element of the kit.

In one specific non-limiting embodiment, a kit may comprise a pair of 10 primers, a probe, microarray, or antibody suitable for detecting the TSC1 Q781* nonsense mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the TSC1 P311fs*4 frameshift mutation biomarker.

15 In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the TSC1 I580fs*7 frameshift biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the TSC1 Q527* 20 nonsense biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the TSC1 S334* nonsense biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of 25 primers, a probe, microarray, or antibody suitable for detecting the TSC2 Q794* nonsense mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the TSC2 R611W missense mutation biomarker.

30 In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the TSC2 S1498N missense mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR Q2223K frameshift mutation biomarker.

5 In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR R2505P mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR L2431P mutation biomarker.

10 In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR S2215F mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR V2406A

15 mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR M2327L mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of

20 primers, a probe, microarray, or antibody suitable for detecting the mTOR L2230V mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR I2228T mutation biomarker.

25 In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR L2220F mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR V2006L

30 mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR T1977K mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR I1973F mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR F1888V, I, and/or L mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR F1888L and L2230V mutation biomarkers.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR C1483F and/or C1483Y mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR L1460P mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR A1459P mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR L1433S mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR A1105P mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR E919V mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting the mTOR K860N mutation biomarker.

In one specific non-limiting embodiment, a kit may comprise a pair of primers, a probe, microarray, or antibody suitable for detecting one or more of the mTOR mutations shown in FIGURE 16.

In certain non-limiting embodiments, where the measurement means in the kit employs an array, the set of biomarkers set forth above may constitute at least 10 percent or at least 20 percent or at least 30 percent or at least 40 percent or at least 50 percent or at least 60 percent or at least 70 percent or at least 80 percent of the species of markers represented on the microarray.

In certain non-limiting embodiments, a biomarker detection kit may comprise one or more detection reagents and other components (e.g. a buffer, enzymes such as DNA polymerases or ligases, chain extension nucleotides such as deoxynucleotide triphosphates, and in the case of Sanger-type DNA sequencing reactions, chain terminating nucleotides, positive control sequences, negative control sequences, and the like) necessary to carry out an assay or reaction to detect a biomarker.

A kit may further contain means for comparing the biomarker with a standard, and can include instructions for using the kit to detect the biomarker of interest. Specifically, the instructions describes that the presence of a biomarker, set forth herein, is indicative of an increased possibility of an anti-cancer effect in a cancer by a rapamycin analog.

6. EXAMPLE: NEXT_GENERATION SEQUENCING REVEALS GENOMIC DETERMINANTS OF LONG-TERM RESPONSE TO mTOR INHIBITORS IN PATIENTS WITH ADVANCED RENAL CELL CARCINOMA

As shown in FIGURE 1, among patients treated with rapamycin analogs (rapalogs) only a relatively small subset of patients receive sufficient therapeutic benefit to support long-term use. This group of "long-term responder" patients was selected for further study in hopes of identifying characteristics which could be used to prospectively assess the likelihood of beneficial therapeutic response. FIGURE 2A and B show, respectively, characteristics of long-term responders and patients who did not substantially benefit from treatment ("poor responders"). DNA from both long-term responders and poor responders was then subjected to Integrated Mutation Profiling of Actionable Cancer Targets ("IMPACT") analysis, which employs bait for 230 cancer genes panel (FIGURE 3A, and see 36). Genes of interest to mTOR pathway are enlarged and in bold in FIGURE 3B.

FIGURE 4 presents a summary of results for responders. Three tumor sites (FIGURE 5B) were analyzed for patient 1, who was diagnosed with clear cell

RCC and had a long-term response to temsirolimus. As shown in FIGURE 5A and C, patient 1 had a single copy of Chromosome 9 and different mutations of TSC1 at different tumor sites (P311fs and Q527). Three tumor sites and one metastasis (FIGURE 6B) were analyzed for patient 2, who was diagnosed with unclassified RCC
5 and had a long-term response to temsirolimus. As shown in FIGURE 6A and C, patient 2 had a 1580fs mutation in TSC1.

Patient 3, diagnosed with clear cell RCC and having a long-term response to everolimus, was found to have a Q781 mutation in TSC1 at two tumor sites of four assayed. Interestingly, the other two sites, while lacking the TSC1
10 mutation, had a Q2223K mutation in mTOR (FIGURE 7A-B. Further study showed that the Q2223K mutation in mTOR resulted in gain-of-function (FIGURE 8B). This mutation maps in the PI3K domain of mTOR (FIGURE 8D).

As shown in FIGURE 9A-D, two tumor sites (FIGURE 9A) were studied in patient 4, who was diagnosed with unclassified RCC and had a long-term
15 response to everolimus. While no mutations were found, site 1 manifested homozygous loss of TSC2. At site 2, a heterozygous deletion, mutation Q794*, was observed (FIGURE 9D).

FIGURE 10 shows a summary of the mutations found and their functional consequences in the various long-term responder patients. As shown in
20 FIGURE 11, there were some mTOR relevant mutations identified in several poor responder patients but the mutations were missense mutations without apparent functional effect.

The foregoing data provides plausible oncogenomic causes for the exceptional treatment responses observed in some, but not all patients. It suggests
25 that identification of mutations alone may not be sufficient without consideration of their biologic effects. It also illustrates that despite of intratumoral heterogeneity, targeted therapy can be successful due to clonal convergence within the pathway.

The foregoing study was advanced further and the results are presented below in Section 7.

30

7. EXAMPLE: PATHWAY CONVERGENT EVOLUTION IS A MAJOR DETERMINANT OF TREATMENT RESPONSE TO mTOR INHIBITORS IN KIDNEY CANCER

7.1 MATERIALS AND METHODS

5 **Patients.** Six RCC cases were retrospectively identified from an institutional database of RCC patients treated with rapalogs at Memorial Sloan-Kettering Cancer Center (MSKCC). All had received either temsirolimus or everolimus as single-agent therapy. Six were selected based on extended therapeutic benefit, evident by treatment duration of ≥ 20 months. We felt this cut-off to be 10 representative of long-term benefit, as the registration trials reported <10% or 0% of patients to be alive and progression-free at 20 months, respectively. As part of our analysis all scans obtained between commencement and discontinuation of rapalogs were retrospectively reviewed by a research radiologist. This protocol was approved by our institutional review board, and all patients had previously provided written 15 consents on an institutional tissue procurement protocol. The access and utilization of the kidney cancer TCGA database for publication were approved by the TCGA Program Office.

Samples. All 6 patients underwent nephrectomy prior to the initiation of rapalog therapy and have frozen specimens. Adjacent normal kidney tissue (n=5) 20 or peripheral blood (n=1) were used for reference. To interrogate intratumor heterogeneity, DNA was extracted from FFPE materials of additional regions within the primary tumors (regions marked as R). Regions were chosen by a dedicated genitourinary pathologist based on interregional differences in histopathologic appearance. Furthermore, fresh frozen specimens of metastasis (marked as M1; 25 patient #2) and a contralateral primary kidney tumor (2 separate tumors marked as T1 and T2, patient #4) were obtained to determine inter-tumor heterogeneity. Previously archived operative specimens were reviewed by an expert genitourinary pathologist to confirm the diagnosis and to identify separate areas of ≥ 70% tumor content and healthy kidney tissues. Macrodissection was performed for each area of interest, and 30 DNA was extracted using the DNeasy tissue kit (Qiagen). DNA was quantified using the Thermo Scientific NanoDropTM 1000 Spectrophotometer and samples with an A260/A280 ratio of 1.8-2.0 and concentration of 135 ng/μL or greater were considered acceptable for further analysis.

Next-generation sequencing. DNA from tumors and matched normal was subjected to an analysis by two next-generation sequencing platforms. The IMPACT assay (Integrated Mutation Profiling of Actionable Cancer Targets) is a customized targeted-exome capture assay of 230 cancer-associated genes with ultra-deep sequencing coverage (>500x) using Illumina HiSeq 2000. Target-specific probes for hybrid selection were designed as previously described to capture all protein-coding exons of a list of oncogenes, tumor suppressor genes, and components of pathways deemed actionable by targeted therapies. The whole-exome capture assay with standard sequencing coverage (~85x) using the Agilent SureSelect XT HumanAllExon 50Mb was performed. Single-nucleotide variants, small insertions and deletions, and copy number alterations (CNA) were interrogated.

The IMPACT Assay. Ultra-deep targeted sequencing of key cancer-associated genes was performed using the IMPACT assay (Integrated Mutation Profiling of Actionable Cancer Targets). We designed target-specific probes to capture all protein-coding exons of 230 genes of interest for hybrid selection (Agilent SureSelect or Nimblegen SeqCap) as previously described (21). This list included commonly implicated oncogenes, tumor suppressor genes, and components of pathways deemed actionable by current targeted therapies (Table 2). Two protocols were followed during the course of the study. For 10 samples, barcoded sequence libraries (Illumina TruSeq) were prepared using 500 ng of input tumor or matched normal DNA according to the manufacturer's instructions. Libraries were pooled at equimolar concentrations (100 ng per library) for a single exon capture reaction (Agilent SureSelect) as previously described (31). For 12 samples, barcoded sequence libraries were prepared using 250 ng of input DNA using a hybrid protocol based on the NEBNext DNA Library Prep Kit (New England Biolabs). Manufacturer's instructions were followed with two substitutions: we used NEXTflex barcoded adapters (Bio Scientific) and HiFi DNA polymerase (Kapa Biosystems). Libraries were pooled at 100 ng per tumor library and 50 ng per normal library for a single exon capture reaction (Nimblegen SeqCap). To prevent off-target hybridization in all capture reactions, we spiked in a pool of blocker oligonucleotides complementary to the full sequences of all barcoded adaptors (to a final total concentration of 10 μM). Hybridized DNA was sequenced on an Illumina HiSeq 2000 to generate paired-end 75-bp reads. Data were demultiplexed using CASAVA, and reads were aligned to the reference human genome (hg19) using the Burrows-Wheeler Alignment tool (32).

Local realignment and quality score recalibration were performed using the Genome Analysis Toolkit (GATK) according to GATK best practices (33). We achieved mean exon sequence coverage of 590x (625x for all tumor samples). Deep sequencing ensured sensitivity for detecting mutations in multiclonal and stroma-admixed samples and enabled accurate determination of mutation allele frequencies.

Sequence data were analyzed to identify three classes of somatic alterations:

single-nucleotide variants, small insertions/deletions (indels), and copy number alterations. Single-nucleotide variants were called using muTect and retained if the variant allele frequency in the tumor was >5 times that in the matched normal. Indels were called using the SomaticIndelDetector tool in GATK. All candidate mutations and indels were reviewed manually using the Integrative Genomics Viewer34. The mean sequence coverage was calculated using the DepthOfCoverage tool in GATK and was used to compute copy number as described previously (22).

Whole-exome capture sequencing. Between 1.9 and 3 μg of high quality genomic DNA was captured by hybridization using the SureSelect XT HumanAllExon 50Mb (Agilent). Samples were prepared according to the manufacturer instructions. PCR amplification of the libraries was carried out for 6 cycles in the pre-capture step and for 10 cycles post capture. Samples were bar-coded and run on a Hiseq 2000 in a 75bp/75bp Paired end run, using the TruSeq SBS Kit v3 (Illumina). Two samples were pooled in a lane, the average number of read pairs per sample was 69 million. All reads were aligned to the reference human genome (NCBI build 37.1 hg19). Exome reads were aligned with BWA 32 which does a gaped alignment for the detection of small indels, as described in below. Samples mapping to the reference genome which mapped uniquely (MAPQ>0) were retained and then converted to SAM format 31 for subsequent analyses and for visualization in the Integrative Genomics Viewer 34. Single nucleotide variants were determined in regions of sufficient coverage. We first removed duplicate reads (using Picard MarkDuplicates) from further analysis, defined here as any read chromosome, start position, strand, and color-space sequence matched another aligned read. Indel realignment, base quality recalibration, variant detection, and variant annotation were performed with the GATK framework (33,35). Specifically, after base quality recalibration for color-space reads, variant detection in exome data was performed with the UnifiedGenotyper. For high-coverage exome experiments, variants were

excluded if their variant quality was <30, genotype quality <5, or if they were associated with either homopolymer runs or excessive strand bias. Novel variants, those not previously identified in either dbSNP ver. 132, were required to be derived from basespace reads not duplicated from non-duplicate color-space reads, were not resident exclusively in higher-error base positions (positions 38-50) and had evidence of the variant allele in reads mapping to both strands. Candidate somatic mutations were those with a variant genotype in the tumor and reference genotype in the normal sample with minimum coverage of ≥10 and 6 reads respectively. Additionally, we required that the tumor variant frequency was ≥10%, and each variant was detected in 4 or more tumor reads. Our pipeline for small insertion and deletion (indel) detection was as follows. Gapped alignment of exome sequencing reads was performed with BWA. The alignment output was sorted and duplicate reads removed with the Picard pipeline and BAM files created and indexed with Samtools. Interval detection, local realignment, indel genotyping, and post-processing were performed with the GATK framework after base quality recalibration, as described above. Retained indels were those with sufficient quality and coverage and not associated with homopolymer runs of 5bp or greater.

Sanger Sequencing. Bidirectional Sanger sequencing for validation was performed for all mTOR pathway mutations using standard techniques with primers provided by the Geoffrey Beene Translational Oncology Core .

Plasmids. Plasmids containing cDNA encoding myc-epitope-tagged S6K (pcDNA3-myc-S6K) and Flag-epitope-tagged Wild-type mTOR (pcDNA3-Flag mTOR) were obtained from Addgene (#26610 and #26603). To generate individual mTOR mutations, a corresponding nucleotide change was introduced via QuikChange site-directed mutagenesis (Stratagene), producing pcDNA3-Flag mTOR mutants. The primers used are shown in Table 7.

Cell Culture, transfection, and immunoblots. HEK293T cells were cultured in DMEM with 10% fetal bovine serum, glutamine, non-essential amino acids, and antibiotics. To assay mTOR activity, pcDNA3-Flag mTOR was transfected alone or with Myc-S6K into HEK293T cells using Lipofectamine 2000, according to manufacturer instructions (Invitrogen). Twenty-four hours after transfection, cells were treated as indicated. Lysates were measured for protein concentration (Pierce BCA assay), and equal amounts of protein were resolved by PAGE and subjected to immunoblotting using the following antibodies against phospho-S6K1(T389), total

S6K, phospho-S6 (S235/236), phospho-AKT (S473) (Cell Signaling #9205, #9202, #4858, #9271), β-Actin (Sigma, AC-15), Flag (Sigma, M2), and c-Myc (Santa Cruz, SC-40).

Computational modeling of mTOR kinase domain. The model was built by HMMHMM (hidden markov-model) comparison, using the HHpred server (http://toolkit.tuebingen.mpg.de) and the x-ray crystal structure of PIK3C3 (pdb: 3ls8) as a template.

7.2 RESULTS

Long-term rapalog treatment responders identified in the MSKCC kidney cancer database. To probe into the genomic determinants underlying long-term rapalog therapeutic benefits, we searched the Memorial Sloan-Kettering Cancer Center (MSKCC) kidney cancer database and identified patients who (1) underwent nephrectomy prior to receiving systemic therapy for metastatic diseases (n=305) with archived fresh frozen tumors available for analysis, (2) were treated with single agent temsirolimus or everolimus, (3) displayed exceptional disease control (partial response or stable disease > 20 months) on rapalogs, and (4) had received sunitinib previously, yet obtained greater clinical benefit with rapalogs. With such criteria, 6 patients were identified who were on average treated with single agent sunitinib for 9 months followed by rapalogs for 29+ months (Table 1).

An integrated next-generation sequencing approach identified genetic mutations involving three core components of the mTORC1 signaling pathway. DNA from primary kidney tumors and matched normal kidney tissues or peripheral blood mononuclear cells was subjected to an integrated next-generation sequencing analysis employing two platforms: the IMPACT (Integrated Mutation Profiling of Actionable Cancer Targets; 19,21,22), and WEC (whole-exome capture) assays (FIGURES 17 and 18). With standard sequencing coverage (~100x), WEC enables us to survey mutational landscapes encompassing all coding exons. On the other hand, the IMPACT assay, a customized targeted-exome capture assay of 230 cancer-associated genes (Table 2) with an ultra-deep sequencing coverage (>500x) provides (5) opportunity to (1) capture genomic events potentially missed by WEC due to tumor impurity and/or heterogeneity, (2) effectively analyze DNA from formalin-fixed paraffinembedded (FFPE) samples, (3) compute copy number

alterations (CNA), and (4) establish a platform which, by means of cost and efficiency, shows promise for future adaptation to a clinical test.

Single-nucleotide variants, small insertions and deletions, and copy number alterations (CNA) were first interrogated with IMPACT on all 6 patients (Table 3) and then with WEC on patients #5 and #6 (Table 4). Pertinent genomic findings are summarized (Table 5) and mutations relevant to our research question were confirmed by orthogonal bidirectional Sanger sequencing (FIGURE 19). Interestingly, this approach identified genetic mutations involving three core components of the mTORC1 pathway, i.e., TSC1, TSC2, and mTOR, through distinct mechanisms, in 4 of 6 (67%) patients.

Complete functional loss of TSC1 or TSC2. For patient #1, a 58 year-old female, the IMPACT analysis of the primary tumor at region 1 (R1) revealed a novel somatic TSC1 single nucleotide deletion (P311fs*4) (FIGURE 12A, FIGURE 19 and Table 5). Copy number analysis of the tumor revealed a single copy of chromosome 9 where the TSC1 gene resides (FIGURE 12E). The frameshift mutation with LOH (loss of heterozygosity) would result in a complete functional impairment of TSC1 in the tumor. For patient #2, a 73 year-old female, the IMPACT analysis of R1 identified another novel somatic TSC1 frameshift mutation (I580fs*7) (FIGURE 12B). Again a concurrent LOH was observed in this patient (FIGURE 12E), indicating a complete functional abrogation of TSC1. For patient #4, a 16 year-old tuberous sclerosis complex 2 male who presented with metastatic disease and multiple (6) primaries of both kidneys, copy number analysis of germline (from peripheral blood) and tumor DNA revealed heterozygous loss of TSC2 in the germline and a bi-allelic TSC2 loss in primary kidney tumor 1 (T1) (FIGURE 12C and FIGURE 20). Complete functional abrogation of either TSC1 or TSC2 would hyperactivate the mTORC1 signaling.

An mTOR kinase domain mutation identified in the tumor of patient #3. For patient #3, a 66 year-old male, the IMPACT analysis identified a novel somatic missense mutation of mTOR (Q2223K) at region 1 (R1) of the primary tumor (FIGURE 12D). Amino acid glutamine at position 2,223 resides in the PI3K-related kinase domain of mTOR. The presence of a Q2223K mutation in a long-term rapalog responder raises a possibility that missense mutations of mTOR in the kinase domain might induce hyperactivity and yet remain sensitive to rapalogs which bind FKBP12 and then target the regulatory FRB domain. For patients #5 and #6, 60 and

50 year-old females, the IMPACT assay did not detect apparent causative oncogenomics events (Table 3). Furthermore, despite capturing a greater number of mutations, WEC (Table 4) also offered no apparent genetic clues concerning the therapeutic benefit of patients #5 and #6 to temsirolimus. Overall, IMPACT assays
5 alone may be sufficient to evaluate the genetic signature of response to rapalogs.

The mTOR (Q2223K) mutant aberrantly activates mTORC1 yet remains sensitive to rapamycin. The discovery of an mTOR (Q2223K) mutant in the kidney tumor of patient #3 suggests that this mTOR kinase mutant may aberrantly activate mTORC1 yet remain sensitive to (7) rapalogs. To examine whether mTOR
10 (Q2223K) affects the mTORC1 signaling, we examined its effect on the threonine 389 phosphorylation of S6K (p70S6 kinase, one of the key substrates of mTORC1). Cells expressing mTOR (Q2223K) displayed stronger S6K phosphorylation than those expressing wild-type mTOR (FIGURE 13A). The observed hyperactivation by mTOR (Q2223K) mutant persisted over lower serum concentrations (FIGURE 13B).
15 Importantly, the mTOR (Q2223K) mutant was sensitive to rapamycin as wildtype mTOR (FIGURE 13C). This contrasts with the hypersensitivity of EGFR activating mutants to small molecule ERFR inhibitors such as gefitinib and erlotinib (23), likely reflecting the intrinsic differences between EGFR tyrosine and PI3K/PI3K-like kinases. When exogenous S6K was co-transfected, a process known to augment
20 mTORC1 signaling, we further demonstrated the hyperactivity of the mTOR (Q2223K) mutant at low serum and affirmed its sensitivity to rapamycin (FIGURE 13D,E). Of note, the serine 473 phosphorylation of AKT, a key post-translational modification mediated by mTORC2, was not enhanced by mTOR (Q2223K), indicating that such mutant has no strong effect on mTORC2 (FIGURE 13D). The
25 lysine substitution of glutamine 2223 of the mTOR kinase domain has created an mTOR that only activates mTORC1 but not mTORC2. Modeling of the mTOR (Q2223K) mutation based on the solved PI3K kinase domain structure suggests that the 2,223 glutamine residue locates right next to the ATP binding site of the catalytic domain (FIGURE 13F).

30 **Clustered, evolutionarily preserved activating mutations of mTOR in kidney cancer.** Our discovery of a hyperactive mTOR (Q2223K) mutant in a long-term rapalog-treated patient suggests that activating mTOR mutations in tumors could be implicative of treatment response to rapalogs. Analysis of the clear cell kidney cancer TCGA database (8)through the cBio Genomics Portal revealed mTOR

mutations in 5.4% of examined cases (23/424) (Table 6). Importantly, all of these are missense mutations, and the majority clusters on either the FAT or kinase domain (FIGURE 14A). Accordingly, we performed functional assessment on most of mTOR mutants identified in TCGA, COSMIC, and MSKCC kidney cancer databases (FIGURE 14A-C). Remarkably, nearly all mutations clustered on FAT or kinase domains exhibited hyperactive mTORC1 activity (FIGURE 14B and FIGURE 16) and were sensitive to rapamycin (FIGURE 14C). The scattered uncommon mutations near the HEAT domains appear to be neutral and likely represent passenger mutations due to the inherent large size of mTOR. Our discovery and subsequent functional validation of clustered hyperactive mTOR mutations in the kidney cancer TCGA database suggests that these are recurrent events in ccRCC. It is highly noteworthy that clusters of activating mTOR mutations around the FAT and kinase domains identified in kidney cancer recapitulate a pattern reported in fission yeast (FIGURE 14A; 24). Using random mutagenesis screens, they identified and functionally validated a large number of similarly clustered activating mutations in TOR2, the yeast equivalent of mTOR (FIGURE 14A). Together, we unveiled a preserved structural/functional evolution/selection of mTOR/TOR in human cancer pathology and unicellular biology.

Thus far, our cancer genomics based on single biopsies of therapeutic outliers was able to successfully provide logical genetic explanations for observed exceptional response to rapalogs in 4 of 6 (67%) patients. All of these mutations would have led to hyperactive mTORC1 signaling. Our findings are in line with the exceptional therapeutic response of imatinib, an Abelson kinase inhibitor, in treating CML bearing the BCR-ABL fusion gene (25), and erlotinib, an EGFR inhibitor, in treating EGFR mutant lung cancer (23). However, recent reports on the complexity of intra-tumor heterogeneity and the branched clonal evolution of RCC raise concerns about the feasibility of single-biopsy genomics in formulating personalized cancer medicine (26,27). To resolve this conundrum, multiregional IMPACT assays were performed on all available additional specimens (spatially separated regions within the primary kidney tumors and metastatic sites whenever are available; and mainly are formalin-fixed paraffin embedded samples) of patients #1 to #4.

Additional 9 regions were chosen based on interregional histopathologic differences. Genomic findings are summarized (FIGURE 15A-D and Table 5).

Intra-tumor heterogeneity with TSC1 intra-genic mTOR pathway convergent evolution. For patient #1, two additional regions (R2, R3) within the primary tumor were examined. Identical to R1 described above, R2 carried a TSC1 (P311fs*4) deletion and a heterozygous loss of chromosome 9 (9−) (FIGURE 15A).
5 Interestingly, analysis of R3 revealed a different nonsense TSC1 (Q527*) mutation with a concurrent heterozygous loss of chromosome 9 (FIGURE 15A and FIGURE 21). Hence, two distinct TSC1 loss-of-function mutations were discovered in spatially separated areas within the same primary tumor. This would simultaneously trigger aberrant mTORC1 activation at different regions of the same tumor, exemplifying an
10 intra-genic (TSC1) clonal convergent evolution of kidney cancer cells in the same patient. For patient #2, the analysis included 2 additional regions within the primary tumor (R2, R3) and one distant metastasis (M1). R2, R3, and M1 all harbored the same TSC1 (I580fs*7) mutation and a concurrent LOH through one copy loss of chromosome 9, which are identical to what discovered in R1 (FIGURE 15B).
15 Matching results across all analyzed specimens support a notion that all examined sites originated from one dominant clone which has a complete functional loss of TSC1.

Inter-tumor heterogeneity with TSC2 intra-genic mTOR pathway convergent evolution. For the tuberous sclerosis patient #4, primary tumors of both
20 kidneys (T1, T2) were analyzed. In addition to the germline heterozygous, chromosomal loss of TSC2 (16p+/−), T1 and T2 harbored distinct genomic events, yet converged on a complete loss of TSC2 function : a large deletion with loss of the 2nd allele of TSC2 in T1 (FIGURE 12C), and a nonsense mutation of TSC2 (Q794*) in T2 (FIGURE 15D and FIGURE 21), exemplifying an inter-tumor (T1 vs. T2),
25 intra-genic (TSC2) convergent evolution of kidney cancers in the same patient.

Intra-tumor heterogeneity with mTOR gain-of-function and TSC1 loss-of-function inter-genic mTOR pathway convergent evolution. For patient #3 whose kidney tumor region 1 (R1) carries an mTOR kinase domain activating mutation, three additional sites (R2, R3, R4) within the nephrectomy specimen were
30 analyzed. R2 carries the same mTOR (Q2223K) mutation as R1 (FIGURE 15C). Strikingly, although R3 and R4 carried the same VHL and MLL3 mutations as R1 and R2, consistent with a shared ancestral clone, R3 and R4 tumors contained a loss-of-function TSC1 (Q781*) mutation and a concurrent LOH through chromosome 9-, resulting in a complete functional impairment of TSC1 ((FIGURE 15C and FIGURES

21 and 22). Hence, three distinct mechanisms, including a missense gain-of-function mutation of growth promoting gene (mTOR), a nonsense loss-of-function mutation of tumor suppressor (TSC1), and another loss-of-function of TSC1 through LOH (9–), were employed by spatially separated cancer clones within the same primary tumor to
5 concurrently activate mTORC1. The presence of different BAP1 splice site mutations between R1/R2 and R3/R4 not only exemplifies their convergent evolution on BAP1 but also supports observed clonal bifurcation (FIGURE 15C). To our knowledge, this represents the first concurrent inter-genic (mTOR and TSC1) pathway convergent evolution (mTORC1 activation) discovered in human cancer.
10

7.3 DISCUSSION

Our multiregional IMPACT study revealed complete loss-of-function of either TSC1 or TSC2 in all tumors tested for patients #1, #2, and #4, and the coexistence of complete functional loss of TSC1 and gain-of-function of mTOR
15 (Q2223K) in spatially separated regions of the same primary tumor in patient #3. Additionally, we discovered that a significant number of clustered activating mutations of mTOR exist in kidney albeit to a lesser extent in other cancers (FIGURE 23). Importantly, mTOR (Q2223K) also occurrs in colon cancer (CRC TCGA) and thus represents a recurrent mutation. Altogether, our study not only suggests
20 uncontrolled mTORC1 signaling as an important contributor to the pathogenesis of kidney cancer but also discovers logical predictive genomic biomarkers for exceptional rapalog response in kidney cancer. Of note, the mTORC1 pathway convergent evolution, through complete functional loss of TSC1 orTSC2, or clustered activating mutations of mTOR discovered in our study, was not present in 5 MSKCC
25 kidney cancer patients whose metastatic cancers progressed within two months despite rapalog treatment (non-responders) (data not shown). Intriguingly,we noticed a heterozygous TSC1 loss in one of the non-responders, suggesting that haploid inactivation of TSC1 alone likely has limited predictive value in kidney cancer. This contrasts with a recent report on bladder cancer where haploid inactivation of TSC1
30 was reported to correlate with response to everolimus in a 14 patient cohort with a median treatment time of 2.6 (1.8-4.1) months, when a long-term responder (33+ months) carrying an additional NF2 mutation was excluded (19). Since mTOR activating mutations are also present in cancers for which rapalogs are not standard of care (FIGURE 23), it might be prudent to conduct a clinical trial administering

rapalogs on selected patients whose tumors carry these pathway convergent mutations.

The accumulation of diverged mutations during individual cancer evolution underscores the propensity of given tumors in achieving higher intra-tumor heterogeneity for the greater robustness of cancer cells (28). Our data are in agreement with recent demonstrations of the existence of a significant number of private mutations in separated regions of primary and metastatic kidney tumors, demonstrating the highly heterogeneous nature in genomics of individual kidney cancers (20). Branching evolution of cancers supports a central tenet that in order to achieve sustainable therapeutic benefit with targeted therapy one must identify and interfere with the earliest mutation events. Under such premises, ensuing genetic ramifications would mitigate the applicability of targeted therapeutic agents. Importantly, despite such an inherent predicament, our data based on kidney cancers suggest that specific tumor types might be prone to evolve around cancer type-specific central pathways (29,30) that contain regulatory circuits consisting of multiple genetic constituents. In our case, multiple distinct mechanisms, including various nonsense mutations, LOH through chromosomal loss, and activating mutations, can all be usurped by kidney cancer cells to activate mTORC1, for example the complete loss of TSC1 or TSC2, and the activating mutation of mTOR. Such pathway convergence in turns signals out converged vulnerability of cancers that can be effectively intervened with pathway inhibitors. On a cautionary note, one kidney cancer patient, reported in a recent article, harbored an activating mTOR (L2431P) mutation in the primary tumor but not metastatic sites (20). This patient progressed after ~7 months of everolimus treatment, explaining the lack of exceptional therapeutic response. Hence, multiple biopsies of tumors at different sites could be advised to discover those converging "Achilles' Heels".

To visualize this concept for treatment planning, we designate "a braided cancer river" to model cancer of a given patient, which branches to illustrate tumor heterogeneity generated by genetic mutations and merges to depict functional convergence through pathway integration. Lastly, it is tempting to speculate that other cancers may also channel through several key tumor type-specific converging pathways that prevalently operate in given cancer types for their robustness, which at the same time provides unique therapeutic vantage points.

Table 1. Patient characteristics of long-term rapalog responders. MSKCC: Memorial Sloan-Kettering Cancer Center Int: intermediate; Fav: favorable; N/A: not applicable; VEGF: vascular endothelial growth factor; TTP: time to progession by RECIST 1.1

	Sex	Age	Histologic subtype	MSKCC risk score	Number of prior regimens	Duration prior treatment with VEGF targeted therapy [months] (agent)	# of metastatic sites	Rapalog	Duration treatment with rapalog [months]
1	F	58	clear	Int	1	14 (sunitinib)	≥3	temsirolimus	27
2	F	73	unclassified	Int	1	3 (sunitinib)	1	temsirolimus	34
3	M	16	unclassified	Int	3	19 (sunitinib)	1	everolimus	36+
4	M	66	clear	Int	2	5 (sunitinib)	≥3	everolimus	20
5	F	60	clear	Fav	3	11 (sunitinib)	≥3	temsirolimus	28
6	F	50	unclassified	Fav	1	2 (sunitinib)	≥3	temsirolimus	33+

Table 2 IMPACT gene list and positions.

Gene Symbol	RefSeq ID	Chromosome
ABL1	NM_005157	9q34.1
ABL2	NM_005158	1q25.2
AKT1	NM_005163	14q32.32-q32.33
AKT2	NM_001626	19q13.1-q13.2
AKT3	NM_005465	1q44
ALK	NM_004304	2p23
ALOX12B	NM_001139	17p13.1
APC	NM_000038	5q21-q22
AR	NM_000044	Xq12
ARAF	NM_001654	Xp11.3-p11.23
ARHGAP26	NM_015071	5q31
ARID1A	NM_006015	1p36.1-p35
ASXL1	NM_015338	20q11
ATM	NM_000051	11q22-q23
ATRX	NM_000489	Xq21.1
AURKA	NM_003600	20q13
BAP1	NM_004656	3p21.31-p21.2
BCL2L1	NM_001191	20q11.21
BCL6	NM_001706	3q27
BIRC2	NM_001166	11q22
BRAF	NM_004333	7q34
BRCA1	NM_007294	17q21-q24
BRCA2	NM_000059	13q12-q13
CARD11	NM_032415	7p22
CBL	NM_005188	11q23.3-qter
CBLB	NM_170662	3q
CBLC	NM_012116	19q13.2
CCND1	NM_053056	11q13
CCNE1	NM_001238	19q12
CD79B	NM_000626	17q23
CDC42EP2	NM_006779	11q13
CDC73	NM_024529	1q25
CDH1	NM_004360	16q22.1
CDK4	NM_000075	12q13
CDK6	NM_001259	7q21-q22
CDK8	NM_001260	13q12
CDKN2A	NM_000077	9p21
CDKN2B	NM_004936	9p21
CDKN2C	NM_001262	1p32.3
CEBPA	NM_004364	19q13.1
CHEK1	NM_001274	11q24.2
CHEK2	NM_007194	22q12.1
CREBBP	NM_004380	16p13.3
CRKL	NM_005207	22q11.21
CRLF2	NM_022148	Xp22.3 and Yp11.3
CSF1R	NM_005211	5q32
CTNNB1	NM_001904	3p21
CYLD	NM_015247	16q12-q13

DAXX	NM_001350	6p21.3
DDR2	NM_006182	1q12-q23
DICER1	NM_030621	14q32.2
DIS3	NM_014953	13q21.32
DNMT1	NM_001379	19p13.2
DNMT3A	NM_022552	2p23
DNMT3B	NM_006892	20q11.2
EGFR	NM_005228	7p12
EIF4EBP1	NM_004095	8p12
EP300	NM_001429	22q13.2
EPHA3	NM_005233	3p11.2
EPHA5	NM_004439	4q13.1
EPHA6	NM_173655	3q12.1
EPHA7	NM_004440	6q16.3
EPHA8	NM_020526	1p36.12
EPHB1	NM_004441	3q21-q23
EPHB4	NM_004444	7q22
EPHB6	NM_004445	7q33-q35
ERBB2	NM_004448	17q11.2-q12
ERBB3	NM_001982	12q13
ERBB4	NM_005235	2q33.3-q34
ERG	NM_004449	21q22.3
ESR1	NM_000125	6q24-q27
ETV1	NM_004956	7p22
ETV6	NM_001987	12p13
EZH2	NM_004456	7q35-q36
FAM123B	NM_152424	Xq11.1
FAM46C	NM_017709	1p12
FAS	NM_000043	10q24.1
FBXW7	NM_018315	4q31.23
FGFR1	NM_015850	8p12
FGFR2	NM_000141	10q25.3-q26
FGFR3	NM_000142	4p16.3
FGFR4	NM_002011	5q33-qter
FH	NM_000143	1q42.1
FLCN	NM_144606	17p11.2
FLT1	NM_002019	13q12
FLT3	NM_004119	13q12
FOXL2	NM_023067	3q23
GATA1	NM_002049	Xp11.23
GATA2	NM_032638	3q21
GATA3	NM_002051	10p15
GNA11	NM_002067	19p13.3
GNAQ	NM_002072	9q21
GNAS	NM_000516	20q13.2-q13.3
GOLPH3	NM_022130	5p13.2
GRIN2A	NM_000833	16p13.2
GSK3B	NM_002093	3q13.3
HDAC2	NM_001527	6q21
HIF1A	NM_001530	14q23.2
HMGA2	NM_003483	12q15
HNF1A	NM_000545	12q24.31

HRAS	NM_005343	11p15.5
HSP90AA1	NM_005348	14q32.33
IDH1	NM_005896	2q32-qter
IDH2	NM_002168	15q21-qter
IGF1R	NM_000875	15q26.3
IGFBP7	NM_001553	4q12
IKBKE	NM_014002	1q31
IKZF1	NM_006060	7pter-7qter
INSR	NM_000208	19p13.3-p13.2
IRS1	NM_005544	2q36
IRS2	NM_003749	13q34
JAK1	NM_002227	1p32.3-p31.3
JAK2	NM_004972	9p24
JAK3	NM_000215	19p13-p12
JUN	NM_002228	1p32-p31
KDM5C	NM_004187	Xp11.22-p11.21
KDM6A	NM_021140	Xp11.2
KDR	NM_002253	4q11-q12
KEAP1	NM_012289	19p13.2
KIT	NM_000222	4q11-q12
KLF6	NM_001300	10p15
KRAS	NM_004985	12p12.1
LDHA	NM_005566	11p15.1
LGR6	NM_021636	1q32.1
MAGI2	NM_012301	7q21
MAP2K1	NM_002755	15q22.1-q22.33
MAP2K2	NM_030662	19p13.3
MAP2K4	NM_003010	17p11.2
MAP3K8	NM_005204	10p11.2
MCL1	NM_021960	1q21
MDM2	NM_002392	12q13-q14
MDM4	NM_002393	1q32
MEN1	NM_000244	11q13
MET	NM_000245	7q31
MITF	NM_000248	3p14.1-p12.3
MLH1	NM_000249	3p22.3
MLL	NM_005933	11q23
MLL2	NM_003482	12q12-q13
MLL3	NM_170606	7q36
MLST8	NM_022372	16p13.3
MPL	NM_005373	1p34
MSH2	NM_000251	2p21
MSH6	NM_000179	2p16
mTOR	NM_004958	1p36
MYB	NM_005375	6q22-q23
MYC	NM_002467	8q24
MYCL1	NM_005376	1p34.3
MYCN	NM_005378	2p24.3
NCOA2	NM_006540	8q13
NF1	NM_000267	17q11.2
NF2	NM_000268	22q12.2
NFE2L2	NM_006164	2q31

NFKB1	NM_003998	4q24
NFKB2	NM_002502	10q24
NKX2-1	NM_003317	14q13.3
NOTCH1	NM_017617	9q34.3
NOTCH2	NM_024408	1p13-p11
NOTCH3	NM_000435	19p13.2-p13.1
NOTCH4	NM_004557	6p21.3
NPM1	NM_002520	5q35.1
NRAS	NM_002524	1p13.2
NTRK1	NM_002529	1q21-q22
NTRK2	NM_006180	9q22.1
NTRK3	NM_002530	15q24-q25
PAK7	NM_020341	20p12
PARK2	NM_004562	6q25.2-q27
PARP1	NM_001618	1q41-q42
PAX5	NM_016734	9p13.2
PBRM1	NM_018165	3p21
PDGFRA	NM_006206	4q12
PDGFRB	NM_002609	5q33.1
PHOX2B	NM_003924	4p13
PIK3C2G	NM_004570	12p12
PIK3CA	NM_006218	3q26.3
PIK3CB	NM_006219	3q21-qter
PIK3CD	NM_005026	1p36.2
PIK3CG	NM_002649	7q22
PIK3R1	NM_181504	5q13.1
PIK3R2	NM_005027	19q13.2-q13.4
PIK3R3	NM_003629	1p34.1
PKM2	NM_002654	15q22-qter
PLK2	NM_006622	5q12.1-q13.2
PNRC1	NM_006813	6q16.1
PREX2	NM_024870	8q13.1
PRKAR1A	NM_002734	17q23-q24
PRKCI	NM_002740	3q26.3
PTCH1	NM_000264	9q22.1-q31
PTEN	NM_000314	10q23
PTPN11	NM_002834	12q24.1
PTPRD	NM_002839	9p24.1-p23
PTPRS	NM_002850	19p13.3
RAF1	NM_002880	3p25
RARA	NM_000964	17q21.1
RB1	NM_000321	13q14.2
REL	NM_002908	2p13-p12
RET	NM_020630	10q11.2
RICTOR	NM_152756	5p13.1
RPTOR	NM_020761	17q25.3
RUNX1	NM_001754	21q22.3
SDHB	NM_003000	1p36.1-p35
SETD2	NM_014159	3p21.31
SHQ1	NM_018130	3p13
SMAD4	NM_005359	18q21.1
SMARCA4	NM_003072	19p13.3

SMARCB1	NM_003073	22q11.23
SMO	NM_005631	7q32.1
SOCS1	NM_003745	16p13.13
SOX2	NM_003106	3q26.3-q27
SPOP	NM_003563	17q21.33
SRC	NM_005417	20q12-q13
STK11	NM_000455	19p13.3
SUFU	NM_016169	10q24.32
TBK1	NM_013254	12q14.2
TEK	NM_000459	9p21
TERT	NM_198253	5p15.33
TET1	NM_030625	10q21
TET2	NM_017628	4q24
TGFBR2	NM_003242	3p22
TMPRSS2	NM_005656	21q22.3
TNFAIP3	NM_006290	6q23-q25
TOP1	NM_003286	20q12-q13.1
TP53	NM_000546	17p13.1
TP63	NM_003722	3q27-q29
TSC1	NM_000368	9q34
TSC2	NM_000548	16p13.3
TSHR	NM_000369	14q24-q31
VHL	NM_000551	3p25.3
WT1	NM_000378	11p13
YAP1	NM_006106	11q13
YES1	NM_005433	18p11.31-p11.21

Table 3. List of all mutations detected by IMPACT assays in individual patient samples.

Gene	Pt	Chr	Genomic Coordinates (GRCh37)	REF	ALT	AA Change	Effect	Transcript ID	Allele Freq %
VHL	Pt 1	3	10183811	G	T	E94*	Nonsense	NM_000551	22
PBRM1	Pt 1	3	52621444	T	A	E991D	Missense	NM_018165	24
PHOX2B	Pt 1	4	41750569	C	A	G20V	Missense	NM_003924	13
NFKB1	Pt 1	4	103527732	T	C	L611P	Missense	NM_003998	16
NFKB1	Pt 1	4	103527768	C	T	A623V	Missense	NM_003998	17
TSC1	Pt 1	9	135786937	G	-	P311fs	Frameshift	NM_000368	22
VHL	Pt 2	3	10188200	C	A	H115N	Missense	NM_000551	61
TP53	Pt 2	17	7577120	C	T	R273H	Missense	NM_000546	59
JAK1	Pt 2	1	65344709	C	-	R110fs	Frameshift	NM_002227	24
IGF1R	Pt 2	15	99467158	-	C	S847fs	Frameshift	NM_000875	37
BAP1	Pt 3	3	52440393	C	A	Splice e9-1	Splice Site	NM_004656	15
VHL	Pt 3	3	10191641	GA	-	G212	Frameshift	NM_000551	12
mTOR	Pt 3	1	11182179	G	T	Q2223K	Missense	NM_004958	15
MLL3	Pt 3	7	151878766	A	G	V2060A	Missense	NM_170606	14
VHL	Pt 5	3	10188210	T	C	L118P	Missense	NM_000551	34
PBRM1	Pt 5	3	52595895	TCACTG CTGAA	-	E1360fs	Frameshift	NM_018165	22
ATM	Pt 5	11	108143312	T	-	N1044fs	Frameshift	NM_000051	23
DAXX	Pt 6	6	33286886	G	A	T684M	Missense	NM_001350	40
KEAP1	Pt 6	19	10610405	G	A	S102L	Missense	NM_012289	41

Table 4. WEC sequencing for patients #5 and #6. (**a**) WEC run statistics. (**b**) WEC mutation detection statistics. (**c**) List of all mutations identified by WEC.

(a)

SAMPLE	TOTAL READS	PF UQ BASES ALIGNED	PCT SELECTED BASES	MEAN TARGET COVERAGE	PCT USABLE BASES ON TARGET	PCT TARGET BASES 2X	PCT TARGET BASES 10X	PCT TARGET BASES 20X	PCT TARGET BASES 30X
Pt 5 (N)	70,182,339	5,123,974,440	99.14%	81.62	80.41%	96.54%	91.96%	86.08%	79.47%
Pt 5 (T)	54,314,779	3,920,678,104	99.18%	63.22	81.17%	95.86%	89.77%	81.73%	72.13%
Pt 6 (N)	77,253,432	5,659,907,427	99.20%	89.00	79.34%	96.39%	91.70%	86.10%	80.08%
Pt 6 (T)	93,018,700	6,812,455,829	99.21%	107.21	79.48%	96.67%	92.90%	88.33%	83.49%

(b)

Sample	Pt 5	Pt 6
DOWNSTREAM	5333	7000
INTERGENIC	2449	2853
INTRON	34314	42840
NON_SYNONYMOUS_CODING	14711	17479
NON_SYNONYMOUS_START	0	0
SPLICE_SITE_ACCEPTOR	48	49
SPLICE_SITE_DONOR	65	80
START_GAINED	185	237
START_LOST	18	17
STOP_GAINED	265	300
STOP_LOST	167	207
SYNONYMOUS_CODING	6262	7901
SYNONYMOUS_START	0	1
SYNONYMOUS_STOP	12	15
UPSTREAM	816	1135
UTR_3_PRIME	3044	4090
UTR_5_PRIME	790	1050
Raw SNP Count	65926	81611
dbSNP	62134	75714

(c)

Gene	Pt ID	Chr	Genomic Coordinates (GRCh37)	REF	ALT	AA Change	Effect	Transcript.ID	Allele Freq %
AKR7A3	Pt 5	1	19611604	A	T	M/K	Missense	NM_012067	27
SLC35A3	Pt 5	1	100487952	C	T	L/F	Missense	NM_012243	21
TROVE2	Pt 5	1	193053996	GA	G	.	Frameshift	NR_033393	20
CAD	Pt 5	2	27455316	C	G	S/R	Missense	NM_004341	31
OXER1	Pt 5	2	42990229	T	A	H/L	Missense	NM_148962	38
RANBP2	Pt 5	2	109381202	A	T	N/Y	Missense	NM_006267	17
ZNF717	Pt 5	3	75786760	TC	T	.	Frameshift	NM_001128223	18
ATP6V1G2-DDX39B	Pt 5	6	3023942	T	C	K/E	Missense	NR_037853	25
ABCF1	Pt 5	6	30553045	T	C	F/S	Missense	NM_001025091	26
ALDH8A1	Pt 5	6	135250302	T	C	S/G	Missense	NM_001193480	24
JARID2	Pt 5	6	15501569	GA	G	.	Frameshift	NM_004973	23
NEUROD6	Pt 5	7	31378243	G	A	P/S	Missense	NM_022728	24
TOPORS	Pt 5	9	32542010	T	C	N/S	Missense	NM_001195622	27
HABP4	Pt 5	9	99250524	G	A	A/T	Missense	NM_014282	28
PBLD	Pt 5	10	70044010	A	T	I/N	Missense	NM_022129	24
FAM171A1	Pt 5	10	15256214	TG	T	.	Frameshift	NM_001010924	22
ATM	Pt 5	11	108143312	AT	A	.	Frameshift	NM_000051	32
KLF5	Pt 5	13	73649885	G	T	W/L	Missense	NM_001730	30
ANKRD20A9P	Pt 5	13	19415894	C	CA	.	Frameshift	NR_027995	17
MIR1197	Pt 5	14	101491918	GA	G	.	Frameshift	NR_031713	29
PLA2G15	Pt 5	16	68293469	T	G	L/W	Missense	NM_012320	22
ITGA3	Pt 5	17	48156815	C	A	P/Q	Missense	NM_002204	31
TMX4	Pt 5	20	7963023	G	A	R/W	Missense	NM_021156	31
C20orf118	Pt 5	20	35515885	T	A	F/I	Missense	NM_080628	21
TSHZ2	Pt 5	20	51871927	A	T	K/*	Nonsense	NM_001193421	25

KIF17	Pt 6	1	21014104	C	A	R/M	Missense	NM_001122819	33
AGL	Pt 6	1	100379220	A	G	K/E	Missense	NM_000028	36
IGSF8	Pt 6	1	160063808	G	T	A/E	Missense	NM_001206665	37
PRG4	Pt 6	1	186278230	A	T	R/*	Nonsense	NM_001127708	33
FBXO2	Pt 6	1	11710779	C	CGCG	A/AP	Frameshift	NM_012168	50
WDR54	Pt 6	2	74650637	A	G	S/G	Missense	NM_032118	40
STAMBP	Pt 6	2	74087188	CT	C	.	Frameshift	NM_006463	36
PVRL3	Pt 6	3	110830925	G	A	W/*	Nonsense	NM_001243286	41
ISY1	Pt 6	3	128853674	C	G	.	Splice Site	NM_020701	25
ISY1-RAB43	Pt 6	3	128853675	G	T	L/I	Missense	NM_001204890	24
C3orf25	Pt 6	3	129121412	T	C	K/E	Missense	NM_207307	38
SI	Pt 6	3	164697187	A	C	V/G	Missense	NM_001041	33
COL7A1	Pt 6	3	48618050	CT	C	.	Frameshift	NM_000094	37
DCP1A	Pt 6	3	53326687	TA	T	.	Frameshift	NM_018403	42
PARP14	Pt 6	3	122419572	T	TAC	.	Frameshift	NM_017554	34
PPEF2	Pt 6	4	76797687	G	T	P/H	Missense	NM_006239	34
DAB2	Pt 6	5	39388912	T	C	K/E	Missense	NM_001244871	37
SSBP2	Pt 6	5	80756906	T	C	R/G	Missense	NM_012446	42
NMUR2	Pt 6	5	151784319	C	T	C/Y	Missense	NM_020167	41
TAP1	Pt 6	6	32821452	G	A	P/S	Missense	NM_000593	29
DAXX	Pt 6	6	33286886	G	A	R/*	Nonsense	NR_024517	44
FTSJD2	Pt 6	6	37419624	G	A	E/K	Missense	NM_015050	41
STL	Pt 6	6	125231574	A	T	Y/N	Missense	NR_026876	32
GTPBP10	Pt 6	7	90012289	A	C	E/A	Missense	NM_001042717	34
SSPO	Pt 6	7	149487383	GC	G	.	Frameshift	NM_198455	47
VCPIP1	Pt 6	8	67577332	T	A	N/I	Missense	NM_025054	35
TJP2	Pt 6	9	71827506	A	T	T/S	Missense	NM_001170414	42
ODF2	Pt 6	9	131256871	A	G	E/G	Missense	NM_001242352	47
NOXA1	Pt 6	9	140327502	G	C	G/R	Missense	NM_006647	32
GAD2	Pt 6	10	26505757	G	A	G/S	Missense	NM_000818	39
ZNF33A	Pt 6	10	38345237	A	G	I/V	Missense	NM_006954	36

MCU	Pt 6	10	74644033	T	C	Y/H	Missense	NM_138357	34
P4HA1	Pt 6	10	74828612	T	C	N/S	Missense	NM_000917	40
KIAA0913	Pt 6	10	75554386	T	C	V/A	Missense	NM_001242487	38
ECHS1	Pt 6	10	135179536	T	G	K/T	Missense	NM_004092	40
AGAP4	Pt 6	10	46342676	CA	C	.	Frameshift	NM_133446	33
IFIT5	Pt 6	10	91178337	G	GT	.	Frameshift	NM_012420	32
NAP1L4	Pt 6	11	2972543	T	G	E/D	Missense	NM_005969	41
SPON1	Pt 6	11	14276269	C	G	P/R	Missense	NM_006108	25
SLC22A24	Pt 6	11	62886396	A	G	F/S	Missense	NM_001136506	43
MALAT1	Pt 6	11	65271721	A	T	K/N	Missense	NR_002819	37
MALAT1	Pt 6	11	65271722	A	T	I/F	Missense	NR_002819	37
FAM138D	Pt 6	12	147968	GT	G	.	Frameshift	NR_026823	100
ATP8A2	Pt 6	13	26594101	A	G	K/R	Missense	NM_016529	24
ANKRD20A9P	Pt 6	13	19415894	C	CA	.	Frameshift	NR_027995	11
MIS18BP1	Pt 6	14	45711551	C	G	D/H	Missense	NM_018353	55
NEMF	Pt 6	14	50292663	G	T	S/*	Nonsense	NM_004713	62
TDP1	Pt 6	14	90456086	G	A	R/Q	Missense	NM_001008744	42
SAV1	Pt 6	14	51132213	GA	G	.	Frameshift	NM_021818	53
SPATA5L1	Pt 6	15	45713319	A	G	T/A	Missense	NM_024063	64
SMYD4	Pt 6	17	1715384	T	A	R/*	Nonsense	NM_052928	38
FLJ90757	Pt 6	17	79005261	C	A	R/M	Missense	NR_026857	29
C19orf28	Pt 6	19	3557268	A	G	L/P	Missense	NM_001042680	37
KEAP1	Pt 6	19	10610405	G	A	S/L	Missense	NM_012289	36
KLK9	Pt 6	19	51509963	G	A	L/F	Missense	NM_012315	33
NLRP12	Pt 6	19	54313633	G	C	T/R	Missense	NM_144687	44
SLC9A8	Pt 6	20	48461621	C	A	P/T	Missense	NM_015266	31
SON	Pt 6	21	34927665	G	A	R/Q	Missense	NM_032195	41
PI4KA	Pt 6	22	21119924	G	A	R/*	Nonsense	NM_058004	35
POM121L8P	Pt 6	22	21649094	AC	A	.	Frameshift	NR_024583	25
TLR8	Pt 6	X	12938246	T	G	F/V	Missense	NM_138636	38
CYBB	Pt 6	X	37665639	G	T	.	Splice Site	NM_000397	32

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Table 5. Summary of oncogenomic findings in patients #1 to #6. CNA: copy number alteration; Chr: chromosome

Patient		Oncongenomic Findings					Proposed Mechanism *for repalog-sensitivity*
1			R1	R2	R3		**Functional loss of Tscl**
	P13K/Akt/MTOR pathway alterations:	Somatic mutations:					
		TSCI frameshift (P311fs*4)	X	X			
		TSCI nonsense (Q527*)			X		
		CNA:					
		Heterozygous loss of Chr 9	X	X	X		
	Other pertinent genomic alterations:	**Somatic mutations:**					
		VHL Nonsense (E94*)	X	X	X		
		PBRMI Missense (E991D)	X	X	X		
		CNA:					
		Heterozygous loss of Chr 3p	X	X	X		
2			R1	R2	R3	M1	**Functional loss of Tscl**
	P13K/Akt/MTOR pathway alterations	Somatic mutations:					
		TSCI Frameshift (1580fs*7)	X	X	X	X	
		CNA:					
		Heterozygous loss of Chr 9	X	X	X	X	
	Other pertinent genomic alterations:	**Somatic mutations:**					
		VHL Misssense (H115N)	X	X	X	X	
		TP53 Missense (R273H)	X	X	X	X	
		CNA:					
3			R1	R2	R3	R4	**Hyperactive MTOR/ Functional loss of Tscl**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**					
		MTOR missense (Q2223K)	x	x	x		
		TSCI nonsense (Q781*)			x	x	
		CNA:					
		Heterozygous loss of Chr 9			x	x	
	Other pertinent genomic alterations:	**Somatic mutations:**					
		VHL frameshift (G212fs)					
		BAPI splice (g220_splice)	x	x	x		
		BAPI splice (Q85_splice)			x	x	
		CNA:					
		Heterozygous loss of Chr 3p					
4			T1	T2			**Functional loss Tsc2**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**					
		TSC2 frameshift (Q794*)		X			
		CNA:					
		Homozygous loss of TSC2	X				
		Heterozygous loss of TSC2		X			
	Other pertinent genomic alterations:						
		Somatic mutations:					
		none					
		CNA:					
		None					
5			R1	M1			**Unclear**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**					
		none					
		CNA:					
		None					

	Other pertinent genomic alterations:	**Somatic mutations:**				
		VHL missense (L118P)	X	X		
		PBRMI frameshift (E1360fs)	X	X		
		CNA:				
		Heterozygous loss of Chr 3p	X	X		
6			**R1**			**Unclear**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**				
		none				
		CNA:				
		None				
	Other pertinent genomic alterations:	**Somatic mutations:**				
		none				
		CNA:				
		None				
7			**R1**			**N/A**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**				
		none				
		CNA:				
		Heterozygous loss of Chr 9	X			
	Other pertinent genomic alterations:	**Somatic mutations:**				
		none				
		CNA:				
		Heterozygous loss of Chr 9	X			
8		**Somatic mutations**	**R1**			**N/A**
	P13K/Akt/MTOR pathway alterations:	MTOR missense (E919V)	X			
		CNA:				
		Heterozygous loss of Chr 9q	X			
	Other pertinent genomic alterations:	**Somatic mutations:**				
		VHL missense (S65L)	X			
		BAP1 splice (e6-1)	X			
		PBRM1 splice (e5-2)	X			
		SETD2 frameshift (E2477fs)	X			
		CNA:				
		Heterozygous loss of Chr 3p	X			
9			**R1**			**N/A**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**				
		TSC2 missense (1475F)	x			
		CNA:				
	Other pertinent genomic alterations:	**Somatic mutations:**				
		None				
		CNA:				
		MAP2K1 amplification	X			
10			**R1**			**N/A**
	P13K/Akt/MTOR pathway alterations:	**Somatic mutations:**				
		PTEN missense (F2001)	X			
		CNA:				
		None				
	Other pertinent genomic alterations:	**Somatic mutations:**				
		None				
		CNA:				
		PDGFRA, KIT amplification	X			

TABLE 6. *mTOR* mutations in clear cell renal cell carcinoma from the TCGA.

ID	Amino Acid	Nucleotide	Genome Start GRCh37	Genome End GRCh37	Source/PUBMED ID
TCGA-AK-3429	G5R	c.13G>C	11319454	11319454	TCGA
TCGA-B0-5119	K860N	c.2580G>C	11291426	11291426	TCGA
TCGA-BP-5001	L1433S	c.4298T>C	11227530	11227530	TCGA
TCGA-CZ-5987	K1452N	c.4356A>C	11217322	11217322	TCGA
TCGA-BP-5176	A1459P	c.4375G>C	11217303	11217303	TCGA
TCGA-B0-5701	L1460P	c.4376T>C	11217299	11217299	TCGA
TCGA-BP-5175	L1460P	c.4376T>C	11217299	11217299	TCGA
TCGA-B0-5697	Y1463S	c.4388A>C	11217290	11217290	TCGA
TCGA-B0-5696	C1483Y	c.4448G>A	11217230	11217230	TCGA
TCGA-CJ-6027	A1519T	c.4555G>A	11210198	11210198	TCGA
TCGA-B0-4846	F1888I	c.5662T>A	11189847	11189847	TCGA
TCGA-CZ-4857	F1888L	c.5662T>C	11189847	11189847	TCGA
TCGA-CZ-4866	F1888L	c.5662T>C	11189847	11189847	TCGA
TCGA-B0-5100	I1973F	c.5917A>T	11188177	11188177	TCGA
TCGA-B0-4827	T1977K	c.5919C>A	11188164	11188164	TCGA
TCGA-CJ-4644	V2006L	c.6016G>C	11188078	11188078	TCGA

Active 15269048.1

TCGA-B0-4852	E2033V	c.6098A>T	11187799	11187799	TCGA
TCGA-B0-4810	A2210P	c.6628G>C	11184589	11184589	TCGA
TCGA-CJ-5679	S2215F	c.6644C>A	11184573	11184573	TCGA
TCGA-CJ-4887	L2230V	c.6688T>G	11182158	11182158	TCGA
TCGA-A3-3347	M2327I	c.6981G>A	11177096	11177096	TCGA
TCGA-B0-5691	L2334V	c.7000T>G	11177077	11177077	TCGA
TCGA-CW-5580	I2500M	c.7500T>G	11169375	11169375	TCGA

TABLE 7. **Primers.** Primers for PCR-mutagenesis are:

Mutation	Primer Sequence
K860N	GAG CCC TAC AGG AAT TAC CCT ACT TTG C
E919V	GTC AGC CTG TCA GTA TCC AAG TCA AGT C
A1105P	CCA GCT GTT TGG CCC CAA CCT GGA TGA C
L1443S	GCG GCC GGA GTG TCA GAA TAT GCC ATG AAA C
A1459P	CAC GAG TGG GAG GAT CCC CTT GTG GCC TAT G
L1460P	GTG GGA GGA TGC CCC TGT GGC CTA TGA CAA G
C1483F	GGG CCG CAT GCG CTT CCT CGA GGC CTT GGG
E1799K	GCA GTG ATG AAC TTC AAA GCT GTG CTA CAC
F1888I	CTG CCG TCC AGG GCA TCT TCC GTT CCA TCT C
F1888L	GCC GTC CAG GGC TTG TTC CGT TCC ATC TCC
F1888V	CTG CCG TCC AGG GCG TCT TCC GTT CCA TCT C
I1973F	CCC CCA GGC CCT CTT CTA CCC ACT GAC AG
T1977K	CAT CTA CCC ACT GAA AGT GGC TTC TAA GTC
V2006L	CAC AGC AAC ACC CTG CTC CAG CAG GCC ATG
S2215F	CCA ATG ACC CAA CAT TTC TTC GGA AAA ACC
L2220F	CAT CTC TTC GGA AAA ACT TCA GCA TCC AGA G
Q2223K	GGA AAA ACC TCA GCA TCA AGA GAT ACG CTG TC
I2228T	GAG ATA CGC TGT CAC CCC TTT ATC GAC C
L2230V	CGC TGT CAT CCC TGT ATC GAC CAA CTC GG
M2327I	GTT CTT TAG CGG TCA TAT CAA TGG TTG GG
V2406A	CAC AGT GAT GGA GGC GCT GCG AGA GCA C
L2431P	GCT GAA CTG GAG GCC GAT GGA CAC AAA TAC C
R2505P	GAT TAT TAA CAG GGT TCC AGA TAA GCT CAC TGG

8. EXAMPLE: PROPERTIES OF mTOR MUTANTS ASSOCIATED WITH THERAPEUTIC RESPONSE TO RAPALOGS

Various experiments were performed to explore the properties of
5 identified mTOR mutants.

To test the ability of cells carrying mTOR mutations to grow in serum-depleted conditions, Hela cells, transfected with Flag-mTOR constructs bearing various mutations, were cultured either without serum (-) or in the presence of 10% serum (+) for 1 hour. Cellular lysates were then subjected to immunoblot analysis to
10 assess phosphorylation of S6K as a measure of mTOR activity. As shown in FIGURE 24, mTOR mutants associated with therapeutic response to rapalogs were found to be more resistant to serum than wild-type mTOR.

Experiments were then performed to test the effect of an AKT inhibitor on the activity of mTOR mutants. Hela cells, transfected with Flag-mTOR constructs
15 carrying various mTOR mutations, were cultured in medium with (+) or without (-) 1 μM MK2206, an AKT inhibitor for 2 hours. Cellular lysates were then subjected to immunoblot analysis analysis to assess phosphorylation of S6K as a measure of mTOR activity. As shown in FIGURE 25, mTOR mutants associated with therapeutic response to rapalogs were found to be more resistant to AKT inhibitor
20 than wild-type mTOR.

The ability of rapamycin and INK128 to inhibit activity of the mTOR mutants was also tested. Transfected Hela cells expressing various mTOR mutants were cultured in medium with (+) or without (-) 25 nM rapamycin or 100 nM INK128 for 2 hours. Cellular lysates were then subjected to immunoblot analysis analysis to
25 assess phosphorylation of S6K as a measure of mTOR activity. As shown in FIGURE 26, mTOR mutants associated with therapeutic response to rapalogs were found to be senstive to rapamycin or to INK128, an ATP-competitive inhibitor of mTORC1 and mTORC2.

9. EXAMPLE: SYNERGISTIC EFFECT OF DOUBLE
30 MUTATION

The effect of concurrent mutations F188L and L2230V on mTOR activity, as reflected by phosphorylation of S6K, was evaluated. In experiments analogous to those described in the preceding section, cells expressing single or double mTOR mutants were prepared. FIGURE 27A depicts the level of

phosphorylation of S6K in the presence of single F1881L and L2230V mutations. FIGURE 27B depicts phosphorylation of S6K where both mutations are present (other single mutants shown for comparison), where phosphorylation levels were substantially higher in the double-mutant mTOR expressing cells. This higher level
5 of mTOR activity was further demonstrated by resistance to serum depletion (FIGURE 27C) and was even observed when cells were cultured in phosphate buffered saline (FIGURE 27D), indicative of a high level of activity.

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Various publications and nucleic acid and amino acid sequence accession numbers are cited herein, the contents and full sequences of which are hereby incorporated by reference herein in their entireties.

WHAT IS CLAIMED IS:

1. A method of producing an anti-cancer effect in a cancer, comprising determining whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where 5 the cancer is renal cell carcinoma, supependymal giant cell astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma, and, where a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is present, administering a therapeutically 10 effective amount of a rapamycin analog to produce an anti-cancer effect.

2. The method of claim 1, where the cancer is renal cell carcinoma.

3. The method of claim 1, where the presence of a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid sequencing.

15 4. The method of claim 3, where nucleic acid complementary to a TSC1 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

5. The method of claim 1, where the biomarker is a mTOR biomarker.

6. The method of claim 5, where the biomarker is Q2223K.

20 7. The method of claim 5, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; 25 increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTORl and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

8. The method of claim 5, where the biomarker is a mutation in one or more residue of amino acid residues 2182-2516 of the amino acid sequence of human 30 mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased

resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

9. The method of claim 5, where the biomarker is selected from the group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I,
5 L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V and K860N.

10. A method of determining whether an anti-cancer effect is likely to be produced in a cancer by a rapamycin analog, comprising determining whether cells of
10 the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where the cancer is renal cell carcinoma, supependymal giant cell astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell
15 lymphoma, or melanoma, where if the TSC1, TSC2, and/or mTOR biomarker is present, it is more likely that a rapamycin analog would have an anti-cancer effect on the cancer.

11. The method of claim 10, where the cancer is renal cell carcinoma.

12. The method of claim 10, where the presence of a TSC1 biomarker, a
20 TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid sequencing.

13. The method of claim 12, where nucleic acid complementary to a TSC1 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

25 14. The method of claim 10, where the biomarker is a mTOR biomarker.

15. The method of claim 14, where the biomarker is Q2223K.

16. The method of claim 14, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity.
30 as indicated by as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR;, and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

17. The method of claim 14, where the biomarker is a mutation in one or more residue of amino acid residues 2182-2516 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by one or more of the following indicators: an increase in
5 phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR,; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

18. The method of claim 14, where the biomarker is selected from the
10 group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F,C1483Y, L1460P, A1459P, L1433S, A1105P, E919V and K860N.

19. A method of treating a subject suffering from a cancer, comprising
15 determining whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof,

where the cancer is renal cell carcinoma, supependymal giant cell astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's
20 lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma, and,

where a TSC1 biomarker, a TCS2 biomarker, and/or a mTOR biomarker is present, treating the subject with a therapeutically effective amount of a rapamycin analog, but

where a TSC1, TSC2 or mTOR biomarker is not present, the subject is not
25 treated with a rapamycin analog but treatment with another modality, for example an alternative chemotherapeutic agent, biologic anticancer agent, or radiation therapy, is administered..

20. The method of claim 19, where the cancer is renal cell carcinoma.

21. The method of claim 19, where the presence of a TSC1 biomarker, a
30 TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid sequencing.

22. The method of claim 21, where nucleic acid complementary to a TSC1 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

23. The method of claim 19, where the biomarker is a mTOR biomarker.

24. The method of claim 23, where the biomarker is Q2223K.

25. The method of claim 23, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR;and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

26. The method of claim 23, where the biomarker is a mutation in one or more residue of amino acid residues 2182-2516 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

27. The method of claim 23, where the biomarker is selected from the group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V and K860N.

28. A method of determining whether an anti-cancer effect is likely to be produced in a cancer by a rapamycin analog, comprising obtaining a sample of the cancer, and determining, in the sample, whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where the cancer is renal cell carcinoma, supependymal giant cell astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma, and, where if the TSC1, TSC2, and/or mTOR biomarker is present, it is more likely that a rapamycin analog would have an anti-cancer effect on the cancer.

29. The method of claim 28, where the cancer is renal cell carcinoma.

30. The method of claim 28, where the presence of a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid sequencing.

31. The method of claim 30, where nucleic acid complementary to a TSC1
5 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

32. The method of claim 28, where the biomarker is a mTOR biomarker.

33. The method of claim 32, where the biomarker is Q2223K.

34. The method of claim 32, where the biomarker is a mutation in one or
10 more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased
15 resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

35. The method of claim 32, where the biomarker is a mutation in one or more residue of amino acid residues 2182-2516 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity.
20 as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

25 36. The method of claim 32, where the biomarker is selected from the group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V and K860N.

30 37 A method of treating a subject suffering from a cancer, comprising obtaining a plurality of samples from different locations of cancer in the subject, determining, in each sample, whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where the cancer is renal cell carcinoma, supependymal giant cell

astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma, and, where a TSC1 biomarker, a TCS2 biomarker, and/or a mTOR biomarker is present in a sample
5 or a plurality of the samples or in all of the samples, treating the subject with a therapeutically effective amount of a rapamycin analog.

38. The method of claim 37, where the cancer is renal cell carcinoma.

39. The method of claim 37, where the presence of a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid
10 sequencing.

40. The method of claim 39, where nucleic acid complementary to a TSC1 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

41. The method of claim 37, where the biomarker is a mTOR biomarker.

15 42. The method of claim 41, where the biomarker is Q2223K.

43. The method of claim 41, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by as indicated by one or more of the following indicators: an increase in
20 phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

44. The method of claim 41, where the biomarker is a mutation in one or
25 more residue of amino acid residues 2182-2516 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased
30 resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

45. The method of claim 41, where the biomarker is selected from the group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I,

F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V and K860N.

46 A method of treating a subject suffering from a cancer, comprising obtaining a plurality of samples from different locations of cancer in the subject, determining, in each sample, whether cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, where the cancer is renal cell carcinoma, supependymal giant cell astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma, and, where one or more of the samples does not contain a TSC1, TSC2 or mTOR biomarker, the subject is not treated with a rapamycin analog but treatment with another modality, for example an alternative chemotherapeutic agent, biologic anticancer agent, or radiation therapy, is administered.

47. The method of claim 46, where the cancer is renal cell carcinoma.

48. The method of claim 46, where the presence of a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid sequencing.

49. The method of claim 48, where nucleic acid complementary to a TSC1 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

50. The method of claim 46, where the biomarker is a mTOR biomarker.

51. The method of claim 50, where the biomarker is Q2223K.

52. The method of claim 50, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

53. The method of claim 50, where the biomarker is a mutation in one or more residue of amino acid residues 2182-2516 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity.

as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be
5 inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

54. The method of claim 50, where the biomarker is selected from the group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P,
10 L1433S, A1105P, E919V and K860N.

55. A rapamycin analog, for use in producing an anti-cancer effect in a cancer, where cells of the cancer contain a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof, and where the cancer is renal cell carcinoma, supependymal giant cell astrocytoma,
15 hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma,

56. The rapamycin analog of claim 55, where the cancer is renal cell carcinoma.

20 57. The rapamycin analog of claim 55, where the presence of a TSC1 biomarker, a TSC2 biomarker, and/or a mTOR biomarker is determined by nucleic acid sequencing.

58. The rapamycin analog of claim 57, where nucleic acid complementary to a TSC1 gene, a TSC2 gene, and/or a gene encoding a mTOR biomarker is
25 amplified and the amplified nucleic acid is subjected to nucleic acid sequencing.

59. The rapamycin analog of claim 55, where the biomarker is a mTOR biomarker.

60. The rapamycin analog of claim 59, where the biomarker is Q2223K.

61. The rapamycin analog of claim 59, where the biomarker is a mutation
30 in one or more residue of amino acid residues 1382-1982 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to

wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

62. The rapamycin analog of claim 59, where the biomarker is a mutation in one or more residue of amino acid residues 2182-2516 of the amino acid sequence of human mTOR set forth in NCBI Accession No. NP_004949 which increases mTOR activity. as indicated by one or more of the following indicators: an increase in phosphporylation of S6K, for example at residue T389, relative to wild type mTOR; increased growth in serum-depleted medium relative to wild type mTOR; increased resistance to AKT inhibition relative to wild type mTOR; and/or the ability to be inhibited by (that is to say, sensitivity to) rapamycin and/or INK128.

63. The rapamycin analog of claim 55, where the biomarker is selected from the group of mutations consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V and K860N.

64. A method of producing an anti-cancer effect in a cancer cell carrying a mTOR biomarker which increases mTOR activity, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 and/or amino acid residues 2182-2516, comprising administering, to a subject having a cancer determined to comprise cancer cells carrying said biomarker. an effective amount of an mTOR inhibitor which may be a rapamycin analog or which may not be a rapamycin analog.

65. An mTOR inhibitor for use in producing an anti-cancer effect in a cancer comprising cells which carry a mTOR biomarker which increases mTOR activity, where the biomarker is a mutation in one or more residue of amino acid residues 1382-1982 and/or amino acid residues 2182-2516.

66. A kit for determining whether an anti-cancer effect is likely to be produced in a cancer by a rapamycin analog, comprising a means for detecting a biomarker selected from a TSC1 biomarker, a TSC2 biomarker, a mTOR biomarker, and a combination thereof.

67. The kit of claim 66, comprising one or more of packaged probe and primer sets (e.g. TaqMan probe/primer sets), arrays/microarrays, biomarker-specific antibodies and/or beads.

68. The kit of claim 66, comprising a pair of oligonucleotide primers, suitable for polymerase chain reaction (PCR) or nucleic acid sequencing, for detecting the biomarker(s) to be identified.

69. The kit of claim 66, comprising at least one nucleic acid probe, suitable
5 for in situ hybridization or fluorescent in situ hybridization, for detecting the biomarker(s) to be identified.

70. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting a TSC1 biomarker.

71. The kit of claim 66, comprising a pair of primers or a nucleic acid-
10 containing probe for detecting a TSC2 biomarker.

72. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting a mTOR biomarker.

73. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC1 Q781* biomarker.

15 74. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC1 P311fs*4 biomarker.

75. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC1 I580fs*7 biomarker.

76. The kit of claim 66, comprising a pair of primers or a nucleic acid-
20 containing probe for detecting the TSC1 Q527* biomarker.

77. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC1 S334* biomarker.

78. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC2 Q794* biomarker.

25 79. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC2 R611W biomarker.

80. The kit of claim 66, comprising a pair of primers or a nucleic acid-containing probe for detecting the TSC2 S1498N biomarker.

81. The kit of claim 66, comprising a pair of primers or a nucleic-acid
30 containing probe for detecting a mTOR biomarker having a mutation selected from the group consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V, K860N and a combination thereof.

82. The kit of claim 81, which comprises pairs of primers or probes for detecting more than one mTOR biomarker having a mutation selected from the group consisting of Q2223K, R2505P, L2431P, S2215F, V2406A, M2327I, L2230V, I2228T, L2220F, V2006L, T1977K, I1973F, F1888V, F1888I, F1888L, F1888L in combination with L2230V, C1483F, C1483Y, L1460P, A1459P, L1433S, A1105P, E919V, K860N and a combination thereof.

83. The kit of any of claims 66-82, for use where the cancer is renal cell carcinoma, supependymal giant cell astrocytoma, hormone-receptor positive, HER-2 negative breast cancer, progressive neuroendocrine tumor of pancreatic origin, Hodgkin's lymphoma, non-Hodgkin's lymphoma, endometrial cancer, mantle-cell lymphoma, or melanoma.

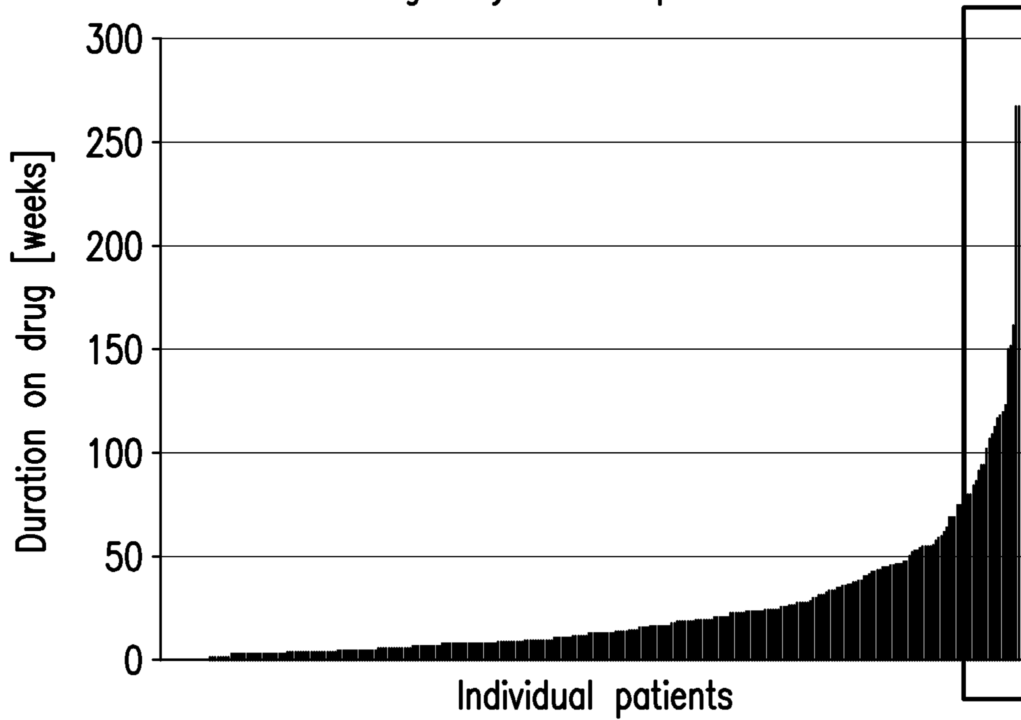


FIG. 1

Patient	Sex	Age	Histologic subtype	Repalog	Duration treatment with rapalog (weeks)	#of metastatic sites	Duration prior treatment with sunitinib	Mutation identified
1	F	58	clear	temsirolimus	117	≥3	60	TSC1
2	F	73	unclassified	temsirolimus	147	1	13	TSC1
3	M	66	clear	everolimus	87	≥3	21	mTOR
4	M	16	unclassified	everolimus	139	1	82	TSC2
5	F	60	clear	temsirolimus	121	≥3	47	NA
6	F	50	unclassified	temsirolimus	126	≥3	9	NA

FIG. 2A

7	papillary	1	≥3	T	1	<1	17 (sorafenib)	
8	clear	1	≥3	E	2	2	2 (sunitinib)	
9	chromophobe	1	2	T	2	3	6 (sunitinib+bev)	
11	chromophobe	1	2	E	1	1	5 (sunitinib)	

FIG. 2B

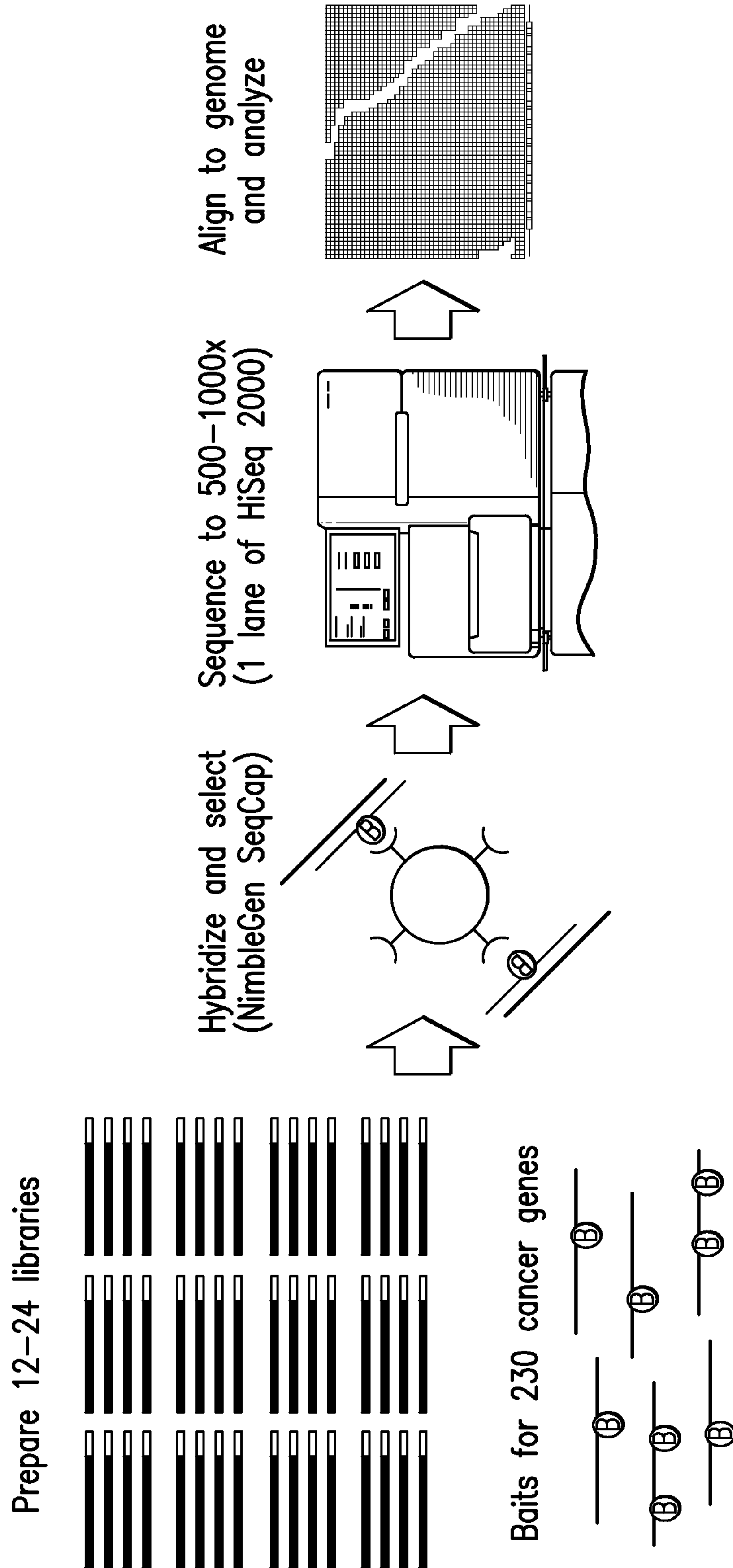


FIG. 3A

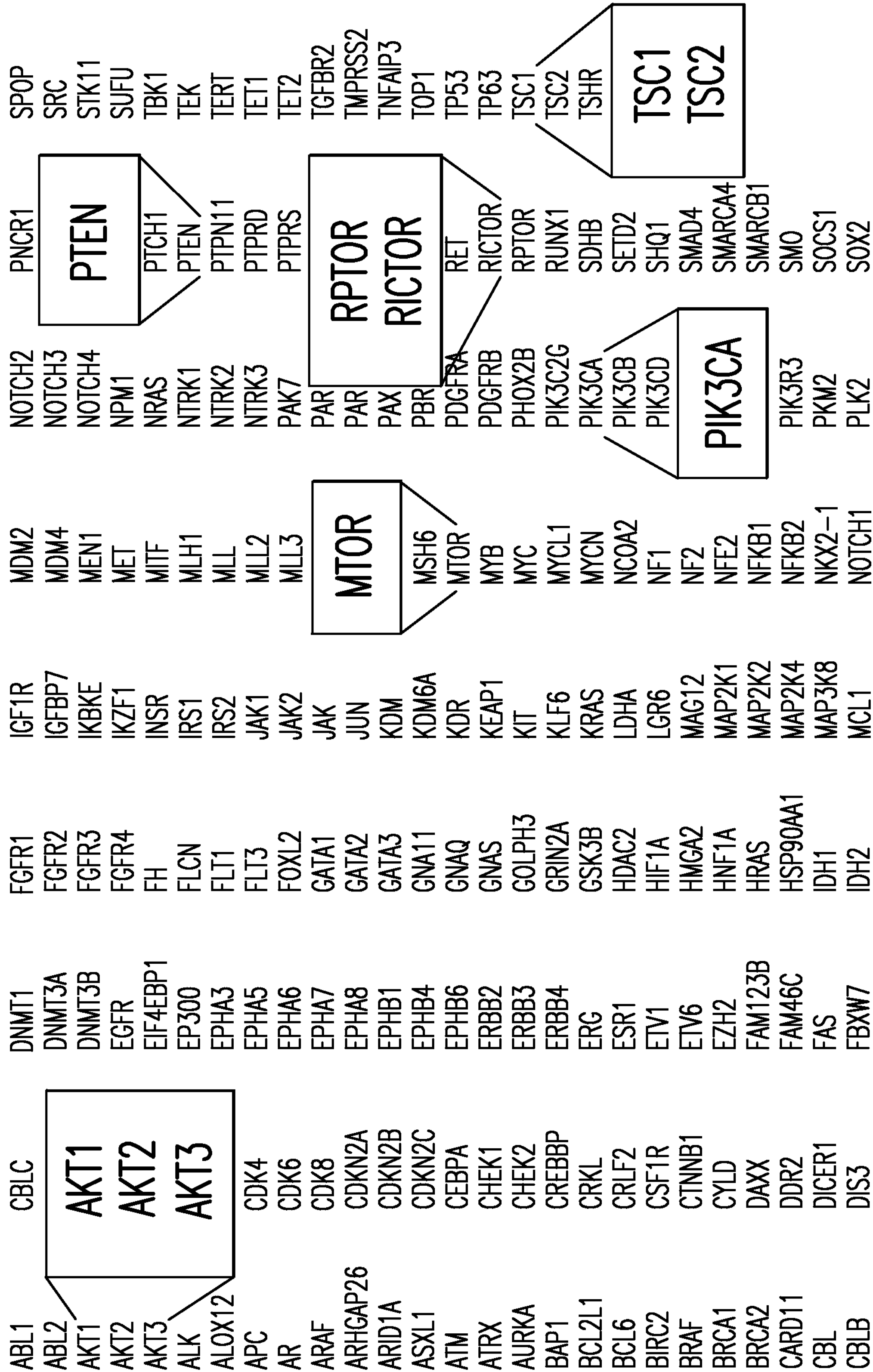


FIG. 3B

	Histologic subtype	mTORi (months)	Relevant Mutations	Relevant CNA	Functional effect on mTOR pathway
1	clear	T (27)	TSC1 Frameshift	Het del Chr 9	LOF TSC1
2	unclassified	T (34)	TSC1 Frameshift	Het del Chr 9	LOF TSC1
3	clear	E (20)	mTOR Missense	–	GOF mTOR
4	unclassified	E (36+)	–	Hom del TSC2	LOF TSC2
5	clear	T (28)	–	–	–
6	unclassified	T (33+)	–	–	–

mTORi: mTOR inhibitor
CNA: copy number alteration
E: everolimus
T: temsirolimus
Hom del: homozygous deletion

Chr: chromosome
LOF: loss of function
GOF: gain of function
Ampl: amplification
Het del: heterozygous deletion

FIG. 4

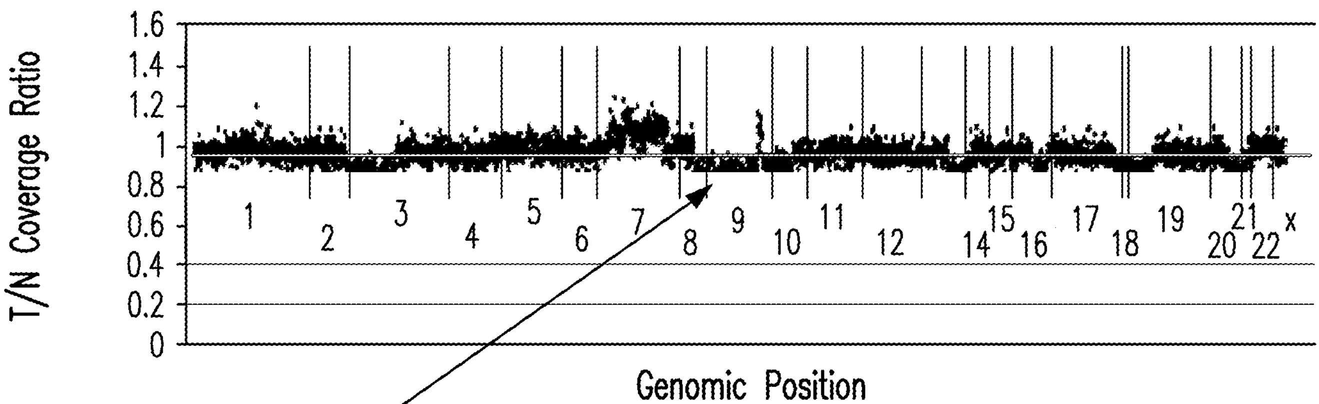


FIG. 5A

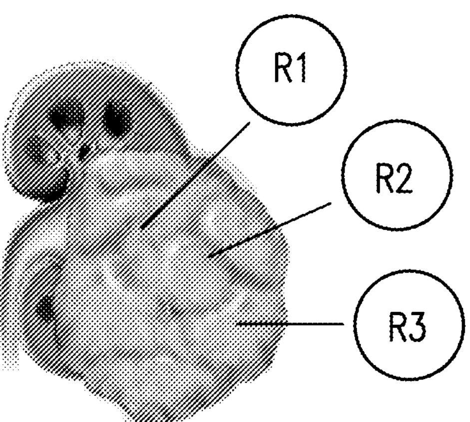


FIG. 5B

Chr	Gene	Protein	R1	R2	R3
3	VHL	p.E94*	0.22	0.25	0.28
3	PBRM1	p.E991D	0.24	0.22	0.26
4	PHOX2B	p.G20V	0.13	0.02	0
4	NFKB1	p.L611P	0.16	0.17	0.18
4	NFKB1	p.A623V	0.17	0.16	0.19
9	TSC1	p.P311fs	0.22	0.22	0
9	TSC1	p.Q527*	0	0	0.20

FIG. 5C

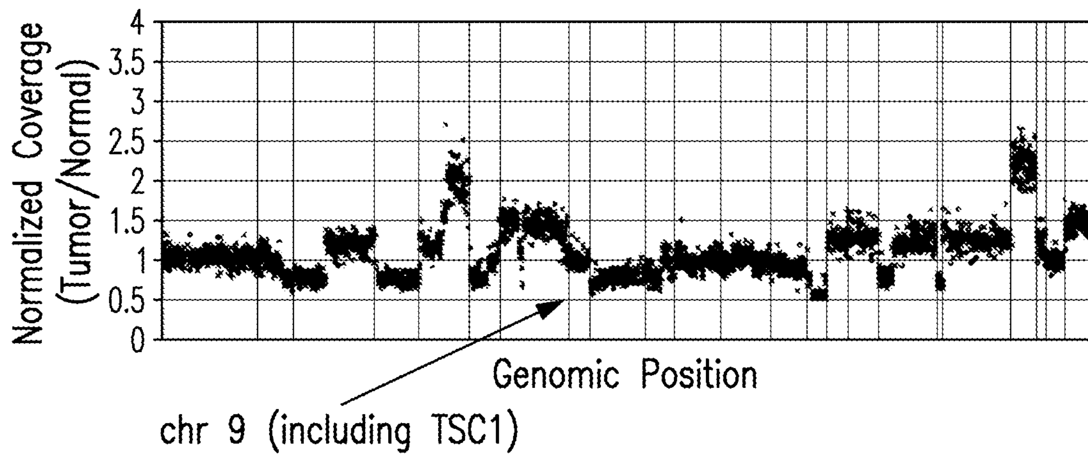


FIG. 6B

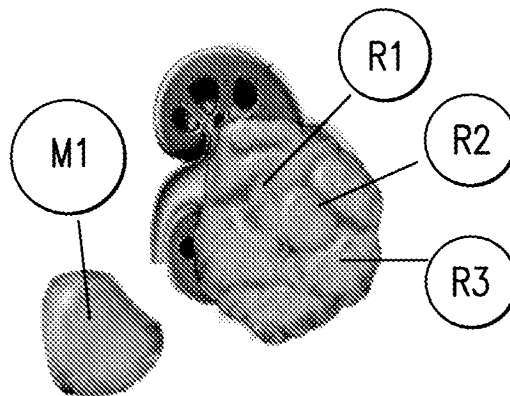


FIG.6C

Chr	Gene	Protein	R1	R2	R3	M1
3	VHL	p.H115N	0.61	0.50	0.30	0.23
17	TP53	p.R273H	0.59	0.52	0.29	0.25
1	JAK1	p.R110fs	0.24	0.22	0.26	0.23
9	TSC1	p.I580fs	0.60	0.44	0.29	0.25
15	IGF1R	p.S847fs	0.37	0.35	0.32	0.24
2	ERBB4	p.T360S	0	0	0	0.11
9	GNAQ	p.T96S	0.03	0.09	0.09	0.06

FIG.6D

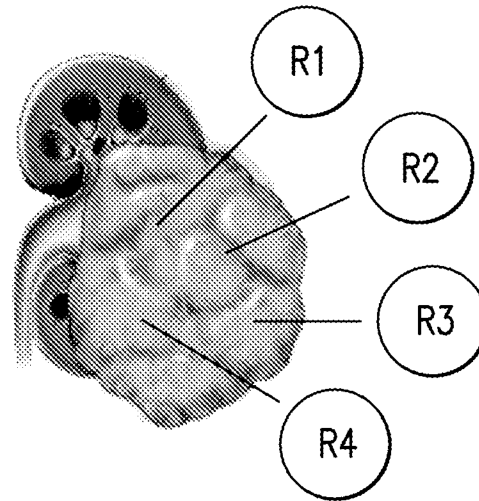


FIG. 7A

Chr	Gene	Protein	R1	R2	R3	R4
1	MTOR	p.Q2223K	0.15	0.20	0.04	0
3	BAP1	p.G220_splice	0.15	0.26	0.03	0.01
3	VHL	p.G212	0.12	0.25	0.29	0.34
7	MLL3	p.V2060A	0.14	0.22	0.28	0.28
3	BAP1	p.Q85_splice	0	0	0.28	0.37
9	NTRK2	p.I511M	0	0	0.08	0
9	TSC1	p.Q781*	0	0	0.24	0.35
19	PIK3R2	p.G3V	0	0	0.09	0

FIG. 7B

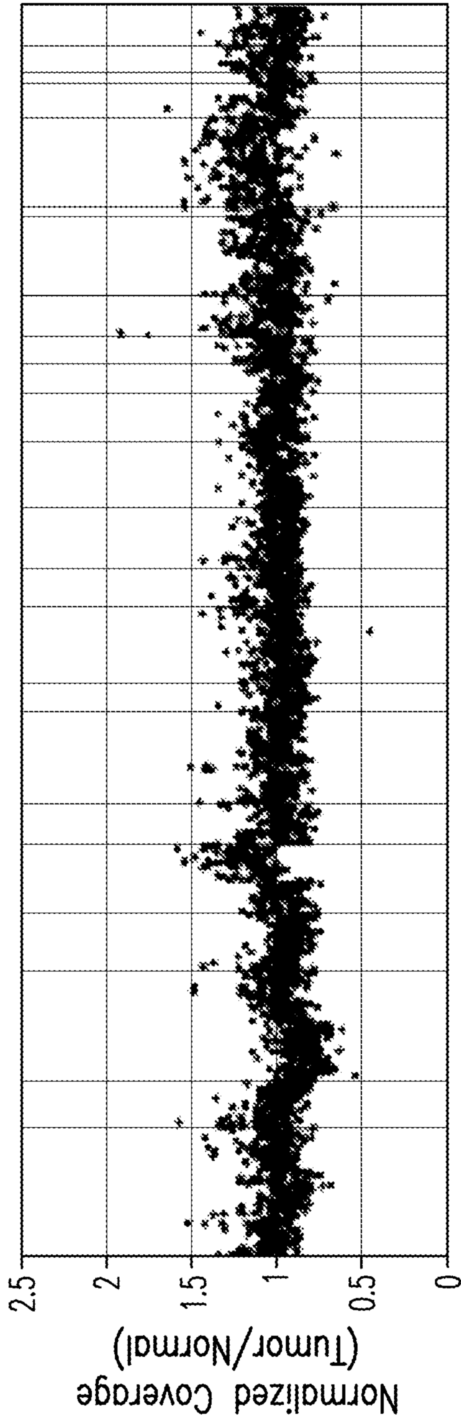


FIG. 8A

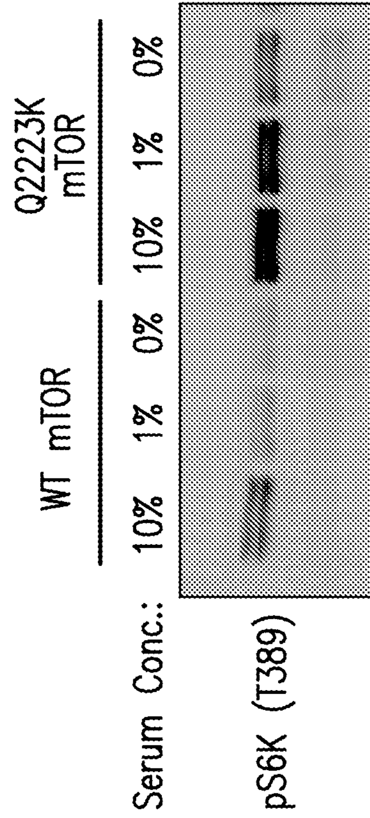


FIG. 8B

MTOR

Chr	Gene	Protein	R1	R2	R3	R4
1	MTOR	p.Q2223K	0.15	0.20	0.04	0

FIG. 8C

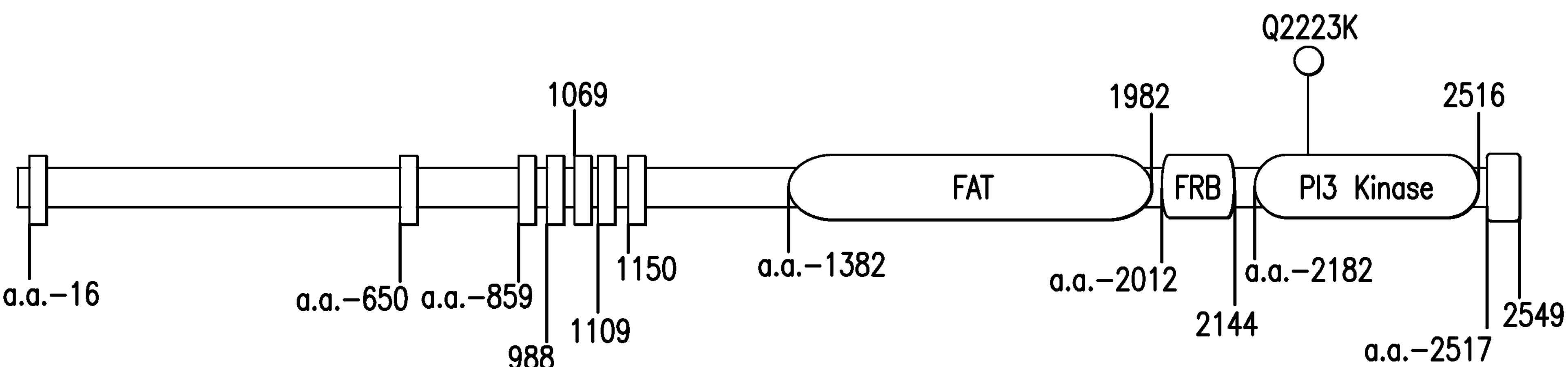


FIG. 8D

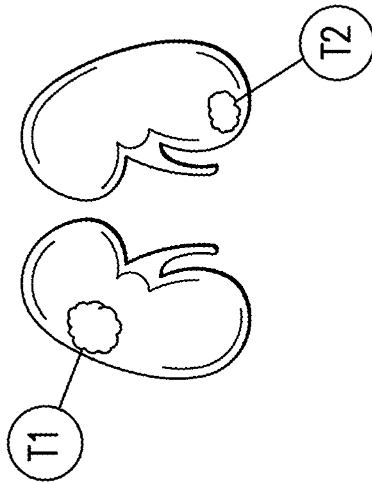


FIG. 9A

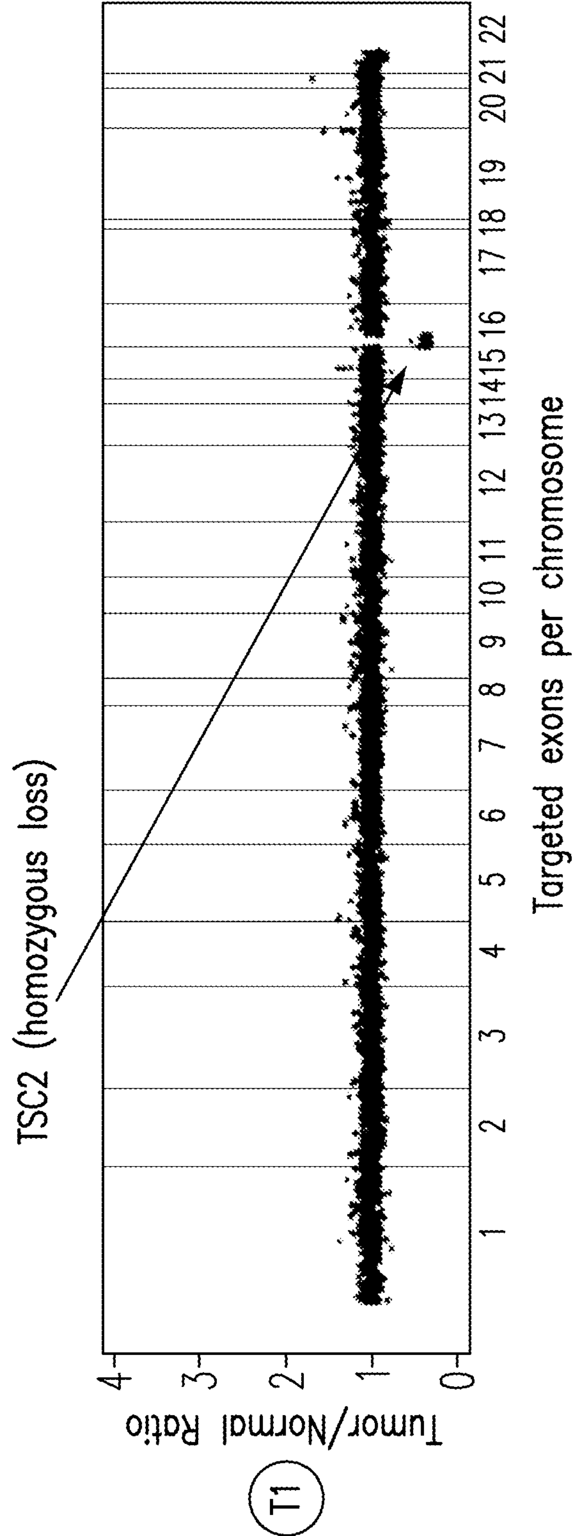


FIG. 9B

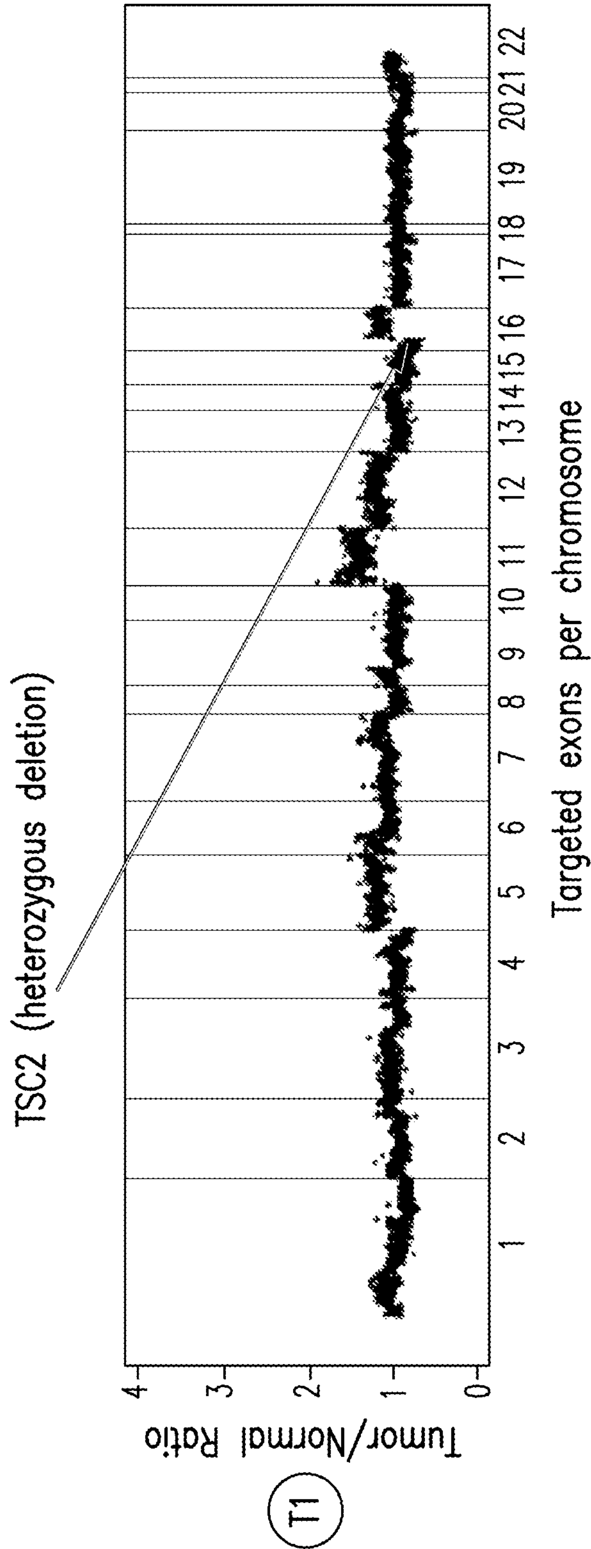


FIG. 9C

T2

Chr	Gene	Protein	T2
16	TSC2	p.Q794*	0.75

FIG. 9D

Summary long-term responders

Pt	mTORi		Mutations	CNA	Functional effect
1	T (27)	R1	TSC1 frameshift (P311fs)	Heterozygous del of TSC1	Functional loss of TSC1
		R2	TSC1 frameshift (P311fs)	Heterozygous del of TSC1	Functional loss of TSC1
		R3	TSC1 nonsense (Q527*)	Heterozygous del of TSC1	Functional loss of TSC1
2	T (34)	R1	TSC1 frameshift (I580fs)	Heterozygous del of TSC1	Functional loss of TSC1
		R2	TSC1 frameshift (I580fs)	Heterozygous del of TSC1	Functional loss of TSC1
		R3	TSC1 frameshift (I580fs)	Heterozygous del of TSC1	Functional loss of TSC1
		M1	TSC1 frameshift (I580fs)	Heterozygous del of TSC1	Functional loss of TSC1
3	E (20)	R1	mTOR missense (Q2223K)	–	Functional gain of mTOR
		R2	mTOR missense (Q2223K)	–	Functional gain of mTOR
		R3	mTOR missense (Q2223K)	–	Functional gain of mTOR
		R4	TSC1 nonsense (Q781*)	Heterozygous del of TSC1	Functional loss of TSC1
4	E (36+)	T1	–	Heterozygous del of TSC2	Functional loss of TSC2
		T2	TSC2 nonsense (p.Q794*)	Heterozygous del of TSC2	Functional loss of TSC2
5	T (28)	T1	–	–	–
		M1	–	–	–
6	E (33+)	T1	–	–	–

mTORi: mTOR inhibitor
CNA: copy number alteration
T: temsirolimus
E: everolimus
del: deletion

FIG. 10

Pt	mTORi		Mutations	CNA	Functional effect
7	T (1)	T1	–	–	–
8	E (2)	T1	mTOR missense (E919V)	–	–
9	T (2)	T1	TSC2 frameshift (1475F)	Ampl MAP2K1	–
10	E (1)	T1	PTEN missense (F2001)	–	–

mTORi: mTOR inhibitor
CNA: copy number alteration
T: temsirolimus
E: everolimus
ampl: amplification

FIG. 11

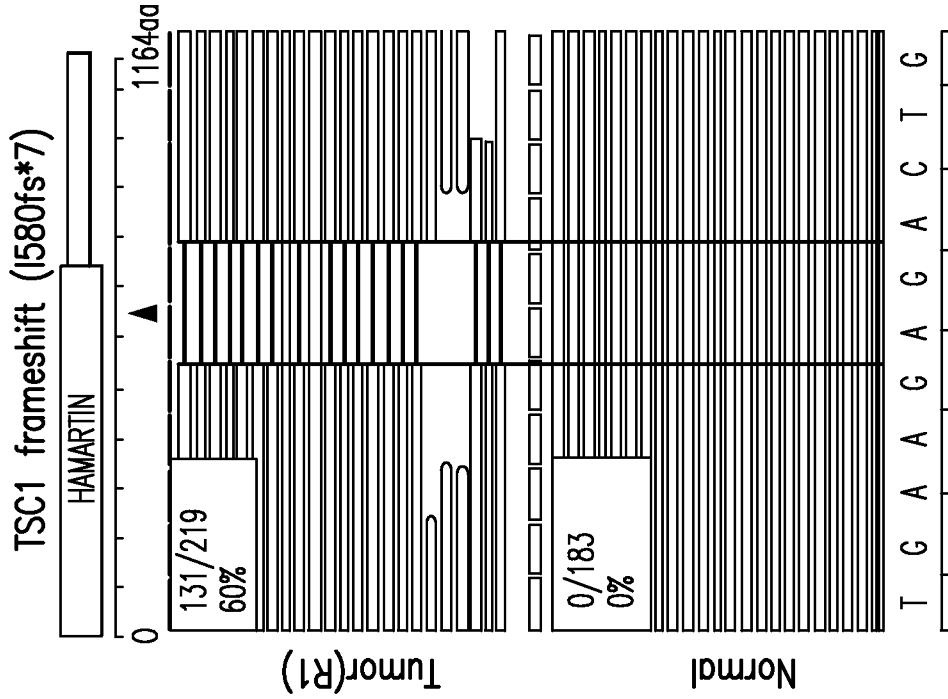


FIG. 12B

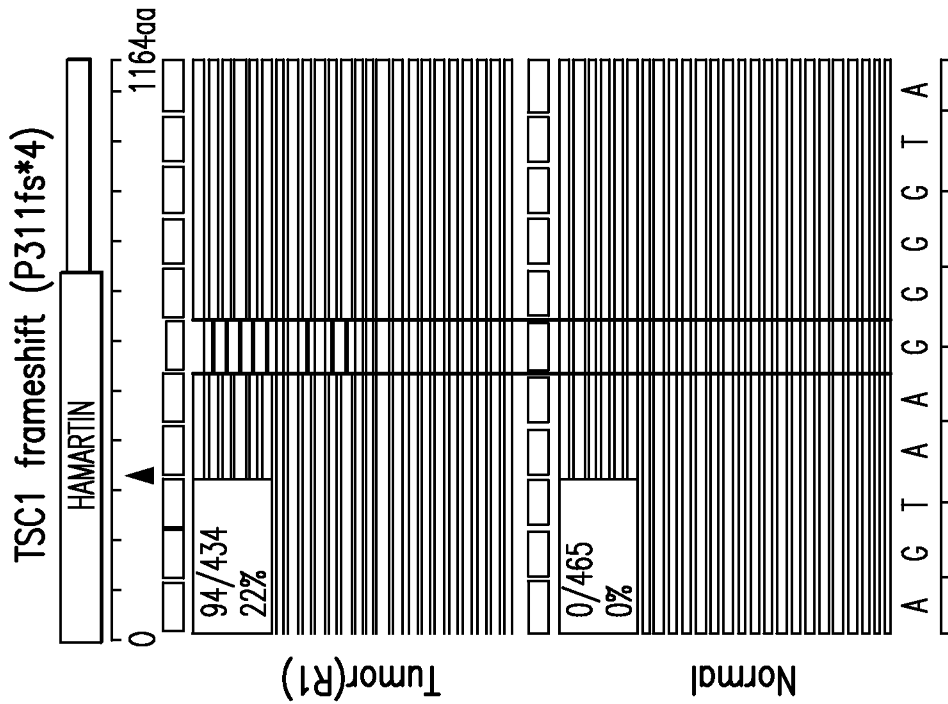


FIG. 12A

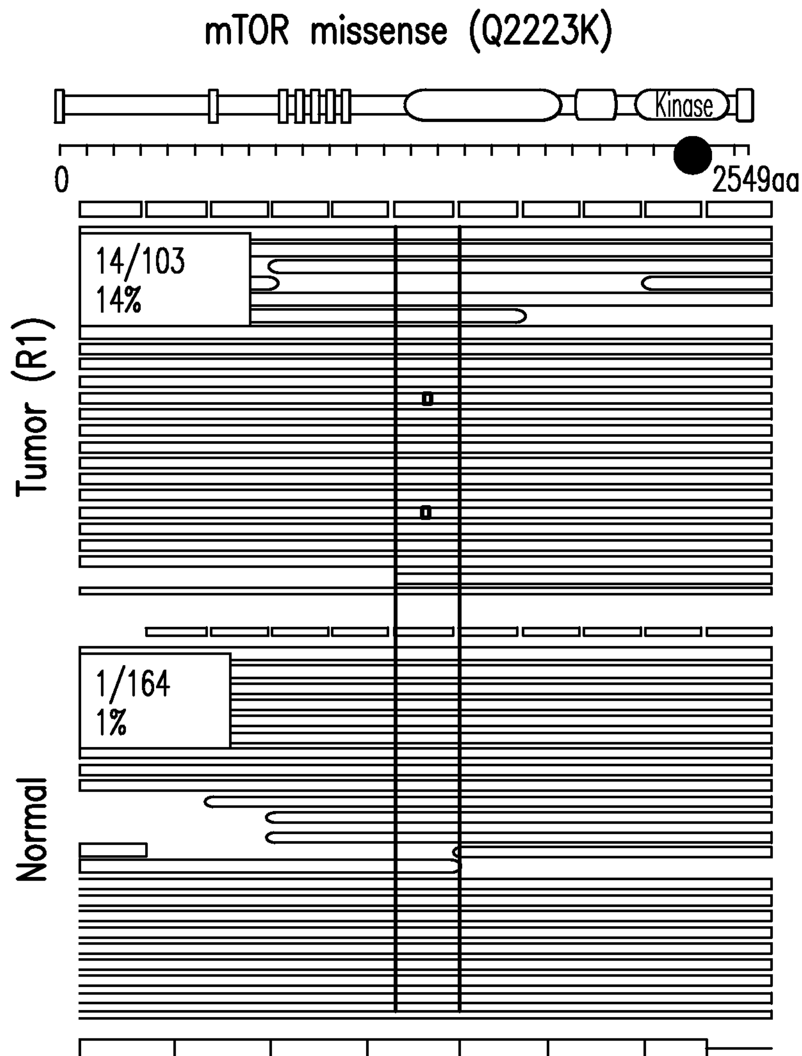


FIG. 12D

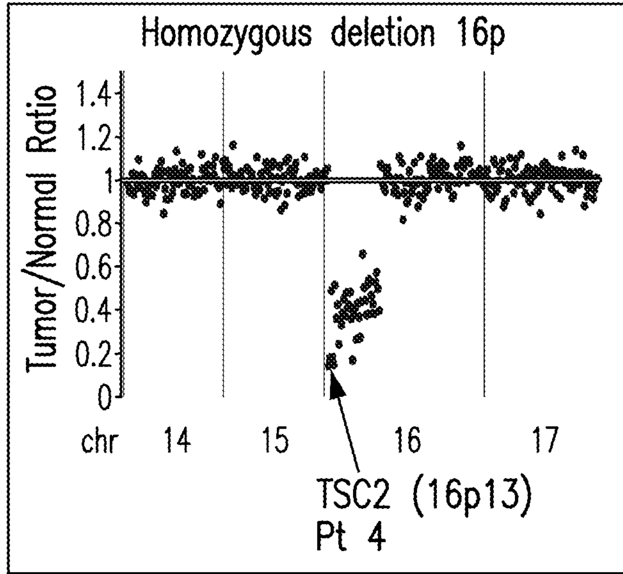


FIG. 12C

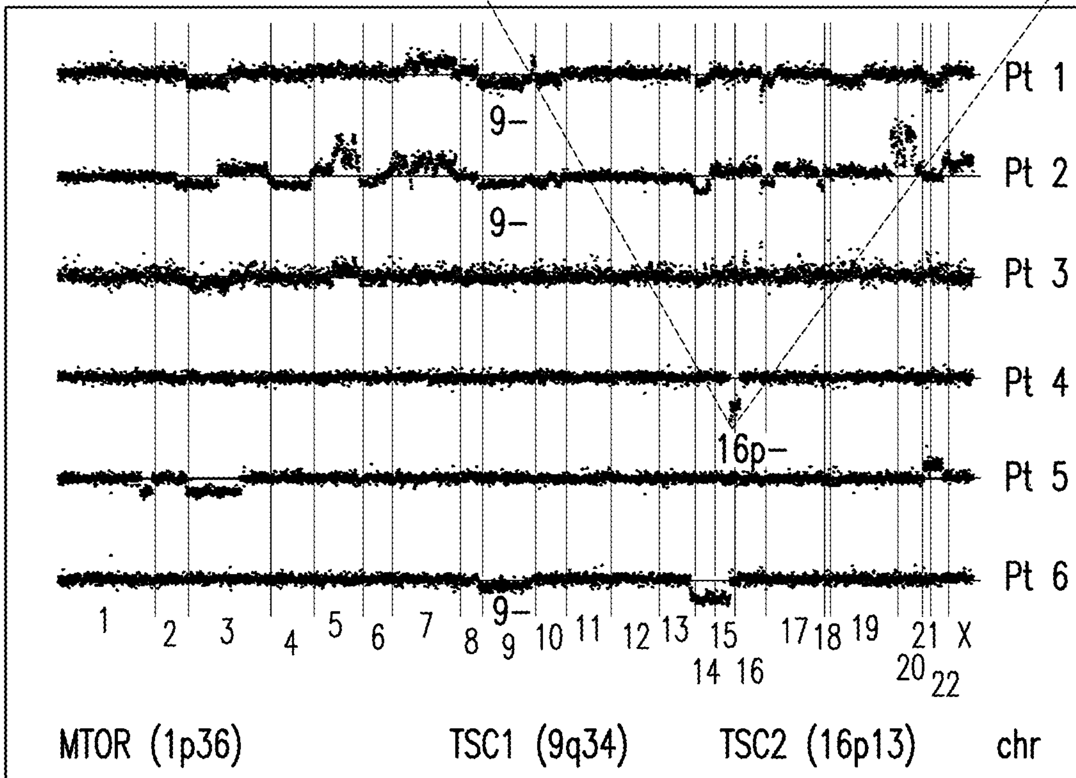


FIG. 12E

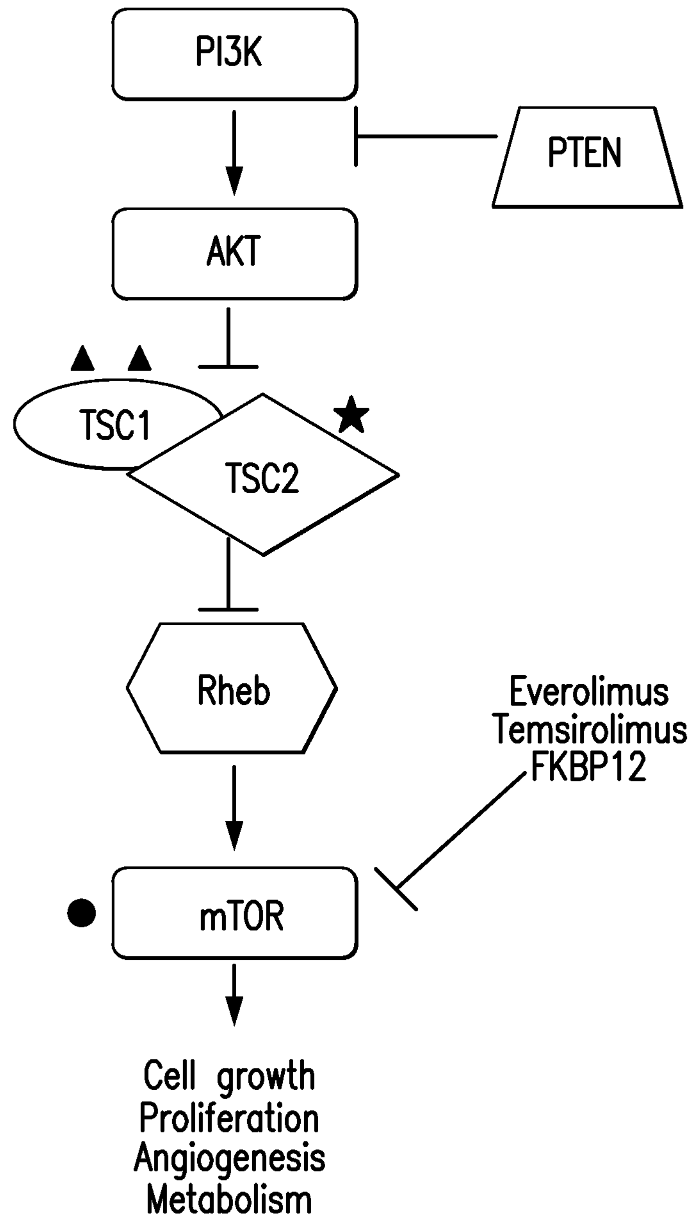


FIG. 12F

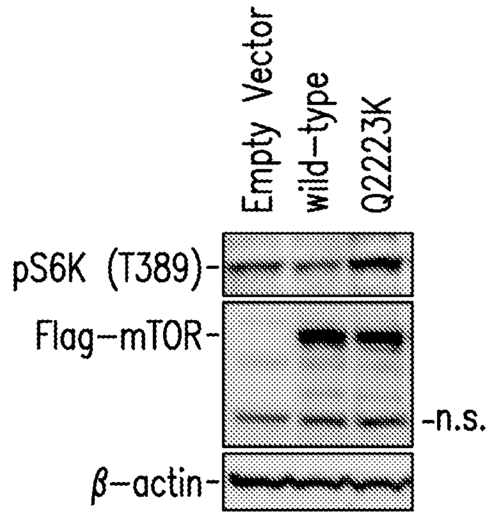


FIG. 13A

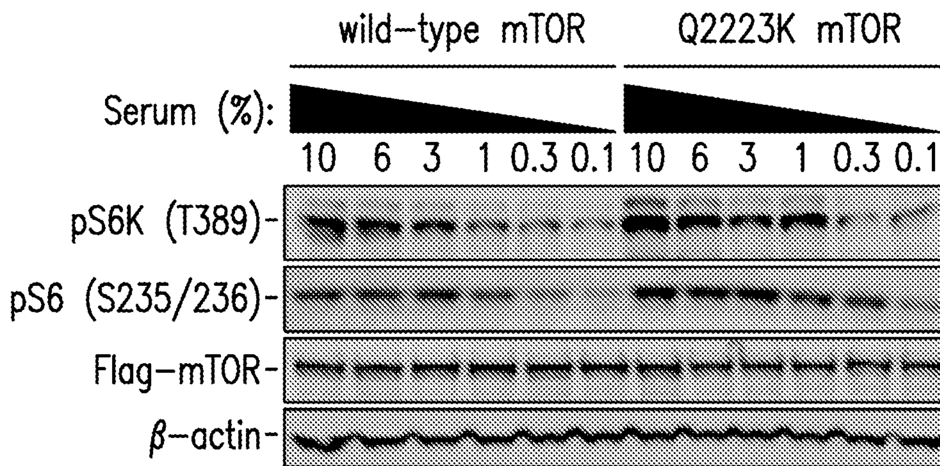


FIG. 13B

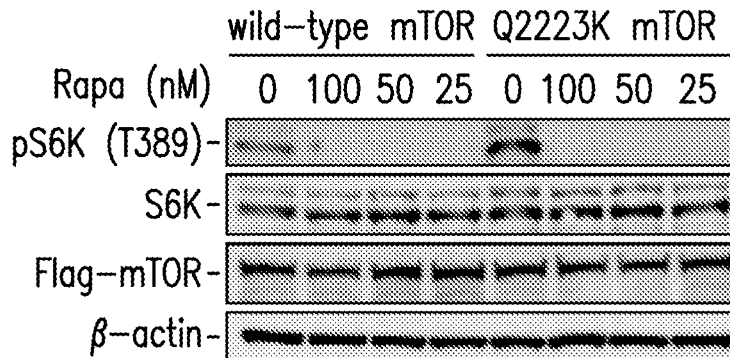


FIG. 13C

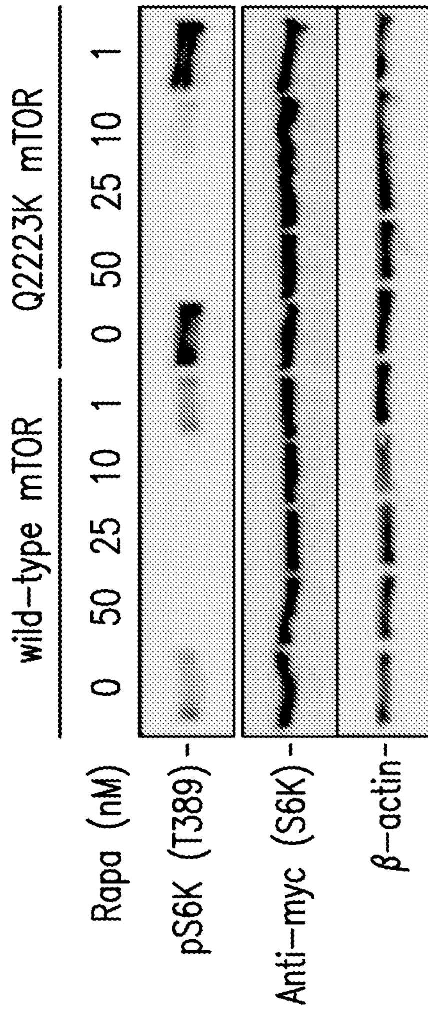


FIG. 13E

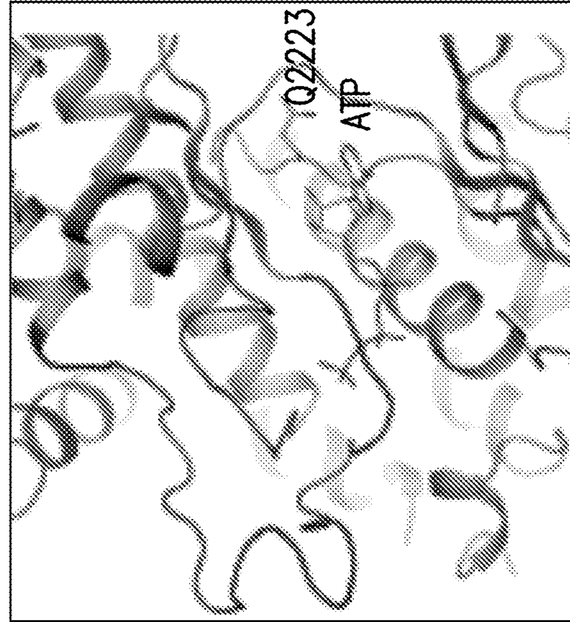


FIG. 13F

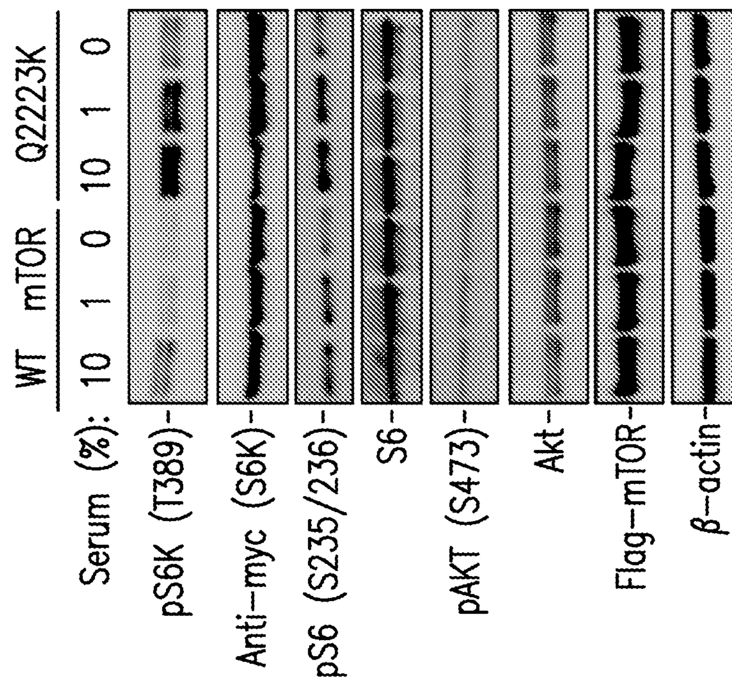


FIG. 13D

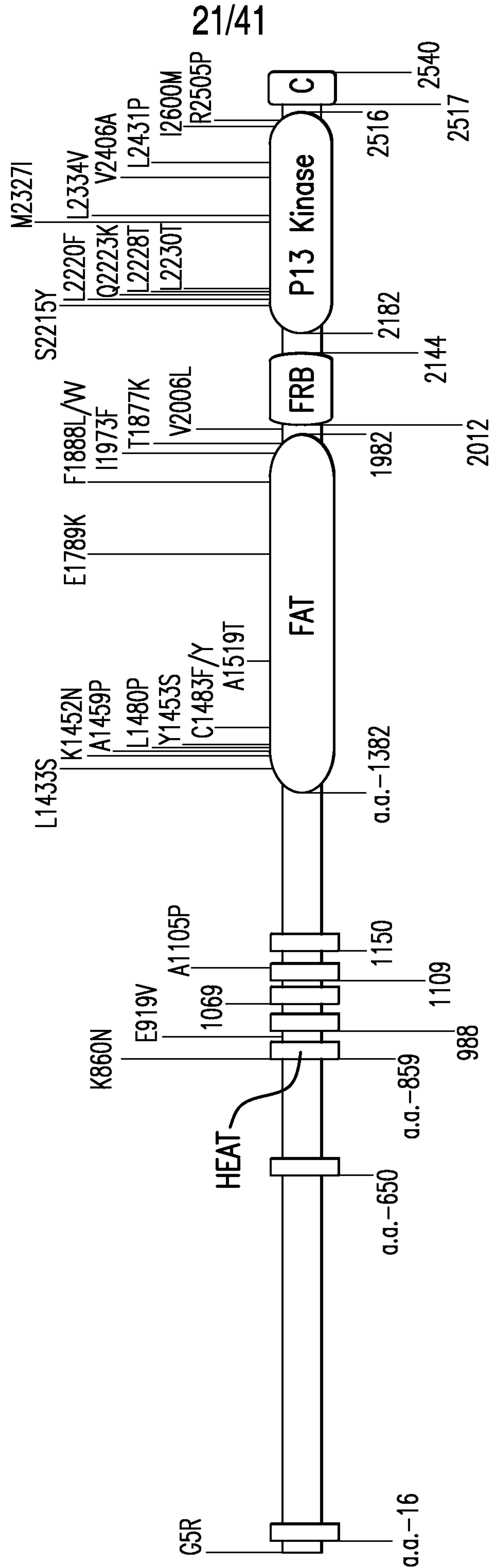


FIG. 14A

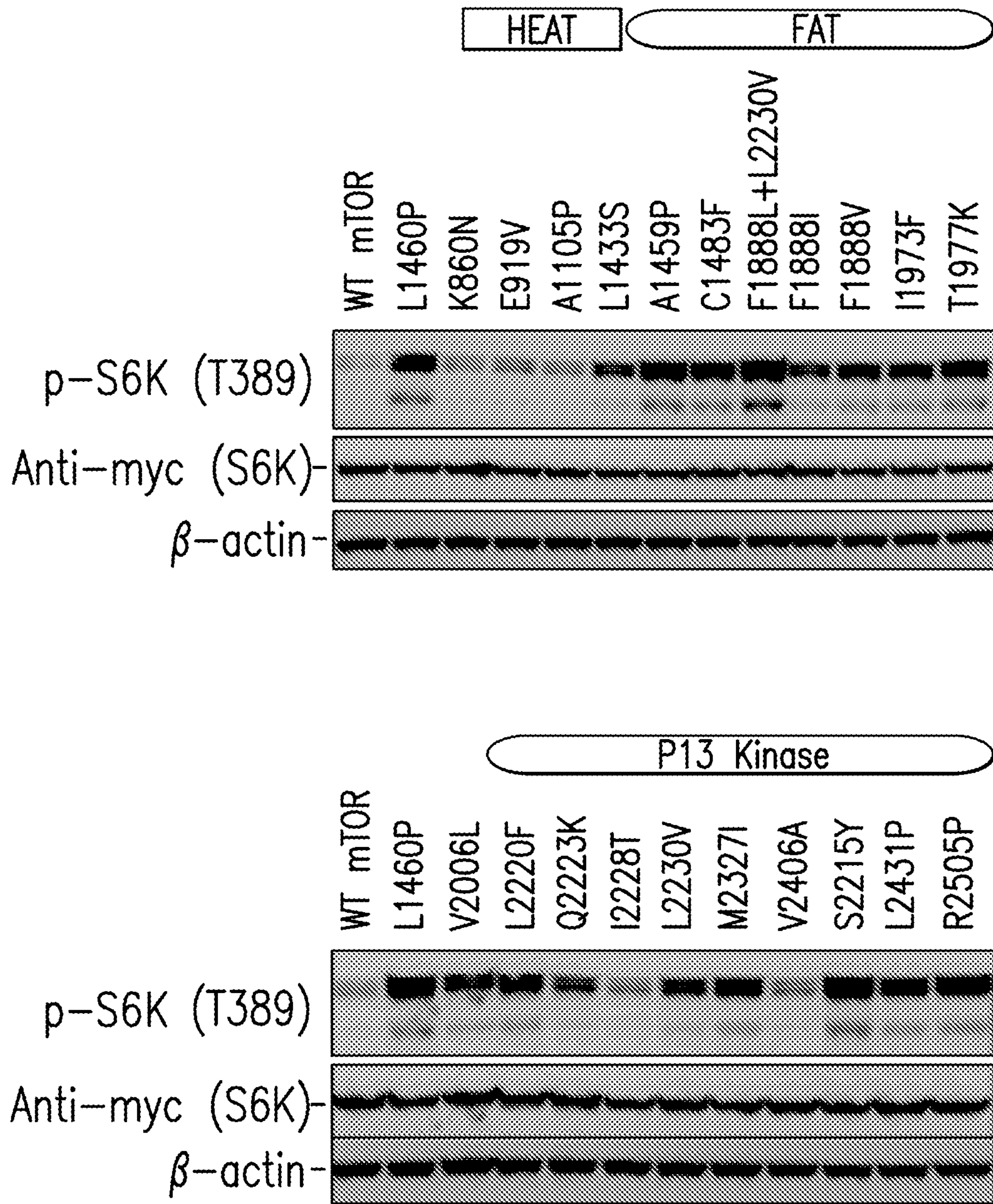


FIG. 14B

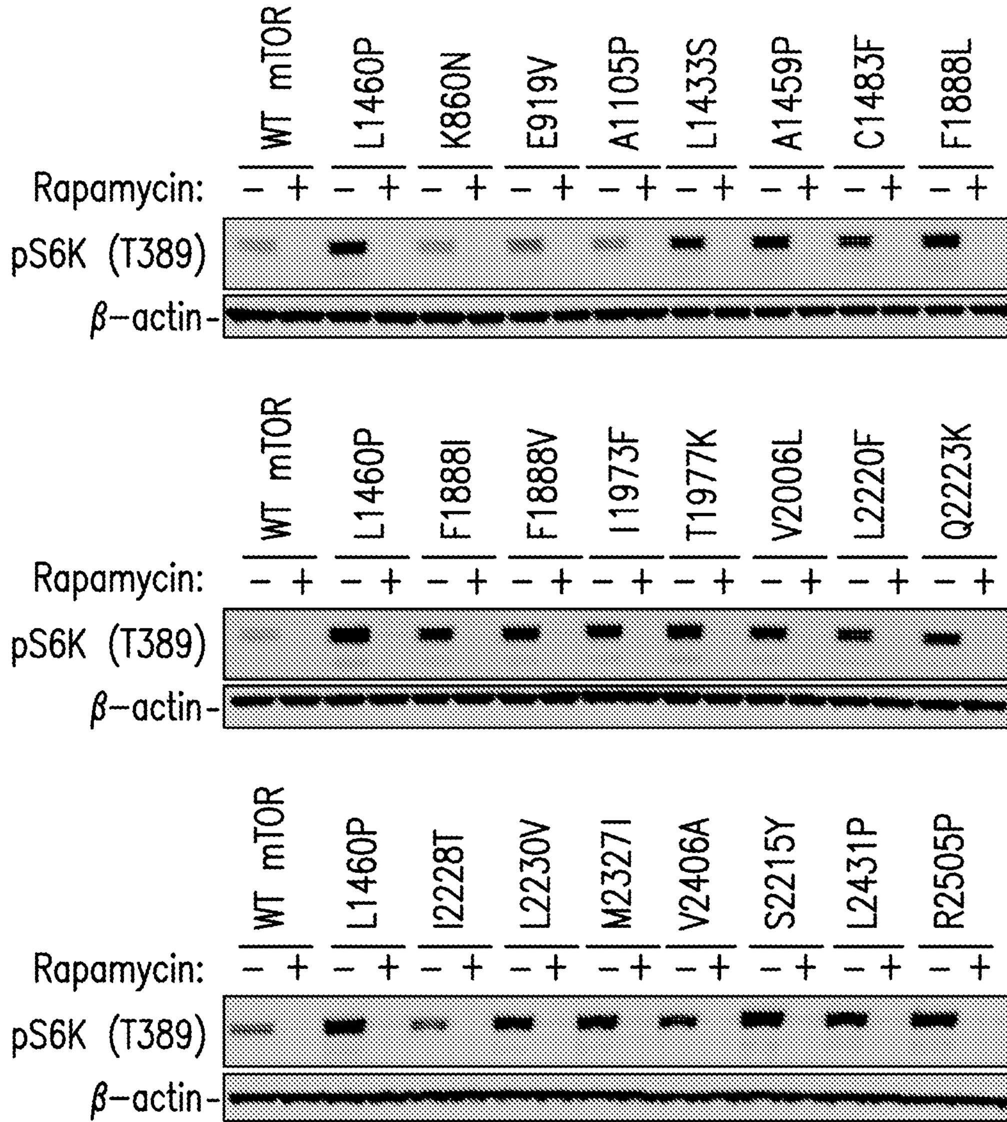
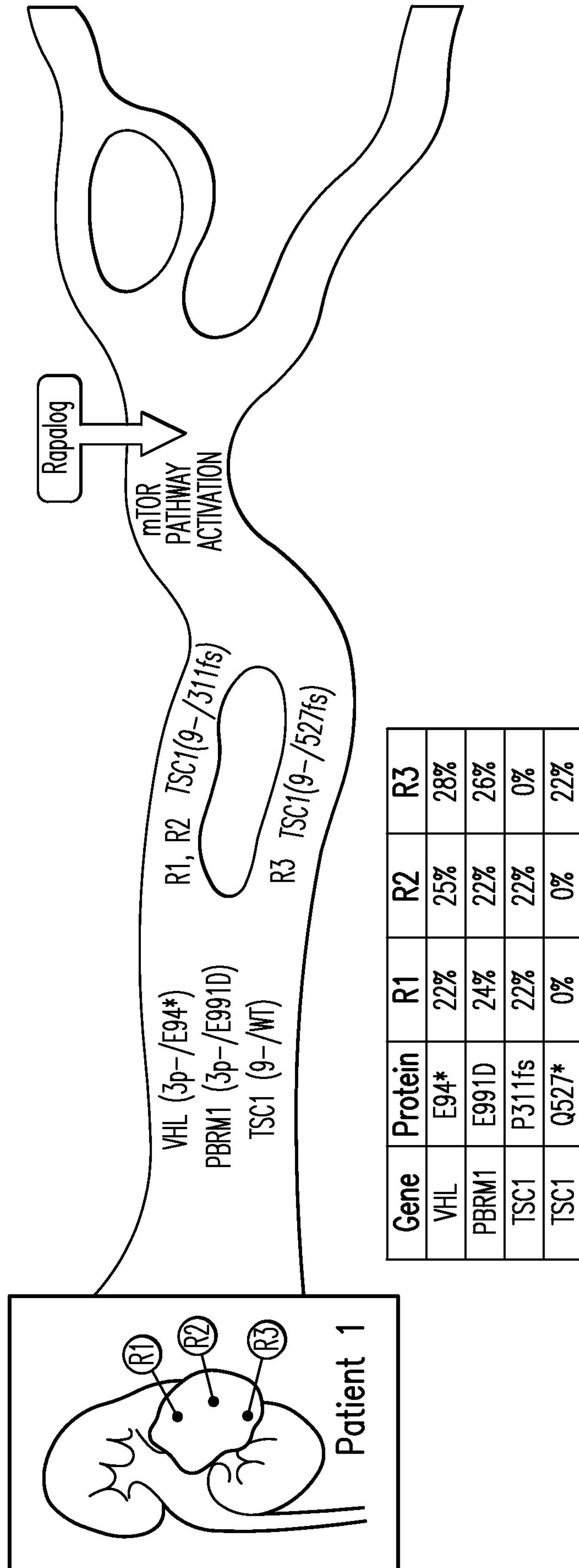
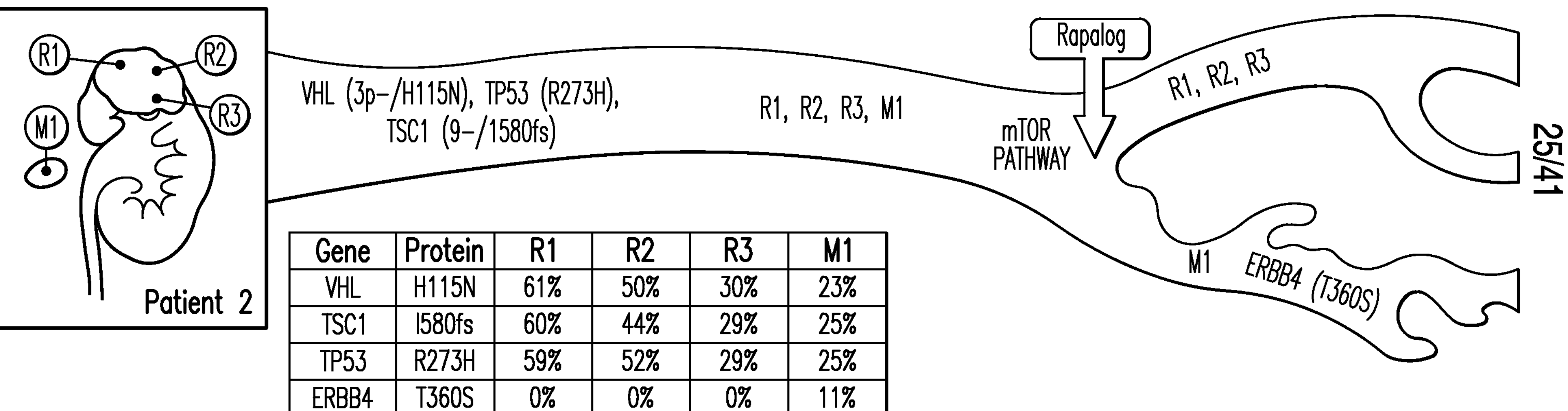


FIG. 14C



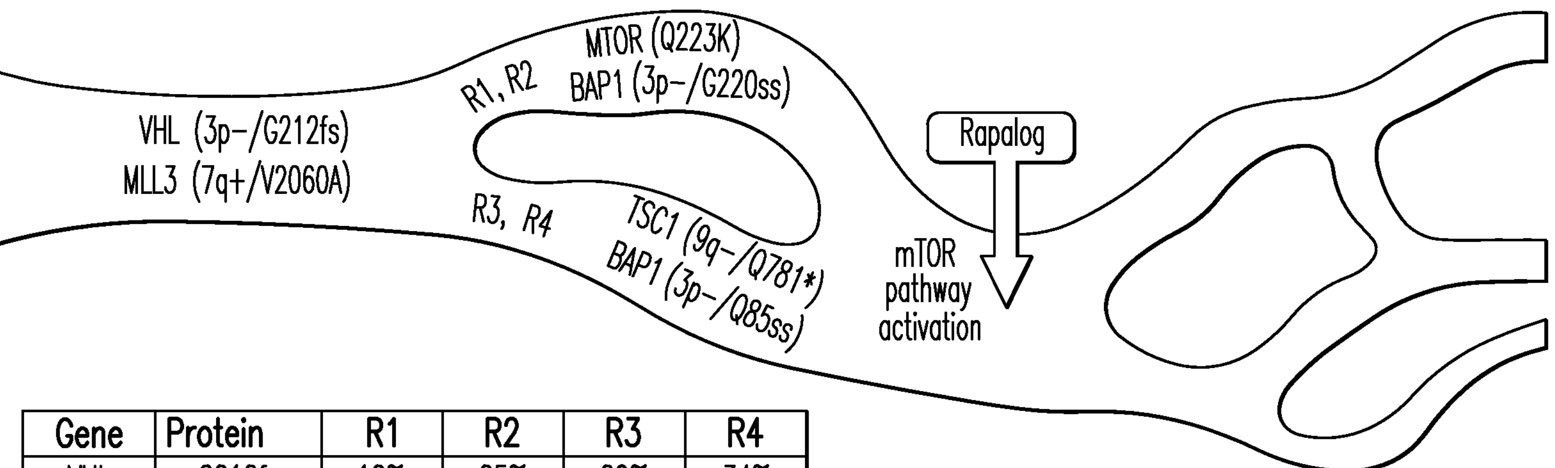
Gene	Protein	R1	R2	R3
VHL	E94*	22%	25%	28%
PBRM1	E991D	24%	22%	26%
TSC1	P311fs	22%	22%	0%
TSC1	Q527*	0%	0%	22%

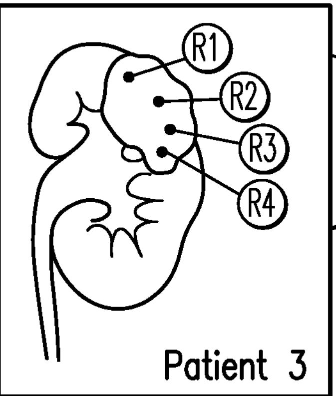
FIG. 15A



Gene	Protein	R1	R2	R3	M1
VHL	H115N	61%	50%	30%	23%
TSC1	I580fs	60%	44%	29%	25%
TP53	R273H	59%	52%	29%	25%
ERBB4	T360S	0%	0%	0%	11%

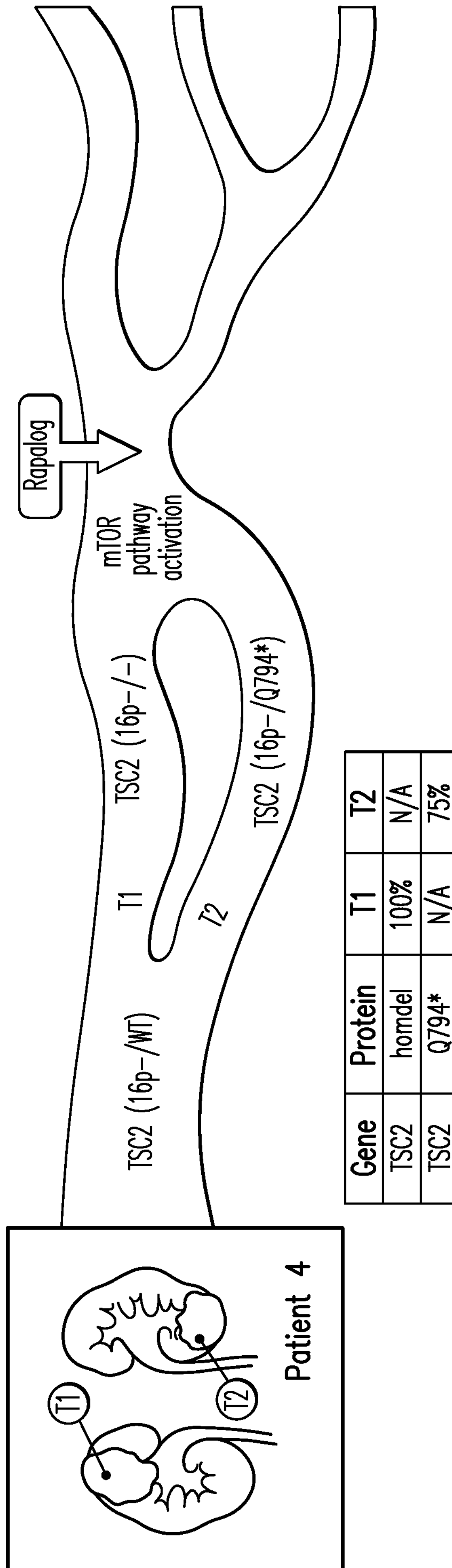
FIG. 15B





Gene	Protein	R1	R2	R3	R4
VHL	G212fs	12%	25%	29%	34%
TSC1	Q781*	0%	0%	24%	35%
MTOR	Q2223K	15%	20%	4%	0%
BAP1	G220_splice	15%	26%	3%	1%
BAP1	Q85_splice	0%	0%	28%	37%
MLL3	V2060A	14%	22%	28%	28%

FIG. 15C



Gene	Protein	T1	T2
TSC2	homdel	100%	N/A
TSC2	Q794*	N/A	75%

FIG. 15D

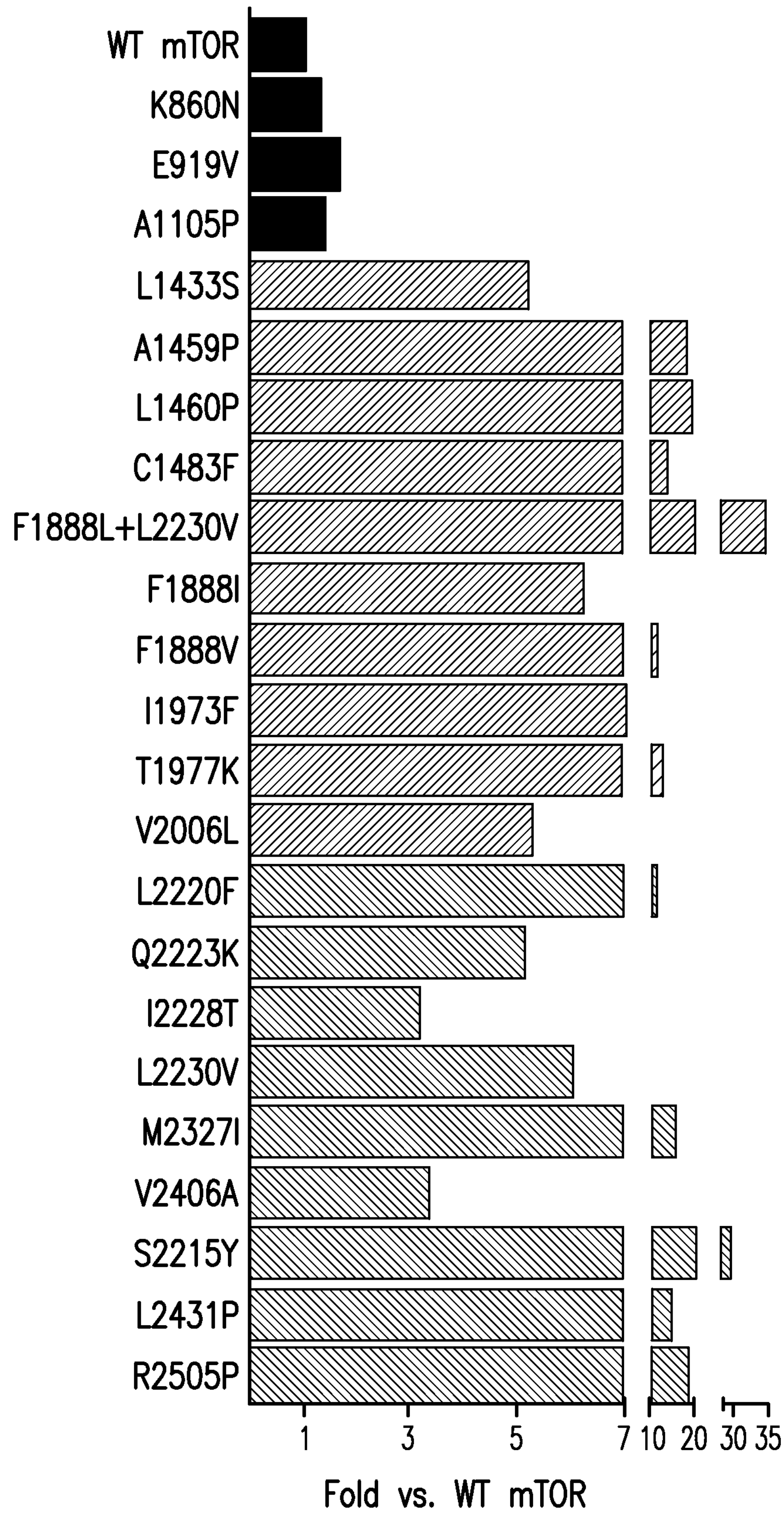


FIG. 16

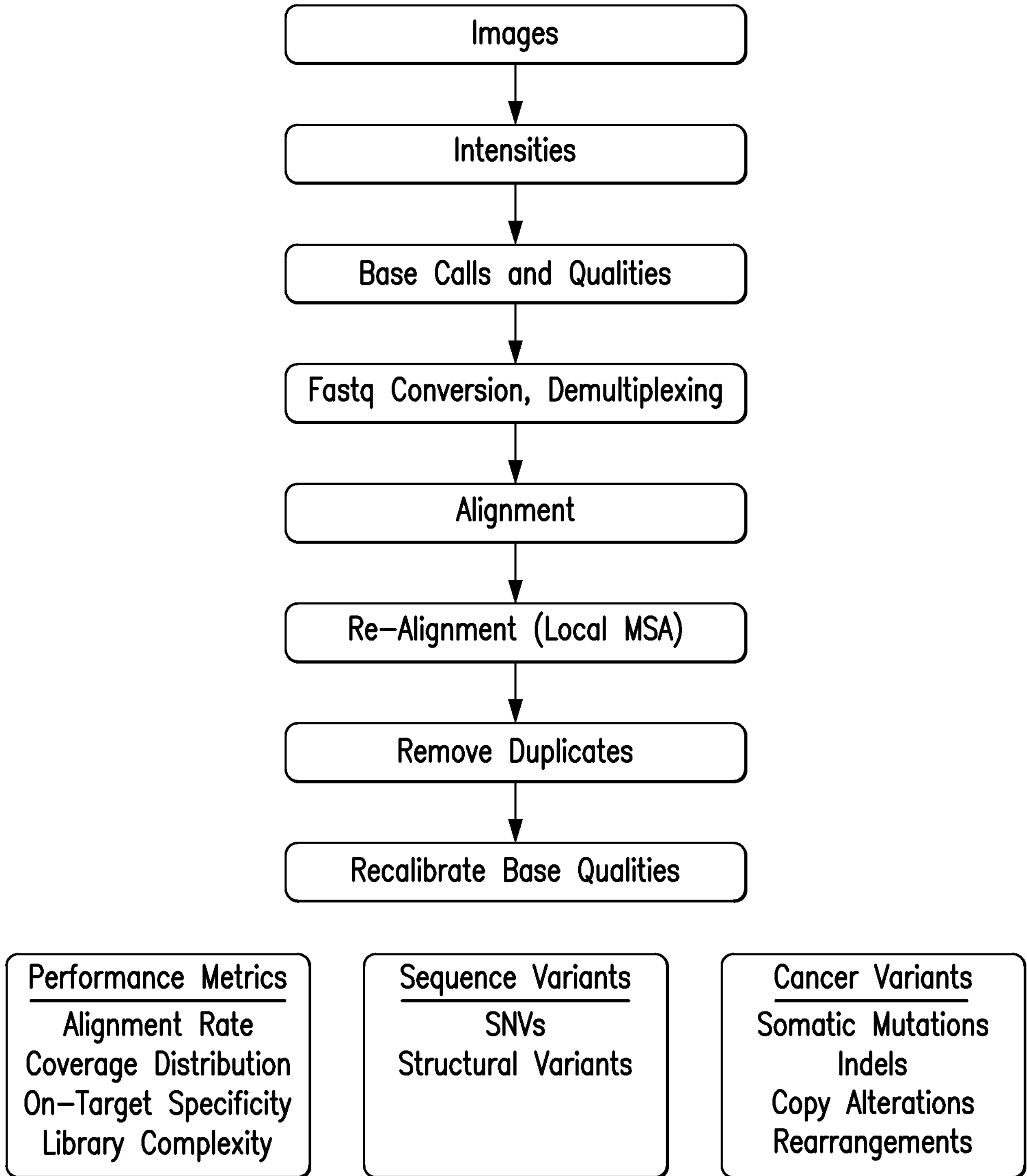


FIG. 17

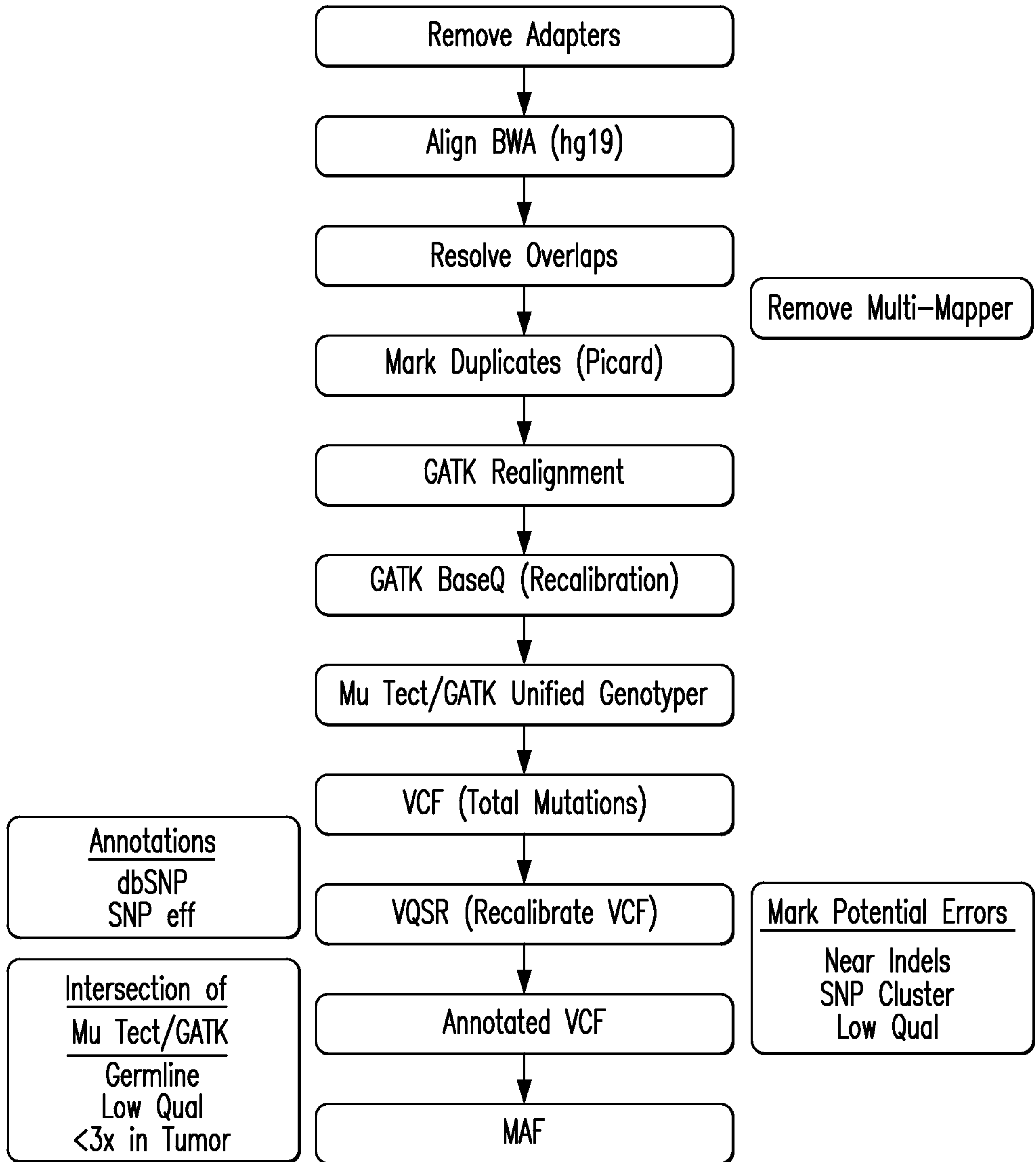


FIG. 18

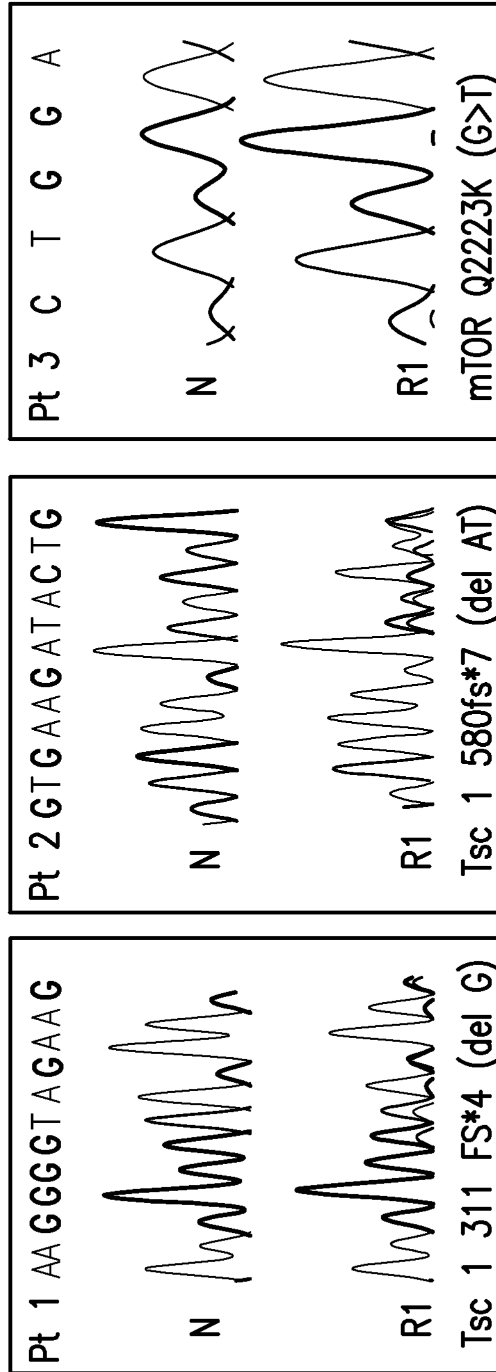


FIG. 19

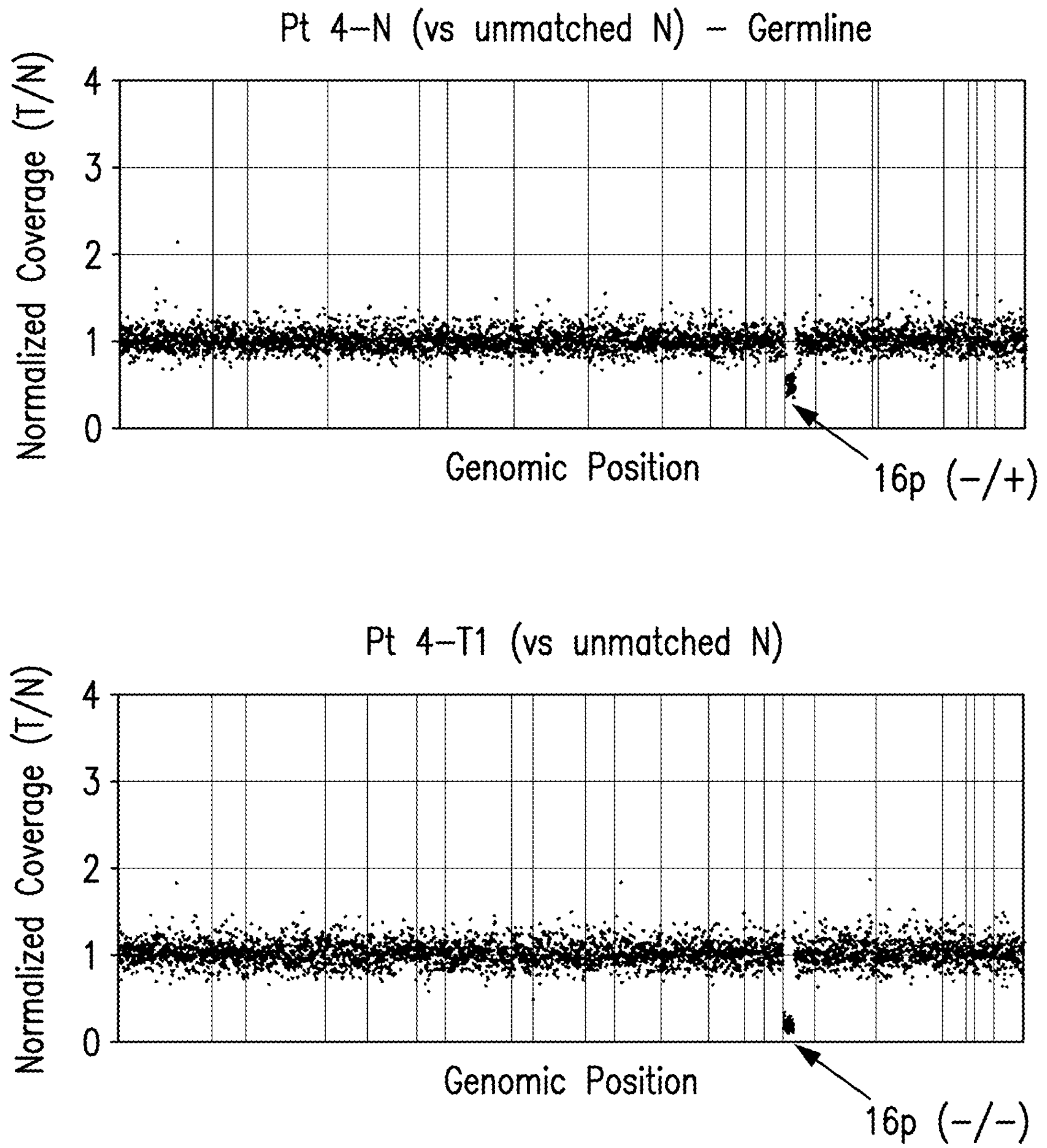
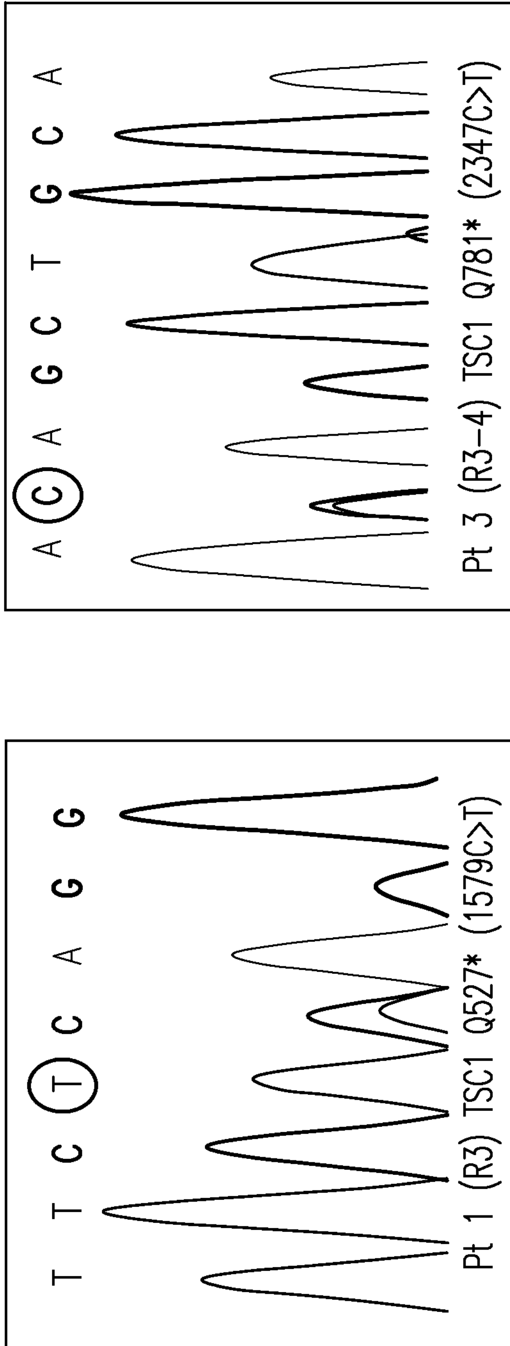


FIG. 20



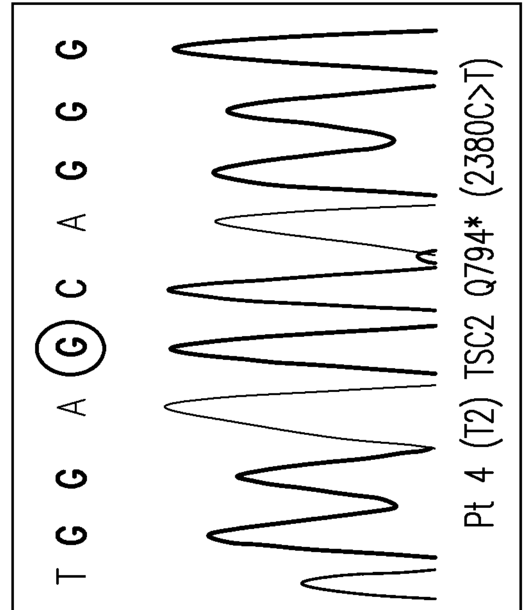


FIG. 21

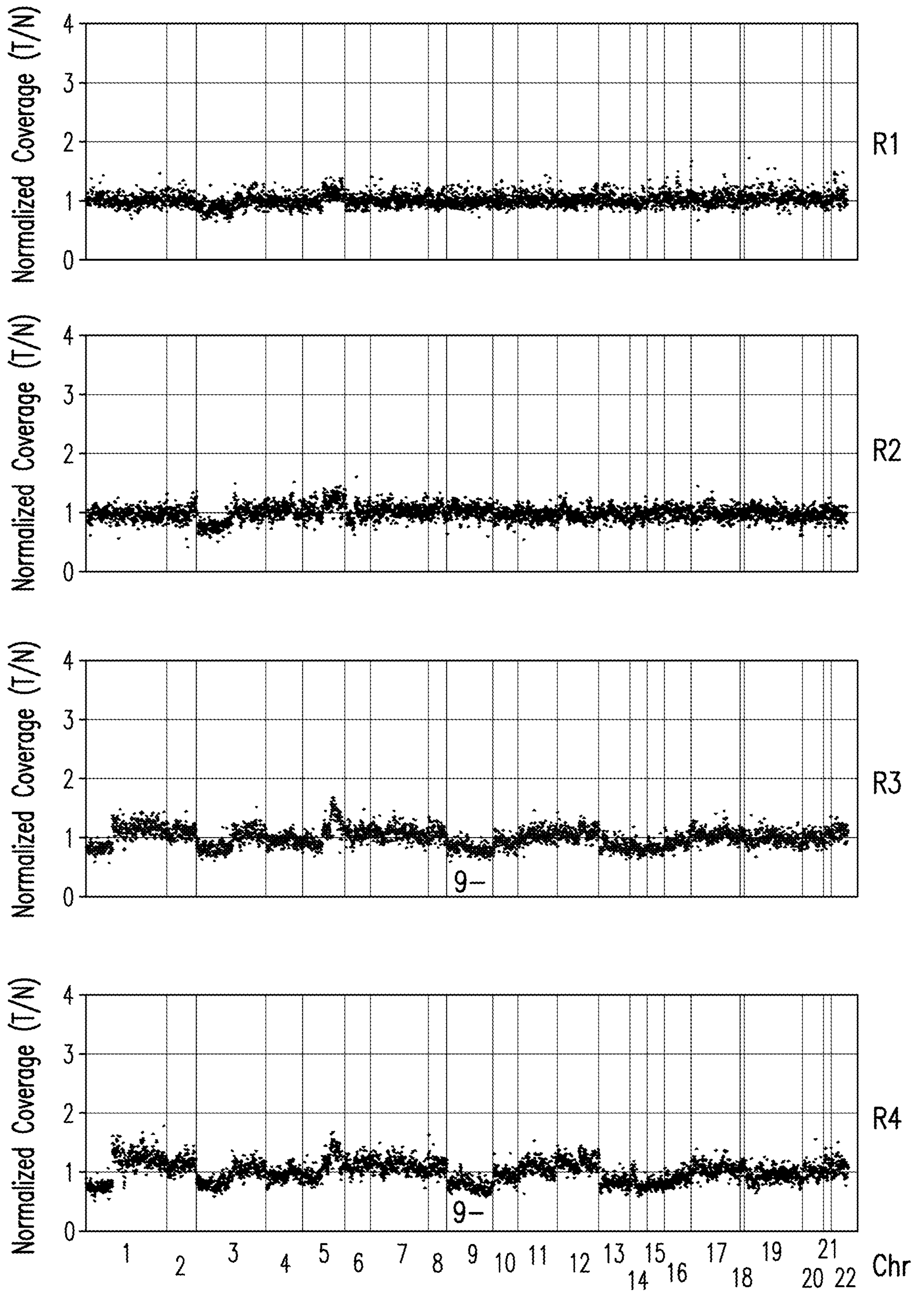


FIG. 22

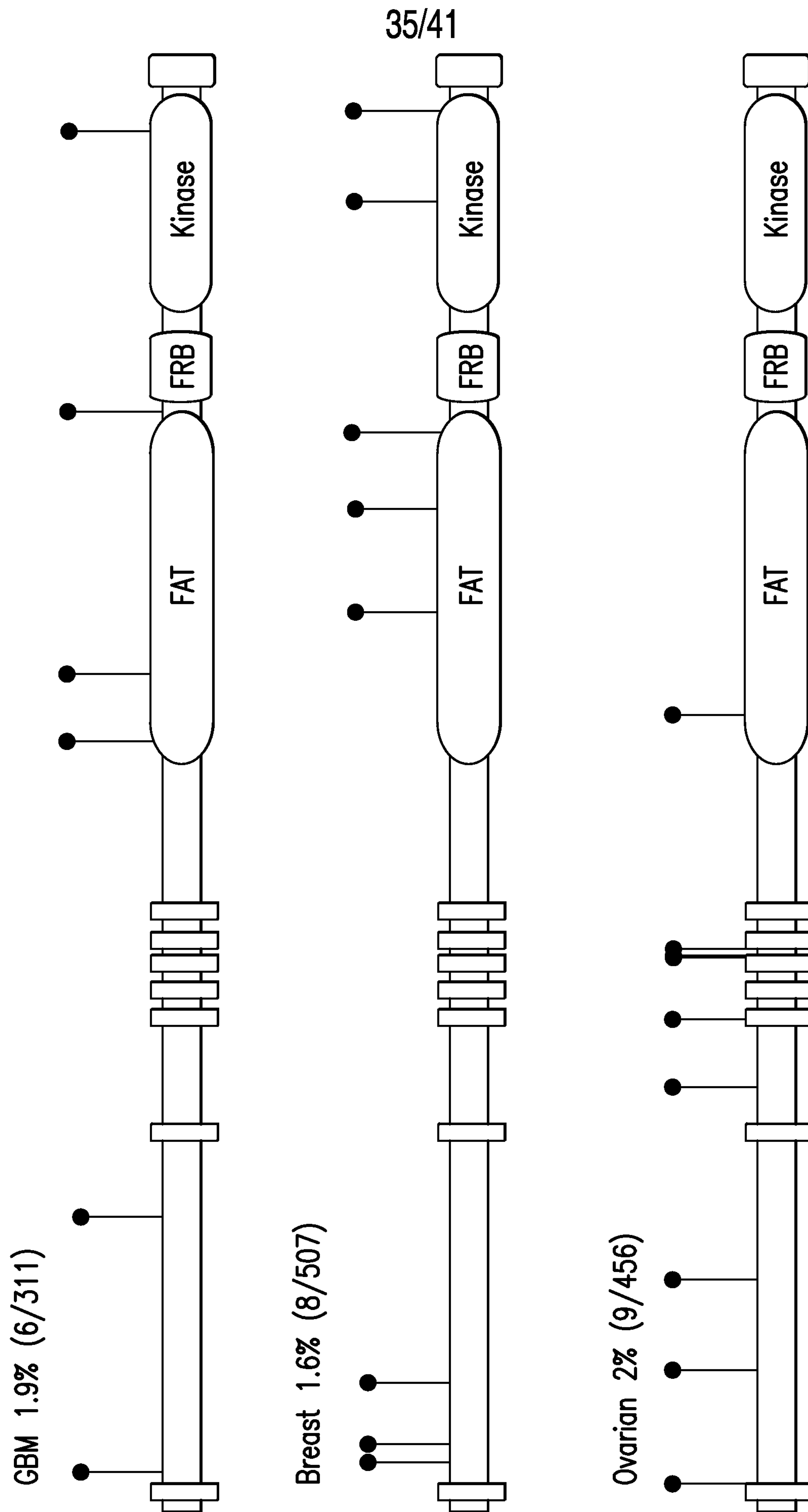


FIG. 23

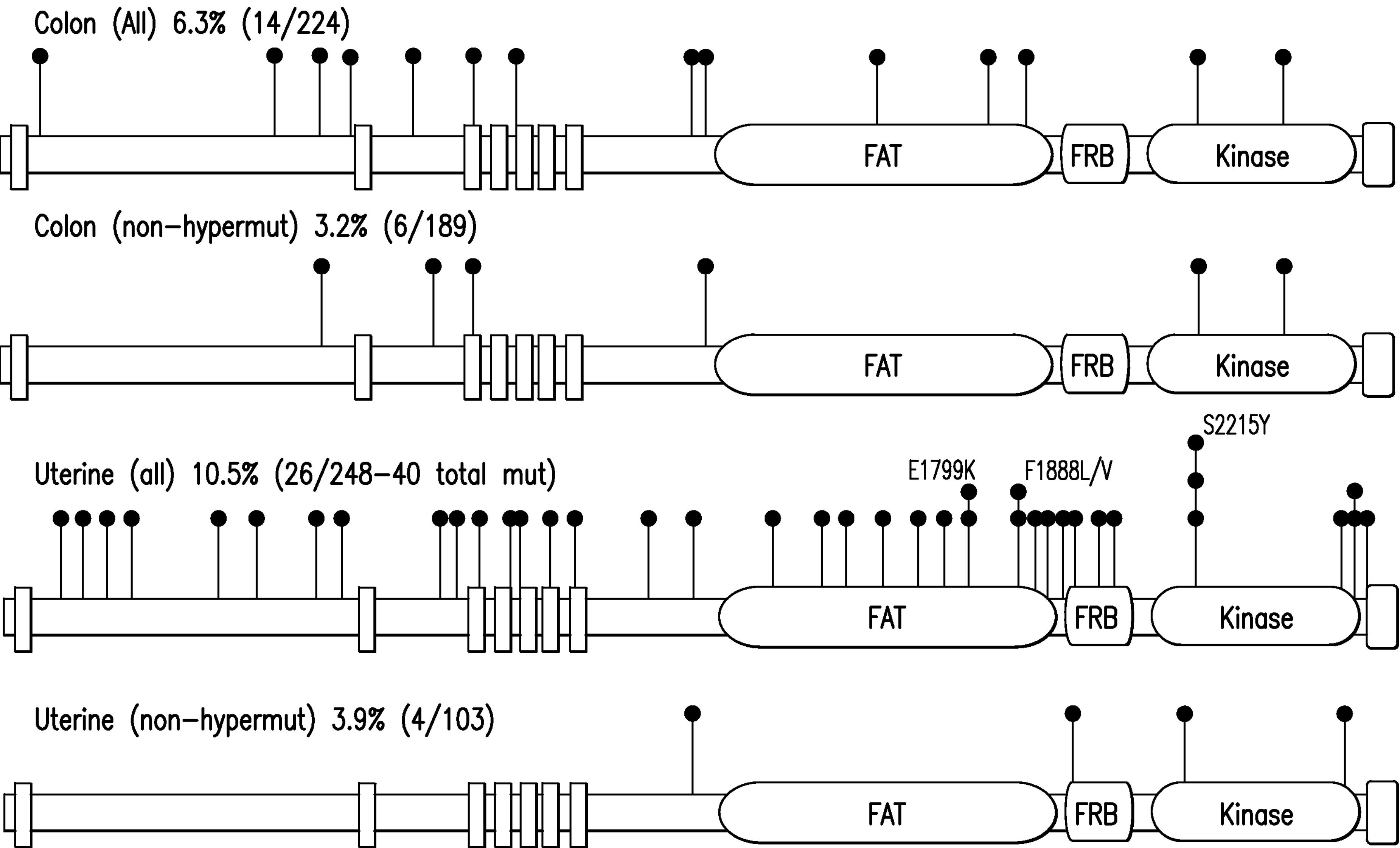


FIG. 23 Continued

Serum
p-T389-S6K
S6K (myc)
β-actin
WT mTOR
L1460P
C1483F
F1888L
WT mTOR
T1977K
S2215Y
L2220F
L2431P

FIG. 24

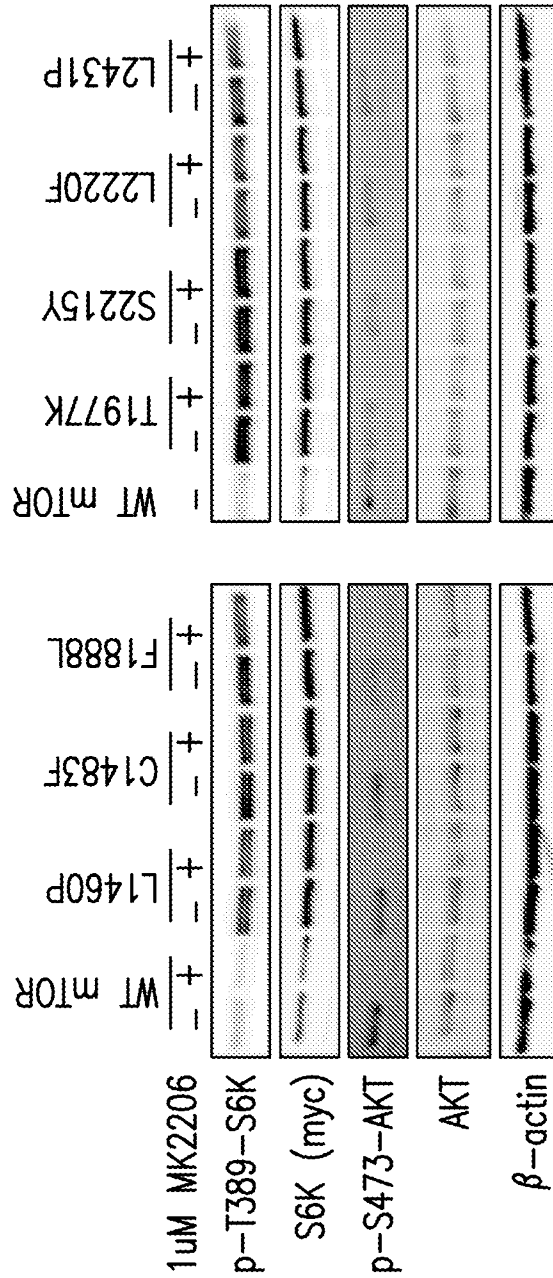


FIG. 25

WT mTOR L1460P C1483F WT mTOR F1888L T1977K S2215Y WT mTOR L2220F L2431P

25nM Rapa

100nM INK128

p–T389–S6K

S6K(myc)

β–actin

FIG. 26

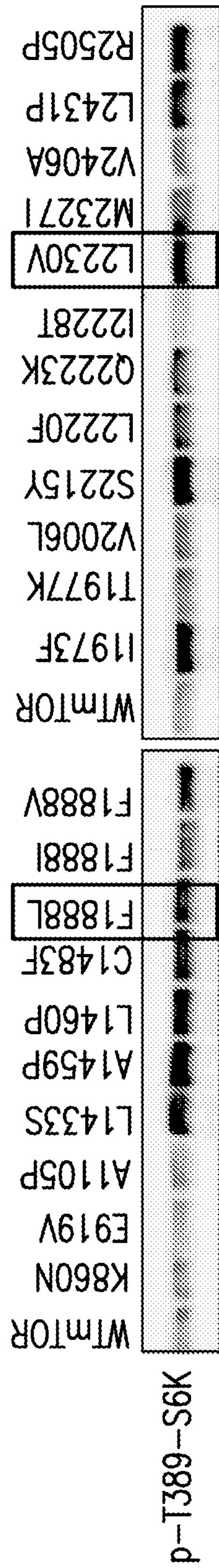


FIG. 27A

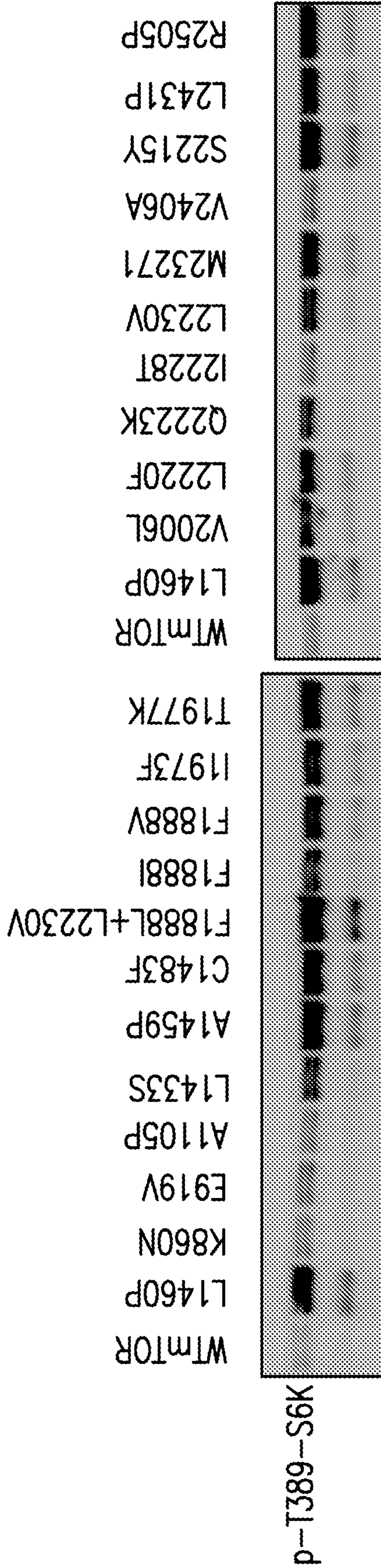


FIG. 27B

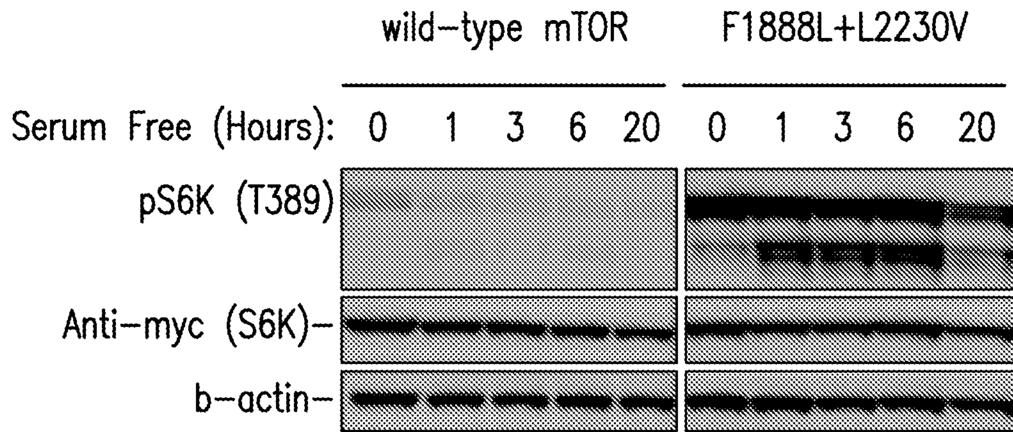


FIG. 27C

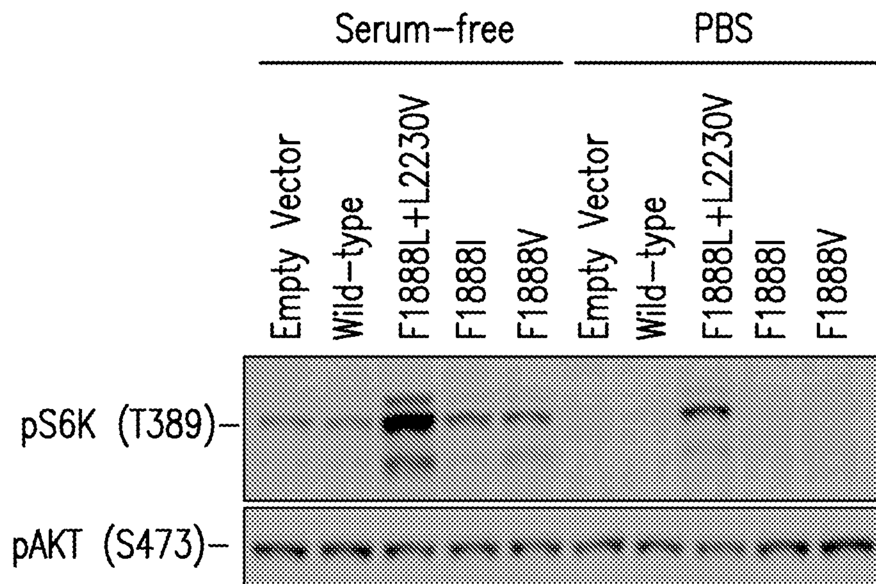


FIG. 27D